National Aeronautics and Space Administration

Genetic Inventory Task Final Report

Volume 2 of 2

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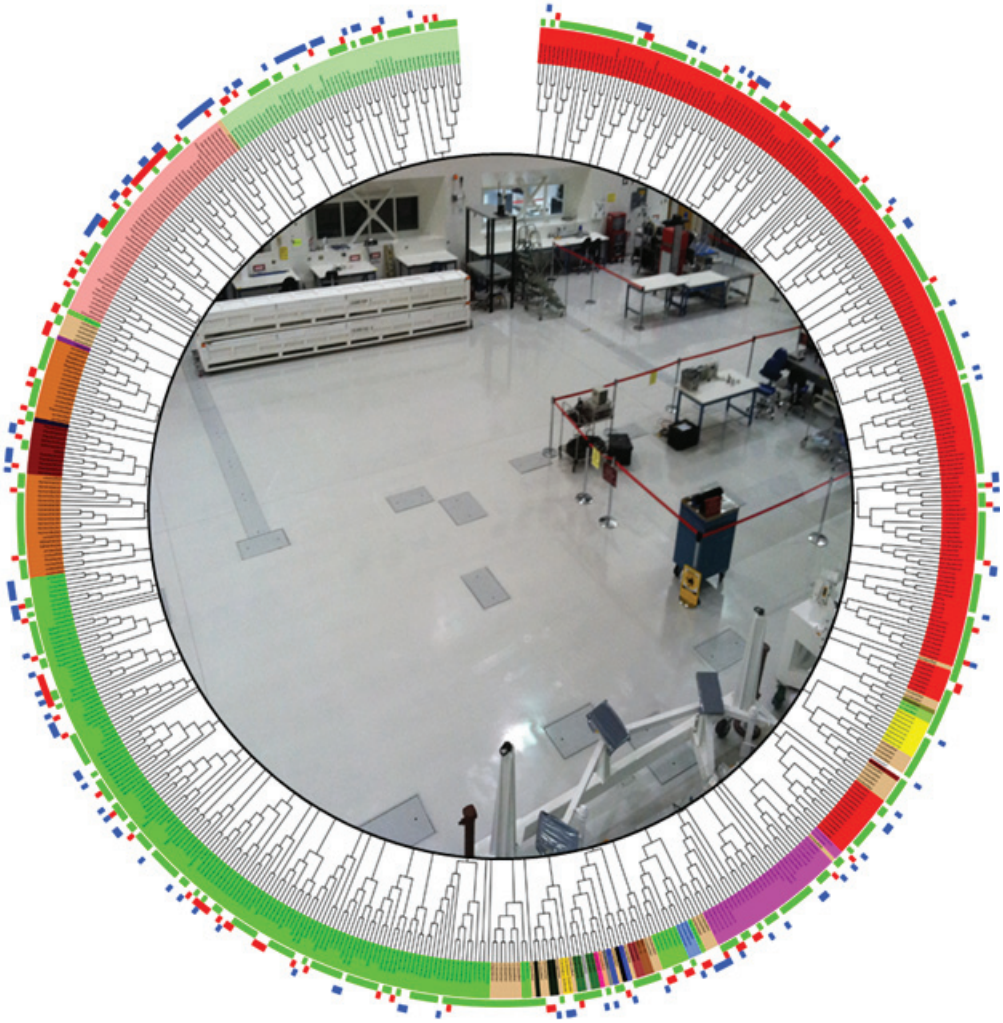

September 2012

National Aeronautics and Space Administration

Jet Propulsion Laboratory
California Institute of Technology
Pasadena, California

www.nasa.gov

JPL Publication 12-12 09/12

This research was carried out at the Jet Propulsion Laboratory, California Institute of Technology, under a contract with the National Aeronautics and Space Administration.

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This report shall be referenced as follows.

For Volume 1:

Venkateswaran, K., La Duc, M. T., and Vaishampayan, P. (2012) Genetic Inventory Task: Final Report, Volume 1, JPL Publication 12-12. Jet Propulsion Laboratory, California Institute of Technology, Pasadena, CA.

For Volume 2:

Venkateswaran, K., La Duc, M. T., and Vaishampayan, P. (2012) Genetic Inventory Task: Final Report, Volume 2, JPL Publication 12-12. Jet Propulsion Laboratory, California Institute of Technology, Pasadena, CA.

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APPENDIX A: SAMPLING OF LOW-BIOMASS SURFACES WITH COTTON AND FLOCKED-NYLON SWABS: LESSONS LEARNED

Appendix A documents the significant lessons learned while working with swabs (primarily cotton and flocked-nylon) in the context of sample collection (cells, biomolecules, etc.) from low-biomass surfaces. This report was prepared by Kasthuri Venkateswaran, Myron T. La Duc, and Parag Vaishampayan, with significant contribution from Emilee Bargoma, Kelly Kwan, and James N. Benardini.

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A.1 INTRODUCTION

A.1.1 Purpose

This report documents the significant lessons learned while working with swabs (primarily cotton and flocked-nylon) in the context of sample collection (cells, biomolecules, etc.) from low-biomass surfaces. The report discusses the advantages and limitations of each swabbing material with regard to sample acquisition, sample retention, background contamination (indigenous biomaterials), and consistency across production lots. The results have been identified over the course of several studies of the Genetic Inventory. Also presented are the results of the subtle differences between cotton and nylon swabs when used to collect nucleic acids from surfaces. Heritage studies, such as those based on the NASA standard spore assay, have focused solely on cultivation-dependent cell collection efficiencies. Here, the efficacy and efficiency of each swab matrix is discussed and compared according to results generated via DNA-dependent assays.

A.1.2 Background and Rationale

The *NASA Technical Handbook for the Microbial Examination of Space Hardware* protocol requires researchers to exclusively use cotton swabs with wood handles to sample small surface areas (NASA 2010). Similarly, the European Space Agency (ESA) has elected to use flocked nylon swabs when downstream analyses are molecular-based (Probst *et al.,* 2010). Because cotton and nylon swabs have been the standard sampling devices, the Genetic Inventory Task team started out focusing on the efficacy and efficiency of swab-based nucleic acid sample collection.

The Genetic Inventory team quickly identified two shortcomings associated with swab-based sample collection:

1. **Indigenous nucleic acid contamination** was concomitant with cotton swabs, due primarily to their organic composition (both cotton matrix and wood shaft).
   - When assayed via quantitative polymerase chain reaction (qPCR) and short-read (~80-bp) 454-tag sequencing, the levels of indigenous DNA associated with cotton swabs oftentimes exceeded the levels of DNA originating from the low-biomass (~10^4 ribosomal RNA [rRNA] gene copies) samples.
   - Enzymatic digestion (DNase) of the swab-associated indigenous DNA was not possible as such processing compromises the integrity of the swab head. Since the cotton swabs were made sterile via gamma radiation, fragmentation of the indigenous DNA molecules (thereby detected by short-read 454 assays) was a problem. To by-pass this issue, longer-read (~400-bp) 454-tag sequencing was successfully used.
   - To circumnavigate the indigenous nucleic acid contamination associated with the various swab materials examined, it is essential to incorporate appropriate controls at all stages of sample collection, processing, and analysis. By experimenting with the controls, it was always possible to differentiate target sample–associated cells and/or molecules from those originating from the swab matrix (or wood handle in the case of cotton).
   - When downstream analyses necessitate sensitive enzymatic-based molecular biological processes (adenosine triphosphate/Limulus amebocyte lysate [ATP/LAL] assays), the organic nature of the cotton and wood swab composition often interferes with the analyses, in which case the cotton swab-borne sample cannot be assessed with emerging analytical methodologies.

2. Swab sampling was found to be unsuitable for collecting samples from low-biomass environments.
   - Due to the limiting surface area able to be collected (~ 25 cm2), it was oftentimes not possible to collect the levels of sample material required to accommodate the sensitivity thresholds of downstream molecular analyses.
   - Given the limited amount of time and resources available, this pitfall fueled the team's decision to shift emphasis away from swabs, towards devices capable of sampling much larger surface areas (e.g., polyester wipes).

In light of these shortcomings, and at the direction of the review committee, the Genetic Inventory team abandoned swab investigation in favor of devices capable of collecting samples from much larger surface areas. The lessons learned in working with swabbing matrices while carrying out routine sample collection and processing procedures for the genetic inventory task will benefit NASA planetary protection efforts by enhancing understanding of the strengths and weaknesses associated with the various swabbing materials currently available for sample collection from spacecraft hardware.

A.2 Physical and Chemical Characteristics of Sampling Materials

A.2.1 Cotton

Cellulose makes up to ~95% of the chemical component found in cotton. Proteins, ash, wax, sugar, organic acids, and other chemicals make up the remaining 5%. High in carbon, hydrogen, oxygen and other polar OH groups, the interactive forces in cotton involve very strong hydrogen bonds. There are roughly 10,000 glucose monomers linked together to form a single molecule of cellulose. These long spiral linear chains are present in each cotton fiber. The outer surface of cotton fibers has a protective barrier of wax, which is made up of long fatty acid chains and alcohols. The higher the wax content present on cotton fibers, the higher the surface area of the cotton. A high surface area is indicative of higher retention during sample collection.

Also present on cotton fibers is cotton sugar, which comes from the cotton plant (in the form of monosaccharides, glucose, and fructose), and from cross pollinators such as insects (e.g., whiteflies). Cotton also contains organic acids (e.g., malic and citric acid), which are present as metabolic residues. Prior to market distribution, manufacturing plants pre-treat cotton with selective solvents such as chloroform, hexanes, sodium hydroxide and non-polar solutions, to remove non-cellulose chemicals. These procedural treatments usually result in 99% cellulose present in cotton post treatment.

The strong hydrogen bonds maximize moisture absorption by cotton swabs. The cotton wax increases the surface of the cotton, thus increasing its absorption capability. In addition, the rigid nature of the wooden shaft allows the researcher to grip the swab and swipe it evenly across the smooth surface of the metal coupon while maintaining uninterrupted direct contact between the swab head and the sampling surface. No droplets were observed on the surface of the swab head following a sampling event, and even fewer water droplets were observed on the surface of the metal after sampling.

A.2.2 Nylon

The nylon-flocked swab has perpendicularly sprayed fibers that allow the brush-like texture to rapidly absorb liquid through capillary action. Most nylon-flocked swabs are commonly used for nasopharyngeal sample collection. The long molecular chain of amides (polyamide) results in high hydrogen bond interactions. Unfortunately, there are certain physical characteristics that limit the effectiveness of nylon-flocked swabs for sampling metal surfaces.. The shaft (handle) of the swab is quite pliant, a design that is necessary for easy maneuverability in tight orifices such as the nasopharyngeal passage. For flat, smooth surfaces such as stainless steel, however, the flexibility of the swab may contribute to the consistently lower recovery efficiency (compared to cotton swabs). The researcher's inability to maintain proper continuous direct-contact swipe across the metal surface with a nylon-flocked swab during sampling may also contribute to the lower recovery. Because the swab is not being maneuvered through a tight orifice, the samples are not adequately absorbed between the perpendicular fibers; rather, they either collect in droplets on the surface of the swab or remain in small puddles on the surface of the metal. We have confirmed a much higher concentration of nucleic acid deposits remaining on the metal surface after sampling with nylon swabs (data not shown).

A.2.3 Macrofoam

The detection of nucleic acids and isolation of microbes depend on the type of pre analytical devices used for sample collection. Subsequently, because the sampling device is in direct contact with the organism to be recovered, the sensitivity of a molecular diagnostic depends on the number of cells successfully released by the sampling device. An ideal sampling device, therefore, must have the ability to both absorb and release as much of the organism as possible from a given surface. Of critical importance are (a) the physical structure of the sampling device material and (b) the type of material that makes up the sampling device. Ultimately, the construction of the device is equally important because it affects the amount of testable specimen recovered.

Low recovery from sampling is usually not due to poor choice in sampling device; rather, it is due to specimen entrapment in the device (Madhusudhan 2009). An ideal sampling device would be designed to collect a majority of the cells on a given surface and to effectively release the sample while conforming to its manufacturer intended use. This is essential, as not all sampling devices are created equal—between manufacturers, between batches or, in some cases, within a given batch. With this sampling capability and design conditions in mind, macrofoam device manufacturers have created a sampling device to overcome the limitations inherent in cotton and nylon swabs.

Aqueous foam is an impermanent form of matter in which a gas, often air, is dispersed in an cluster of bubbles that are separated from one another by a film of liquid that is mostly water and surfactants, alcohols and polymers (Archuleta 1995). The ability to successfully control the formation and potential sizes of these jumbled bubble masses puts us closer to attaining that "ideal sampling device." Levels of non-toxic ammonium-neutralized sulfate esters, fatty acid alcohols, and phosphate salts in aqueous foam are manipulated to turn aqueous foam into macrofoam sponge. The controlled spray-pump application of the aqueous foam allows the macrofoam sponge to dry in such a way that the bubble-pore sizes are uniform in shape and size. This increases efficiency in sample collection and release, while lowering retention rates because there are no strong electrostatic forces, due to the inherent antistatic nature of the sponge, that would hold or retain the samples during an expunging step. When the sponge is dry, its coarse composition boosts the scouring of the metal surface. Therefore, macrofoam sponge is most effective as a large-surface sampling device: the larger the surface area (i.e., more pores), the greater the sample collection efficiency.

A.2.4 Polyester

Polyester (polyethylene terephthalate, PET) fibers are made up of long polymers of ester-containing chains. They are double-knitted, continuous filaments that have higher absorbency and particulate retention characteristics than other fabrics. Polyester fabrics provide specific advantages over cotton and wool in that they have higher wrinkle resistance and color retention. The carbon conductive nature of these fibers makes the wipe an electrostatic dissipater, which is important when sampling metal surfaces. Additionally, the non-porous, tightly woven nature of these fibers renders them highly efficient in sample collection. Unfortunately, the sample retention rate of these fibers is significantly higher than their sample release rate. As polyester devices are used to sample microbes and/or naked nucleic acids from surfaces, the long continuous filamentous interlocked fibers trap the cells, rendering the amount of sampled material released, following extraction, to be very low. What makes this material ideal for keeping cleanrooms clean and debris-free, is, unfortunately, an encumbrance for the purposes of sample release following collection.

A.3 Experimental Conditions

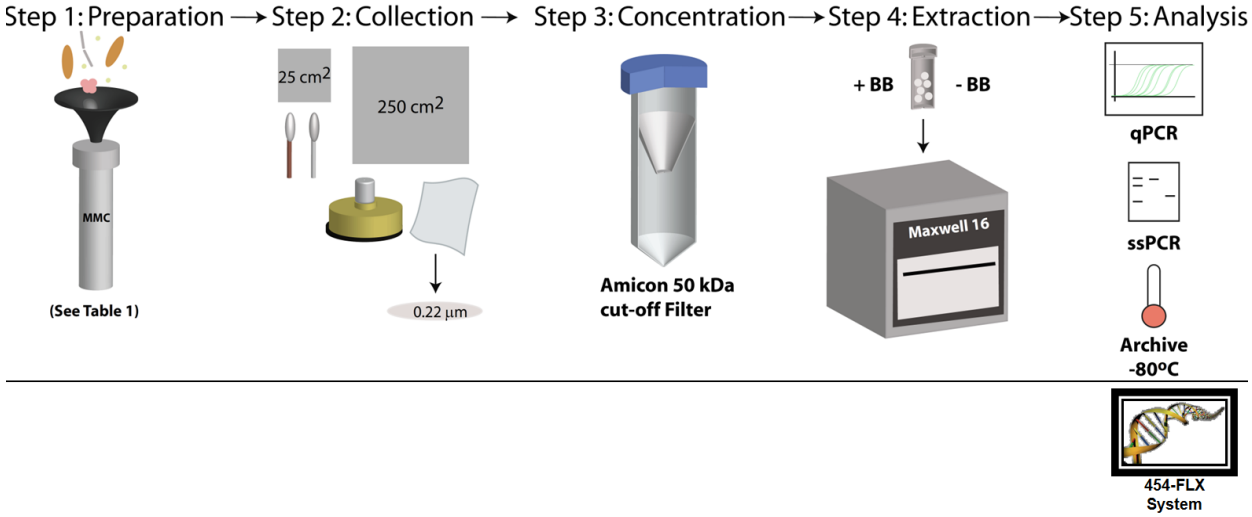

Figure A.3-1. A schematic representation of the various procedures involved in the preparation of purified spore and MMC suspensions, followed by deposition onto metal surfaces, 24 h drying, and sample collection, processing, and analyses.

Legend:
BB = mechanical cell membrane rupture by bead beating
qPCR = quantitative polymerase chain reaction
ssPCR = species-specific polymerase chain reaction
ss-qPCR = species-specific quantitative polymerase chain reaction.

Note: All of the findings discussed below are based on the results of controlled laboratory experiments where a known quantity of cells, spores, or rRNA genes was artificially deposited onto a surface, allowed to dry, and subsequently sampled with the various devices under examination.

A.3.1 Desiccation and Recovery

Previously published findings have shown that it is important to consider the amount of time the model microbial community (MMC) spends in a completely desiccated state on the metal surface. By applying tape-lifting and/or polyvinyl alcohol coating techniques, effective removal of bacterial spores from metal surfaces has been demonstrated, with recoveries as high as 90% for up to 18 months of desiccation (Tauscher *et al.,* 2006). **With regard to vegetative cells, however, previous unpublished studies have shown that recovery from metal surfaces correlates significantly (negatively) with time. In those studies, fewer vegetative cells were recovered as the length of time that the MMC spent desiccated on the metal surfaces or swab head increased (from a few to 24 hours).** Since the length of time is clearly a significant variable, the team ensured that it was consistent during the study. In order to accurately mimic the conditions of a typical humidity-controlled cleanroom (RH = ~40-55%, facility-dependent) and at the same time remain consistent, all MMC suspensions were deposited and allowed to dry for 24 hours on the metal surface prior to sample collection.

A.3.2 Sonication and Concentration

There are several variables to examine with regard to the collection and processing of recovered MMC samples. Subjecting sample-laden collection devices (e.g., cotton swab) to a NASA-approved ultrasonic water bath with added resuspension solution (sterile water or PBS) has been shown to promote the release of cells and spores from cotton, foam, and polyester matrices (Puleo *et al.,* 1967). In our studies, sonication did not dramatically hinder the cultivation of MMC strains (~80% cultivable after sonication), nor did it compromise the integrity of sample DNA molecules. As

different sampling devices required different volumes of resuspension fluid (~45 mL to 600 mL) for optimum recovery, the sample eluates underwent centrifugal concentration in Amicon filters (Millipore) after sonication. This concentration of cells, spores, and all other materials of biotic origin proved very effective and facilitated molecular biological downstream analyses that would not have otherwise been possible, due to the low concentrations of biomass. The percent recovery of DNA (~60%) achieved using Amicon centrifugal filters was superior to all other available concentration protocols. Previously, DNA loss as high as 90% was reported when ~10-mL sample volumes were directly subjected to standard phenol/chloroform-based DNA extraction procedures. This loss was likely attributable in large part to the direct processing of large sample volumes (>10 mL) without prior concentration (La Duc *et al.,* 2009; Sambrook *et al.,* 1989). Other studies have also confirmed the necessity of centrifugation or filtration of large sample volumes prior to downstream DNA processing and analysis (Buttner *et al.,* 2001). The Amicon centrifugal filtration procedure adopted and advocated here proved extremely effective and yielded reproducible results for sample volumes up to 45 mL. In cases where the authors processed ~600 mL sample volumes collected with polyester wipes, the entire volume was first subjected to 0.22 µm membrane filtration and then further concentrated via Amicon centrifugal filters.

A.3.3 Sample Processing

To achieve thorough and effective lysis of the most highly diverse and robust microbial cell walls and outer membranes, both automated and manual alkaline lysis-based DNA purification procedures are oftentimes augmented with some form of mechanical abrasion (Sambrook *et al.,* 1989). For the genetic inventory task, a simple bead-beating of the sample volume prior to nucleic acid extraction was necessary to lyse open extremely resilient actinobacterial cells and bacterial spores (La Duc *et al.,* 2009; Wilson *et al.,* 2002). However, bead-beating or any other form of mechanical abrasion could result in the inadvertent shearing and/or degradation of large nucleic acid polymers from the less resilient organisms (La Duc *et al.,* 2009). To avoid biases in this regard, the samples collected in the genetic inventory study were split into two equivalent fractions. One fraction was subjected to bead-beating prior to undergoing nucleic acid extraction, and the other portion was not subjected to mechanical abrasion prior to purification of nucleic acids. Both portions were then pooled together and subjected to automated DNA extraction as one sample volume (La Duc *et al.,* 2009). The findings of our studies confirmed previous recommendations that automated methods are preferred to traditional manual phenol/chloroform-based DNA extraction techniques; therefore, automated methods were employed during the genetic inventory study so as to maximize reproducibility and avoid technician-based variability (La Duc *et al.,* 2009).

A.4 RESULTS

1. *Polyester swab disqualification*. Three different swab materials were tested in the early stages of the genetic inventory task: cotton, polyester, and macrofoam. Materials data and vendor specifications detailing locations to procure these sampling devices are provided in [REF]. *Bacillus subtilis* 168 spores were deposited onto precision-cleaned spacecraft-qualified aluminum 6061 coupons (5 × 5 cm), which were then air-dried for 24 hours prior to sample collection procedures. Appropriate controls that had not been seeded with spores were also included to measure the background noise (indigenous, contaminant CFU) associated with the coupons. Initially, the NASA standard spore assay was performed to measure the spore recovery percentage of the various swabs according to routine protocol. As shown in Figure A.4-1, cotton (9 to 20%) and macrofoam (6 to 13%) swabs performed roughly equivalently, while polyester swabs (0 to 0.9%) recovered fewer spores. For this reason polyester swabs were omitted from further consideration. Since the recovery of cultivable spores was no better with macrofoam swabs than cotton, the Genetic Inventory team elected to focus on cotton swabs, as these are the standard NASA sampling device.

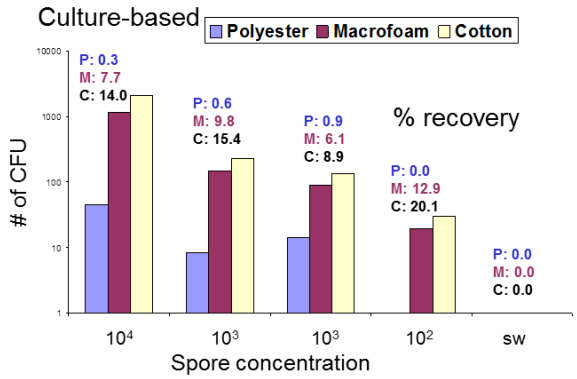

Figure A.4-1. Recovery performance of cotton, macrofoam, and polyester swabs.

2. *Recovery and yield of DNA: cotton vs. nylon swabs*. Recently, a comparative evaluation of cotton swabs with other swab varieties concluded that nylon-flocked swabs were superior to cotton swabs for the collection of *Bacillus* spores from stainless steel and other surfaces (Probst *et al.,* 2010). In a similar vein, the use of nylon-flocked swabs resulted in a more efficient recovery of cultivable contaminants on pharmaceutically relevant surfaces (Dalmaso *et al.,* 2008). To date, the literature is devoid of reports similar to that of the Genetic Inventory investigation, which focused on evaluating procedures for the effective and efficient collection and processing of not only intact microorganisms, but also nucleic acids from cleanroom surfaces. The results (Figure A.4-2) of numerous experiments carried out in the Genetic Inventory study showed that nylon-flocked swabbing material was comparable to cotton for removing intact cultivable cells and spores from small (~25 cm^2) metal surfaces [≤1% recovery; (Kwan *et al.,* 2011)]. However, cotton swabs consistently yielded a greater recovery of rRNA gene copies than nylon-flocked swabs (10-fold more). When nylon-flocked swabs were used to collect samples, 62 out of 89 replicates recovered less than 9.9% of the rDNA seeded onto the

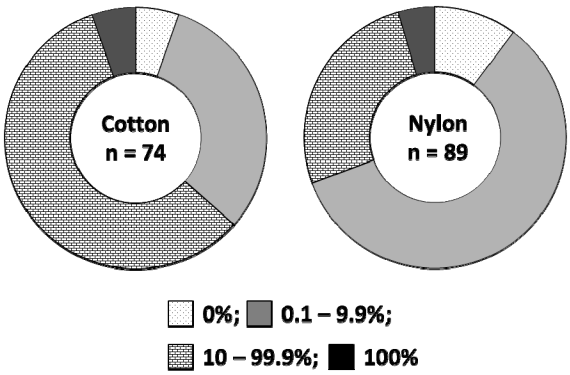

Figure A.4-2. Categorical percent recovery efficiency of cotton and nylon-swabs

metal surfaces. Cotton swabs proved much more effective in sample recovery, as 48 of the 74 cotton swab sampling replicates yielded recovery greater than 10%.

3. *Recovery of a diverse suite of microbes: cotton vs. nylon swabs*:

a. *Species-specific quantitative-PCR*: Resulting MMC-strain-based recovery efficiencies associated with the two sampling materials tested are depicted in Figure A.4-3. The initial amount of rDNA of each MMC constituent present in one ml of MMC suspension was calculated and used as the reference point for determining percent recovery. Cotton swabs enabled the recovery of rDNA from all nine MMC constituent microbes assayed, whereas nylon-flocked swabs failed to recover three of the MMC members, including the archaeaon *M. formicicum* (Fig. A.4-1). In addition, cotton swabs recovered considerable levels of rDNA of several MMC constituents that had been totally unaccounted for when sampled via nylon-flocked swabs. Of the nine MMC constituents assayed, cotton recovered at least 25% of the originally deposited rDNA from *C. metallidurans* (34.5%), *C. sporosphaeroides* (36.7%), *M. luteus* (29.1%), *S. warneri* (31.8%), and *M. formicicum* (24.8%). In contrast, nylon-flocked swabs recovered the rDNA of *S. warneri* at 18.6%, and the rDNA of five additional MMC-strains at 7% or less. Both swab materials had difficulty recovering the rDNA of *D. radiodurans* (<1% each).

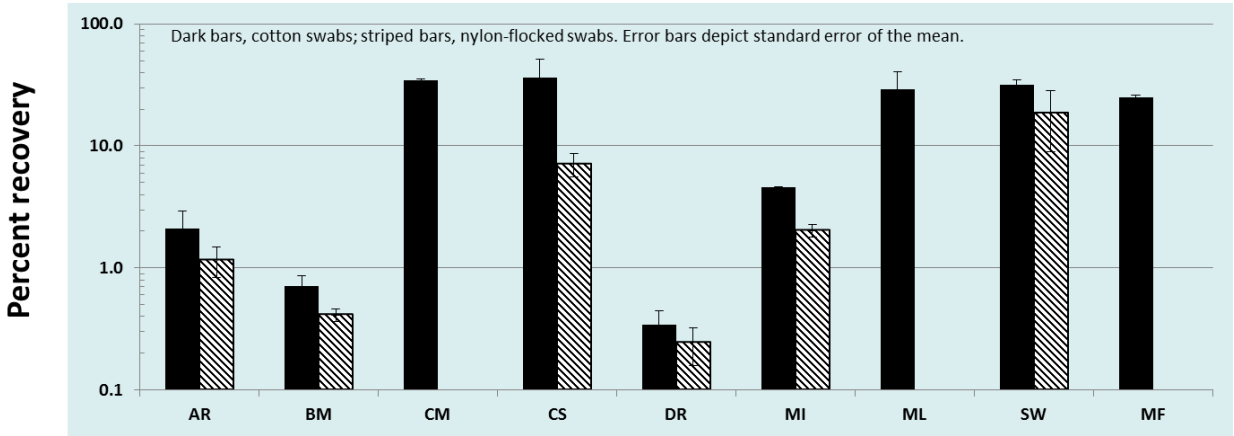

Figure A.4-3. Resulting MMC-strain-based recovery efficiencies associated with cotton swabs (dark bars) and nylon-flocked swabs (striped bars).

b. *Tag-encoded FLX PCR-amplicon Pyrosequencing*: Table A.4-1 identifies the MMC-strain-based

Table A.4-1. Effectiveness of swabs in the retrieval of 16S rRNA genes from metal surface using pyrosequencing technology

Microbial taxa	Pyrosequences retrieved from cotton swab	Pyrosequences retrieved from nylon swab	Fold increase (Cotton/ Nylon)
Acinetobacter radioresistens	82	26	**3.15**
Bacillus megaterium	4,424	2,397	**1.85**
Bacillus pumilus	2,631	817	**3.22**
Cupriavidus metallidurans	431	292	**1.48**
Deinococcus radiodurans	2,204	535	**4.12**
Microbacterium imperialae	27	8	**3.38**
Micrococcus luteus	271	79	**3.43**
Staphylococcus warneri	365	198	**1.84**
Methanobacterium formicicum (archaeon)	4,471	2,009	**2.23**

recovery efficiencies associated with swab materials assessed via 454-tag-encoded pyrosequencing. As was the case with ss-qPCR, the results of pyrosequencing processing and analysis clearly demonstrated that cotton swabs rendered superior recovery over nylon swabs. Both swab types facilitated the generation of pyrotag reads from all nine of the MMC constituent microbes; however, cotton swabs consistently gave rise to more pyrotag reads than nylon swabs (1.5- to 4-fold increase).

4. *Variability*: Even though all of the sampling devices for each material originated from the same lot, both cotton and nylon-flocked swabs exhibited remarkably high variability in resulting qPCR values for sampling blank controls and across sample replicates (Bargoma *et al.,* 2012). Such inconsistency (up to 2 logs in the case of nylon-flocked swab replicates) could be indicative of a notable degree of variation in sampling material composition within the same lot, and it merits further investigation. In addition, the signal-to-noise ratios for nylon-flocked swabs were surprisingly low, suggestive of indigenous DNA associated with each sampling device.

A.5 LESSONS LEARNED

1. **Ultimately, how one goes about selecting and tailoring materials and processes factors immensely into the experimental outcome.**

   Recommendation: The results of experiments conducted over the course of the Genetic Inventory Task lead the team to stress the importance of selecting and tailoring sample collection and processing approaches based on the desired target within the sample, as well as the level of detection/resolution required. The team therefore recommends that a thorough analysis of preferred and ideal markers and/or targets be performed prior to embarking on any initiative to ascertain biological sample characteristics, be they subtle or robust. A well-planned study would then avoid pitfalls arising from failure to use the right tool, or assayable target, for the task at hand.

2. **The time that a given biological sample is allowed to dry and sit in a desiccated state is a variable that matters.**

   Recommendation: The Genetic Inventory team recommends that consistency is maintained throughout a study, as was the case for the Genetic Inventory study wherein all samples were set to dry and held in a desiccated state for 24 hours.

3. **Cotton swabs outperform flocked-nylon swabs in collecting biomaterials from samples extremely low in total biomass.**

   Recommendation: The Genetic Inventory team recommends the use of cotton swabs for the collection of biomaterials (e.g., nucleic acids) from environmental surfaces extremely low in biomass, such as those found on 100K (or cleaner) class cleanroom floors or spacecraft hardware intended for a Planetary Protection Category IVa/IVc[1] mission to Mars (e.g., Mars Science Laboratory).

4. **Cotton swabs are superior to flocked-nylon swabs in recovering the greatest breadth of biological materials, from diverse cultivable intact cells to rRNA gene proxies.**

   Recommendation: Cotton swabs are recommended for use when a given survey is more interested in the entire spectrum of microbial diversity (e.g., genetic inventory) than the total yield of cultivable entities.

[1] Mars landers not carrying instruments designed to search for evidence of extant Martian life are designated Category Iva; their biological burden is restricted to a level no greater than the Viking-lander pre-sterilization level. Mars landers carrying instruments designed to search for evidence of extant Martian life are designated Category IVb and subject to more stringent sterilization requirements: the entire landed system must be sterilized at least to Viking Lander post-sterilization biological burden levels or to levels of biological burden reduction driven by the nature and sensitivity of the particular life-detection experiments, whichever are more stringent Mars lander missions intended to explore so-called "special regions," areas where liquid water is present or likely to occur are designated Category IVc and subject to stringent sterilization requirements, determined by the parameters of the mission, such as landing method, landing site, rover mobility.

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APPENDIX B: PROCEDURES AND PROTOCOLS FOR COLLECTING, PROCESSING, AND ARCHIVING SAMPLES FROM SPACECRAFT AND ASSOCIATED SURFACES

Appendix B documents procedures and protocols for collecting, processing, and archiving samples from spacecraft and associated surfaces. This document was prepared by Kasthuri Venkateswaran, Myron T. La Duc, and Parag Vaishampayan, with significant contribution from Emilee Bargoma, Kelly Kwan, and James N. Benardini. This work was performed from the start of the Genetic Inventory Task (FY'07) on through to completion in FY'11.

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Required Materials and Equipment

This section lists the materials that will be required to prepare the positive control microbial strains which will be deposited (Section B.1) onto metal surfaces and subsequently collected (Section B.2) for processing (Section B.3). Also listed are all the supporting labware, consumables, laboratory equipment and reagents needed to carry out the procedures herein described.

***Note**: To minimize lot-lot variation, procured materials are ordered in bulk so that the experiment is completed from beginning to end using consumables, labware, and reagents from the same lot numbers.*

Laboratory Equipment and Supplies	
4	Biological hoods
1	4°C refrigerator for short-term storage
4	−80°C freezers for long-term storage
1	Autoclave
1	New Brunswick Scientific Incubator Shaker (Cat. # Innova-4430)
1	Petroff-Hausser counting chamber
1	Olympus Microscope (BX60)
1	Calculator (TI-36X Solar)
2	Welch Ashcroft electric pumps (Model # 2545B-01. 115v, 60Hz, 3.6A)
5	Sterile pump tubing (≥ 2.5 ft)
4	Stir plates
1–5	Genie-II Vortex mixers
1	Eppendorf rotating/swing bucket centrifuge (Model # 5804)
960	Rainin LTS tips (Cat. # RT-L200F)
1	Rainin EDP3+ electronic LTS pipette (Cat. # E8-200)
1	Ultrasonic bath for ultrasonication (Cat. # Branson-8510)
40	MP Bio Lysing Matrix E microbeads (Cat. # 6914-100-9472)
1	MP Bio FastPrep-24 Bead-beating instrument
1	Maxwell-16 Automated DNA/RNA Purification System
1	Brady-IP300 thermal printer
Labware	
4	2-L glass bottles
8	250-mL vented Corning Erlenmeyer flasks (Cat. # 431144)
6	1-L glass bottles (Cat. # 430518)
5	Magnetic stir bars, sterile
1	5-L glass bottle
5	Fisher Scientific sterile manual and serological pipettes (Cat. # 1072-5410)
2	Sterile 1-L beakers for waste collection
6	Instaware 22″ × 22″ roasting pan (Cat. # JRO-3781)
1	Ice bucket (4.5 L capacity)
5–30	Sterile metal forceps
Consumables	
1–5	Clean laboratory smocks
10–20	Hairnets
10–20	Sterile gloves
120	Fischer Scientific 15-mm plastic Petri dishes, raised edges (Cat. # 08-757-12)
11	Sterile disposable streakers
20	Corning disposable polystyrene 250-mL flasks (Cat. # 430281)
40	Fisher sealable autoclave envelopes (Chem-all II, Cat. # 024014)
96	Extended length 1000-µL pipette tips
100	BD Falcon 50-mL conical polypropylene centrifuge tubes (Cat. # 352070)
60	Millipore Amicon 50-kDa cut-off centrifugal filters (Cat. # UFC905024)
24–40	Equal-size metal test tube caps
20	Fisher Microscope cover slips (Cat. #12-540C, 25 mm)
1 roll	Aluminum foil
5	VistaLab disposable reagent reservoirs (Cat. # ISO 9001)
37	Eppendorf 1.7-mL micro-centrifuge tubes
37	0.5-mL elution tubes
37	BioExpress skirted screw cap 0.5-mL tubes (Cat. # C-3273-1)
2 rolls	Brady Thermatab Markers thermal labels (Cat. # THT-127-461-3)
4000	Fisher cryogenic storage vials (Cat. # 10-500-26)
46	Thermo Scientific Nalgene cryogenic storage boxes (Cat. # 15-350-107B)
5	VWR non-hazardous autoclavable waste bags (36 x 45 in., Cat. # 14220-044)

Stainless Steel Metal	
24	Spacecraft surface stainless-steel coupons, grade 304-020, 5 × 5 cm
12	Spacecraft surface stainless-steel sheets, grade 304-020, 50 × 50 cm
Sampling Devices	
12	Puritan cotton swabs (Cat. # 25-806 1 WC)
12	Copan nylon-flocked swabs (Cat. # 552C.US)
12	ITW polyester wipes, 4 × 4 in, (Cat. # TX1004)*
8	Quicksilver Analytics BiSKits (BIS-4C001A)
Reagents and Media	
5 g	Tryptone
30 g	Yeast extract (100%, Cat. # 8013012)
1 g	D(+)-Glucose (Cat. 4074-2)
5 L	Gibco UltraPure Distilled Water (Cat.# 10977)
3 g	Noble agar (1.5%, Cat. # 0142-15)
8 g	Nutrient Broth (Difco/BD)
~50 mL	DSMZ medium 78
~50 mL	DSMZ medium 119
2 L	MoBio UltraClean pH 7.4, 1X PBS (Cat. # 17330-500)
50–100 mL	Ethanol, 70% (Cat.# E1424)
30–200 mL	Kleenol-30 strong alkaline-based detergent (Cat. # 118030)
10–20 mL	0.5% Amphyl surface disinfectant spray bottle solution (Cardinal Health, Cat. # 3624195101)
1 bottle	Fisher Scientific RNase/DNA remover solution (Cat. # 04-355-138)
1 bag	Ice chips (to fill 4.5 L ice bucket)
10 mL	Tween-80, 0.02%

Microbial Strains
Culture stock strains are on cryogenic beads in −80 °C

- *Aureobasidium pullulans* 28v1 (AP, NRRL 58992): Eukaryotic yeast
- *Acinetobacter radioresistans* 50v1 (AR, NRRL B-59417): g-proteobacteria
- *Bacillus megaterium* KL-197 (BM, NRRL B-59415): Gram-positive, spore-forming bacteria
- *Cupriavidus metallidurans* CH34 (CM, ATCC 43123): non-spore-forming b-proteobacteria (received from C. Moissl, University of Regensburg, Germany, who procured the culture from N. Leys, Belgium)
- *Deinococcus radiodurans* R1 (DR, ATCC 13939; NRRL B-59418): Gram-positive, non-spore-forming bacteria
- *Microbacterium imperiale* 47v1 (MI, NRRL B-59416): Gram-positive, actinobacteria
- *Micrococcus luteus* (ML, ATCC 4698; NRRL B-59413): Gram-positive, actinobacteria
- *Staphylococcus warneri* 82-4 (SW, NRRL B-59414): Gram-positive, non-spore-forming bacteria
- *Bacillus pumilus* SAFR-032 spores (BP, ATCC PTA-7603; NRRL B-30938): Gram-positive bacteria
- *Clostridium sporosphaeroides* (CS, ATCC 25781; DSMZ 1294): Gram-positive, spore-forming anaerobe culture (received from C. Moissl, University of Regensburg, Germany)
- *Methanobacterium formicicum* (MF, ATCC 33274; DSMZ 1535): Anaerobic archaea culture (received from C. Moissl, University of Regensburg, Germany)

*Note: *Initially, 9 x 9 in (Cat. # TX1009) ITW alpha polyester wipes were employed for sample collection. However, due to the large surface area of these wipes (162 in^2), ~600 mL of eluent liquid was required to effectively release collected materials, which required vacuum-based filtration through a 0.22-μm membrane prior to Amicon centrifugal concentration. Collectively, all of this extra processing led to more sample loss. The Genetic Inventory team was advised to avoid these additional steps by using smaller polyester wipes (4 x 4 in; 32 in^2 total surface area), which can be completely immersed in 15 mL of eluent liquid to effectively release collected particulates.*

B.1 Model Microbial Community Preparation and Deposition onto Metal Surfaces

B.1.1 Purpose

This section details the steps needed to create a reference model microbial community (MMC) of known composition for future method comparison and validation. MMC serves as the positive control in this laboratory controlled experiment. The procedures and protocols described herein were developed and subsequently executed to determine the most effective methodology approach for seeding these reference strains onto stainless-steel surface areas, using various sampling matrices to collect the seeded strains, and applying the latest molecular approaches to investigate efficacies in total and differential recovery of these reference strains.

B.1.2 Approach

MMC is used as a laboratory positive control in this experiment to optimize the sample collection efficiency of the sampling devices tested. Stainless-steel coupons (25 cm^2) and sheets (2,500 cm^2) are used to test the efficacy of the sampling devices in collecting seeded MMC from small and large surface areas, respectively.

***Note**: In this and all sections to follow, strict aseptic conditions apply, with all procedures performed wearing sterile gloves, a hairnet, and a clean laboratory smock. Additionally, all autoclave sterilizations are performed at 121°C, 15 Pa N/m^2, for 30 min.*

B.1.2.1 Preparation and Inoculation

B.1.2.1.1 Preparation

1. Use a 2-L glass bottle to prepare 1 L of Tryptone Yeast Glucose (TYG) agar as described in Table B.1-1 below.

Table B.1-1. 1-L preparations of Tryptone Yeast Glucose (TYG) broth (steps 1–4) and agar (steps 1–5).

Step	Amount	Ingredient
1	5 g	Tryptone
2	3 g	Yeast Extract
3	1 g	Glucose
4	1 L (total volume)	UltraPure water
5	15 g	Noble Agar

2. Use a 2-L glass bottle to prepare 1 L of Nutrient Agar as described in Table B.1-2 below.

Table B.1-2. 1-L preparations Nutrient Broth (steps 1–2) and Agar plate (steps 1–3).

Step	Amount	Ingredient
1	8 g	Nutrient Broth powder
2	1 L (total volume)	UltraPure water
3	15 g	Noble Agar

3. Tightly cap each glass bottle and mix the agar preparation by gently inverting the bottles up and down several times.
4. Loosen both bottle caps to allow gas to escape from the pressure build-up in the bottles.

5. Autoclave both media preparations.
6. Allow the liquid agars to cool to touch (~40°C).
7. Pour ~20 mL of each liquid agar into ~50 sterile plastic petri dishes arranged on the flat surface of the biological hood.
8. Allow the agar plates to solidify in the biological hood—at room temperature with the fan on—with the plate lids partially ajar.
9. Once solidified, store the agar plates stacked—no more than 12 plates/stack—and inverted in a petri-dish sleeve or a petri-dish plastic bag at 4°C until ready for use.
10. Remove the 11 MMC strains (listed in Table B.1-3) that have been archived and stored at −80°C on cryogenic beads.
11. Prepare 11 pure culture-streak plates using the agar plates.
    a. Remove 10 TYG agar plates from the 4°C storage.
    b. Streak *only 1* bead of AP, AR, BM, CM, DR, MI, SW, BP, CS, and MF onto the 10 plates, respectively.
    c. Remove 1 Nutrient Agar plate from the 4°C storage.
    d. Streak *only 1* ML cryobead onto the Nutrient Agar plate.
12. Incubate all 11 plates, respectively, as indicated in Table B.1-3.

Table B.1-3. Optimal incubation time (h) and growth conditions for each model microbial community constituent.

Strain	Plate Growth Conditions	Plate Growth Time from Bead (h)	Broth Growth Conditions	Broth Growth Time from Pure Plate Colony to 10^8 cells/mL (h)	Total Growth Time (h)
Aureobasidium pullulans 28v1	TYG agar, 30°C	40	TYG broth, 30°C	46	86
Acinetobacter radioresistens 50v1	TYG agar, 32°C	40	TYG broth, 32°C	20	60
Bacillus megaterium KL-197	TYG agar, 32°C	18	TYG broth, 32°C	20	38
Cupriavidus metallidurans CH34	TYG agar, 32°C	40	TYG broth, 32°C	20	60
Deinococcus radiodurans R1, ATCC 13939	TYG agar, 32°C	40	TYG broth, 32°C	20	60
Microbacterium imperiale 47v1	TYG agar, 32°C	40	TYG broth, 32°C	20	60
Micrococcus luteus ATCC 4698	Nutrient agar, 32°C	40	Nutrient broth, 32°C	20	60
Staphylococcus warneri 82-4	TYG agar, 32°C	20	TYG broth, 32°C	20	40
Bacillus pumilus SAFR-032	TYG agar, 32°C	24	TYG, 32°C	24	48
Clostridium sporosphaeroides DSM 1294	TYG agar, 37°C	40	DSMZ medium 78, 37°C	20	60
Methanobacterium formicicum DSM 1535	TYG agar, 37°C	32	DSMZ medium 119, 37°C	40	72

13. Procure DSMZ medium 78 for the CS broth culture.
14. Procure DSMZ medium 119 for the MF broth culture.
15. Use a 2-L glass bottle to prepare 1 L of TYG broth as described in Table B.1-1.
16. Use a 2-L glass bottle to prepare 1 L of Nutrient Broth as described in Table B.1-2.
17. Autoclave both broth preparations.
18. Allow the broths to cool to touch in a biological hood—at room temperature with the fan on.
19. Pour ~50 mL of the TYG broth into eight sterile disposable 250-mL vented Corning Erlenmeyer flasks labeled AP, AR, BM, CM, DR, MI, SW, and BP.
20. Pour ~50 mL of Nutrient Broth into a sterile Corning Erlenmeyer flask labeled ML.
21. Pour ~50 mL of DSMZ medium 78 into a sterile Corning Erlenmeyer flask labeled CS.
22. Pour ~50 mL of DSMZ medium 119 into a sterile Corning Erlenmeyer flask labeled MF.
23. Broth media can now be inoculated with the MMC strains.

B.1.2.1.2 Inoculation

1. As the incubation period is completed for each microbial strain agar plate, remove the plate from incubation.
2. Select one pure isolated colony from the agar plate to inoculate its respectively assigned broth media in the Erlenmeyer flasks.
3. Inoculate the eight 50-mL TYG broths with AP, AR, BM, BP, DR, MI, CM, and SW, respectively.
4. Inoculate the 50-mL Nutrient Broth flask with ML.
5. Incubate—while rotating at 125 rpm—each strain flask, respectively, as indicated in Table B.1-3.
6. The remaining unused TYG, Nutrient, medium 119, and medium 78 broths will serve as media blanks.

B.1.2.2 Determination of Cell Concentrations

B.1.2.2.1 Preparation

1. Pull one flask at a time from the shaker incubator as the incubation periods end for each strain.
2. Pipette 10 µL of liquid culture onto the center grid of a Petroff-Hausser counting chamber.
3. Cover the drop with the counting chamber cover slip and observe under a microscope at 400 × total magnification.
4. The volume of one small Petroff-Hausser square is 0.20 mm × 0.20 mm × 0.02 mm (1/20,000 mm^3). The volume of a large double-lined square is 1/1,250,000 cm^3. There are 16 small squares in the large double-lined squares. Count with the Petroff-Hausser as follows:
   a. Count the number of bacteria in the five large double-lined squares.
   b. Divide the total counted by five to obtain the average number of bacteria per large square.
   c. Multiply the average by 1,250,000 to determine the total number of organisms per cm^3 (mL) in the original sample.

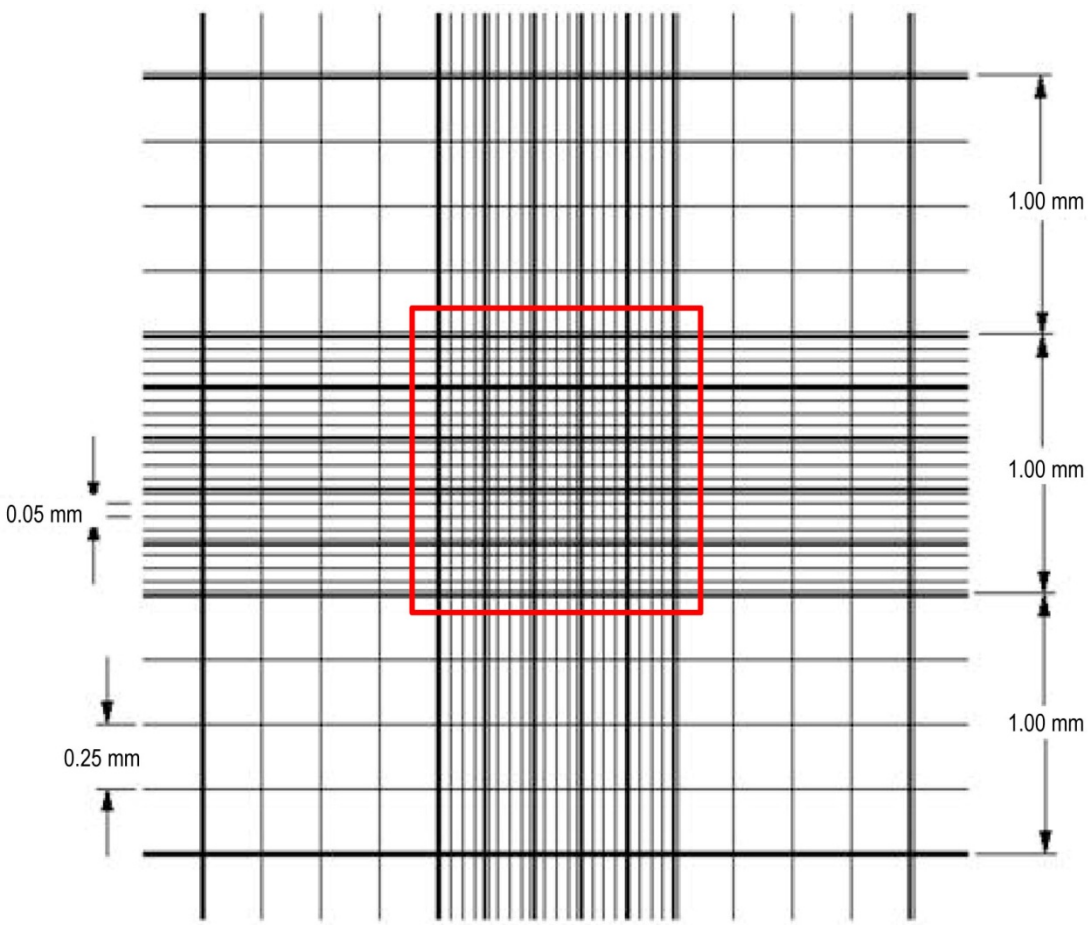


Figure B.1-1. Petroff-Hausser counting chamber. The counting area comprises the larger 5 x 5 squares outlined in red.

5. Ensure that each small square contains no more than an average of three cells. If more cells are present:
   a. Perform a serial dilution by adding 1 mL of liquid culture to 9 mL of phosphate buffered saline (PBS). Repeat if necessary.
   b. Record the dilutions made and factor them into the final calculations.
   c. Record the total number of cells in five large squares.
6. Remove the cover slip, and wash the counting chamber and cover slip with 70% ethanol.
7. For each sample, perform duplicate counts.
   a. Calculate the average cell concentration of the ten counted large squares for each sample.
   b. All liquid cultures should contain $\geq 10^8$ cells/mL.
8. Repeat the cell counts for all flasks until the cell concentration has been estimated for each community strain.
9. Also perform the Petroff-Hausser counting steps for the media blanks.

B.1.2.3 Assembly of the Model Microbial Community

B.1.2.3.1 Materials Preparation

1. *Day one:* Three days prior to the MMC assembly, thoroughly clean four biological hoods in the following order:
   a. Wash with strong alkaline-based detergent (e.g. Kleenol-30).
   b. Spray down with 0.5% Amphyl disinfectant.
   c. Wipe down with RNase/DNA remover solution.
   d. Expose with UV for 30 min.
2. Place three TYG agar plates, at different locations, in each hood.
3. Fully remove the lids and expose the plates.
4. Leave the plates overnight.
5. *Day two:* Close the lids of each plate.
6. Leave the plates in the biological hoods.
7. Incubate the plates at room temperature for an additional 24 h.
8. *Day three:* Begin preparing the assembly equipment.

B.1.2.3.2 Equipment Preparation

1. Collect five electric pumps capable of dispensing precise-volume aliquots of 1.2 mL from the liquid culture. Set vacuum pressure to ≥ 20-in Hg.
2. Equip each pump with tubing capable of extending into a Corning 1-L glass bottle.
3. Collect five sterile magnetic stir bars.
4. Rinse the equipment with a strong alkaline-based detergent, followed by a 0.5% Amphyl disinfectant spray, and finally, an RNase/DNA remover wipe down.
5. Place each item into an individual sealable autoclave envelope.
6. Autoclave.
7. Clean the biological hoods as described earlier.
8. Place two stir plates in each hood.

B.1.2.3.3 Cryogenic Vial Preparation and Labeling

1. Procure the following items:
   a. 4000 Fisher cryogenic storage vials
   b. 46 Thermo Scientific Nalgene cryogenic storage boxes
   c. Two rolls of Brady Thermatab Markers thermal labels
2. Print and affix labels to the cryogenic vials for the MMCs (numbered MMC-0001 to MMC-3700) and the cryogenic vials for the media blanks (numbered MB-001 to MB-300).
3. Place the cryogenic vials, with corresponding labels affixed, into the cryogenic boxes for easy use on the day of MMC assembly.

B.1.2.3.4 Preparation of Phosphate Buffered Solution

1. Thoroughly wash a 5-L glass bottle.
2. Rinse the bottle several times with filtered (18 Meg-Ohm/cm^2) water before washing it in the dishwasher.
3. Sterilize the bottles by autoclaving.
4. Pour 4 L of sterile PBS into the sterile 5-L glass bottle.
5. Use the formula $M_1V_1 = M_2V_2$ to determine the appropriate mix ratio of cells to PBS, such that each of the 11 community strains will have an individual final cell concentration of 10^5 cells/mL in the 4-L solution.
   a. The desired total cell concentration in the entire solution is 1.1×10^6 cells/mL (11 strains $\times 10^5$ cells/mL per strain).
   b. Volumes of individual strain cultures added to meet the 10^5 cells/mL/strain requirement must be $\geq$ 0.500 mL and $\leq$ 20 mL.
6. Perform the appropriate serial dilutions by adding 1 mL of liquid culture to 9 mL of sterile PBS, such that each individual-strain mixing volume is within the acceptable range.
7. Calculate the total volume of liquid culture to be added to the 4 L of PBS and use a sterile serological pipette to remove this volume from the 4 L of PBS. (This will ensure that the final volume of MMC solution remains 4 L.)

B.1.2.3.5 Addition of the Model Microbial Community Strains

1. In a biological hood, use the predetermined mixing ratio values and a pipette (manual or serological, depending on the volume of culture required) to add the appropriate volume from each individual liquid culture into the PBS for a total volume of 4 L.
2. Cap the bottle and invert it a few times for a thorough mix.
3. Aseptically dispense approximately 1 L of the 4-L MMC-PBS suspension into four separate sterile Corning 1-L glass bottles.
4. Place one bottle in each of the four biological hoods.

B.1.2.3.6 Preparation of Representative Media Blank

1. Prepare a media blank with the same ratios of media used to culture the MMC.
2. Use the final mixing ratios of individual strain cultures to calculate the volume of media broths to add to PBS for a final volume of 500 mL.
3. Store the media blank mix in a sterile Corning 1-L glass bottle.
4. Cap the bottle and invert it a few times for a thorough mix.
5. Place the bottle in any of the biological hoods containing the stir plates.

B.1.2.3.7 Dispensing of MMC

1. In the biological hoods, place one Corning 1-L glass bottle (containing either one of the MMC mix or the lone media blank) on a stir plate.
2. Open the autoclave bag containing the sterile stir bars.
3. Place one stir bar into each bottle.

4. Open the autoclave bag containing the assembled pump system.
5. Attach the pump tubing to the bottle.
6. Turn on the stir function on the stir plate (no heat).
7. Set the plate to stir at a constant high speed.
8. Prime the pump of each MMC-mix bottle using sterile beakers to collect the fluid. *Wait to prime the media blank pump until all MMC cryogenic vials have been filled.*
9. Working with two people per hood, have one person handle the cryogenic vials while the other operates the electric pump.
10. Dispense 1.2-mL volume aliquots into each designated cryogenic vial until most of the MMC mix has been used.
11. Prime the pump of the media blank model into a sterile beaker designated for waste.
12. Dispense 1.2-mL volume aliquots into each designated cryogenic vial until most of the media blank has been used.
13. Immediately store all cryogenic boxes in −80°C, taking record of each box's location for future use.

B.1.2.4 Deposition of Model Microbial Communities onto Stainless-Steel Surfaces

This section provides a step-by-step description of the technique employed in depositing the prepared MMC onto sterile stainless-steel surfaces. 10^6 cells/mL are deposited onto 25 cm^2 and 2500 cm^2 metal surfaces, respectively, for the experimental purpose of determining sample recovery and detection. The following procedures shall be performed in a Class 100K cleanroom.

B.1.2.4.1 Preparation

Cleaning of Stainless-Steel Coupons and Sheets

1. Procure precision-cleaned, individually packaged, double-bagged, and heat-sealed (in electrostatic bags) stainless-steel coupons (24 count) and sheets (12 count). *Precision cleaning is performed by a non-GI JPL group as outlined in Detail Specification, General Cleaning of Materials, Rev. F, JPL Rules 35576, and per the specifications of Precision Cleanliness Requirements for Spacecraft Propulsion Subsystems and Support Equipment, Rev. D, JPL Rules 35263.*

Washing and Suspension of Model Microbial Community Cells in UltraPure Water

1. Remove 35 MMC aliquots from −80°C storage.
2. Thaw and aseptically transfer each aliquot into the same sterile, 50-mL conical tube to a total volume of 42 mL.
3. Use a marker to draw a thin line on the tube to indicate the fluid level of ~42 mL.
4. Vortex the aliquot mixture for 10 s at maximum speed.
5. Use a serological pipette to aseptically transfer 15 mL of MMC into each of three Amicon 50-kDa cut-off centrifugal filters (Figure B.1-2).
6. Centrifuge filters at 5000 × g for 4 min.
7. Discard only the flow-through.
8. Use a sterile pipette tip to remove the MMC concentrate from each filter and transfer all three concentrates into the pre-marked 50-mL conical tube.
9. Aseptically add UltraPure water to the tube up to the pre-marked ~42 mL fluid line.
10. Tightly cap the tube and place it into a sealable autoclave bag.
11. Place the bagged sample on ice in an ice bucket.

Figure B.1-2. Amicon 50-kDa molecular weight cut-off centrifugal filter being placed into a swinging bucket centrifuge.

Source: EMD Millipore. www.millipore.com

B.1.2.4.2 Model Microbial Community Deposition

Preparation

1. *Day one:* Three days prior to MMC deposition, prepare 24–40 test tube caps in the following manner:
   a. Rinse each cap with a strong alkaline-based detergent.
   b. Wipe caps with RNase/DNA remover solution.
   c. Place each cap into an individual sealable autoclave bag.
   d. Autoclave.
2. Place six roasting pans into large non-hazardous autoclave waste bags.

3. Autoclave. *Leave pans in the autoclave bags and save for downstream use.*
4. Thoroughly clean a biological hood as follows:
   a. Wash with a strong alkaline-based detergent.
   b. Follow with a disinfectant spray of 0.5% Amphyl.
   c. Wipe down with RNase/DNA remover solution.
   d. Expose to UV for 30 min.
5. Place three TYG agar plates at different locations within the hood.
6. Remove the lid of each plate.
7. Expose the plates overnight to UV.
8. *Day two:* Turn off the UV.
9. Incubate plates at room temperature for 24 h.
10. Tear 22 strips (10 in × 3 in) of aluminum foil.
11. Fold each strip lengthwise into thirds.
12. Place each strip into a sterile Petri dish, with both ends of the foil hanging over the rim of the dish (Figure B.1-3).
13. Carefully cut open the electrostatic packages of 24 stainless-steel coupons. *Save these electrostatic bags for future use.*
14. Gently place one stainless-steel coupon in each Petri dish.
15. Cover each Petri dish.
16. Remove the prepared roasting pans from the autoclave bags.
17. Line each pan with aluminum foil, being sure to cover the entire bottom and all sides of the pan.
18. Keep the six roasting pans in the biological hood. If necessary, stack them on top of each other.

Figure B.1-3. Aluminum foil-lined Petri dish with stainless-steel coupon inside. The foil overhang makes it easy to handle the coupon without touching it.

Deposition onto Stainless-Steel Sheets

1. Program the Rainin EDP3+ to dispense five 20-µL spots for a total of 10 times per sheet.
2. Pause at least 5 s in between the deposition of each row of spots.
3. Label the side of a sterile reagent reservoir "Water" and add 10 mL of UltraPure water.
4. Label the side of the second sterile reagent reservoir "Mix."
5. Working within the biological hood and with one stainless-steel sheet at a time, remove the sheet from its electrostatic packaging and place it on a foil-lined roasting pan.
6. Secure five pipette tips onto the EDP3+.
7. Vortex the conical tube containing the 42 mL of MMC mix prepared earlier.
8. Pour 3 mL of MMC into the "Mix" reagent reservoir.

9. Load 1 mL of the mix into the EDP3+.
10. Deposit the first row of five 20-µL spots, leaving at least an 8-cm border around the outside of the sheet for handling.
11. Deposit the second row of five 20-µL spots in the same manner.
12. Continue sample deposition until all 10 rows have been deposited.
13. Replace the pipette tips with a new set of five.
14. Load 1 mL of water from the "Water" reagent reservoir into the EDP3+.
15. Deposit the first row of five 20-µL water spots.
16. Randomly move the pipette to another location on the sheet, leaving at least an 8-cm border around the outside of the sheet for handling, and deposit the second row of five 20-µL water spots.
17. Continue depositions until all 10 rows have been deposited. *(The water spots will serve to decrease human bias toward sampling a sample-spotted area more heavily than a bare area).*
18. See Figure B.1-4 for a diagram of how the MMC and water spots are to be deposited onto the stainless-steel surfaces.
19. Place one sterile test tube cap, prepared earlier, at the four corners of the sheet.
20. Lay a large piece of foil over the test tube caps so that the ends of the foil hang over the rim of the roasting pan.

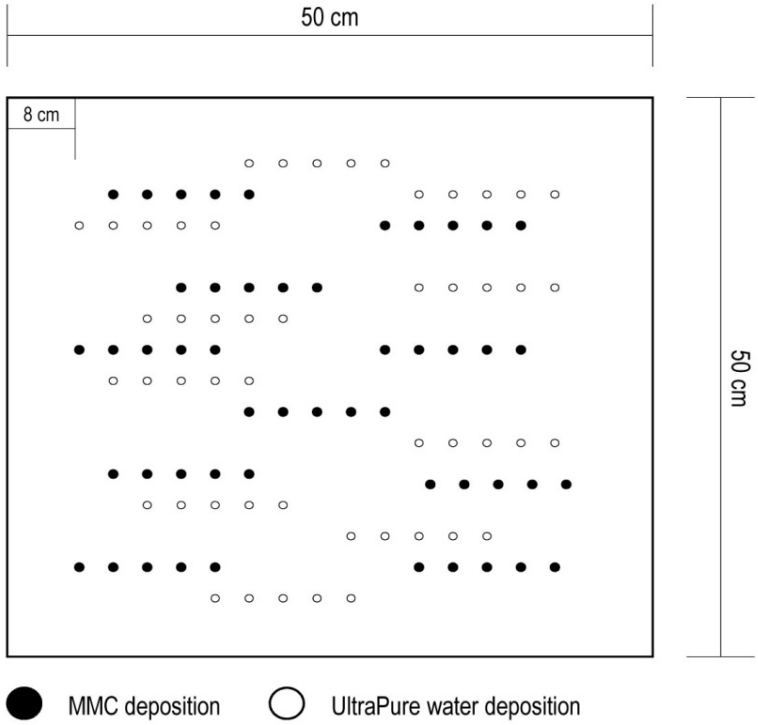


Figure B.1-4. Deposition schematic for stainless-steel sheets. Open circles represent water spots; closed circles represent the model microbial community mix. Leave 8 cm around all four edges of the sheet to allow for handling space without compromising the deposited sample.

21. To maximize the limited hood space, unwrap a second sheet and place it on top of the test tube cap-balanced foil, which is protecting the first sheet.
22. Perform "Mix" and "Water" deposition for the second sheet as described for the first sheet. As with the first sheet, place four test tube caps at the four corners of the sheet and cover the entire pan with another piece of foil.
23. Repeat the deposition and foil protection steps until all 10 sheets have been doped with the MMC mix and water. Continue to stack the pans on top of each other as necessary to conserve space within the hood.
24. Onto two sterile sheets, deposit only "Water" spots, no MMC mix. *These two water-only sheets will serve as sampling controls; one for the BiSKit samples, the other for the polyester wipes.*
25. As with the sheets spotted with the MMC mix, also stack these control sheets on a foil-lined roasting pan and cover with foil.

Deposition onto Stainless-Steel Coupons

1. Program the Rainin EDP+ pipette to dispense five 50-µL spots for a total of four times per coupon, pausing at least 5 s between depositions.
2. Secure five pipette tips onto the EDP3+.
3. Vortex the conical tube containing the MMC mix.
4. Pour 3 mL into the "Mix" reagent reservoir.
5. Load 1 mL of the mix into the EDP3+.
6. Working within the biological hood and with one stainless-steel coupon at a time, remove the Petri dish lid covering the coupon.
7. Leave an approximate ½-centimeter border around the coupon for handling.
8. Deposit the first row of five 50-µL spots.
9. Continue until all four rows of the MMC mix have been deposited. See Figure B.1-5 for a deposition schematic of the 25 cm^2 coupons.
10. Replace the Petri dish lid.

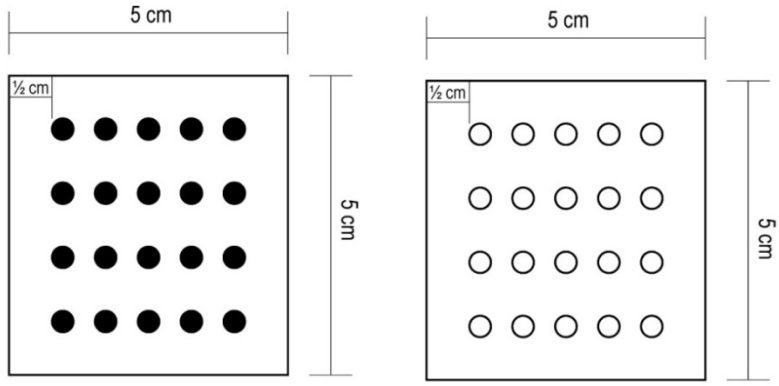


Figure B.1-5. Deposition schematic for stainless-steel coupons. Closed circles represent 50 µL deposits of model microbial community mix; open circles represent 50 µL deposits of UltraPure water. Leave 1/2 cm around all four edges of the coupon to allow for handling space without compromising the deposited sample.

11. Carefully slide the Petri dish toward the opposite side of the hood.
12. Repeat the sample deposition and handling steps until 20 coupons have been seeded with the MMC mix. *Vortex and pour additional MMC into the "Mix" reagent reservoir as necessary to maintain at least 3 mL until the 20 coupons have been seeded.*
13. Repeat the deposition steps for 2 coupons using the "Water" reagent reservoir instead of the "Mix" reservoir. *One water control coupon will serve as the sampling blank for cotton swabs, and the other for nylon-flocked swabs.*
14. Leave the 2 remaining coupons exposed to the biological hood sampling environment for the duration of the experiment—from MMC deposition to sampling. One coupon will serve as the cotton "Witness" coupon, and the other as the nylon's. *Witness coupons are exposed to the sampling environment to collect any free-falling particles that may be present in the environment.*
15. Label the 20 Petri dishes, containing the coupons spotted with the "Mix" samples, as follows: C-1, C-2, C-3, C-4, C-5, C-6, C-7, C-8, C-9, and C-10 representing the 10 **C**otton replicates; and N-1, N-2, N-3, N-4, N-5, N-6, N-7, N-8, N-9, and N-10 representing the 10 **N**ylon-flocked replicates. *This replicate count for both cotton and nylon-flocked samples may be adjusted (increase or reduce replicates) to accommodate the experiment at hand.*
16. Label the two Petri dishes containing the coupons spotted with only the "Water" sample, as C-SB to represent the **C**otton **S**ampling **B**lank, and N-SB to represent the **N**ylon-flocked **S**ampling **B**lank.
17. Label the two petri dishes containing the witness coupons as C-W to represent **C**otton **W**itness, and N-W to represent **N**ylon **W**itness.
18. Stack the Petri dishes, if necessary, in order to conserve space in the hood.

Drying

1. Make sure all Petri dishes and roasting pans are covered.
2. Allow each stainless-steel surface—either sheet or coupon—to dry in the biological hood for 24 h. *For optimal drying, position the Petri dishes toward the air blowers in the biological hood.*
3. The dried metal surfaces (Figure B.1-6) are now ready for sampling.

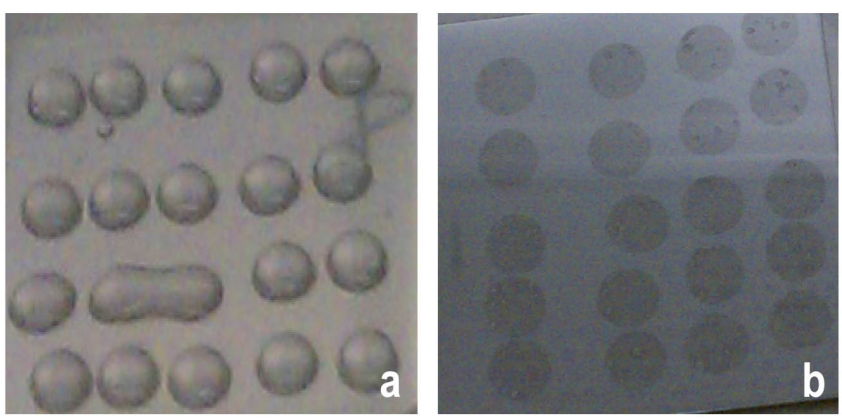


Figure B.1-6. Stainless-steel surface seeded with MMC a) before 24-h drying and b) following 24-h drying in a biological hood at room temperature.

B.2 Sample Collection

B.2.1 Purpose

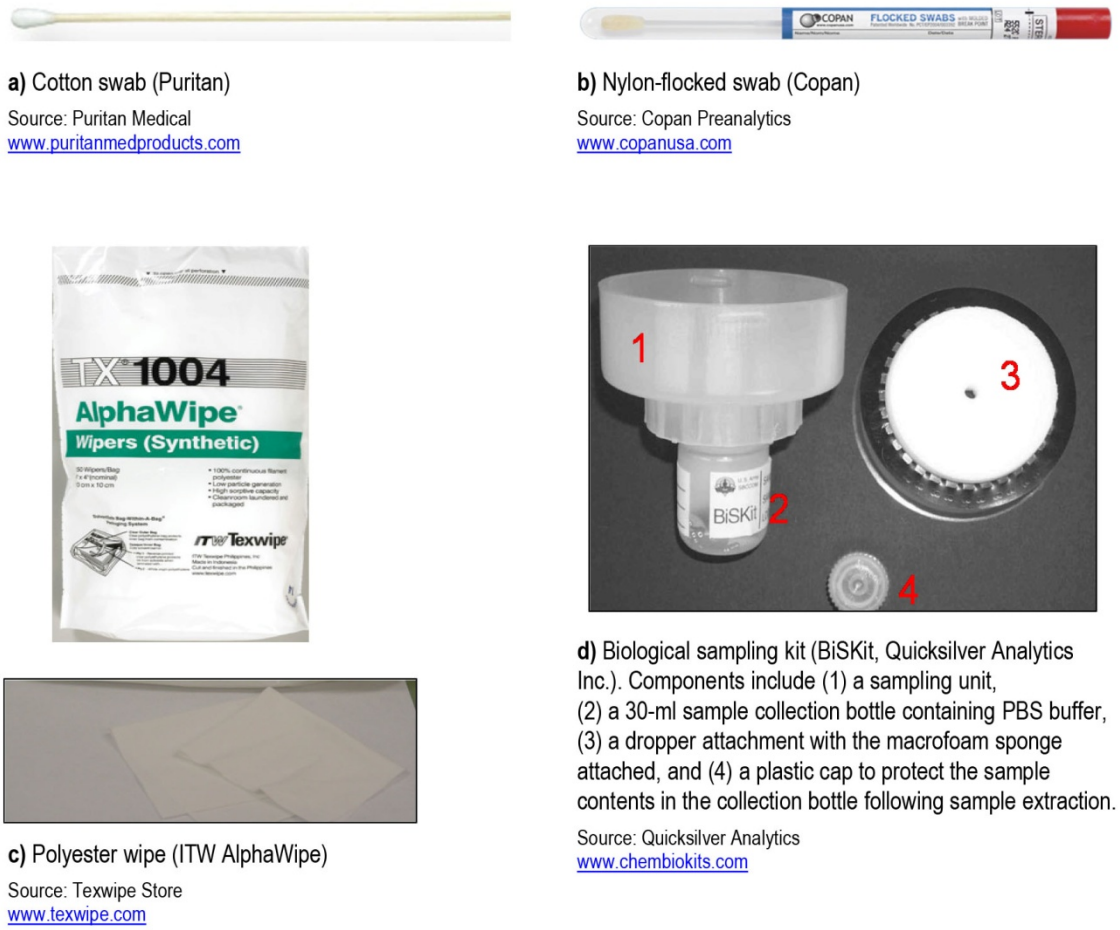
This section details the steps needed to prepare sampling materials prior to sample collection and processing. It also describes the respective procedures for sampling stainless-steel surfaces using cotton swabs, nylon-flocked swabs, polyester wipes, and biological sampling kits (BiSKits). The procedures and protocols described in this laboratory controlled experimental setup are also applicable for collecting samples from spacecraft and associated environments. It should be cautioned that not all sampling devices used in this controlled experimental setup are certified for use in collecting samples from spacecraft surfaces.

B.2.2 Approach

The model microbial community (MMC) (prepared as detailed in Appendix B.1.2.1) is used as a laboratory control in this experiment to optimize the sample collection efficiency of the sampling devices tested. Stainless-steel coupons (25 cm^2) and sheets (2,500 cm^2) are used to test the efficacy of the sampling devices in collecting seeded MMC from small and large surface areas, respectively. A detailed schematic diagram illustrating the process flow for all four sampling matrices can be found in Appendix B.3.2 (Figure B.3-1) of this document.

B.2.2.1 Preparation of Sampling Materials

Figure B.2-1 shows the four material types used in sampling—cotton swabs, nylon-flocked swabs, polyester wipes, and a BiSKit.



a) Cotton swab (Puritan)
Source: Puritan Medical
www.puritanmedproducts.com

b) Nylon-flocked swab (Copan)
Source: Copan Preanalytics
www.copanusa.com

c) Polyester wipe (ITW AlphaWipe)
Source: Texwipe Store
www.texwipe.com

d) Biological sampling kit (BiSKit, Quicksilver Analytics Inc.). Components include (1) a sampling unit, (2) a 30-ml sample collection bottle containing PBS buffer, (3) a dropper attachment with the macrofoam sponge attached, and (4) a plastic cap to protect the sample contents in the collection bottle following sample extraction.
Source: Quicksilver Analytics
www.chembiokits.com

Figure B.2-1. Four sampling matrices: a) cotton swab, b) nylon-flocked swab, c) polyester wipe, and d) BiSKit.

B.2.2.1.1 Cotton Swabs

1. Label thirteen 50-mL Falcon tubes as follows: C-1, C-2, C-3, C-4, C-5, C-6, C-7, C-8, C-9, C-10, C-Neg, C-HC, and C-SB for **C**otton replicates **1–10**, **C**otton **Neg**ative control, **C**otton **H**andling **C**ontrol, and **C**otton **S**ampling **B**lank, respectively. *If using more or fewer samples (whether controlled or environmental), adjust accordingly and label the tubes in the same fashion described above.*
2. Add 15 mL of PBS to each labeled tube.

B.2.2.1.2 Nylon-flocked Swabs

1. Label thirteen 50-mL Falcon tubes N-1, N-2, N-3, N-4, N-5, N-6, N-7, N-8, N-9, N-10, N-Neg, N-HC, and N-SB for **N**ylon-flocked replicates **1–10**, **N**ylon-flocked **Neg**ative control, **N**ylon-flocked **H**andling **C**ontrol, and **N**ylon-flocked **S**ampling **B**lank, respectively. *If using more or fewer samples (whether controlled or environmental), adjust accordingly and label the tubes in the same fashion described above.*
2. Add 15 mL of PBS to each labeled tube.

B.2.2.1.3 Polyester Wipes

1. Label four 50-mL Falcon tubes—which will later on contain wipes used to sample stainless-steel surfaces—as follows: PW-1, PW-2, PW-3, and PW-4 for **P**olyester **W**ipe replicates **1–4**, respectively.
2. Label three 50-ml Falcon tubes PW-Neg, PW-HC, and PW-SB for **P**olyester wipe **Neg**ative control, **P**olyester wipe **H**andling **C**ontrol, and **P**olyester wipe **S**ampling **B**lank, respectively. *If using more or fewer samples (whether controlled or environmental), adjust accordingly and label the tubes in the same fashion described above.*
3. Use sterile metal forceps to remove wipes, one at a time, from packaging.
4. Use sterile gloves to fold each wipe in half.
5. Roll one wipe into each of the pre-labeled 50-mL Falcon tubes.
6. Add 5 mL of water to each tube.
7. Autoclave wipes.

B.2.2.1.4 BiSKits

Note: BiSKits are factory-equipped with 15 mL of sterile PBS in the sample collection bottle (see Figure B.2-1). Because factory-provided PBS is inconsistent in its genetic signature, the Genetic Inventory team chooses instead to use molecular grade DNA-free PBS procured from MoBio Laboratories, Inc. A special order request may be placed for the vendor to ship BiSKit orders with the sterile collection bottles empty.

1. If the BiSKit units were procured from the vendor with PBS in the collection bottle:
   a. Discard the factory-provided PBS.
   b. Rinse the bottle twice with ~10 mL of MoBio UltraPure DNA-free PBS.
2. Add 15 mL of PBS to the collection bottle.
3. Attach the collection bottle to the dropper attachment.
4. Invert the BiSKit unit bottle-side-up (Figure B.2-1).
5. Turn the dropper attachment handle to allow the PBS to soak into the macrofoam sponge.
6. Swirl the unit to boost absorption of PBS into the macrofoam sponge.
7. Invert the BiSKit unit back to the bottle-side-down position.
8. Allow all the excess liquid to flow back into the sample collection bottle.
9. Turn the dropper attachment to expel the PBS, soaked in the macrofoam sponge, back into the collection bottle.
10. Detach the sample collection bottle from the sampling unit.
11. Pour the liquid contents into a sterile 50-mL Falcon tube. *As the BiSKits are prepared for sampling, these rinse samples will be pooled for all BiSKits to serve as the negative lab control (B-Neg).*
12. Add 15 mL of sterile PBS into the sample collection bottle.
13. Reattach the collection bottle onto the sampling unit.
14. Invert the unit bottle-side-up.
15. Turn the dropper attachment to allow the PBS in the bottle to soak into the macrofoam sponge.

16. Store and/or transport the BiSKit in this manner until ready to sample.
17. Repeat the BiSKit preparatory steps until five BiSKit units have been processed.
18. Pool all negative lab controls together and mix well. These pooled samples will eventually be processed as one control lab sample.
19. Label the pooled negative control samples B-Neg for **B**iSKit **Neg**ative control. *Because only a maximum of 45 mL sample can be processed in one filtration unit, multiple B-Neg replicates may be necessary to filter the entire B-Neg sample pool.*
20. Label six BiSKit units B-1, B-2, B-3, B-4, B-HC, and B-SB for **B**iSKit replicates **1–4**, **B**iSKit **H**andling **C**ontrol, and **B**iSKit **S**ampling **B**lank, respectively. *If using more or less samples (whether controlled or environmental), then adjust accordingly and label the tubes in the same fashion described above.*

B.2.2.2 Metal Surface Sampling Procedures

Figure B.2-2 shows the metal surface sampling schematic used for all four sampling matrices—cotton swab sampling, nylon-flocked swab sampling, polyester wipe sampling, and BiSKit sampling.

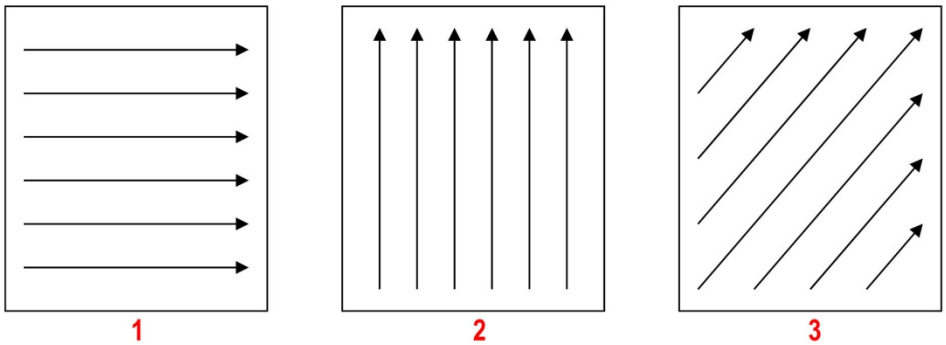


Figure B.2-2. Metal surface sampling schematic for all four sampling matrices.

B.2.2.2.1 Cotton Swab Sampling

1. Remove the protective swab wrapping—only immediately before sample acquisition—being careful not to touch the sterile swab head.
2. Process one sample at a time.
3. Dip the swab into the Falcon tube prepared in Appendix B.2.2.1.1. *This is to moisten the swab before sampling.*
4. Press and roll the swab head against the inside wall of the tube to expel excess fluid.
5. Sample the stainless-steel coupon (prepared in Appendix B.1.2.4), with the swab, in a unidirectional horizontal (left-to-right) manner while holding the swab at an approximate 30° angle (see Figure B.2-2[1]).
6. Rotate the swab head to expose a new surface.
7. Sample in a unidirectional vertical (bottom-to-top) manner (see Figure B.2-2[2]).
8. Finally, rotate the swab head to expose a new surface.
9. Sample in a unidirectional diagonal (bottom-corner-to-top) manner (see Figure B.2-2[3]).
10. Place the swab into its correspondingly labeled 50-mL Falcon tube.
11. Use the underside cap of the tube to snap off the swab head, separating it from the shaft and submerging it in PBS.
12. Discard the remainder of the swab shaft.
13. Repeat the sampling steps for all coupons or, if taking environmental samples, until an adequate representation of the surface area (≥10%) has been sampled. Be sure to place each swab sample into its respective tube.
14. Collect sampling blank samples by sampling the surfaces of sterile, unseeded coupons.
15. Process the sampling blank samples in the same manner as with the other samples.
16. Collect handling control samples by exposing the swab to the sampling environment for the average time duration of one real sampling event. *Do not allow the swab to touch any surface.*

17. Use the underside cap of its correspondingly labeled sample tube to snap off the swab head, separating it from the shaft and submerging it in PBS.
18. Process the handling control samples in the same manner as with the other samples.

B.2.2.2.2 Nylon-Flocked Swab Sampling

1. Remove the swab from its protective tube by twisting the tube cap to break the protective seal, being careful not to touch the sterile swab head.
2. Moisten the swab head in its corresponding Falcon tube (Appendix B.2.2.1.2), which contains 15 mL of PBS.
3. Press the swab head against the inside walls of the tube to expel excess fluid.
4. Sample the stainless-steel coupon (prepared in Appendix B.1.2.4), with the swab, in a unidirectional horizontal (left-to-right) manner while holding the swab at an approximate 30° angle (see Figure B.2-2[1]).
5. Rotate the swab head to expose a new surface.
6. Sample in a unidirectional vertical (bottom-to-top) manner (see Figure B.2-2[2]).
7. Finally, rotate the swab head to expose a new surface.
8. Sample in a unidirectional diagonal (bottom-to-top) manner (see Figure B.2-2[3]).
9. Place the swab into its corresponding Falcon tube.
10. Use the underside cap of the tube to snap off the swab head, separating it from the shaft and submerging it in PBS.
11. Discard the remainder of the swab shaft.
12. Repeat the sampling steps for all coupons or, if taking environmental samples, until an adequate representation of the surface area (≥10%) has been sampled. Be sure to place each swab sample into its respectively labeled tube.
13. Collect sampling blank samples by sampling the surfaces of sterile, unseeded coupons.
14. Process the sampling blank samples in the same manner as with the other samples.
15. Collect handling control samples by exposing the swab to the sampling environment for the average time duration of one real sampling event. *Do not touch any surface with this swab.*
16. Use the underside cap of its corresponding tube to snap off the swab head, separating it from the shaft and submerging it in PBS.
17. Process the handling control samples in the same manner as with the other samples.

B.2.2.2.3 Polyester Wipe Sampling

1. Use sterile metal forceps to remove the autoclaved wipes from the Falcon tubes. Work with one wipe at a time.
2. Handle the polyester wipes with sterile gloves.
3. Unroll the wipe and fold it in half.
4. Using one exposed side, wipe the stainless-steel sheet (prepared in Appendix B.1.2.4) in a unidirectional horizontal (left-to-right) manner (see Figure B.2-2[1]).

5. Turn the folded wipe over to expose a clean surface and wipe the sampling area in a unidirectional vertical (bottom-to-top) manner (see Figure B.2-2[2]).
6. Fold the wipe so that the two used sides are touching, thus exposing two new clean sides.
7. Wipe the sampling area in a unidirectional diagonal (bottom-to-top) manner (see Figure B.2-2[3]).
8. Carefully return the polyester wipe to its corresponding Falcon tube.
9. Add 15 mL of PBS to the tube.
10. Repeat the sampling steps for all wipe samples, taking care to sample as much of the sampling sheet surface as possible, or within a maximum sampling surface area of 1 m^2, if taking environmental samples.
11. Collect the handling control sample by exposing the wipe to the sampling environment for the average time duration of one real sampling event. *Do not touch any surface with this wipe.*
12. Collect sampling blank samples by sampling the surfaces of sterile, unseeded sheets.
13. Process both the handling control and the sampling blank samples in the same manner as with the MMC-seeded samples.

B.2.2.2.4 BiSKit Sampling

1. Remove the BiSKit unit from its protective travel/storage plastic bag.
2. Detach the dropper attachment, exposing the macrofoam sponge.
3. Within the maximum sampling surface area of 2500 cm^2 of the metal sheet (or 1 m^2 if taking environmental samples), wipe the sheet with the sponge in a unidirectional horizontal (left-to right) manner (see Figure B.2-2[1]).
4. Rotate the dropper attachment and wipe the sampling area in a unidirectional vertical (bottom-to-top) manner (see Figure B.2-2[2]).
5. Rotate the dropper attachment and wipe the sampling area in a unidirectional diagonal (bottom-to-top) manner (see Figure B.2-2[3]).
6. Reconnect the dropper attachment to the sampling unit.
7. Place the BiSKit unit back into its original bag for storage/transportation.
8. Repeat the sampling steps for all BiSKits.
9. Collect the sampling blank sample by sampling the surface of a sterile, unseeded sheet.
10. Remove the BiSKit handling control unit (B-HC) from its sterile storage bag.
11. Remove the dropper attachment from the sampling unit.
12. Expose the macrofoam sponge to the sampling environment for the average time duration of one real sampling event. *Do not touch any surface with this BiSKit.*
13. Reattach the dropper attachment to the sampling unit.
14. Place the B-HC back into its storage bag.

B.2.2.3 Controls

Appropriate controls are incorporated into each step of the sampling, analysis, and procedures. The controls are as follows:

1. Positive controls:
   a. DNA from total MMC for qPCR assay.
   b. Purified DNA arising from each MMC constituent strain used for ss-qPCR assays.
2. Negative controls:
   a. Sample device control (SD): Sampling device moistened with PBS only.
   b. Handling control (HC): Sampling device pre-moistened with PBS and exposed to the ambient sampling environment (without any contact with the metal surfaces).
   c. Sampling blank (SB): Sampling device pre-moistened with PBS and exposed to the surfaces of sterile, unseeded stainless steel.
   d. Sampling surface (stainless-steel) control: Sample collected from sonicated sterile, unseeded metal.
   e. Nuclease-free UltraPure water: Sterile water used for all analysis steps.
   f. Sterile PBS: Buffer used for all processing steps.
   g. Media blank (MB): Sterile culture media prepared for inoculation with MMC (or environmental sample).
   h. Maxwell DNA extraction reagent blanks: DNA extraction system reagent control.
   i. No DNA template control (NTC): qPCR reagent assay control. Included in every qPCR assay as a means of evaluating melt curves and detecting primer-dimer amplification (multiple melt peaks).
3. False-negative check: Samples that rendered no PCR amplification, spiked with positive-control DNA (e.g., *Bacillus pumilus* SAFR-032) as a means of checking for false negatives that may have resulted from inhibitory substances.

B.3 Sample Processing

B.3.1 Purpose

The low biomass nature of spacecraft and associated surfaces warrants the collection and subsequent processing of large sample volumes. Before subjecting samples to downstream molecular analyses, several steps must be taken to concentrate the sample down (from 45 mL) to a smaller, more manageable volume (1.0 mL) for DNA extraction. In selecting the most suitable approach for DNA extraction, the Genetic Inventory team opted for the automated DNA method due to its simplicity, reliability, consistency, reproducibility, and robustness in extracting DNA from low-biomass samples. This section details how to render biomolecules from the sampling matrices and provides a means for a unified, automated DNA extraction methodology.

B.3.2 Approach

The model microbial community (MMC) (10^6 rRNA gene copies), prepared as detailed in Appendix B.1, is used as a laboratory positive control to optimize the sample collection and DNA extraction efficiency. Stainless-steel coupons (25 cm^2) and sheets (2,500 cm^2) are used to test the efficacy of the sampling devices in collecting seeded MMC from small and large surface areas, respectively. The detailed schematic diagrammed in Figure B.3-1 illustrates the process flow for sample concentration and DNA extraction.

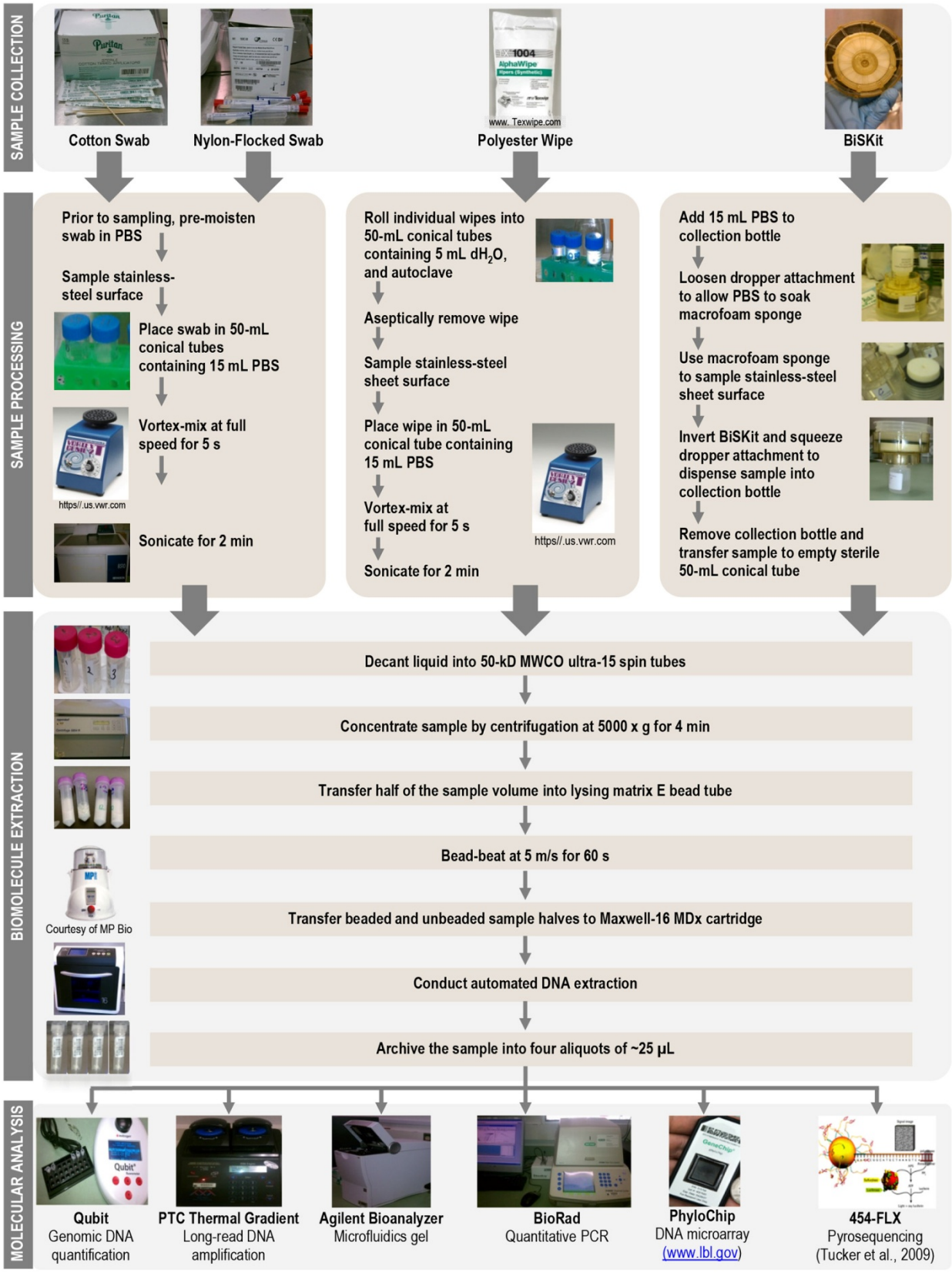


Figure B.3-1. Schematic diagram for end-to-end sample collection, processing, and analyses by four different sampling materials.

B.3.2.1 Sample Concentration

The large volume (45 mL) collected for each sample must first be concentrated down to a smaller, more manageable volume (1.0 mL), thus minimizing variability while increasing consistency and efficiency following downstream functions such as DNA extraction. All samples, regardless of the sampling matrix used in collecting the sample, are concentrated using a 50-kD molecular weight cut-off filtration unit (Figure B.3-2). Concentrating each sample to a smaller volume will increase DNA yield following extraction.

Figure B.3-2. Amicon Ultra-15 Filter unit includes 1) a 50-kD MWCO filter membrane inside 2) a 50-mL conical collection tube.

Source: EMD Millipore
www.millipore.com

B.3.2.1.1 Cotton Swab Sample Concentration

1. Prepare an ultrasonic bath filled to normal capacity. Frequency shall be 19–27 kHz; rated power output in relation to the bottom surface area of the bath should be at least 0.35 w/cm^2. Bath fluid shall be an aqueous solution of 0.02% volume-to-volume Tween-80; solution shall be prepared fresh each day, with a temperature range of 20°C–32°C.
2. De-gas the bath fluid by running the bath—*without any samples*—for 5 min.
3. Vortex-mix each sample (from Appendix B.2) at maximum speed for 5 s.
4. Suspend sample tubes into the water bath.
5. Ensure that the water bath level matches that of the fluid level in the tubes.
6. Sonicate for 2 min.
7. Transfer only the liquid sample—not the swab—from the Falcon tube directly into a Millipore Amicon Ultra-15 50-kDa MWCO centrifugal filtration device. Save the Falcon tubes containing the swabs.
8. *Perform a total of three extractions per sample.*
9. Spin the samples at 5,000 × g for 4 min.
10. Aseptically remove the filter from the Amicon filtration unit. *Take extreme caution as the sample concentrate is in the filter.*
11. Decant the flow-through and re-cap the tube.
12. *The total volume filtered is now 15 mL.*
13. Add 15 mL of PBS to each of the Falcon tubes containing a swab head.
14. Vortex-mix each sample at maximum speed for 5 s.
15. Sonicate each sample for 2 min.
16. Decant only the liquid sample—avoiding the swab—into its respective Amicon filtration tube.
17. Spin at 5,000 × g for 4 min.
18. Aseptically, and gently, remove the filter from the Amicon filtration unit.
19. Decant the flow-through and re-cap the tube.

20. *The total volume filtered is now 30 mL.*
21. Add 15 mL of PBS to each of the Falcon tubes containing a swab head.
22. Vortex-mix each sample at maximum speed for 5 s.
23. Sonicate each sample for 2 min.
24. Decant only the liquid sample—avoiding the swab—into its respective Amicon filtration tube.
25. Spin at 5,000 × g for 4 min.
26. Aseptically remove the filter from the Amicon filtration unit.
27. Decant the flow-through and re-cap the tube.
28. *The total final volume filtered is 45 mL.*
29. The ideal concentrate volume for each sample is 250–400 μL.
30. Gently remove the filter from the Amicon filtration unit.
31. Do not discard the final flow-through.
32. Pipette out the concentrated sample from the filter into a sterile Eppendorf micro-centrifuge tube.
33. Use the final flow-through of each sample to top-off the sample volume to 1.0 mL.
34. Discard both the flow-through and the filtration unit.
35. Samples are now ready for bead-beating (Appendix B.3.2.2.1).

B.3.2.1.2 Nylon-Flocked Swab Sample Concentration

1. Prepare an ultrasonic bath filled to normal capacity. Frequency shall be 19–27 kHz; rated power output in relation to the bottom surface area of the bath should be at least 0.35 w/cm^2. Bath fluid shall be an aqueous solution of 0.02% volume-to-volume Tween-80; solution shall be prepared fresh each day, with a temperature range of 20°C–32°C.
2. De-gas the bath fluid by running the bath—*without any samples*—for 5 min.
3. Vortex-mix each sample (from Appendix B.2) at maximum speed for 5 s.
4. Suspend the sample tubes into the water bath.
5. Ensure that the water bath level matches that of the fluid level in the tubes.
6. Sonicate for 2 min.
7. Transfer only the liquid sample—not the swab—from the Falcon tube directly into a Millipore Amicon Ultra-15 50-kDa MWCO centrifugal filtration device. Save the Falcon tubes containing the swabs.
8. *Perform a total of three extractions per sample.*
9. Spin at 5,000 × g for 4 min.
10. Aseptically remove the filter from the Amicon filtration unit. *Take extreme caution as the sample concentrate is in the filter.*
11. Decant the flow-through and re-cap the tube.

12. *The total volume filtered is now 15 mL.*
13. Add 15 mL of PBS to each of the Falcon tubes containing a swab head.
14. Vortex-mix each sample at maximum speed for 5 s.
15. Sonicate each sample for 2 min.
16. Decant only the liquid sample—avoiding the swab—into its respective Amicon filtration tube.
17. Spin at 5,000 × g for 4 min.
18. Aseptically, and gently, remove the filter from the Amicon filtration unit.
19. Decant the flow-through and re-cap the tube.
20. *The total volume filtered is now 30 mL.*
21. Add 15 mL of PBS to each of the Falcon tubes containing a swab head.
22. Vortex-mix each sample at maximum speed for 5 s.
23. Sonicate each sample for 2 min.
24. Decant only the liquid sample—avoiding the swab—into its respective Amicon filtration tube.
25. Spin at 5,000 × g for 4 min.
26. Aseptically remove the filter from the Amicon filtration unit.
27. Decant the flow-through and re-cap the tube.
28. *The total final volume filtered is 45 mL.*
29. The ideal concentrate volume for each sample is 250–400 µL.
30. Gently remove the filter from the Amicon filtration unit.
31. Do not discard the final flow-through.
32. Pipette out the concentrated sample from the filter into a sterile Eppendorf micro-centrifuge tube.
33. Use the final flow-through of each sample to top-off the sample volume to 1.0 mL.
34. Discard both the flow-through and the filtration unit.
35. Samples are now ready for bead-beating (Appendix B.3.2.2.1).

B.3.2.1.3 Polyester Wipes Sample Concentration

1. Prepare an ultrasonic bath filled to normal capacity. Frequency shall be 19–27 kHz; rated power output in relation to the bottom surface area of the bath should be at least 0.35 w/cm^2. Bath fluid shall be an aqueous solution of 0.02% volume-to-volume Tween-80; solution shall be prepared fresh each day, with a temperature range of 20°C–32°C.
2. De-gas the bath fluid by running the bath—*without any samples*—for 5 min.
3. Vortex-mix each sample (from Appendix B.2) at maximum speed for 5 s.
4. Suspend the sample tubes into the water bath.
5. Ensure that the water bath level matches that of the fluid level in the tubes.

6. Sonicate for 2 min.
7. Transfer only the liquid sample—not the wipe—from the Falcon tube directly into a Millipore Amicon Ultra-15 50-kDa MWCO centrifugal filtration device. Save the Falcon tubes containing the wipes.
8. *Perform a total of three extractions per sample.*
9. Spin at 5,000 × g for 4 min.
10. Aseptically remove the filter from the Amicon filtration unit. *Take extreme caution as the sample concentrate is in the filter.*
11. Decant the flow-through and re-cap the tube.
12. *The total volume filtered is now 15 mL.*
13. Add 15 mL of PBS to each of the Falcon tubes containing a wipe.
14. Vortex-mix each sample at maximum speed for 5 s.
15. Sonicate each sample for 2 min.
16. Decant only the liquid sample—avoiding the wipe—into its respective Amicon filtration tube.
17. Spin at 5,000 × g for 4 min.
18. Aseptically, and gently, remove the filter from the Amicon filtration unit.
19. Decant the flow-through and re-cap the tube.
20. *The total volume filtered is now 30 mL.*
21. Add 15 mL of PBS to each of the Falcon tubes containing a wipe.
22. Vortex-mix each sample at maximum speed for 5 s.
23. Sonicate each sample for 2 min.
24. Decant only the liquid sample—avoiding the wipe—into its respective Amicon filtration tube.
25. Spin at 5,000 × g for 4 min.
26. Aseptically remove the filter from the Amicon filtration unit.
27. Decant the flow-through and re-cap the tube.
28. *The total final volume filtered is 45 mL.*
29. The ideal concentrate volume for each sample is 250–400 μL.
30. Gently remove the filter from the Amicon filtration unit.
31. Do not discard the final flow-through.
32. Pipette out the concentrated sample from the filter into a sterile Eppendorf micro-centrifuge tube.
33. Use the final flow-through of each sample to top-off the sample volume to 1.0 mL.
34. Discard both the flow-through and the filtration unit.
35. Samples are now ready for bead-beating (Appendix B.3.2.2.1).

B.3.2.1.4 BiSKit Sample Concentration

1. Remove the BiSKit from its storage/transport bag.
2. Hold the unit bottle-side-down.
3. Turn the dropper attachment handle to expel the sample, soaked in the macrofoam, into the collection bottle.
4. Detach the collection bottle from the unit.
5. Decant ~15 mL of the sample into an appropriately labeled 50-mL Falcon tube.
6. *The total volume expelled from the BiSKit is now ~15 mL.*
7. Dispense 15 mL of PBS into the collection tube.
8. Attach the collection bottle to the BiSKit unit, while holding the unit bottle-side-down.
9. Invert the unit bottle-side-up.
10. Gently turn the handle on the dropper attachment to release the PBS into the macrofoam.
11. Swirl the unit to ensure even distribution of PBS over the macrofoam.
12. Invert the unit bottle-side-down.
13. Gently turn the handle on the dropper attachment to release the PBS into the macrofoam.
14. Detach the collection bottle from the unit.
15. Decant ~15 mL of the sample into the same 50-mL Falcon tube.
16. *The total volume expelled from the BiSKit is now ~30 mL.*
17. Attach the collection bottle—while holding the unit bottle-side-down—to the BiSKit unit.
18. Invert the unit bottle-side-up.
19. Gently turn the handle on the dropper attachment to release the PBS into the macrofoam.
20. Swirl the unit to ensure even distribution of PBS over the macrofoam.
21. Invert the unit bottle-side-down.
22. Gently turn the handle on the dropper attachment to release the PBS into the macrofoam.
23. Detach the collection bottle from the unit.
24. Decant ~15 mL of the sample into the same 50-mL Falcon tube.
25. *The total final volume expelled from the BiSKit is ~45 mL*
26. If less than 45 mL of the sample was collected from the BiSKit, top the sample volume to 45 mL using PBS.
27. Vortex-mix the sample at maximum speed for 5 s.
28. Dispense 15 mL of the sample into an appropriately labeled Amicon filtration unit.
29. Spin at 5,000 × g for 4 min.
30. *The total volume filtered is now 15 mL.*
31. Aseptically remove the filter from the Amicon filtration unit.
32. Discard the flow-through.

33. Return the filter to the tube.
34. Dispense an additional 15 mL of the sample into the same tube.
35. Spin at 5,000 × g for 4 min.
36. *The final volume filtered is now 30 mL.*
37. Aseptically remove the filter from the Amicon filtration unit.
38. Discard the flow-through.
39. Return the filter to the tube.
40. Dispense the final 15 mL of the sample into the same tube.
41. Spin at 5,000 × g for 4 min.
42. *The total final volume filtered is 45 mL.*
43. Gently remove the filter from the Amicon filtration unit.
44. Do not discard the final flow-through.
45. Pipette out the concentrated sample from the filter into a sterile Eppendorf micro-centrifuge tube.
46. Use the final flow-through of each sample to top-off the sample volume to 1.0 mL.
47. Discard both the flow-through and the filtration unit.
48. Samples are now ready for bead-beating (Appendix B.3.2.2.1).

B.3.2.2 DNA Extraction

Concentrated samples (using the methods described in Appendix B.3.2.1) must now undergo cell lysis in order for DNA to be extracted. To eliminate variability introduced by laboratory-operator technique, an automated DNA extraction system is used. To increase differential recovery and MMC constituent strain detection—without subjecting the entire sample volume to potential DNA damage caused by over agitation—half the volume of each sample is subjected to mechanical cell lysis by bead-beating. Figure B.3-3 is an illustration of the automated system used for DNA extraction. This system is used for its consistency in generating high DNA yield with low variability.

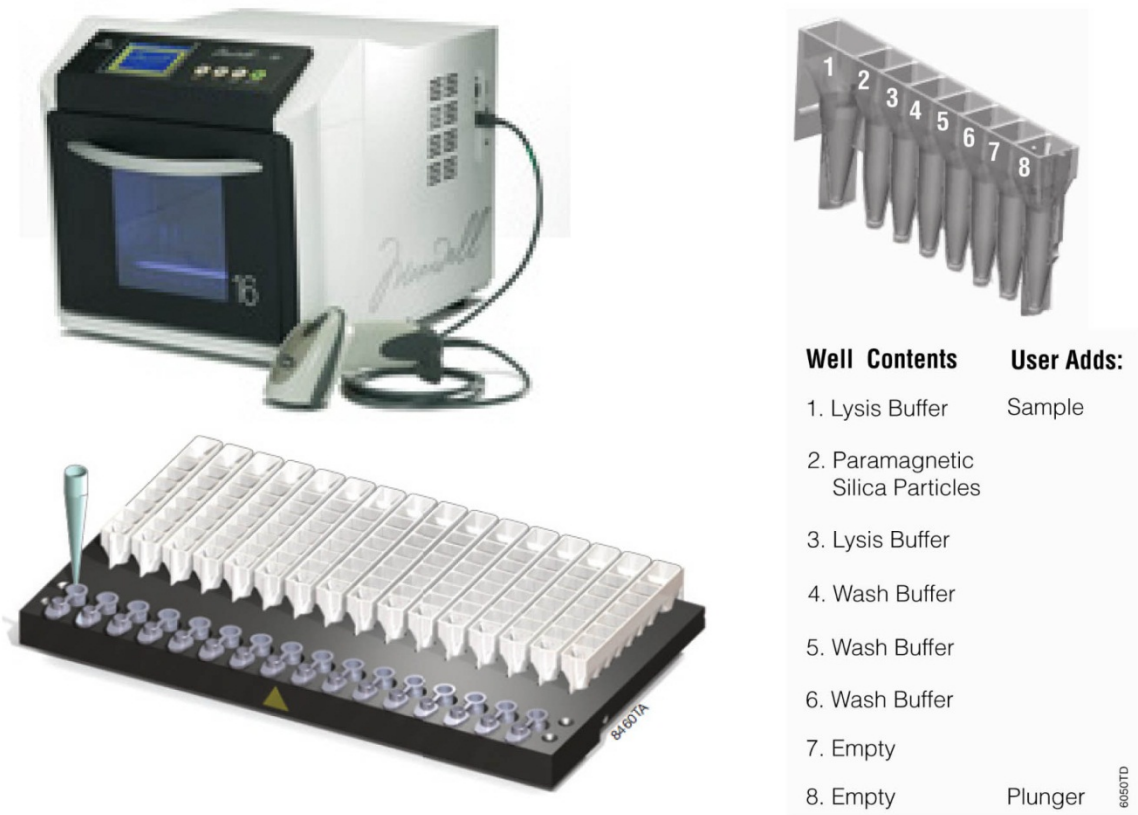


Figure B.3-3. Maxwell-16 Automated DNA/RNA Purification System (*top left*), LEV DNA/RNA extraction cartridge (*right*), and cartridge rack showing both cartridges and elution tubes loaded (*bottom left*).

Source: Images courtesy of Promega Corp. www.promega.com.

B.3.2.2.1 Bead-Beating

1. Vortex-mix samples at maximum speed for 5 s.
2. Pipette 500 µL of each sample concentrate into MP Bio Lysing Matrix E microbeads.
3. Save the other half of each sample.
4. Load and secure the samples onto the MP Bio bead-beating instrument
5. Bead-beat at a rate of 5.0 m/s for 60 s.

B.3.2.2.2 Extraction

1. Follow the prompts on the screen of the Maxwell-16 Automated DNA/RNA Purification System (see Figure B.3-3) to initiate setup for the extraction process.
2. When prompted by the machine, open the door to remove the cartridge rack for sample loading.
3. Load the appropriate number of cartridges onto the cartridge rack.
4. Designate one cartridge for each sample.
5. Carefully remove the seal from each cartridge.
6. Transfer all ~500 µL of sample supernatant from the lysing tube into its respectively assigned Maxwell-16 DNA extraction cartridge.
7. Transfer all ~500 µL of the non-beated half of the same sample into the same DNA cartridge as its bead-beated half.
8. Carefully load plungers into position 8 of each cartridge, taking care not to touch the plunger tip.
9. Label and securely load elution tubes into the tube holder of the cartridge rack.
10. Pipette 100 µL of UltraPure Gibco water into each elution tube.
11. Leave the elution tubes un-capped.
12. Run a Maxwell-16 reagent control by including a cartridge that contains no added sample.
13. Place the cartridge rack back into the Maxwell-16 system.
14. Run the program as prompted by the system.
15. When the program is complete, follow the prompts to retrieve samples.
16. Aliquot each sample into four 25 µL smaller sample sizes, in 0.5-mL screw cap cryovials.
17. Store the aliquot that will be used for analysis in −20°C until the analysis is complete, then transfer the sample to −80°C.
18. Archive the remaining three sample aliquots in three different locations at −80°C.

B.3.2.3 Archiving

Each archived sample must possess a sample name and barcode identification that is unique to the particular sample. It is important to archive the genetic inventory samples in such a manner that allows for easy identification and retrieval following long-term storage. Archiving the genetic inventory samples preserves the samples for future use when more advanced technologies have been developed for more comprehensive, high-throughput molecular analyses.

The Biomatrica SampleWare system meets all of the following criteria:

- Quickly and efficiently organizes samples for tracking, storage, and retrieval
- Uploads and tracks samples efficiently
- Customizes the database to match sample types
- Attaches data and image files to individual samples
- Transfers sample data between departments
- Can be installed, learned, and used in minutes

SampleWare Archiving Steps

1. Enter the new sample name in the **SampleWare Excel Master List** document as follows:
   a. Sample ID
   b. Sample barcode (sequentially assigned)
   c. Sample source
   d. Experiment
   e. Date archived
   f. Metadata (includes images, accession no, and publication links)
2. Transport the sample information from the master list to Biomatrica's **Sampleware** archive software program.
3. Use the LabelMark software to create labels, and the Brady printer to print the labels.
   a. On the desktop of the computer dedicated to the label printer, double click the **Archive Label Maker** folder.
   b. In that folder, double click **Labelmark 5**.
   c. Double click the **LabelMark 5 program**. This will open the LabelMark software program. *The "SampleWare" folder in the "Archive Label Maker" folder contains all the sample databases. The "Archive Containers" excel spreadsheet file contains databases of label information for each container of samples.*
   d. Under **File** select **New**.
   e. The **Create New/Open** menu will pop up.
   f. Select **A New Label File based on an existing template.** This will bring up a list of all available templates.
   g. Select **GI_DNA Archive Template.l5t**
   h. Click **OK**.

i. With the template open, select **Insert** from the menu.

j. Select **External Data.**

k. **Data Import** box will pop onto screen.

l. Select **Use Advanced Options to Import Data** and click **Next.**

m. In the **Select Type of Data Source** window, click **Microsoft Excel Spreadsheet.**

n. Click **Select File** and from the pop-up dialogue box; **Open** the document of interest.

o. Click **Next** to select the container of interest.

p. Click **Select Visual Element.**

q. To match the columns with the appropriate data field in the template, click the option **Edit in A New Window.**

r. Highlight a column name, and click the **Link to Existing Shape** icon . In the label preview to the right, click the field to which you would like to link the data. Do this for every column.

s. When finished, click **Close.**

t. When back at the "Select Visual Element" screen, click **Next** to go to the **Data Placement** menu.

u. Configure and apply the desired settings, then click **Finish.**

v. Ensure that all the fields in each label contain the correct information. On the bottom half of the screen, where it says "Errors and Information," click on **Auto Fit All** to ensure that all text fits within the text field.

w. Ensure all label objects are within the margins and look satisfactory. Readjust object and text positioning if necessary.

x. Adjust the font size for the label text if necessary. Do this by clicking the text field and adjusting the font size on the right side menu where it says "Label Object Properties."

y. Under the **File** menu, select **Print**. A menu for various print options will display on screen. Configure the desired print options accordingly. To print only certain labels or a range of labels, under the *"Labels to Print"* submenu, select either *"Selected Labels Only"* or *"Range of Labels."*

z. When all printing requirements are configured, click **Print**. If desired, select **Print Preview** under the **File** menu.

4. Once printed, affix the labels to their respective cryogenic storage vials:

   a. Affix the labels along the *length* of the vial. (This will make the label too long for the vial and the transparent part of the label will hang over the bottom edge of the vial.)

   b. Cut off the excess transparent part of the label and use it to protect the printing (from rubbing or peeling off during handling or storage) by placing it back over the label.

5. Place each cryovial in its designated position in a pre-labeled (complete with container name and unique identification number and barcode) 9 × 9 freezer storage box.

B.3.3 Glossary of Terms

acinetobacter radioresistans 50v1 (AR)
Aerobic gram negative g-proteobacteria. In the Genetic Inventory experiment, 1 of 11 MMC constituents.

aureobasidium pullulans 28v1 (AP)
Eukaryotic yeast. In the Genetic Inventory experiment, 1 of 11 MMC constituents.

autoclave
To sterilize equipment or supplies by subjecting the items to high-pressure saturated steam in a device known as an autoclave. All autoclave sterilizations for the Genetic Inventory experiment are performed at 121°C, 15 Pa N/m^2, for 30 min.

bacillus megaterium KL-197 (BM)
Gram-positive, spore-forming bacteria. In the Genetic Inventory experiment, 1 of 11 MMC constituents.

bacillus pumilus SAFR-032 spores (BP)
Gram-positive spore-forming bacteria. In the Genetic Inventory experiment, 1 of 11 MMC constituents.

bead-beating
A process used to complete cell lysis by employing mechanical agitation.

biological sampling kit (BiSKit)
A foam material sampling device, which is protectively encased in a sterile plastic unit meant to minimize potential risk of sampling device contamination. In the Genetic Inventory experiment, it serves as one of two materials used for sample collection of large surface areas (i.e., stainless-steel sheets).

clostridium sporosphaeroides (CS)
Gram-positive, spore-forming anaerobe culture. In the Genetic Inventory experiment, 1 of 11 MMC constituents; received from C. Moissl, University of Regensburg, Germany, who procured the culture from DSMZ [1294].

cotton swab
An organic cellulose-rich (>95%) material that is wrapped around one end of a wooden stick, and used to serve as a metal surface sampling device. In the Genetic Inventory experiment, it serves as one of two materials used for sample collection of small surface areas (i.e., stainless-steel coupons).

cupriavidus metallidurans CH34 (CM)
Non-spore-forming b-proteobacteria. In this laboratory controlled experiment, 1 of 11 MMC constituents; received from C. Moissl, University of Regensburg, Germany, who procured the culture from N. Leys, Belgium.

decant
To gently pour a supernatant liquid from one vessel to another without disturbing the pellet formed at the bottom of the original vessel.

deinococcus radiodurans R1 (DR, ATCC 13939)
Gram-positive, non-spore-forming bacteria. In the Genetic Inventory experiment, 1 of 11 MMC constituents.

DNA extraction

A process used to extract DNA from a sample for the purpose of purifying it for downstream molecular analyses. The Genetic Inventory experiment uses the automated DNA method due to its simplicity, reliability, consistency, reproducibility, and robustness in extracting DNA from low-biomass samples.

DSMZ medium 119

A special growth medium used to specifically foster the growth of *M. formicum* (MF) during a 72-h 37°C incubation period in the Genetic Inventory experiment.

DSMZ medium 78

A special growth medium used to specifically foster the growth of *C. sporosphaeroides* (CS) during a 60-h 37°C incubation period in the Genetic Inventory experiment.

false-positive/false-negative

A false positive occurs when signal amplification is observed—following a qPCR run—in a sample containing the target species primer set, but lacking the target species itself. A false negative occurs when no signal amplification is observed in a sample that contains both the target species and its corresponding primer set. A false-negative check involves spiking samples that rendered no PCR amplification, with the target species (e.g., *Bacillus pumilus* SAFR-032) as a means of checking for false negatives that may result from inhibitory substances.

handling control (HC)

A sampling device pre-moistened with PBS and exposed to the ambient sampling environment (without any contact with the metal surfaces). The Genetic Inventory experiment uses this as a negative control.

macrofoam

A sponge provided as part of the BisKit. In the Genetic Inventory experiment, the macrofoam sponge is used to sample large surface areas such as 2500 cm^2 stainless-steel sheets.

Maxwell DNA extraction reagent blank

A DNA extraction system reagent control. This is the reagent content of the Maxwell-16 cartridge processed as is, without the addition of samples or UltraPure water. The Genetic Inventory experiment uses this as a negative control.

media blank (MB)

A sterile culture medium prepared for inoculation with MMC (or environmental sample). The Genetic Inventory experiment uses this as a negative control.

methanobacterium formicicum (MF)

Anaerobic archaea culture. In the Genetic Inventory experiment, 1 of 11 MMC constituents; received from C. Moissl, University of Regensburg, Germany, who procured the culture from DSMZ [1535].

microbacterium imperiale 47v1 (MI)

Gram-positive, actinobacteria. In the Genetic Inventory experiment, 1 of 11 MMC constituents.

micrococcus luteus (ML, ATCC 4698)

Gram-positive, actinobacteria. In the Genetic Inventory experiment, 1 of 11 MMC constituents.

model microbial community (MMC)

A sample of known phylogenetic composition and cellular/endospore density. In the Genetic Inventory experiment, MMC is synthesized to serve as the positive control, and is comprised of 11 constituents (AP, AR, BM, CM, DR, MI, ML, SW, BP, CS, and MF).

negative control
A group in a scientific experiment in which the results are known to be negative; used to isolate any variables from the experiment results. In the Genetic Inventory experiment, negative controls include SB, SD, HC, sampling surface stainless-steel control, nuclease-free UltraPure water, sterile PBS, MB, Maxwell DNA extraction reagent blanks, and NTC.

no-DNA template control (NTC)
A qPCR reagent assay control. NTC is included in every qPCR assay as a means of evaluating melt curves and detecting primer-dimer amplification (multiple melt peaks). The Genetic Inventory experiment uses this as a negative control.

nuclease-free UltraPure water
Sterile water. The Genetic Inventory experiment uses this as a negative control.

Nutrient Agar (NA)
Universal growth medium for short-term (≤ 24 h) incubation. In the Genetic Inventory experiment, Nutrient Agar is used as a growth medium for the MMC constituent, ML.

Nutrient Broth (NB)
Universal growth medium for short-term (≤ 24 h) incubation. In the Genetic Inventory experiment, Nutrient Broth is used as a growth medium for the MMC constituent, ML.

nylon-flocked swab
A plastic stick—with a scored neck for easier breakage—with liquid nylon sprayed perpendicular to one end of the stick and allowed to dry onto the stick. In the Genetic Inventory experiment, it serves as one of two materials used for sample collection of small surface areas (i.e., stainless-steel coupons).

Petroff-Hausser counting chamber
A counting chamber designed to count bacteria up to 1,000× magnification for qualitative and quantitative analysis. In the Genetic Inventory experiment, the chamber is used to determine the total number of organisms per cm^3 (mL) in a sample.

polyester wipe
A 4" × 4" continuous material with the long fibers tightly interweaved for use in cleanroom environments. In the Genetic Inventory experiment, it serves as one of two materials used for sample collection of large surface areas (i.e., stainless-steel sheets).

positive control
A group in a scientific experiment in which the results are known to be positive; used to isolate any variables from the experiment results. In the Genetic Inventory experiment, positive controls include DNA from total MMC for qPCR assay, and purified DNA arising from each MMC constituent strain used for ssPCR assays

sample device control (SD)
A sampling device moistened with PBS only. The Genetic Inventory experiment uses this as a negative control.

sampling blank (SB)
A sampling device pre-moistened with PBS and exposed to the surfaces of sterile, unseeded stainless steel. The Genetic Inventory experiment uses this as a negative control.

sampling matrices
Materials used in sample collection. In the Genetic Inventory experiment, the four sampling matrices are the cotton swab, nylon-flocked swab, polyester wipe, and BiSKit.

sampling surface (stainless-steel) control
A sample collected from sonicated sterile, unseeded metal. The Genetic Inventory experiment uses this as a negative control.

sonicate
To use high-frequency sound waves to break down the sample cells.

stainless-steel coupons
A medium used to test the efficacy of the sampling devices in collecting seeded MMC; 25 cm^2 in surface area.

stainless-steel sheets
A medium used to test the efficacy of the sampling devices in collecting seeded MMC; 2,500 cm^2 in surface area.

staphylococcus warneri 82-4 (SW)
Gram-positive, non-spore-forming bacteria. In the Genetic Inventory experiment, 1 of 11 MMC constituents.

sterile phosphate buffered saline (PBS)
A buffer used for all processing steps. The Genetic Inventory experiment uses this as a negative control.

Tryptone Yeast Glucose (TYG) agar
A growth agar containing Tryptone, yeast, and glucose for the enumeration of bacteria onto a semisolid growth media surface. In the Genetic Inventory experiment, TYG agar is used as a growth medium for the MMC constituents, AP, AR, BM, CM, DR, MI, SW, BP, CS, and MF.

Tryptone Yeast Glucose (TYG) broth
A growth broth containing Tryptone, yeast, and glucose for the enumeration of bacteria in liquid suspension growth media. In the Genetic Inventory experiment, TYG broth is used as a growth medium for the MMC constituents, AP, AR, BM, CM, DR, MI, SW, and BP.

ultrasonic bath
A device that cleans items using ultrasound and cleaning solvent to release cells from their attached surfaces (i.e., metal).

vortex-mix
To mix tubes of liquid samples using a device known as a vortex mixer, which creates a vortex by transmitting motion inside the liquid of a test tube by adjacent oscillation of a rubber piece.

APPENDIX C: PEER-REVIEWED PUBLICATIONS

This appendix includes abstracts of papers published as a result of the Genetic Inventory research. The peer-reviewed publications are listed below.

Publications in Support of Achieving Objective 1

1. Evaluation of Procedures for the Collection, Processing, and Analysis of Biomolecules from Low-Biomass Surfaces
2. Comparative Analysis of Methods for the Purification of DNA from Low-Biomass Samples Based on Total Yield and Conserved Microbial Diversity
3. Differential Recovery of Phylogenetically Disparate Microbes from Spacecraft-Qualified Metals

Publications in Support of Achieving Objective 2

1. Comprehensive Census of Bacteria in Clean Rooms by Using DNA Microarray and Cloning Methods
2. Comparison of Innovative Molecular Approaches and Standard Spore Assays for Assessment of Surface Cleanliness
3. Pyrosequencing-Derived Bacterial, Archaeal, and Fungal Diversity of Spacecraft Hardware Destined for Mars
4. Diversity of Anaerobic Microbes in Spacecraft Assembly Clean Rooms
5. New Perspectives on Viable Microbial Communities in Low-Biomass Environments

Applied and Environmental Microbiology, May 2011, 77(9): 2943–2953
http://aem.asm.org/content/77/9/2943.full.pdf+html (free full AEM version)

SUMMARY

Evaluation of Procedures for the Collection, Processing, and Analysis of Biomolecules from Low-Biomass Surfaces

Kwan, K., Cooper, M., La Duc, M. T., Vaishampayan, P., Stam, C., Benardini, J. N., Scalzi, G., Moissl-Eichinger, C., and Venkateswaran, K.

Planetary protection requirements for robotic probe and orbiter missions address concerns over the potential for forward contamination (i.e., the inadvertent contamination of extraterrestrial environments with terrestrial organic and biological matter) and backward contamination (i.e., the inadvertent exposure of the terrestrial biosphere to extraterrestrial material). NASA's techniques for monitoring biological contamination of spacecraft and spacecraft assembly clean-room (SAC) surfaces have been largely based on 1970s Viking-related studies. From the Viking era to the present, NASA has employed cotton swabs to collect biological materials from spacecraft and SAC surfaces. However, research has shown that the sole use of a cotton swab does not provide an accurate assessment of the microbial diversity on SAC surfaces.

The goal of this study was to rigorously assess microbial diversity and abundance using molecular analysis–based methods. The researchers evaluated and standardized protocols and procedures for collecting, processing, and analyzing contaminant biomolecules—intact microorganisms as well as a wide spectrum of biomaterials (from cells to nucleic acid remnants)—from SAC surfaces. While several protocols are available to sample low-biomass surfaces, few are based on molecular analysis, and most experiment only with one or two test organisms. In this study, researchers created a model microbial community (MMC) to represent a sample typical of the low-biomass microbial populations found in cleanroom environments. The MMC included strains from all three microbial domains and, whenever possible, strains isolated directly from spacecraft and SAC surfaces; the MMC was used to assess how each sampling method was affected by variables in sampling devices, target cell density and molecule concentration, and cryogenic storage.

Precision-cleaned, sterile stainless steel coupons (25 cm^2) and sheets (2,500 cm^2) served as surrogate spacecraft surfaces. A known amount (aliquot) of MMC was deposited onto the coupons and sheets, the coupons and sheets were allowed to dry, and the aliquots were stored at (−80 °C) for various periods of time. A variety of sampling devices (cotton and nylon-flocked swabs for the coupons, and polyester wipes and biological sampling kits [BiSKits] for the sheets) were then used to recover cells and biomolecules, which were analyzed using two molecular analysis–based methods: quantitative polymerase chain reaction (qPCR) and species-specific polymerase chain reaction (ssPCR) techniques.

The qPCR analysis showed that cotton swabs were superior to nylon-flocked swabs for sampling small surface areas; for larger surfaces, BiSKits significantly outperformed polyester wipes. ssPCR assays engineered for each MMC strain revealed that the sampling device affected the type of species recovered from each coupon or sheet. In addition, this molecular technique was not at all affected by the considerable levels of indigenous DNA associated with sampling materials. Several of the MMC constituents most frequently detected via ssPCR were among those still cultivable after 90 days of storage at −80°C. These bacterial species were apparently the most resistant to drying and cryogenic storage. While cryogenic storage for up to 90 days had little or no effect on total cell/spore counts, the cultivability of MMC constituents decreased as much as 3 orders of magnitude When MMC aliquots were removed from −80 °C storage at various time points, subjected directly to DNA extraction protocols, and assessed via qPCR, the total DNA yield increased with increased storage time through 8 days, at which time it remained constant for up to 90 days at −80°C.

These results stress the importance of selecting sample collection and processing approaches based on the desired target and the required level of detection. If an investigation is examining the presence of intact, cultivable cells, nylon-flocked swabs would likely be the better sampling device. If a survey is more interested in the entire spectrum of microbial diversity on a given surface, then the preferred sampling instrument would be either cotton swabs or BiSKits, depending on the surface area. The results of this study empower current and future molecular analysis–based microbial sampling and processing methodologies.

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Journal of Rapid Methods and Automation in Microbiology, 2009, 17(3): 350–368
http://onlinelibrary.wiley.com/doi/10.1111/j.1745-4581.2009.00153.x/abstract (restricted access; fee is applicable)

SUMMARY

Comparative Analysis of Methods for the Purification of DNA from Low-Biomass Samples Based on Total Yield and Conserved Microbial Diversity

La Duc, M.T., Osman, S. and Venkateswaran, K.

Even with significant advances in molecular biological technologies, the ability to efficiently detect, collect, and purify nucleic acids from low-biomass samples remains a tremendous challenge for researchers who must accurately describe the total yield as well as the true microbial diversity of the samples. These limitations are relevant to many industries—including pharmaceutical, ecological, medical, and semiconductor—as well as to the space program.

To limit the likelihood of forward contamination of Mars, Europa, and other extraterrestrial environments, the National Aeronautics and Space Administration (NASA) has established rigorous standards for clean room design and maintenance to ensure that spacecraft assembly environments are largely free of microbial contamination. However, the rigorous cleaning protocols do not eradicate microbial contaminants completely; bioburden associated with the surfaces of a spacecraft, albeit low, could potentially lead to forward contamination and the confounding of future life-detection missions. To achieve NASA's planetary protection objectives for future missions, scientists should identify the nucleic acids from these contaminants to ensure that microbial contaminants from the spacecraft assembly environment could not later be misconstrued as the discovery of extraterrestrial life.

As with any low-biomass sample, analyses of spacecraft and associated surfaces necessitate novel, highly efficient nucleic acid extraction strategies before the downstream use of state-of-the-art molecular techniques. The surface area of a spacecraft is fixed, and much of it is not amenable to sampling; it is not possible to simply increase the sample size to improve yield. It is therefore critical to ensure that current methods of purifying biomolecules from these precious samples are optimized to both maximize total yield and conserve the true microbial diversity of the sampled environment.

The objective of this study was to determine the most effective DNA purification regime for routine assessment of microbial contamination and diversity in low-biomass samples. A total of nine bacterial strains were used; eight of the strains were isolated from Class 100K clean room or co-located spacecraft surfaces. One organism, *Bacillus pumilus*, was examined in the form of purified spores. The other eight strains were grown in appropriate culture conditions, and a sample of each culture was suspended in 50% phosphate buffered saline; these eight samples are referred to as the test Bacterial Bisque. Using six 10-mL Bacterial Bisque subsamples for each method, five distinct DNA purification methods for extracting nucleic acids were tested in parallel: (1) A "gold-standard," solvent-based manual DNA extraction method, (2) a commercial MoBio UltraClean Microbial DNA Isolation Kit, (3) a commercial Promega Wizard Genomic DNA Purification Kit, (4) A simple, fully automated method using an Axcyte AutoLyser (AA), and (5) the AA method with bead-beating agitation (bbAA), an extraction method devised to more efficiently disrupt the cellular structure of hardier cell types than the AA method could lyse alone.

DNA products from each of these five methods were then subjected to polymerase chain reaction (PCR) (to generate multiple copies of the DNA sequence), 16S rRNA[1] clone library analysis and bidirectional DNA sequencing, and quantitative PCR using commercial TaqMan probe technology. Novel 16S sequences (approximately 1,400 nucleotides) were aligned with known sequences using the public ARB database and software suite, and the results were statistically analyzed using software specific for each assay or with the Microsoft Excel 2000 software package.

Researchers concluded that the automated Axcyte AutoLyser (without bbAA) outperformed all other purification regimes examined. This automated method consistently yielded the highest concentration of PCR-amplifiable DNA, and it also reported species composition most consistent with the starting solution.

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[1] 16S refers to the rate of sedimentation, in Svedberg units, of the RNA molecule in a centrifugal field. 16S rRNA is the region of DNA that most reliably reveals similarities between organisms, or evolutionary relatedness.

SUMMARY

Differential Recovery of Phylogenetically Disparate Microbes from Spacecraft-Qualified Metal

Bargoma, E., La Duc, M. T., Kwan, K., Vaishampayan, P., and Venkateswaran, K.

Despite a growing understanding of the diverse microbial population on spacecraft-associated surfaces, it is still challenging to predict the true risk that terrestrial organisms could compromise the scientific integrity of space exploration missions. As not all lineages of microbial life pose an equivalent threat of forward contamination, understanding which taxa are of greatest concern, and the frequency at which these microbes are encountered in spacecraft-associated samples, would significantly empower strategies to accurately assess the risk of forward contamination. However, before a comprehensive census of the microbes present within spacecraft-associated surfaces can be achieved, researchers need to identify and optimize sample collection methodologies capable of recovering a diverse range of targeted microbial cells and associated biomolecules.

The primary focus of this investigation is an in-depth assessment of effective and efficient strategies for the collection of biological samples from low-biomass surfaces typical of those found in spacecraft assembly cleanrooms. In this study, experiments were designed and executed to (a) test the effectiveness of four sampling devices in recovering cells and naked nucleic acids from metal surfaces and (b) use species-specific quantitative polymerase chain reaction (ss-qPCR) techniques to assess the recovery of rDNA of members of a model microbial community (MMC). The MMC comprised 11 distinct microbial species that spanned all three domains of life as well as a variety of metabolisms, modes of respiration, and cellular morphotypes. Most of the MMC cell lines had been isolated from spacecraft and associated cleanroom surfaces; some were procured. Experiments were devised to test the performance of the four sampling devices in recovering the rDNA of nine targeted MMC bacterial strains. (Two strains were included in the MMC to elucidate the effect of nontargeted strains on recovery efficiencies.)

Known cell densities (10^6 cells) of the MMC were deposited onto small metal coupons (25 cm^2) and large metal sheets (2500 cm^2), and the metal surfaces were air dried at room temperature. Subsequently, samples were collected from each surface, using cotton and nylon-flocked swabs for the small coupons and biological sampling kits (BiSKits) and polyester wipes for the large sheets. The sample collection materials were processed to extract sample volumes, which were further processed to extract DNA for analysis. In order to discern differences in the recovery of ribosomal RNA (rRNA) genes of the various microbes present in the MMC positive control, ss-qPCR assays were designed and carried out targeting each MMC constituent. All rRNA gene copy measurements were determined in triplicate, and controls were included in all qPCR runs. Excel-based statistical calculations were charted and compared, and standard statistical techniques were applied to each sample to determine the reliability of the results.

The qPCR analyses revealed that cotton swabs were superior to nylon-flocked swabs for recovering biomolecules from small metal surface areas. Similarly, BiSKits outperformed polyester wipes for sampling large metal surface areas. Species-specific qPCR results showed that the type of sampling device employed influenced the recovery of rRNA genes for each of the nine targeted MMC strains. Both cotton swabs and BiSKits recovered the rDNA of all nine of the targeted MMC strains, whereas nylon-flocked swabs and polyester wipes recovered the rDNA of only six and four of these MMC strains, respectively.

The findings of this study demonstrate the importance of molecular techniques in gauging the effectiveness and efficiency of various modes of biological sample collection from metal surfaces. The study demonstrates that universal and ss-qPCR–based methods are essential tools for surveying microbial abundance and diversity in samples of extremely low total biomass.

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Applied and Environmental Microbiology, October 2009, 75(20): 6559–6567
http://aem.asm.org/content/75/20/6559.full.pdf+html (free full AEM version)

SUMMARY

Comprehensive Census of Bacteria in Clean Rooms by Using DNA Microarray and Cloning Methods

La Duc, M.T., Osman, S., Vaishampayan, P., Piceno, Y., Andersen, G., Spry, J. A., and Venkateswaran, K.

To ensure that missions do not inappropriately contaminate solar system bodies with terrestrial biological material (forward contamination), NASA's planetary protection requirements mandate that spacecraft be assembled and readied for launch in controlled cleanroom environments. In spite of rigorous cleaning protocols, a variety of organisms are repeatedly found in spacecraft assembly clean rooms (SACs). NASA needs to know which microbes are present in SACs in order to assess the threat of forward contamination as well as to control and eradicate microorganisms present on spacecraft being readied for launch. One approach to achieving this objective is to routinely survey and catalog the genetic microbial inventory in SACs.

There are several methods available to scientists to create a genetic microbial inventory. Factors to consider in choosing an appropriate methodology include cost, time, labor intensity, and reproducibility; however, to meet planetary protection goals, the bias and accuracy of a given approach are perhaps the most important considerations. In theory, cloning and sequencing 16S ribosomal genes from each and every cell present would be the ideal method; however, the full-length sequencing of all 16S ribosomal ribonucleic acid (rRNA) genes from environmental samples is prohibitively expensive, so the approach is not feasible for generating comprehensive profiles of the complex microbial communities found in SACs. Less-expensive classic cloning methods are time-intensive, and they have proven to be insufficient for detecting organisms that may be present in clean rooms in very small quantities. A third approach is to use DNA microarray PhyloChip methodologies, which are highly sensitive and can quickly detect organisms present in very small amounts (below 10^{-4} abundance of the total sample); therefore, PhyloChip may prove to be the best way to meet NASA's requirements.

This study compares the microbial diversity profiles resulting from DNA microarray analyses with profiles resulting from conventional cloning and sequencing of 16S rRNA genes. An extensive census of the microbial communities was conducted on the surfaces in three NASA SACs: Lockheed Martin Aeronautics' Multiple Testing Facility (LMA-MTF), the Kennedy Space Center's Payload Hazardous Servicing Facility (KSC-PHSF), and the Jet Propulsion Laboratory's Spacecraft Assembly Facility (JPL-SAF). Each of the facilities examined was a certified class 100K or ISO 8 clean room. The three SACs were supporting two missions: Phoenix and Mars Science Laboratory, during 10 sampling events over an 18-month period (April 2007–August 2008). Researchers used biological sampling kits (BiSKits) to collect 107 samples. To compensate for limitations associated with processing samples of such extremely low biomass, individual samples from each sampling event were pooled for further analysis; the 10 pooled samples represented three categories: samples collected from SACs in the presence of spacecraft hardware (Category A), samples collected within SACs devoid of spacecraft (Category B), and samples collected from an SAC during spacecraft assembly (Category C). Subsamples from each sampling event were subjected to both DNA microarray protocols and to conventional cloning and sequencing of 16S rRNA genes.

PhyloChip microarray analyses were found to be superior to conventional 16S rRNA gene cloning and sequencing strategies in all aspects of microbial diversity analysis except one: the detection of novel microbial taxa. PhyloChip identified >90% of all 16S rRNA sequence types identified by the more expensive clone library method. Perhaps the greatest advantage of cloning-based biodiversity analysis was the ability to identify the number and coverage of different species in the samples, which provided an invaluable approximation of just how representative each sample was of its true environment. PhyloChip DNA microarrays detected a much broader biodiversity than clone libraries, especially for samples from SACs that housed spacecraft hardware (32- to 70-fold) than for vacant SACs (9- to 16-fold). The rapidity, repeatability, comprehensiveness, and sensitivity of the PhyloChip for surveying entire bacterial communities suggest that the approach could significantly advance microbial detection and monitoring in a wide range of scientific, electronics, homeland security, medical, and pharmaceutical ventures.

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Applied and Environmental Microbiology, August 2011, 77(15): 5438–5444
http://aem.asm.org/content/77/15/5438.full.pdf+html (free full AEM version)

SUMMARY

Comparison of Innovative Molecular Approaches and Standard Spore Assays for Assessment of Surface Cleanliness

Cooper, M., La Duc, M. T., Probst, A., Vaishampayan, P., Stam, C., Benardini, J. N., Piceno, Y. M., Andersen, G. L., and Venkateswaran, K.

Future NASA missions will likely include life detection instruments that could be compromised if appropriate tools and standards are not in place to reduce the probability of transferring terrestrial microorganisms to Mars, Europa, and other icy satellites. The biomedical industry has developed advanced molecular methods that give NASA the opportunity to update its standards and to augment traditional, cultivation-based procedures (spore assay) for surveying, archiving, and quantifying microbial burden associated with low-biomass environments such as spacecraft surfaces and cleanrooms.

Earlier research confirmed that microbial diversity will go undetected by the standard spore assay alone. In addition, earlier research showed that forward contamination risk cannot be assessed by DNA assay alone because the DNA method does not reveal which microbes are physiologically active (and which are inactive). Hence, traditional spore assays and DNA assays are complementary.

Using the same set of samples, the two methods—a standard bacterial spore assay and a molecular PhyloChip generation 3 (G3) DNA microarray method—were compared to determine the ability of each to assess relative spacecraft surface cleanliness with regard to microbial diversity and total cell numbers. Following NASA sampling protocol, polyester wipes were used to collect samples from the surfaces of 107 flight hardware components. A standard spore assay was carried out within 2 h of sample collection. The 107 samples were divided into three categories based on the number of spores counted at the time the sample was collected (category A, 0 spores; category B, 1 to 50 spores; and category C, >50 spores).The samples were further subdivided and pooled based on spore counts, sampling location, or both. The samples were processed to cultivate aerobic spores for DNA-based analyses, and colony-forming units (CFU) were counted at 24 h, 48 h, and 72 h of growth.

Colony counts derived from the NASA standard spore assay were extremely low for spacecraft surfaces. However, the PhyloChip generation 3 (G3) DNA microarray revealed a highly diverse suite of 16S rRNA genes in the same sample set. This study clearly demonstrated that there is not a statistically significant correlation between the cultivable spore counts obtained from a sample and the likely degree of bacterial diversity present. The study verified that standard spore assay alone will fail to account for the presence of a certain subset of the microbial population. This underestimation of bioburden (microorganism contamination) would, in turn, increase the probability of transferring terrestrial microorganisms to Mars.

The results demonstrate that validated state-of-the-art molecular techniques, such as DNA microarrays, can be utilized in parallel with classical culture-based methods to improve assessments of spacecraft surface cleanliness. The combination of the classical method with biomolecular technology will have valuable implications in other fields, including food, medical, pharmaceutical, aeronautical, and homeland security industries.

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Applied and Environmental Microbiology, August 2012, 78(16): 5912–5922
http://aem.asm.org/content/early/2012/06/10/AEM.01435-12.abstract (free abstract; full version free 12 months after publication)

SUMMARY

Pyrosequencing-Derived Bacterial, Archaeal, and Fungal Diversity of Spacecraft Hardware Destined for Mars

La Duc, M. T., Vaishampayan, P., Nilsson, H. R., Torok, T., and Venkateswaran, K.

If terrestrial microorganisms are inadvertently introduced in extraterrestrial settings, there could be significant consequences to the scientific integrity of in situ and sample return life detection experiments. Researchers must be able to distinguish between terrestrial microbes and organisms that may have originated on an extraterrestrial body. To meet this challenge, NASA is supporting efforts to validate technologies that could provide a comprehensive census of the microbes present on spacecraft surfaces.

Historically, bacterial endospores have been considered most likely to survive interplanetary transport. Recent research has shown that fungal cells can also withstand space conditions for extended periods of time. Similarly, researchers suspect that archaeal cells may be capable of tolerating the Martian environment. Therefore, researchers should expand the scope of spacecraft-associated microbial diversity assessments in order to achieve a comprehensive microbial census. High-throughput next-generation sequencing and phylogenetic microarray techniques have dramatically increased the resolution and detectable spectrum of diverse microbes from environmental samples. This study uses the massively parallel capability of tag-encoded FLX 80 amplicon pyrosequencing (TEFAP) technique to reveal the bacterial, archaeal, and fungal diversity associated with extremely low-biomass spacecraft surfaces.

Samples were collected from spacecraft hardware of a recent Mars mission as well as from two Jet Propulsion Laboratory Class 100K spacecraft assembly cleanroom floors and ground support equipment. Samples were grouped into four categories for analysis: Category I to examine the effect of cleanroom cleanliness levels; Category II to assess the impact of cleaning procedures; Category III to evaluate the correlation between the endospore burden on spacecraft hardware and the resulting TEFAP sequence and molecular taxonomic unit (MOTU) abundance; Category IV to investigate how TEFAP results differ across various mission components. Samples were processed to prepare DNA extracts, which were stored at −20 °C. TEFAP procedures were then performed in accordance with established protocols. Of the millions of pyrosequences generated, 203,852 were high quality. Bioinformatic analyses revealed correlations between pyrosequence and/or MOTU abundance and certain sample characteristics, such as source (cleanroom floor, ground support equipment, or spacecraft hardware), cleaning regimen applied, and location about the facility or spacecraft.

TEFAP analyses supported the general trends observed in other research: the greatest microbial diversity was encountered in ordinary room facilities (159 to 654 distinct bacterial MOTUs), with less diversity on cleanroom floors (122 MOTU), and the least diversity (1 to 45 MOTU) on spacecraft components. The results of this TEFAP study underscore that (a) continued monitoring and biosignature detection needs to be extended throughout all three domains (Bacteria, Archaea, and Eukarya) of microbial life and that (b) a shift towards high-throughput, data-rich molecular assays with significant bioinformatic analysis is inevitable in microbial community analyses.

This study provides important insights into the benefits and limitations of innovative molecular approaches for assessing the microbial diversity associated with extremely low–biomass samples. The findings are relevant to current and future NASA endeavors, as well as to homeland security, medical, pharmaceutical, and superconductor fabrication industries. Coupling TEFAP techniques with other emerging molecular methodologies could lead to radically improved approaches for monitoring and mitigating diverse microbial populations associated with ultra-clean environments.

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Applied and Environmental Microbiology, May 2010, 76(9): 2837–2845
http://aem.asm.org/content/76/9/2837.full.pdf+html (free full AEM version)

SUMMARY

Diversity of Anaerobic Microbes in Spacecraft Assembly Clean Rooms

Probst, A., Vaishampayan, P., Osman, S., Moissl-Eichinger, C., Andersen, G. L., and Venkateswaran, K.

The diversity of cultivable and noncultivable microbes in spacecraft assembly clean rooms has been documented using both conventional and state-of-the-art molecular techniques; however, scientists are still unsure to what extent obligate anaerobes[1] occur in clean rooms. Recent use of molecular microbial community analyses on clean-room samples has revealed a much higher biodiversity (aerobic and anaerobic) than is revealed by NASA's standard assay procedure alone, with approximately 0 to 8% of retrieved genetic sequences belonging to obligate anaerobes. This low percentage might be due to the fact that clone library construction is generally limited to hundreds or thousands of sequences, which has proven to be insufficient for detecting low-abundance organisms, including anaerobes. Mars Science Laboratory (MSL) will search for habitable environments in new sites on Mars using highly sensitive biosensors that require high cleanliness control to prevent false positives; therefore, the study of anaerobes is particularly important, since the proliferation of microbes adapted to Mars-like environments would increase the risk of contaminating the planet and would compromise sensitive life-detection activities.

To overcome limitations in clone library construction, this study used a two-step approach to characterize the obligate anaerobic bacterial communities of the three clean-room facilities used for the MSL rover assembly: samples were collected and enriched in liquid and solid media suitable for anaerobes, and the samples were subjected to both culture-dependent and culture-independent molecular analyses.

Anaerobic bacteria were cultured on several media (liquid and solid), and DNA was extracted from the anaerobic enrichments and examined with conventional 16S rRNA[2] gene clone library, as well as with high-density phylogenetic 16S rRNA gene microarray (PhyloChip) technologies. Clone libraries were generated from the samples that were pre-enriched for obligate or facultative anaerobes; the enrichment approach suppressed aerobes and increased the efficiency of retrieving 16S rRNA gene sequences of both facultative and strict anaerobes. High-quality sequences were analyzed using statistical techniques and DNA microarray-based microbial analyses; to ensure sampling and processing were correctly performed, appropriate negative controls were included in each step.

The 16S rRNA gene sequences retrieved from clone libraries revealed distinct microbial populations associated with each clean-room facility, clustered exclusively within gram-positive[3] organisms. PhyloChip analysis detected a greater microbial diversity, spanning many phyla of bacteria, and provided a deeper insight into the microbial community structure of the clean-room facilities. The culture-dependent analyses predominantly showed the presence of strains that may not be able to germinate or thrive on Mars; however, the strains' spores are able to resist heat, chemicals, and UV irradiation, which may allow them to survive during space flight. Therefore, these strains could cause forward contamination that could compromise life-detection experiments.

Study results reveal that highly diverse anaerobic bacterial populations persist in the clean rooms even after the imposition of rigorous maintenance programs. The anaerobic bacteria will pose a challenge to planetary protection implementation activities. Although the results of this study are of particular interest to space-faring nations, the study will also benefit a wide range of scientific, electronic, homeland security, medical, and pharmaceutical ventures that produce sensitive products or assemble products in clean rooms.

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[1] An obligate anaerobe (also called a strict anaerobe) is an organism that has a very difficult time living (and in fact many species cannot), much less propagating in the presence of molecular oxygen. A facultative anaerobe is an organism that can live in the absence as well as in the presence of atmospheric oxygen. An aerobe requires oxygen for growth.

[2] 16S refers to the rate of sedimentation, in Svedberg units, of the RNA molecule in a centrifugal field. 16S rRNA is the region of DNA that most reliably reveals similarities between organisms, or evolutionary relatedness.

[3] The Gram staining test reveals information about the external structure of the bacterium; this information helps the researcher identify the type of bacteria found in the culture.

SUMMARY

New Perspectives on Viable Microbial Communities in Low-Biomass Environments

Vaishampayan, P., Probst, A. J., La Duc, M. T., Bargoma, E., Benardini, J. N., Andersen, G. L., and Venkateswaran, K.

Microbial cells are traditionally classified as either viable (maintaining active metabolism and membrane integrity), viable but dormant (due to external pressures), or non-viable (dead). The ability to identify living microbes on surfaces is essential to minimize contamination in, for example, hospital operating rooms, pharmaceutical manufacturing and packaging facilities, superconductor fabrication, and spacecraft assembly cleanrooms.

Advanced molecular approaches minimize the amount of time needed to determine viability; however, these approaches have an inherent risk of overestimating the number of viable cells. DNA-based molecular technologies alone have yet to be validated for assessing cell viability across varying phylogenetic lineages in a complex microbial assemblage. Methods probing RNA as an alternative to DNA also assess viability, but these, too, come with complications. This study is the first effort to assess cell viability and correlate it with phylogenetic lineage. This pioneering effort couples propidium monoazide (PMA) treatment with PhyloChip DNA microarray and bacterial tag-encoded FLX amplicon pyrosequencing (bTEFAP) methodologies to assess the viable bacterial population present in a typical low-biomass environmental sample. The results help scientists better understand the frequency, diversity, and distribution of viable bacteria in spacecraft assembly cleanrooms and other critical environments.

Thirty-six samples were collected from the floors and ground support equipment in two Jet Propulsion Laboratory Class 100K cleanrooms, one of which housed spacecraft flight hardware at the time of sample collection. Each 1 m^2 sample was collected using a biological sampling kit (BiSKit). Sample volumes were then extracted from the BiSKit devices; and samples from the same general location were pooled together and further concentrated, filtered, and separated into two aliquots. One aliquot was subjected to PMA pretreatment (viability assessment), and the other served as a null environmental sample. DNA was extracted from all samples, and bacterial 16S rRNA[1] genes were amplified from each sample. Total bacterial burden in each sample was assessed by quantitative polymerase chain reaction (qPCR) analysis. All samples were analyzed using PhyloChip generation 3 (G3) techniques and bTEFAP pyrosequence discrimination analyses. bTEFAP-based pyrosequence discrimination results were binned into molecular operational taxonomic units (MOTU) to improve the accuracy of the results. Several statistical analyses were performed to study the differences between the PMA-treated samples and the non-PMA–treated samples.

The bTEFAP sequencing method was able to generate high-quality pyrosequences from low-biomass samples, where conventional gene cloning and sequencing techniques may fail to yield meaningful data. Sample fractions not treated with PMA, which were indicative of the presence of both live and dead cells, yielded a great abundance (27,449) of highly diverse bacterial pyrosequences. In contrast, PMA pretreatment resulted in the generation of only 2,827 pyrosequences in the same samples. The results of PhyloChip analyses of PMA-treated and untreated sample fractions were in agreement with those of pyrosequencing. The viable bacterial population detected in a cleanroom devoid of spacecraft hardware was far more diverse than that observed in a cleanroom that housed spacecraft flight hardware. The latter was dominated by hardy, robust organisms previously reported to survive in cleanroom environments.

The findings of this study provide important insights into the benefits and limitations of innovative molecular approaches for measuring and monitoring viable microbial diversity and burden. Coupling the PMA-linked bTEFAP/PhyloChip technologies developed in this study with other emerging molecular detection methodologies could lead to radically improved approaches for monitoring and mitigating the total viable microbial burden of low-biomass environments.

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[1] 16S refers to the rate of sedimentation, in Svedberg units, of the RNA molecule in a centrifugal field. 16S rRNA is the region of DNA that most reliably reveals similarities between organisms, or evolutionary relatedness.

APPENDIX D: PRESENTATIONS AND POSTERS

This appendix includes abstracts for all presentations and posters published as a result of the Genetic Inventory task. A citation for each poster or presentation is provided as a header at the top of each page. For each poster, a reduced-sized image is provided. Although these pages are not set up to be legible if printed, the posters can be enlarged on screen to view information.

Presentations and Posters in Support of Achieving Objective 1

1. Standardization of Sampling and Sample Processing Techniques for Spacecraft and Associated Clean Rooms
2. Development of a Model Community to Evaluate Efficient Removal of Genetic Signatures from Spacecraft Surfaces: Issues Pertaining to Sampling, Sample Processing, and Analysis
3. Efficient Removal of Genetic Materials From Low-Biomass Surfaces: Issues Pertaining to Sampling, Sample Processing, and Analysis
4. Species-Specific qPCR Analysis of Recovery Efficiency and Indigenous Contaminants Associated with Various Sampling Matrices
5. Comparative Analyses of Molecular Approaches and a NASA Standard Spore Assay in Assessing the Cleanliness of Spacecraft
6. Methods in Planetary Protection—A Tightrope Walk
7. Greengenes 16S Ribosomal RNA Gene Database Update For 2011—HMP Reference Sets and Tools
8. Species-specific qPCR to Assess the Differential Recovery of Microorganisms by Various Sampling Materials
9. Significance of Effective Sampling from Low-Biomass Surfaces and Challenges Involved in Nucleic Acid-Based Phylogenetic Analyses

Presentations and Posters in Support of Achieving Objective 2

1. State-of-the-Art Molecular Approaches to Elucidate the Genetic Inventory about the Surfaces of Spacecraft and Associated Environments.
2. Genetic Inventory of Phoenix Spacecraft and Associated Environments via Conventional Cloning and Sequencing Analysis
3. Microbial Diversity of Anaerobes from Spacecraft Associated Surfaces
4. Predictive Risk Assessment of Spacecraft Contamination with Computational Analysis
5. Viable Bacterial, Archaeal, and Fungal Diversity of Spacecraft-Associated Clean Rooms Using a Novel DNA Intercalating Agent
6. Development and Implementation of Molecular Tools for Assessing the Viability of Microbes on Spacecraft and Associated Surfaces
7. Viability Assessment of Microbial Communities Using State-of-the-Art Molecular Techniques
8. Assessing Bacterial, Archaeal, and Fungal Diversity of Spacecraft-Associated Surfaces via Tag-Encoded FLX Amplicon Pyrosequencing
9. Bacterial, Archaeal, and Fungal Diversity of Spacecraft-Associated Surfaces

ABSTRACT *[Presentation]*

Standardization of Sampling and Sample Processing Techniques for Spacecraft and Associated Clean Rooms

Kwan, K., La Duc, M. L., Cooper, M., Stam, C., Vaishampayan, P., Scalzi, G., Benardini, J. N., Moissl, C., Andersen, G., Spry, J. A., and Venkateswaran, K.

As a result of stringent cleaning procedures, the microbial burden of a typical spacecraft assembly clean room is lower when compared to other indoor environments. This presents a challenge in the recovery of microorganisms and biomolecules from spacecraft surfaces. In order to obtain samples that are representative of both the richness and diversity of microbial species which persist on spacecraft and associated clean room surfaces, current sampling and sample processing techniques needed to be evaluated for their efficiency in recovering microorganism and targeted biomolecules. The effectiveness of several sampling systems and processing techniques were analyzed by doping a known concentration of microbial cells on a surrogate spacecraft surface. The model microbial community used in this study consists of 11 species of extremophiles present in spacecraft assembly clean rooms and represents spore-forming and non-spore-forming bacterial strains, an anaerobic archaeal strain, and a fungal strain. Additionally, the community organisms possess multiple survival characteristics, such as resistance to gamma and UV radiation, desiccation, and hydrogen peroxide. The model community was analyzed at 0 hours and subsequent time points for cultivability, viability, cell concentration, DNA concentration, and species richness. Stainless steel coupons were spiked with equal aliquots of the model community, dried, and then sampled at different time points using a variety of sampling devices (swabs, wipes, and macrofoam sponges) for comparison. Reaction mixtures extracted from each sampling device underwent the same downstream analysis as performed on the model community, specifically including colony/microscopic counts, ATP assay, a novel live-dead DNA intercalating dye analysis, rrn gene (16S and 18S) Q-PCR, and species-specific PCR. Results from this study will optimize current sampling and sample processing techniques while enabling planetary protection to obtain samples which are representative of spacecraft and associated surfaces. In addition to NASA astrobiology/planetary protection programs, the outcome of this research will be useful for the control of microbial contamination in the pharmaceutical, medical, and food processing industries where clean rooms are essential.

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ABSTRACT *[Presentation]*

Development of a Model Community to Evaluate Efficient Removal of Genetic Signatures from Spacecraft Surfaces: Issues Pertaining to Sampling, Sample Processing, and Analysis

La Duc, M. T., Kwan, K., Cooper, M., Stam, C., Vaishampayan, P., Scalzi, G., Benardini, J. N., Moissl, C., Andersen, G., Spry, J. A., and Venkateswaran, K.

Despite advances in the specificity and sensitivity of molecular biological technologies, the efficient recovery of DNA from low-biomass samples remains extremely challenging. Optimal methods to extract these biomolecules should 1) achieve the greatest total yield; 2) reflect comprehensive microbial diversity of the sampled environment; and 3) assert reproducible results. For an in-depth assessment of the wide spectrum of microorganisms present in the low-biomass spacecraft assembly clean room environment, technologies facilitating efficient collection, sample processing, and analysis are needed. To this end, a homogenous mixture of equal concentrations of 11 distinct microbial lineages having significant relevance to planetary protection (bacteria, archaea, and fungi; aerobes and anaerobes; cells and spores; rods and cocci) was prepared. Suitable aliquots of this "model" community were then characterized using a parallel set of downstream molecular analyses which revealed the level of microbial DNA, extracellular DNA, dissolved organic matter, and particulate non-microbial substances present in the community. Appropriate subsamples of this model community were dried on stainless steel metal surfaces, and procedures targeting the efficient removal and recovery of community member DNAs were evaluated. The collection and release of genetic materials from cotton and flocked nylon swabs were compared. Several automated nucleic acid extraction methods were assessed for both total DNA yield and conservation of microbial community structure. Universal small subunit rrn Q-PCR, species-specific Q-PCR, and DNA microarray methodologies were used in concert to estimate the recovery of both individual members, and the community as a whole. Results of this study will enable consideration of future planetary protection policy amendments based on modern molecular methods.

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ABSTRACT *[Poster]*

Efficient Removal of Genetic Materials from Low-Biomass Surfaces: Issues Pertaining to Sampling, Sample Processing, and Analysis

Kwan, K., Cooper, M., Stam, C., Vaishampayan, P., La Duc, M. T., Spry, J. A., and Venkateswaran, K.

For analysis of the complete spectrum of microbial diversity from low biomass surfaces, there is a general consensus that the target biomolecules are not being collected in great enough abundance for much of the downstream molecular processing and analysis to be robust and/or reproducible. Although theoretical calculations suggest detection of as low as one copy of a given target molecule to be possible, signal-to-noise ratios require that target molecules are present to in excess of 103 copy numbers (due for example to indigenous DNA contaminants in reagents and sampling materials). Hence our decision was made to concentrate samples (ca. 103 initial gene copies of the target per reaction) to reproducibly assess microbial diversity. Furthermore it is obvious that optimizing representative sample collection of biomolecules is critical and has not received enough attention. Research focused on improving detection limits of sample analyses were published but with insufficient emphasis on collection and processing of representative samples of biomolecules from low biomass environments. To understand the problems associated with sample collection, it needs to be appreciated that most of the previous studies were conducted concentrating on use of spores, with only a few additional studies using vegetative cells as target microbes. A comprehensive method for the culture and molecular-based evaluation of the effectiveness of the sampling for low-biomass surfaces using a model microbial community of vegetative cells and spores, and species representing all domains of life will be presented. Standardization and optimization of sample collection and processing biomolecules will be beneficial to the pharmaceutical, medical, semi-conductor, and aerospace industries in addition to other government agencies such as Homeland Security.

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Efficient removal of genetic materials from low-biomass surfaces: issues pertaining to sampling, sample processing, and analysis

K. Kwan[1], M. Cooper[1], C. Stam[1], P. Vaishampayan[1], G. Scalzi[1], J.N. Benardini[1], C. Moissl[2], G. Andersen[3], M.T. La Duc[1], J.A. Spry[1], and K. Venkateswaran[1]*

[1]Jet Propulsion Laboratory, California Institute of Technology, Pasadena, CA 91109, USA
[2]Institute for Microbiology, Regensburg University, Regensburg, 93053, Germany
[3]Center for Environmental Biotechnology, Lawrence Berkeley National Lab, Berkeley, CA 94720

Rationale | Process | Results

Assembly

Rationale

- Reliable cultivation- and molecular-based methods are needed to evaluate efficiency of sampling low-biomass environments.
- Microbial populations dominant on spacecraft and associated clean room surfaces served as a representative model community (MC).
- As the objective of this study was to evaluate sampling efficiency from low-biomass environments, a mere $1x10^5$ CFU/mL of each strain (11 strains in total) was included in the MC matrix.

Process

MC

1. *Aureobasidium pullulans* 28v1
2. *Acinetobacter radioresistens* 50V1
3. *Bacillus megaterium* KL-197
4. *Bacillus pumilus* SAFR-032
5. *Deinococcus radiodurans* R1
6. *Microbacterium imperiale* 47v1
7. *Staphylococcus warneri* 82-4
8. *Micrococcus luteus*
9. *Cupriavidus metallidurans* CH34
10. *Clostridium sporosphaeroides*
11. *Methanobacterium formicicum*

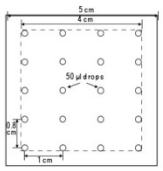
Results

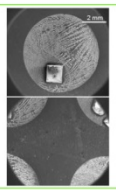
Doping

Rationale

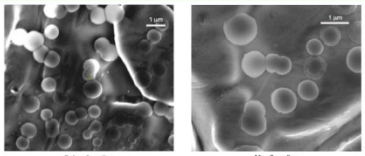
- Prior to deposition on stainless steel surfaces, MC samples were removed from PBS storage and re-suspended in water as to circumvent crystal formation.
- Model Community samples were then doped on precision-cleaned stainless steel surfaces via multi-channel manual pipetting.

Process





Results



Before Sampling | After Sampling

Both nylon-flocked and cotton swabs left behind detectable numbers of microbes on metal surfaces after sampling.

Sampling

Rationale

- Standardization and optimization of sample collection and processing of biomolecules in low-biomass environments must be investigated in further detail.
- NASA-approved standard sampling devices (used for culture-based analysis) and commercial kits were evaluated in this study.

Process

Cotton Swab

Biological Sampling Kit (BiSKit)

Nylon-Flocked Copan Swab

Polyester Wipe

Spacecraft and associated surface sampling

Results

Small surface area ($1x10^6$ cells; 25 cm^2): Cotton vs Copan (n=30)

- Cotton swabs were superior (~8-fold) in removing 16S rRNA gene copies from the stainless steel surfaces than Nylon flocked swabs.
  - Cotton: 32.80% recovery
  - Nylon-Flocked Copan swabs: 4.29% recovery
- Nylon-Flocked Copan swabs (n=30) yielded fewer outliers than Cotton swabs

vs.

Larger surface area ($1x10^6$ cells; 250 cm^2): BiSKit vs Wipes (n=21)

- Two-fold higher recovery of biomolecules by BiSKits than polyester wipes.
  - BiSKits: 41.91% recovery
  - Polyester wipe: 26.69% recovery
- Blank values for Nylon-flocked and BiSKits both revealed a signal-to-noise ratio near or below 1 (0.57 and 1.10 respectively), indicating a high level of indigenous DNA associated with the sampling devices.

vs.

Conc.

Rationale

- To measure the complete spectrum of microbial diversity from low biomass surfaces, target biomolecules must first be concentrated in great enough abundance to render downstream molecular analyses significant and reproducible.

Process

Extracted sample

Amicon 50 kDa cut-off Filter

Spin for 15 minutes at 4000rpm

Results

- Amicon filters can withstand 3 centrifuge spins and the design of Amicon filter allows to release trapped DNA effectively.
- Recovery rate of 63% after filtration.
- This concentration step has aided in processing large volumes of samples (~45 mL).

Extraction

Rationale

- Samples underwent bead-beating protocols prior to DNA extraction to significantly increase DNA recovery efficiency.
- To account for maximum diversity, portions of each sample were subjected to DNA extraction sans bead-beating and later combined with the bead-beaten portion.

Process

Maxwell 16 Automated DNA extraction

Extracted DNA

Archive -80°C

Analysis

Results

Previous analysis of methods for the purification of DNA from low-biomass samples reveal that the percentage of DNA amplifiable by PCR based on the DNA extraction method is:

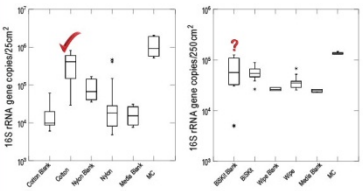
- Manual (Promega Wizard kit): 75%
- Manual (MoBio Ultraclean methods): 63%
- Automated DNA extraction: 90%

La Duc, M. T., D. Osman, et al. (2009). "COMPARATIVE ANALYSIS OF METHODS FOR THE PURIFICATION OF DNA FROM LOW-BIOMASS SAMPLES BASED ON TOTAL YIELD AND CONSERVED MICROBIAL DIVERSITY." Journal of Rapid Methods & Automation in Microbiology 17(3): 350-366.

Analysis

Rationale

- Signal-to-noise ratios demand that target molecules exist in excess of 10^3 copy numbers (due to indigenous DNA in reagents and sampling materials).
- While in theory, a single DNA molecule should suffice, efforts were made to concentrate samples (ca. 10^3 initial gene copies of the target per reaction) to reproducibly assess microbial diversity.



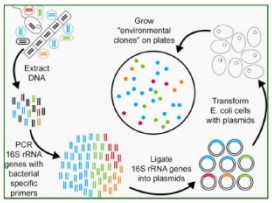
Process

qPCR analysis

TGA AGC ACT TGA GAA ATT
TGC TGC AAA GAA AAT

Species Specific PCR - ssPCR

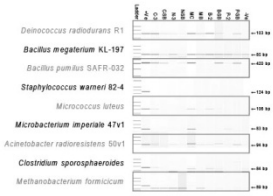
PhyloChip DNA Microarray



Cloning of amplified PCR products

Results

- CFU: Three-logs reduction in cultivability after 16-days at -80°C.
- Cell concentration, as determined by microscopy counts, remained above 10^6 cells/mL for all time points (90 d) analyzed.
- "As-is" samples have the highest 16S *rrn* copy number yield 72 hrs - 90 days of storage, and are recommended as the storage method for the model community.
- Freeze-thaw (at -80°C) may be the reason why high DNA yield is noticed from 72 hours onwards.
- 10 out of 11 species are optimized for ssPCR.
- PhyloChip and cloning methodologies are being used to validate the species specific primers and PCR conditions.



Disclaimer: NASA does not endorse the products listed in this poster
Part of the research described in this poster was carried out by the Jet Propulsion Laboratory, California Institute of Technology, under contract with the National Aeronautics and Space Administration.

ABSTRACT *[Poster]*

Species-Specific qPCR Analysis of Recovery Efficiency and Indigenous Contaminants Associated with Various Sampling Matrices

Kwan, K., La Duc, M.T., Bargoma, E., Cooper, M., Vaishampayan, P., and Venkateswaran, K.

To better understand the limitations and challenges of measuring microbial burden in low-biomass environments, standard techniques for sample acquisition and downstream processing were evaluated to examine the efficacy, in depth, of processing techniques and numerous sampling devices (cotton and nylon-flocked swabs, polyester wipes, and macrofoam biological sampling kits). The control sample, Model Microbial Community (MMC), consisted of a predetermined and well established cell/spore density. MMC constituents are 11 distinct species of extremotolerant bacteria, archaea, and fungi. The recovery of each MMC constituent was assayed via species-specific quantitative PCR (ss-qPCR). Designed and synthesized oligonucleotide DNA primers of specific sequence homology to the rRNA genes of each MMC constituent. After exhaustive trial-and-error experimentation, ss-qPCR thermal cycling parameters were optimized for each MMC-constituent species. Experiments were devised to examine and quantify the levels of contaminant, indigenous DNA molecules associated with the various reagents used and sampling materials tested. This provided a more thorough understanding of the sensitivity of each sampling device in recovering microbes from surfaces.

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Species-Specific qPCR Analysis of Recovery Efficiency and Indigenous Contaminants Associated with Various Sampling Matrices

K. Kwan, M.T. La Duc, E. Bargoma, M. Cooper, P. Vaishampayan, and K. Venkateswaran*

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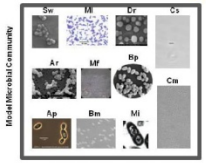
Abstract

- **Objectives**:
  - To better understand the limitations and challenges of measuring microbial burden in low-biomass environments, standard techniques for sample acquisition and downstream processing were evaluated.
  - To examine the efficacy, in depth, of processing techniques and numerous sampling devices (cotton and nylon-flocked swabs, polyester wipes, and macrofoam biological sampling kits).
- **Methods**:
  - The control sample, Model Microbial Community (MMC), consisted of a predetermined and well established cell/spore density
    - MMC constituents are 11 distinct species of extremotolerant bacteria, archaea, and fungi .
  - The recovery of each MMC constituent was assayed via species-specific quantitative PCR (ss-qPCR).
    - Designed and synthesized oligonucleotide DNA primers of specific sequence homology to the rRNA genes of each MMC constituent.
- **Results**:
  - After exhaustive trial-and-error experimentation, ss-qPCR thermal cycling parameters were optimized for each MMC-constituent species.
  - Experiments were devised to examine and quantify the levels of contaminant, indigenous DNA, molecules associated with the various reagents used and sampling materials tested.
    - This provided a more thorough understanding of the sensitivity of each sampling device in recovering microbes from surfaces.

Methods



I. **Model Microbial Community Preparation:**
- Mixed in equal concentrations
- Stored (at -80C) in 1.2 mL aliquots of PBS cell suspension.

II. **Deposition onto Stainless Steel Surfaces:**

- MMC aliquots were manually deposited onto several replicates of stainless steel coupons (25cm²) and sheets (2,500cm²).
- Allowed to dry at RT for 24 hours.

III. **Sampling (Kwan et al., 2011):**
- MMC-deposited steel coupons were sampled with Puritan cotton and Copan Diagnostics nylon-flocked swabs.
- MMC-deposited steel sheets were sampled with ITW Texwipe polyester wipes and QuickSilver Analytics biological sampling kits (BiSKits).

IV. **Sample Processing:**
- 3 extractions per sampling device, including: vortex mixing and sonication (swabs and polyester wipes), or manual extraction (BiSKits).
- Extraction fluids concentrated via Amicon 50kDa centrifugal filter.
- Extraction fluids resuspended in 500 uL PBS.
- Half volume of each sample extract subjected to bead-beating.
- DNA extraction with Maxwell-16 purification kit and system.
- Sample analysis via Species-specific PCR and qPCR.

Conclusions

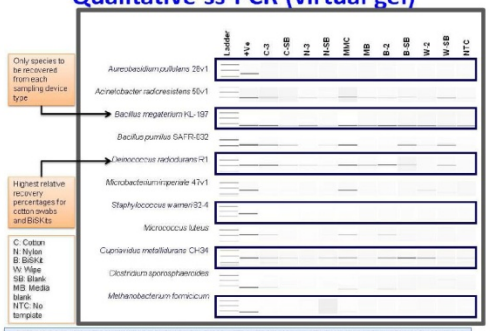
- Due to overwhelming inherent bias and limitations in sensitivity, traditional, cultivation-dependent methodologies are not ideal for testing sample acquisition and processing technologies. Rather, molecular techniques proved more valuable for accomplishing this goal.
- Measuring total microbial burden using molecular methods was complicated by the presence of indigenous DNA in each sterile sampling device.
- Once optimized, species-specific PCR proved invaluable in assessing the differential recovery of MMC-constituents by the various sampling matrices tested.
- Such analyses also provided a more comprehensive understanding of the background levels of contaminant DNA associated with each sampling device.
- The findings of this study help drive, and lend credence and support to, ongoing policy- and decision-making with regards to the optimal manner in which to collect and process samples such that they more accurately represent the true microbial phylogenetic breadth housed on spacecraft and associated surfaces.
- Research of this nature will prove valuable in devising superior methods of controlling microbial contamination in pharmaceutical, medical, food processing, and other cleanroom-dependent industries.

Limits of detection of ss-PCR for model community constituents

	Microbes	Presence of amplicons when initial inoculum (cells or spores/mL) was:						Detection Limit[2]
		10^{6}	10^{5}	10^{4}	10^{3}	10^{2}	10^{1}	
Ap	*Aureobasidium pullulans 25v1*	+						9.0×10^{6}
Ar	*Acinetobacter radioresistens 50v1*	+	+	+	+			3.4×10^{3}
Bm	*Bacillus megaterium KL-197*	+	+	+	+	+		2.1×10^{3}
Bp	*Bacillus pumilus SAFR-032 spores*	+	+	+	+	+	+	4.6×10^{3}
Dr	*Deinococcus radiodurans ATCC 13939*	+	+	+				1.6×10^{4}
Mi	*Microbacterium imperiale 47v1*	+	+	+	+			5.6×10^{3}
Sw	*Staphylococcus warneri 82-4*	+	+	+				4.3×10^{4}
Ml	*Micrococcus luteus ATCC 4698*	+	+	+				4.5×10^{4}
Cm	*Cupriavidus metallidurans CH34*	+	+	+	+			4.7×10^{3}
Cs	*Clostridium sporosphaeroides DSM1294*[3]	+	+					7.7×10^{6}
Mf	*Methanobacterium formicicum DSM11535*[3]	+	+					1.4×10^{6}

[1]Number of cells was determined via microscopic counts. After serially diluted, DNA from the reaction mixtures was extracted.
[2]The PCR set was scored positive (+) when the amplified products were ≥0.25 ng/µL, as quantified by Bioanalyzer.
[3]DNA, instead of whole cells, was serially diluted for these strains.

Qualitative ss-PCR (virtual gel)



Gels showing relative band intensities and semi-quantitative recovery percentages using Bioanalyzer-calculated DNA concentrations (>0.25ng is scored as positive) were used to compare the relative abundance of each species present in each sample.

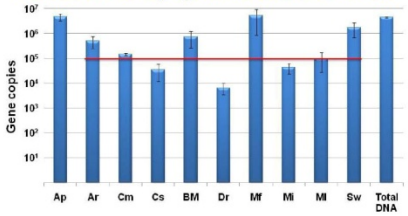
Presence/absence of specific MMC constituents using ss-PCR

Presence/absence of microbes after sampling by various matrices

Microbes[1]	Limit of Detection 16S rRNA copies	Cotton swab replicates	Nylon flocked swab replicates	BiSKit replicates	Polyester wipe replicates
		C1 C2 C3 C4 C5 C6 C7	N1 N2 N3 N4 N5 N6 N7	B1 B2 B3 B4 B5 B6 B7	W1 W2 W3 W4 W5 W6 W7
Optimization of uPCR for *Aureobasidium pullulans* primer/probe development	5.00×10^{6}	51 positive for cotton	57 positive for nylon	45 positive for BiSKit	51 positive for wipes
Acinetobacter radioresistens 50v1	3.40×10^{3}	+ + + + + + +	+ + + + + + +	+ + + + + + +	+ + + + + + +
Bacillus megaterium KL-197	2.00×10^{3}	+ + + + + + +	+ + + + + + +	+ + + + + + +	+ + + + + + +
Bacillus pumilus SAFR-032	4.60×10^{3}	+ + + + + + +	+ + + + + + +	+ + + + + + +	+ + + + + + +
Deinococcus radiodurans ATCC 13939	1.60×10^{4}	+ + + + + + +	+ + + + + + +	+ + + + + + +	+ + + + + + +
Microbacterium imperiale 47v1	5.60×10^{3}	+ + + + + + +	+ + + + + + +	+ + + + + + +	+ + + + + + +
Optimization of uPCR for *Staphylococcus warneri* primer/probe development	4.25×10^{4}				
Micrococcus luteus ATCC 4698	4.40×10^{4}	+ + + +	+ + + + + + +	+ + + + + + +	+ + + + + + +
Cupriavidus metallidurans CH34	4.67×10^{3}	+ + + + + + +	+ + + + + + +	+ + + + + + +	+ + + + + + +
Clostridium sporosphaeroides DSM1294	7.60×10^{6}	+ + + + + + +	+ + + + + + +	+ + + + + + +	
Methanobacterium formicicum DSM1535	1.40×10^{6}	+		+	

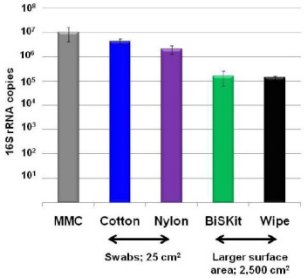
[1]*A. pullulans* and *S. warneri* were not detected in any of the sampling materials.
[2]The PCR set was scored positive (+) when the amplified products were ≥0.25 ng/µL, as quantified by Bioanalyzer.

Abundance of MMC constituents as measured by quantitative ss-PCR



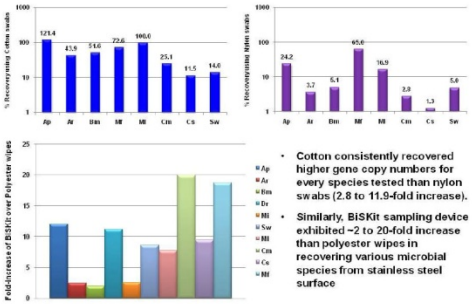
- *A. pullulans* was measured using rRNA ITS region
- All other 10 members of bacteria or archaea were mixed in equal concentrations (1.0 x 10^{5} cells or spores; red line). However, the 16S rRNA copy numbers vary between each species.

Recovery of *Staphylococcus warneri* as measured by quantitative ss-PCR



- Quantitative ss-PCR conditions were standardized for 10 out of 11 constituents of MMC (except for *B. pumilus*)
- Quantitative ss-PCR revealed that the sampling devices were devoid of MMC constituents.

Recovery of Various Species



- Cotton consistently recovered higher gene copy numbers for every species tested than nylon swabs (2.8 to 11.9-fold increase).
- Similarly, BiSKit sampling device exhibited ~2 to 20-fold increase than polyester wipes in recovering various microbial species from stainless steel surface

The research described herein was carried out at the Jet Propulsion Laboratory, California Institute of Technology, under a contract with the National Aeronautics and Space Administration.

ABSTRACT *[Poster]*

Comparative Analyses of Molecular Approaches and a NASA Standard Spore Assay in Assessing the Cleanliness of Spacecraft

Cooper, M., La Duc, M.T., Probst, A., Vaishampayan, P., Stam, C., Benardini, J. B., Piceno, Y.M., Andersen, G.L., and Venkateswaran, K.

While it is illogical to gauge the relative cleanliness of a spacecraft, which is almost entirely dependent on associated microbial abundance and diversity, on spore-counts resulting from selective assays alone. It is equally unrealistic to assess the risk of forward contamination by DNA-based molecular methods alone without an indication of who is alive (and who is dead). Both assays are necessary and complimentary. Whereas NASA standard spore assays are extremely limited in sensitivity and detection of phylogenetic breadth, PhyloChip DNA microarrays are able to provide detailed information on microbial diversity and composition, and can detect the presence of low-abundance and even singleton taxa. In this study, the relative cleanliness of spacecraft surfaces, in the context of bacterial abundance and diversity, was assessed by both a NASA standard bacterial spore assay and PhyloChip G3 molecular DNA microarray.

Samples were collected using Texwipe TX1009 polyester wipes and were rinsed as per the NASA sampling protocol (1). Aliquots were divided into portions which were plated and those subjected to downstream DNA-based analyses. Details concerning PhyloChip G3 target fragmentation, biotin labeling, PhyloChip hybridization, and more are given in Hazen et al.

Approximately 60% of the samples analyzed via standard spore assays failed to yield any detectable spore counts, whereas PhyloChip G3 DNA microarrays resolved the genetic signatures of more than 100 distinct microbial phylotypes in the very same samples. Furthermore, samples that yielded a greater abundance of cultivable spores were not necessarily richer in microbial diversity, as might have been expected. Gammaproteobacteria was the most prevalent phylum (2,081 OTUs) encountered from spacecraft surfaces. The presence of Firmicutes (20% of the subfamilies detected) and Actinobacterial (11%) OTUs supports earlier hypotheses which posit that the primary source of contamination of spacecraft assembly cleanrooms is humans and the exterior environment. Based on the findings of this study, it is clear that molecular techniques such as DNA microarrays can and should be coupled with traditional culture-based methods to more accurately assess the relative cleanliness of spacecraft surfaces.

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Comparative Analyses of Molecular Approaches and a NASA Standard Spore Assay in Assessing the Cleanliness of Spacecraft Surfaces

M. Cooper[1], M.T. La Duc[1], Alexander Probst[1], P. Vaishampayan[1], C. Stam[1], J.N. Benardini[1], Y. M. Piceno[2], G. Andersen[2], and K. Venkateswaran[1]

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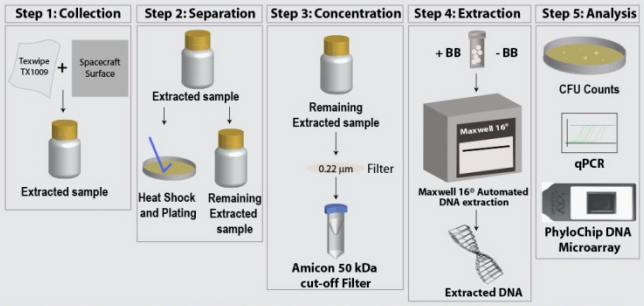
Background

- Standards have been established which attempt to monitor and limit the microbial population introduced by contamination sources such as un-gloved hands(1-3), water(4-5), cosmetics(6), and air(7).
- NASA monitors the microbial bioburden of spacecraft to limit the transfer of terrestrial microorganisms to other planetary bodies (forward contamination) where life may exist.
- The standard practice of evaluating microbial quality of spacecraft surfaces is the NASA standard spore assay (8).
- The use of a spore-selective assay alone is not a realistic way to assess the risk of forward contamination, as they are extremely limited in sensitivity and detection of phylogenetic breadth.
- The PhyloChip DNA microarrays are able to provide detailed information on microbial diversity and composition for low-abundance and even singleton taxa.
- In this study, the relative cleanliness of spacecraft surfaces, in the context of bacterial abundance and diversity, was assessed by both a NASA standard bacterial spore assay and PhyloChip G3 molecular DNA microarray.

Methods

- Samples were collected using Texwipe TX1009 polyester wipes and were rinsed as per the NASA sampling protocol (11).
- Aliquots were divided into portions which were plated and those subjected to downstream DNA-based analyses.



- Details concerning PhyloChip G3 target fragmentation, biotin labeling, PhyloChip hybridization, and more are given in Hazen et al. (13).

Results and Discussion

- Samples were pooled and labled based on the spore counts resulting from the standard spore assay. Results were grouped by category: Cat A: 0 spores; Cat B: 1-50 spores; Cat C: >50 spores; and Blank: experimental control.

Table 1. Categorical grouping of spacecraft samples based on spore population, as determined by the NASA Standard Spore Assay (8).

Sample		Sampling category	No. of wipes pooled	Total surface area sampled [m^2]	Total spore count/m^2	Total 16s rRNA gene copies/m^2	16S rRNA amplicons used in the DNA microarray analyses whose: initial concentration [ng/µL]	mass added to the PhyloChip [ng]
Cat A								
	GI-15	S	9	5.7	0	$4.56x10^8$	468	350
	GI-16	S	6	4.2	0	$2.74x10^5$	BDL	NMA
	GI-17	S	10	7	0	$2.94x10^6$	188.2	350
	GI-25	S	8	7	0	$1.64x10^5$	7.4	281
	GI-26	S	7	3.9	0	$3.69x10^5$	24.8	350
	GI-27	S	4	7.8	0	BDL	4.8	183
	GI-28	S	6	3.3	0	BDL	3.7	141
	GI-b	NC	14	0	0	$1.02x10^6$	BDL	NMA
Cat B								
	GI-18b	HC	3	0		BDL	BDL	NMA
	GI-18	S	10	8.5	1.2	BDL	BDL	NMA
	GI-19b	HC	3	0		BDL	BDL	NMA
	GI-19	S	14	9.9	2.8	$1.22x10^5$	17.5	350
	GI-20b	HC	1	0		BDL	3.8	144
	GI-20	S	5	3.4	10.3	BDL	6.7	256
	GI-21	S	4	2.8	15.7	$8.86x10^5$	39.8	350
	GI-22	S	1	0.7	45.7	BDL	BDL	NMA
Cat C								
	GI-23	S	1	0.7	84.3	$6.70x10^7$	548.4	350
	GI-24	S	1	0.7	215.7	$5.13x10^6$	36.1	350

Abbreviations: NC-negative control, S- spacecraft surfaces, and HC-handling control, BDL- below detection limit, NMA-no measured amplicon but the products were processed for PhyloChip analysis

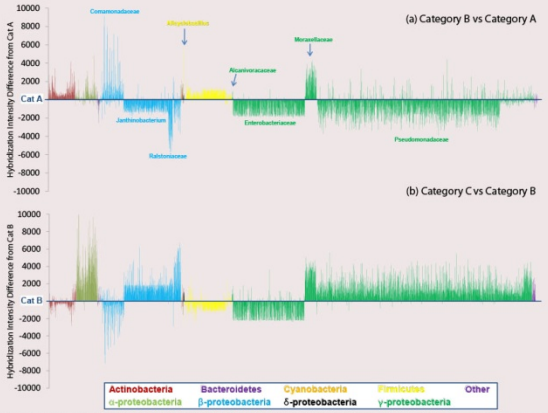


Fig. 1. PhyloChip analysis of hybridization intensity difference of the three spore abundance categories. (a) Hybridization intensity difference of at B (1-50 spores) compared to Cat A (0 spores). (b) Hybridization intensity difference of Cat C (>50 spores) compared to Cat B. Bars above the zero line represent bacteria that increased in abundance relative to Cat A and Cat B for Fig. 1a and Fig. 1b, respectively; bars below represent those bacterial DNAs that declined in abundance.

- Approximately 60% of the samples analyzed via standard spore assays failed to yield any detectable spore counts, whereas PhyloChip G3 DNA microarrays resolved the genetic signatures of more than 100 distinct microbial phylotypes in the very same samples.
- Furthermore, samples that yielded a greater abundance of cultivable spores were not necessarily richer in microbial diversity.
- Gammaproteobacteria was the most prevalent phylum (2,081 OTUs) encountered from spacecraft surfaces.
- The presence of Firmicutes (20% of the subfamilies detected) and Actinobacterial (11%) OTUs supports earlier hypotheses which posit that the primary source of contamination of spacecraft assembly cleanrooms is humans and the exterior environment.

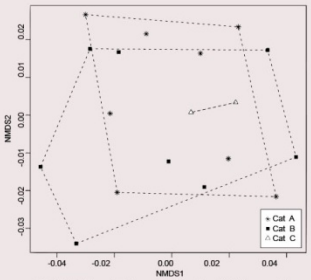


Fig. 2. NMDS analysis based on Bray Curtis distcance of abundance values reveal the spore categorical groupings are from a similar community structure.

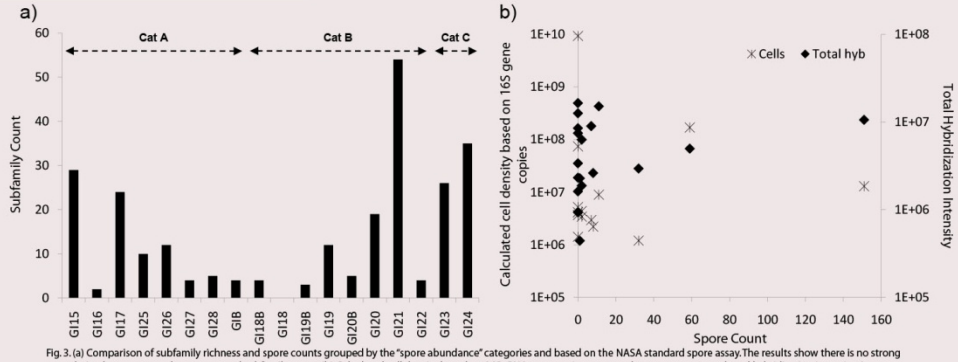


Fig. 3. (a) Comparison of subfamily richness and spore counts grouped by the "spore abundance" categories and based on the NASA standard spore assay. The results show there is no strong correlation between sample category and subfamily count. (b) Calculated cell density based on 16S rRNA gene copies compared to spore counts and total hybridization intensity. Average 16S rRNA gene copies are 3.6 per cell (14). Gene copies correlate similarly to hybridization intensities but show no correlation to spore counts.

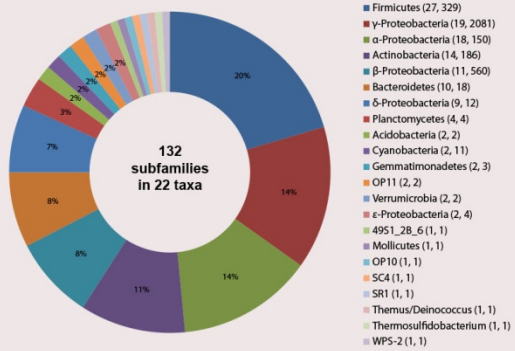


Fig. 4. Overall microbial diversity grouped by taxa. Number of subfamilies and OTUs detected per taxon are given in the parenthesis. Percentages lower than 2% are not displayed.

Conclusions

- The NASA Standard Spore Assay is a helpful tool to assess the level of compliance to the planetary protection and COSPAR regulations; however, it lacks the ability to fully assess the level of microbial diversity.
- Although current standards are set based on the spore population, there are many hardy vegetative microorganisms known to resist the harsh conditions of space (vacuum, cosmic radiation, extreme temperature fluctuations, etc.)
- Based on the findings of this study, it is clear that molecular techniques such as DNA microarrays can and should be used in tandem with traditional culture-based methods to more accurately assess the relative cleanliness of spacecraft surfaces and forward contamination risk.

Part of the research described in this poster was carried out by the Jet Propulsion Laboratory, California Institute of Technology, under contract with the National Aeronautics and Space Administration.

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ABSTRACT *[Presentation]*

Methods in Planetary Protection—A Tightrope Walk

Probst, A., Cooper, M., Venkateswaran, K., Andersen, G., and Moissl-Eichinger, C.

Spacecraft sent to foreign celestial bodies are assembled in clean rooms and undergo regular decontamination and cleanliness control to ensure the scientific integrity of present and future life detection missions. Since the early 70s the bioburden of a spacecraft and its surrounding clean room environment has been controlled by culturing heterotrophic, mesophilic and aerobic spore formers. However, space agency's protocols have not significantly changed until today, although very recent approaches have shown the availability of much more efficient methods—for sampling, detection and cultivation. Hence, the European Space Agency has recently evaluated a novel nylon-flocked-swab protocol for recovery of spores from spacecraft surfaces and proven its superiority over the NASA standard cotton-swab assay (Probst et al 2010a). Furthermore, our group was able to show that the recovery of spores is strongly affected by the porosity of the spacecraft material sampled, which can pose a threat to the cleanliness control of space missions (Probst et al 2011). Nevertheless, other non-spore forming microbes have also been demonstrated highly resistant and must be considered when estimating planetary protection risk (La Duc et al 2007). In the wide field of microbial ecology, however, much more sensitive methods have been developed detecting molecular signatures of microorganisms. Although most of these methods require higher amounts of biomass (e.g. proteomics, metatranscriptomics), some DNA-based methods have increased our knowledge about the microorganisms associated with spacecraft related surfaces. One standard method for detection of 16S rRNA genes is the generation of clone libraries and sequencing of hundreds of clones. This method gives scientist the opportunity to reconstruct the phylogeny of detected microorganisms and estimate their diversity. Nevertheless, much more sensitive methodologies have been designed in recent times: Partial Ribosomal Amplification and Pyrosequencing (PRAP) and 16S rDNA based microarrays, so called PhyloChips. While no study has appeared to elucidate the potential of PRAP to clean room diversity, the latter has resulted in many high quality publications demonstrating it a powerful tool. Interestingly, when comparing the NASA standard assay and the PhyloChip G3 technology as well as qPCR data, no correlation of spore counts with diversity or abundance of microbes could be found. This emphasizes that standard cultivation methods are unfeasible to estimate the cleanliness of a spacecraft (Cooper et al submitted). Extraordinary cultivation methods have, however, shown the presence of (strictly) anaerobic but also autotrophic bacteria in clean rooms and provide access to study isolates, their resistances and estimate their risk for planetary protection considerations (Probst et al 2010b, Stieglmeier et al 2009). This talk will give a short but comprehensive overview of the advantages and disadvantages of the current methods used in the field of planetary protection that necessitate attention and discussion among the scientific community.

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ABSTRACT *[Poster]*

Greengenes 16S Ribosomal RNA Gene Database Update for 2011—HMP Reference Sets and Tools

DeSantis, T., Singh, N., Andersen, G., Werner, J., Koren, M., Ley, R., McDonald, D., Knight, R., Probst, A., Kelly, S., Venkateswaran, K., White, O., Pei, Z., and Hugenholtz, P.

Due to global interest in the human microbiome's role in health and disease, a diverse community of international researchers from the medical, microbiological and computational fields have recently converged to address questions in microbial ecology. Activities such as describing community structure, portraying population dynamics, and depicting diagnostic test candidates all benefit from mapping assay data to high-quality reference sets with useful nomenclature. In popular workflows, ribosomal gene segments are hybridized to probes or sequenced with NGS technology. Annotating the matches to both cultured and vetted uncultured clades reveals trends overlooked by sole reliance on cultured references. The 2011 Greengenes 16S rRNA Taxonomy was created from Infernal-improved NAST alignments, FastTree-validated tree topology, nomenclature reconciliation with NCBI for cultured strains, and manual curation of thousands of yet-to-be cultured groups. The effort resulted in standardized or proposed names for >4000 hierarchical taxonomic nodes. From these relations, existing datasets from 454 (Roche), HiSeq (Illumina), and PhyloChip Assay (Second Genome) and expected datasets from PGM (Ion Torrent) and PacBioRS (Pacific Biosciences) have the opportunity to be compared. Files are available for download in their complete forms as well as subsets suitable for metagenomic pipeline tools. Furthermore, a chromatogram processing and capture tool has been established those desiring to contribute to future reference sets. The Greengenes database is supported by grant UH3CA140233 from HMP of the NIH Roadmap Initiative and National Cancer Institute and NIH common fund contract U01-HG004866, a Data Analysis and Coordination Center for the Human Microbiome Project.

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Greengenes 16S Ribosomal RNA Gene Database Update For 2011 HMP Reference Sets And Tools

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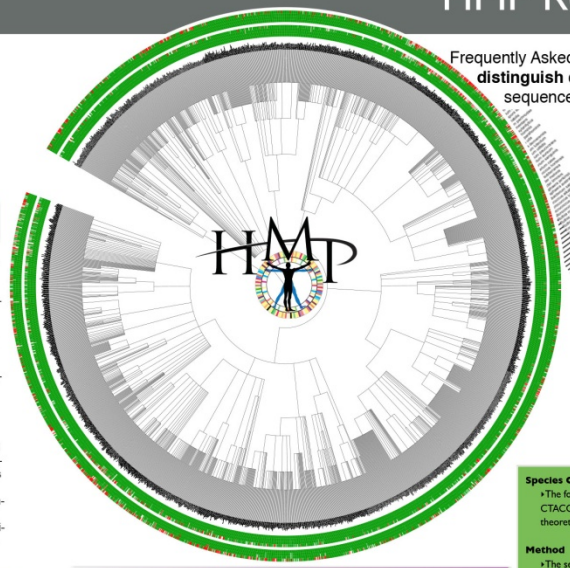
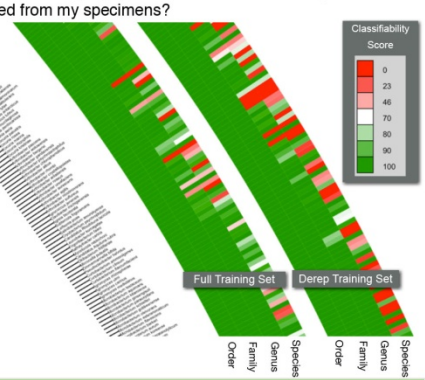


Frequently Asked Question: "Which **species** should I expect to **confidently distinguish** considering **my** subsection of the 16S rRNA gene sequenced from my specimens?



ABSTRACT

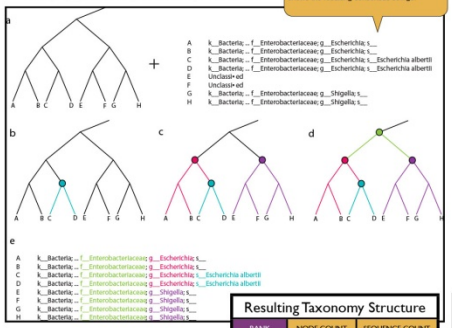
Due to global interest in the human microbiome's role in health and disease, a diverse community of international researchers from the medical, microbiological and computational fields have recently converged to address questions in microbial ecology. Activities such as describing community structure, portraying population dynamics, and depicting diagnostic test candidates all benefit from mapping assay data to high-quality reference sets with useful nomenclature. In popular workflows, ribosomal gene segments are hybridized to probes or sequenced with NGS technology. Annotating the matches to both cultured and vetted uncultured clades reveals trends overlooked by sole reliance on cultured references. The 2011 Greengenes 16S rRNA Taxonomy was created from Infernal-improved NAST alignments, FastTree-validated tree topology, nomenclature reconciliation with NCBI for cultured strains, and manual curation of thousands of yet-to-be cultured groups. The effort resulted in standardized or proposed names for >4000 hierarchical taxonomic nodes. From these relations, existing datasets from 454 (Roche), HiSeq (Illumina), and PhyloChip Assay (Second Genome) and expected datasets from PGM (Ion Torrent) and PacBioRS (Pacific Biosciences) have the opportunity to be compared. Files are available for download in their complete forms as well as subsets suitable for metagenomic pipeline tools. Furthermore, a chromatogram processing and capture tool has been established those desiring to contribute to future reference sets. The Greengenes database is supported by grant UH3CA140233 from HMP of the NIH Roadmap Initiative and National Cancer Institute and NIH common fund contract U01-HG004866, a Data Analysis and Coordination Center for the Human Microbiome Project.

NOVEL TREE - RICH TAXONOMY

- **Methods**
- Infernal alignment of full length sequences (Nawrocki, 2010)
- Hypervariable lane mask (Lane, 1991)
- Uchime chimera filter (Edgar, 2010)
- Chimera Slayer chimera filter (Haas, submitted)
- Dual Study Heuristic filter
- FastTree de-novo tree construction from 407K seqs (Price, 2010)
- tax2tree node re-mapping (McDonald, in prep)
  - nomenclature mapping from NCBI
  - nomenclature mapping from Greengenes
  - Precision/Recall name conflict resolution
  - Back-filling classifier for unnamed nodes
  - Back-propagation to collapse redundantly named nodes

Overview of the tax2tree workflow. Panel a: Inputs are a phylogenetic tree + taxonomy strings for some (or all) of the tips in the tree including two Unclassified tips (E,F). The taxonomy mapping can optionally have rank abbreviations already appended on (k__, p__, etc. .). Note, the consensus strings are shortened (...) for brevity.

Panels b, c, and d: Assignment of species, genus and family nodes, respectively. When decorating genus, we are able to infer in this case that tips E and F are under g__Shigella as the lowest common ancestor with tips G and H has >= 50% relative abundance of the genus name. Panel e) shows the resulting consensus strings.



Resulting Taxonomy Structure

RANK	NODE COUNT	SEQUENCE COUNT
Kingdom	2	407K
Phylum	90	407K
Class	179	407K
Order	253	402K
Family	460	395K
Genus	1365	314K
Species	2488	112K

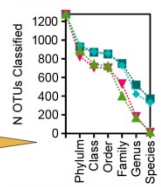
Examples of important nomenclature updates:

Anaerocellum_thermophilum	=>	*Caldicellulosiruptor bescii*
Brevibacterium stationis	=>	*Corynebacterium stationis*
Desulfomicrobium terraneus	=>	*Desulfomicrobium thermophilum*
Marinibacillus marinus	=>	*Jeotgalibacillus marinus*
Clostridium orbiscindens	=>	*Flavonifractor plautii*
Thermoanaerobacter tengcongensis	=>	*Caldanaerobacter subterraneus*
Rhodoferax ferrireducens	=>	*Albidiferax ferrireducens*
Vibrio fischeri	=>	*Aliivibrio fischeri*

CLASSIFIABILITY

- **Test by classifying 1,200 sequence clusters from human feces against GG and other reference sets.**
- 407K GG reference sequences
  - Derep at 99 or 91.3
  - Trim to amplicon span
  - Train Bayesian classifier
  - Compare number of pyrosequenced OTUs classified at each rank against using GG or other reference sets.

New Greengenes taxonomy allows taxonomic nomenclature to be applied to a significantly greater number of NGS sequences.



Species Classifiability Example

- The foregut microbiome amplicon of interest is 347F (5'-GGAGGCAGCAGTRRGGAAT) to 803R (5'-CTACCRGGGTATCTAATCC) (Nossa, 2010). For each known bacterial species, how confidently could the theoretical amplicon distinguish it from all other nodes (named or not).

Method

- The search pattern, GGAGGCAGCAGTRRGGAATJGGATTAGATACCCYGGTAG, was used in conjunction to the greengenes online sub-alignement locator (http://greengenes.lbl.gov/cgi-bin/nph-probe_locator.cgi) to determine the coordinates of the theoretical amplicon at position 1882 to 4081 (inclusive of both primers). A subsequence from 1917 to 4048 gathers all the DNA sequence exclusive of the primers.
- 407K sub-sequences were obtained.
  - http://greengenes.lbl.gov/Download/Sequence_Data/Fasta_data_files/
    - 347to803_gz_norm_unaligned.fasta.gz
- Train the Mothur (Schloss, 2009) classifier using all 407K sequences (Full Training Set) or a non-redundant set of 176K sequences (Derep Training Set).
- 2. Classify each sequence from the training set and record the confidence at each taxonomic rank.
- Find average "classifiability" for each node as the mean confidence of classification to that node divided by the set of sequences *belonging* to that node.
- Plot the classifiability of the named species as a heat map using ITOL (Letunic, 2006).

Observations

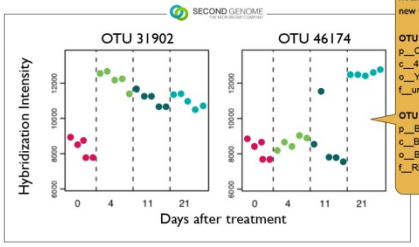
- Family-level classification was highly confident throughout the tree.
- Genus and species level confidence is dependent on the genus and species.
- Confidence was greater using the Full Training Set compared to the Derep Training Set.

For Further Discussion

- Within the trained model the count of taxonomy-by-word intersections will not differ across the two methods but the priors will change.
- More redundant sequences in one node than another affects the model's view of the distribution of a given 8mer across taxonomic nodes.

PHYLOCHIP™ ASSAY ANNOTATION

- **New Greengenes taxonomy facilitates PhyloChip results annotation.**
- 1,016,064 probes
- 59K OTUs, each tracked with multiple probe pairs
- Overcomes sampling effort problem encountered with NGS approaches
  - typical 16S rRNA gene PCR yields 500 to 1,000 ng in a 20 uL volume
    - 1500bp @ 660 g/mole/bp ➡ 5E-14 moles / uL ➡ 3E+10 molecules /uL ➡ 6E+11 total sequences ➡ 600 billion sequences per PCR sample
  - How many should we observe? 600? 60,000 (1 out of every 10 million)?
- Hybridize them all on to a PhyloChip ...
  - Dominant populations do not occlude minority populations



Example output from a PhyloChip (Second Genome, Inc.) experiment tracking bacterial population dynamics in hindgut for 21 days after a specific medical treatment. OTU annotations are mapped from the new Greengenes taxonomy:

OTU 31902:
p__Cyanobacteria;
c__4C0d-2;
o__YS2;
f__unclassified

OTU 46174:
p__Bacteroidetes;
c__Bacteroidia;
o__Bacteroidales;
f__Rikinellaceae;

GREENGENES SUBSETS

- All named isolates
- All HMP Genome Strains
- Knight, Caporaso: QIIME-ready reference sets
- Current aligned Core Set for NAST templates
  - 36,550 genes represents the known 16S diversity.
- Older Core Sets
- VISIT: http://greengenes.lbl.gov/Download/Sequence_Data/Fasta_data_files

GENOMES QC

Contigs from genome projects finished or unfinished can be quality filtered using the Greengenes Core Set. Surprisingly over 50 genomes contain zero full-length16S rRNA genes. Finishing effort will be needed to assemble 16S genes in these projects for use as references for future trees.

ACKNOWLEDGMENTS

This study was supported in part by grant UH2/UH3CA140233 from the Human Microbiome Project of the NIH Roadmap Initiative and National Cancer Institute and by NIH common fund contract U01-HG004866, a Data Analysis and Coordination Center for the Human Microbiome Project. Work performed at Lawrence Berkeley National Laboratory is under the U.S. Department of Energy contract number DE-AC02-05CH11231. Manual taxonomic nomenclature verification was supported in part by Second Genome, Inc (San Francisco, CA)

SECOND GENOME THE MICROBIOME COMPANY

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ABSTRACT *[Poster]*

Species-Specific qPCR to Assess the Differential Recovery of Microorganisms by Various Sampling Materials

Bargoma, E., La Duc, M.T., Kwan, K., Vaishampayan, P., and Venkateswaran, K.

Universal and species-specific quantitative polymerase chain reaction (PCR)-based methods were employed to compare the effectiveness of four distinct materials used to collect biological samples from metal surfaces. Known cell densities of a model microbial community (MMC) were deposited onto metal surfaces and subsequently collected using cotton and nylon-flocked swabs for small surface areas, and biological sampling kits (BiSKits) and polyester wipes for large surface areas. Ribosomal RNA gene-based quantitative PCR (qPCR) analyses revealed that cotton swabs were superior to nylon-flocked swabs for recovering biomolecules from small surface areas. Similarly, BiSKits outperformed polyester wipes for sampling large surface areas. Species-specific qPCR results showed a differential recovery of rRNA genes of the various MMC constituents, seemingly dependent on the type of sampling device employed. Both cotton swabs and BiSKits recovered the rDNA of all nine of the MMC constituent microbes assayed, whereas nylon-flocked swabs and polyester wipes recovered the rDNA of only six and four of these MMC strains, respectively. The findings of this study demonstrate the importance and proficiency of molecular techniques in gauging the effectiveness and efficiency of various modes of biological sample collection from metal surfaces.

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Species-specific qPCR to Assess the Differential Recovery of Microorganisms by Various Sampling Materials

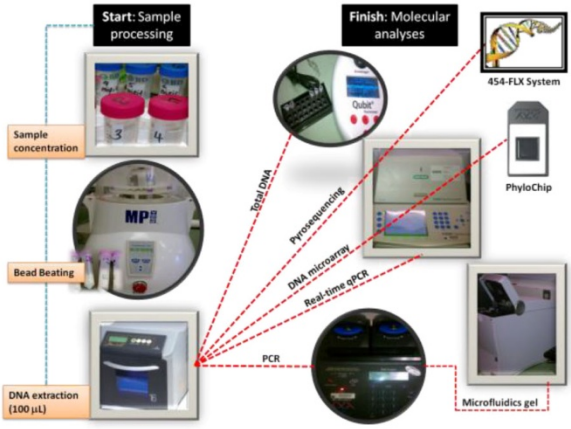
E. Bargoma, M.T. La Duc, K. Kwan, P. Vaishampayan, and K. Venkateswaran*

Jet Propulsion Laboratory, California Institute of Technology, Pasadena, CA 91109

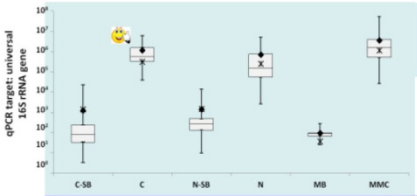
Abstract

- Universal and species-specific quantitative polymerase chain reaction (PCR)-based methods were employed to compare the effectiveness of four distinct materials used to collect biological samples from metal surfaces.
- Known cell densities of a model microbial community (MMC) were deposited onto metal surfaces and subsequently collected using cotton and nylon-flocked swabs for small surface areas, and biological sampling kits (BiSKits) and polyester wipes for large surface areas.
- Ribosomal RNA gene-based quantitative PCR (qPCR) analyses revealed that cotton swabs were superior to nylon-flocked swabs for recovering biomolecules from small surface areas. Similarly, BiSKits outperformed polyester wipes for sampling large surface areas.
- Species-specific qPCR results showed a differential recovery of rRNA genes of the various MMC constituents, seemingly dependent on the type of sampling device employed. Both cotton swabs and BiSKits recovered the rDNA of all nine of the MMC constituent microbes assayed, whereas nylon-flocked swabs and polyester wipes recovered the rDNA of only six and four of these MMC strains, respectively.
- The findings of this study demonstrate the importance and proficiency of molecular techniques in gauging the effectiveness and efficiency of various modes of biological sample collection from metal surfaces.

Analyses

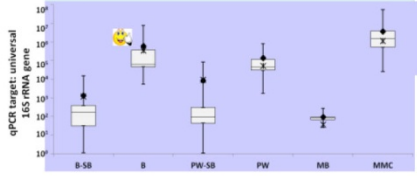


Recovery of total 16S rRNA gene fragments from metal surfaces with various sampling materials



Resulting rRNA gene recovery when metal surfaces artificially seeded with MMC were sampled with cotton (C) and nylon-flocked (N) swabs.

Box plots represent the mean (closed diamonds), confidence intervals (95%, asterisks) and upper and lower quartiles. Error bars depict the standard error of the mean in box plot format.

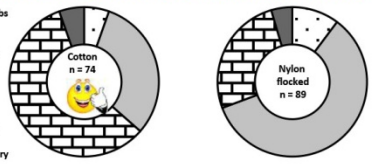


Resulting rRNA gene recovery when metal surfaces artificially seeded with MMC were sampled with BiSKits (B) and polyester wipes (PW).

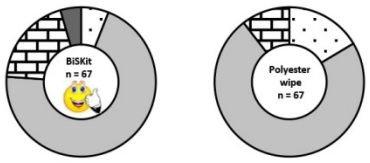
C:	Cotton swabs
N:	Nylon swabs
B:	BiSKit
PW:	Polyester wipes
SB:	Sampling device blank
MB:	Media control
MMC:	Model microbial community

Categorical percent recovery efficiency of various sampling matrices

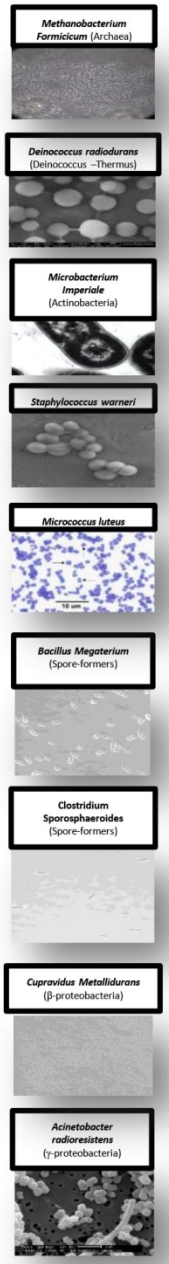
When nylon-flocked swabs were used to collect samples, 62 out of 89 replicates recovered less than 9.9% of the rDNA seeded onto the metal surfaces. Cotton swabs proved much more effective in sample recovery, as 48 of the 74 cotton swab sampling replicates yielded recovery greater than 10%.



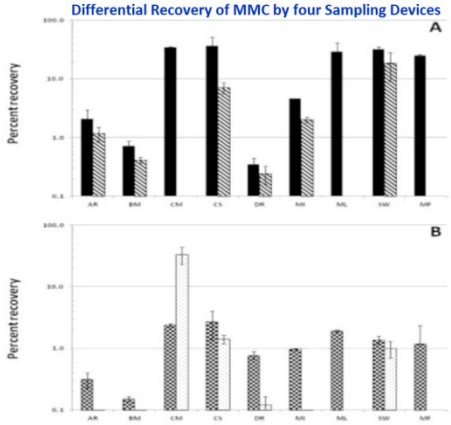
When BiSKits were used for sample collection 13 of 67 replicates exhibited >20% recovery (equivalent ~10^5 16S rRNA gene copies), whereas only 2 of 67 polyester wipe samplings yielded recovery this high.



10 – 99.9%; 100% 0%; 0.1 – 9.9%;

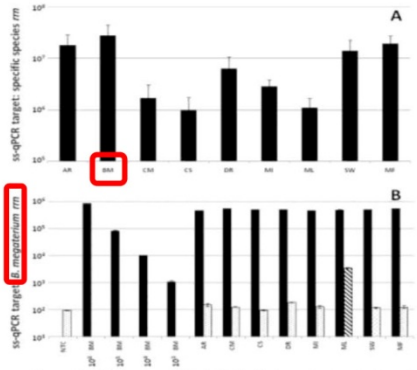


Differential Recovery of MMC by four Sampling Devices



Differential recovery of cells and rDNA of MMC constituents from metal surfaces by various sampling devices. Error bars depict standard error of the mean. Bars: Solid = Cotton swabs; Striped = Nylon-Flocked swabs; Checkered = BiSKits; Stippled = Polyester wipes

Species-specific-quantitative PCR Primer Specificity

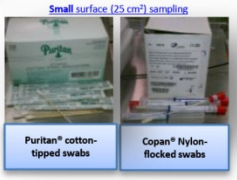


Performance and specificity of ss-qPCR assays developed in this study. (A) Performance of ss-various qPCR primer sets in amplifying their respective component of the model microbial community. Error bars depict standard error of the mean.

Effectiveness of swabs in the retrieval of 16S rRNA genes from metal surface using 454-FLX technology

Microbial taxa	Total number of pyrosequences generated from:				
	Model Microbial Community (before inoculation)	Metal surface after sampling with:		Swab heads that are:	
		Cotton	Nylon	Cotton	Nylon
Acinetobacter radioresistens	894	39	756	↑ 82	26
Bacillus flexus-megaterium	18,216	642	14,906	↑ 4,424	2,397
Bacillus pumilus	5,827	338	5,589	↑ 2,631	817
Cupriavidus metallidurans	1,911	78	2,578	↑ 431	292
Deinococcus radiodurans	5,675	491	4,816	↑ 2,204	535
Microbacterium sp.	149	4	177	↑ 27	8
Micrococcus luteus	1,023	46	681	↑ 271	79
Staphylococcus sp.	1,556	71	1,758	↑ 365	198
Methanobacterium formicicum (archaeon)	6,115	66	3,916	↑ 4,471	2,009

Small surface (25 cm²) sampling



Large surface (10000 cm²) sampling

Summary

Ribosomal RNA gene-based quantitative PCR (qPCR) analyses revealed that **cotton swabs** were **superior** to nylon-flocked swabs for recovering biomolecules from **small surface areas**.

Similarly, **BiSKits outperformed** polyester wipes for sampling **large surface areas**.

Species-specific qPCR results showed a **differential recovery** of rRNA genes of the various MMC constituents, seemingly **dependent on the type of sampling device** employed.

Both **cotton swabs and BiSKits** recovered the rDNA of **all nine** of the MMC constituent microbes assayed.

Nylon-flocked swabs and polyester wipes recovered the rDNA of **only six and four** of these MMC strains, respectively.

*kjvenkat@jpl.nasa.gov

ABSTRACT *[Presentation]*

Significance of Effective Sampling from Low-Biomass Surfaces and Challenges Involved in Nucleic Acid-Based Phylogenetic Analyses

Bargoma, E., Kwan, K., La Duc, M. T., Vaishampayan, P., and Venkateswaran, K.

To comprehensively assess microbial diversity and abundance via molecular-based methods, procedures for sample collection, processing, and analysis were evaluated in depth. To date, there are very few published reports that share the primary focus of this investigation, which is the in-depth assessment of effective and efficient strategies for the collection of representative biological samples from low-biomass surfaces. Experiments were designed and executed to: a) test the effectiveness of several sampling devices in recovering cells and naked nucleic acids from surfaces, and b) assess the differential recovery of rDNA members of a model microbial community (MMC) via species-specific quantitative PCR. Known cell densities of MMC were deposited onto metal surfaces and after drying, four sampling devices were used to recover cells and biomolecules. Ribosomal RNA gene-based quantitative PCR (qPCR) analyses revealed that cotton swabs were quantitatively superior to nylon-flocked swabs for recovering biomolecules from small surface areas. Similarly, BiSKits outperformed polyester wipes for sampling large surface areas. Species-specific qPCR results showed a differential recovery of rRNA genes of the various MMC constituents, seemingly dependent on the type of sampling device employed. Both cotton swabs and BiSKits recovered the rDNA of all nine of the MMC constituent microbes assayed, whereas nylon-flocked swabs and polyester wipes recovered the rDNA of only six and four of these MMC strains, respectively. The findings of this study demonstrate the importance of molecular techniques in gauging the efficiency and effectiveness of various modes of biological sample collection from low-biomass surfaces.

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ABSTRACT *[Presentation]*

State-of-the-Art Molecular Approaches to Elucidate the Genetic Inventory about the Surfaces of Spacecraft and Associated Environments

La Duc, M.T., Spry, A., Osman, S., Huber, J., Andersen, G., Sogin, M., and Venkateswaran, K.

Scientific literature teems with reports of microbial diversity from seemingly every niche imaginable, from deep within Antarctic ice to ocean-floor hydrothermal systems. Day after day novel approaches are thrust forward promising ever-increasing specificity and robustness in elucidating microbial diversity. The fields of applied microbiology and molecular biology have made enormous technological advancements over the past decade, from the development of PCR-amplification of DNA to the forensic detection of what many consider to be "miniscule" amounts of blood and other such biomatter. Despite advances in the specificity and sensitivity of molecular biological technologies, the ability to efficiently sample and extract nucleic acids from low-biomass matrices, and accurately describe the true microbial diversity housed in such samples remains a significant, ominous challenge. To minimize the likelihood of forward contamination of Mars, Europa, or any other extraterrestrial environment, utmost effort is put forth to ensure that environments in which spacecraft are assembled are maintained appropriately and kept as free of microbial contamination as possible. To this end, routine analyses, largely based on spore-counts and cultivation-based approaches, are carried out to validate the cleanliness of such surfaces. However, only by applying the most efficient and accurate molecular means of analysis can conclusions on the actual bioburden and microbial diversity associated with these environments be drawn. For any measure of sample-derived bioburden, a large portion is inevitably lost in sampling. Furthermore, a 90% loss is typical when extracting nucleic acids from a known concentration of bacterial cells. This loss is insignificant for samples rich in biomass, but those working with low-biomass samples cannot afford to merely discount such a loss. Since the surface area of a spacecraft is fixed, it is not possible to simply increase sample size to improve yield. It is therefore critical to assure that current methods of purification of biomolecules from these precious allotments are 1) optimal for achieving total yield and 2) conserving of the true microbial diversity of the sampled environment. This project focuses on the development of capabilities to effectively and efficiently generate a genetic inventory of microbes present about the surfaces of spacecraft and associated clean-room facilities. This entails the evaluation and optimization of molecular-based strategies designed to assess microbial burden and diversity arising from samples of low biomass. Such strategies include conventional clone library analysis, DNA microarray screening, and 454 Tag Sequencing. The data arising from such an array of molecular approaches will enable NASA to establish and maintain a genetic inventory capable of mitigating the ramifications of any detected contaminant terrestrial biosignatures on life detection missions.

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ABSTRACT *[Presentation]*

Genetic Inventory of Phoenix Spacecraft and Associated Environments via Conventional Cloning and Sequencing Analysis

La Duc, M. T., Osman, S., Chen, F., Spry, J. A., and Venkateswaran, K.

The bacterial diversity arising from surfaces of the Phoenix spacecraft and associated facilities was analyzed during assembly at the Multiple Testing Facility (MTF), Lockheed Martin Aeronautics and prior to the launch at the Payload Hazard Servicing Facility (PHSF), Kennedy Space Center. Spacecraft and facility surfaces were sampled with macrofoam, material that contained low levels of indigenous DNA compared to conventional cotton. An automated nucleic acid extraction device capable of high DNA yield and efficient bacterial diversity recovery was employed. Conventional methods of gene amplification, cloning, and sequencing were implemented, and several thousand (I prefer a real number) clones were analyzed. Despite the arid, nutrient bare conditions within these clean rooms, a broad diversity of bacteria was detected, covering all major bacterial phyla (be more specific). Furthermore, bacterial communities were significantly different between the MTF and PHSF, with but a few microorganisms common to both locations. Spacecraft surface samples showed a richer diversity comparing with facility surface samples, indicative of the need for additional or alternative analyses to determine whether facility samples are indeed appropriate surrogates for spacecraft surfaces. This approach facilitates downstream research to further (to a degree acceptable for planetary protection purposes) our understanding of the microbial population on and around spacecraft surfaces. In turn, this knowledge will allow the Mars Program to develop capabilities that achieve compliance with both current and anticipated planetary protection requirements at the earliest stages of future missions.

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ABSTRACT *[Poster]*

Microbial Diversity of Anaerobes from Spacecraft Associated Surfaces

Probst, A., Vaishampayan, P., Moissl, C., and Venkateswaran, K.

Inadvertent introduction of terrestrial microbes into some solar system bodies could significantly compromise the scientific integrity of future life-detection missions. Hence, spacecraft targeted to such extraterrestrial environments are assembled in clean rooms under stringent quality controlled conditions to minimize biological burden of spacecraft components. Under NASA policy, the heterotrophic mesophilic aerobic bacterial spore burden of spacecraft surfaces serves as a conservative proxy indicator for cleanliness and planetary protection risk. However, information about the presence of anaerobic microorganisms in such facilities (including spore formers) is sparse. Since spores can tolerate a variety of stresses, including the space environment, they are considered the primary risk for introduction to and survival in extraterrestrial environmental conditions. Such abilities can be predicted for Clostridium and other anaerobic spore formers. In this study, an in depth survey of the cultured and uncultured anaerobic microbial population of spacecraft associated environment was attempted. Samples were collected and processed from three different clean room facility environments where the Mars Science Laboratory spacecraft subsystems were being assembled. Cultivation based studies revealed the presence of Propionibacterium and Clostridium spp. In addition to the culturing, DNA was extracted from the subset of the anaerobic enrichment and the 16S rRNA genes were amplified, cloned, and sequenced to elucidate the anaerobic microbial inventory. The anaerobic microbial diversity profile suggested the influence of human activities and also showed presence of soil-associated anaerobes. This study provides the first detailed account of the anaerobic bacterial diversity of spacecraft associated surfaces, which informs strategic planning for planetary protection implementation in future missions. The data is also relevant to other fields of study, such as medical-related clean rooms and bio-threat detection, where the presence and abundance of anaerobic microorganisms may also be of concern.

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Microbial Diversity of Anaerobes from Spacecraft Associated Surfaces

N-006

Alexander Probst[1,2], Parag Vaishampayan[1], Christine Moissl[2], and Kasthuri Venkateswaran[1]

[1]Jet Propulsion Laboratory, California Institute of Technology, Pasadena, CA, USA [2]Regensburg University, Department of Microbiology and Archaea Centre, Regensburg, Germany; Email: Alexander.Probst@biologie.uni-regensburg.de

Jet Propulsion Laboratory
California Institute of Technology

Regensburg University
Department for Microbiology and Archaea Centre

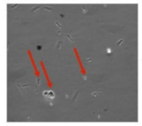
Introduction

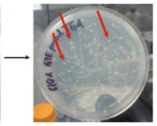
- Reduction of microbial load of spacecraft and their hardware are necessary to prevent forward contamination of the exploring planets. Failure to contain microbial burden on the spacecraft surfaces will compromise the science involved in the life detection missions (Planetary Protection [PP]; A key Astrobiology Principle).
- It is mandated to assemble any components of spacecraft in clean rooms to keep the bioload at appropriate level
  - Since the humidity and temperature are kept constant, nutirents levels are low, and the air particulates are controlled through advanced engineering systems the clean rooms are considered as „extreme environment."
- As per the UN Treaty NASA and other space faring nations clean the spacecraft surface based on the counts of aerobic sporeformers and mesophilic bacteria.
- Molecular approaches of the last decade revealed a high diversity in clean rooms including strictly anaerobic microorganisms.
- Since most possible survivors in the extraterrestrial environments are the anearobes due the absence or low concentration of oxygen (e.g. Mars 0.13 %), it is absolutely necessary to describe the anaerobic biodiversity during spacecraft assembly.
- In this study we present the anaerobic diversity of three facilities of the Jet Propulsion Laboratory (JPL) where the majority of the Mars Science Laboratory (MSL) mission hardware are being assembled.
- Cultivation based techniques combined with molecular analysis using 16S rRNA gene sequencing were conducted to elucidate the anaerobic bacterial diversity.

1

Isolation of strict anaerobes

- Enrichment cultures were checked for growth and purity by phase contrast light microscopy
- Appropriate aliquots were aseptically spread plated on solid anaerobic media in anaerobic glove box





- Each strain was passed through several times to obtain pure culture.
- Purified strains that were not able to grow in the presence of oxygen were grown in liquid medium, cells harvested, and 16S rRNA gene sequenced.
- Sequences were compared to publicly available databases

4

Molecular Community Analysis of Anaerobes

Phylum / Family	Genus and species (of closest relative type strain)	Percentage of similarity	Number of clones retrieved from facilities that are: JPL-SAF-A gradient PCR (61)	Bldg-233-B standard PCR (74)	Bldg-233-B gradient PCR (55)	JPL-SAF-C standard PCR (59)	JPL-SAF-C gradient PCR (51)	BDL-D standard PCR (58)	BDL-D gradient PCR (69)
Actinobacteria									
Cellulomonadaceae	*Oerskovia paurometabola* DSM14281, AJ314851	98-99%				1	1		
Dermabacteraceae	*Dermabacter hominis* DSM7083, X91034	94-98%						5	5
Propionibacteriaceae	*Propionibacterium acnes* DSM1897, X53218	96-97%	24	18	12				
	Propionibacterium propionicum DSM43307, AJ003058	93-97%	4						
Firmicutes									
Bacillaceae	*Bacillus licheniformis* DSM13, X68416	94-100%		3				41	30
	Bacillus thuringiensis ATTC10792, AF290545	96-99%				2	13		
	Bacillus weihenstephanensis DSM11821, AB021199	96-99%				23	3		
Carnobacteriaceae	*Granulicatella adiacens* GIFU12706, D50540 AF016390	98%	1						
Clostridiaceae	*Clostridium colicanis* 13634, AJ420008	94-99%		9	11				
	Sarcina ventriculi DSM286, X76649	94-99%		20	16				
Leuconostocaceae	*Leuconostoc lactis* DSM8581, AF175403	98%		1					
Paenibacillaceae	*Paenibacillus borealis* KK19, AJ011322	97-98%		2	1				
	Paenibacillus odorifer TOD45, AJ223990	97%		1					
Staphylococcaceae	*Staphylococcus capitis* subsp. *capitis* ATCC 49326T, AB009937	95-99%	1	1	1				1
	Staphylococcus caprae ATTC 35538T, AB009935	94-98%		1		3	4	2	2
	Staphylococcus epidermidis ATCC 14990T, D83363	95-99%	29	16	12	30	30	10	31
	Staphylococcus lugdunensis ATTC 43809T, AB009941	98%			1				
	Staphylococcus saccharolyticus L37602	97-99%	1	1					
	Staphylococcus warneri L37603	98-99%		1	1				
Streptococcaceae	*Streptococcus parasanguinis* ATCC 15912, AF003933	95%	1						

7

For each sampling event standard and gradient PCR were performed. Numbers of high quality sequences are given in brackets. The high quality 16S rRNA gene sequences were compared to publicly available data (NCBI, BLAST).

Sampling

- Sampling methods
  - Biological Sampling Kits (BisKits)
  - Wipes accoring to NASA standard protocols
- Sampling locations and events
  Same locations at the Jet Propulsion Laboratory, Pasadena, CA, USA. Class 100 K (ISO 8) clean room facilities:
  - **Spacecraft assembly facility (JPL-SAF-A)**
  - **Building 233 (Bldg-233-B)**
  - **Spacecraft assembly facility (JPL-SAF-C)**
  - **Biomolecule Detection Lab (BDL-D)**

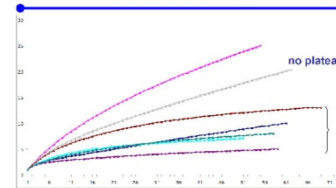
- Samples
  - Clean room floors using BisKit (1 m^2 surface area; 10 locations)
  - Several Ground Support Equipment (GSE) of JPL-SAF-A/B were sampled with BisKits or Wipes

2

Molecular community analysis of enrichment cultures

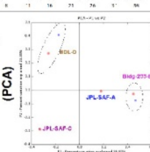
- Appropriate aliquots of enrichment cultures were pooled and DNA was extracted using bead beating and Axcyte Genomics Autolyser
- Standard and gradient PCR with bacterial 16S primer set: B27F and 1492R were carried out
- PCR products of standard (55°C) and gradient PCR (48 to 57.5°C) were used to construct two clone libraries for each sampling event
- 96 clones were sequenced from each clone library and high quality sequences were used for further analysis.
- Anaerobic diversity
  - number of OTUs (>97.5% sequence similarities)
  - Coverage (C) values (coverage of rare species)
  - rarefaction analysis (sampling efficiency)

All Anaerobic Species Covered?



- Two sampling events at Bldg-233-B exhibited the highest diversity, no plateau in rarefaction analysis and low coverage value indicating the uncomplete sampling.
- All other sampling events revealed high coverage values and a plateau. Hence, a complete coverage of anaerobic biodiversity can be considered.

UniFrac :Principal Coordinates Analysis (PCA)



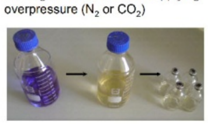
Facility	Coverage
JPL-SAF-A gradient PCR	89%
Bldg-233-B standard PCR	73%
Bldg-233-B-gradient PCR	78%
JPL-SAF-C standard PCR	96%
JPL-SAF-C gradient PCR	97%
BDL-D-standard PCR	94%
BDL-D-gradient PCR	95%

Sampling efficiency as revealed by the coverage values

Hungate technology

Preparation of anaerobic media:

- Mixing ingrediences and adding resazurine as oxygen indicator
- Purging the mixture with nitrogen for 20 minutes
- Adjusting pH to 7.2
- Reducing medium with sodium-thioglycollate and L-cystein decoloring resazurine by removing bound oxygen
- Aliquoting into serum bottles under anaerobic conditions
- Sealing serum bottles and applying overpressure (N_2 or CO_2)



Anaerobic media:

TSB – Trypticase soy liquid medium
- commercially available, rich medium

TG – Thioglycollate liquid medium
- non commercially, rich medium

Modified American Type Culture Collection (ATCC) **medium 591**
- Specific medium for isolation of microbes of the genus *Clostridium*.
- Since 16S rRNA gene sequences of *Clostridium* spp. were retrieved from the NASA clean room facilities (Moissl et al., 2007. FEMS Microbiol. Ecol. **61**:509), we attempted a medium specific to promote the growth of this species.

3

Cultivable Anaerobes

Phylum/ Family	Closest relatives*	%	# of isolates	Sample location**	Sampling facility
Firmicutes/ Clostridiaceae	*Clostridium colicanis 13634*	99	8	Floor	Bldg-233-B
	Clostridium perfringens SM101	99	1	GSE	JPL-SAF-C
	Clsotridium saccharolyticum DSM 2544	96-98	3	GSE	JPL-SAF-C
	Clostridium botulinum A ATCC 19397	99	3	GSE	JPL-SAF-A
				GSE	JPL-SAF-C
				Floor	BDL-D
Actinobacteria/ Propioni-bacteriaceae	*Propionibacterium acnes* KPA 171202	99	3	Floor	JPL-SAF-A
				10 floor samples pooled	JPL-SAF-A
				GSE	JPL-SAF-A

*based on 16S rRNA gene sequence analysis; **GSE: ground support equipment; %: percentage similarity with the 16S rRNA gene sequence of the closely related type strain.

- The JPL-SAF-C isolate exhibited only 96% 16S rRNA gene similarity with *Clostridium saccharolyticum* type strain and may be a novel species
- All isolates were sporeformers or associated with human
- Some strains were considered to be human pathogens

6

Conclusions

- Sequences of the strict anaerobes isolated during this study were also present in clone libraries indicating the validity of the implemented method.
- All faciltlies sampled are from the same premise (within few meters) and also maintained by the same personnel but still shared only one common species (*Stapylococcus epidermis*).
  - Skin microflora?
  - Contamination may be due to the human activity and maintenance.
- Anaerobic diversity was predominated by gram positive bacteria.
- Most anaerobes present in clean room facilities were human associated or sporeformes, some were human pathogens (*Propionibacterium*, *Clostridium*).
- Presence of anaerobic sporeformes in clean room facilities pose serious threat of forward contamination and can jeopardise integrity of future life detection missions, since spores are known to survive radiation, dessication and heat more than most other forms of microorganisms.
- It is recommended based on this study that space-faring nations should consider screening and/or estimating the anaerobic microbes during spacecraft assembly.
- This study represents the first anaerobical screening while having strict Planetary Protection implementations due to MSL assembly. 9

Part of the research described in this poster was carried out by the Jet Propulsion Laboratory, California Institute of Technology, under contract with the National Aeronautics and Space Administration. We thank J.A. Spry and K. Buxbaum for valuable advice and encouragement.

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Picture: Google Earth

ABSTRACT *[Poster]*

Predictive Risk Assessment of Spacecraft Contamination with Computational Analysis

Vaishampayan, P., Osman, S., LaDuc, M., and Venkateswaran, K.

Clean-room environments are oligotrophic (low nutrient level), desiccated, clean (low particle per square foot air) and dry, conditions aimed at reducing microbial populations and sometimes referred as 'extreme'. These facilities are periodically cleaned with chemical disinfectants and maintained with appropriate environmental control engineering system. In spite of these harsh conditions, a subset of tenacious microbes has been shown to survive in this 'extreme' condition. Not all microorganisms pose an equivalent threat to forward contamination and the confounding of life-detection experiments. Understanding which taxa are of greatest concern, coupled with data pertaining to the rate at which each are encountered, would factor significantly in the ability to accurately assess risk. Routine planetary protection assays of MER, Phoenix, and MSL spacecraft and associated facilities have amassed an immense amount of contaminant bacterial 16s rDNA sequence data. This data, along with that generated from ongoing sampling events being carried out by JPL's Biotechnology and Planetary Protection group, was subjected to numerous computational analysis that will divulge total microbial diversity, species richness and divergence estimates within, and between, each sample. We have also verified whether the sampling surveys are sufficiently comprehensive. Computational modeling of spacecraft-associated microbial population dynamics was carried out to predict the complete spectrum of bacteria present, thereby developing the ability to accurately assess the risk of forward contamination based on resistance and recurrence. We have performed comparative analysis of microbial population between different spacecraft assembly facilities to understand impact of geographical location. We have also compared microbial population during different stages of spacecraft assembly to understand impact of facility cleaning protocols and human activities. It is very important to note that a limited number of bacterial genera representing a large percentage of the total bacterial population of the clean room survive throughout the assembly process. These compelling evidences strongly suggested that certain bacterial population adapted, survived and persisted in clean room 'extreme conditions'. As environmental conditions and maintenance procedures differ from one clean room facility to other, it is possible to have characteristics bacterial population unique to each clean room facility. Understanding the real threat to space missions due to forward contamination requires an in depth survey and computational analysis of total microbial load and persistent hardy population.

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National Aeronautics and Space Administration

N-003

Predictive Risk Assessment of Spacecraft Contamination with Computational Analysis

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Abstract

Rationale:

- One of the prime functions of the National Aeronautics and Space Administration (NASA) planetary protection policies is to prevent the inadvertent introduction of organic matter (e.g. cells or cellular remnants) originating from Earth to the exploring extraterrestrial surface (forward contamination). Accordingly, current planetary protection protocols require that spacecraft be assembled and readied for launch in closed, near-sterile, ultra-clean facilities.
- Yet despite these harsh conditions experienced in cleanrooms, a subset of tenacious microbes is known to exist[1,2]. It is documented that not all microorganisms pose an equivalent threat to forward contamination and compromise life-detection experiments but recurrent isolation of certain microbes was reported.
- To date, no comprehensive analysis is available that describes the variations, dynamics, and composition of bacterial diversity in a NASA clean room before, during, and after hardware assembly.

Approach:

- The bacterial diversity and comparative community structure of the Kennedy Space Center Payload Hazardous Servicing Facility (PHSF), assembling the Phoenix (PHX) lander , was characterized throughout the spacecraft assembly process using 16S rRNA gene sequencing and DNA microarray (PhyloChip) technologies.

Results:

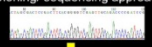
- Computational modeling of spacecraft-associated bacterial population dynamics was carried out to predict the complete spectrum of bacteria present, thereby developing the ability to accurately assess the recurrence of certain bacterial types to avoid risk of forward contamination.
- This approach will enable to predict model microbes, thus developing stringent control measures to eradicate the recurrent bacterial types in these spacecraft assembly facility.

Sample collection from Kennedy Space Center Payload Hazardous Servicing Facility (PHSF)

Sample sets (~10 each) were collected from the PHSF surfaces at three time points:

1: Before Phoenix assembly (PHX-B)
2: During Phoenix assembly (PHX-D)
3: After Phoenix moved out (PHX-A)

Cloning/ sequencing approach

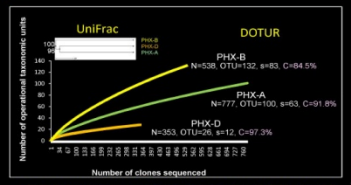


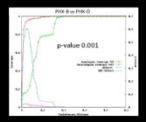
DNA microarray (PhyloChip) approach

Data obtained from both the approaches was subjected to series of computational algorithms to elucidate complete spectrum of microbial diversity and community dynamics.

Methodologies are described in Q-235 (poster board # 728); May 19th 1:00 PM

Computational algorithms to elucidate functional aspects of Microbial monitoring



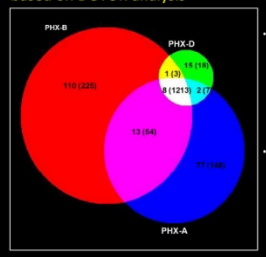


- PHX-B library exhibited the greatest number of OTUs (n=132) but the steep rarefaction curve and low coverage value (c=84.5%) indicates insufficient sampling.
- PHX-D library showed least number of OTU's (n=26) but highest coverage value (c= 97.4%)
- UniFrac and LIBSHUFF analysis indicated that the Before-Phoenix environment contained statistically different bacterial diversity when compared to the During and After-Phoenix environments .

The coverage of clone libraries was calculated using the equation: C= [1-(n1/N)]*100, where C is the homologous coverage, *n1* is the number of OTU's appearing only once in the library, and N is the total number of clones examined.

Computational analysis to estimate recurring microbial population

Algorithm: Determine fraction of OTUs shared by communities based on DOTUR analysis



- Bacterial diversity and abundance was reduced dramatically during Phoenix (PHX-D) components were assembled.
- 73% of all clones (1,213 sequences) belonged to a limited number of species (8 OTUs) that appear to dominate within the PHSF throughout the spacecraft assembly process.
  - These overlapping OTUs were: two OTUs of *Acinetobacter*, one OTU each of *Ralstonia*, *Streptococcus*, *Brevundimonas*, *Sphingomonas*, *Delfia*, and *Pseudomonas*.
- The decrease in bacterial abundance and community complexity in the samples collected before Phoenix arrived (PHX-B) to during Phoenix (PHX-D) and subsequent recurrence of these organisms in samples collected after Phoenix left (PHX-A) indicate that stringent air processing, more intense cleaning regimens, or greater operator care result in "cleaner" clean rooms during spacecraft assembly.

In-house developed computational tool enable to rapidly identify problematic microbial species

Clone	Isolates	%similarity	Phenotypic trait	Species
1P-3-2-C17	1P09AB	99	Alkalophiles	*B. pumilus*
	3P01AB	99	Alkalophiles	
	3P01AA	99	Alkalophiles	
	3P01Ma	99	Mesophiles	
	1P04MA	99	Mesophiles	
	1P09SC	99	Spore former	
	3P04SA	99	Spore former	
	1P09SA	99	Spore former	
	3P03SA	99	Spore former	
	1P09SB	99	Spore former	
	1P09TA	98	Thermophiles	
	3P07UA	98	UV resistance	

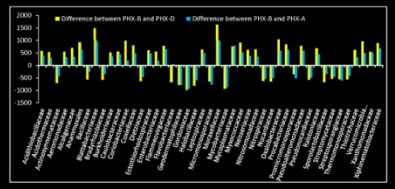
Alkalophile: pH 9.5; Mesophile: 25°C; Spore former: 80°C-15 min.; Thermophile: 62°C; UV resistance: 1,000 J/m2

Identification of "problematic" species that could grow under variety of environmental stresses encountered during space transport

Comparative analysis of total observed microbial diversity measured at family-level by DNA-microarray and cloning

- PhyloChip analysis found high bacterial diversity when compared to cloning approach in all three sampling events of the KSC PHSF.
- Significant decrease in the number of bacterial families was noticed during Phoenix assembly (PHX-D) than in the PHSF samples collected before Phoenix arrived (PHX-B).

Relative abundance of bacteria during clean regimes (during [PHX-D] and after [PHX-A] Phoenix assembly) when compared to the period before the arrival of Phoenix (PHX-B), based on PhyloChip fluorescence intensity



- Fluorescence intensity data, indicated identical trends of shift in bacterial abundance during clean regimes (PHX-D and PHX-A) as compared to PHX-B sampling.
- The number of unique taxa detected in samples decreased by nearly 40% between PHX-B (1,817 OTUs) and PHX-D (1,094 OTUs).
- Over 53% of OTUs (1,030 of 1,922) were detected across all three sampling events.
- The widespread detection of a core set of organisms, both in clone libraries, and on the PhyloChip underscore the challenges in eliminating contaminants completely.

Conclusions

- This was the first investigation to observe the impact that a spacecraft assembly (cleaning?) has on a clean room's bacterial community.
- Contrary to expectations that human activities during spacecraft assembly would lead to elevated bacterial counts, evidence suggests that the lowest bacterial diversity actually occurred during the assembly period (PHX-D). Trends in population structures similar to those observed in clone libraries were also noticed during microarray analysis.
- Cloning approach indicate that a limited number of bacterial genera representing a large percentage of the total bacterial population of the clean room survive throughout the assembly process. Apparent reductions in complexity between clone libraries may indicate that clean room operation conditions select for a core set of organisms.
- Microarray findings suggest that this core set of microbes is much more diverse than can be measured by clone libraries alone. Microarrays found surprising resilience in the PHSF microbial community after the departure of the Phoenix, presumably due to a return to "normal" operations.
- This case study confirms the ability of computational analysis to understand microbial community dynamics during spacecraft assembly phases for predictive risk assessment.

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Acknowledgements

The research described herein was carried out at the Jet Propulsion Laboratory, California Institute of Technology, under a contract with the National Aeronautics and Space Administration and ROSES-06 NRA award for KV. We are indebted to Yuki Salinas (JPL), Randy Sumner (Bionetics Corp.), Dennis Vaughn (LMA), and Buzz Petsos (KSC) for facilitating sample collection at KSC-PHSF.

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ABSTRACT *[Poster]*

Viable Bacterial, Archaeal, and Fungal Diversity of Spacecraft-Associated Clean Rooms Using a Novel DNA Intercalating Agent

Stam, C. N., Scalzi, G., Schwendner, P., Cooper, M., Kwan, K. M., Tom, L., Piceno, Y., Andersen, G., Onofri, S., LaDuc, M. L., Benardini, J. N., and Venkateswaran, K.

Several molecular based methods have been used to identify microbial communities associated with NASA spacecraft surfaces. However, it is still not known what proportion of these genetic signatures come from viable organisms. By knowing which signatures are from viable organisms it is possible to tailor specific eradication processes, if they pose a potential threat for forward contamination of extraterrestrial environments, thereby improving current sterilization methods for spacecraft surfaces. Molecular based nucleic acid amplification approaches such as polymerase chain reaction (PCR) have been used in a wide range of microbial detection applications. Real-time PCR methods are particularly promising, as these methods can be used for quantification of environmental microbial populations. Currently, nucleic acid based methods are limited, because DNA from dead bacterial cells is highly stable and hence DNA based methods fail to discriminate between live and dead microorganisms. To circumvent the issues associated with the persistence of DNA from dead cells, a fluorescent DNA intercalating agent, which only penetrates the membranes of dead cells, will be used. Therefore we can rapidly detect and identify viable microorganisms present that have a high potential for surviving spacecraft flight. Environmental samples were collected from ground support equipment and floors of the spacecraft assembly facility. Samples were concentrated to a final volume of <500 μL using a 50 kDa filter. Each sample was divided and one half was treated with 12.5 mg/ml PMA. DNA was extracted from each sample, and PCR was performed using universal primers targeting bacterial, archaeal, and eukaryotic rRNA. Diversity was further characterized using 16S rRNA gene sequencing and DNA microarray (PhyloChip and MycoChip) technologies. Excellent PCR amplification of bacterial, fungal, and archaeal DNA was obtained from the environmental samples. PMA treated archaeal samples did not amplify however, PMA treated bacterial and fungal DNA was still PCR amplifiable. Further PhyloChip and MycoChip analyses will be used to determine the microbial diversity of the samples.

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Viable Bacterial, Archaeal, and Fungal Diversity of Spacecraft-Associated Clean Rooms Using a Novel DNA Intercalating Agent

CN Stam[1], G Scalzi[1], P Schwendner[1], M Cooper[1], KM Kwan[1], L Tom[3], Y Piceno[3], T DeSantis[3], MT LaDuc[1], JN Benardini[1], S Onofri[2], G Andersen[3], K Venkateswaran[1]

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Abstract

Several molecular based methods have been used to identify microbial communities associated with NASA spacecraft surfaces. However, it is still not known what proportion of these genetic signatures come from viable organisms. By knowing which signatures are from viable organisms it is possible to tailor specific eradication processes, if they pose a potential threat for forward contamination of extraterrestrial environments, thereby improving current sterilization methods for spacecraft surfaces. Molecular based nucleic acid amplification approaches such as polymerase chain reaction (PCR) have been used in a wide range of microbial detection applications. Real-time PCR methods are particularly promising, as these methods can be used for quantification of environmental microbial populations. Currently, nucleic acid based methods are limited, because DNA from dead bacterial cells is highly stable and hence DNA based methods fail to discriminate between live and dead microorganisms. To circumvent the issues associated with the persistence of DNA from dead cells, a fluorescent DNA intercalating agent, which only penetrates the membranes of dead cells, will be used. Therefore we can rapidly detect and identify viable microorganisms present that have a high potential for surviving spacecraft flight. Environmental samples were collected from ground support equipment and floors of the spacecraft assembly facility. Samples were concentrated to a final volume of <500 µL using a 50 kDa filter. Each sample was divided and one half was treated with 12.5 mg/ml PMA. DNA was extracted from each sample, and PCR was performed using universal primers targeting bacterial, archaeal, and eukaryotic rRNA. Diversity was further characterized using 16S rRNA gene sequencing and DNA microarray (PhyloChip and MycoChip) technologies. Excellent PCR amplification of bacterial, fungal, and archaeal DNA was obtained from the environmental samples. PMA treated archaeal samples did not amplify however, PMA treated bacterial and fungal DNA was still PCR amplifiable. Further PhyloChip and MycoChip analyses will be used to determine the microbial diversity of the samples.

Introduction

There is a continuing need for the development and application of a sensitive, rapid method that will detect and enumerate total viable microorganisms. Culture-based plating methods, including the NASA standard assay, have remained the "gold standard," even though such methods are both laborious and time consuming. Nucleic-acid-based amplification approaches such as the polymerase chain reaction (PCR) have shown promise for improving time to detection for a wide range of applications. Real-time quantitative-PCR (qPCR) methods are particularly promising, since these methods can be used to measure microbial burden. Nonetheless, PCR-based methods are rarely used for process validation, largely because the DNA from dead bacterial cells is highly stable, and hence DNA-based amplification methods fail to discriminate between live and inactivated microorganisms.

DNA intercalating agents such as ethidium monoazide (EMA) and propidium monoazide (PMA) have been used to selectively distinguish between viable and dead bacterial cells. Previous work has demonstrated that these dyes can only penetrate the membrane of dead cells (Rudi et al., 2005; Nogva et al., 2003). Once penetrated, they intercalate the DNA and, upon photolysis using visible light, produce stable DNA monoadducts (Rudi et al., 2005b; Rueckert et al., 2005). Once the DNA is cross-linked, it becomes insoluble and is lost during genomic DNA preparation (Nocker and Camper, 2006). Theoretically, if PMA is used to treat bacterial cells prior to DNA extraction, only the DNA of viable cells should be available for PCR amplification (Nocker et al., 2007).

Materials and Methods

Sample Collection:

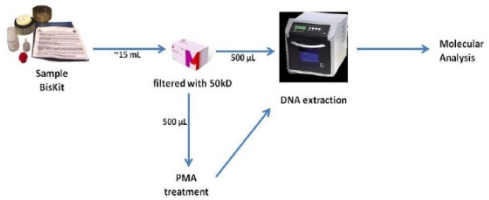
The BiSKit (QuickSilver Analytics; Abingdon, MD) was used for all sampling of ground support equipment and floors in the spacecraft clean room. A volume of 15mL of PBS is added to the BiSKit, the BiSKit module is then inverted so as to allow the 15mL buffer to soak into the macrofoam sponge of the BiSKit unit. Samples are collected by traversing the surface area first in a horizontal manner, then vertical, and finally in a diagonal sampling pattern. The PBS solution is then collected from the BiSKit by squeezing the BiSKit sampling unit. The expelled buffer is emptied into a sterile 50 mL Falcon tube, and this is repeated two additional times.

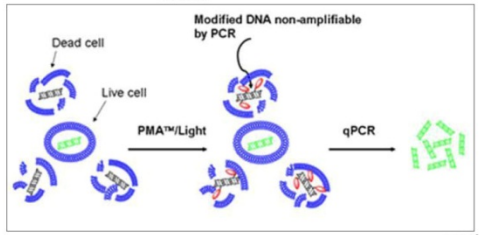
Sample Processing:

Samples are filtered using Amicon Ultra-15 Ultracel centrifugal filter (Millipore; Billerica, MA). All amicon filter samples are divided into separate aliquots, one to be treated with PMA and the other to be used as a control. DNA is extracted using the Maxwell 16 automated system (Promega Corp.; Madison, WI), and samples are stored at -20 ° C until use.

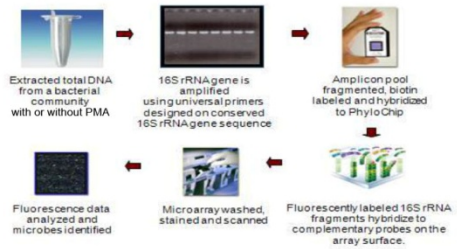
DNA Amplification:

DNA extracts were amplified using an 8-temperature PCR gradient with Bacterial (27F, 1492R), Archaeal (4fa, 1492R), or fungal (ITS1F, TW13) primers. Bacterial products were analyzed using PhyloChip microarrays.





Microarray sample processing

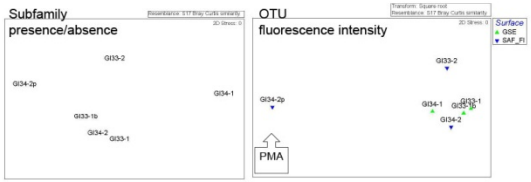


Results

Surface Type	PCR Products (N = nested) Bacteria	Archaea	Fungi	Samples (Pooled) p=PMA
GSE 1 & 2	+	- (N-)	+	GI33-1
GSE 1 & 2	-	- (N-)	+	GI33-1p
GSE field blank	+	- (N-)	+	GI33-1b
GSE field blank	-	- (N-)	+	GI33-1bp
SAF floor	+	- (N-)	-	GI33-2
SAF floor	-	- (N-)	+	GI33-2p
SAF floor field blank	-	- (N-)	+	GI33-2b
SAF floor field blank	-	- (N-)	+	GI33-2bp
GSE	+	- (N-)	+	GI34-1
GSE	+ *	- (N-)	+	GI34-1p
SAF floor	+	- (N+)*	+	GI34-2
SAF floor	+	- (N-)	+	GI34-2p
Biskit field blank	-	- (N-)	+	GI34-3
Biskit field blank	-	- (N-)	+	GI34-3p

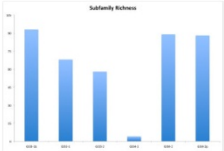
GSE = ground support equipment * not enough product for a chip

Table 1. Results from 8-temp. gradient PCR using regular and/or nested PCR, as indicated.



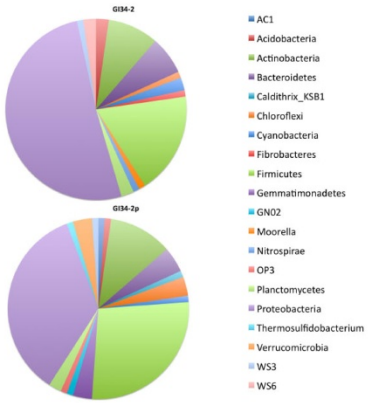
NMDS plots show that adding PMA prior to DNA extraction had a greater effect on the microbial community detected than did the location or time of sampling. *Note: very few (4) subfamilies were detected in sample GI34-1, and so it is well-separated from the other non-PMA samples when the data were reduced to presence or absence of subfamilies.*

Number of Subfamilies Detected Using 70%TPR and 0.5% FPR cutoffs.



As only one PMA-treated sample had enough PCR product to analyze, detailed comparisons were made only with GI34-2 and 2p.

Effect of PMA on Community Structure



Subfamily richness summarized at Phylum.

Proteobacteria were more prevalent in the non-PMA samples, whereas Firmicutes were more prevalent in the PMA-treated sample (live bacteria).

Many of the OTU associated with the PMA sample had been found previously in arid environments (especially soils (24) and indoor or outdoor air (5), including a JPL clean room) and in marine waters (6) and a few were human-associated (2).

Families in Phylum Proteobacteria	GI34 2	GI34 2p
Azospira_FM	1	1
Comamonadaceae	1	1
Janthinobacterium_FM	1	1
Legionella_FM	1	1
Methylobacteriaceae	1	1
Ralstoniaceae	1	1
Sphingomonas_FM	1	1
Desulfovibrionaceae	2	0
Enterobacteriales_Enterobacteriaceae	2	0
Polyangiaceae	2	0
Alcaligenaceae	1	0
Bradyrhizobium_FM	1	0
Brevundimonas_FM	1	0
Burkholderiaceae	1	0
Devosia_FM	1	0
Halomonadaceae	1	0
Hyphomicrobium_FM	1	0
Labrys_FM	1	0
Magnetospirillum_FM	1	0
Methylococcaceae	1	0
Moraxellaceae	1	0
Porphyrobacter_FM	1	0
Pseudomonadaceae	1	0
Rhodoplanaceae	1	0
Rhodospirillum_FM	1	0
Rhodovulum_FM	1	0
Spirillaceae	1	0
Acetobacteraceae	0	1
Azospirillaceae	0	1
Bacteriovorax_FM	0	1
Caedibacteraceae	0	1
Oleomonas_FM	0	1
Rhizobiaceae	0	1
Rhodovibrio_FM	0	1
Roseomonas_FM	0	1
SAR11_FM	0	1

Families in Phylum Firmicutes	GI34 2	GI34 2p
Peptostreptococcaceae	2	3
Paenibacillaceae	1	2
Ruminococcus_FM	1	2
Bacillus_FM	1	1
Clostridiaceae	1	1
Clostridium_FM	1	1
Planococcaceae	1	1
Staphylococcaceae	1	1
Catabacter_FM	1	0
Marinococcus_FM	1	0
Sporolactobacillus_FM	1	0
Streptococcaceae	1	0
Acidaminococcaceae	0	1
Desulfotomaculum_FM	0	1
Geobacillus_FM	0	1
Halobacillus_FM	0	1
Mycoplasma_FM	0	1
Symbiobacterium_FM	0	1

Conclusions

- PMA treatment reduces the amount of amplifiable DNA and PCR product formation, indicating it is selecting against some part of the total recoverable DNA.
- PhyloChip analysis indicates a difference in the bacterial community structure between PMA- and non-PMA-treated samples, such as reducing the diversity of proteobacteria detected in PMA-treated samples.
- There was insufficient Archaeal DNA extracted from these surfaces for analysis, with or without nested amplification.

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Part of the research described in this poster was carried out by the Jet Propulsion Laboratory, California Institute of Technology, under contract with the National Aeronautics and Space Administration

ABSTRACT *[Presentation]*

Development and Implementation of Molecular Tools for Assessing the Viability of Microbes on Spacecraft and Associated Surfaces

Vaishampayan, P., La Duc, M. T., and Venkateswaran, K.

The development of molecular methods to selectively detect the living portion of microbial population resident on spacecraft surfaces, to the exclusion of dead biomass, is of immense importance to planetary protection imposed bioburden assessment, in addition to probabilistic calculations of forward contamination. A firefly luciferase bioluminescence assay method that differentiates free extracellular ATP (cellular debris, etc.) from intracellular ATP (viable microbes) was used to determine the viable microbial burden of various cleanroom facilities. A large fraction of the samples analyzed were positive for intracellular ATP, which was measured after enzymatically degrading the sample's exogenous ATP, despite the fact that no colonies arose on agar plates. Subsequently, total genomic DNA was isolated directly from selected samples and 16S rRNA gene fragments were cloned and sequenced. The nearest neighbors to many of these sequenced rRNA genes were known to be non-cultivable in/on the media employed. Treating samples with the DNA-intercalating dye propidium monoazide (PMA) prior to downstream PCR-based detection has become an increasingly popular means of differentiating the living (viable) and dead (non-viable) portions of a given microbial assemblage. Surface samples were processed with and without PMA treatment, subjected to DNA extraction and PCR amplification with universal primers, and analyzed via 454-pyrosequencing, PhyloChip DNA microarrays, and quantitative PCR. A marked decrease was observed in the diversity and total number of microbes in PMA treated samples, indicative of the expected low proportions of viable cells in cleanroom environments. Furthermore, a greatly diminished viable microbial population was observed in samples collected from mission-critical cleanrooms, in comparison to samples retrieved from non-mission cleanrooms where cleaning regimens were less stringent. The coupling of compatible PMA-PhyloChip/pyrosequencing techniques is an attractive methodology for detecting viable microbes in spacecraft-associated environments, which is of crucial importance to practices aimed at reducing the abundance of spacecraft-borne microbial contaminants.

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ABSTRACT *[Poster]*

Viability Assessment of Microbial Communities Using State-of-the-Art Molecular Techniques

Vaishampayan, P., Probst, A., La Duc, M.T., Bargoma, E., Benardini, J.N., Andersen, G., and Venkateswaran, K.

The advent of phylogenetic microarrays and high-throughput pyrosequencing has dramatically increased the resolvable spectrum of microbial lineages from environmental samples. Despite an expanding array of methods detecting the presence of microbes in a sample, means of assessing the differential viability of cells remain elusive. The development of molecular methods to selectively detect the viable microbial population resident on spacecraft surfaces is of immense importance to planetary protection imposed bioburden limitations, in addition to probabilistic calculations of forward contamination. Treating cell suspensions with the DNA-intercalating dye propidium monoazide (PMA) prior to downstream PCR-based detection has become an increasingly popular means of differentiating the viable and dead (non-viable) portions of a given microbial assemblage. PMA permeates the compromised membranes of dead cells, and thus selectively targets non-viable bacterial cells by intercalating, and upon photoactivation covalently cross linking DNA, thus precluding downstream PCR. Here, emerging molecular techniques were employed in a concerted manner to better understand the diversity and distribution of viable microbes in spacecraft assembly cleanrooms. Surface samples were processed with and without PMA treatment, subjected to DNA extraction and PCR amplification with universal primers, and analyzed via Titanium 454-pyrosequencing, PhyloChip DNA microarrays, and quantitative PCR. A marked decrease was observed in the diversity and total number of microbes in PMA treated samples, indicative of the expected low proportions of viable cells in cleanroom environments. Furthermore, a greatly diminished viable microbial population was observed in samples collected from mission-critical cleanrooms, in comparison to samples retrieved from non-mission cleanrooms where cleaning regimens were less stringent. The coupling of compatible PMA-PhyloChip/pyrosequencing techniques is an attractive methodology for detecting viable microbes in spacecraft-associated environments, which is of crucial importance to practices aimed at reducing the abundance of spacecraft-borne microbial contaminants.

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Viability Assessment Of Microbial Communities Using State-of-the-Art Molecular Techniques

Parag Vaishampayan[1*], Alexander J Probst[2], Myron T. La Duc[1], Emilee Bargoma[1], James N. Benardini[1], Gary L. Andersen[3] and Kasthuri Venkateswaran[1]

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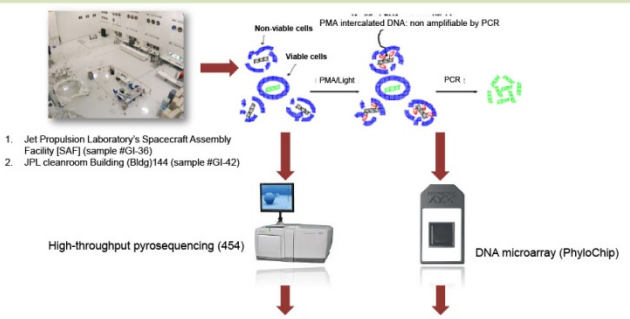
Abstract

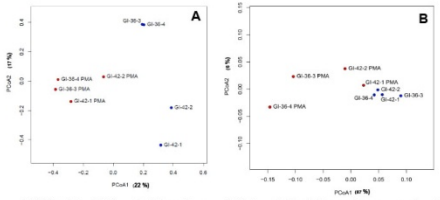
The advent of phylogenetic microarrays and high-throughput pyrosequencing has dramatically increased the resolvable spectrum of microbial lineages from environmental samples. Despite an expanding array of methods detecting the presence of microbes in a sample, means of assessing the differential viability of cells remain elusive. The development of molecular methods to selectively detect the viable microbial population resident on spacecraft surfaces, is of immense importance to planetary protection imposed bioburden limitations, in addition to probabilistic calculations of forward contamination.
Here, emerging molecular techniques were employed in a concerted manner to better understand the diversity and distribution of viable microbes in spacecraft assembly cleanrooms.

Methodology



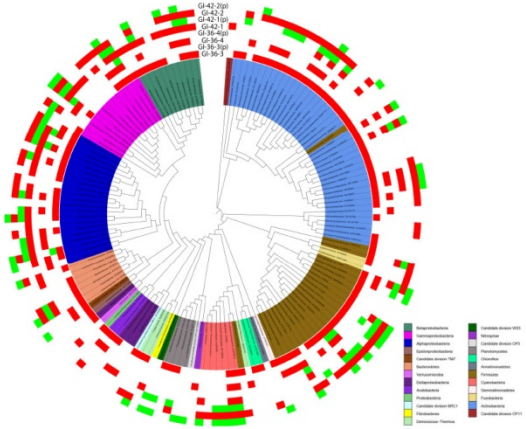
Data obtained from both the approaches was subjected to series of computational algorithms to elucidate complete spectrum of microbial diversity and community dynamics.

- Principal Coordinate Analysis (PCoA) based on: (A) number of pyrosequences per MOTU and (B) PhyloChip-derived transformed hybridization scores of each PTU.
- All of the samples analyzed *without* PMA-treatment clustered together, indicative of their relatively similar community structure, compared to their coinciding PMA-treated sample fractions.

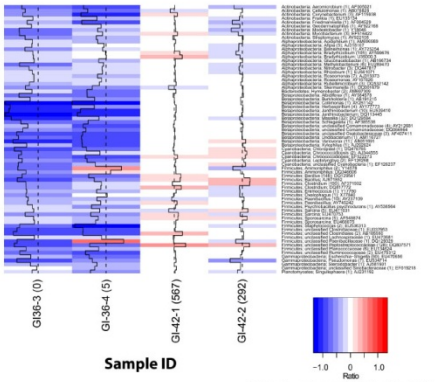


Red and Blue dots represents PMA treated and PMA-non treated samples respectively. Percent values in the parentheses represents explained variance.

A phylogenetic tree based on the PhyloChip PTU grouped at the family level and their presence in each sample was depicted.

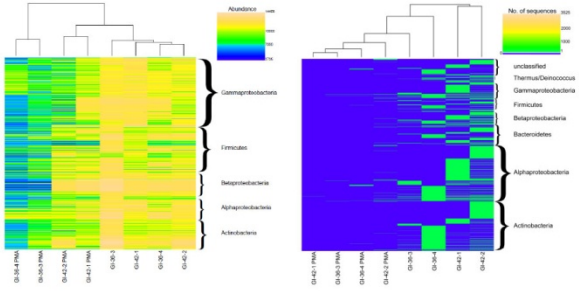


- Heatmap of PTU that increased in transformed hybridization intensities in PMA treated samples compared to non-PMA treated samples and were called present in at least one of the PMA-treated samples.
- An increase in PMA treated sample is reflected as a positive ratio.
- Representatives of all genera with the most drastic changes for each sample pair are displayed.



Numbers in parentheses are the total number of PTU.

- Heatmap based on number of sequences and transformed hybridization scores of all PTU detected in at least one of the samples was analyzed.
- The dendogram (based on Euclidean distance measure) groups all non-PMA treated samples as a separate cluster, which indicates a similar microbial community structure among these samples.
- An observed increase in the transformed hybridization intensity of a given PTU following PMA treatment would likely stem from PCR bias in non-PMA-treated samples, where high levels of DNA originating from non-viable cells are co-amplified.



Conclusions

- A dramatic decrease in the total number of bacterial genera was observed in all samples upon pre-treatment with PMA.
- Based on the multiple statistical approaches employed [Multi Response Permutation Procedure (MRPP) , a Euclidean-distance based dendogram, Adonis based on Bray-Curtis distance, Diversity indices (Shannon-Wiener), ADONIS test and an ordination (PCoA) analyses] it was clear that PMA-treated samples and non-PMA samples were dissimilar with respect to diversity in bacterial community profiles.
- The results of this study suggests that hitherto, the breadth of diversity enveloped within the viable fraction(s) of typical spacecraft-associated microbial communities have been overestimated.
- Coupling the PMA-linked bTEFAP/PhyloChip technologies developed in this study could lead to drastically improved approaches for monitoring the total viable microbial burden of an environment.

Acknowledgement

Part of the research described in this study was carried out at the Jet Propulsion Laboratory, California Institute of Technology, under contract with the National Aeronautics and Space Administration. A. Probst's contribution was supported by the German National Academic Foundation (Studienstiftung des deutschen Volkes). The authors are grateful to T. DeSantis, L. Tom, for PhyloChip analyses, S. Westcott and P. Schloss, for pyrosequence analysis, J. Andy Spry and K. Buxbaum for valuable advice and guidance. The authors also thank M. Cooper and C. Stam for assistance with sample collection and processing.

ABSTRACT *[Poster]*

Assessing Bacterial, Archaeal, and Fungal Diversity of Spacecraft-Associated Surfaces via Tag-Encoded FLX Amplicon Pyrosequencing

La Duc, M. T., Vaishampayan, P., Nilsson, H.R., Torok, T., and Venkateswaran, K.

The introduction of contaminant microbiota to extraterrestrial settings could have profound repercussions to the scientific integrity of in-situ and sample-return based life detection experiments, and thus a key challenge lies in providing a comprehensive account of the genetic signatures of microbes resident on spacecraft hardware. The advent of high-throughput massively parallel tag-encoded FLX amplicon pyrosequencing (TEFAP) has dramatically increased the resolution of detection of distinct microbial lineages in mixed microbial assemblages. DNA microarray approaches alone are unlikely to achieve an all-inclusive account of the microbial phylotypes present in a given sample, since they cannot account for unknown species and are limited to those present in pre-existing databases. In contrast, TEFAP approaches are not predicated on a priori information, and thus yield far more comprehensive results. To date, a comprehensive census of the total microbial population associated with spacecraft hardware has yet to be provided. Surface areas of 250 m2 were collected from spacecraft hardware and assembly cleanrooms, and total genomic DNA was extracted. Variable regions of the 16S rRNA gene (bacteria and archaea) and ITS region (fungi) were targeted and PCR amplified, and a minimum of 3,000 reads were obtained for each 250 m2 sample. A MOTHUR-based bioinformatics pipeline was used to process gene sequences and generate microbial diversity profiles for each of the various types of spacecraft associated samples. Analysis of the TEFAP data enabled cogent inferences to be drawn regarding the complete phylogenetic spectrum of microbes present. Computational population modeling then facilitated predictions about the proportions of innocuous/resistant, transient/recurrent, and ecologically inconsequential/dominant taxa present about the spacecraft surface, thereby empowering forward contamination risk assessments based on microbial recurrence. The successful application of emerging technologies to a spacecraft-relevant microbial census is encouraging, and TEFAP approaches in particular are of immense potential for future analyses of fluctuations in spacecraft-associated microbial populations.

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Assessing Bacterial, Archaeal, and Fungal Diversity of Spacecraft-Associated Surfaces via Tag-Encoded FLX Amplicon Pyrosequencing

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ABSTRACT

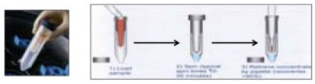
The introduction of microbiota to extraterrestrial settings could have profound repercussions on the scientific integrity of in-situ and sample-return based life detection experiments, and thus a key challenge lies in providing a comprehensive account of the genetic signatures of microbes resident on spacecraft hardware. The advent of high-throughput massively parallel tag-encoded FLX amplicon pyrosequencing (TEFAP) has dramatically increased the resolution of detection of distinct microbial lineages in mixed communities. DNA microarray approaches alone are unlikely to achieve an all-inclusive account of the microbial phylotypes present in a sample, since they cannot fully account for unknown species and are limited to those present in pre-existing databases. In contrast, TEFAP approaches are not predicated on *a priori* information, and thus yield far more comprehensive results. To date, a comprehensive census of the total microbial population associated with spacecraft hardware has yet to be provided.

Surface areas of 250 m^2 were collected from spacecraft hardware and assembly cleanrooms, and total genomic DNA was extracted. Variable regions of the 16S rRNA gene (bacteria and archaea) and ITS region (fungi) were targeted and PCR amplified, and a minimum of 3,000 reads were obtained for each 250 m^2 sample. A MOTHUR-based bioinformatics approach was used to process gene sequences and generate microbial diversity profiles for each of the various types of spacecraft associated samples. Analysis of the TEFAP data enabled cogent inferences to be drawn regarding the complete phylogenetic spectrum of microbes present. Computational population modeling then facilitated predictions about the proportions of innocuous/resistant, transient/recurrent, and ecologically inconsequential/dominant taxa present about the spacecraft surface, thereby empowering forward contamination risk assessments based on microbial recurrence. The successful application of emerging technologies to a spacecraft-relevant microbial census is encouraging, and TEFAP approaches in particular are of immense potential for future analyses of fluctuations in spacecraft-associated microbial populations.

SAMPLE COLLECTION & PROCESSING

Sample Collection. Samples were collected from spacecraft hardware via sampling 1 m^2 surface areas with sterile, water-moistened polyester wipes (Texwipe, Upper Saddle River, NJ). Samples (1m^2) were collected from spacecraft assembly cleanroom floors and ground support equipment via wet-surface sampling with BiSKit devices (QuickSilver Analytics, Abingdon, MD).

Pooling and Concentration of Samples. As spacecraft-associated samples are extremely low in biomass and seldom yield detectable PCR products (Moissl, et al., 2008), the authors pooled multiple samples from each sampling event and/or vicinity. All samples were filter-concentrated using Amicon Ultra-50 Ultracel centrifugal filters (Millipore, Billerica, MA). Each unit has a molecular mass cutoff of 50 kDa, which facilitates the concentration of bacterial cells, spores, and exogenous nucleic acid fragments greater than 100 bp into a final volume of 500 µl.



DNA Purification. Samples were divided into equivalent fractions, one of which was subjected to bead-beating in a FastPrep instrument (MP Biomedicals, Santa Ana, CA). After bead-beating, the fractions were recombined and subjected to total DNA purification via the Maxwell MDx automated nucleic acid extraction system (Promega, Madison, WI).

Table 1. Sample characteristics of various spacecraft and associated surfaces

Sample (total area sampled)	Sample ID	Sampling devices	Sample type	Area (m2)	Cleanroom type	Description
Cleanroom types (53 m^2)						
GI-37	139	BiSKit	Floor-70A	10	Non-NASA Cleanroom	Non-NASA cleanroom (LBNL; #70A)
GI-35-6	143	BiSKit	Entrance floor	1	Ordinary room	Ordinary room adjacent to JPL-SAF
GI-35-4	141	BiSKit	Shoe Cleaner	1	Ordinary room	Ordinary room adjacent to JPL-SAF
GI-35-7	144	BiSKit	Floor 1	1	Ordinary room	Ordinary room adjacent to JPL-SAF
GI-35-8	145	BiSKit	Floor 2	1	Ordinary room	Ordinary room adjacent to JPL-SAF
GI-35-5	142	BiSKit	Air-lock	1	Ordinary room	Ordinary room adjacent to JPL-SAF
GI-36-3	146	BiSKit	JPL-SAF GSE	9	Class 100K	During spacecraft assembly (JPL-SAF)
GI-36-4	148	BiSKit	JPL-SAF Floor	9	Class 100K	During spacecraft assembly (JPL-SAF)
Cleaning vs. prior to cleaning (38 m^2)						
GI-42-1	155	BiSKit	Floor	9	Class 100K	JPL-144 cleanroom prior to cleaning
GI-42-2	157	BiSKit	GSE	9	Class 100K	JPL-144 cleanroom prior to cleaning
GI-43-1	159	Polyester wipe	Floor	10	Class 100K	JPL-144 cleanroom after cleaning
GI-43-2	161	Polyester wipe	GSE	10	Class 100K	JPL-144 cleanroom after cleaning
Spacecraft surfaces (early ATLO; spore count-based (110 m^2))						
GI-16	124	Polyester wipe	spacecraft	6	Class 100K	No spore count
GI-17	125	Polyester wipe	spacecraft	10	Class 100K	No spore count
GI-25	133	Polyester wipe	spacecraft	8	Class 100K	No spore count
GI-26	134	Polyester wipe	spacecraft	7	Class 100K	No spore count
GI-27	135	Polyester wipe	spacecraft	4	Class 100K	No spore count
GI-28	136	Polyester wipe	spacecraft	6	Class 100K	No spore count
GI-29	137	Polyester wipe	spacecraft	18	Class 100K	No spore count
GI-18	126	Polyester wipe	spacecraft	10	Class 100K	1 to 5 spores per m2
GI-19	127	Polyester wipe	spacecraft	14	Class 100K	1 to 5 spores per m2
GI-20	128	Polyester wipe	spacecraft	5	Class 100K	1 to 5 spores per m2
GI-21	129	Polyester wipe	spacecraft	4	Class 100K	1 to 5 spores per m2
GI-22	130	Polyester wipe	spacecraft	1	Class 100K	1 to 5 spores per m2
GI-30	138	Polyester wipe	spacecraft	13	Class 100K	1 to 5 spores per m2
GI-32	140	Polyester wipe	spacecraft	3	Class 100K	5 to 10 spores per m2
GI-24	132	Polyester wipe	spacecraft	1	Class 100K	300 spores per m2
Spacecraft surfaces (late ATLO; component-based (52 m^2))						
GI-38	151	Polyester wipe	spacecraft	26	Class 100K	Component C5 (0.2 spores per m2)
GI-39	152	Polyester wipe	spacecraft	9	Class 100K	Component D5 (0.4 spores per m2)
GI-40	153	Polyester wipe	spacecraft	16	Class 100K	Component R (0.3 spores per m2)
GI-41	154	Polyester wipe	spacecraft	1	Class 100K	Non-flight samples (14 spores per m2)

JPL-SAF: Jet Propulsion Laboratory-Spacecraft Assembly Facility; LBNL: Lawrence Berkeley National Laboratory

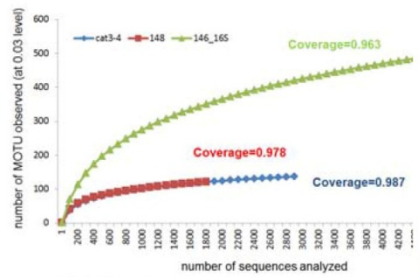
ANALYSIS

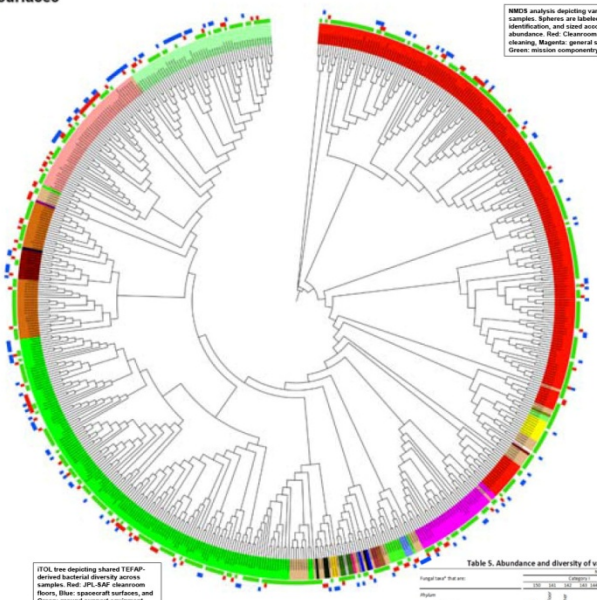
Tag Encoded FLX Amplicon Pyrosequencing (TEFAP). Bacterial-biased primers 28F and 519R, and archaeal-biased 341F and 958R primers were used to PCR amplify ~550 bp 16S rRNA gene fragments from bacteria and archaea, respectively. Fungal-biased ITS1F and ITS4R primers were employed to amplify ~600 bp fragments of the ITS region. Primer pairs were tailored for TEFAP by adding a fusion linker and a proprietary barcode sequence at the 5' end of the forward primer, and a biotin and fusion linker sequence at the 5' end of the reverse primer (Dowd, et al., 2008). A HotStarTaq Plus master mix kit (QIAGEN) was used to catalyze the PCR under the following thermal cycling conditions: initial denaturing at 95ºC for 5 min, followed by 35 cycles of denaturing at 95ºC for 30 s, annealing at 54ºC for 40 s, and extension at 72ºC for 1 min, finalized by a 10-minute elongation at 72ºC. Resulting PCR products were purified via Rapid Tips (Diffinity Genomics, Inc, West Henrietta, NY), and were pooled accordingly. Small fragments were removed with Ampure Beads (Beckman Coulter, CA). For FLX-Titanium sequencing (Roche, Nutley, New Jersey), resulting PCR amplicon fragment size and concentration were measured with DNA chips using an Experion automated electrophoresis station (Bio-Rad) and a TBS-380 Fluorometer (Turner Biosystems, CA). The total volume of initial PCR product used for subsequent emulsion PCR was 2 uL for strong positives, 5 uL for weak positives, and 20 uL for samples that failed to yield PCR products. This normalization step helped to ensure minimal bias favoring downstream amplification from initially strong PCR products. Approximately 9.6 x 10^6DNA molecules of ~ 600 bp double-stranded DNA were combined with 9.6 x 10^6DNA capture beads, and then subjected to emulsion PCR conditions. Following recovery and enrichment, bead-attached DNA molecules were denatured with NaOH and sequencing primers were annealed. A four-region TEFAP run was performed on a GS PicoTiterPlate (PTP) using the Genome Sequencer FLX System in accordance with manufacturer's instructions. Twenty-four to 30 tagged samples were applied to each quarter region of the PTP. All TEFAP procedures were performed at the Research and Testing Laboratory (Lubbock, TX) according to well established protocols (Dowd, et al., 2008).

Bioinformatic analyses. Bacterial and archaeal pyrosequences were processed and analyzed using MOTHUR software (Schloss *et al.* 2009), with the AmpliconNoise algorithm implemented to reduce error. Sequences were removed from consideration if they (a) did not contain the primer sequence, (b) contained an uncorrectable barcode, (c) were < 200 nt in length, or (d) had a quality score < 25. Unique sequences were aligned using the SILVA reference alignment (Schloss, 2009) and trimmed such that only regions of overlapping columns of sequence data were considered. Filtered sequences were assigned to samples according to their barcode. After removing chimeras, sequences were classified in accordance with the new Greengenes training set and taxonomy (McDonald, et al., 2011, Werner, et al., 2012), and clustered into operational taxonomic units at the 0.03 level. The full-length ITS1 sub-region was extracted from the fungal ITS dataset using ITS Extractor v. 1.1 (Nilsson et al., 2010), dismissing entires for which not both of the 3' end of the SSU gene and the 5' end of the 5.8S gene were found. The ITS1 sequences were clustered in CrunchClust v. 43 (Hartmann et al., in press) with pyrosequencing homopolymer correction enabled and at a Levenshtein distance of 7 (approximately 97% sequence similarity, a threshold value known to perform well for a wide range of fungi in terms of ITS distances (Nilsson et al., 2008)). A representative sequence from each OTU as designated by CrunchClust was annotated for taxonomic affiliation using the ITS 454 pipeline of Tedersoo et al. (2010) against the UNITE (Abarenkov et al., 2010) and INSD (Karsch-Mizachi et al., 2012) databases. The results were verified manually for each molecular taxonomic unit (MOTU). An entry was deemed identified to species level if it produced a ≥ 97% match over the full length of the sequence to a fully identified reference sequence whose name was not contradicted by other, equally good matches. The corresponding values for tentative generic and ordinal affiliation were 85% and 70%, respectively; they were deliberately set to be high to avoid false-positive inclusions. In the case of competing names for which neither synonymy nor anamorph-teleomorph relationships could be established through MycoBank (Crous et al., 2004), the least inclusive parent nomenclatural level was used (e.g., *Penicillium* sp.).

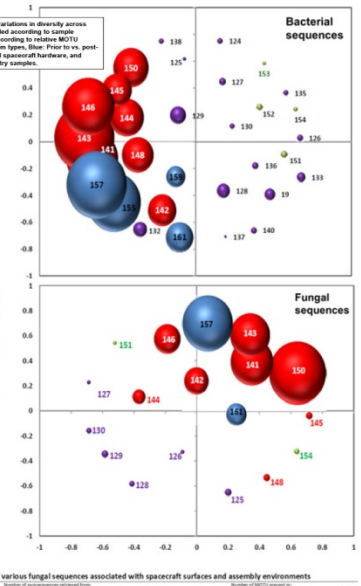
RESULTS

Rarefaction analysis: JPL-SAF floors, GSE, and spacecraft surfaces





iTOL tree depicting shared TEFAP-derived bacterial diversity across samples. Red: JPL-SAF cleanroom floors, Blue: spacecraft surfaces, and Green: ground support equipment.



NMDS analysis depicting variations in diversity across samples. Spheres are labeled according to sample identification, and sized according to relative MOTU abundance. Red: Cleanroom types, Blue: Prior to vs. post-cleaning, Magenta: general spacecraft hardware, and Green: mission componentry samples.

146_165	148_165	cat3	Class	Genus
11	1	26	Actinobacteria(100)	Corynebacterium(100)
77	4	14		Modestobacter(100)
38	3	2		Arthrobacter(100)
317	218	97		Propionibacterium(100)
89	39	65	Bacilli(100)	Staphylococcus(100)
34	64	5		Staphylococcus(100)
10	71	9	Alphaproteobacteria(100)	Brevundimonas(98)
201	47	57		Blastobacter(56)
83	1	25		Methylobacterium(100)
29	9	8		Methylobacterium(100)
42	15	3		Rubellimicrobium(100)
9	7	91		unclassified(100)
4	9	4		unclassified(100)
15	2	13	Gammaproteobacteria(100)	unclassified(95)
3	4	48		Escherichia(68)
7	45	8		Acinetobacter(100)
1	48	50		Acinetobacter(100)
2	180	170		Acinetobacter(100)
24	26	59		Pseudomonas(100)

19 common MOTU

Table 3. Bacterial MOTU retrieved from various spacecraft and associated surfaces

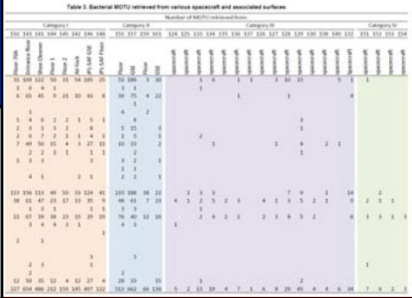
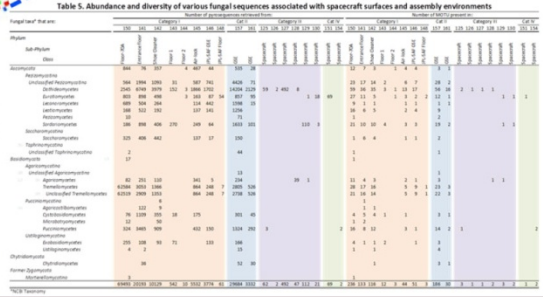


Table 4. Archaeal pyrosequences and MOTU retrieved from various spacecraft and associated surfaces

Archaeal taxa	Number of archaeal pyrosequences/MOTU from: Category I: Floor (150)	Entrance floor (143)	Shoe Cleaner (141)	Air-lock (142)	JPL-GSE (148)	Cat II: GSE (157)	GSE (161)	Category III: Spacecraft (124)	Spacecraft (126)	Spacecraft (127)	Spacecraft (128)	Spacecraft (130)	Spacecraft (132)
Nitrosphaeraceae - SCA114-1	17		35	47		5	2						
Nitrosphaeraceae - SCA114-2			1										
Nitrosphaeraceae - SCA117		6											
Methanobacteriaceae - 1								1	2	7	3	16	1
Methanobacteriaceae - 3												1	
Number of archaeal MOTUs	1	1	2	1		1	1	1	1	1	1	2	1

Table 5. Abundance and diversity of various fungal sequences associated with spacecraft surfaces and assembly environments



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Part of the research described here was carried out at the Jet Propulsion Laboratory, California Institute of Technology, under a contract with the National Aeronautics and Space Administration.

ABSTRACT *[Presentation]*

Bacterial, Archaeal, and Fungal Diversity of Spacecraft-Associated Surfaces

La Duc, M. T., Vaishampayan, P., and Venkateswaran, K.

The introduction of contaminant microbiota to extraterrestrial settings could have profound repercussions on the scientific integrity of in-situ and sample-return based life detection experiments. Thus a key challenge lies in providing a comprehensive account of the molecular signatures of microorganisms resident on spacecraft hardware. It will be essential to know which organisms pose the greatest threat of contamination based on recurrent isolation and/or detection on spacecraft associated surfaces, so that their presence can be preferably eliminated, or at least recognized and discriminated from any authentic extraterrestrial biosignatures. The advent of high-throughput molecular biological methodologies has dramatically increased the resolution and sensitivity of detection of various microbial lineages in mixed assemblages. At present, NASA is developing such enabling technologies capable of providing a detailed, comprehensive census of the microorganisms present on spacecraft surfaces. Establishing such a genetic inventory will prove invaluable when working to meet the anticipated requirements for potential future missions to return samples from Mars.

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APPENDIX E: MOLECULAR ANALYSIS DATA

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E.1 DNA Archive: Metadata

Table E.1-1. Characteristics of Genetic Inventory Task DNA samples archived at JPL (Bldg 98).

Sample ID	Sample Description	Sample Source	Sampling Device	Date	Mission	Samples Pooled	Barcode	GI-Container	Row	Column	Sample Volume	16S rRNA Gene Copies
GI1-1	BIG Control	Buffer control	PBS	01/03/07	Phoenix at LMA		000308	1	A	1	15	
GI1-2	1-MTF-1B	Floor	BiSKit	01/03/07	Phoenix at LMA		Samples not listed in SampleWare database					
GI1-3	1-MTF-2B	Floor	BiSKit	01/03/07	Phoenix at LMA		Samples not listed in SampleWare database					
GI1-4	1-MTF-3B	Floor	BiSKit	01/03/07	Phoenix at LMA		Samples not listed in SampleWare database					
GI1-5	1-MTF-4B	Floor	BiSKit	01/03/07	Phoenix at LMA		Samples not listed in SampleWare database					
GI1-6	1-MTF-5B	Floor	BiSKit	01/03/07	Phoenix at LMA		Samples not listed in SampleWare database					
GI1-7	1-MTF-6B	Floor	BiSKit	01/03/07	Phoenix at LMA		Samples not listed in SampleWare database					
GI1-8	1-MTF-7B	Floor	BiSKit	01/03/07	Phoenix at LMA		Samples not listed in SampleWare database					
GI1-9	1-MTF-8B	Floor	BiSKit	01/03/07	Phoenix at LMA		000309	1	A	2	10	
GI1-10	1-MTF-9B	Floor	BiSKit	01/03/07	Phoenix at LMA		000310	1	A	3	15	
GI1-11	1-MTF-10B	Floor	BiSKit	01/03/07	Phoenix at LMA		000311	1	A	4	10	
GI1-12	1-MTF-BLNK	Blank	BiSKit	01/03/07	Phoenix at LMA		Sample not listed in SampleWare database					
GI1-13	PHX swab BLNK 10 pooled	Blank	Cotton swab	01/03/07	Phoenix at LMA		000312	1	A	5	10	1.22E+02
GI1-14	MTF Swab BLNK9 pooled	Blank	Cotton swab	01/03/07	Phoenix at LMA		000313	1	A	6	10	1.45E+02
GI1-15	MTF Swab 9 pooled	Floor	Cotton swab	01/03/07	Phoenix at LMA		000314	1	A	7	0	1.60E+04
GI1-16	PHX s/c swab10 pooled	Spacecraft	Cotton swab	01/03/07	Phoenix at LMA		000315	1	A	8	0	1.47E+04
GI2-1	SSB-1B	Floor	BiSKit	02/03/07	Phoenix s/c not in SSB		000316	1	A	9	10	
GI2-2	SSB-2B	Floor	BiSKit	02/03/07	Phoenix s/c not in SSB		000317	1	B	1	15	
GI2-3	SSB-3B	Floor	BiSKit	02/03/07	Phoenix s/c not in SSB		000318	1	B	2	10	
GI2-4	SSB-4B	Floor	BiSKit	02/03/07	Phoenix s/c not in SSB		000319	1	B	3	10	
GI2-5	SSB-5B	Floor	BiSKit	02/03/07	Phoenix s/c not in SSB		000320	1	B	4	10	
GI2-6	SSB Swab 10 pooled	Floor	Cotton swab	02/03/07	Phoenix s/c not in SSB		000321	1	B	5	0	1.00E+05
GI2-7	SSB Swab BLNK 10 pooled	Blank	Cotton swab	02/03/07	Phoenix s/c not in SSB		000322	1	B	6	10	
GI3-1	PHSF W1	Floor	BiSKit	04/24/07	Before Phoenix		000323	1	B	7	15	
GI3-2	PHSF W2-SE	Floor	BiSKit	04/24/07	Before Phoenix		000324	1	B	8	15	
GI3-3	PHSF W3-Center	Floor	BiSKit	04/24/07	Before Phoenix		000325	1	B	9	10	
GI3-4	PHSF W4-NW	Floor	BiSKit	04/24/07	Before Phoenix		000326	1	C	1	15	
GI3-5	PHSF B5-SW	Floor	BiSKit	04/24/07	Before Phoenix		000327	1	C	2	15	
GI3-6	PHSF B6-E	Floor	BiSKit	04/24/07	Before Phoenix		000329	1	C	3	10	
GI3-7	PHSF B7-W	Floor	BiSKit	04/24/07	Before Phoenix		000330	1	C	4	15	
GI3-8	PHSF B8-N	Floor	BiSKit	04/24/07	Before Phoenix		000331	1	C	5	15	
GI3-9	PHSF B9-S	Floor	BiSKit	04/24/07	Before Phoenix		000332	1	C	6	15	
GI3-10	PHSF B10-Wall	Floor	BiSKit	04/24/07	Before Phoenix		000333	1	C	7	10	1.57E+05
GI3-FC1	BiSKit Field Control #1	Field control	BiSKit	04/24/07	Before Phoenix		000334	1	C	8	10	
GI3-BRC1	BiSKit PBS Control #1	Buffer control	PBS	04/24/07	Before Phoenix		000335	1	C	9	10	1.40E+02
GI3-BIG	Autolyser Cartridge Control	Buffer control	PBS	04/24/07	Before Phoenix		000336	1	D	1	10	1.26E+02
GI4-1	IP1-GI (BiSKit samples)	Floor	BiSKit	06/27/07	During Phoenix		000337	1	D	2	15	
GI4-2	IP2-GI	Floor	BiSKit	06/27/07	During Phoenix		000338	1	D	3	15	
GI4-3	IP3-GI	Floor	BiSKit	06/27/07	During Phoenix		000339	1	D	4	10	
GI4-5	IP5-GI	Floor	BiSKit	06/27/07	During Phoenix		000340	1	D	5	10	
GI4-6	IP6-GI	Floor	BiSKit	06/27/07	During Phoenix		000341	1	D	6	15	
GI4-7	IP7-GI	Floor	BiSKit	06/27/07	During Phoenix		000342	1	D	7	20	
GI4-8	IP8-GI	Floor	BiSKit	06/27/07	During Phoenix		000343	1	D	8	10	8.79E+05
GI4-1-blnk	IP1-GI-blnk (in 15 ml tubes)	Blank	BiSKit	06/27/07	During Phoenix		000344	1	D	9	15	1.45E+02
GI4-2-blnk	IP2-GI-blnk	Blank	BiSKit	06/27/07	During Phoenix		000345	1	E	1	20	
GI4-3-blnk	IP3-GI-blnk	Blank	BiSKit	06/27/07	During Phoenix		000346	1	E	2	15	
GI4-5-blnk	IP5-GI-blnk	Blank	BiSKit	06/27/07	During Phoenix		000347	1	E	3	15	
GI4-6-blnk	IP6-GI-blnk	Blank	BiSKit	06/27/07	During Phoenix		000348	1	E	4	15	

Sample ID	Sample Description	Sample Source	Sampling Device	Date	Mission	Samples Pooled	Barcode	GI-Container	Row	Column	Sample Volume	16S rRNA Gene Copies
GI4-7-blnk	IP7-GI-blnk	Blank	BiSKit	06/27/07	During Phoenix		000349	1	E	5	15	
GI4-8-blnk	IP8-GI-blnk	Blank	BiSKit	06/27/07	During Phoenix		000350	1	E	6	15	
GI4-BIG(-)		Buffer control	PBS	06/27/07	During Phoenix		000351	1	E	7	15	1.47E+02
GI5-1	PPO-PHSF-1B	Floor	BiSKit	07/20/07	Post-Phoenix		000352	1	E	8	15	
GI5-2	PPO-PHSF-2B	Floor	BiSKit	07/20/07	Post-Phoenix		000353	1	E	9	15	
GI5-3	PPO-PHSF-3B	Floor	BiSKit	07/20/07	Post-Phoenix		000354	1	F	1	15	
GI5-4	PPO-PHSF-4B	Floor	BiSKit	07/20/07	Post-Phoenix		000355	1	F	2	10	
GI5-5	PPO-PHSF-5B	Floor	BiSKit	07/20/07	Post-Phoenix		000356	1	F	3	15	
GI5-6	PPO-PHSF-6B	Floor	BiSKit	07/20/07	Post-Phoenix		000357	1	F	4	10	
GI5-7	PPO-PHSF-7B	Floor	BiSKit	07/20/07	Post-Phoenix		000358	1	F	5	10	
GI5-8	PPO-PHSF-8B	Floor	BiSKit	07/20/07	Post-Phoenix		000359	1	F	6	10	
GI5-9	PPO-PHSF-9B	Floor	BiSKit	07/20/07	Post-Phoenix		000360	1	F	7	10	
GI5-10	PPO-PHSF-10B	Floor	BiSKit	07/20/07	Post-Phoenix		000361	1	F	8	15	
GI5-12	PPO-PHSF-12B	Floor	BiSKit	07/20/07	Post-Phoenix		000362	1	F	9	15	
GI5-13	PPO-PHSF-13B	Floor	BiSKit	07/20/07	Post-Phoenix		000363	1	G	1	15	
GI5-14	PPO-PHSF-14B	Floor	BiSKit	07/20/07	Post-Phoenix		000364	1	G	2	15	
GI5-15	PPO-PHSF-15B	Floor	BiSKit	07/20/07	Post-Phoenix		000365	1	G	3	15	
GI5-16	PPO-PHSF-16B	Floor	BiSKit	07/20/07	Post-Phoenix		000366	1	G	4	10	
GI5-17	PPO-PHSF-17B	Floor	BiSKit	07/20/07	Post-Phoenix		000367	1	G	5	15	
GI5-18	PPO-PHSF-18B	Floor	BiSKit	07/20/07	Post-Phoenix		000368	1	G	6	20	
GI5-19	PPO-PHSF-19B	Floor	BiSKit	07/20/07	Post-Phoenix		000369	1	G	7	15	
GI5-20	PPO-PHSF-20B	Floor	BiSKit	07/20/07	Post-Phoenix		000370	1	G	8	15	1.80E+05
GI6-1	PHSF-1B	Floor	BiSKit	08/02/07	Post Phoenix		000775	1	G	9	5	0.00E+00
GI6-2	PHSF-2B	Floor	BiSKit	08/02/07	Post Phoenix		000371	1	H	1	15	
GI6-3	PHSF-3B	Floor	BiSKit	08/02/07	Post Phoenix		000776	1	H	2	0	1.02E+08
GI6-4	PHSF-4B	Floor	BiSKit	08/02/07	Post Phoenix		000372	1	H	3	15	
GI6-5	PHSF-5B	Floor	BiSKit	08/02/07	Post Phoenix		000373	1	H	4	15	
GI6-6	PHSF-6B	Floor	BiSKit	08/02/07	Post Phoenix		000374	1	H	5	15	
GI6-7	PHSF-7B	Floor	BiSKit	08/02/07	Post Phoenix		000789	1	H	6	0	0.00E+00
GI6-8	PHSF-8B	Floor	BiSKit	08/02/07	Post Phoenix		000375	1	H	7	15	
GI6-9	PHSF-9B	Floor	BiSKit	08/02/07	Post Phoenix		Samples not listed in SampleWare database					
GI6-10	PHSF-10B	Floor	BiSKit	08/02/07	Post Phoenix		Samples not listed in SampleWare database					
GI6-1blnk	PHSF-1-blnk	Blank	BiSKit	08/02/07	Post Phoenix		Samples not listed in SampleWare database					
GI6-2blnk	PHSF-2-blnk	Blank	BiSKit	08/02/07	Post Phoenix		000376	1	H	8	15	
GI6-3blnk	PHSF-3-blnk	Blank	BiSKit	08/02/07	Post Phoenix		Samples not listed in SampleWare database					2.92E+02
GI6-4blnk	PHSF-4-blnk	Blank	BiSKit	08/02/07	Post Phoenix		000377	1	H	9	15	
GI6-5blnk	PHSF-5-blnk	Blank	BiSKit	08/02/07	Post Phoenix		000378	1	I	1	15	
GI6-6blnk	PHSF-6-blnk	Blank	BiSKit	08/02/07	Post Phoenix		000379	1	I	2	15	
GI6-7blnk	PHSF-7-blnk	Blank	BiSKit	08/02/07	Post Phoenix		Samples not listed in SampleWare database					1.05E+02
GI6-8blnk	PHSF-8-blnk	Blank	BiSKit	08/02/07	Post Phoenix		000380	1	I	3	15	
GI6-9blnk	PHSF-9-blnk	Blank	BiSKit	08/02/07	Post Phoenix		Samples not listed in SampleWare database					2.04E+02
GI6-10blnk	PHSF-10-blnk	Blank	BiSKit	08/02/07	Post Phoenix		Samples not listed in SampleWare database					2.37E+02
GI6-FC	PHFS-field control BiSKit	Field control	BiSKit	08/02/07	Post Phoenix		000381	1	I	4	15	
GI6-FCblnk	PHFS-field control blank	FC blank	BiSKit	08/02/07	Post Phoenix		000382	1	I	5	15	
GI7-B-1	9C-E	Floor	BiSKit	11/28/07	During Dawn		000383	1	I	6	10	2.75E+05
GI7-B-2	9C-G	Floor	BiSKit	11/28/07	During Dawn		000384	1	I	7	10	
GI7-B-3	9C-D	Floor	BiSKit	11/28/07	During Dawn		000385	1	I	8	10	7.72E+03
GI7-B-4	9C-A	Floor	BiSKit	11/28/07	During Dawn		000386	1	I	9	15	
GI7-B-5	9C Level	Floor	BiSKit	11/28/07	During Dawn		000387	2	A	1	10	1.26E+03
GI7-B-6	9C stair	Floor	BiSKit	11/28/07	During Dawn		000388	2	A	2	15	
GI7-B-7	9C-F	Floor	BiSKit	11/28/07	During Dawn		000389	2	A	3	15	
GI7-B-8	9C by B Central east of s/c	Floor	BiSKit	11/28/07	During Dawn		000390	2	A	4	10	3.09E+03
GI7-B-9	9C D/E	Floor	BiSKit	11/28/07	During Dawn		000391	2	A	5	15	

Sample ID	Sample Description	Sample Source	Sampling Device	Date	Mission	Samples Pooled	Barcode	GI-Container	Row	Column	Sample Volume	16S rRNA Gene Copies
GI7-B-10	Field control @9C	Field control	BiSKit	11/28/07	During Dawn		000392	2	A	6	15	
GI7-B-11	11	Floor	BiSKit	11/28/07	During Dawn		000393	2	A	7	10	1.10E+03
GI7-B-12	12	Floor	BiSKit	11/28/07	During Dawn		000394	2	A	8	15	
GI7-B-13	13	Floor	BiSKit	11/28/07	During Dawn		000395	2	A	9	10	
GI7-B-14	14	Floor	BiSKit	11/28/07	During Dawn		000396	2	B	1	15	
GI7-B-15	15	Floor	BiSKit	11/28/07	During Dawn		000397	2	B	2	10	
GI7-B-16	16	Floor	BiSKit	11/28/07	During Dawn		000398	2	B	3	15	
GI7-B-17	17	Floor	BiSKit	11/28/07	During Dawn		000399	2	B	4	15	
GI7-B-18	18	Floor	BiSKit	11/28/07	During Dawn		000400	2	B	5	15	
GI7-B-19	19	Floor	BiSKit	11/28/07	During Dawn		000401	2	B	6	15	
GI7-B-20	20	Floor	BiSKit	11/28/07	During Dawn		000402	2	B	7	15	
GI7-B-21	B-9/17-1	Floor	BiSKit	11/28/07	During Dawn		000403	2	B	8	0	
GI7-B-22	B-9/17-2	Floor	BiSKit	11/28/07	During Dawn		000404	2	B	9	0	
GI7-B-23	B-9/17-3	Floor	BiSKit	11/28/07	During Dawn		000405	2	C	1	15	
GI7-B-24	B-9/17-4	Floor	BiSKit	11/28/07	During Dawn		000406	2	C	2	15	
GI7-BLNK-1	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		000407	2	C	3	10	1.66E+02
GI7-BLNK-2	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		000408	2	C	4	15	
GI7-BLNK-3	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		000409	2	C	5	15	0.00E+00
GI7-BLNK-4	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		000411	2	C	6	15	
GI7-BLNK-5	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		000412	2	C	7	10	2.17E+02
GI7-BLNK-6	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		000413	2	C	8	15	
GI7-BLNK-7	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		000414	2	C	9	15	
GI7-BLNK-8	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		000415	2	D	1	10	7.51E+02
GI7-BLNK-9	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		000416	2	D	2	15	
GI7-BLNK-10	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		000417	2	D	3	15	
GI7-BLNK-11	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		000418	2	D	4	5	
GI7-BLNK-12	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		000419	2	D	5	15	
GI7-BLNK-13	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		000420	2	D	6	15	
GI7-BLNK-14	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		000421	2	D	7	15	
GI7-BLNK-15	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		000422	2	D	8	15	
GI7-BLNK-16	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		000423	2	D	9	15	
GI7-BLNK-17	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		000424	2	E	1	15	
GI7-BLNK-18	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		000425	2	E	2	15	
GI7-BLNK-19	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		000426	2	E	3	15	
GI7-BLNK-20	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		000427	2	E	4	15	
GI8-1	JPL SAF pooled samples 10 BiSKits)	Floor	BiSKit	10/08/07	During MSL @ JPL SAF		000428	2	E	5	5	8.74E+04
GI8-2	Pooled blanks (10 BiSKits)	Blank	BiSKit	10/08/07	During MSL @ JPL SAF		000429	2	E	6	0	1.19E+02
GI8-3	PBS/BIG	Buffer control	PBS	10/08/07	During MSL @ JPL SAF		000430	2	E	7	10	
GI10-1	JPL SAF pooled samples (20 BiSKits)	Floor	BiSKit	01/22/08	During MSL @ JPL SAF		Samples not listed in SampleWare database					9.51E+07
GI10-2	Pooled blanks (20 BiSKits)	Blank	BiSKit	01/22/08	During MSL @ JPL SAF		Samples not listed in SampleWare database					0.00E+00

Sample ID	Sample Description	Sample Source	Sampling Device	Date	Mission	Samples Pooled	Barcode	GI-Container	Row	Column	Sample Volume	16S rRNA Gene Copies
GI10-3	PBS/BIG	Buffer control	PBS	01/22/08	During MSL @ JPL SAF		Samples not listed in SampleWare database					
GI11-1	JPL SAF pooled samples (20 BiSKits)	Floor	BiSKit	02/12/08	During MSL @ JPL SAF		Samples not listed in SampleWare database					1.44E+07
GI11-2	Pooled blanks (20 BiSKits)	Blank	BiSKit	02/12/08	During MSL @ JPL SAF		Samples not listed in SampleWare database					
GI11-3	PBS/BIG	Buffer control	PBS	02/12/08	During MSL @ JPL SAF		Samples not listed in SampleWare database					
GI12-1	JPL SAF pooled samples (20 BiSKits)	Floor	BiSKit	04/01/08	During MSL @ JPL SAF		000431	2	E	8	0	4.78E+05
GI12-2	Pooled blanks (20 BiSKits)	Blank	BiSKit	04/01/08	During MSL @ JPL SAF		000432	2	E	9	0	
GI12-3	PBS/BIG	Buffer control	PBS	04/01/08	During MSL @ JPL SAF		000433	2	F	1	10	
GI13-1	JPL SAF pooled samples (20 BiSKits)	Floor	BiSKit	06/04/08	During MSL @ JPL SAF		Samples not listed in SampleWare database					1.01E+08
GI13-2	Pooled blanks (20 BiSKits)	Blank	BiSKit	06/04/08	During MSL @ JPL SAF		Samples not listed in SampleWare database					
GI13-3	PBS/BIG	Buffer control	PBS	06/04/08	During MSL @ JPL SAF		Samples not listed in SampleWare database					
GI14	JPL SAF pooled samples (20 BiSKits)	Floor	BiSKit	08/05/08	During MSL @ JPL SAF		000434	2	F	2	15	3.96E+05
GI14BLNK	Pooled blanks (20 BiSKits)	Blank	BiSKit	08/05/08	During MSL @ JPL SAF		000435	2	F	3	15	0.00E+00
GI15	See MSL sample ID for detail	Surface	Polyester wipe	09/05/08	MSL		000436	2	F	4	15	3.64E+09
GI16	See MSL sample ID for detail	Surface	Polyester wipe	09/23/08	MSL		000437	2	F	5	0	8.28E+02
GI17	See MSL sample ID for detail	Surface	Polyester wipe	10/02/08	MSL		000438	2	F	6	10	1.77E+04
GI18	See MSL sample ID for detail	Surface	Polyester wipe	9/23/08 - 12/8/08	MSL		000439	2	F	7	10	6.37E+03
GI19	See MSL sample ID for detail	Surface	Polyester wipe	9/19/08 - 12/8/08	MSL		000440	2	F	8	10	1.22E+03
GI20	See MSL sample ID for detail	Surface	Polyester wipe	9/18/08 - 12/8/08	MSL		000441	2	F	9	5	1.91E+03
GI21	See MSL sample ID for detail	Surface	Polyester wipe	10/21/08 - 12/1/08	MSL		000442	2	G	1	10	6.76E+04
GI22	See MSL sample ID for detail	Surface	Polyester wipe	11/19/08 - 12/8/08	MSL		000443	2	G	2	0	6.83E+03
GI23	See MSL sample ID for detail	Surface	Polyester wipe	09/23/08	MSL		000444	2	G	3	10	2.74E+05
GI24	See MSL sample ID for detail	Surface	Polyester wipe	12/01/08	MSL		000445	2	G	4	10	2.06E+04
GI25	See MSL sample ID for detail	Surface	Polyester wipe	9/8/08 - 9/19/08	MSL		000446	2	G	5	10	1.44E+03
GI26	See MSL sample ID for detail	Surface	Polyester wipe	9/24/08 - 10/6/08	MSL		000447	2	G	6	10	7.78E+03
GI27	See MSL sample ID for detail	Surface	Polyester wipe	10/21/08 - 10/27/08	MSL		000448	2	G	7	0	5.56E+03
GI28	See MSL sample ID for detail	Surface	Polyester wipe	10/30/08 - 11/25/08	MSL		000449	2	G	8	10	9.95E+02
GIblnk	See MSL sample ID for detail	Negative control	PBS	09/05/08	MSL blank		000450	2	G	9	0	
GI18blnk	See MSL sample ID for detail	Handling Control (HC)	Polyester wipe	9/29/08 - 10/13/08	MSL blank		000451	2	H	1	10	1.47E+02
GI19blnk	See MSL sample ID for detail	Handling Control (HC)	Polyester wipe	9/30/08 - 12/8/08	MSL blank		000452	2	H	2	0	1.77E+02
GI20blnk	See MSL sample ID for detail	Handling Control (HC)	Polyester wipe	10/27/08	MSL blank		000453	2	H	3	15	1.67E+02
GI29	See MSL sample ID for detail	Floor	Polyester wipe	03/09/09	MSL		000247	2	H	4	10	3.45E+01
GI30	See MSL sample ID for detail	Floor	Polyester wipe	03/10/09	MSL		000248	2	H	5	10	5.12E+03
GI31	See MSL sample ID for detail	Floor	Polyester wipe	03/11/09	MSL		000249	2	H	6	10	2.90E+02
GI32	See MSL sample ID for detail	Floor	Polyester wipe	03/12/09	MSL		000250	2	H	7	15	5.81E+03
GI29-32blnk	See MSL sample ID for detail	Blank	Polyester wipe	03/13/09	MSL blank		000251	2	H	8	15	1.05E+02
GI-33-1		GSE 1 & 2	Polyester wipe		MSL		000252	2	H	9	15	
GI-33-1b		GSE FB	Polyester wipe		MSL		000253	2	I	1	15	
GI-33-1bp		GSE FB PMA	Polyester wipe		MSL		000254	2	I	2	15	

Sample ID	Sample Description	Sample Source	Sampling Device	Date	Mission	Samples Pooled	Barcode	GI-Container	Row	Column	Sample Volume	16S rRNA Gene Copies
GI-33-1p		GSE 1 & 2 PMA	Polyester wipe		MSL		000255	2	I	3	15	
GI-33-2		SAF Sample	Polyester wipe		MSL		000256	2	I	4	15	
GI-33-2b		SAF FB	Polyester wipe		MSL		000257	2	I	5	15	
GI-33-2bp		SAF FB PMA	Polyester wipe		MSL		000258	2	I	6	15	
GI-33-2p		SAF Sample PMA	Polyester wipe		MSL		000259	2	I	7	15	
GI-34-1		GSE	Polyester wipe		MSL		000260	2	I	8	15	
GI-34-1p		GSE PMA	Polyester wipe		MSL		000261	2	I	9	15	
GI-34-2		SAF Sample	Polyester wipe		MSL		000262	3	A	1	15	
GI-34-2p		SAF PMA	Polyester wipe		MSL		000263	3	A	2	15	
GI-34-3		FB	Polyester wipe		MSL		000264	3	A	3	15	
GI-34-3p		FB PMA	Polyester wipe		MSL		000265	3	A	4	15	
GI-35-1	External to SAF. See sheet 2. Archaea	Blank	Polyester wipe	04/06/10	MSL	1	000001	3	A	5	10	3.36E+02
GI-35-2	External to SAF. See sheet 2. Archaea	Buffer control	PBS	04/06/10	MSL	1	000002	3	A	6	0	4.81E+02
GI-35-3	External to SAF. See sheet 2. Archaea	Environmental Control	Polyester wipe	04/06/10	MSL	1	000003	3	A	7	10	
GI-35-4	External to SAF. See sheet 2. Archaea	Shoe Cleaner	Polyester wipe	04/06/10	MSL	1	000004	3	A	8	0	5.31E+04
GI-35-5	External to SAF. See sheet 2. Archaea	ARD	Polyester wipe	04/06/10	MSL	1	000005	3	A	9	0	1.11E+04
GI-35-6	External to SAF. See sheet 2. Archaea	EF	Polyester wipe	04/06/10	MSL	1	000006	3	B	1	0	7.26E+04
GI-35-7	External to SAF. See sheet 2. Archaea	CR1	Polyester wipe	04/06/10	MSL	1	000007	3	B	2	0	5.16E+04
GI-35-8	External to SAF. See sheet 2. Archaea	CR2	Polyester wipe	04/06/10	MSL	1	000008	3	B	3	0	1.30E+04
GI-36-1lc	BiSKit samples. See Sheet 3 for locations	Lab Control (LC)	BiSKit	06/08/10	MSL	20	000009	3	B	4	20	2.01E+03
GI-36-1lcp	BiSKit samples. See Sheet 3 for locations	LC PMA	BiSKit	06/08/10	MSL	20	000010	3	B	5	10	7.38E+01
GI-36-2b	BiSKit samples. See Sheet 3 for locations	FB	BiSKit	06/08/10	MSL	2	000011	3	B	6	0	5.11E+02
GI-36-2bp	BiSKit samples. See Sheet 3 for locations	FB PMA	BiSKit	06/08/10	MSL	2	000012	3	B	7	0	2.45E+02
GI-36-3	BiSKit samples. See Sheet 3 for locations	GSE	BiSKit	06/08/10	MSL	9	000013	3	B	8	0	7.45E+02
GI-36-3p	BiSKit samples. See Sheet 3 for locations	GSE PMA	BiSKit	06/08/10	MSL	9	000014	3	B	9	0	2.70E+03
GI-36-4	BiSKit samples. See Sheet 3 for locations	FLR	BiSKit	06/08/10	MSL	9	000015	3	C	1	0	1.88E+04
GI-36-4p	BiSKit samples. See Sheet 3 for locations	FLR PMA	BiSKit	06/08/10	MSL	9	000016	3	C	2	0	1.27E+03
GI-37lc	LBNL/Nick Palaio Cleanroom, rm 70A	B: Blank	BiSKit	05/25/10	Non-NASA Cleanroom	10	000017	3	C	3	50	4.64E+02
GI-37b	LBNL/Nick Palaio Cleanroom, rm 70A	FB: Field Blank (1 BiSKit)	BiSKit	05/25/10	Non-NASA Cleanroom	1	000018	3	C	4	15	4.97E+02
GI-37	LBNL Cleanroom, rm 70A	S: Sample (9 BiSKits)	BiSKit	05/25/10	Non-NASA Cleanroom	9	000019	3	C	5	35	8.33E+04
GI-38b	CS	Blank	Polyester wipe	3/15/2010 - 5/27/2010	MSL	10	000020	3	C	6	15	1.58E+02

Sample ID	Sample Description	Sample Source	Sampling Device	Date	Mission	Samples Pooled	Barcode	GI-Container	Row	Column	Sample Volume	16S rRNA Gene Copies
GI-38	CS	CS	Polyester wipe	3/15/2010 - 5/27/2010	MSL	26	000021	3	C	7	15	1.30E+03
GI-39b	DS	Blank	Polyester wipe	3/10/2010 - 4/29/2010	MSL	3	000022	3	C	8	15	1.57E+02
GI-39	DS	DS	Polyester wipe	3/10/2010 - 4/29/2010	MSL	9	000023	3	C	9	15	1.68E+02
GI-40b	RVR	Blank	Polyester wipe	3/8/2010 - 6/2/2010	MSL	5	000024	3	D	1	0	1.61E+02
GI-40	RVR	RVR	Polyester wipe	3/8/2010 - 6/2/2010	MSL	16	000025	3	D	2	10	1.11E+03
GI-41b	Nonflight - Cleanroom wipe control	Blank	Polyester wipe	5/17/2010	MSL	1	000026	3	D	3	10	1.84E+02
GI-41	Non-flight wipe used to support Tc bundle	Non-flight	Polyester wipe	5/13/2010	MSL	1	000027	3	D	4	10	1.33E+03
Blank	26 wipes procured from Nick (200 mL x 26)	Blank	Polyester wipe	5/13/2010	MSL	26	000028	3	D	5	5	1.96E+02
GI-42lc	Bldg 144 cleanroom prior to cleaning	Lab control	BiSKit	06/15/10	MSL	20	000029	3	D	6	10	9.35E+02
GI-42lcp	Bldg 144 cleanroom prior to cleaning	Lab control PMA	BiSKit	06/15/10	MSL	20	000030	3	D	7	10	1.36E+02
GI-42b	Bldg 144 cleanroom prior to cleaning	FB	BiSKit	06/15/10	MSL	1	000031	3	D	8	10	8.52E+02
GI-42bp	Bldg 144 cleanroom prior to cleaning	FB PMA	BiSKit	06/15/10	MSL	1	000032	3	D	9	10	1.50E+02
GI-42-1	Bldg 144 cleanroom prior to cleaning	FLR Sample	BiSKit	06/15/10	MSL	9	000033	3	E	1	10	1.03E+06
GI-42-1p	Bldg 144 cleanroom prior to cleaning	FLR Sample PMA	BiSKit	06/15/10	MSL	9	000034	3	E	2	10	3.94E+05
GI-42-2	Bldg 144 cleanroom prior to cleaning	GSE Sample	BiSKit	06/15/10	MSL	9	000035	3	E	3	10	1.33E+05
GI-42-2p	Bldg 144 cleanroom prior to cleaning	GSE Sample PMA	BiSKit	06/15/10	MSL	9	000036	3	E	4	10	5.66E+04
GI-43lc	Bldg 144 cleanroom after cleaning	Lab control	Polyester wipe	06/16/10	MSL	21	000037	3	E	5	10	1.84E+02
GI-43lcp	Bldg 144 cleanroom after cleaning	Lab control PMA	Polyester wipe	06/16/10	MSL	21	000038	3	E	6	10	1.44E+02
GI-43b	Bldg 144 cleanroom after cleaning	Field Blank	Polyester wipe	06/16/10	MSL	2	000039	3	E	7	10	1.72E+02
GI-43bp	Bldg 144 cleanroom after cleaning	Field Blank PMA	Polyester wipe	06/16/10	MSL	2	000040	3	E	8	15	1.36E+02
GI-43-1	Bldg 144 cleanroom after cleaning	FLR Sample	Polyester wipe	06/16/10	MSL	9	000041	3	E	9	10	1.74E+05
GI-43-1p	Bldg 144 cleanroom after cleaning	FLR Sample PMA	Polyester wipe	06/16/10	MSL	9	000042	3	F	1	10	4.58E+05
GI-43-2	Bldg 144 cleanroom after cleaning	GSE Sample	Polyester wipe	06/16/10	MSL	9	000043	3	F	2	15	4.79E+05
GI-43-2p	Bldg 144 cleanroom after cleaning	GSE Sample PMA	Polyester wipe	06/16/10	MSL	9	000044	3	F	3	15	5.05E+03
GI-44			Polyester Wipe				000627	3	F	4	15	
GI-44b		Blank	Polyester Wipe				000628	3	F	5	10	
GI-45			Polyester Wipe				000625	3	F	6	15	

Sample ID	Sample Description	Sample Source	Sampling Device	Date	Mission	Samples Pooled	Barcode	GI-Container	Row	Column	Sample Volume	16S rRNA Gene Copies
GI-45b		Blank	Polyester Wipe				000626	3	F	7	15	
GI-46			Polyester Wipe				000624	3	F	8	10	
GI-47			Polyester Wipe				000622	3	F	9	10	
GI-47b		Blank	Polyester Wipe				000623	3	G	1	20	
GI-48			Polyester Wipe				000620	3	G	2	20	
GI-48b		Blank	Polyester Wipe				000621	3	G	3	20	
GI-49			Polyester Wipe	11/28/2011	MSL @ KSC	7	001483	3	G	4	15	2.22E+02
GI-49b,52b…60b		Blank	Polyester Wipe	11/28/2011	MSL @ KSC	13	001480	3	G	5	15	2.70E+00
GI-50			Polyester Wipe	11/28/2011	MSL @ KSC	3	001484	3	G	6	15	5.53E+02
GI-50b		Blank	Polyester Wipe	11/28/2011	MSL @ KSC	1	001481	3	G	7	15	7.88E+00
GI-51			Polyester Wipe	11/28/2011	MSL @ KSC	7	001485	3	G	8	15	8.60E+02
GI-51b		Blank	Polyester Wipe	11/28/2011	MSL @ KSC	1	001482	3	G	9	15	1.03E+01
GI-52			Polyester Wipe	11/28/2011	MSL @ KSC	6	001486	3	H	1	15	1.24E+03
GI-53			Polyester Wipe	11/28/2011	MSL @ KSC	7	001487	3	H	2	15	6.52E+01
GI-54			Polyester Wipe	11/28/2011	MSL @ KSC	5	001488	3	H	3	15	6.55E+02
GI-55			Polyester Wipe	11/28/2011	MSL @ KSC	9	001489	3	H	4	15	4.40E+02
GI-56			Polyester Wipe	11/28/2011	MSL @ KSC	2	001490	3	H	5	15	6.99E+02
GI-57			Polyester Wipe	11/28/2011	MSL @ KSC	2	001491	3	H	6	15	8.94E+02
GI-58			Polyester Wipe	11/28/2011	MSL @ KSC	5	001492	3	H	7	15	8.73E+02
GI-59			Polyester Wipe	11/28/2011	MSL @ KSC	11	001493	3	H	8	15	1.05E+03
GI-60			Polyester Wipe	11/28/2011	MSL @ KSC	6	001494	3	H	9	15	1.46E+03
GI-61			Polyester Wipe	12/17/2011	MSL @ KSC	4	001497	3	I	1	15	1.31E+05
GI-61b		Blank	Polyester Wipe	12/17/2011	MSL @ KSC	1	001554	3	I	2	15	4.63E+02
GI-62			Polyester Wipe	12/17/2011	MSL @ KSC	6	001498	3	I	3	15	5.54E+04
GI-62b		Blank	Polyester Wipe	12/17/2011	MSL @ KSC	2	001555	3	I	4	15	1.35E+03
GI-63			Polyester Wipe	12/17/2011	MSL @ KSC	8	01499	3	I	5	15	1.34E+05
GI-63b		Blank	Polyester Wipe	12/17/2011	MSL @ KSC	2	001556	3	I	6	15	3.28E+02
GI-64			Polyester Wipe	12/17/2011	MSL @ KSC	6	001500	3	I	7	15	7.50E+04
GI-64b		Blank	Polyester Wipe	12/17/2011	MSL @ KSC	1	001557	3	I	8	15	3.46E+02
GI-65			Polyester Wipe	12/17/2011	MSL @ KSC	3	001501	3	I	9	15	1.67E+05
GI-65b		Blank	Polyester Wipe	12/17/2011	MSL @ KSC	1	001559	4	A	1	15	3.20E+02
GI-66			Polyester Wipe	12/17/2011	MSL @ KSC	Water only-Place holder	001502	4	A	2	15	No Sample - water only
GI-66b		Blank	Polyester Wipe	12/17/2011	MSL @ KSC	Water only-Place holder	001560	4	A	3	15	No Sample - water only
GI-67			Polyester Wipe	12/17/2011	MSL @ KSC	2	001503	4	A	4	15	2.32E+04
GI-67b		Blank	Polyester Wipe	12/17/2011	MSL @ KSC	1	001561	4	A	5	15	5.42E+02
GI-68			Polyester Wipe	12/17/2011	MSL @ KSC	2	001504	4	A	6	15	7.17E+04
GI-68b		Blank	Polyester Wipe	12/17/2011	MSL @ KSC	Water only-Place holder	001562	4	A	7	15	No Sample - water only
GI-69			Polyester Wipe	12/17/2011	MSL @ KSC	Water only-Place holder	001505	4	A	8	15	No Sample - water only
GI-69b		Blank	Polyester Wipe	12/17/2011	MSL @ KSC	Water only-Place holder	001563	4	A	9	15	No Sample - water only
GI-70			Polyester Wipe	12/17/2011	MSL @ KSC	5	001506	4	B	1	15	3.45E+04
GI-70b		Blank	Polyester Wipe	12/17/2011	MSL @ KSC	2	001564	4	B	2	15	4.51E+02
GI-71			Polyester Wipe	12/17/2011	MSL @ KSC	2	001507	4	B	3	15	5.14E+04
GI-71b		Blank	Polyester Wipe	12/17/2011	MSL @ KSC	1	001565	4	B	4	15	5.37E+02
GI-72			Polyester Wipe	12/17/2011	MSL @ KSC	6	001508	4	B	5	15	1.05E+05
GI-72b		Blank	Polyester Wipe	12/17/2011	MSL @ KSC	2	001566	4	B	6	15	7.94E+02
GI-73			Polyester Wipe	12/18/2011	MSL @ KSC	2	001509	4	B	7	15	9.71E+03

Sample ID	Sample Description	Sample Source	Sampling Device	Date	Mission	Samples Pooled	Barcode	GI-Container	Row	Column	Sample Volume	16S rRNA Gene Copies
GI-73b		Blank	Polyester Wipe	12/18/2011	MSL @ KSC	Water only-Place holder	001567	4	B	8	15	No Sample - water only
GI-74			Polyester Wipe	12/18/2011	MSL @ KSC	11	001510	4	B	9	15	1.63E+04
GI-74b		Blank	Polyester Wipe	12/18/2011	MSL @ KSC	4	001568	4	C	1	15	1.54E+02
GI-75			Polyester Wipe	12/18/2011	MSL @ KSC	3	001511	4	C	2	15	1.25E+04
GI-75b		Blank	Polyester Wipe	12/18/2011	MSL @ KSC	2	001569	4	C	3	15	9.35E+01
GI-76			Polyester Wipe	12/18/2011	MSL @ KSC	4	001512	4	C	4	15	7.93E+03
GI-76b		Blank	Polyester Wipe	12/18/2011	MSL @ KSC	2	001570	4	C	5	15	9.84E+01
GI-77			Polyester Wipe	12/18/2011	MSL @ KSC	2	001513	4	C	6	15	1.14E+04
GI-77b		Blank	Polyester Wipe	12/18/2011	MSL @ KSC	1	001571	4	C	7	15	6.83E+01
GI-78			Polyester Wipe	12/18/2011	MSL @ KSC	1	001514	4	C	8	15	8.16E+03
GI-78b		Blank	Polyester Wipe	12/18/2011	MSL @ KSC	1	001572	4	C	9	15	5.54E+01
GI-79			Polyester Wipe	12/18/2011	MSL @ KSC	2	001515	4	D	1	15	7.54E+03
GI-79b		Blank	Polyester Wipe	12/18/2011	MSL @ KSC	1	001573	4	D	2	15	1.14E+02
GI-80			Polyester Wipe	12/18/2011	MSL @ KSC	6	001516	4	D	3	15	1.09E+04
GI-80b		Blank	Polyester Wipe	12/18/2011	MSL @ KSC	3	001574	4	D	4	15	1.48E+02
GI-81			Polyester Wipe	12/18/2011	MSL @ KSC	2	001517	4	D	5	15	9.93E+03
GI-81b		Blank	Polyester Wipe	12/18/2011	MSL @ KSC	1	001575	4	D	6	15	1.29E+02
GI-82			Polyester Wipe	12/18/2011	MSL @ KSC	1	001518	4	D	7	15	6.47E+03
GI-82b		Blank	Polyester Wipe	12/18/2011	MSL @ KSC	1	001576	4	D	8	15	2.47E+02
GI-83			Polyester Wipe	12/18/2011	MSL @ KSC	3	001519	4	D	9	15	1.14E+04
GI-83b		Blank	Polyester Wipe	12/18/2011	MSL @ KSC	1	001577	4	E	1	15	9.54E+01
GI-84			Polyester Wipe	12/18/2011	MSL @ KSC	3	001520	4	E	2	15	8.08E+03
GI-84b		Blank	Polyester Wipe	12/18/2011	MSL @ KSC	2	001578	4	E	3	15	2.12E+02
GI-85			Polyester Wipe	12/19/2011	MSL @ KSC	10	001521	4	E	4	15	7.86E+04
GI-85b		Blank	Polyester Wipe	12/19/2011	MSL @ KSC	5	001579	4	E	5	15	1.66E+02
GI-86			Polyester Wipe	12/19/2011	MSL @ KSC	1	001522	4	E	6	15	1.05E+04
GI-86b		Blank	Polyester Wipe	12/19/2011	MSL @ KSC	1	001580	4	E	7	15	9.10E+01
GI-87			Polyester Wipe	12/19/2011	MSL @ KSC	2	001523	4	E	8	15	1.76E+04
GI-87b		Blank	Polyester Wipe	12/19/2011	MSL @ KSC	1	'001581	4	E	9	15	1.25E+02
GI-88			Polyester Wipe	12/19/2011	MSL @ KSC	2	001524	4	F	1	15	2.51E+04
GI-88b		Blank	Polyester Wipe	12/19/2011	MSL @ KSC	1	001582	4	F	2	15	7.03E+01
GI-89			Polyester Wipe	12/19/2011	MSL @ KSC	4	001525	4	F	3	15	3.30E+04
GI-89b		Blank	Polyester Wipe	12/19/2011	MSL @ KSC	1	001583	4	F	4	15	1.10E+02
GI-90			Polyester Wipe	12/19/2011	MSL @ KSC	20	001526	4	F	5	15	1.13E+04
GI-90b		Blank	Polyester Wipe	12/19/2011	MSL @ KSC	5	001584	4	F	6	15	9.54E+02
GI-91			Polyester Wipe	12/19/2011	MSL @ KSC	4	001527	4	F	7	15	1.82E+04
GI-91b		Blank	Polyester Wipe	12/19/2011	MSL @ KSC	1	001585	4	F	8	15	7.16E+01
GI-92			Polyester Wipe	12/19/2011	MSL @ KSC	2	001528	4	F	9	15	2.79E+04
GI-92b		Blank	Polyester Wipe	12/19/2011	MSL @ KSC	1	001586	4	G	1	15	1.57E+02
GI-93			Polyester Wipe	12/19/2011	MSL @ KSC	6	001529	4	G	2	15	1.20E+07
GI-93b		Blank	Polyester Wipe	12/19/2011	MSL @ KSC	2	001587	4	G	3	15	1.20E+02
GI-94			Polyester Wipe	12/19/2011	MSL @ KSC	10	001530	4	G	4	15	3.76E+04
GI-94b		Blank	Polyester Wipe	12/19/2011	MSL @ KSC	1	001588	4	G	5	15	9.35E+01
GI-95			Polyester Wipe	12/19/2011	MSL @ KSC	7	001531	4	G	6	15	1.13E+05
GI-95b		Blank	Polyester Wipe	12/19/2011	MSL @ KSC	2	001589	4	G	7	15	4.08E+02
GI-96			Polyester Wipe	12/19/2011	MSL @ KSC	3	001532	4	G	8	15	2.37E+04
GI-96b		Blank	Polyester Wipe	12/19/2011	MSL @ KSC	1	001590	4	G	9	15	6.06E+02
GI-97			Polyester Wipe	12/20/2011	MSL @ KSC	1	001533	4	H	1	15	3.04E+04
GI-97b		Blank	Polyester Wipe	12/20/2011	MSL @ KSC	1	001591	4	H	2	15	2.54E+02
GI-98			Polyester Wipe	12/20/2011	MSL @ KSC	1	001534	4	H	3	15	3.48E+04
GI-98b		Blank	Polyester Wipe	12/20/2011	MSL @ KSC	1	001592	4	H	4	15	2.56E+02
GI-99			Polyester Wipe	12/20/2011	MSL @ KSC	8	001535	4	H	5	15	9.12E+03

Sample ID	Sample Description	Sample Source	Sampling Device	Date	Mission	Samples Pooled	Barcode	GI-Container	Row	Column	Sample Volume	16S rRNA Gene Copies
GI-99b		Blank	Polyester Wipe	12/20/2011	MSL @ KSC	1	001593	4	H	6	15	3.42E+02
GI-100			Polyester Wipe	12/20/2011	MSL @ KSC	3	001536	4	H	7	15	2.47E+04
GI-100b		Blank	Polyester Wipe	12/20/2011	MSL @ KSC	1	001594	4	H	8	15	1.72E+02
GI-101			Polyester Wipe	12/20/2011	MSL @ KSC	3	001537	4	H	9	15	4.63E+04
GI-101b		Blank	Polyester Wipe	12/20/2011	MSL @ KSC	1	001595	4	I	1	15	3.03E+02
GI-102			Polyester Wipe	12/20/2011	MSL @ KSC	3	001538	4	I	2	15	4.84E+04
GI-102b		Blank	Polyester Wipe	12/20/2011	MSL @ KSC	1	001596	4	I	3	15	2.53E+02
GI-103			Polyester Wipe	12/20/2011	MSL @ KSC	2	001539	4	I	4	15	4.53E+04
GI-103b		Blank	Polyester Wipe	12/20/2011	MSL @ KSC	1	001597	4	I	5	15	1.85E+02
GI-104			Polyester Wipe	12/20/2011	MSL @ KSC	2	001540	4	I	6	15	3.96E+04
GI-104b		Blank	Polyester Wipe	12/20/2011	MSL @ KSC	1	001598	4	I	7	15	2.38E+02
GI-105			Polyester Wipe	12/20/2011	MSL @ KSC	1	001541	4	I	8	15	2.84E+04
GI-105b		Blank	Polyester Wipe	12/20/2011	MSL @ KSC	1	001599	4	I	9	15	2.71E+02
GI-106			Polyester Wipe	12/20/2011	MSL @ KSC	6	001542	5	A	1	15	2.66E+04
GI-106b		Blank	Polyester Wipe	12/20/2011	MSL @ KSC	2	001600	5	A	2	15	2.58E+02
GI-107			Polyester Wipe	12/20/2011	MSL @ KSC	3	001543	5	A	3	15	4.13E+04
GI-107b		Blank	Polyester Wipe	12/20/2011	MSL @ KSC	1	001601	5	A	4	15	2.56E+02
GI-108			Polyester Wipe	12/20/2011	MSL @ KSC	3	001544	5	A	5	15	2.36E+04
GI-108b		Blank	Polyester Wipe	12/20/2011	MSL @ KSC	Water only-Place holder	001602	5	A	6	15	No Sample - water only
GI-109			Polyester Wipe	12/16/2011	MSL @ KSC	2	001545	5	A	7	15	2.01E+04
GI-109b		Blank	Polyester Wipe	12/16/2011	MSL @ KSC	1	001603	5	A	8	15	1.71E+02
GI-110			Polyester Wipe	12/16/2011	MSL @ KSC	2	001546	5	A	9	15	2.26E+04
GI-110b		Blank	Polyester Wipe	12/16/2011	MSL @ KSC	1	001604	5	B	1	15	2.81E+02
GI-111			Polyester Wipe	12/16/2011	MSL @ KSC	4	001547	5	B	2	15	3.75E+04
GI-111b		Blank	Polyester Wipe	12/16/2011	MSL @ KSC	1	001605	5	B	3	15	3.44E+02
GI-112			Polyester Wipe	12/16/2011	MSL @ KSC	8	001548	5	B	4	15	3.61E+04
GI-112b		Blank	Polyester Wipe	12/16/2011	MSL @ KSC	2	001606	5	B	5	15	1.73E+02
GI-113			Polyester Wipe	12/16/2011	MSL @ KSC	2	001549	5	B	6	15	1.63E+04
GI-113b		Blank	Polyester Wipe	12/16/2011	MSL @ KSC	1	001607	5	B	7	15	2.29E+02
GI-114			Polyester Wipe	12/16/2011	MSL @ KSC	1	001550	5	B	8	15	3.83E+04
GI-114b		Blank	Polyester Wipe	12/16/2011	MSL @ KSC	1	001608	5	B	9	15	4.62E+02
GI-115			Polyester Wipe	12/16/2011	MSL @ KSC	2	001551	5	C	1	15	9.67E+03
GI-115b		Blank	Polyester Wipe	12/16/2011	MSL @ KSC	1	001609	5	C	2	15	2.09E+01
GI-116			Polyester Wipe	12/16/2011	MSL @ KSC	22	001552	5	C	3	15	2.25E+06
GI-116b		Blank	Polyester Wipe	12/16/2011	MSL @ KSC	3	001610	5	C	4	15	1.89E+02
GI-117			BiSKit	12/16/2011	MSL @ KSC	23	001553	5	C	5	15	0.00E+00
GI-117b		Blank	BiSKit	12/16/2011	MSL @ KSC	4	001611	5	C	6	15	2.19E+02
GI-Max-28		Reagent Control	Maxwell Control	12/16/2011	MSL		001612	5	C	7	15	3.16E+01
GI-KSC-PBS-23		Buffer Control JPL	Buffer Control	12/16/2011	MSL		001613	5	C	8	15	1.44E+02
GI-JPL-PBS-24		Buffer Control KSC	Buffer Control	12/16/2011	MSL		001614	5	C	9	15	5.57E+01

Table E.1-2. Characteristics of Genetic Inventory Task DNA samples archived at JPL (Bldg 244).

Sample ID	Sample Description	Sample Source	Sampling Device	Date	Mission	Samples Pooled	Barcode	GI-Container	Row	Column	Sample Volume	16S rRNA Gene Copies
GI1-1	BIG Control	Buffer control	PBS	01/03/07	Phoenix at LMA			6	A	1	0	
GI1-2	1-MTF-1B	Floor	BiSKit	01/03/07	Phoenix at LMA		Samples not listed in SampleWare database					
GI1-3	1-MTF-2B	Floor	BiSKit	01/03/07	Phoenix at LMA		Samples not listed in SampleWare database					
GI1-4	1-MTF-3B	Floor	BiSKit	01/03/07	Phoenix at LMA		Samples not listed in SampleWare database					
GI1-5	1-MTF-4B	Floor	BiSKit	01/03/07	Phoenix at LMA		Samples not listed in SampleWare database					
GI1-6	1-MTF-5B	Floor	BiSKit	01/03/07	Phoenix at LMA		Samples not listed in SampleWare database					
GI1-7	1-MTF-6B	Floor	BiSKit	01/03/07	Phoenix at LMA		Samples not listed in SampleWare database					
GI1-8	1-MTF-7B	Floor	BiSKit	01/03/07	Phoenix at LMA		Samples not listed in SampleWare database					
GI1-9	1-MTF-8B	Floor	BiSKit	01/03/07	Phoenix at LMA			6	A	2	0	
GI1-10	1-MTF-9B	Floor	BiSKit	01/03/07	Phoenix at LMA			6	A	3	0	
GI1-11	1-MTF-10B	Floor	BiSKit	01/03/07	Phoenix at LMA		005464	6	A	4	10	
GI1-12	1-MTF-BLNK	Blank	BiSKit	01/03/07	Phoenix at LMA		Sample not listed in SampleWare database					
GI1-13	PHX swab BLNK 10 pooled	Blank	Cotton swab	01/03/07	Phoenix at LMA			6	A	5	0	1.22E+02
GI1-14	MTF Swab BLNK9 pooled	Blank	Cotton swab	01/03/07	Phoenix at LMA			6	A	6	0	1.45E+02
GI1-15	MTF Swab 9 pooled	Floor	Cotton swab	01/03/07	Phoenix at LMA			6	A	7	0	1.60E+04
GI1-16	PHX s/c swab10 pooled	Spacecraft	Cotton swab	01/03/07	Phoenix at LMA			6	A	8	0	1.47E+04
GI2-1	SSB-1B	Floor	BiSKit	02/03/07	Phoenix s/c not in SSB			6	A	9	0	
GI2-2	SSB-2B	Floor	BiSKit	02/03/07	Phoenix s/c not in SSB			6	B	1	0	
GI2-3	SSB-3B	Floor	BiSKit	02/03/07	Phoenix s/c not in SSB		005465	6	B	2	10	
GI2-4	SSB-4B	Floor	BiSKit	02/03/07	Phoenix s/c not in SSB		005466	6	B	3	10	
GI2-5	SSB-5B	Floor	BiSKit	02/03/07	Phoenix s/c not in SSB		005467	6	B	4	10	
GI2-6	SSB Swab 10 pooled	Floor	Cotton swab	02/03/07	Phoenix s/c not in SSB			6	B	5	0	1.00E+05
GI2-7	SSB Swab BLNK 10 pooled	Blank	Cotton swab	02/03/07	Phoenix s/c not in SSB			6	B	6	0	
GI3-1	PHSF W1	Floor	BiSKit	04/24/07	Before Phoenix		000456	6	B	7	15	
GI3-2	PHSF W2-SE	Floor	BiSKit	04/24/07	Before Phoenix		000457	6	B	8	15	
GI3-3	PHSF W3-Center	Floor	BiSKit	04/24/07	Before Phoenix		000458	6	B	9	10	
GI3-4	PHSF W4-NW	Floor	BiSKit	04/24/07	Before Phoenix		000459	6	C	1	15	
GI3-5	PHSF B5-SW	Floor	BiSKit	04/24/07	Before Phoenix		000460	6	C	2	15	
GI3-6	PHSF B6-E	Floor	BiSKit	04/24/07	Before Phoenix		000461	6	C	3	10	
GI3-7	PHSF B7-W	Floor	BiSKit	04/24/07	Before Phoenix		000462	6	C	4	10	
GI3-8	PHSF B8-N	Floor	BiSKit	04/24/07	Before Phoenix		000463	6	C	5	10	
GI3-9	PHSF B9-S	Floor	BiSKit	04/24/07	Before Phoenix		000464	6	C	6	10	
GI3-10	PHSF B10-Wall	Floor	BiSKit	04/24/07	Before Phoenix		000465	6	C	7	10	1.57E+05
GI3-FC1	BiSKit Field Control #1	Field control	BiSKit	04/24/07	Before Phoenix		000657	6	C	8	10	
GI3-BRC1	BiSKit PBS Control #1	Buffer control	PBS	04/24/07	Before Phoenix		000466	6	C	9	10	1.40E+02
GI3-BIG	Autolyser Cartridge Control	Buffer control	PBS	04/24/07	Before Phoenix		000467	6	D	1	10	1.26E+02
GI4-1	IP1-GI (BiSKit samples)	Floor	BiSKit	06/27/07	During Phoenix		000468	6	D	2	10	
GI4-2	IP2-GI	Floor	BiSKit	06/27/07	During Phoenix		000514	6	D	3	10	
GI4-3	IP3-GI	Floor	BiSKit	06/27/07	During Phoenix		000469	6	D	4	15	
GI4-5	IP5-GI	Floor	BiSKit	06/27/07	During Phoenix		000470	6	D	5	10	
GI4-6	IP6-GI	Floor	BiSKit	06/27/07	During Phoenix		000471	6	D	6	15	
GI4-7	IP7-GI	Floor	BiSKit	06/27/07	During Phoenix		000472	6	D	7	10	
GI4-8	IP8-GI	Floor	BiSKit	06/27/07	During Phoenix		000473	6	D	8	15	8.79E+05
GI4-1-blnk	IP1-GI-blnk (in 15 ml tubes)	Blank	BiSKit	06/27/07	During Phoenix		000474	6	D	9	15	1.45E+02
GI4-2-blnk	IP2-GI-blnk	Blank	BiSKit	06/27/07	During Phoenix		000475	6	E	1	15	
GI4-3-blnk	IP3-GI-blnk	Blank	BiSKit	06/27/07	During Phoenix		000476	6	E	2	15	
GI4-5-blnk	IP5-GI-blnk	Blank	BiSKit	06/27/07	During Phoenix		000477	6	E	3	15	
GI4-6-blnk	IP6-GI-blnk	Blank	BiSKit	06/27/07	During Phoenix		000478	6	E	4	15	
GI4-7-blnk	IP7-GI-blnk	Blank	BiSKit	06/27/07	During Phoenix		000479	6	E	5	15	
GI4-8-blnk	IP8-GI-blnk	Blank	BiSKit	06/27/07	During Phoenix		000480	6	E	6	15	
GI4-BIG(-)		Buffer control	PBS	06/27/07	During Phoenix		000481	6	E	7	10	1.47E+02

Sample ID	Sample Description	Sample Source	Sampling Device	Date	Mission	Samples Pooled	Barcode	GI-Container	Row	Column	Sample Volume	16S rRNA Gene Copies
GI5-1	PPO-PHSF-1B	Floor	BiSKit	07/20/07	Post-Phoenix		000482	6	E	8	10	
GI5-2	PPO-PHSF-2B	Floor	BiSKit	07/20/07	Post-Phoenix		000483	6	E	9	10	
GI5-3	PPO-PHSF-3B	Floor	BiSKit	07/20/07	Post-Phoenix		000484	6	F	1	15	
GI5-4	PPO-PHSF-4B	Floor	BiSKit	07/20/07	Post-Phoenix		000485	6	F	2	15	
GI5-5	PPO-PHSF-5B	Floor	BiSKit	07/20/07	Post-Phoenix		000486	6	F	3	15	
GI5-6	PPO-PHSF-6B	Floor	BiSKit	07/20/07	Post-Phoenix		000487	6	F	4	15	
GI5-7	PPO-PHSF-7B	Floor	BiSKit	07/20/07	Post-Phoenix		000488	6	F	5	15	
GI5-8	PPO-PHSF-8B	Floor	BiSKit	07/20/07	Post-Phoenix		000489	6	F	6	15	
GI5-9	PPO-PHSF-9B	Floor	BiSKit	07/20/07	Post-Phoenix		000490	6	F	7	15	
GI5-10	PPO-PHSF-10B	Floor	BiSKit	07/20/07	Post-Phoenix		000491	6	F	8	15	
GI5-12	PPO-PHSF-12B	Floor	BiSKit	07/20/07	Post-Phoenix		000493	6	F	9	15	
GI5-13	PPO-PHSF-13B	Floor	BiSKit	07/20/07	Post-Phoenix		000494	6	G	1	15	
GI5-14	PPO-PHSF-14B	Floor	BiSKit	07/20/07	Post-Phoenix		000495	6	G	2	15	
GI5-15	PPO-PHSF-15B	Floor	BiSKit	07/20/07	Post-Phoenix		000496	6	G	3	15	
GI5-16	PPO-PHSF-16B	Floor	BiSKit	07/20/07	Post-Phoenix		000497	6	G	4	15	
GI5-17	PPO-PHSF-17B	Floor	BiSKit	07/20/07	Post-Phoenix		000498	6	G	5	15	
GI5-18	PPO-PHSF-18B	Floor	BiSKit	07/20/07	Post-Phoenix		000499	6	G	6	15	
GI5-19	PPO-PHSF-19B	Floor	BiSKit	07/20/07	Post-Phoenix		000500	6	G	7	15	
GI5-20	PPO-PHSF-20B	Floor	BiSKit	07/20/07	Post-Phoenix		000501	6	G	8	15	1.80E+05
GI6-1	PHSF-1B	Floor	BiSKit	08/02/07	Post Phoenix		000783	6	G	9	0	0.00E+00
GI6-2	PHSF-2B	Floor	BiSKit	08/02/07	Post Phoenix		000502	6	H	1	15	
GI6-3	PHSF-3B	Floor	BiSKit	08/02/07	Post Phoenix		000785	6	H	2	0	1.02E+08
GI6-4	PHSF-4B	Floor	BiSKit	08/02/07	Post Phoenix		000503	6	H	3	15	
GI6-5	PHSF-5B	Floor	BiSKit	08/02/07	Post Phoenix		000504	6	H	4	15	
GI6-6	PHSF-6B	Floor	BiSKit	08/02/07	Post Phoenix		000505	6	H	5	15	
GI6-7	PHSF-7B	Floor	BiSKit	08/02/07	Post Phoenix			6	H	6	0	0.00E+00
GI6-8	PHSF-8B	Floor	BiSKit	08/02/07	Post Phoenix		000506	6	H	7	15	
GI6-9	PHSF-9B	Floor	BiSKit	08/02/07	Post Phoenix		Samples not listed in SampleWare database					
GI6-10	PHSF-10B	Floor	BiSKit	08/02/07	Post Phoenix		Samples not listed in SampleWare database					
GI6-1blnk	PHSF-1-blnk	Blank	BiSKit	08/02/07	Post Phoenix		Samples not listed in SampleWare database					
GI6-2blnk	PHSF-2-blnk	Blank	BiSKit	08/02/07	Post Phoenix		000507	6	H	8	15	
GI6-3blnk	PHSF-3-blnk	Blank	BiSKit	08/02/07	Post Phoenix		Samples not listed in SampleWare database					2.92E+02
GI6-4blnk	PHSF-4-blnk	Blank	BiSKit	08/02/07	Post Phoenix		000508	6	H	9	15	
GI6-5blnk	PHSF-5-blnk	Blank	BiSKit	08/02/07	Post Phoenix		000509	6	I	1	15	
GI6-6blnk	PHSF-6-blnk	Blank	BiSKit	08/02/07	Post Phoenix		000510	6	I	2	15	
GI6-7blnk	PHSF-7-blnk	Blank	BiSKit	08/02/07	Post Phoenix		Samples not listed in SampleWare database					1.05E+02
GI6-8blnk	PHSF-8-blnk	Blank	BiSKit	08/02/07	Post Phoenix		000511	6	I	3	15	
GI6-9blnk	PHSF-9-blnk	Blank	BiSKit	08/02/07	Post Phoenix		Samples not listed in SampleWare database					2.04E+02
GI6-10blnk	PHSF-10-blnk	Blank	BiSKit	08/02/07	Post Phoenix		Samples not listed in SampleWare database					2.37E+02
GI6-FC	PHFS-field control BiSKit	Field control	BiSKit	08/02/07	Post Phoenix		000512	6	I	4	15	
GI6-FCblnk	PHFS-field control blank	FC blank	BiSKit	08/02/07	Post Phoenix		000513	6	I	5	15	
GI7-B-1	9C-E	Floor	BiSKit	11/28/07	During Dawn		000515	6	I	6	5	2.75E+05
GI7-B-2	9C-G	Floor	BiSKit	11/28/07	During Dawn		000516	6	I	7	15	
GI7-B-3	9C-D	Floor	BiSKit	11/28/07	During Dawn		000517	6	I	8	0	7.72E+03
GI7-B-4	9C-A	Floor	BiSKit	11/28/07	During Dawn		000518	6	I	9	15	
GI7-B-5	9C Level	Floor	BiSKit	11/28/07	During Dawn		000519	7	A	1	5	1.26E+03
GI7-B-6	9C stair	Floor	BiSKit	11/28/07	During Dawn		000520	7	A	2	15	
GI7-B-7	9C-F	Floor	BiSKit	11/28/07	During Dawn		000521	7	A	3	10	
GI7-B-8	9C by B Central east of s/c	Floor	BiSKit	11/28/07	During Dawn		000522	7	A	4	5	3.09E+03
GI7-B-9	9C D/E	Floor	BiSKit	11/28/07	During Dawn		000523	7	A	5	10	
GI7-B-10	Field control @9C	Field control	BiSKit	11/28/07	During Dawn		000524	7	A	6	15	
GI7-B-11	11	Floor	BiSKit	11/28/07	During Dawn		000525	7	A	7	5	1.10E+03
GI7-B-12	12	Floor	BiSKit	11/28/07	During Dawn		000526	7	A	8	15	

Sample ID	Sample Description	Sample Source	Sampling Device	Date	Mission	Samples Pooled	Barcode	GI-Container	Row	Column	Sample Volume	16S rRNA Gene Copies
GI7-B-13	13	Floor	BiSKit	11/28/07	During Dawn		000527	7	A	9	15	
GI7-B-14	14	Floor	BiSKit	11/28/07	During Dawn		000528	7	B	1	15	
GI7-B-15	15	Floor	BiSKit	11/28/07	During Dawn		000529	7	B	2	15	
GI7-B-16	16	Floor	BiSKit	11/28/07	During Dawn		000530	7	B	3	15	
GI7-B-17	17	Floor	BiSKit	11/28/07	During Dawn		000531	7	B	4	15	
GI7-B-18	18	Floor	BiSKit	11/28/07	During Dawn		000532	7	B	5	15	
GI7-B-19	19	Floor	BiSKit	11/28/07	During Dawn		000533	7	B	6	15	
GI7-B-20	20	Floor	BiSKit	11/28/07	During Dawn		000534	7	B	7	15	
GI7-B-21	B-9/17-1	Floor	BiSKit	11/28/07	During Dawn			7	B	8	0	
GI7-B-22	B-9/17-2	Floor	BiSKit	11/28/07	During Dawn			7	B	9	0	
GI7-B-23	B-9/17-3	Floor	BiSKit	11/28/07	During Dawn		000535	7	C	1	15	
GI7-B-24	B-9/17-4	Floor	BiSKit	11/28/07	During Dawn		000536	7	C	2	15	
GI7-BLNK-1	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		000537	7	C	3	10	1.66E+02
GI7-BLNK-2	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		000538	7	C	4	15	
GI7-BLNK-3	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		000539	7	C	5	10	0.00E+00
GI7-BLNK-4	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		000540	7	C	6	15	
GI7-BLNK-5	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		000541	7	C	7	0	2.17E+02
GI7-BLNK-6	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		000542	7	C	8	15	
GI7-BLNK-7	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		000543	7	C	9	15	
GI7-BLNK-8	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		000544	7	D	1	15	7.51E+02
GI7-BLNK-9	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		000545	7	D	2	15	
GI7-BLNK-10	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		000546	7	D	3	15	
GI7-BLNK-11	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn			7	D	4	0	
GI7-BLNK-12	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		000547	7	D	5	15	
GI7-BLNK-13	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		000548	7	D	6	15	
GI7-BLNK-14	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		000549	7	D	7	15	
GI7-BLNK-15	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		000550	7	D	8	15	
GI7-BLNK-16	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		000551	7	D	9	10	
GI7-BLNK-17	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		000552	7	E	1	10	
GI7-BLNK-18	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		000553	7	E	2	10	
GI7-BLNK-19	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		000554	7	E	3	10	
GI7-BLNK-20	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		000555	7	E	4	15	
GI8-1	JPL SAF pooled samples 10 BiSKits)	Floor	BiSKit	10/08/07	During MSL, JPL SAF			7	E	5	0	8.74E+04

Sample ID	Sample Description	Sample Source	Sampling Device	Date	Mission	Samples Pooled	Barcode	GI-Container	Row	Column	Sample Volume	16S rRNA Gene Copies
GI8-2	Pooled blanks (10 BiSKits)	Blank	BiSKit	10/08/07	During MSL, JPL SAF			7	E	6	0	1.19E+02
GI8-3	PBS/BIG	Buffer control	PBS	10/08/07	During MSL, JPL SAF		005527	7	E	7	10	
GI10-1	JPL SAF pooled samples (20 BiSKits)	Floor	BiSKit	01/22/08	During MSL, JPL SAF		Samples not listed in SampleWare database					9.51E+07
GI10-2	Pooled blanks (20 BiSKits)	Blank	BiSKit	01/22/08	During MSL, JPL SAF		Samples not listed in SampleWare database					0.00E+00
GI10-3	PBS/BIG	Buffer control	PBS	01/22/08	During MSL, JPL SAF		Samples not listed in SampleWare database					
GI11-1	JPL SAF pooled samples (20 BiSKits)	Floor	BiSKit	02/12/08	During MSL, JPL SAF		Samples not listed in SampleWare database					1.44E+07
GI11-2	Pooled blanks (20 BiSKits)	Blank	BiSKit	02/12/08	During MSL, JPL SAF		Samples not listed in SampleWare database					
GI11-3	PBS/BIG	Buffer control	PBS	02/12/08	During MSL, JPL SAF		Samples not listed in SampleWare database					
GI12-1	JPL SAF pooled samples (20 BiSKits)	Floor	BiSKit	04/01/08	During MSL, JPL SAF			7	E	8	0	4.78E+05
GI12-2	Pooled blanks (20 BiSKits)	Blank	BiSKit	04/01/08	During MSL, JPL SAF			7	E	9	0	
GI12-3	PBS/BIG	Buffer control	PBS	04/01/08	During MSL, JPL SAF		005528	7	F	1	10	
GI13-1	JPL SAF pooled samples (20 BiSKits)	Floor	BiSKit	06/04/08	During MSL, JPL SAF		Samples not listed in SampleWare database					1.01E+08
GI13-2	Pooled blanks (20 BiSKits)	Blank	BiSKit	06/04/08	During MSL, JPL SAF		Samples not listed in SampleWare database					
GI13-3	PBS/BIG	Buffer control	PBS	06/04/08	During MSL, JPL SAF		Samples not listed in SampleWare database					
GI14	JPL SAF pooled samples (20 BiSKits)	Floor	BiSKit	08/05/08	During MSL, JPL SAF			7	F	2	10	3.96E+05
GI14BLNK	Pooled blanks (20 BiSKits)	Blank	BiSKit	08/05/08	During MSL, JPL SAF			7	F	3	0	0.00E+00
GI15	See MSL sample ID for detail	Surface	Polyester wipe	09/05/08	MSL		000825	7	F	4	10	3.64E+09
GI16	See MSL sample ID for detail	Surface	Polyester wipe	09/23/08	MSL			7	F	5	0	8.28E+02
GI17	See MSL sample ID for detail	Surface	Polyester wipe	10/02/08	MSL		000827	7	F	6	10	1.77E+04
GI18	See MSL sample ID for detail	Surface	Polyester wipe	9/23/08 - 12/8/08	MSL		000829	7	F	7	10	6.37E+03
GI19	See MSL sample ID for detail	Surface	Polyester wipe	9/19/08 - 12/8/08	MSL		005530	7	F	8	10	1.22E+03
GI20	See MSL sample ID for detail	Surface	Polyester wipe	9/18/08 - 12/8/08	MSL		000830	7	F	9	0	1.91E+03
GI21	See MSL sample ID for detail	Surface	Polyester wipe	10/21/08 - 12/1/08	MSL		005531	7	G	1	10	6.76E+04
GI22	See MSL sample ID for detail	Surface	Polyester wipe	11/19/08 - 12/8/08	MSL		000834	7	G	2	0	6.83E+03
GI23	See MSL sample ID for detail	Surface	Polyester wipe	09/23/08	MSL		005532	7	G	3	10	2.74E+05
GI24	See MSL sample ID for detail	Surface	Polyester wipe	12/01/08	MSL		005533	7	G	4	10	2.06E+04
GI25	See MSL sample ID for detail	Surface	Polyester wipe	9/8/08 - 9/19/08	MSL		005534	7	G	5	10	1.44E+03
GI26	See MSL sample ID for detail	Surface	Polyester wipe	9/24/08 - 10/6/08	MSL		005535	7	G	6	10	7.78E+03
GI27	See MSL sample ID for detail	Surface	Polyester wipe	10/21/08 - 10/27/08	MSL			7	G	7	0	5.56E+03
GI28	See MSL sample ID for detail	Surface	Polyester wipe	10/30/08 - 11/25/08	MSL		005536	7	G	8	10	9.95E+02
GIblnk	See MSL sample ID for detail	Negative control	PBS	09/05/08	MSL blank			7	G	9	0	
GI18blnk	See MSL sample ID for detail	Handling Control (HC)	Polyester wipe	9/29/08 - 10/13/08	MSL blank		005537	7	H	1	10	1.47E+02
GI19blnk	See MSL sample ID for detail	Handling Control (HC)	Polyester wipe	9/30/08 - 12/8/08	MSL blank		000581	7	H	2	0	1.77E+02
GI20blnk	See MSL sample ID for detail	Handling Control (HC)	Polyester wipe	10/27/08	MSL blank		000831	7	H	3	0	1.67E+02
GI29	See MSL sample ID for detail	Floor	Polyester wipe	03/09/09	MSL		000632	7	H	4	10	3.45E+01
GI30	See MSL sample ID for detail	Floor	Polyester wipe	03/10/09	MSL		000631	7	H	5	10	5.12E+03
GI31	See MSL sample ID for detail	Floor	Polyester wipe	03/11/09	MSL		000630	7	H	6	10	2.90E+02

Sample ID	Sample Description	Sample Source	Sampling Device	Date	Mission	Samples Pooled	Barcode	GI-Container	Row	Column	Sample Volume	16S rRNA Gene Copies
GI32	See MSL sample ID for detail	Floor	Polyester wipe	03/12/09	MSL		000629	7	H	7	15	5.81E+03
GI29-32blnk	See MSL sample ID for detail	Blank	Polyester wipe	03/13/09	MSL blank		000633	7	H	8	10	1.05E+02
GI-33-1		GSE 1 & 2	Polyester wipe		MSL			7	H	9	0	
GI-33-1b		GSE FB	Polyester wipe		MSL			7	I	1	0	
GI-33-1bp		GSE FB PMA	Polyester wipe		MSL			7	I	2	0	
GI-33-1p		GSE 1 & 2 PMA	Polyester wipe		MSL			7	I	3	0	
GI-33-2		SAF Sample	Polyester wipe		MSL			7	I	4	0	
GI-33-2b		SAF FB	Polyester wipe		MSL			7	I	5	0	
GI-33-2bp		SAF FB PMA	Polyester wipe		MSL			7	I	6	0	
GI-33-2p		SAF Sample PMA	Polyester wipe		MSL			7	I	7	0	
GI-34-1		GSE	Polyester wipe		MSL			7	I	8	0	
GI-34-1p		GSE PMA	Polyester wipe		MSL			7	I	9	0	
GI-34-2		SAF Sample	Polyester wipe		MSL			8	A	1	0	
GI-34-2p		SAF PMA	Polyester wipe		MSL			8	A	2	0	
GI-34-3		FB	Polyester wipe		MSL			8	A	3	0	
GI-34-3p		FB PMA	Polyester wipe		MSL			8	A	4	0	
GI-35-1	External to SAF. See sheet 2. Archaea	Blank	Polyester wipe	04/06/10	MSL	1	000268	8	A	5	10	3.36E+02
GI-35-2	External to SAF. See sheet 2. Archaea	Buffer control	PBS	04/06/10	MSL	1	000269	8	A	6	0	4.81E+02
GI-35-3	External to SAF. See sheet 2. Archaea	Environmental Control	Polyester wipe	04/06/10	MSL	1	000270	8	A	7	0	
GI-35-4	External to SAF. See sheet 2. Archaea	Shoe Cleaner	Polyester wipe	04/06/10	MSL	1	000271	8	A	8	0	5.31E+04
GI-35-5	External to SAF. See sheet 2. Archaea	ARD	Polyester wipe	04/06/10	MSL	1	000272	8	A	9	0	1.11E+04
GI-35-6	External to SAF. See sheet 2. Archaea	EF	Polyester wipe	04/06/10	MSL	1	000273	8	B	1	0	7.26E+04
GI-35-7	External to SAF. See sheet 2. Archaea	CR1	Polyester wipe	04/06/10	MSL	1	000274	8	B	2	0	5.16E+04
GI-35-8	External to SAF. See sheet 2. Archaea	CR2	Polyester wipe	04/06/10	MSL	1	000275	8	B	3	0	1.30E+04
GI-36-1lc	BiSKit samples. See Sheet 3 for locations	Lab Control (LC)	BiSKit	06/08/10	MSL	20	000276	8	B	4	20	2.01E+03
GI-36-1lcp	BiSKit samples. See Sheet 3 for locations	LC PMA	BiSKit	06/08/10	MSL	20	000277	8	B	5	10	7.38E+01
GI-36-2b	BiSKit samples. See Sheet 3 for locations	FB	BiSKit	06/08/10	MSL	2	000278	8	B	6	0	5.11E+02
GI-36-2bp	BiSKit samples. See Sheet 3 for locations	FB PMA	BiSKit	06/08/10	MSL	2	000279	8	B	7	0	2.45E+02
GI-36-3	BiSKit samples. See Sheet 3 for locations	GSE	BiSKit	06/08/10	MSL	9	000280	8	B	8	0	7.45E+02
GI-36-3p	BiSKit samples. See Sheet 3 for locations	GSE PMA	BiSKit	06/08/10	MSL	9	000281	8	B	9	0	2.70E+03
GI-36-4	BiSKit samples. See Sheet 3 for locations	FLR	BiSKit	06/08/10	MSL	9	000282	8	C	1	0	1.88E+04
GI-36-4p	BiSKit samples. See Sheet 3 for locations	FLR PMA	BiSKit	06/08/10	MSL	9	000283	8	C	2	0	1.27E+03
GI-37lc	LBNL/Nick Palaio Cleanroom, rm 70A	B: Blank	BiSKit	05/25/10	Non-NASA Cleanroom	10	000284	8	C	3	50	4.64E+02
GI-37b	LBNL/Nick Palaio Cleanroom, rm 70A	FB: Field Blank (1 BiSKit)	BiSKit	05/25/10	Non-NASA Cleanroom	1	000285	8	C	4	15	4.97E+02

Sample ID	Sample Description	Sample Source	Sampling Device	Date	Mission	Samples Pooled	Barcode	GI-Container	Row	Column	Sample Volume	16S rRNA Gene Copies
GI-37	LBNL Cleanroom, rm 70A	S: Sample (9 BiSKits)	BiSKit	05/25/10	Non-NASA Cleanroom	9	000286	8	C	5	35	8.33E+04
GI-38b	CS	Blank	Polyester wipe	3/15/2010 - 5/27/2010	MSL	10	000287	8	C	6	15	1.58E+02
GI-38	CS	CS	Polyester wipe	3/15/2010 - 5/27/2010	MSL	26	000288	8	C	7	15	1.30E+03
GI-39b	DS	Blank	Polyester wipe	3/10/2010 - 4/29/2010	MSL	3	000289	8	C	8	15	1.57E+02
GI-39	DS	DS	Polyester wipe	3/10/2010 - 4/29/2010	MSL	9	000290	8	C	9	15	1.68E+02
GI-40b	RVR	Blank	Polyester wipe	3/8/2010 - 6/2/2010	MSL	5	000291	8	D	1	0	1.61E+02
GI-40	RVR	RVR	Polyester wipe	3/8/2010 - 6/2/2010	MSL	16	000292	8	D	2	10	1.11E+03
GI-41b	Nonflight - Cleanroom wipe control	Blank	Polyester wipe	5/17/2010	MSL	1	000293	8	D	3	10	1.84E+02
GI-41	Non-flight wipe used to support Tc bundle	Non-flight	Polyester wipe	5/13/2010	MSL	1	000294	8	D	4	10	1.33E+03
Blank	26 wipes procured from Nick (200 mL x 26)	Blank	Polyester wipe	5/13/2010	MSL	26	000295	8	D	5	0	1.96E+02
GI-42lc	Bldg 144 cleanroom prior to cleaning	Lab control	BiSKit	06/15/10	MSL	20	000296	8	D	6	10	9.35E+02
GI-42lcp	Bldg 144 cleanroom prior to cleaning	Lab control PMA	BiSKit	06/15/10	MSL	20	000297	8	D	7	15	1.36E+02
GI-42b	Bldg 144 cleanroom prior to cleaning	FB	BiSKit	06/15/10	MSL	1	000298	8	D	8	10	8.52E+02
GI-42bp	Bldg 144 cleanroom prior to cleaning	FB PMA	BiSKit	06/15/10	MSL	1	000299	8	D	9	10	1.50E+02
GI-42-1	Bldg 144 cleanroom prior to cleaning	FLR Sample	BiSKit	06/15/10	MSL	9	000300	8	E	1	0	1.03E+06
GI-42-1p	Bldg 144 cleanroom prior to cleaning	FLR Sample PMA	BiSKit	06/15/10	MSL	9	000301	8	E	2	0	3.94E+05
GI-42-2	Bldg 144 cleanroom prior to cleaning	GSE Sample	BiSKit	06/15/10	MSL	9	000302	8	E	3	0	1.33E+05
GI-42-2p	Bldg 144 cleanroom prior to cleaning	GSE Sample PMA	BiSKit	06/15/10	MSL	9	000303	8	E	4	0	5.66E+04
GI-43lc	Bldg 144 cleanroom after cleaning	Lab control	Polyester wipe	06/16/10	MSL	21	000304	8	E	5	10	1.84E+02
GI-43lcp	Bldg 144 cleanroom after cleaning	Lab control PMA	Polyester wipe	06/16/10	MSL	21	000305	8	E	6	10	1.44E+02
GI-43b	Bldg 144 cleanroom after cleaning	Field Blank	Polyester wipe	06/16/10	MSL	2	000306	8	E	7	0	1.72E+02
GI-43bp	Bldg 144 cleanroom after cleaning	Field Blank PMA	Polyester wipe	06/16/10	MSL	2	000307	8	E	8	10	1.36E+02
GI-43-1	Bldg 144 cleanroom after cleaning	FLR Sample	Polyester wipe	06/16/10	MSL	9	000639	8	E	9	10	1.74E+05
GI-43-1p	Bldg 144 cleanroom after cleaning	FLR Sample PMA	Polyester wipe	06/16/10	MSL	9	000638	8	F	1	10	4.58E+05
GI-43-2	Bldg 144 cleanroom after cleaning	GSE Sample	Polyester wipe	06/16/10	MSL	9	000637	8	F	2	10	4.79E+05
GI-43-2p	Bldg 144 cleanroom after cleaning	GSE Sample PMA	Polyester wipe	06/16/10	MSL	9	000636	8	F	3	0	5.05E+03
GI-44			Polyester Wipe				001447	8	F	4	10	
GI-44b		Blank	Polyester Wipe				001446	8	F	5	15	

Sample ID	Sample Description	Sample Source	Sampling Device	Date	Mission	Samples Pooled	Barcode	GI-Container	Row	Column	Sample Volume	16S rRNA Gene Copies
GI-45			Polyester Wipe				001449	8	F	6	10	
GI-45b		Blank	Polyester Wipe				001448	8	F	7	15	
GI-46			Polyester Wipe				001450	8	F	8	10	
GI-47			Polyester Wipe				001452	8	F	9	10	
GI-47b		Blank	Polyester Wipe				001451	8	G	1	20	
GI-48			Polyester Wipe				001454	8	G	2	20	
GI-48b		Blank	Polyester Wipe				001453	8	G	3	20	
GI-49			Polyester Wipe	11/28/2011	MSL, KSC	7	002688	8	G	4	25	2.22E+02
GI-49b,52b…60b		Blank	Polyester Wipe	11/28/2011	MSL, KSC	13	002625	8	G	5	25	2.70E+00
GI-50			Polyester Wipe	11/28/2011	MSL, KSC	3	002689	8	G	6	25	5.53E+02
GI-50b		Blank	Polyester Wipe	11/28/2011	MSL, KSC	1	002626	8	G	7	25	7.88E+00
GI-51			Polyester Wipe	11/28/2011	MSL, KSC	7	002690	8	G	8	25	8.60E+02
GI-51b		Blank	Polyester Wipe	11/28/2011	MSL, KSC	1	002627	8	G	9	25	1.03E+01
GI-52			Polyester Wipe	11/28/2011	MSL, KSC	6	002691	8	H	1	25	1.24E+03
GI-53			Polyester Wipe	11/28/2011	MSL, KSC	7	002692	8	H	2	25	6.52E+01
GI-54			Polyester Wipe	11/28/2011	MSL, KSC	5	002693	8	H	3	25	6.55E+02
GI-55			Polyester Wipe	11/28/2011	MSL, KSC	9	002694	8	H	4	25	4.40E+02
GI-56			Polyester Wipe	11/28/2011	MSL, KSC	2	002695	8	H	5	25	6.99E+02
GI-57			Polyester Wipe	11/28/2011	MSL, KSC	2	002696	8	H	6	25	8.94E+02
GI-58			Polyester Wipe	11/28/2011	MSL, KSC	5	002697	8	H	7	25	8.73E+02
GI-59			Polyester Wipe	11/28/2011	MSL, KSC	11	002698	8	H	8	25	1.05E+03
GI-60			Polyester Wipe	11/28/2011	MSL, KSC	6	002699	8	H	9	25	1.46E+03
GI-61			Polyester Wipe	12/17/2011	MSL, KSC	4	002700	8	I	1	25	1.31E+05
GI-61b		Blank	Polyester Wipe	12/17/2011	MSL, KSC	1	002628	8	I	2	25	4.63E+02
GI-62			Polyester Wipe	12/17/2011	MSL, KSC	6	002701	8	I	3	25	5.54E+04
GI-62b		Blank	Polyester Wipe	12/17/2011	MSL, KSC	2	002629	8	I	4	25	1.35E+03
GI-63			Polyester Wipe	12/17/2011	MSL, KSC	8	002702	8	I	5	25	1.34E+05
GI-63b		Blank	Polyester Wipe	12/17/2011	MSL, KSC	2	002630	8	I	6	25	3.28E+02
GI-64			Polyester Wipe	12/17/2011	MSL, KSC	6	002703	8	I	7	25	7.50E+04
GI-64b		Blank	Polyester Wipe	12/17/2011	MSL, KSC	1	002631	8	I	8	25	3.46E+02
GI-65			Polyester Wipe	12/17/2011	MSL, KSC	3	002704	8	I	9	25	1.67E+05
GI-65b		Blank	Polyester Wipe	12/17/2011	MSL, KSC	1	002632	9	A	1	25	3.20E+02
GI-66			Polyester Wipe	12/17/2011	MSL, KSC	Water only-Place holder	002705	9	A	2	25	No Sample - water only
GI-66b		Blank	Polyester Wipe	12/17/2011	MSL, KSC	Water only-Place holder	002633	9	A	3	25	No Sample - water only
GI-67			Polyester Wipe	12/17/2011	MSL, KSC	2	002707	9	A	4	25	2.32E+04
GI-67b		Blank	Polyester Wipe	12/17/2011	MSL, KSC	1	002634	9	A	5	25	5.42E+02
GI-68			Polyester Wipe	12/17/2011	MSL, KSC	2	002708	9	A	6	25	7.17E+04
GI-68b		Blank	Polyester Wipe	12/17/2011	MSL, KSC	Water only-Place holder	002635	9	A	7	25	No Sample - water only
GI-69			Polyester Wipe	12/17/2011	MSL, KSC	Water only-Place holder	002709	9	A	8	25	No Sample - water only
GI-69b		Blank	Polyester Wipe	12/17/2011	MSL, KSC	Water only-Place holder	002636	9	A	9	25	No Sample - water only
GI-70			Polyester Wipe	12/17/2011	MSL, KSC	5	002710	9	B	1	25	3.45E+04
GI-70b		Blank	Polyester Wipe	12/17/2011	MSL, KSC	2	002637	9	B	2	25	4.51E+02
GI-71			Polyester Wipe	12/17/2011	MSL, KSC	2	002711	9	B	3	25	5.14E+04
GI-71b		Blank	Polyester Wipe	12/17/2011	MSL, KSC	1	002638	9	B	4	25	5.37E+02
GI-72			Polyester Wipe	12/17/2011	MSL, KSC	6	002712	9	B	5	25	1.05E+05
GI-72b		Blank	Polyester Wipe	12/17/2011	MSL, KSC	2	002639	9	B	6	25	7.94E+02

Sample ID	Sample Description	Sample Source	Sampling Device	Date	Mission	Samples Pooled	Barcode	GI-Container	Row	Column	Sample Volume	16S rRNA Gene Copies
GI-73			Polyester Wipe	12/18/2011	MSL, KSC	2	002713	9	B	7	25	9.71E+03
GI-73b		Blank	Polyester Wipe	12/18/2011	MSL, KSC	Water only-Place holder	002640	9	B	8	25	No Sample - water only
GI-74			Polyester Wipe	12/18/2011	MSL, KSC	11	002714	9	B	9	25	1.63E+04
GI-74b		Blank	Polyester Wipe	12/18/2011	MSL, KSC	4	002641	9	C	1	25	1.54E+02
GI-75			Polyester Wipe	12/18/2011	MSL, KSC	3	002715	9	C	2	25	1.25E+04
GI-75b		Blank	Polyester Wipe	12/18/2011	MSL, KSC	2	002642	9	C	3	25	9.35E+01
GI-76			Polyester Wipe	12/18/2011	MSL, KSC	4	002716	9	C	4	25	7.93E+03
GI-76b		Blank	Polyester Wipe	12/18/2011	MSL, KSC	2	002643	9	C	5	25	9.84E+01
GI-77			Polyester Wipe	12/18/2011	MSL, KSC	2	002717	9	C	6	25	1.14E+04
GI-77b		Blank	Polyester Wipe	12/18/2011	MSL, KSC	1	002644	9	C	7	25	6.83E+01
GI-78			Polyester Wipe	12/18/2011	MSL, KSC	1	002718	9	C	8	25	8.16E+03
GI-78b		Blank	Polyester Wipe	12/18/2011	MSL, KSC	1	002645	9	C	9	25	5.54E+01
GI-79			Polyester Wipe	12/18/2011	MSL, KSC	2	002719	9	D	1	25	7.54E+03
GI-79b		Blank	Polyester Wipe	12/18/2011	MSL, KSC	1	002646	9	D	2	25	1.14E+02
GI-80			Polyester Wipe	12/18/2011	MSL, KSC	6	002720	9	D	3	25	1.09E+04
GI-80b		Blank	Polyester Wipe	12/18/2011	MSL, KSC	3	002647	9	D	4	25	1.48E+02
GI-81			Polyester Wipe	12/18/2011	MSL, KSC	2	002721	9	D	5	25	9.93E+03
GI-81b		Blank	Polyester Wipe	12/18/2011	MSL, KSC	1	002648	9	D	6	25	1.29E+02
GI-82			Polyester Wipe	12/18/2011	MSL, KSC	1	002722	9	D	7	25	6.47E+03
GI-82b		Blank	Polyester Wipe	12/18/2011	MSL, KSC	1	002649	9	D	8	25	2.47E+02
GI-83			Polyester Wipe	12/18/2011	MSL, KSC	3	002723	9	D	9	25	1.14E+04
GI-83b		Blank	Polyester Wipe	12/18/2011	MSL, KSC	1	002650	9	E	1	25	9.54E+01
GI-84			Polyester Wipe	12/18/2011	MSL, KSC	3	002724	9	E	2	25	8.08E+03
GI-84b		Blank	Polyester Wipe	12/18/2011	MSL, KSC	2	002652	9	E	3	25	2.12E+02
GI-85			Polyester Wipe	12/19/2011	MSL, KSC	10	002725	9	E	4	25	7.86E+04
GI-85b		Blank	Polyester Wipe	12/19/2011	MSL, KSC	5	002652	9	E	5	25	1.66E+02
GI-86			Polyester Wipe	12/19/2011	MSL, KSC	1	002726	9	E	6	25	1.05E+04
GI-86b		Blank	Polyester Wipe	12/19/2011	MSL, KSC	1	002653	9	E	7	25	9.10E+01
GI-87			Polyester Wipe	12/19/2011	MSL, KSC	2	002727	9	E	8	25	1.76E+04
GI-87b		Blank	Polyester Wipe	12/19/2011	MSL, KSC	1	002654	9	E	9	25	1.25E+02
GI-88			Polyester Wipe	12/19/2011	MSL, KSC	2	002728	9	F	1	25	2.51E+04
GI-88b		Blank	Polyester Wipe	12/19/2011	MSL, KSC	1	002655	9	F	2	25	7.03E+01
GI-89			Polyester Wipe	12/19/2011	MSL, KSC	4	002729	9	F	3	25	3.30E+04
GI-89b		Blank	Polyester Wipe	12/19/2011	MSL, KSC	1	002656	9	F	4	25	1.10E+02
GI-90			Polyester Wipe	12/19/2011	MSL, KSC	20	002730	9	F	5	25	1.13E+04
GI-90b		Blank	Polyester Wipe	12/19/2011	MSL, KSC	5	002657	9	F	6	25	9.54E+02
GI-91			Polyester Wipe	12/19/2011	MSL, KSC	4	002731	9	F	7	25	1.82E+04
GI-91b		Blank	Polyester Wipe	12/19/2011	MSL, KSC	1	002658	9	F	8	25	7.16E+01
GI-92			Polyester Wipe	12/19/2011	MSL, KSC	2	002732	9	F	9	25	2.79E+04
GI-92b		Blank	Polyester Wipe	12/19/2011	MSL, KSC	1	002659	9	G	1	25	1.57E+02
GI-93			Polyester Wipe	12/19/2011	MSL, KSC	6	002733	9	G	2	25	1.20E+07
GI-93b		Blank	Polyester Wipe	12/19/2011	MSL, KSC	2	002660	9	G	3	25	1.20E+02
GI-94			Polyester Wipe	12/19/2011	MSL, KSC	10	002734	9	G	4	25	3.76E+04
GI-94b		Blank	Polyester Wipe	12/19/2011	MSL, KSC	1	002661	9	G	5	25	9.35E+01
GI-95			Polyester Wipe	12/19/2011	MSL, KSC	7	002735	9	G	6	25	1.13E+05
GI-95b		Blank	Polyester Wipe	12/19/2011	MSL, KSC	2	002662	9	G	7	25	4.08E+02
GI-96			Polyester Wipe	12/19/2011	MSL, KSC	3	002736	9	G	8	25	2.37E+04
GI-96b		Blank	Polyester Wipe	12/19/2011	MSL, KSC	1	002663	9	G	9	25	6.06E+02
GI-97			Polyester Wipe	12/20/2011	MSL, KSC	1	002737	9	H	1	25	3.04E+04
GI-97b		Blank	Polyester Wipe	12/20/2011	MSL, KSC	1	002664	9	H	2	25	2.54E+02
GI-98			Polyester Wipe	12/20/2011	MSL, KSC	1	002738	9	H	3	25	3.48E+04
GI-98b		Blank	Polyester Wipe	12/20/2011	MSL, KSC	1	002665	9	H	4	25	2.56E+02

Sample ID	Sample Description	Sample Source	Sampling Device	Date	Mission	Samples Pooled	Barcode	GI-Container	Row	Column	Sample Volume	16S rRNA Gene Copies
GI-99			Polyester Wipe	12/20/2011	MSL, KSC	8	002739	9	H	5	25	9.12E+03
GI-99b		Blank	Polyester Wipe	12/20/2011	MSL, KSC	1	002666	9	H	6	25	3.42E+02
GI-100			Polyester Wipe	12/20/2011	MSL, KSC	3	002740	9	H	7	25	2.47E+04
GI-100b		Blank	Polyester Wipe	12/20/2011	MSL, KSC	1	002667	9	H	8	25	1.72E+02
GI-101			Polyester Wipe	12/20/2011	MSL, KSC	3	002741	9	H	9	25	4.63E+04
GI-101b		Blank	Polyester Wipe	12/20/2011	MSL, KSC	1	002668	9	I	1	25	3.03E+02
GI-102			Polyester Wipe	12/20/2011	MSL, KSC	3	002742	9	I	2	25	4.84E+04
GI-102b		Blank	Polyester Wipe	12/20/2011	MSL, KSC	1	002669	9	I	3	25	2.53E+02
GI-103			Polyester Wipe	12/20/2011	MSL, KSC	2	002743	9	I	4	25	4.53E+04
GI-103b		Blank	Polyester Wipe	12/20/2011	MSL, KSC	1	002670	9	I	5	25	1.85E+02
GI-104			Polyester Wipe	12/20/2011	MSL, KSC	2	002745	9	I	6	25	3.96E+04
GI-104b		Blank	Polyester Wipe	12/20/2011	MSL, KSC	1	002671	9	I	7	25	2.38E+02
GI-105			Polyester Wipe	12/20/2011	MSL, KSC	1	002746	9	I	8	25	2.84E+04
GI-105b		Blank	Polyester Wipe	12/20/2011	MSL, KSC	1	002672	9	I	9	25	2.71E+02
GI-106			Polyester Wipe	12/20/2011	MSL, KSC	6	002746	10	A	1	25	2.66E+04
GI-106b		Blank	Polyester Wipe	12/20/2011	MSL, KSC	2	002675	10	A	2	25	2.58E+02
GI-107			Polyester Wipe	12/20/2011	MSL, KSC	3	002747	10	A	3	25	4.13E+04
GI-107b		Blank	Polyester Wipe	12/20/2011	MSL, KSC	1	002674	10	A	4	25	2.56E+02
GI-108			Polyester Wipe	12/20/2011	MSL, KSC	3	002748	10	A	5	25	2.36E+04
GI-108b		Blank	Polyester Wipe	12/20/2011	MSL, KSC	Water only-Place holder	002675	10	A	6	25	No Sample - water only
GI-109			Polyester Wipe	12/16/2011	MSL, KSC	2	002749	10	A	7	25	2.01E+04
GI-109b		Blank	Polyester Wipe	12/16/2011	MSL, KSC	1	002676	10	A	8	25	1.71E+02
GI-110			Polyester Wipe	12/16/2011	MSL, KSC	2	002750	10	A	9	25	2.26E+04
GI-110b		Blank	Polyester Wipe	12/16/2011	MSL, KSC	1	002677	10	B	1	25	2.81E+02
GI-111			Polyester Wipe	12/16/2011	MSL, KSC	4	002751	10	B	2	25	3.75E+04
GI-111b		Blank	Polyester Wipe	12/16/2011	MSL, KSC	1	002678	10	B	3	25	3.44E+02
GI-112			Polyester Wipe	12/16/2011	MSL, KSC	8	002752	10	B	4	25	3.61E+04
GI-112b		Blank	Polyester Wipe	12/16/2011	MSL, KSC	2	002679	10	B	5	25	1.73E+02
GI-113			Polyester Wipe	12/16/2011	MSL, KSC	2	002753	10	B	6	25	1.63E+04
GI-113b		Blank	Polyester Wipe	12/16/2011	MSL, KSC	1	002680	10	B	7	25	2.29E+02
GI-114			Polyester Wipe	12/16/2011	MSL, KSC	1	002754	10	B	8	25	3.83E+04
GI-114b		Blank	Polyester Wipe	12/16/2011	MSL, KSC	1	002681	10	B	9	25	4.62E+02
GI-115			Polyester Wipe	12/16/2011	MSL, KSC	2	002755	10	C	1	25	9.67E+03
GI-115b		Blank	Polyester Wipe	12/16/2011	MSL, KSC	1	002683	10	C	2	25	2.09E+01
GI-116			Polyester Wipe	12/16/2011	MSL, KSC	22	002756	10	C	3	25	2.25E+06
GI-116b		Blank	Polyester Wipe	12/16/2011	MSL, KSC	3	002683	10	C	4	25	1.89E+02
GI-117			BiSKit	12/16/2011	MSL, KSC	23	002757	10	C	5	25	0.00E+00
GI-117b		Blank	BiSKit	12/16/2011	MSL, KSC	4	002684	10	C	6	25	2.19E+02
GI-Max		Reagent Control	Maxwell Control	12/16/2011	MSL		002685	10	C	7	25	3.16E+01
GI-JPL-PBS		Buffer Control JPL	Buffer Control	12/16/2011	MSL		002686	10	C	8	25	1.44E+02
GI-KSC-PBS		Buffer Control KSC	Buffer Control	12/16/2011	MSL		002687	10	C	9	25	5.57E+01

Table E.1-3. Characteristics of Genetic Inventory Task DNA samples archived at TBD location-1.

Sample ID	Sample Description	Sample Source	Sampling Device	Date	Mission	Samples Pooled	Barcode	GI-Container	Row	Column	Sample Volume	16S rRNA Gene copies
	BIG Control	Buffer control	PBS	01/03/07	Phoenix at LMA			11	A	1	0	
GI1-2	1-MTF-1B	Floor	BiSKit	01/03/07	Phoenix at LMA		Samples not listed in SampleWare database					
GI1-3	1-MTF-2B	Floor	BiSKit	01/03/07	Phoenix at LMA		Samples not listed in SampleWare database					
GI1-4	1-MTF-3B	Floor	BiSKit	01/03/07	Phoenix at LMA		Samples not listed in SampleWare database					
GI1-5	1-MTF-4B	Floor	BiSKit	01/03/07	Phoenix at LMA		Samples not listed in SampleWare database					
GI1-6	1-MTF-5B	Floor	BiSKit	01/03/07	Phoenix at LMA		Samples not listed in SampleWare database					
GI1-7	1-MTF-6B	Floor	BiSKit	01/03/07	Phoenix at LMA		Samples not listed in SampleWare database					
GI1-8	1-MTF-7B	Floor	BiSKit	01/03/07	Phoenix at LMA		Samples not listed in SampleWare database					
GI1-9	1-MTF-8B	Floor	BiSKit	01/03/07	Phoenix at LMA			11	A	2	0	
GI1-10	1-MTF-9B	Floor	BiSKit	01/03/07	Phoenix at LMA			11	A	3	0	
GI1-11	1-MTF-10B	Floor	BiSKit	01/03/07	Phoenix at LMA			11	A	4	0	
GI1-12	1-MTF-BLNK	Blank	BiSKit	01/03/07	Phoenix at LMA		Samples not listed in SampleWare database					
GI1-13	PHX swab BLNK 10 pooled	Blank	Cotton swab	01/03/07	Phoenix at LMA			11	A	5	0	1.22E+02
GI1-14	MTF Swab BLNK9 pooled	Blank	Cotton swab	01/03/07	Phoenix at LMA			11	A	6	0	1.45E+02
GI1-15	MTF Swab 9 pooled	Floor	Cotton swab	01/03/07	Phoenix at LMA			11	A	7	0	1.60E+04
GI1-16	PHX s/c swab10 pooled	Spacecraft	Cotton swab	01/03/07	Phoenix at LMA			11	A	8	0	1.47E+04
GI2-1	SSB-1B	Floor	BiSKit	02/03/07	Phoenix s/c not in SSB			11	A	9	0	
GI2-2	SSB-2B	Floor	BiSKit	02/03/07	Phoenix s/c not in SSB			11	B	1	0	
GI2-3	SSB-3B	Floor	BiSKit	02/03/07	Phoenix s/c not in SSB			11	B	2	0	
GI2-4	SSB-4B	Floor	BiSKit	02/03/07	Phoenix s/c not in SSB			11	B	3	0	
GI2-5	SSB-5B	Floor	BiSKit	02/03/07	Phoenix s/c not in SSB			11	B	4	0	
GI2-6	SSB Swab 10 pooled	Floor	Cotton swab	02/03/07	Phoenix s/c not in SSB			11	B	5	0	1.00E+05
GI2-7	SSB Swab BLNK 10 pooled	Blank	Cotton swab	02/03/07	Phoenix s/c not in SSB			11	B	6	0	
GI3-1	PHSF W1	Floor	BiSKit	04/24/07	Before Phoenix		005468	11	B	7	10	
GI3-2	PHSF W2-SE	Floor	BiSKit	04/24/07	Before Phoenix		005470	11	B	8	10	
GI3-3	PHSF W3-Center	Floor	BiSKit	04/24/07	Before Phoenix			11	B	9	0	
GI3-4	PHSF W4-NW	Floor	BiSKit	04/24/07	Before Phoenix		005472	11	C	1	10	
GI3-5	PHSF B5-SW	Floor	BiSKit	04/24/07	Before Phoenix		005474	11	C	2	10	
GI3-6	PHSF B6-E	Floor	BiSKit	04/24/07	Before Phoenix		005475	11	C	3	10	
GI3-7	PHSF B7-W	Floor	BiSKit	04/24/07	Before Phoenix		005477	11	C	4	10	
GI3-8	PHSF B8-N	Floor	BiSKit	04/24/07	Before Phoenix		005478	11	C	5	10	
GI3-9	PHSF B9-S	Floor	BiSKit	04/24/07	Before Phoenix		005479	11	C	6	10	
GI3-10	PHSF B10-Wall	Floor	BiSKit	04/24/07	Before Phoenix		005480	11	C	7	10	1.57E+05
GI3-FC1	BiSKit Field Control #1	Field control	BiSKit	04/24/07	Before Phoenix		000733	11	C	8	0	
GI3-BRC1	BiSKit PBS Control #1	Buffer control	PBS	04/24/07	Before Phoenix		000735	11	C	9	10	1.40E+02
GI3-BIG	Autolyser Cartridge Control	Buffer control	PBS	04/24/07	Before Phoenix		000734	11	D	1	0	1.26E+02
GI4-1	IP1-GI (BiSKit samples)	Floor	BiSKit	06/27/07	During Phoenix		000736	11	D	2	10	
GI4-2	IP2-GI	Floor	BiSKit	06/27/07	During Phoenix		000737	11	D	3	10	
GI4-3	IP3-GI	Floor	BiSKit	06/27/07	During Phoenix		000739	11	D	4	10	
GI4-5	IP5-GI	Floor	BiSKit	06/27/07	During Phoenix		000740	11	D	5	10	
GI4-6	IP6-GI	Floor	BiSKit	06/27/07	During Phoenix		000741	11	D	6	10	
GI4-7	IP7-GI	Floor	BiSKit	06/27/07	During Phoenix		000742	11	D	7	10	
GI4-8	IP8-GI	Floor	BiSKit	06/27/07	During Phoenix		000743	11	D	8	10	8.79E+05
GI4-1-blnk	IP1-GI-blnk (in 15 ml tubes)	Blank	BiSKit	06/27/07	During Phoenix		000744	11	D	9	0	1.45E+02
GI4-2-blnk	IP2-GI-blnk	Blank	BiSKit	06/27/07	During Phoenix		000745	11	E	1	10	
GI4-3-blnk	IP3-GI-blnk	Blank	BiSKit	06/27/07	During Phoenix		000746	11	E	2	10	
GI4-5-blnk	IP5-GI-blnk	Blank	BiSKit	06/27/07	During Phoenix		000756	11	E	3	10	
GI4-6-blnk	IP6-GI-blnk	Blank	BiSKit	06/27/07	During Phoenix		000757	11	E	4	10	
GI4-7-blnk	IP7-GI-blnk	Blank	BiSKit	06/27/07	During Phoenix		000758	11	E	5	0	
GI4-8-blnk	IP8-GI-blnk	Blank	BiSKit	06/27/07	During Phoenix		000759	11	E	6	15	
GI4-BIG(-)		Buffer control	PBS	06/27/07	During Phoenix		000752	11	E	7	10	1.47E+02

Sample ID	Sample Description	Sample Source	Sampling Device	Date	Mission	Samples Pooled	Barcode	GI-Container	Row	Column	Sample Volume	16S rRNA Gene copies
GI5-1	PPO-PHSF-1B	Floor	BiSKit	07/20/07	Post-Phoenix		000760	11	E	8	10	
GI5-2	PPO-PHSF-2B	Floor	BiSKit	07/20/07	Post-Phoenix		000761	11	E	9	10	
GI5-3	PPO-PHSF-3B	Floor	BiSKit	07/20/07	Post-Phoenix		000762	11	F	1	10	
GI5-4	PPO-PHSF-4B	Floor	BiSKit	07/20/07	Post-Phoenix		000763	11	F	2	10	
GI5-5	PPO-PHSF-5B	Floor	BiSKit	07/20/07	Post-Phoenix		000764	11	F	3	10	
GI5-6	PPO-PHSF-6B	Floor	BiSKit	07/20/07	Post-Phoenix		000765	11	F	4	10	
GI5-7	PPO-PHSF-7B	Floor	BiSKit	07/20/07	Post-Phoenix		000766	11	F	5	10	
GI5-8	PPO-PHSF-8B	Floor	BiSKit	07/20/07	Post-Phoenix		000767	11	F	6	15	
GI5-9	PPO-PHSF-9B	Floor	BiSKit	07/20/07	Post-Phoenix		005481	11	F	7	10	
GI5-10	PPO-PHSF-10B	Floor	BiSKit	07/20/07	Post-Phoenix		000768	11	F	8	15	
GI5-12	PPO-PHSF-12B	Floor	BiSKit	07/20/07	Post-Phoenix		000769	11	F	9	15	
GI5-13	PPO-PHSF-13B	Floor	BiSKit	07/20/07	Post-Phoenix		000792	11	G	1	15	
GI5-14	PPO-PHSF-14B	Floor	BiSKit	07/20/07	Post-Phoenix		000793	11	G	2	15	
GI5-15	PPO-PHSF-15B	Floor	BiSKit	07/20/07	Post-Phoenix		000794	11	G	3	15	
GI5-16	PPO-PHSF-16B	Floor	BiSKit	07/20/07	Post-Phoenix		000795	11	G	4	10	
GI5-17	PPO-PHSF-17B	Floor	BiSKit	07/20/07	Post-Phoenix		000796	11	G	5	10	
GI5-18	PPO-PHSF-18B	Floor	BiSKit	07/20/07	Post-Phoenix		000797	11	G	6	10	
GI5-19	PPO-PHSF-19B	Floor	BiSKit	07/20/07	Post-Phoenix		000798	11	G	7	10	
GI5-20	PPO-PHSF-20B	Floor	BiSKit	07/20/07	Post-Phoenix		000799	11	G	8	10	1.80E+05
GI6-1	PHSF-1B	Floor	BiSKit	08/02/07	Post Phoenix		000700	11	G	9	0	0.00E+00
GI6-2	PHSF-2B	Floor	BiSKit	08/02/07	Post Phoenix		000784	11	H	1	10	
GI6-3	PHSF-3B	Floor	BiSKit	08/02/07	Post Phoenix		000702	11	H	2	0	1.02E+08
GI6-4	PHSF-4B	Floor	BiSKit	08/02/07	Post Phoenix		000786	11	H	3	15	
GI6-5	PHSF-5B	Floor	BiSKit	08/02/07	Post Phoenix		000787	11	H	4	10	
GI6-6	PHSF-6B	Floor	BiSKit	08/02/07	Post Phoenix		000788	11	H	5	10	
GI6-7	PHSF-7B	Floor	BiSKit	08/02/07	Post Phoenix			11	H	6	0	0.00E+00
GI6-8	PHSF-8B	Floor	BiSKit	08/02/07	Post Phoenix		005482	11	H	7	10	
GI6-9	PHSF-9B	Floor	BiSKit	08/02/07	Post Phoenix		Samples not listed in SampleWare database					
GI6-10	PHSF-10B	Floor	BiSKit	08/02/07	Post Phoenix		Samples not listed in SampleWare database					
GI6-1blnk	PHSF-1-blnk	Blank	BiSKit	08/02/07	Post Phoenix		Samples not listed in SampleWare database					
GI6-2blnk	PHSF-2-blnk	Blank	BiSKit	08/02/07	Post Phoenix		005483	11	H	8	10	
GI6-3blnk	PHSF-3-blnk	Blank	BiSKit	08/02/07	Post Phoenix		Samples not listed in SampleWare database					2.92E+02
GI6-4blnk	PHSF-4-blnk	Blank	BiSKit	08/02/07	Post Phoenix		005484	11	H	9	10	
GI6-5blnk	PHSF-5-blnk	Blank	BiSKit	08/02/07	Post Phoenix		005485	11	I	1	10	
GI6-6blnk	PHSF-6-blnk	Blank	BiSKit	08/02/07	Post Phoenix		005486	11	I	2	10	
GI6-7blnk	PHSF-7-blnk	Blank	BiSKit	08/02/07	Post Phoenix		Samples not listed in SampleWare database					1.05E+02
GI6-8blnk	PHSF-8-blnk	Blank	BiSKit	08/02/07	Post Phoenix		005487	11	I	3	10	
GI6-9blnk	PHSF-9-blnk	Blank	BiSKit	08/02/07	Post Phoenix		Samples not listed in SampleWare database					2.04E+02
GI6-10blnk	PHSF-10-blnk	Blank	BiSKit	08/02/07	Post Phoenix		Samples not listed in SampleWare database					2.37E+02
GI6-FC	PHFS-field control BiSKit	Field control	BiSKit	08/02/07	Post Phoenix		005488	11	I	4	10	
GI6-FCblnk	PHFS-field control blank	FC blank	BiSKit	08/02/07	Post Phoenix		005489	11	I	5	10	
GI7-B-1	9C-E	Floor	BiSKit	11/28/07	During Dawn			11	I	6	0	2.75E+05
GI7-B-2	9C-G	Floor	BiSKit	11/28/07	During Dawn		005490	11	I	7	10	
GI7-B-3	9C-D	Floor	BiSKit	11/28/07	During Dawn			11	I	8	0	7.72E+03
GI7-B-4	9C-A	Floor	BiSKit	11/28/07	During Dawn		005491	11	I	9	10	
GI7-B-5	9C Level	Floor	BiSKit	11/28/07	During Dawn			12	A	1	0	1.26E+03
GI7-B-6	9C stair	Floor	BiSKit	11/28/07	During Dawn		005492	12	A	2	10	
GI7-B-7	9C-F	Floor	BiSKit	11/28/07	During Dawn		005493	12	A	3	10	
GI7-B-8	9C by B Central east of s/c	Floor	BiSKit	11/28/07	During Dawn			12	A	4	0	3.09E+03
GI7-B-9	9C D/E	Floor	BiSKit	11/28/07	During Dawn		005494	12	A	5	10	
GI7-B-10	Field control @9C	Field control	BiSKit	11/28/07	During Dawn		005495	12	A	6	10	
GI7-B-11	11	Floor	BiSKit	11/28/07	During Dawn			12	A	7	0	1.10E+03
GI7-B-12	12	Floor	BiSKit	11/28/07	During Dawn		005496	12	A	8	10	

Sample ID	Sample Description	Sample Source	Sampling Device	Date	Mission	Samples Pooled	Barcode	GI-Container	Row	Column	Sample Volume	16S rRNA Gene copies
GI7-B-13	13	Floor	BiSKit	11/28/07	During Dawn		005497	12	A	9	10	
GI7-B-14	14	Floor	BiSKit	11/28/07	During Dawn		005498	12	B	1	10	
GI7-B-15	15	Floor	BiSKit	11/28/07	During Dawn		005499	12	B	2	10	
GI7-B-16	16	Floor	BiSKit	11/28/07	During Dawn		005500	12	B	3	10	
GI7-B-17	17	Floor	BiSKit	11/28/07	During Dawn		005501	12	B	4	10	
GI7-B-18	18	Floor	BiSKit	11/28/07	During Dawn			12	B	5	0	
GI7-B-19	19	Floor	BiSKit	11/28/07	During Dawn		005502	12	B	6	10	
GI7-B-20	20	Floor	BiSKit	11/28/07	During Dawn		005503	12	B	7	10	
GI7-B-21	B-9/17-1	Floor	BiSKit	11/28/07	During Dawn			12	B	8	0	
GI7-B-22	B-9/17-2	Floor	BiSKit	11/28/07	During Dawn			12	B	9	0	
GI7-B-23	B-9/17-3	Floor	BiSKit	11/28/07	During Dawn		005504	12	C	1	10	
GI7-B-24	B-9/17-4	Floor	BiSKit	11/28/07	During Dawn		005505	12	C	2	10	
GI7-BLNK-1	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn			12	C	3	0	1.66E+02
GI7-BLNK-2	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		005507	12	C	4	10	
GI7-BLNK-3	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		005509	12	C	5	10	0.00E+00
GI7-BLNK-4	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		005510	12	C	6	10	
GI7-BLNK-5	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn			12	C	7	0	2.17E+02
GI7-BLNK-6	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		005512	12	C	8	10	
GI7-BLNK-7	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		005514	12	C	9	10	
GI7-BLNK-8	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn			12	D	1	0	7.51E+02
GI7-BLNK-9	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		005516	12	D	2	10	
GI7-BLNK-10	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		005517	12	D	3	10	
GI7-BLNK-11	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn			12	D	4	0	
GI7-BLNK-12	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		005518	12	D	5	10	
GI7-BLNK-13	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		005519	12	D	6	10	
GI7-BLNK-14	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		005520	12	D	7	10	
GI7-BLNK-15	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		005521	12	D	8	10	
GI7-BLNK-16	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		005522	12	D	9	10	
GI7-BLNK-17	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		005523	12	E	1	10	
GI7-BLNK-18	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		005524	12	E	2	10	
GI7-BLNK-19	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		005525	12	E	3	10	
GI7-BLNK-20	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		005526	12	E	4	10	
GI8-1	JPL SAF pooled samples 10 BiSKits)	Floor	BiSKit	10/08/07	During MSL, JPL SAF			12	E	5	0	8.74E+04

Sample ID	Sample Description	Sample Source	Sampling Device	Date	Mission	Samples Pooled	Barcode	GI-Container	Row	Column	Sample Volume	16S rRNA Gene copies
GI8-2	Pooled blanks (10 BiSKits)	Blank	BiSKit	10/08/07	During MSL, JPL SAF			12	E	6	0	1.19E+02
GI8-3	PBS/BIG	Buffer control	PBS	10/08/07	During MSL, JPL SAF			12	E	7	0	
GI10-1	JPL SAF pooled samples (20 BiSKits)	Floor	BiSKit	01/22/08	During MSL, JPL SAF		Samples not listed in SampleWare database					9.51E+07
GI10-2	Pooled blanks (20 BiSKits)	Blank	BiSKit	01/22/08	During MSL, JPL SAF		Samples not listed in SampleWare database					0.00E+00
GI10-3	PBS/BIG	Buffer control	PBS	01/22/08	During MSL, JPL SAF		Samples not listed in SampleWare database					
GI11-1	JPL SAF pooled samples (20 BiSKits)	Floor	BiSKit	02/12/08	During MSL, JPL SAF		Samples not listed in SampleWare database					1.44E+07
GI11-2	Pooled blanks (20 BiSKits)	Blank	BiSKit	02/12/08	During MSL, JPL SAF		Samples not listed in SampleWare database					
GI11-3	PBS/BIG	Buffer control	PBS	02/12/08	During MSL, JPL SAF		Samples not listed in SampleWare database					
GI12-1	JPL SAF pooled samples (20 BiSKits)	Floor	BiSKit	04/01/08	During MSL, JPL SAF			12	E	8	0	4.78E+05
GI12-2	Pooled blanks (20 BiSKits)	Blank	BiSKit	04/01/08	During MSL, JPL SAF			12	E	9	0	
GI12-3	PBS/BIG	Buffer control	PBS	04/01/08	During MSL, JPL SAF			12	F	1	0	
GI13-1	JPL SAF pooled samples (20 BiSKits)	Floor	BiSKit	06/04/08	During MSL, JPL SAF		Samples not listed in SampleWare database					1.01E+08
GI13-2	Pooled blanks (20 BiSKits)	Blank	BiSKit	06/04/08	During MSL, JPL SAF		Samples not listed in SampleWare database					
GI13-3	PBS/BIG	Buffer control	PBS	06/04/08	During MSL, JPL SAF		Samples not listed in SampleWare database					
GI14	JPL SAF pooled samples (20 BiSKits)	Floor	BiSKit	08/05/08	During MSL, JPL SAF			12	F	2	0	3.96E+05
GI14BLNK	Pooled blanks (20 BiSKits)	Blank	BiSKit	08/05/08	During MSL, JPL SAF			12	F	3	0	0.00E+00
GI15	See MSL sample ID for detail	Surface	Polyester wipe	09/05/08	MSL		000566	12	F	4	10	3.64E+09
GI16	See MSL sample ID for detail	Surface	Polyester wipe	09/23/08	MSL			12	F	5	0	8.28E+02
GI17	See MSL sample ID for detail	Surface	Polyester wipe	10/02/08	MSL		000567	12	F	6	10	1.77E+04
GI18	See MSL sample ID for detail	Surface	Polyester wipe	9/23/08 - 12/8/08	MSL		000568	12	F	7	0	6.37E+03
GI19	See MSL sample ID for detail	Surface	Polyester wipe	9/19/08 - 12/8/08	MSL		000569	12	F	8	0	1.22E+03
GI20	See MSL sample ID for detail	Surface	Polyester wipe	9/18/08 - 12/8/08	MSL			12	F	9	0	1.91E+03
GI21	See MSL sample ID for detail	Surface	Polyester wipe	10/21/08 - 12/1/08	MSL		000570	12	G	1	0	6.76E+04
GI22	See MSL sample ID for detail	Surface	Polyester wipe	11/19/08 - 12/8/08	MSL			12	G	2	0	6.83E+03
GI23	See MSL sample ID for detail	Surface	Polyester wipe	09/23/08	MSL		000571	12	G	3	0	2.74E+05
GI24	See MSL sample ID for detail	Surface	Polyester wipe	12/01/08	MSL		000572	12	G	4	0	2.06E+04
GI25	See MSL sample ID for detail	Surface	Polyester wipe	9/8/08 - 9/19/08	MSL		000573	12	G	5	0	1.44E+03
GI26	See MSL sample ID for detail	Surface	Polyester wipe	9/24/08 - 10/6/08	MSL		000576	12	G	6	0	7.78E+03
GI27	See MSL sample ID for detail	Surface	Polyester wipe	10/21/08 - 10/27/08	MSL			12	G	7	0	5.56E+03
GI28	See MSL sample ID for detail	Surface	Polyester wipe	10/30/08 - 11/25/08	MSL			12	G	8	0	9.95E+02
GIblnk	See MSL sample ID for detail	Negative control	PBS	09/05/08	MSL blank			12	G	9	0	
GI18blnk	See MSL sample ID for detail	Handling Control (HC)	Polyester wipe	9/29/08 - 10/13/08	MSL blank		000578	12	H	1	0	1.47E+02
GI19blnk	See MSL sample ID for detail	Handling Control (HC)	Polyester wipe	9/30/08 - 12/8/08	MSL blank		000579	12	H	2	0	1.77E+02
GI20blnk	See MSL sample ID for detail	Handling Control (HC)	Polyester wipe	10/27/08	MSL blank		000580	12	H	3	0	1.67E+02
GI29	See MSL sample ID for detail	Floor	Polyester wipe	03/09/09	MSL		000557	12	H	4	10	3.45E+01
GI30	See MSL sample ID for detail	Floor	Polyester wipe	03/10/09	MSL		000558	12	H	5	10	5.12E+03
GI31	See MSL sample ID for detail	Floor	Polyester wipe	03/11/09	MSL		000559	12	H	6	10	2.90E+02

Sample ID	Sample Description	Sample Source	Sampling Device	Date	Mission	Samples Pooled	Barcode	GI-Container	Row	Column	Sample Volume	16S rRNA Gene copies
GI32	See MSL sample ID for detail	Floor	Polyester wipe	03/12/09	MSL		000560	12	H	7	15	5.81E+03
GI29-32blnk	See MSL sample ID for detail	Blank	Polyester wipe	03/13/09	MSL blank		000556	12	H	8	0	1.05E+02
GI-33-1		GSE 1 & 2	Polyester wipe		MSL			12	H	9	0	
GI-33-1b		GSE FB	Polyester wipe		MSL			12	I	1	0	
GI-33-1bp		GSE FB PMA	Polyester wipe		MSL			12	I	2	0	
GI-33-1p		GSE 1 & 2 PMA	Polyester wipe		MSL			12	I	3	0	
GI-33-2		SAF Sample	Polyester wipe		MSL			12	I	4	0	
GI-33-2b		SAF FB	Polyester wipe		MSL			12	I	5	0	
GI-33-2bp		SAF FB PMA	Polyester wipe		MSL			12	I	6	0	
GI-33-2p		SAF Sample PMA	Polyester wipe		MSL			12	I	7	0	
GI-34-1		GSE	Polyester wipe		MSL			12	I	8	0	
GI-34-1p		GSE PMA	Polyester wipe		MSL			12	I	9	0	
GI-34-2		SAF Sample	Polyester wipe		MSL			13	A	1	0	
GI-34-2p		SAF PMA	Polyester wipe		MSL			13	A	2	0	
GI-34-3		FB	Polyester wipe		MSL			13	A	3	0	
GI-34-3p		FB PMA	Polyester wipe		MSL			13	A	4	0	
GI-35-1	External to SAF. See sheet 2. Archaea	Blank	Polyester wipe	04/06/10	MSL	1	001408	13	A	5	10	3.36E+02
GI-35-2	External to SAF. See sheet 2. Archaea	Buffer control	PBS	04/06/10	MSL	1		13	A	6	0	4.81E+02
GI-35-3	External to SAF. See sheet 2. Archaea	Environmental Control	Polyester wipe	04/06/10	MSL	1		13	A	7	0	
GI-35-4	External to SAF. See sheet 2. Archaea	Shoe Cleaner	Polyester wipe	04/06/10	MSL	1		13	A	8	0	5.31E+04
GI-35-5	External to SAF. See sheet 2. Archaea	ARD	Polyester wipe	04/06/10	MSL	1		13	A	9	0	1.11E+04
GI-35-6	External to SAF. See sheet 2. Archaea	EF	Polyester wipe	04/06/10	MSL	1		13	B	1	0	7.26E+04
GI-35-7	External to SAF. See sheet 2. Archaea	CR1	Polyester wipe	04/06/10	MSL	1		13	B	2	0	5.16E+04
GI-35-8	External to SAF. See sheet 2. Archaea	CR2	Polyester wipe	04/06/10	MSL	1		13	B	3	0	1.30E+04
GI-36-1lc	BiSKit samples. See Sheet 3 for locations	Lab Control (LC)	BiSKit	06/08/10	MSL	20	001423	13	B	4	20	2.01E+03
GI-36-1lcp	BiSKit samples. See Sheet 3 for locations	LC PMA	BiSKit	06/08/10	MSL	20	001438	13	B	5	15	7.38E+01
GI-36-2b	BiSKit samples. See Sheet 3 for locations	FB	BiSKit	06/08/10	MSL	2		13	B	6	0	5.11E+02
GI-36-2bp	BiSKit samples. See Sheet 3 for locations	FB PMA	BiSKit	06/08/10	MSL	2		13	B	7	0	2.45E+02
GI-36-3	BiSKit samples. See Sheet 3 for locations	GSE	BiSKit	06/08/10	MSL	9	001422	13	B	8	0	7.45E+02
GI-36-3p	BiSKit samples. See Sheet 3 for locations	GSE PMA	BiSKit	06/08/10	MSL	9	001437	13	B	9	0	2.70E+03
GI-36-4	BiSKit samples. See Sheet 3 for locations	FLR	BiSKit	06/08/10	MSL	9	001420	13	C	1	0	1.88E+04
GI-36-4p	BiSKit samples. See Sheet 3 for locations	FLR PMA	BiSKit	06/08/10	MSL	9	001421	13	C	2	0	1.27E+03
GI-37lc	LBNL/Nick Palaio Cleanroom, rm 70A	B: Blank	BiSKit	05/25/10	Non-NASA Cleanroom	10	001425	13	C	3	30	4.64E+02
GI-37b	LBNL/Nick Palaio Cleanroom, rm 70A	FB: Field Blank (1 BiSKit)	BiSKit	05/25/10	Non-NASA Cleanroom	1	001415	13	C	4	15	4.97E+02

Sample ID	Sample Description	Sample Source	Sampling Device	Date	Mission	Samples Pooled	Barcode	GI-Container	Row	Column	Sample Volume	16S rRNA Gene copies
GI-37	LBNL Cleanroom, rm 70A	S: Sample (9 BiSKits)	BiSKit	05/25/10	Non-NASA Cleanroom	9	001412	13	C	5	45	8.33E+04
GI-38b	CS	Blank	Polyester wipe	3/15/2010 - 5/27/2010	MSL	10	001416	13	C	6	15	1.58E+02
GI-38	CS	CS	Polyester wipe	3/15/2010 - 5/27/2010	MSL	26	001429	13	C	7	5	1.30E+03
GI-39b	DS	Blank	Polyester wipe	3/10/2010 - 4/29/2010	MSL	3	001431	13	C	8	10	1.57E+02
GI-39	DS	DS	Polyester wipe	3/10/2010 - 4/29/2010	MSL	9	001432	13	C	9	15	1.68E+02
GI-40b	RVR	Blank	Polyester wipe	3/8/2010 - 6/2/2010	MSL	5	001927	13	D	1	0	1.61E+02
GI-40	RVR	RVR	Polyester wipe	3/8/2010 - 6/2/2010	MSL	16	001442	13	D	2	10	1.11E+03
GI-41b	Nonflight - Cleanroom wipe control	Blank	Polyester wipe	5/17/2010	MSL	1	001428	13	D	3	10	1.84E+02
GI-41	Non-flight wipe used to support Tc bundle	Non-flight	Polyester wipe	5/13/2010	MSL	1	001417	13	D	4	10	1.33E+03
Blank	26 wipes procured from Nick (200 mL x 26)	Blank	Polyester wipe	5/13/2010	MSL	26	001426	13	D	5	0	1.96E+02
GI-42lc	Bldg 144 cleanroom prior to cleaning	Lab control	BiSKit	06/15/10	MSL	20	001444	13	D	6	10	9.35E+02
GI-42lcp	Bldg 144 cleanroom prior to cleaning	Lab control PMA	BiSKit	06/15/10	MSL	20	001424	13	D	7	10	1.36E+02
GI-42b	Bldg 144 cleanroom prior to cleaning	FB	BiSKit	06/15/10	MSL	1	001440	13	D	8	15	8.52E+02
GI-42bp	Bldg 144 cleanroom prior to cleaning	FB PMA	BiSKit	06/15/10	MSL	1	001445	13	D	9	15	1.50E+02
GI-42-1	Bldg 144 cleanroom prior to cleaning	FLR Sample	BiSKit	06/15/10	MSL	9	001434	13	E	1	0	1.03E+06
GI-42-1p	Bldg 144 cleanroom prior to cleaning	FLR Sample PMA	BiSKit	06/15/10	MSL	9	001427	13	E	2	0	3.94E+05
GI-42-2	Bldg 144 cleanroom prior to cleaning	GSE Sample	BiSKit	06/15/10	MSL	9	001441	13	E	3	0	1.33E+05
GI-42-2p	Bldg 144 cleanroom prior to cleaning	GSE Sample PMA	BiSKit	06/15/10	MSL	9	001439	13	E	4	0	5.66E+04
GI-43lc	Bldg 144 cleanroom after cleaning	Lab control	Polyester wipe	06/16/10	MSL	21	001436	13	E	5	15	1.84E+02
GI-43lcp	Bldg 144 cleanroom after cleaning	Lab control PMA	Polyester wipe	06/16/10	MSL	21	001418	13	E	6	10	1.44E+02
GI-43b	Bldg 144 cleanroom after cleaning	Field Blank	Polyester wipe	06/16/10	MSL	2	001926	13	E	7	0	1.72E+02
GI-43bp	Bldg 144 cleanroom after cleaning	Field Blank PMA	Polyester wipe	06/16/10	MSL	2	001435	13	E	8	15	1.36E+02
GI-43-1	Bldg 144 cleanroom after cleaning	FLR Sample	Polyester wipe	06/16/10	MSL	9	001419	13	E	9	10	1.74E+05
GI-43-1p	Bldg 144 cleanroom after cleaning	FLR Sample PMA	Polyester wipe	06/16/10	MSL	9	001443	13	F	1	10	4.58E+05
GI-43-2	Bldg 144 cleanroom after cleaning	GSE Sample	Polyester wipe	06/16/10	MSL	9	001433	13	F	2	0	4.79E+05
GI-43-2p	Bldg 144 cleanroom after cleaning	GSE Sample PMA	Polyester wipe	06/16/10	MSL	9	001430	13	F	3	0	5.05E+03
GI-44			Polyester Wipe				001462	13	F	4	10	
GI-44b		Blank	Polyester Wipe				001463	13	F	5	15	

Sample ID	Sample Description	Sample Source	Sampling Device	Date	Mission	Samples Pooled	Barcode	GI-Container	Row	Column	Sample Volume	16S rRNA Gene copies
GI-45			Polyester Wipe				001460	13	F	6	10	
GI-45b		Blank	Polyester Wipe				001461	13	F	7	15	
GI-46			Polyester Wipe				001459	13	F	8	10	
GI-47			Polyester Wipe				001457	13	F	9	10	
GI-47b		Blank	Polyester Wipe				001458	13	G	1	10	
GI-48			Polyester Wipe				001455	13	G	2	10	
GI-48b		Blank	Polyester Wipe				001456	13	G	3	10	
GI-49			Polyester Wipe	11/28/2011	MSL, KSC	7	004000	13	G	4	25	2.22E+02
GI-49b,52b…60b		Blank	Polyester Wipe	11/28/2011	MSL, KSC	13	003937	13	G	5	25	2.70E+00
GI-50			Polyester Wipe	11/28/2011	MSL, KSC	3	004001	13	G	6	25	5.53E+02
GI-50b		Blank	Polyester Wipe	11/28/2011	MSL, KSC	1	003938	13	G	7	25	7.88E+00
GI-51			Polyester Wipe	11/28/2011	MSL, KSC	7	004002	13	G	8	25	8.60E+02
GI-51b		Blank	Polyester Wipe	11/28/2011	MSL, KSC	1	003939	13	G	9	25	1.03E+01
GI-52			Polyester Wipe	11/28/2011	MSL, KSC	6	004003	13	H	1	25	1.24E+03
GI-53			Polyester Wipe	11/28/2011	MSL, KSC	7	004004	13	H	2	25	6.52E+01
GI-54			Polyester Wipe	11/28/2011	MSL, KSC	5	004005	13	H	3	25	6.55E+02
GI-55			Polyester Wipe	11/28/2011	MSL, KSC	9	004006	13	H	4	25	4.40E+02
GI-56			Polyester Wipe	11/28/2011	MSL, KSC	2	004007	13	H	5	25	6.99E+02
GI-57			Polyester Wipe	11/28/2011	MSL, KSC	2	004008	13	H	6	25	8.94E+02
GI-58			Polyester Wipe	11/28/2011	MSL, KSC	5	004009	13	H	7	25	8.73E+02
GI-59			Polyester Wipe	11/28/2011	MSL, KSC	11	004010	13	H	8	25	1.05E+03
GI-60			Polyester Wipe	11/28/2011	MSL, KSC	6	004011	13	H	9	25	1.46E+03
GI-61			Polyester Wipe	12/17/2011	MSL, KSC	4	004012	13	I	1	25	1.31E+05
GI-61b		Blank	Polyester Wipe	12/17/2011	MSL, KSC	1	003940	13	I	2	25	4.63E+02
GI-62			Polyester Wipe	12/17/2011	MSL, KSC	6	004013	13	I	3	25	5.54E+04
GI-62b		Blank	Polyester Wipe	12/17/2011	MSL, KSC	2	003941	13	I	4	25	1.35E+03
GI-63			Polyester Wipe	12/17/2011	MSL, KSC	8	004014	13	I	5	25	1.34E+05
GI-63b		Blank	Polyester Wipe	12/17/2011	MSL, KSC	2	003942	13	I	6	25	3.28E+02
GI-64			Polyester Wipe	12/17/2011	MSL, KSC	6	004015	13	I	7	25	7.50E+04
GI-64b		Blank	Polyester Wipe	12/17/2011	MSL, KSC	1	003943	13	I	8	25	3.46E+02
GI-65			Polyester Wipe	12/17/2011	MSL, KSC	3	004016	13	I	9	25	1.67E+05
GI-65b		Blank	Polyester Wipe	12/17/2011	MSL, KSC	1	003944	14	A	1	25	3.20E+02
GI-66			Polyester Wipe	12/17/2011	MSL, KSC	Water only-Place holder	004017	14	A	2	25	No Sample - water only
GI-66b		Blank	Polyester Wipe	12/17/2011	MSL, KSC	Water only-Place holder	003945	14	A	3	25	No Sample - water only
GI-67			Polyester Wipe	12/17/2011	MSL, KSC	2	004019	14	A	4	25	2.32E+04
GI-67b		Blank	Polyester Wipe	12/17/2011	MSL, KSC	1	003946	14	A	5	25	5.42E+02
GI-68			Polyester Wipe	12/17/2011	MSL, KSC	2	004020	14	A	6	25	7.17E+04
GI-68b		Blank	Polyester Wipe	12/17/2011	MSL, KSC	Water only-Place holder	003947	14	A	7	25	No Sample - water only
GI-69			Polyester Wipe	12/17/2011	MSL, KSC	Water only-Place holder	004021	14	A	8	25	No Sample - water only
GI-69b		Blank	Polyester Wipe	12/17/2011	MSL, KSC	Water only-Place holder	003948	14	A	9	25	No Sample - water only
GI-70			Polyester Wipe	12/17/2011	MSL, KSC	5	004022	14	B	1	25	3.45E+04
GI-70b		Blank	Polyester Wipe	12/17/2011	MSL, KSC	2	003949	14	B	2	25	4.51E+02
GI-71			Polyester Wipe	12/17/2011	MSL, KSC	2	004023	14	B	3	25	5.14E+04
GI-71b		Blank	Polyester Wipe	12/17/2011	MSL, KSC	1	003950	14	B	4	25	5.37E+02
GI-72			Polyester Wipe	12/17/2011	MSL, KSC	6	004024	14	B	5	25	1.05E+05
GI-72b		Blank	Polyester Wipe	12/17/2011	MSL, KSC	2	003951	14	B	6	25	7.94E+02

Sample ID	Sample Description	Sample Source	Sampling Device	Date	Mission	Samples Pooled	Barcode	GI-Container	Row	Column	Sample Volume	16S rRNA Gene copies
GI-73			Polyester Wipe	12/18/2011	MSL, KSC	2	004025	14	B	7	25	9.71E+03
GI-73b		Blank	Polyester Wipe	12/18/2011	MSL, KSC	Water only-Place holder	003952	14	B	8	25	No Sample - water only
GI-74			Polyester Wipe	12/18/2011	MSL, KSC	11	004026	14	B	9	25	1.63E+04
GI-74b		Blank	Polyester Wipe	12/18/2011	MSL, KSC	4	003953	14	C	1	25	1.54E+02
GI-75			Polyester Wipe	12/18/2011	MSL, KSC	3	004027	14	C	2	25	1.25E+04
GI-75b		Blank	Polyester Wipe	12/18/2011	MSL, KSC	2	003954	14	C	3	25	9.35E+01
GI-76			Polyester Wipe	12/18/2011	MSL, KSC	4	004028	14	C	4	25	7.93E+03
GI-76b		Blank	Polyester Wipe	12/18/2011	MSL, KSC	2	003955	14	C	5	25	9.84E+01
GI-77			Polyester Wipe	12/18/2011	MSL, KSC	2	004029	14	C	6	25	1.14E+04
GI-77b		Blank	Polyester Wipe	12/18/2011	MSL, KSC	1	003956	14	C	7	25	6.83E+01
GI-78			Polyester Wipe	12/18/2011	MSL, KSC	1	004030	14	C	8	25	8.16E+03
GI-78b		Blank	Polyester Wipe	12/18/2011	MSL, KSC	1	003957	14	C	9	25	5.54E+01
GI-79			Polyester Wipe	12/18/2011	MSL, KSC	2	004031	14	D	1	25	7.54E+03
GI-79b		Blank	Polyester Wipe	12/18/2011	MSL, KSC	1	003958	14	D	2	25	1.14E+02
GI-80			Polyester Wipe	12/18/2011	MSL, KSC	6	004032	14	D	3	25	1.09E+04
GI-80b		Blank	Polyester Wipe	12/18/2011	MSL, KSC	3	003959	14	D	4	25	1.48E+02
GI-81			Polyester Wipe	12/18/2011	MSL, KSC	2	004033	14	D	5	25	9.93E+03
GI-81b		Blank	Polyester Wipe	12/18/2011	MSL, KSC	1	003960	14	D	6	25	1.29E+02
GI-82			Polyester Wipe	12/18/2011	MSL, KSC	1	004034	14	D	7	25	6.47E+03
GI-82b		Blank	Polyester Wipe	12/18/2011	MSL, KSC	1	003961	14	D	8	25	2.47E+02
GI-83			Polyester Wipe	12/18/2011	MSL, KSC	3	004035	14	D	9	25	1.14E+04
GI-83b		Blank	Polyester Wipe	12/18/2011	MSL, KSC	1	003962	14	E	1	25	9.54E+01
GI-84			Polyester Wipe	12/18/2011	MSL, KSC	3	004036	14	E	2	25	8.08E+03
GI-84b		Blank	Polyester Wipe	12/18/2011	MSL, KSC	2	003964	14	E	3	25	2.12E+02
GI-85			Polyester Wipe	12/19/2011	MSL, KSC	10	004037	14	E	4	25	7.86E+04
GI-85b		Blank	Polyester Wipe	12/19/2011	MSL, KSC	5	003964	14	E	5	25	1.66E+02
GI-86			Polyester Wipe	12/19/2011	MSL, KSC	1	004038	14	E	6	25	1.05E+04
GI-86b		Blank	Polyester Wipe	12/19/2011	MSL, KSC	1	003965	14	E	7	25	9.10E+01
GI-87			Polyester Wipe	12/19/2011	MSL, KSC	2	004039	14	E	8	25	1.76E+04
GI-87b		Blank	Polyester Wipe	12/19/2011	MSL, KSC	1	003966	14	E	9	25	1.25E+02
GI-88			Polyester Wipe	12/19/2011	MSL, KSC	2	004040	14	F	1	25	2.51E+04
GI-88b		Blank	Polyester Wipe	12/19/2011	MSL, KSC	1	003967	14	F	2	25	7.03E+01
GI-89			Polyester Wipe	12/19/2011	MSL, KSC	4	004041	14	F	3	25	3.30E+04
GI-89b		Blank	Polyester Wipe	12/19/2011	MSL, KSC	1	003968	14	F	4	25	1.10E+02
GI-90			Polyester Wipe	12/19/2011	MSL, KSC	20	004042	14	F	5	25	1.13E+04
GI-90b		Blank	Polyester Wipe	12/19/2011	MSL, KSC	5	003969	14	F	6	25	9.54E+02
GI-91			Polyester Wipe	12/19/2011	MSL, KSC	4	004043	14	F	7	25	1.82E+04
GI-91b		Blank	Polyester Wipe	12/19/2011	MSL, KSC	1	003970	14	F	8	25	7.16E+01
GI-92			Polyester Wipe	12/19/2011	MSL, KSC	2	004044	14	F	9	25	2.79E+04
GI-92b		Blank	Polyester Wipe	12/19/2011	MSL, KSC	1	003971	14	G	1	25	1.57E+02
GI-93			Polyester Wipe	12/19/2011	MSL, KSC	6	004045	14	G	2	25	1.20E+07
GI-93b		Blank	Polyester Wipe	12/19/2011	MSL, KSC	2	003972	14	G	3	25	1.20E+02
GI-94			Polyester Wipe	12/19/2011	MSL, KSC	10	004046	14	G	4	25	3.76E+04
GI-94b		Blank	Polyester Wipe	12/19/2011	MSL, KSC	1	003973	14	G	5	25	9.35E+01
GI-95			Polyester Wipe	12/19/2011	MSL, KSC	7	004047	14	G	6	25	1.13E+05
GI-95b		Blank	Polyester Wipe	12/19/2011	MSL, KSC	2	003974	14	G	7	25	4.08E+02
GI-96			Polyester Wipe	12/19/2011	MSL, KSC	3	004048	14	G	8	25	2.37E+04
GI-96b		Blank	Polyester Wipe	12/19/2011	MSL, KSC	1	003975	14	G	9	25	6.06E+02
GI-97			Polyester Wipe	12/20/2011	MSL, KSC	1	004049	14	H	1	25	3.04E+04
GI-97b		Blank	Polyester Wipe	12/20/2011	MSL, KSC	1	003976	14	H	2	25	2.54E+02
GI-98			Polyester Wipe	12/20/2011	MSL, KSC	1	004050	14	H	3	25	3.48E+04
GI-98b		Blank	Polyester Wipe	12/20/2011	MSL, KSC	1	003977	14	H	4	25	2.56E+02

Sample ID	Sample Description	Sample Source	Sampling Device	Date	Mission	Samples Pooled	Barcode	GI-Container	Row	Column	Sample Volume	16S rRNA Gene copies
GI-99			Polyester Wipe	12/20/2011	MSL, KSC	8	004051	14	H	5	25	9.12E+03
GI-99b		Blank	Polyester Wipe	12/20/2011	MSL, KSC	1	003978	14	H	6	25	3.42E+02
GI-100			Polyester Wipe	12/20/2011	MSL, KSC	3	004052	14	H	7	25	2.47E+04
GI-100b		Blank	Polyester Wipe	12/20/2011	MSL, KSC	1	003979	14	H	8	25	1.72E+02
GI-101			Polyester Wipe	12/20/2011	MSL, KSC	3	004053	14	H	9	25	4.63E+04
GI-101b		Blank	Polyester Wipe	12/20/2011	MSL, KSC	1	003980	14	I	1	25	3.03E+02
GI-102			Polyester Wipe	12/20/2011	MSL, KSC	3	004054	14	I	2	25	4.84E+04
GI-102b		Blank	Polyester Wipe	12/20/2011	MSL, KSC	1	003981	14	I	3	25	2.53E+02
GI-103			Polyester Wipe	12/20/2011	MSL, KSC	2	004055	14	I	4	25	4.53E+04
GI-103b		Blank	Polyester Wipe	12/20/2011	MSL, KSC	1	003982	14	I	5	25	1.85E+02
GI-104			Polyester Wipe	12/20/2011	MSL, KSC	2	004057	14	I	6	25	3.96E+04
GI-104b		Blank	Polyester Wipe	12/20/2011	MSL, KSC	1	003983	14	I	7	25	2.38E+02
GI-105			Polyester Wipe	12/20/2011	MSL, KSC	1	004058	14	I	8	25	2.84E+04
GI-105b		Blank	Polyester Wipe	12/20/2011	MSL, KSC	1	003984	14	I	9	25	2.71E+02
GI-106			Polyester Wipe	12/20/2011	MSL, KSC	6	004058	15	A	1	25	2.66E+04
GI-106b		Blank	Polyester Wipe	12/20/2011	MSL, KSC	2	003985	15	A	2	25	2.58E+02
GI-107			Polyester Wipe	12/20/2011	MSL, KSC	3	004059	15	A	3	25	4.13E+04
GI-107b		Blank	Polyester Wipe	12/20/2011	MSL, KSC	1	003986	15	A	4	25	2.56E+02
GI-108			Polyester Wipe	12/20/2011	MSL, KSC	3	004060	15	A	5	25	2.36E+04
GI-108b		Blank	Polyester Wipe	12/20/2011	MSL, KSC	Water only-Place holder	003987	15	A	6	25	No Sample - water only
GI-109			Polyester Wipe	12/16/2011	MSL, KSC	2	004061	15	A	7	25	2.01E+04
GI-109b		Blank	Polyester Wipe	12/16/2011	MSL, KSC	1	003988	15	A	8	25	1.71E+02
GI-110			Polyester Wipe	12/16/2011	MSL, KSC	2	004062	15	A	9	25	2.26E+04
GI-110b		Blank	Polyester Wipe	12/16/2011	MSL, KSC	1	003989	15	B	1	25	2.81E+02
GI-111			Polyester Wipe	12/16/2011	MSL, KSC	4	004063	15	B	2	25	3.75E+04
GI-111b		Blank	Polyester Wipe	12/16/2011	MSL, KSC	1	003990	15	B	3	25	3.44E+02
GI-112			Polyester Wipe	12/16/2011	MSL, KSC	8	004064	15	B	4	25	3.61E+04
GI-112b		Blank	Polyester Wipe	12/16/2011	MSL, KSC	2	003991	15	B	5	25	1.73E+02
GI-113			Polyester Wipe	12/16/2011	MSL, KSC	2	004065	15	B	6	25	1.63E+04
GI-113b		Blank	Polyester Wipe	12/16/2011	MSL, KSC	1	003992	15	B	7	25	2.29E+02
GI-114			Polyester Wipe	12/16/2011	MSL, KSC	1	004066	15	B	8	25	3.83E+04
GI-114b		Blank	Polyester Wipe	12/16/2011	MSL, KSC	1	003993	15	B	9	25	4.62E+02
GI-115			Polyester Wipe	12/16/2011	MSL, KSC	2	004067	15	C	1	25	9.67E+03
GI-115b		Blank	Polyester Wipe	12/16/2011	MSL, KSC	1	003994	15	C	2	25	2.09E+01
GI-116			Polyester Wipe	12/16/2011	MSL, KSC	22	004068	15	C	3	25	2.25E+06
GI-116b		Blank	Polyester Wipe	12/16/2011	MSL, KSC	3	003995	15	C	4	25	1.89E+02
GI-117			BiSKit	12/16/2011	MSL, KSC	23	004069	15	C	5	25	0.00E+00
GI-117b		Blank	BiSKit	12/16/2011	MSL, KSC	4	003996	15	C	6	25	2.19E+02
GI-Max		Reagent Control	Maxwell Control	12/16/2011	MSL		003997	15	C	7	25	3.16E+01
GI-JPL-PBS		Buffer Control JPL	Buffer Control	12/16/2011	MSL		003998	15	C	8	25	1.44E+02
GI-KSC-PBS		Buffer Control KSC	Buffer Control	12/16/2011	MSL		003999	15	C	9	25	5.57E+01

Table E.1-4. Characteristics of Genetic Inventory Task DNA samples archived at TBD location-2.

Sample ID	Sample Description	Sample Source	Sampling Device	Date	Mission	Samples Pooled	Barcode	GI-Container	Row	Column	Sample Volume	16S rRNA Gene Copies
GI1-1	BIG Control	Buffer control	PBS	01/03/07	Phoenix at LMA			16	A	1	0	
GI1-2	1-MTF-1B	Floor	BiSKit	01/03/07	Phoenix at LMA		Samples not listed in SampleWare database					
GI1-3	1-MTF-2B	Floor	BiSKit	01/03/07	Phoenix at LMA		Samples not listed in SampleWare database					
GI1-4	1-MTF-3B	Floor	BiSKit	01/03/07	Phoenix at LMA		Samples not listed in SampleWare database					
GI1-5	1-MTF-4B	Floor	BiSKit	01/03/07	Phoenix at LMA		Samples not listed in SampleWare database					
GI1-6	1-MTF-5B	Floor	BiSKit	01/03/07	Phoenix at LMA		Samples not listed in SampleWare database					
GI1-7	1-MTF-6B	Floor	BiSKit	01/03/07	Phoenix at LMA		Samples not listed in SampleWare database					
GI1-8	1-MTF-7B	Floor	BiSKit	01/03/07	Phoenix at LMA		Samples not listed in SampleWare database					
GI1-9	1-MTF-8B	Floor	BiSKit	01/03/07	Phoenix at LMA			16	A	2	0	
GI1-10	1-MTF-9B	Floor	BiSKit	01/03/07	Phoenix at LMA			16	A	3	0	
GI1-11	1-MTF-10B	Floor	BiSKit	01/03/07	Phoenix at LMA			16	A	4	0	
GI1-12	1-MTF-BLNK	Blank	BiSKit	01/03/07	Phoenix at LMA		Sample not listed in SampleWare database					
GI1-13	PHX swab BLNK 10 pooled	Blank	Cotton swab	01/03/07	Phoenix at LMA			16	A	5	0	1.22E+02
GI1-14	MTF Swab BLNK9 pooled	Blank	Cotton swab	01/03/07	Phoenix at LMA			16	A	6	0	1.45E+02
GI1-15	MTF Swab 9 pooled	Floor	Cotton swab	01/03/07	Phoenix at LMA			16	A	7	0	1.60E+04
GI1-16	PHX s/c swab10 pooled	Spacecraft	Cotton swab	01/03/07	Phoenix at LMA			16	A	8	0	1.47E+04
GI2-1	SSB-1B	Floor	BiSKit	02/03/07	Phoenix s/c not in SSB			16	A	9	0	
GI2-2	SSB-2B	Floor	BiSKit	02/03/07	Phoenix s/c not in SSB			16	B	1	0	
GI2-3	SSB-3B	Floor	BiSKit	02/03/07	Phoenix s/c not in SSB			16	B	2	0	
GI2-4	SSB-4B	Floor	BiSKit	02/03/07	Phoenix s/c not in SSB			16	B	3	0	
GI2-5	SSB-5B	Floor	BiSKit	02/03/07	Phoenix s/c not in SSB			16	B	4	0	
GI2-6	SSB Swab 10 pooled	Floor	Cotton swab	02/03/07	Phoenix s/c not in SSB			16	B	5	0	1.00E+05
GI2-7	SSB Swab BLNK 10 pooled	Blank	Cotton swab	02/03/07	Phoenix s/c not in SSB			16	B	6	0	
GI3-1	PHSF W1	Floor	BiSKit	04/24/07	Before Phoenix		005469	16	B	7	10	
GI3-2	PHSF W2-SE	Floor	BiSKit	04/24/07	Before Phoenix		005471	16	B	8	10	
GI3-3	PHSF W3-Center	Floor	BiSKit	04/24/07	Before Phoenix			16	B	9	0	
GI3-4	PHSF W4-NW	Floor	BiSKit	04/24/07	Before Phoenix		005473	16	C	1	10	
GI3-5	PHSF B5-SW	Floor	BiSKit	04/24/07	Before Phoenix			16	C	2	0	
GI3-6	PHSF B6-E	Floor	BiSKit	04/24/07	Before Phoenix		005476	16	C	3	10	
GI3-7	PHSF B7-W	Floor	BiSKit	04/24/07	Before Phoenix			16	C	4	0	
GI3-8	PHSF B8-N	Floor	BiSKit	04/24/07	Before Phoenix			16	C	5	0	
GI3-9	PHSF B9-S	Floor	BiSKit	04/24/07	Before Phoenix			16	C	6	0	
GI3-10	PHSF B10-Wall	Floor	BiSKit	04/24/07	Before Phoenix			16	C	7	0	1.57E+05
GI3-FC1	BiSKit Field Control #1	Field control	BiSKit	04/24/07	Before Phoenix			16	C	8	0	
GI3-BRC1	BiSKit PBS Control #1	Buffer control	PBS	04/24/07	Before Phoenix		000659	16	C	9	0	1.40E+02
GI3-BIG	Autolyser Cartridge Control	Buffer control	PBS	04/24/07	Before Phoenix		000658	16	D	1	0	1.26E+02
GI4-1	IP1-GI (BiSKit samples)	Floor	BiSKit	06/27/07	During Phoenix		000800	16	D	2	10	
GI4-2	IP2-GI	Floor	BiSKit	06/27/07	During Phoenix		000661	16	D	3	0	
GI4-3	IP3-GI	Floor	BiSKit	06/27/07	During Phoenix		000801	16	D	4	0	
GI4-5	IP5-GI	Floor	BiSKit	06/27/07	During Phoenix		000802	16	D	5	0	
GI4-6	IP6-GI	Floor	BiSKit	06/27/07	During Phoenix		000803	16	D	6	10	
GI4-7	IP7-GI	Floor	BiSKit	06/27/07	During Phoenix		000804	16	D	7	10	
GI4-8	IP8-GI	Floor	BiSKit	06/27/07	During Phoenix		000805	16	D	8	0	8.79E+05
GI4-1-blnk	IP1-GI-blnk (in 15 ml tubes)	Blank	BiSKit	06/27/07	During Phoenix		000753	16	D	9	0	1.45E+02
GI4-2-blnk	IP2-GI-blnk	Blank	BiSKit	06/27/07	During Phoenix		000754	16	E	1	10	
GI4-3-blnk	IP3-GI-blnk	Blank	BiSKit	06/27/07	During Phoenix		000755	16	E	2	0	
GI4-5-blnk	IP5-GI-blnk	Blank	BiSKit	06/27/07	During Phoenix		000672	16	E	3	10	
GI4-6-blnk	IP6-GI-blnk	Blank	BiSKit	06/27/07	During Phoenix		000673	16	E	4	0	
GI4-7-blnk	IP7-GI-blnk	Blank	BiSKit	06/27/07	During Phoenix		000674	16	E	5	0	
GI4-8-blnk	IP8-GI-blnk	Blank	BiSKit	06/27/07	During Phoenix		000675	16	E	6	10	
GI4-BIG(-)		Buffer control	PBS	06/27/07	During Phoenix		000668	16	E	7	0	1.47E+02

Sample ID	Sample Description	Sample Source	Sampling Device	Date	Mission	Samples Pooled	Barcode	GI-Container	Row	Column	Sample Volume	16S rRNA Gene Copies
GI5-1	PPO-PHSF-1B	Floor	BiSKit	07/20/07	Post-Phoenix		000676	16	E	8	0	
GI5-2	PPO-PHSF-2B	Floor	BiSKit	07/20/07	Post-Phoenix		000677	16	E	9	0	
GI5-3	PPO-PHSF-3B	Floor	BiSKit	07/20/07	Post-Phoenix		000678	16	F	1	0	
GI5-4	PPO-PHSF-4B	Floor	BiSKit	07/20/07	Post-Phoenix		000679	16	F	2	0	
GI5-5	PPO-PHSF-5B	Floor	BiSKit	07/20/07	Post-Phoenix		000680	16	F	3	0	
GI5-6	PPO-PHSF-6B	Floor	BiSKit	07/20/07	Post-Phoenix		000681	16	F	4	10	
GI5-7	PPO-PHSF-7B	Floor	BiSKit	07/20/07	Post-Phoenix		000682	16	F	5	0	
GI5-8	PPO-PHSF-8B	Floor	BiSKit	07/20/07	Post-Phoenix		000683	16	F	6	10	
GI5-9	PPO-PHSF-9B	Floor	BiSKit	07/20/07	Post-Phoenix			16	F	7	0	
GI5-10	PPO-PHSF-10B	Floor	BiSKit	07/20/07	Post-Phoenix		000790	16	F	8	0	
GI5-12	PPO-PHSF-12B	Floor	BiSKit	07/20/07	Post-Phoenix		000791	16	F	9	10	
GI5-13	PPO-PHSF-13B	Floor	BiSKit	07/20/07	Post-Phoenix			16	G	1	0	
GI5-14	PPO-PHSF-14B	Floor	BiSKit	07/20/07	Post-Phoenix		000770	16	G	2	15	
GI5-15	PPO-PHSF-15B	Floor	BiSKit	07/20/07	Post-Phoenix		000771	16	G	3	15	
GI5-16	PPO-PHSF-16B	Floor	BiSKit	07/20/07	Post-Phoenix		000779	16	G	4	10	
GI5-17	PPO-PHSF-17B	Floor	BiSKit	07/20/07	Post-Phoenix		000780	16	G	5	10	
GI5-18	PPO-PHSF-18B	Floor	BiSKit	07/20/07	Post-Phoenix		000781	16	G	6	10	
GI5-19	PPO-PHSF-19B	Floor	BiSKit	07/20/07	Post-Phoenix		000782	16	G	7	15	
GI5-20	PPO-PHSF-20B	Floor	BiSKit	07/20/07	Post-Phoenix		000774	16	G	8	15	1.80E+05
GI6-1	PHSF-1B	Floor	BiSKit	08/02/07	Post Phoenix		000692	16	G	9	0	0.00E+00
GI6-2	PHSF-2B	Floor	BiSKit	08/02/07	Post Phoenix		000701	16	H	1	0	
GI6-3	PHSF-3B	Floor	BiSKit	08/02/07	Post Phoenix		000693	16	H	2	0	1.02E+08
GI6-4	PHSF-4B	Floor	BiSKit	08/02/07	Post Phoenix		000777	16	H	3	10	
GI6-5	PHSF-5B	Floor	BiSKit	08/02/07	Post Phoenix		000704	16	H	4	10	
GI6-6	PHSF-6B	Floor	BiSKit	08/02/07	Post Phoenix		000705	16	H	5	0	
GI6-7	PHSF-7B	Floor	BiSKit	08/02/07	Post Phoenix		000706	16	H	6	0	0.00E+00
GI6-8	PHSF-8B	Floor	BiSKit	08/02/07	Post Phoenix			16	H	7	0	
GI6-9	PHSF-9B	Floor	BiSKit	08/02/07	Post Phoenix		Samples not listed in SampleWare database					
GI6-10	PHSF-10B	Floor	BiSKit	08/02/07	Post Phoenix		Samples not listed in SampleWare database					
GI6-1blnk	PHSF-1-blnk	Blank	BiSKit	08/02/07	Post Phoenix		Samples not listed in SampleWare database					
GI6-2blnk	PHSF-2-blnk	Blank	BiSKit	08/02/07	Post Phoenix			16	H	8	0	
GI6-3blnk	PHSF-3-blnk	Blank	BiSKit	08/02/07	Post Phoenix		Samples not listed in SampleWare database					2.92E+02
GI6-4blnk	PHSF-4-blnk	Blank	BiSKit	08/02/07	Post Phoenix			16	H	9	0	
GI6-5blnk	PHSF-5-blnk	Blank	BiSKit	08/02/07	Post Phoenix			16	I	1	0	
GI6-6blnk	PHSF-6-blnk	Blank	BiSKit	08/02/07	Post Phoenix			16	I	2	0	
GI6-7blnk	PHSF-7-blnk	Blank	BiSKit	08/02/07	Post Phoenix		Samples not listed in SampleWare database					1.05E+02
GI6-8blnk	PHSF-8-blnk	Blank	BiSKit	08/02/07	Post Phoenix			16	I	3	0	
GI6-9blnk	PHSF-9-blnk	Blank	BiSKit	08/02/07	Post Phoenix		Samples not listed in SampleWare database					2.04E+02
GI6-10blnk	PHSF-10-blnk	Blank	BiSKit	08/02/07	Post Phoenix		Samples not listed in SampleWare database					2.37E+02
GI6-FC	PHFS-field control BiSKit	Field control	BiSKit	08/02/07	Post Phoenix			16	I	4	0	
GI6-FCblnk	PHFS-field control blank	FC blank	BiSKit	08/02/07	Post Phoenix			16	I	5	0	
GI7-B-1	9C-E	Floor	BiSKit	11/28/07	During Dawn			16	I	6	0	2.75E+05
GI7-B-2	9C-G	Floor	BiSKit	11/28/07	During Dawn			16	I	7	0	
GI7-B-3	9C-D	Floor	BiSKit	11/28/07	During Dawn			16	I	8	0	7.72E+03
GI7-B-4	9C-A	Floor	BiSKit	11/28/07	During Dawn			16	I	9	0	
GI7-B-5	9C Level	Floor	BiSKit	11/28/07	During Dawn			17	A	1	0	1.26E+03
GI7-B-6	9C stair	Floor	BiSKit	11/28/07	During Dawn			17	A	2	0	
GI7-B-7	9C-F	Floor	BiSKit	11/28/07	During Dawn			17	A	3	0	
GI7-B-8	9C by B Central east of s/c	Floor	BiSKit	11/28/07	During Dawn			17	A	4	0	3.09E+03
GI7-B-9	9C D/E	Floor	BiSKit	11/28/07	During Dawn			17	A	5	0	
GI7-B-10	Field control @9C	Field control	BiSKit	11/28/07	During Dawn			17	A	6	0	
GI7-B-11	11	Floor	BiSKit	11/28/07	During Dawn			17	A	7	0	1.10E+03
GI7-B-12	12	Floor	BiSKit	11/28/07	During Dawn			17	A	8	0	

Sample ID	Sample Description	Sample Source	Sampling Device	Date	Mission	Samples Pooled	Barcode	GI-Container	Row	Column	Sample Volume	16S rRNA Gene Copies
GI7-B-13	13	Floor	BiSKit	11/28/07	During Dawn			17	A	9	0	
GI7-B-14	14	Floor	BiSKit	11/28/07	During Dawn			17	B	1	0	
GI7-B-15	15	Floor	BiSKit	11/28/07	During Dawn			17	B	2	0	
GI7-B-16	16	Floor	BiSKit	11/28/07	During Dawn			17	B	3	0	
GI7-B-17	17	Floor	BiSKit	11/28/07	During Dawn			17	B	4	0	
GI7-B-18	18	Floor	BiSKit	11/28/07	During Dawn			17	B	5	0	
GI7-B-19	19	Floor	BiSKit	11/28/07	During Dawn			17	B	6	0	
GI7-B-20	20	Floor	BiSKit	11/28/07	During Dawn			17	B	7	0	
GI7-B-21	B-9/17-1	Floor	BiSKit	11/28/07	During Dawn			17	B	8	0	
GI7-B-22	B-9/17-2	Floor	BiSKit	11/28/07	During Dawn			17	B	9	0	
GI7-B-23	B-9/17-3	Floor	BiSKit	11/28/07	During Dawn			17	C	1	0	
GI7-B-24	B-9/17-4	Floor	BiSKit	11/28/07	During Dawn			17	C	2	0	
GI7-BLNK-1	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn			17	C	3	0	1.66E+02
GI7-BLNK-2	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		005508	17	C	4	10	
GI7-BLNK-3	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn			17	C	5	0	0.00E+00
GI7-BLNK-4	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		005511	17	C	6	10	
GI7-BLNK-5	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn			17	C	7	0	2.17E+02
GI7-BLNK-6	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		005513	17	C	8	10	
GI7-BLNK-7	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		005515	17	C	9	10	
GI7-BLNK-8	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn			17	D	1	0	7.51E+02
GI7-BLNK-9	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn			17	D	2	0	
GI7-BLNK-10	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn			17	D	3	0	
GI7-BLNK-11	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn			17	D	4	0	
GI7-BLNK-12	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn			17	D	5	0	
GI7-BLNK-13	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn			17	D	6	0	
GI7-BLNK-14	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn			17	D	7	0	
GI7-BLNK-15	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn		005529	17	D	8	0	
GI7-BLNK-16	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn			17	D	9	0	
GI7-BLNK-17	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn			17	E	1	0	
GI7-BLNK-18	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn			17	E	2	0	
GI7-BLNK-19	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn			17	E	3	0	
GI7-BLNK-20	BiSKit blank	Blank	BiSKit	11/28/07	During Dawn			17	E	4	0	
GI8-1	JPL SAF pooled samples 10 BiSKits)	Floor	BiSKit	10/08/07	During MSL, JPL SAF			17	E	5	0	8.74E+04

Sample ID	Sample Description	Sample Source	Sampling Device	Date	Mission	Samples Pooled	Barcode	GI-Container	Row	Column	Sample Volume	16S rRNA Gene Copies
GI8-2	Pooled blanks (10 BiSKits)	Blank	BiSKit	10/08/07	During MSL, JPL SAF			17	E	6	0	1.19E+02
GI8-3	PBS/BIG	Buffer control	PBS	10/08/07	During MSL, JPL SAF			17	E	7	0	
GI10-1	JPL SAF pooled samples (20 BiSKits)	Floor	BiSKit	01/22/08	During MSL, JPL SAF		Samples not listed in SampleWare database					9.51E+07
GI10-2	Pooled blanks (20 BiSKits)	Blank	BiSKit	01/22/08	During MSL, JPL SAF		Samples not listed in SampleWare database					0.00E+00
GI10-3	PBS/BIG	Buffer control	PBS	01/22/08	During MSL, JPL SAF		Samples not listed in SampleWare database					
GI11-1	JPL SAF pooled samples (20 BiSKits)	Floor	BiSKit	02/12/08	During MSL, JPL SAF		Samples not listed in SampleWare database					1.44E+07
GI11-2	Pooled blanks (20 BiSKits)	Blank	BiSKit	02/12/08	During MSL, JPL SAF		Samples not listed in SampleWare database					
GI11-3	PBS/BIG	Buffer control	PBS	02/12/08	During MSL, JPL SAF		Samples not listed in SampleWare database					
GI12-1	JPL SAF pooled samples (20 BiSKits)	Floor	BiSKit	04/01/08	During MSL, JPL SAF			17	E	8	0	4.78E+05
GI12-2	Pooled blanks (20 BiSKits)	Blank	BiSKit	04/01/08	During MSL, JPL SAF			17	E	9	0	
GI12-3	PBS/BIG	Buffer control	PBS	04/01/08	During MSL, JPL SAF			17	F	1	0	
GI13-1	JPL SAF pooled samples (20 BiSKits)	Floor	BiSKit	06/04/08	During MSL, JPL SAF		Samples not listed in SampleWare database					1.01E+08
GI13-2	Pooled blanks (20 BiSKits)	Blank	BiSKit	06/04/08	During MSL, JPL SAF		Samples not listed in SampleWare database					
GI13-3	PBS/BIG	Buffer control	PBS	06/04/08	During MSL, JPL SAF		Samples not listed in SampleWare database					
GI14	JPL SAF pooled samples (20 BiSKits)	Floor	BiSKit	08/05/08	During MSL, JPL SAF			17	F	2	0	3.96E+05
GI14BLNK	Pooled blanks (20 BiSKits)	Blank	BiSKit	08/05/08	During MSL, JPL SAF			17	F	3	0	0.00E+00
GI15	See MSL sample ID for detail	Surface	Polyester wipe	09/05/08	MSL			17	F	4	10	3.64E+09
GI16	See MSL sample ID for detail	Surface	Polyester wipe	09/23/08	MSL			17	F	5	0	8.28E+02
GI17	See MSL sample ID for detail	Surface	Polyester wipe	10/02/08	MSL			17	F	6	0	1.77E+04
GI18	See MSL sample ID for detail	Surface	Polyester wipe	9/23/08 - 12/8/08	MSL			17	F	7	0	6.37E+03
GI19	See MSL sample ID for detail	Surface	Polyester wipe	9/19/08 - 12/8/08	MSL			17	F	8	0	1.22E+03
GI20	See MSL sample ID for detail	Surface	Polyester wipe	9/18/08 - 12/8/08	MSL			17	F	9	0	1.91E+03
GI21	See MSL sample ID for detail	Surface	Polyester wipe	10/21/08 - 12/1/08	MSL			17	G	1	0	6.76E+04
GI22	See MSL sample ID for detail	Surface	Polyester wipe	11/19/08 - 12/8/08	MSL			17	G	2	0	6.83E+03
GI23	See MSL sample ID for detail	Surface	Polyester wipe	09/23/08	MSL			17	G	3	0	2.74E+05
GI24	See MSL sample ID for detail	Surface	Polyester wipe	12/01/08	MSL			17	G	4	0	2.06E+04
GI25	See MSL sample ID for detail	Surface	Polyester wipe	9/8/08 - 9/19/08	MSL			17	G	5	0	1.44E+03
GI26	See MSL sample ID for detail	Surface	Polyester wipe	9/24/08 - 10/6/08	MSL			17	G	6	0	7.78E+03
GI27	See MSL sample ID for detail	Surface	Polyester wipe	10/21/08 - 10/27/08	MSL			17	G	7	0	5.56E+03
GI28	See MSL sample ID for detail	Surface	Polyester wipe	10/30/08 - 11/25/08	MSL			17	G	8	0	9.95E+02
GIblnk	See MSL sample ID for detail	Negative control	PBS	09/05/08	MSL blank			17	G	9	0	
GI18blnk	See MSL sample ID for detail	Handling Control (HC)	Polyester wipe	9/29/08 - 10/13/08	MSL blank			17	H	1	0	1.47E+02
GI19blnk	See MSL sample ID for detail	Handling Control (HC)	Polyester wipe	9/30/08 - 12/8/08	MSL blank			17	H	2	0	1.77E+02
GI20blnk	See MSL sample ID for detail	Handling Control (HC)	Polyester wipe	10/27/08	MSL blank			17	H	3	0	1.67E+02
GI29	See MSL sample ID for detail	Floor	Polyester wipe	03/09/09	MSL		000562	17	H	4	10	3.45E+01
GI30	See MSL sample ID for detail	Floor	Polyester wipe	03/10/09	MSL		000563	17	H	5	15	5.12E+03
GI31	See MSL sample ID for detail	Floor	Polyester wipe	03/11/09	MSL		000564	17	H	6	15	2.90E+02

Sample ID	Sample Description	Sample Source	Sampling Device	Date	Mission	Samples Pooled	Barcode	GI-Container	Row	Column	Sample Volume	16S rRNA Gene Copies
GI32	See MSL sample ID for detail	Floor	Polyester wipe	03/12/09	MSL		000565	17	H	7	10	5.81E+03
GI29-32blnk	See MSL sample ID for detail	Blank	Polyester wipe	03/13/09	MSL blank		000561	17	H	8	0	1.05E+02
GI-33-1		GSE 1 & 2	Polyester wipe		MSL			17	H	9	0	
GI-33-1b		GSE FB	Polyester wipe		MSL			17	I	1	0	
GI-33-1bp		GSE FB PMA	Polyester wipe		MSL			17	I	2	0	
GI-33-1p		GSE 1 & 2 PMA	Polyester wipe		MSL			17	I	3	0	
GI-33-2		SAF Sample	Polyester wipe		MSL			17	I	4	0	
GI-33-2b		SAF FB	Polyester wipe		MSL			17	I	5	0	
GI-33-2bp		SAF FB PMA	Polyester wipe		MSL			17	I	6	0	
GI-33-2p		SAF Sample PMA	Polyester wipe		MSL			17	I	7	0	
GI-34-1		GSE	Polyester wipe		MSL			17	I	8	0	
GI-34-1p		GSE PMA	Polyester wipe		MSL			17	I	9	0	
GI-34-2		SAF Sample	Polyester wipe		MSL			18	A	1	0	
GI-34-2p		SAF PMA	Polyester wipe		MSL			18	A	2	0	
GI-34-3		FB	Polyester wipe		MSL			18	A	3	0	
GI-34-3p		FB PMA	Polyester wipe		MSL			18	A	4	0	
GI-35-1	External to SAF. See sheet 2. Archaea	Blank	Polyester wipe	04/06/10	MSL	1		18	A	5	0	3.36E+02
GI-35-2	External to SAF. See sheet 2. Archaea	Buffer control	PBS	04/06/10	MSL	1		18	A	6	0	4.81E+02
GI-35-3	External to SAF. See sheet 2. Archaea	Environmental Control	Polyester wipe	04/06/10	MSL	1		18	A	7	0	
GI-35-4	External to SAF. See sheet 2. Archaea	Shoe Cleaner	Polyester wipe	04/06/10	MSL	1		18	A	8	0	5.31E+04
GI-35-5	External to SAF. See sheet 2. Archaea	ARD	Polyester wipe	04/06/10	MSL	1		18	A	9	0	1.11E+04
GI-35-6	External to SAF. See sheet 2. Archaea	EF	Polyester wipe	04/06/10	MSL	1		18	B	1	0	7.26E+04
GI-35-7	External to SAF. See sheet 2. Archaea	CR1	Polyester wipe	04/06/10	MSL	1		18	B	2	0	5.16E+04
GI-35-8	External to SAF. See sheet 2. Archaea	CR2	Polyester wipe	04/06/10	MSL	1		18	B	3	0	1.30E+04
GI-36-1lc	BiSKit samples. See Sheet 3 for locations	Lab Control (LC)	BiSKit	06/08/10	MSL	20	005538	18	B	4	20	2.01E+03
GI-36-1lcp	BiSKit samples. See Sheet 3 for locations	LC PMA	BiSKit	06/08/10	MSL	20	005539	18	B	5	10	7.38E+01
GI-36-2b	BiSKit samples. See Sheet 3 for locations	FB	BiSKit	06/08/10	MSL	2		18	B	6	0	5.11E+02
GI-36-2bp	BiSKit samples. See Sheet 3 for locations	FB PMA	BiSKit	06/08/10	MSL	2		18	B	7	0	2.45E+02
GI-36-3	BiSKit samples. See Sheet 3 for locations	GSE	BiSKit	06/08/10	MSL	9		18	B	8	0	7.45E+02
GI-36-3p	BiSKit samples. See Sheet 3 for locations	GSE PMA	BiSKit	06/08/10	MSL	9		18	B	9	0	2.70E+03
GI-36-4	BiSKit samples. See Sheet 3 for locations	FLR	BiSKit	06/08/10	MSL	9		18	C	1	0	1.88E+04
GI-36-4p	BiSKit samples. See Sheet 3 for locations	FLR PMA	BiSKit	06/08/10	MSL	9		18	C	2	0	1.27E+03
GI-37lc	LBNL/Nick Palaio Cleanroom, rm 70A	B: Blank	BiSKit	05/25/10	Non-NASA Cleanroom	10	001409	18	C	3	30	4.64E+02
GI-37b	LBNL/Nick Palaio Cleanroom, rm 70A	FB: Field Blank (1 BiSKit)	BiSKit	05/25/10	Non-NASA Cleanroom	1	005540	18	C	4	15	4.97E+02

Sample ID	Sample Description	Sample Source	Sampling Device	Date	Mission	Samples Pooled	Barcode	GI-Container	Row	Column	Sample Volume	16S rRNA Gene Copies
GI-37	LBNL Cleanroom, rm 70A	S: Sample (9 BiSKits)	BiSKit	05/25/10	Non-NASA Cleanroom	9	001413	18	C	5	40	8.33E+04
GI-38b	CS	Blank	Polyester wipe	3/15/2010 - 5/27/2010	MSL	10		18	C	6	0	1.58E+02
GI-38	CS	CS	Polyester wipe	3/15/2010 - 5/27/2010	MSL	26		18	C	7	0	1.30E+03
GI-39b	DS	Blank	Polyester wipe	3/10/2010 - 4/29/2010	MSL	3		18	C	8	0	1.57E+02
GI-39	DS	DS	Polyester wipe	3/10/2010 - 4/29/2010	MSL	9		18	C	9	0	1.68E+02
GI-40b	RVR	Blank	Polyester wipe	3/8/2010 - 6/2/2010	MSL	5		18	D	1	0	1.61E+02
GI-40	RVR	RVR	Polyester wipe	3/8/2010 - 6/2/2010	MSL	16		18	D	2	0	1.11E+03
GI-41b	Nonflight - Cleanroom wipe control	Blank	Polyester wipe	5/17/2010	MSL	1	005541	18	D	3	10	1.84E+02
GI-41	Non-flight wipe used to support Tc bundle	Non-flight	Polyester wipe	5/13/2010	MSL	1		18	D	4	0	1.33E+03
Blank	26 wipes procured from Nick (200 mL x 26)	Blank	Polyester wipe	5/13/2010	MSL	26		18	D	5	0	1.96E+02
GI-42lc	Bldg 144 cleanroom prior to cleaning	Lab control	BiSKit	06/15/10	MSL	20		18	D	6	0	9.35E+02
GI-42lcp	Bldg 144 cleanroom prior to cleaning	Lab control PMA	BiSKit	06/15/10	MSL	20		18	D	7	0	1.36E+02
GI-42b	Bldg 144 cleanroom prior to cleaning	FB	BiSKit	06/15/10	MSL	1		18	D	8	0	8.52E+02
GI-42bp	Bldg 144 cleanroom prior to cleaning	FB PMA	BiSKit	06/15/10	MSL	1		18	D	9	0	1.50E+02
GI-42-1	Bldg 144 cleanroom prior to cleaning	FLR Sample	BiSKit	06/15/10	MSL	9		18	E	1	0	1.03E+06
GI-42-1p	Bldg 144 cleanroom prior to cleaning	FLR Sample PMA	BiSKit	06/15/10	MSL	9		18	E	2	0	3.94E+05
GI-42-2	Bldg 144 cleanroom prior to cleaning	GSE Sample	BiSKit	06/15/10	MSL	9		18	E	3	0	1.33E+05
GI-42-2p	Bldg 144 cleanroom prior to cleaning	GSE Sample PMA	BiSKit	06/15/10	MSL	9		18	E	4	0	5.66E+04
GI-43lc	Bldg 144 cleanroom after cleaning	Lab control	Polyester wipe	06/16/10	MSL	21		18	E	5	0	1.84E+02
GI-43lcp	Bldg 144 cleanroom after cleaning	Lab control PMA	Polyester wipe	06/16/10	MSL	21		18	E	6	0	1.44E+02
GI-43b	Bldg 144 cleanroom after cleaning	Field Blank	Polyester wipe	06/16/10	MSL	2		18	E	7	0	1.72E+02
GI-43bp	Bldg 144 cleanroom after cleaning	Field Blank PMA	Polyester wipe	06/16/10	MSL	2		18	E	8	0	1.36E+02
GI-43-1	Bldg 144 cleanroom after cleaning	FLR Sample	Polyester wipe	06/16/10	MSL	9		18	E	9	0	1.74E+05
GI-43-1p	Bldg 144 cleanroom after cleaning	FLR Sample PMA	Polyester wipe	06/16/10	MSL	9		18	F	1	0	4.58E+05
GI-43-2	Bldg 144 cleanroom after cleaning	GSE Sample	Polyester wipe	06/16/10	MSL	9		18	F	2	0	4.79E+05
GI-43-2p	Bldg 144 cleanroom after cleaning	GSE Sample PMA	Polyester wipe	06/16/10	MSL	9		18	F	3	0	5.05E+03
GI-44			Polyester Wipe				004070	18	F	4	0	
GI-44b		Blank	Polyester Wipe				001922	18	F	5	0	

Sample ID	Sample Description	Sample Source	Sampling Device	Date	Mission	Samples Pooled	Barcode	GI-Container	Row	Column	Sample Volume	16S rRNA Gene Copies
GI-45			Polyester Wipe				005542	18	F	6	10	
GI-45b		Blank	Polyester Wipe				005543	18	F	7	10	
GI-46			Polyester Wipe				005544	18	F	8	10	
GI-47			Polyester Wipe				005545	18	F	9	10	
GI-47b		Blank	Polyester Wipe				005546	18	G	1	10	
GI-48			Polyester Wipe				005547	18	G	2	10	
GI-48b		Blank	Polyester Wipe				005548	18	G	3	10	
GI-49			Polyester Wipe	11/28/2011	MSL, KSC	7	005394	18	G	4	25	2.22E+02
GI-49b,52b…60b		Blank	Polyester Wipe	11/28/2011	MSL, KSC	13	005331	18	G	5	25	2.70E+00
GI-50			Polyester Wipe	11/28/2011	MSL, KSC	3	005395	18	G	6	25	5.53E+02
GI-50b		Blank	Polyester Wipe	11/28/2011	MSL, KSC	1	005332	18	G	7	25	7.88E+00
GI-51			Polyester Wipe	11/28/2011	MSL, KSC	7	005396	18	G	8	25	8.60E+02
GI-51b		Blank	Polyester Wipe	11/28/2011	MSL, KSC	1	005333	18	G	9	25	1.03E+01
GI-52			Polyester Wipe	11/28/2011	MSL, KSC	6	005397	18	H	1	25	1.24E+03
GI-53			Polyester Wipe	11/28/2011	MSL, KSC	7	005398	18	H	2	25	6.52E+01
GI-54			Polyester Wipe	11/28/2011	MSL, KSC	5	005399	18	H	3	25	6.55E+02
GI-55			Polyester Wipe	11/28/2011	MSL, KSC	9	005400	18	H	4	25	4.40E+02
GI-56			Polyester Wipe	11/28/2011	MSL, KSC	2	005401	18	H	5	25	6.99E+02
GI-57			Polyester Wipe	11/28/2011	MSL, KSC	2	005402	18	H	6	25	8.94E+02
GI-58			Polyester Wipe	11/28/2011	MSL, KSC	5	005403	18	H	7	25	8.73E+02
GI-59			Polyester Wipe	11/28/2011	MSL, KSC	11	005404	18	H	8	25	1.05E+03
GI-60			Polyester Wipe	11/28/2011	MSL, KSC	6	005405	18	H	9	25	1.46E+03
GI-61			Polyester Wipe	12/17/2011	MSL, KSC	4	005406	18	I	1	25	1.31E+05
GI-61b		Blank	Polyester Wipe	12/17/2011	MSL, KSC	1	005334	18	I	2	25	4.63E+02
GI-62			Polyester Wipe	12/17/2011	MSL, KSC	6	005407	18	I	3	25	5.54E+04
GI-62b		Blank	Polyester Wipe	12/17/2011	MSL, KSC	2	005335	18	I	4	25	1.35E+03
GI-63			Polyester Wipe	12/17/2011	MSL, KSC	8	005408	18	I	5	25	1.34E+05
GI-63b		Blank	Polyester Wipe	12/17/2011	MSL, KSC	2	005336	18	I	6	25	3.28E+02
GI-64			Polyester Wipe	12/17/2011	MSL, KSC	6	005409	18	I	7	25	7.50E+04
GI-64b		Blank	Polyester Wipe	12/17/2011	MSL, KSC	1	005337	18	I	8	25	3.46E+02
GI-65			Polyester Wipe	12/17/2011	MSL, KSC	3	005410	18	I	9	25	1.67E+05
GI-65b		Blank	Polyester Wipe	12/17/2011	MSL, KSC	1	005338	19	A	1	25	3.20E+02
GI-66			Polyester Wipe	12/17/2011	MSL, KSC	Water only-Place holder	005411	19	A	2	25	No Sample - water only
GI-66b		Blank	Polyester Wipe	12/17/2011	MSL, KSC	Water only-Place holder	005339	19	A	3	25	No Sample - water only
GI-67			Polyester Wipe	12/17/2011	MSL, KSC	2	005413	19	A	4	25	2.32E+04
GI-67b		Blank	Polyester Wipe	12/17/2011	MSL, KSC	1	005340	19	A	5	25	5.42E+02
GI-68			Polyester Wipe	12/17/2011	MSL, KSC	2	005414	19	A	6	25	7.17E+04
GI-68b		Blank	Polyester Wipe	12/17/2011	MSL, KSC	Water only-Place holder	005341	19	A	7	25	No Sample - water only
GI-69			Polyester Wipe	12/17/2011	MSL, KSC	Water only-Place holder	005415	19	A	8	25	No Sample - water only
GI-69b		Blank	Polyester Wipe	12/17/2011	MSL, KSC	Water only-Place holder	005342	19	A	9	25	No Sample - water only
GI-70			Polyester Wipe	12/17/2011	MSL, KSC	5	005416	19	B	1	25	3.45E+04
GI-70b		Blank	Polyester Wipe	12/17/2011	MSL, KSC	2	005343	19	B	2	25	4.51E+02
GI-71			Polyester Wipe	12/17/2011	MSL, KSC	2	005417	19	B	3	25	5.14E+04
GI-71b		Blank	Polyester Wipe	12/17/2011	MSL, KSC	1	005344	19	B	4	25	5.37E+02
GI-72			Polyester Wipe	12/17/2011	MSL, KSC	6	005418	19	B	5	25	1.05E+05
GI-72b		Blank	Polyester Wipe	12/17/2011	MSL, KSC	2	00534	19	B	6	25	7.94E+02

Sample ID	Sample Description	Sample Source	Sampling Device	Date	Mission	Samples Pooled	Barcode	GI-Container	Row	Column	Sample Volume	16S rRNA Gene Copies
GI-73			Polyester Wipe	12/18/2011	MSL, KSC	2	005419	19	B	7	25	9.71E+03
GI-73b		Blank	Polyester Wipe	12/18/2011	MSL, KSC	Water only-Place holder	005346	19	B	8	25	No Sample - water only
GI-74			Polyester Wipe	12/18/2011	MSL, KSC	11	005420	19	B	9	25	1.63E+04
GI-74b		Blank	Polyester Wipe	12/18/2011	MSL, KSC	4	005347	19	C	1	25	1.54E+02
GI-75			Polyester Wipe	12/18/2011	MSL, KSC	3	005421	19	C	2	25	1.25E+04
GI-75b		Blank	Polyester Wipe	12/18/2011	MSL, KSC	2	005348	19	C	3	25	9.35E+01
GI-76			Polyester Wipe	12/18/2011	MSL, KSC	4	005422	19	C	4	25	7.93E+03
GI-76b		Blank	Polyester Wipe	12/18/2011	MSL, KSC	2	005349	19	C	5	25	9.84E+01
GI-77			Polyester Wipe	12/18/2011	MSL, KSC	2	005423	19	C	6	25	1.14E+04
GI-77b		Blank	Polyester Wipe	12/18/2011	MSL, KSC	1	005350	19	C	7	25	6.83E+01
GI-78			Polyester Wipe	12/18/2011	MSL, KSC	1	005424	19	C	8	25	8.16E+03
GI-78b		Blank	Polyester Wipe	12/18/2011	MSL, KSC	1	005351	19	C	9	25	5.54E+01
GI-79			Polyester Wipe	12/18/2011	MSL, KSC	2	005425	19	D	1	25	7.54E+03
GI-79b		Blank	Polyester Wipe	12/18/2011	MSL, KSC	1	005352	19	D	2	25	1.14E+02
GI-80			Polyester Wipe	12/18/2011	MSL, KSC	6	005426	19	D	3	25	1.09E+04
GI-80b		Blank	Polyester Wipe	12/18/2011	MSL, KSC	3	005353	19	D	4	25	1.48E+02
GI-81			Polyester Wipe	12/18/2011	MSL, KSC	2	005427	19	D	5	25	9.93E+03
GI-81b		Blank	Polyester Wipe	12/18/2011	MSL, KSC	1	005354	19	D	6	25	1.29E+02
GI-82			Polyester Wipe	12/18/2011	MSL, KSC	1	005428	19	D	7	25	6.47E+03
GI-82b		Blank	Polyester Wipe	12/18/2011	MSL, KSC	1	005355	19	D	8	25	2.47E+02
GI-83			Polyester Wipe	12/18/2011	MSL, KSC	3	005429	19	D	9	25	1.14E+04
GI-83b		Blank	Polyester Wipe	12/18/2011	MSL, KSC	1	005356	19	E	1	25	9.54E+01
GI-84			Polyester Wipe	12/18/2011	MSL, KSC	3	005430	19	E	2	25	8.08E+03
GI-84b		Blank	Polyester Wipe	12/18/2011	MSL, KSC	2	005358	19	E	3	25	2.12E+02
GI-85			Polyester Wipe	12/19/2011	MSL, KSC	10	005431	19	E	4	25	7.86E+04
GI-85b		Blank	Polyester Wipe	12/19/2011	MSL, KSC	5	005358	19	E	5	25	1.66E+02
GI-86			Polyester Wipe	12/19/2011	MSL, KSC	1	005432	19	E	6	25	1.05E+04
GI-86b		Blank	Polyester Wipe	12/19/2011	MSL, KSC	1	005359	19	E	7	25	9.10E+01
GI-87			Polyester Wipe	12/19/2011	MSL, KSC	2	005433	19	E	8	25	1.76E+04
GI-87b		Blank	Polyester Wipe	12/19/2011	MSL, KSC	1	005360	19	E	9	25	1.25E+02
GI-88			Polyester Wipe	12/19/2011	MSL, KSC	2	005434	19	F	1	25	2.51E+04
GI-88b		Blank	Polyester Wipe	12/19/2011	MSL, KSC	1	005361	19	F	2	25	7.03E+01
GI-89			Polyester Wipe	12/19/2011	MSL, KSC	4	005435	19	F	3	25	3.30E+04
GI-89b		Blank	Polyester Wipe	12/19/2011	MSL, KSC	1	005362	19	F	4	25	1.10E+02
GI-90			Polyester Wipe	12/19/2011	MSL, KSC	20	005436	19	F	5	25	1.13E+04
GI-90b		Blank	Polyester Wipe	12/19/2011	MSL, KSC	5	005363	19	F	6	25	9.54E+02
GI-91			Polyester Wipe	12/19/2011	MSL, KSC	4	005437	19	F	7	25	1.82E+04
GI-91b		Blank	Polyester Wipe	12/19/2011	MSL, KSC	1	005364	19	F	8	25	7.16E+01
GI-92			Polyester Wipe	12/19/2011	MSL, KSC	2	005438	19	F	9	25	2.79E+04
GI-92b		Blank	Polyester Wipe	12/19/2011	MSL, KSC	1	005365	19	G	1	25	1.57E+02
GI-93			Polyester Wipe	12/19/2011	MSL, KSC	6	005439	19	G	2	25	1.20E+07
GI-93b		Blank	Polyester Wipe	12/19/2011	MSL, KSC	2	005366	19	G	3	25	1.20E+02
GI-94			Polyester Wipe	12/19/2011	MSL, KSC	10	005440	19	G	4	25	3.76E+04
GI-94b		Blank	Polyester Wipe	12/19/2011	MSL, KSC	1	005367	19	G	5	25	9.35E+01
GI-95			Polyester Wipe	12/19/2011	MSL, KSC	7	005441	19	G	6	25	1.13E+05
GI-95b		Blank	Polyester Wipe	12/19/2011	MSL, KSC	2	005368	19	G	7	25	4.08E+02
GI-96			Polyester Wipe	12/19/2011	MSL, KSC	3	005442	19	G	8	25	2.37E+04
GI-96b		Blank	Polyester Wipe	12/19/2011	MSL, KSC	1	005369	19	G	9	25	6.06E+02
GI-97			Polyester Wipe	12/20/2011	MSL, KSC	1	005443	19	H	1	25	3.04E+04
GI-97b		Blank	Polyester Wipe	12/20/2011	MSL, KSC	1	005370	19	H	2	25	2.54E+02
GI-98			Polyester Wipe	12/20/2011	MSL, KSC	1	005444	19	H	3	25	3.48E+04
GI-98b		Blank	Polyester Wipe	12/20/2011	MSL, KSC	1	005371	19	H	4	25	2.56E+02

Sample ID	Sample Description	Sample Source	Sampling Device	Date	Mission	Samples Pooled	Barcode	GI-Container	Row	Column	Sample Volume	16S rRNA Gene Copies
GI-99			Polyester Wipe	12/20/2011	MSL, KSC	8	005445	19	H	5	25	9.12E+03
GI-99b		Blank	Polyester Wipe	12/20/2011	MSL, KSC	1	005372	19	H	6	25	3.42E+02
GI-100			Polyester Wipe	12/20/2011	MSL, KSC	3	005446	19	H	7	25	2.47E+04
GI-100b		Blank	Polyester Wipe	12/20/2011	MSL, KSC	1	005373	19	H	8	25	1.72E+02
GI-101			Polyester Wipe	12/20/2011	MSL, KSC	3	005447	19	H	9	25	4.63E+04
GI-101b		Blank	Polyester Wipe	12/20/2011	MSL, KSC	1	005374	19	I	1	25	3.03E+02
GI-102			Polyester Wipe	12/20/2011	MSL, KSC	3	005448	19	I	2	25	4.84E+04
GI-102b		Blank	Polyester Wipe	12/20/2011	MSL, KSC	1	005375	19	I	3	25	2.53E+02
GI-103			Polyester Wipe	12/20/2011	MSL, KSC	2	005449	19	I	4	25	4.53E+04
GI-103b		Blank	Polyester Wipe	12/20/2011	MSL, KSC	1	005376	19	I	5	25	1.85E+02
GI-104			Polyester Wipe	12/20/2011	MSL, KSC	2	005451	19	I	6	25	3.96E+04
GI-104b		Blank	Polyester Wipe	12/20/2011	MSL, KSC	1	005377	19	I	7	25	2.38E+02
GI-105			Polyester Wipe	12/20/2011	MSL, KSC	1	005452	19	I	8	25	2.84E+04
GI-105b		Blank	Polyester Wipe	12/20/2011	MSL, KSC	1	005378	19	I	9	25	2.71E+02
GI-106			Polyester Wipe	12/20/2011	MSL, KSC	6	005452	20	A	1	25	2.66E+04
GI-106b		Blank	Polyester Wipe	12/20/2011	MSL, KSC	2	005379	20	A	2	25	2.58E+02
GI-107			Polyester Wipe	12/20/2011	MSL, KSC	3	005453	20	A	3	25	4.13E+04
GI-107b		Blank	Polyester Wipe	12/20/2011	MSL, KSC	1	005380	20	A	4	25	2.56E+02
GI-108			Polyester Wipe	12/20/2011	MSL, KSC	3	005454	20	A	5	25	2.36E+04
GI-108b		Blank	Polyester Wipe	12/20/2011	MSL, KSC	Water only-Place holder	005381	20	A	6	25	No Sample - water only
GI-109			Polyester Wipe	12/16/2011	MSL, KSC	2	005455	20	A	7	25	2.01E+04
GI-109b		Blank	Polyester Wipe	12/16/2011	MSL, KSC	1	005382	20	A	8	25	1.71E+02
GI-110			Polyester Wipe	12/16/2011	MSL, KSC	2	005456	20	A	9	25	2.26E+04
GI-110b		Blank	Polyester Wipe	12/16/2011	MSL, KSC	1	005383	20	B	1	25	2.81E+02
GI-111			Polyester Wipe	12/16/2011	MSL, KSC	4	005457	20	B	2	25	3.75E+04
GI-111b		Blank	Polyester Wipe	12/16/2011	MSL, KSC	1	005384	20	B	3	25	3.44E+02
GI-112			Polyester Wipe	12/16/2011	MSL, KSC	8	005458	20	B	4	25	3.61E+04
GI-112b		Blank	Polyester Wipe	12/16/2011	MSL, KSC	2	005385	20	B	5	25	1.73E+02
GI-113			Polyester Wipe	12/16/2011	MSL, KSC	2	005459	20	B	6	25	1.63E+04
GI-113b		Blank	Polyester Wipe	12/16/2011	MSL, KSC	1	005386	20	B	7	25	2.29E+02
GI-114			Polyester Wipe	12/16/2011	MSL, KSC	1	005460	20	B	8	25	3.83E+04
GI-114b		Blank	Polyester Wipe	12/16/2011	MSL, KSC	1	005387	20	B	9	25	4.62E+02
GI-115			Polyester Wipe	12/16/2011	MSL, KSC	2	005461	20	C	1	25	9.67E+03
GI-115b		Blank	Polyester Wipe	12/16/2011	MSL, KSC	1	005388	20	C	2	25	2.09E+01
GI-116			Polyester Wipe	12/16/2011	MSL, KSC	22	005462	20	C	3	25	2.25E+06
GI-116b		Blank	Polyester Wipe	12/16/2011	MSL, KSC	3	005389	20	C	4	25	1.89E+02
GI-117			BiSKit	12/16/2011	MSL, KSC	23	005463	20	C	5	25	0.00E+00
GI-117b		Blank	BiSKit	12/16/2011	MSL, KSC	4	005390	20	C	6	25	2.19E+02
GI-Max		Reagent Control	Maxwell Control	12/16/2011	MSL		005391	20	C	7	25	3.16E+01
GI-JPL-PBS		Buffer Control JPL	Buffer Control	12/16/2011	MSL		005392	20	C	8	25	1.44E+02
GI-KSC-PBS		Buffer Control KSC	Buffer Control	12/16/2011	MSL		005393	20	C	9	25	5.57E+01

E.2 PhyloChip: Metadata

E.2.1 Generation 2 (G2) PhyloChip

E.2.1.1 G2 Summary

Not available.

E.2.1.2 Sample Data

Set 1-1

Family (Phy-Subphy-Order-Family) (57 families)

Actinobacteria_Actinobacteridae_Frankineae_Frankineae
Actinobacteria_Actinobacteridae_Gordoniaceae_Gordoniaceae
Actinobacteria_Actinobacteridae_Micromonosporaceae_Micromonosporaceae
Actinobacteria_Actinobacteridae_Propionibacterineae_Propionibacterineae
Actinobacteria_Actinobacteridae_Streptomycineae_Streptomycineae
Actinobacteria_Actinobacteridae_Streptosporangineae_Streptosporangineae
Actinobacteria_Actinobacteridae_Uncl_Uncl
Bacteroidetes_Flexibacterales_Flexibacterales_Roseivirga_FM
Bacteroidetes_Flexibacterales_Flexibacterales_Uncl
Bacteroidetes_PC1-9_Uncl_Uncl
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Bacteroidetes_Uncl_Uncl_Uncl
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Firmicutes_Bacilli_Bacillus_Bacillus_FM

Firmicutes_Bacilli_Halobacillus_Halobacillus_FM
Firmicutes_Bacilli_Lactobacillales_Aerococcaceae
Firmicutes_Bacilli_Lactobacillales_Streptococcaceae
Firmicutes_Bacilli_Staphylococcaceae_Staphylococcaceae
Firmicutes_Bacilli_Uncl_Uncl
Firmicutes_Clostridia_Clostridiales_Uncl
Firmicutes_Clostridia_Peptostreptococcaceae_Peptostreptococcaceae
OP10_CH21_Uncl_Uncl
OP10_Uncl_Uncl_Uncl
Planctomycetes_Planctomycetacia_Planctomycetales_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Bradyrhizobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Xanthobacteraceae
Proteobacteria_Alphaproteobacteria_Caulobacterales_Uncl
Proteobacteria_Alphaproteobacteria_Rhizobiaceae_Rhizobiaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacter_FM
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodovulum_FM
Proteobacteria_Alphaproteobacteria_Schlegelella_Schlegelella_FM
Proteobacteria_Alphaproteobacteria_Stappia_Stappia_FM
Proteobacteria_Alphaproteobacteria_Uncl_Uncl
Proteobacteria_Deltaproteobacteria_Geobacter_Geobacter_FM
Proteobacteria_Epsilonproteobacteria_Arcobacteraceae_Arcobacteraceae
Proteobacteria_Epsilonproteobacteria_Nautilliales_Nautillaceae
Proteobacteria_Epsilonproteobacteria_Sulfuricurvales_Sulfuricurvaceae
Proteobacteria_Gammaproteobacteria_Alteromonadales_Alteromonas_FM
Proteobacteria_Gammaproteobacteria_Alteromonadales_Rheinheimeraceae
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacteriales_Enterobacteriaceae
Proteobacteria_Gammaproteobacteria_Gammaproteobacteria_Uncl
Proteobacteria_Gammaproteobacteria_Legionellales_Uncl
Proteobacteria_Gammaproteobacteria_Neisseriales_Chromobacterium_FM
Proteobacteria_Gammaproteobacteria_Nitrosomonadales_Uncl
Proteobacteria_Gammaproteobacteria_Pasteurellaceae_Pasteurellaceae
Proteobacteria_Gammaproteobacteria_Pseudomonadaceae_Pseudomonadaceae
Proteobacteria_Gammaproteobacteria_Rhodocyclales_Accumulibacter_FM
Proteobacteria_Gammaproteobacteria_Rhodocyclales_Uncl
Proteobacteria_Gammaproteobacteria_SBR1001_Uncl
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Vibrionaceae_Vibrionaceae
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Uncl
Sulfobacilli_Sulfobacillus_Sulfobacillus_Sulfobacillus_FM

Set 1-2

Family (Phy-Subphy-Order-Family) (111 families)
ABY1_OD1_WCHB1-58_Uncl_Uncl
Actinobacteria_Actinobacteridae_Actinomycineae_Actinomycineae
Actinobacteria_Actinobacteridae_Agromyces_Agromyces_FM
Actinobacteria_Actinobacteridae_Curtobacterium_Curtobacterium_FM
Actinobacteria_Actinobacteridae_Frankineae_Frankineae
Actinobacteria_Actinobacteridae_Micromonosporaceae_Micromonosporaceae
Actinobacteria_Actinobacteridae_Propionibacterineae_Propionibacterineae
Actinobacteria_Actinobacteridae_Pseudonocardiaceae_Pseudonocardiaceae
Actinobacteria_Actinobacteridae_Streptomycineae_Streptomycineae
Actinobacteria_Actinobacteridae_Streptosporangineae_Streptosporangineae
Actinobacteria_Actinobacteridae_Uncl_Uncl
Actinobacteria_Rubrobacteridae_Rubrobacteraceae_Rubrobacteraceae
Actinobacteria_Rubrobacteridae_Thermoleiphilaceae_Thermoleiphilaceae
Bacteroidetes_Bacteroidales_Bacteroidales_Bacteroidaceae
Bacteroidetes_Flavobacteriales_Flavobacteriales_Flavobacteriaceae
Bacteroidetes_Flexibacterales_Flexibacterales_Roseivirga_FM
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Bacteroidetes_Sphingobacteriaceae_Sphingobacteriaceae_Sphingobacteriaceae
Caldithrix_KSB1_Caldithrixales_Caldithrixales_Uncl
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Cyanobacteria_Chloroplasts_Uncl_Uncl
Firmicutes_Acidaminococcaceae_Acidaminococcaceae_Acidaminococcaceae
Firmicutes_Bacilli_Bacillus_Bacillus_FM
Firmicutes_Bacilli_Exiguobacterium_Exiguobacterium_FM
Firmicutes_Bacilli_Halobacillus_Halobacillus_FM
Firmicutes_Bacilli_Lactobacillales_Aerococcaceae
Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae
Firmicutes_Bacilli_Lactobacillales_Leuconostoc_FM
Firmicutes_Bacilli_Lactobacillales_Streptococcaceae
Firmicutes_Bacilli_Lactobacillales_Uncl
Firmicutes_Bacilli_Paenibacillaceae_Paenibacillaceae
Firmicutes_Bacilli_Staphylococcaceae_Staphylococcaceae
Firmicutes_Bacilli_Uncl_Uncl
Firmicutes_Clostridia_Clostridiales_RF6_FM
Firmicutes_Clostridia_Peptostreptococcaceae_Peptostreptococcaceae
Firmicutes_Clostridia_Uncl_Uncl
Firmicutes_Desulfotomaculum_Desulfotomaculum_Desulfotomaculum_FM
Firmicutes_Mollicutes_Uncl_Uncl
Fusobacteria_Fusobacteriaceae_Fusobacteriaceae_Fusobacteriaceae
Fusobacteria_Leptotrichales_Leptotrichales_Streptobacilliaceae
Fusobacteria_Uncl_Uncl_Uncl
Haloanaerobiales_Halanaerobiaceae_Halanaerobiaceae_Halanaerobiaceae
Marine_group_AA714017_Uncl_Uncl
Nitrospirae_Thermodesulfovibrionales_Thermodesulfovibrionales_Thermodesulfovibrionaceae
OP10_CH21_Uncl_Uncl
OP10_Uncl_Uncl_Uncl
Planctomycetes_Planctomycetacia_Planctomycetales_Uncl
Proteobacteria_Alphaproteobacteria_Acetobacterales_Acetobacteraceae
Proteobacteria_Alphaproteobacteria_alpha_proteobacterium_MBIC1474_Uncl
Proteobacteria_Alphaproteobacteria_Azospirillaceae_Azospirillaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Bradyrhizobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacteriaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Pleomorphomonas_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Rhodoplanaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Caedibacteraceae_Caedibacteraceae
Proteobacteria_Alphaproteobacteria_Caulobacterales_Brevundimonas_FM
Proteobacteria_Alphaproteobacteria_Caulobacterales_Uncl
Proteobacteria_Alphaproteobacteria_Phyllobacteriaceae_Phyllobacteriaceae
Proteobacteria_Alphaproteobacteria_Rhizobiaceae_Rhizobiaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Hyphomonadaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacter_FM
Proteobacteria_Alphaproteobacteria_Rhodobacterales_S36_FM
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Uncl
Proteobacteria_Alphaproteobacteria_Rickettsiales_Wolbachia_FM
Proteobacteria_Alphaproteobacteria_Schlegelella_Schlegelella_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Porphyrobacter_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingobium_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonas_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingosinicella_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Uncl
Proteobacteria_Alphaproteobacteria_Uncl_Uncl
Proteobacteria_Deltaproteobacteria_Desulfovibrio_Desulfovibrio_FM
Proteobacteria_Deltaproteobacteria_Myxococcales_Polyangiaceae
Proteobacteria_Deltaproteobacteria_Myxococcales_Uncl
Proteobacteria_Deltaproteobacteria_Syntrophaceae_Syntrophaceae
Proteobacteria_Desulfovibrionales_Desulfovibrionales_Desulfovibrionaceae
Proteobacteria_Epsilonproteobacteria_Arcobacteraceae_Arcobacteraceae
Proteobacteria_Epsilonproteobacteria_Sulfuricurvales_Sulfuricurvaceae
Proteobacteria_Gammaproteobacteria_Alcaligenaceae_Alcaligenaceae
Proteobacteria_Gammaproteobacteria_Alteromonadales_Pseudoalteromonadaceae
Proteobacteria_Gammaproteobacteria_Alteromonadales_Rheinheimeraceae
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Ellin339_Uncl
Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacteriales_Enterobacteriaceae
Proteobacteria_Gammaproteobacteria_Halomonadaceae_Halomonadaceae
Proteobacteria_Gammaproteobacteria_Legionellales_Legionella_FM
Proteobacteria_Gammaproteobacteria_Legionellales_Uncl
Proteobacteria_Gammaproteobacteria_Marinobacter_Marinobacter_FM
Proteobacteria_Gammaproteobacteria_Methylococcaceae_Methylococcaceae
Proteobacteria_Gammaproteobacteria_Methylophilales_Uncl
Proteobacteria_Gammaproteobacteria_Moraxellaceae_Moraxellaceae
Proteobacteria_Gammaproteobacteria_Neisseriales_Chromobacterium_FM
Proteobacteria_Gammaproteobacteria_Oceanospirillales_Uncl
Proteobacteria_Gammaproteobacteria_Pasteurellaceae_Pasteurellaceae
Proteobacteria_Gammaproteobacteria_Pseudomonadaceae_Pseudomonadaceae
Proteobacteria_Gammaproteobacteria_Rhodocyclales_Accumulibacter_FM
Proteobacteria_Gammaproteobacteria_Rhodocyclales_Uncl
Proteobacteria_Gammaproteobacteria_SBR1001_Uncl
Proteobacteria_Gammaproteobacteria_Shewanellaceae_Shewanellaceae
Proteobacteria_Gammaproteobacteria_Sutterellaceae_Sutterellaceae
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Vibrionaceae_Vibrionaceae
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Uncl
Proteobacteria_Gammaproteobacteria_ZA3605c_Uncl
Proteobacteria_Gammaproteobacteria_ZD0433_Uncl
Thermi_Thermales_Thermales_Thermaceae
TM6_Uncl_Uncl_Uncl
Verrucomicrobia_Pedosphaerae_Uncl_Uncl

Set 1-3

Family (Phy-Subphy-Order-Family) (94 families)

ABY1_OD1_WCHB1-58_Uncl_Uncl
Actinobacteria_Acidimicrobidae_JTB31_BD2-10_FM
Actinobacteria_Acidimicrobidae_Uncl_Uncl
Actinobacteria_Actinobacteridae_Bifidobacteriaceae_Bifidobacteriaceae
Actinobacteria_Actinobacteridae_Brachybacterium_Brachybacterium_FM
Actinobacteria_Actinobacteridae_Frankineae_Frankineae
Actinobacteria_Actinobacteridae_Gordoniaceae_Gordoniaceae
Actinobacteria_Actinobacteridae_Propionibacterineae_Propionibacterineae
Actinobacteria_Actinobacteridae_Streptomycineae_Streptomycineae
Actinobacteria_Actinobacteridae_Streptosporangineae_Streptosporangineae
Actinobacteria_Actinobacteridae_Uncl_Uncl
Actinobacteria_Coriobacteridae_Coriobacteriales_Collinsella_FM
Actinobacteria_WCHB1-81_Uncl_Uncl
Bacteroidetes_Bacteroidales_Bacteroidales_Uncl
Bacteroidetes_Flavobacteriales_Flavobacteriales_Cytophaga_FM
Bacteroidetes_Flavobacteriales_Flavobacteriales_Sporocytophaga_FM
Bacteroidetes_Flexibacterales_Flexibacterales_Roseivirga_FM
Bacteroidetes_Hymenobacterales_Hymenobacterales_Pontibacteraceae
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Bacteroidetes_SHA-94_Bacteroidales_Uncl
Bacteroidetes_Sphingobacteriaceae_Sphingobacteriaceae_Sphingobacteriaceae
Bacteroidetes_Uncl_Uncl_Uncl
Chlorobi_Uncl_Uncl_Uncl
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Cyanobacteria_Chloroplasts_Uncl_Uncl
Cyanobacteria_Uncl_Uncl_Uncl
Elusimicrobia_TG1_Uncl_Uncl_Uncl
Firmicutes_Acidaminococcaceae_Acidaminococcaceae_Acidaminococcaceae
Firmicutes_Bacilli_Halobacillus_Halobacillus_FM
Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae
Firmicutes_Bacilli_Lactobacillales_Streptococcaceae
Firmicutes_Bacilli_Lactobacillales_Uncl
Firmicutes_Bacilli_Paenibacillaceae_Paenibacillaceae
Firmicutes_Bacilli_Staphylococcaceae_Staphylococcaceae
Firmicutes_Bacilli_Uncl_Uncl
Firmicutes_Clostridia_Clostridiales_Ruminococcus_FM
Firmicutes_Clostridia_Clostridiales_Uncl
Firmicutes_Mollicutes_Uncl_Uncl
Firmicutes_Syntrophomonadaceae_Syntrophomonadaceae_Syntrophomonadaceae
Haloanaerobiales_Halanaerobiaceae_Halanaerobiaceae_Halanaerobiaceae
Marine_group_AA714017_Uncl_Uncl
OP10_CH21_Uncl_Uncl
OP10_CL500-48_Uncl_Uncl
Planctomycetes_Planctomycetacia_Planctomycetales_Uncl
Proteobacteria_Alphaproteobacteria_Azospirillaceae_Azospirillaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Bradyrhizobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Hyphomicrobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacteriaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Rhodoplanaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Caedibacteraceae_Caedibacteraceae
Proteobacteria_Alphaproteobacteria_Caulobacterales_Brevundimonas_FM
Proteobacteria_Alphaproteobacteria_Caulobacterales_Uncl
Proteobacteria_Alphaproteobacteria_Labrys_Labrys_FM
Proteobacteria_Alphaproteobacteria_Pseudochrobactrum_Pseudochrobactrum_FM
Proteobacteria_Alphaproteobacteria_Rhizobiaceae_Rhizobiaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Hyphomonadaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacter_FM
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodovulum_FM
Proteobacteria_Alphaproteobacteria_Schlegelella_Schlegelella_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Porphyrobacter_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingobium_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonas_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Uncl
Proteobacteria_Alphaproteobacteria_Uncl_Uncl
Proteobacteria_Deltaproteobacteria_Bdellovibrio_Bdellovibrio_FM
Proteobacteria_Deltaproteobacteria_Desulfovibrio_Desulfovibrio_FM
Proteobacteria_Desulfovibrionales_Desulfovibrionales_Desulfovibrionaceae
Proteobacteria_Epsilonproteobacteria_Sulfuricurvales_Sulfuricurvaceae
Proteobacteria_Gammaproteobacteria_Alcaligenaceae_Alcaligenaceae
Proteobacteria_Gammaproteobacteria_Alteromonadales_Rheinheimeraceae
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Ellin339_Uncl
Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacteriales_Enterobacteriaceae
Proteobacteria_Gammaproteobacteria_Legionellales_Legionella_FM
Proteobacteria_Gammaproteobacteria_Legionellales_Uncl
Proteobacteria_Gammaproteobacteria_Methylococcaceae_Methylococcaceae
Proteobacteria_Gammaproteobacteria_Microbulbifer_Microbulbifer_FM
Proteobacteria_Gammaproteobacteria_MND1_mle1-7_FM
Proteobacteria_Gammaproteobacteria_Moraxellaceae_Moraxellaceae
Proteobacteria_Gammaproteobacteria_Neisseriales_Uncl
Proteobacteria_Gammaproteobacteria_obligately_oligotrophic_bacteria_KI89C_Uncl
Proteobacteria_Gammaproteobacteria_Pseudomonadaceae_Pseudomonadaceae
Proteobacteria_Gammaproteobacteria_Rhodocyclales_Accumulibacter_FM
Proteobacteria_Gammaproteobacteria_Rhodocyclales_Uncl
Proteobacteria_Gammaproteobacteria_Sutterellaceae_Sutterellaceae
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Uncl
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Xylella_FM
Proteobacteria_Gammaproteobacteria_ZA3605c_Uncl
Spirochaetes_Leptospirales_Leptospirales_Leptospiraceae
Thermi_Thermales_Thermales_Thermaceae
Thermotogae_A2_Uncl_Uncl

Set 1-4

Family (Phy-Subphy-Order-Family) (77 families)

Acidobacteria_iii1-8_Uncl_Uncl
Acidobacteria_OS-K_Uncl_Uncl
Actinobacteria_Acidimicrobidae_Acidimicrobineae_Acidimicrobineae
Actinobacteria_Acidimicrobidae_JTB31_BD2-10_FM
Actinobacteria_Actinobacteridae_Actinomycineae_Actinomycineae
Actinobacteria_Actinobacteridae_Agromyces_Agromyces_FM
Actinobacteria_Actinobacteridae_Frankineae_Frankineae
Actinobacteria_Actinobacteridae_Gordoniaceae_Gordoniaceae
Actinobacteria_Actinobacteridae_Propionibacterineae_Propionibacterineae
Actinobacteria_Actinobacteridae_Streptomycineae_Streptomycineae
Actinobacteria_Actinobacteridae_Uncl_Uncl
Bacteroidetes_Flavobacteriales_Flavobacteriales_Flavobacteriaceae
Bacteroidetes_Flexibacterales_Flexibacterales_Roseivirga_FM
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Bacteroidetes_Uncl_Uncl_Uncl
Chlorobi_Uncl_Uncl_Uncl
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Cyanobacteria_Chloroplasts_Uncl_Uncl
Cyanobacteria_Uncl_Uncl_Uncl
Firmicutes_Bacilli_Halobacillus_Halobacillus_FM
Firmicutes_Bacilli_Lactobacillales_Aerococcaceae
Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae
Firmicutes_Bacilli_Lactobacillales_Uncl
Firmicutes_Bacilli_Staphylococcaceae_Staphylococcaceae
Firmicutes_Bacilli_Uncl_Uncl
Firmicutes_Clostridia_Clostridiales_Uncl
Firmicutes_Clostridia_Peptostreptococcaceae_Peptostreptococcaceae
Firmicutes_Mollicutes_Uncl_Uncl
Firmicutes_Symbiobacteria_Uncl_Uncl
Nitrospirae_Nitrospirales_Nitrospirales_Uncl
OP10_CH21_Uncl_Uncl
OP10_Uncl_Uncl_Uncl
Planctomycetes_Planctomycetacia_Planctomycetales_Uncl
Poribacteria_Uncl_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_Acetobacterales_Acetobacteraceae
Proteobacteria_Alphaproteobacteria_alpha_proteobacterium_MBIC1474_Uncl
Proteobacteria_Alphaproteobacteria_Azospirillaceae_Azospirillaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Beijerinckiaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Bradyrhizobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Rhodoplanaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Xanthobacteraceae
Proteobacteria_Alphaproteobacteria_Oleomonas_Oleomonas_FM
Proteobacteria_Alphaproteobacteria_Phyllobacteriaceae_Phyllobacteriaceae
Proteobacteria_Alphaproteobacteria_Rhizobiaceae_Rhizobiaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacter_FM
Proteobacteria_Alphaproteobacteria_Rickettsiales_Uncl
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingobium_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Uncl
Proteobacteria_Alphaproteobacteria_Uncl_Uncl
Proteobacteria_Epsilonproteobacteria_Arcobacteraceae_Arcobacteraceae
Proteobacteria_Epsilonproteobacteria_Sulfuricurvales_Sulfuricurvaceae
Proteobacteria_Gammaproteobacteria_Acidithiobacillales_Uncl
Proteobacteria_Gammaproteobacteria_Alteromonadales_Pseudoalteromonadaceae
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacteriales_Enterobacteriaceae
Proteobacteria_Gammaproteobacteria_Legionellales_Uncl
Proteobacteria_Gammaproteobacteria_Methylococcaceae_Methylococcaceae
Proteobacteria_Gammaproteobacteria_Moraxellaceae_Moraxellaceae
Proteobacteria_Gammaproteobacteria_Neisseriales_Chromobacterium_FM
Proteobacteria_Gammaproteobacteria_Oceanospirillales_Uncl
Proteobacteria_Gammaproteobacteria_Pseudomonadaceae_Pseudomonadaceae
Proteobacteria_Gammaproteobacteria_Rhodocyclales_Uncl
Proteobacteria_Gammaproteobacteria_Sutterellaceae_Sutterellaceae
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Vibrionaceae_Vibrionaceae
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Stenotrophomonas_FM
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Uncl
Spirochaetes_Spirochaetales_Spirochaetales_Spirochaetaceae
Sulfobacilli_Sulfobacillus_Sulfobacillus_Sulfobacillus_FM
Thermi_Deinococcales_Deinococcales_Deinococcaceae
Thermi_Thermales_Thermales_Meiothermaceae
Thermi_Thermales_Thermales_Thermaceae
TM7_Uncl_Uncl_Uncl
Verrucomicrobia_Verrucomicrobiae_Uncl_Uncl

Set 1-5

Family (Phy-Subphy-Order-Family) (51 families)

Actinobacteria_Actinobacteridae_Actinomycineae_Actinomycineae
Actinobacteria_Actinobacteridae_Bifidobacteriaceae_Bifidobacteriaceae
Actinobacteria_Actinobacteridae_Micromonosporaceae_Micromonosporaceae
Actinobacteria_WCHB1-81_Uncl_Uncl
Bacteroidetes_Bacteroidales_Bacteroidales_Uncl
Bacteroidetes_Flexibacterales_Flexibacterales_Roseivirga_FM
Bacteroidetes_FukuN24_Saprospirales_Uncl
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Chlorobi_Uncl_Uncl_Uncl
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Chloroflexi_Ktedonobacteria_Uncl_Uncl
Cyanobacteria_Uncl_Uncl_Uncl
Entotheonella_Uncl_Uncl_Uncl
Firmicutes_Bacilli_Bacillus_Bacillus_FM
Firmicutes_Bacilli_Thermoactinomycetaceae_Thermoactinomycetaceae
Firmicutes_Bacilli_Uncl_Uncl
Firmicutes_Clostridia_Clostridiales_Gracilibacter_FM
Firmicutes_Clostridia_Peptostreptococcaceae_Peptostreptococcaceae
OP10_CH21_Uncl_Uncl
OP10_Uncl_Uncl_Uncl
OP11_OP11-3_Uncl_Uncl
OP8_OP8_1_Uncl_Uncl
Planctomycetes_Planctomycetacia_Planctomycetales_Uncl
Poribacteria_Uncl_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Beijerinckiaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Rhodoplanaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Caulobacterales_Brevundimonas_FM
Proteobacteria_Alphaproteobacteria_Oleomonas_Oleomonas_FM
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacter_FM
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodovulum_FM
Proteobacteria_Alphaproteobacteria_Rickettsiales_Uncl
Proteobacteria_Alphaproteobacteria_Schlegelella_Schlegelella_FM
Proteobacteria_Epsilonproteobacteria_Arcobacteraceae_Arcobacteraceae
Proteobacteria_Epsilonproteobacteria_Nautilliales_Nautillaceae
Proteobacteria_Epsilonproteobacteria_Sulfuricurvales_Sulfuricurvaceae
Proteobacteria_Gammaproteobacteria_Alcaligenaceae_Alcaligenaceae
Proteobacteria_Gammaproteobacteria_Alteromonadales_Alteromonas_FM
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Ellin339_Uncl
Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacteriales_Enterobacteriaceae
Proteobacteria_Gammaproteobacteria_Legionellales_Uncl
Proteobacteria_Gammaproteobacteria_Neisseriales_Chromobacterium_FM
Proteobacteria_Gammaproteobacteria_Rhodocyclales_Accumulibacter_FM
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Stenotrophomonas_FM
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Uncl
Spirochaetes_Treponemaceae_Treponemaceae_Treponemaceae
SR1_BD2-14_Uncl_Uncl
Thermi_Thermales_Thermales_Thermaceae

Set 1-6

Family (Phy-Subphy-Order-Family) (50 families)

Acidobacteria_OS-K_Uncl_Uncl
Actinobacteria_Actinobacteridae_Streptomycineae_Streptomycineae
Bacteroidetes_Flexibacterales_Flexibacterales_Roseivirga_FM
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Bacteroidetes_SHA-94_Bacteroidales_Uncl
Cyanobacteria_Chloroplasts_Uncl_Uncl
Cyanobacteria_YS2_Uncl_Uncl
Firmicutes_Acidaminococcaceae_Acidaminococcaceae_Acidaminococcaceae
Firmicutes_Bacilli_Halobacillus_Halobacillus_FM
Firmicutes_Bacilli_Staphylococcaceae_Staphylococcaceae
Firmicutes_Clostridia_Clostridiales_Uncl
Firmicutes_Clostridia_Peptostreptococcaceae_Peptostreptococcaceae
Firmicutes_Mollicutes_Uncl_Uncl
Planctomycetes_Planctomycetacia_Planctomycetales_A24_FM
Planctomycetes_Planctomycetacia_Planctomycetales_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Hyphomicrobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Rhodoplanaceae
Proteobacteria_Alphaproteobacteria_Caedibacteraceae_Caedibacteraceae
Proteobacteria_Alphaproteobacteria_Caulobacterales_Brevundimonas_FM
Proteobacteria_Alphaproteobacteria_Nordella_Nordella_FM
Proteobacteria_Alphaproteobacteria_Pseudochrobactrum_Pseudochrobactrum_FM
Proteobacteria_Alphaproteobacteria_Rhizobiaceae_Rhizobiaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_S36_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingobium_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonas_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Uncl
Proteobacteria_Alphaproteobacteria_Uncl_Uncl
Proteobacteria_Deltaproteobacteria_Bdellovibrio_Bdellovibrio_FM
Proteobacteria_Epsilonproteobacteria_Sulfuricurvales_Sulfuricurvaceae
Proteobacteria_Epsilonproteobacteria_Sulfurovumales_Sulfurovumaceae
Proteobacteria_Gammaproteobacteria_Alcaligenaceae_Alcaligenaceae
Proteobacteria_Gammaproteobacteria_Alteromonadales_Rheinheimeraceae
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Ellin339_Uncl
Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacteriales_Enterobacteriaceae
Proteobacteria_Gammaproteobacteria_Legionellales_Legionella_FM
Proteobacteria_Gammaproteobacteria_Legionellales_Uncl
Proteobacteria_Gammaproteobacteria_Neisseriales_Uncl
Proteobacteria_Gammaproteobacteria_Nitrosomonadales_Uncl
Proteobacteria_Gammaproteobacteria_Pseudomonadaceae_Pseudomonadaceae
Proteobacteria_Gammaproteobacteria_Rhodocyclales_Accumulibacter_FM
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Lysobacter_FM
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Uncl
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Xylella_FM
Thermi_Thermales_Thermales_Thermaceae
Thermodesulfobacteria_Thermodesulfobacteriaceae_Thermodesulfobacteriaceae_Thermodesulfobacteriaceae
Verrucomicrobia_Pedosphaerae_Uncl_Uncl

Set 1-7

Family (Phy-Subphy-Order-Family) (47 families)

Actinobacteria_Actinobacteridae_Frankineae_Frankineae
Actinobacteria_Actinobacteridae_Streptosporangineae_Streptosporangineae
Bacteroidetes_Flavobacteriales_Flavobacteriales_Flavobacteriaceae
Bacteroidetes_PHOS-HE21_Flexibacterales_Uncl
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Cyanobacteria_Chloroplasts_Uncl_Uncl
Cyanobacteria_Stigonematales_Stigonematales_Uncl
Firmicutes_Acidaminococcaceae_Acidaminococcaceae_Acidaminococcaceae
Firmicutes_Bacilli_Exiguobacterium_Exiguobacterium_FM
Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae
Firmicutes_Bacilli_Lactobacillales_Leuconostoc_FM
Firmicutes_Bacilli_Lactobacillales_Streptococcaceae
Firmicutes_Bacilli_Lactobacillales_Uncl
Firmicutes_Bacilli_Uncl_Uncl
Firmicutes_Clostridia_Clostridiales_Ruminococcus_FM
Firmicutes_Clostridia_Clostridiales_Uncl
Firmicutes_Clostridia_Peptostreptococcaceae_Peptostreptococcaceae
Firmicutes_Mollicutes_Uncl_Uncl
OP10_CH21_Uncl_Uncl
Planctomycetes_Planctomycetacia_Planctomycetales_Uncl
Poribacteria_Uncl_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Bradyrhizobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Rhodoplanaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Consistiales_SAR11_FM
Proteobacteria_Alphaproteobacteria_Rhizobiaceae_Rhizobiaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacter_FM
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodovulum_FM
Proteobacteria_Alphaproteobacteria_Schlegelella_Schlegelella_FM
Proteobacteria_Alphaproteobacteria_Uncl_Uncl
Proteobacteria_Epsilonproteobacteria_Sulfurovumales_Sulfurovumaceae
Proteobacteria_Gammaproteobacteria_Alcaligenaceae_Alcaligenaceae
Proteobacteria_Gammaproteobacteria_Alteromonadales_Rheinheimeraceae
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacteriales_Enterobacteriaceae
Proteobacteria_Gammaproteobacteria_Legionellales_Uncl
Proteobacteria_Gammaproteobacteria_Neisseriales_Chromobacterium_FM
Proteobacteria_Gammaproteobacteria_Pseudomonadaceae_Pseudomonadaceae
Proteobacteria_Gammaproteobacteria_Sutterellaceae_Sutterellaceae
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Uncl
Sulfobacilli_Sulfobacillus_Sulfobacillus_Sulfobacillus_FM
Thermodesulfobacteria_Thermodesulfobacteriaceae_Thermodesulfobacteriaceae_Thermodesulfobacteriaceae
Thermotogae_Geotogaceae_Geotogaceae_Geotogaceae

Set 1-8

Family (Phy-Subphy-Order-Family) (14 families)

Actinobacteria_Actinobacteridae_Gordoniaceae_Gordoniaceae
Aquificae_Hydrogenothermaceae_Hydrogenothermaceae_Hydrogenothermaceae
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Chlorobi_SJA-28_Uncl_Uncl
Chloroflexi_Chloroflexi-4_Uncl_Uncl
Cyanobacteria_Chloroplasts_Gelidium_Gelidium_FM
Cyanobacteria_Chloroplasts_Uncl_Uncl
Marine_group_AZA3648c_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_Rickettsiales_Uncl
Proteobacteria_Deltaproteobacteria_Myxococcales_Uncl
Proteobacteria_Gammaproteobacteria_Moraxellaceae_Moraxellaceae
Proteobacteria_Gammaproteobacteria_Ralstoniaceae_Ralstoniaceae
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
TM7_Uncl_Uncl_Uncl

Set 1-9

Family (Phy-Subphy-Order-Family) (80 families)

ABY1_OD1_WCHB1-58_Uncl_Uncl
Acidobacteria_Solibacteres_Solibacteraceae_Solibacteraceae
Actinobacteria_Acidimicrobidae_Microthrixineae_Microthrixineae
Actinobacteria_Actinobacteridae_Brachybacterium_Brachybacterium_FM
Actinobacteria_Actinobacteridae_Propionibacterineae_Propionibacterineae
Actinobacteria_Actinobacteridae_Streptomycineae_Streptomycineae
Actinobacteria_Actinobacteridae_Streptosporangineae_Streptosporangineae
Actinobacteria_Actinobacteridae_Uncl_Uncl
Bacteroidetes_Bacteroidales_Bacteroidales_Bacteroidaceae
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Bacteroidetes_Sphingobacteriaceae_Sphingobacteriaceae_Sphingobacteriaceae
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Cyanobacteria_Chloroplasts_Uncl_Uncl
Cyanobacteria_YS2_Uncl_Uncl
Elusimicrobia_TG1_Uncl_Uncl_Uncl
Firmicutes_Acidaminococcaceae_Acidaminococcaceae_Acidaminococcaceae
Firmicutes_Bacilli_Halobacillus_Halobacillus_FM
Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae
Firmicutes_Bacilli_Staphylococcaceae_Staphylococcaceae
Firmicutes_Bacilli_Uncl_Uncl
Firmicutes_Clostridia_Clostridiales_RF6_FM
Firmicutes_Clostridia_Clostridiales_Uncl
Firmicutes_Mollicutes_Acholeplasmatales_Uncl
Firmicutes_Mollicutes_Uncl_Uncl
Haloanaerobiales_Halanaerobiaceae_Halanaerobiaceae_Halanaerobiaceae
Marine_group_AA714017_Uncl_Uncl
Nitrospirae_Thermodesulfovibrionales_Thermodesulfovibrionales_Thermodesulfovibrionaceae
Planctomycetes_Planctomycetacia_Gemmatales_Gemmata_FM
Planctomycetes_Planctomycetacia_Planctomycetales_Uncl
Planctomycetes_WPS-1_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_Azospirillaceae_Azospirillaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Bradyrhizobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Hyphomicrobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacteriaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Caedibacteraceae_Caedibacteraceae
Proteobacteria_Alphaproteobacteria_Caulobacterales_Brevundimonas_FM
Proteobacteria_Alphaproteobacteria_Caulobacterales_Uncl
Proteobacteria_Alphaproteobacteria_Phyllobacteriaceae_Phyllobacteriaceae
Proteobacteria_Alphaproteobacteria_Pseudochrobactrum_Pseudochrobactrum_FM
Proteobacteria_Alphaproteobacteria_Rhizobiaceae_Rhizobiaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Hyphomonadaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacter_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Porphyrobacter_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingobium_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonas_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Uncl
Proteobacteria_Alphaproteobacteria_Uncl_Uncl
Proteobacteria_Deltaproteobacteria_Desulfovibrio_Desulfovibrio_FM
Proteobacteria_Deltaproteobacteria_Syntrophaceae_Syntrophaceae
Proteobacteria_Desulfovibrionales_Desulfovibrionales_Desulfovibrionaceae
Proteobacteria_Epsilonproteobacteria_Arcobacteraceae_Arcobacteraceae
Proteobacteria_Epsilonproteobacteria_Sulfuricurvales_Sulfuricurvaceae
Proteobacteria_Gammaproteobacteria_Alteromonadales_Rheinheimeraceae
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Ellin339_Uncl
Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacteriales_Enterobacteriaceae
Proteobacteria_Gammaproteobacteria_environmental_sequence_ZA3913c_FM
Proteobacteria_Gammaproteobacteria_Legionellales_Legionella_FM
Proteobacteria_Gammaproteobacteria_Legionellales_Uncl
Proteobacteria_Gammaproteobacteria_Moraxellaceae_Moraxellaceae
Proteobacteria_Gammaproteobacteria_Nitrosomonadales_Uncl
Proteobacteria_Gammaproteobacteria_obligately_oligotrophic_bacteria_KI89C_Uncl
Proteobacteria_Gammaproteobacteria_Pasteurellaceae_Pasteurellaceae
Proteobacteria_Gammaproteobacteria_Pseudomonadaceae_Pseudomonadaceae
Proteobacteria_Gammaproteobacteria_Rhodocyclales_Accumulibacter_FM
Proteobacteria_Gammaproteobacteria_Rhodocyclales_Uncl
Proteobacteria_Gammaproteobacteria_Thiotrichales_Thiothrix_FM
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Lysobacter_FM
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Uncl
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Xylella_FM
Proteobacteria_Gammaproteobacteria_ZA3605c_Uncl
Proteobacteria_Zetaproteobacteria_Uncl_Uncl
Thermi_Thermales_Thermales_Thermaceae
Verrucomicrobia_Pedosphaerae_Uncl_Uncl
VHS-B5-50_Uncl_Uncl_Uncl
WS5_Uncl_Uncl_Uncl

Set 1-10

Family (Phy-Subphy-Order-Family) (67 families)

Acidobacteria_iii1-15_Uncl_Uncl
Actinobacteria_Actinobacteridae_Bifidobacteriaceae_Bifidobacteriaceae
Actinobacteria_Actinobacteridae_Frankineae_Frankineae
Actinobacteria_Actinobacteridae_Gordoniaceae_Gordoniaceae
Bacteroidetes_Bacteroidales_Bacteroidales_Bacteroidaceae
Bacteroidetes_Flexibacterales_Flexibacterales_Roseivirga_FM
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Bacteroidetes_Sphingobacteriaceae_Sphingobacteriaceae_Sphingobacteriaceae
Bacteroidetes_Uncl_Uncl_Uncl
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Cyanobacteria_Chloroplasts_Uncl_Uncl
Cyanobacteria_YS2_Uncl_Uncl
Firmicutes_Bacilli_Staphylococcaceae_Staphylococcaceae
Firmicutes_Bacilli_Uncl_Uncl
Firmicutes_Clostridia_Clostridiales_Uncl
Firmicutes_Mollicutes_Uncl_Uncl
Marine_group_AA714017_Uncl_Uncl
OP10_CH21_Uncl_Uncl
Planctomycetes_Planctomycetacia_Planctomycetales_Uncl
Proteobacteria_Alphaproteobacteria_Azospirillaceae_Azospirillaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Beijerinckiaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Bradyrhizobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Hyphomicrobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacteriaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Pleomorphomonas_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Rhodoplanaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Caedibacteraceae_Caedibacteraceae
Proteobacteria_Alphaproteobacteria_Caulobacterales_Brevundimonas_FM
Proteobacteria_Alphaproteobacteria_Caulobacterales_Uncl
Proteobacteria_Alphaproteobacteria_Oleomonas_Oleomonas_FM
Proteobacteria_Alphaproteobacteria_Rhizobiaceae_Rhizobiaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Hyphomonadaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacter_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Porphyrobacter_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingobium_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonas_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Uncl
Proteobacteria_Alphaproteobacteria_Stappia_Stappia_FM
Proteobacteria_Alphaproteobacteria_Uncl_Uncl
Proteobacteria_Deltaproteobacteria_Desulfobacteraceae_Desulfobacteraceae
Proteobacteria_Deltaproteobacteria_Desulfovibrio_Desulfovibrio_FM
Proteobacteria_Desulfovibrionales_Desulfovibrionales_Desulfovibrionaceae
Proteobacteria_Epsilonproteobacteria_Sulfuricurvales_Sulfuricurvaceae
Proteobacteria_Gammaproteobacteria_Alteromonadaceae_Alteromonadaceae
Proteobacteria_Gammaproteobacteria_Alteromonadales_Rheinheimeraceae
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Ellin339_Uncl
Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacteriales_Enterobacteriaceae
Proteobacteria_Gammaproteobacteria_Gammaproteobacteria_Uncl
Proteobacteria_Gammaproteobacteria_Halomonadaceae_Halomonadaceae
Proteobacteria_Gammaproteobacteria_Legionellales_Legionella_FM
Proteobacteria_Gammaproteobacteria_Legionellales_Uncl
Proteobacteria_Gammaproteobacteria_Marinobacter_Marinobacter_FM
Proteobacteria_Gammaproteobacteria_Microbulbifer_Microbulbifer_FM
Proteobacteria_Gammaproteobacteria_Moraxellaceae_Moraxellaceae
Proteobacteria_Gammaproteobacteria_Neisseriales_Uncl
Proteobacteria_Gammaproteobacteria_Pseudomonadaceae_Pseudomonadaceae
Proteobacteria_Gammaproteobacteria_Ralstoniaceae_Ralstoniaceae
Proteobacteria_Gammaproteobacteria_Rhodocyclales_Accumulibacter_FM
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Lysobacter_FM
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Uncl
Proteobacteria_Gammaproteobacteria_ZA3605c_Uncl
Thermi_Thermales_Thermales_Thermaceae
VHS-B5-50_Uncl_Uncl_Uncl

Set 1-11

Family (Phy-Subphy-Order-Family) (75 families)

Acidobacteria_Chloracidobacteria_Uncl_Uncl
Acidobacteria_iii1-15_Uncl_Uncl
Actinobacteria_Acidimicrobidae_Uncl_Uncl
Actinobacteria_Actinobacteridae_Actinomycineae_Actinomycineae
Actinobacteria_Actinobacteridae_Bifidobacteriaceae_Bifidobacteriaceae
Actinobacteria_Actinobacteridae_Gordoniaceae_Gordoniaceae
Actinobacteria_Actinobacteridae_Propionibacterineae_Propionibacterineae
Actinobacteria_Actinobacteridae_Streptosporangineae_Streptosporangineae
Actinobacteria_Actinobacteridae_Uncl_Uncl
Bacteroidetes_Flexibacterales_Flexibacterales_Roseivirga_FM
Bacteroidetes_FukuN24_Saprospirales_Uncl
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Bacteroidetes_Saprospirales_Saprospirales_Uncl
Bacteroidetes_Sphingobacteriaceae_Sphingobacteriaceae_Sphingobacteriaceae
Chlorobi_Uncl_Uncl_Uncl
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Cyanobacteria_Chloroplasts_Uncl_Uncl
Cyanobacteria_Uncl_Uncl_Uncl
Firmicutes_Bacilli_Halobacillus_Halobacillus_FM
Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae
Firmicutes_Bacilli_Lactobacillales_Streptococcaceae
Firmicutes_Bacilli_Lactobacillales_Uncl
Firmicutes_Bacilli_Paenibacillaceae_Paenibacillaceae
Firmicutes_Bacilli_Staphylococcaceae_Staphylococcaceae
Firmicutes_Clostridia_Clostridiales_Acetivibrio_FM
Firmicutes_Clostridia_Clostridiales_Uncl
Firmicutes_Clostridia_Peptostreptococcaceae_Peptostreptococcaceae
Firmicutes_Mollicutes_Uncl_Uncl
Firmicutes_Syntrophomonadaceae_Syntrophomonadaceae_Syntrophomonadaceae
Haloanaerobiales_Halanaerobiaceae_Halanaerobiaceae_Halanaerobiaceae
Marine_group_AA714017_Uncl_Uncl
Nitrospirae_Thermodesulfovibrionales_Thermodesulfovibrionales_Thermodesulfovibrionaceae
OP10_CH21_Uncl_Uncl
Planctomycetes_Planctomycetacia_Planctomycetales_Uncl
Proteobacteria_Alphaproteobacteria_Acetobacterales_Roseomonas_FM
Proteobacteria_Alphaproteobacteria_Azospirillaceae_Azospirillaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Beijerinckiaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacteriaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Rhodoplanaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Xanthobacteraceae
Proteobacteria_Alphaproteobacteria_Caedibacteraceae_Caedibacteraceae
Proteobacteria_Alphaproteobacteria_Caulobacterales_Brevundimonas_FM
Proteobacteria_Alphaproteobacteria_Rhizobiaceae_Rhizobiaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Hyphomonadaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacter_FM
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodovulum_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingobium_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonas_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Uncl
Proteobacteria_Alphaproteobacteria_Uncl_Uncl
Proteobacteria_Desulfovibrionales_Desulfovibrionales_Desulfovibrionaceae
Proteobacteria_Epsilonproteobacteria_Sulfuricurvales_Sulfuricurvaceae
Proteobacteria_Gammaproteobacteria_Alteromonadales_Alteromonas_FM
Proteobacteria_Gammaproteobacteria_Alteromonadales_Rheinheimeraceae
Proteobacteria_Gammaproteobacteria_bacterium_Ellin6067_Uncl
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Ellin339_Uncl
Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacteriales_Enterobacteriaceae
Proteobacteria_Gammaproteobacteria_Legionellales_Legionella_FM
Proteobacteria_Gammaproteobacteria_Legionellales_Uncl
Proteobacteria_Gammaproteobacteria_Moraxellaceae_Moraxellaceae
Proteobacteria_Gammaproteobacteria_Neisseriales_Chromobacterium_FM
Proteobacteria_Gammaproteobacteria_Pasteurellaceae_Pasteurellaceae
Proteobacteria_Gammaproteobacteria_Pseudomonadaceae_Pseudomonadaceae
Proteobacteria_Gammaproteobacteria_Rhodocyclales_Accumulibacter_FM
Proteobacteria_Gammaproteobacteria_Sutterellaceae_Sutterellaceae
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Uncl
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Xylella_FM
Thermi_Deinococcales_Deinococcales_Deinococcaceae
Thermi_Thermales_Thermales_Thermaceae
Verrucomicrobia_Pedosphaerae_Uncl_Uncl

Set 1-12

Family (Phy-Subphy-Order-Family) (66 families)

ABY1_OD1_WCHB1-58_Uncl_Uncl
Acidobacteria_Chloracidobacteria_Uncl_Uncl
Actinobacteria_Actinobacteridae_Bifidobacteriaceae_Bifidobacteriaceae
Actinobacteria_Actinobacteridae_Brachybacterium_Brachybacterium_FM
Actinobacteria_Actinobacteridae_Frankineae_Frankineae
Actinobacteria_Actinobacteridae_Micromonosporaceae_Micromonosporaceae
Actinobacteria_Actinobacteridae_Propionibacterineae_Propionibacterineae
Bacteroidetes_Flavobacteriales_Flavobacteriales_Sporocytophaga_FM
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Bacteroidetes_Sphingobacteriaceae_Sphingobacteriaceae_Sphingobacteriaceae
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Cyanobacteria_Chloroplasts_Uncl_Uncl
Cyanobacteria_YS2_Uncl_Uncl
Firmicutes_Bacilli_Lactobacillales_Streptococcaceae
Firmicutes_Bacilli_Staphylococcaceae_Staphylococcaceae
Firmicutes_Clostridia_Clostridiales_Uncl
Firmicutes_Clostridia_Uncl_Uncl
Firmicutes_Mollicutes_Uncl_Uncl
Marine_group_AA714017_Uncl_Uncl
Nitrospirae_Thermodesulfovibrionales_Thermodesulfovibrionales_Thermodesulfovibrionaceae
Planctomycetes_Planctomycetacia_Planctomycetales_Uncl
Proteobacteria_Alphaproteobacteria_Azospirillaceae_Azospirillaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Bradyrhizobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Hyphomicrobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacteriaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Pleomorphomonas_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Caedibacteraceae_Caedibacteraceae
Proteobacteria_Alphaproteobacteria_Caulobacterales_Brevundimonas_FM
Proteobacteria_Alphaproteobacteria_Caulobacterales_Uncl
Proteobacteria_Alphaproteobacteria_Rhizobiaceae_Rhizobiaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Hyphomonadaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacter_FM
Proteobacteria_Alphaproteobacteria_Rhodobacterales_S36_FM
Proteobacteria_Alphaproteobacteria_Rickettsiales_Uncl
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Porphyrobacter_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingobium_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonas_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Uncl
Proteobacteria_Alphaproteobacteria_Uncl_Uncl
Proteobacteria_Deltaproteobacteria_Desulfovibrio_Desulfovibrio_FM
Proteobacteria_Desulfovibrionales_Desulfovibrionales_Desulfovibrionaceae
Proteobacteria_Epsilonproteobacteria_Sulfuricurvales_Sulfuricurvaceae
Proteobacteria_Gammaproteobacteria_Alteromonadaceae_Alteromonadaceae
Proteobacteria_Gammaproteobacteria_Alteromonadales_Rheinheimeraceae
Proteobacteria_Gammaproteobacteria_bacterium_Ellin6067_Uncl
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Ellin339_Uncl
Proteobacteria_Gammaproteobacteria_endosymbiont_RT7_of_Lyrodus_pedicellatus_Uncl
Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacteriales_Enterobacteriaceae
Proteobacteria_Gammaproteobacteria_Hydrogenophilales_Petrobacter_FM
Proteobacteria_Gammaproteobacteria_Legionellales_Legionella_FM
Proteobacteria_Gammaproteobacteria_Legionellales_Uncl
Proteobacteria_Gammaproteobacteria_Marinobacter_Marinobacter_FM
Proteobacteria_Gammaproteobacteria_Moraxellaceae_Moraxellaceae
Proteobacteria_Gammaproteobacteria_Pseudomonadaceae_Pseudomonadaceae
Proteobacteria_Gammaproteobacteria_Rhodocyclales_Accumulibacter_FM
Proteobacteria_Gammaproteobacteria_Sutterellaceae_Sutterellaceae
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Uncl
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Xylella_FM
Proteobacteria_Gammaproteobacteria_ZA3605c_Uncl
Thermi_Thermales_Thermales_Thermaceae
Thermotogae_A2_Uncl_Uncl
Verrucomicrobia_Pedosphaerae_Uncl_Uncl

Set 1-13

Family (Phy-Subphy-Order-Family) (68 families)

ABY1_OD1_WCHB1-58_Uncl_Uncl
Actinobacteria_Actinobacteridae_Frankineae_Frankineae
Actinobacteria_Actinobacteridae_Gordoniaceae_Gordoniaceae
Actinobacteria_Actinobacteridae_Propionibacterineae_Propionibacterineae
Actinobacteria_Actinobacteridae_Streptomycineae_Streptomycineae
Actinobacteria_Actinobacteridae_Streptosporangineae_Streptosporangineae
Actinobacteria_Actinobacteridae_Uncl_Uncl
Bacteroidetes_Bacteroidales_Bacteroidales_Bacteroidaceae
Bacteroidetes_Flexibacterales_Flexibacterales_Roseivirga_FM
Bacteroidetes_Hymenobacterales_Hymenobacterales_Hymenobacteraceae
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Bacteroidetes_Sphingobacteriaceae_Sphingobacteriaceae_Sphingobacteriaceae
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Cyanobacteria_Chloroplasts_Uncl_Uncl
Elusimicrobia_TG1_Uncl_Uncl_Uncl
Firmicutes_Acidaminococcaceae_Acidaminococcaceae_Acidaminococcaceae
Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae
Firmicutes_Bacilli_Lactobacillales_Streptococcaceae
Firmicutes_Bacilli_Lactobacillales_Uncl
Firmicutes_Bacilli_Planococcaceae_Planococcaceae
Firmicutes_Bacilli_Staphylococcaceae_Staphylococcaceae
Firmicutes_Bacilli_Uncl_Uncl
Firmicutes_Clostridia_Clostridiales_Uncl
Firmicutes_Mollicutes_Uncl_Uncl
Marine_group_AA714017_Uncl_Uncl
OP10_CH21_Uncl_Uncl
Planctomycetes_Planctomycetacia_Planctomycetales_Uncl
Planctomycetes_Planctomycetacia_Rhodopirellulaceae_Rhodopirellulaceae
Proteobacteria_Alphaproteobacteria_Azospirillaceae_Azospirillaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Bradyrhizobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Hyphomicrobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacteriaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Caedibacteraceae_Caedibacteraceae
Proteobacteria_Alphaproteobacteria_Caulobacterales_Brevundimonas_FM
Proteobacteria_Alphaproteobacteria_Caulobacterales_Uncl
Proteobacteria_Alphaproteobacteria_Rhizobiaceae_Rhizobiaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Hyphomonadaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacter_FM
Proteobacteria_Alphaproteobacteria_Rhodobacterales_S36_FM
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Uncl
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Porphyrobacter_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingobium_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonas_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Uncl
Proteobacteria_Alphaproteobacteria_Uncl_Uncl
Proteobacteria_Deltaproteobacteria_Desulfovibrio_Desulfovibrio_FM
Proteobacteria_Deltaproteobacteria_JG37-AG-2_Uncl
Proteobacteria_Epsilonproteobacteria_Arcobacteraceae_Arcobacteraceae
Proteobacteria_Epsilonproteobacteria_Sulfuricurvales_Sulfuricurvaceae
Proteobacteria_Gammaproteobacteria_Alcaligenaceae_Alcaligenaceae
Proteobacteria_Gammaproteobacteria_Alteromonadales_Rheinheimeraceae
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Ellin339_Uncl
Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacteriales_Enterobacteriaceae
Proteobacteria_Gammaproteobacteria_Legionellales_Legionella_FM
Proteobacteria_Gammaproteobacteria_Legionellales_Uncl
Proteobacteria_Gammaproteobacteria_Neisseriales_Uncl
Proteobacteria_Gammaproteobacteria_Pseudomonadaceae_Pseudomonadaceae
Proteobacteria_Gammaproteobacteria_Rhodocyclales_Accumulibacter_FM
Proteobacteria_Gammaproteobacteria_SBR1001_Uncl
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Uncl
Proteobacteria_Gammaproteobacteria_ZA3605c_Uncl
Thermi_Thermales_Thermales_Thermaceae
Verrucomicrobia_Pedosphaerae_Uncl_Uncl

Set 1-14

Family (Phy-Subphy-Order-Family) (77 families)

ABY1_OD1_WCHB1-58_Uncl_Uncl
Acidobacteria_Chloracidobacteria_Uncl_Uncl
Actinobacteria_Acidimicrobidae_JTB31_BD2-10_FM
Actinobacteria_Actinobacteridae_Gordoniaceae_Gordoniaceae
Actinobacteria_Actinobacteridae_Propionibacterineae_Propionibacterineae
Bacteroidetes_Flavobacteriales_Flavobacteriales_Sporocytophaga_FM
Bacteroidetes_Flexibacterales_Flexibacterales_Roseivirga_FM
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Bacteroidetes_Sphingobacteriaceae_Sphingobacteriaceae_Sphingobacteriaceae
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Cyanobacteria_Chloroplasts_Uncl_Uncl
Firmicutes_Acidaminococcaceae_Acidaminococcaceae_Acidaminococcaceae
Firmicutes_Bacilli_Bacillus_Bacillus_FM
Firmicutes_Bacilli_Paenibacillaceae_Paenibacillaceae
Firmicutes_Bacilli_Planococcaceae_Planococcaceae
Firmicutes_Bacilli_Staphylococcaceae_Staphylococcaceae
Firmicutes_Bacilli_Uncl_Uncl
Firmicutes_Clostridia_Clostridiales_Uncl
Firmicutes_Mollicutes_Acholeplasmatales_Uncl
Firmicutes_Mollicutes_Uncl_Uncl
Marine_group_AA714017_Uncl_Uncl
Nitrospirae_Thermodesulfovibrionales_Thermodesulfovibrionales_Thermodesulfovibrionaceae
OP10_Uncl_Uncl_Uncl
Planctomycetes_Planctomycetacia_Planctomycetales_Uncl
Proteobacteria_Alphaproteobacteria_Azospirillaceae_Azospirillaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Bradyrhizobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Hyphomicrobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacteriaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Pleomorphomonas_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Rhodoplanaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Caedibacteraceae_Caedibacteraceae
Proteobacteria_Alphaproteobacteria_Caulobacterales_Brevundimonas_FM
Proteobacteria_Alphaproteobacteria_Caulobacterales_Uncl
Proteobacteria_Alphaproteobacteria_Phyllobacteriaceae_Phyllobacteriaceae
Proteobacteria_Alphaproteobacteria_Pseudochrobactrum_Pseudochrobactrum_FM
Proteobacteria_Alphaproteobacteria_Rhizobiaceae_Rhizobiaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Hyphomonadaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacter_FM
Proteobacteria_Alphaproteobacteria_Rhodobacterales_S36_FM
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Uncl
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Porphyrobacter_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingobium_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonas_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Uncl
Proteobacteria_Alphaproteobacteria_Uncl_Uncl
Proteobacteria_Deltaproteobacteria_Desulfovibrio_Desulfovibrio_FM
Proteobacteria_Desulfovibrionales_Desulfovibrionales_Desulfovibrionaceae
Proteobacteria_Epsilonproteobacteria_Hydrogenimonaceae_Hydrogenimonaceae
Proteobacteria_Epsilonproteobacteria_Sulfuricurvales_Sulfuricurvaceae
Proteobacteria_Gammaproteobacteria_Alteromonadaceae_Alteromonadaceae
Proteobacteria_Gammaproteobacteria_Alteromonadales_Rheinheimeraceae
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Ellin339_Uncl
Proteobacteria_Gammaproteobacteria_endosymbiont_RT7_of_Lyrodus_pedicellatus_Uncl
Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacteriales_Enterobacteriaceae
Proteobacteria_Gammaproteobacteria_Hydrogenophilales_Petrobacter_FM
Proteobacteria_Gammaproteobacteria_Legionellales_Legionella_FM
Proteobacteria_Gammaproteobacteria_Legionellales_Uncl
Proteobacteria_Gammaproteobacteria_Marinobacter_Marinobacter_FM
Proteobacteria_Gammaproteobacteria_Neisseriales_Uncl
Proteobacteria_Gammaproteobacteria_Nitrosomonadales_Uncl
Proteobacteria_Gammaproteobacteria_Pseudomonadaceae_Pseudomonadaceae
Proteobacteria_Gammaproteobacteria_Rhodocyclales_Accumulibacter_FM
Proteobacteria_Gammaproteobacteria_SBR1001_Uncl
Proteobacteria_Gammaproteobacteria_Spirillaceae_Spirillaceae
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Lysobacter_FM
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Uncl
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Xylella_FM
Proteobacteria_Gammaproteobacteria_ZA3605c_Uncl
Thermi_Thermales_Thermales_Thermaceae
TM7_Uncl_Uncl_Uncl
Verrucomicrobia_Pedosphaerae_Uncl_Uncl
VHS-B5-50_Uncl_Uncl_Uncl

Set 1-15

Family (Phy-Subphy-Order-Family) (66 families)

ABY1_OD1_WCHB1-58_Uncl_Uncl
Actinobacteria_Actinobacteridae_Frankineae_Frankineae
Actinobacteria_Actinobacteridae_Gordoniaceae_Gordoniaceae
Actinobacteria_Actinobacteridae_Propionibacterineae_Propionibacterineae
Bacteroidetes_Bacteroidales_Bacteroidales_Bacteroidaceae
Bacteroidetes_Flavobacteriales_Flavobacteriales_Sporocytophaga_FM
Bacteroidetes_Flexibacterales_Flexibacterales_Roseivirga_FM
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Bacteroidetes_Sphingobacteriaceae_Sphingobacteriaceae_Sphingobacteriaceae
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Cyanobacteria_Chloroplasts_Uncl_Uncl
Cyanobacteria_YS2_Uncl_Uncl
Firmicutes_Acidaminococcaceae_Acidaminococcaceae_Acidaminococcaceae
Firmicutes_Bacilli_Paenibacillaceae_Paenibacillaceae
Firmicutes_Bacilli_Staphylococcaceae_Staphylococcaceae
Firmicutes_Clostridia_Clostridiales_Clostridiaceae
Firmicutes_Clostridia_Clostridiales_Uncl
Firmicutes_Clostridia_Peptostreptococcaceae_Peptostreptococcaceae
Firmicutes_Mollicutes_Uncl_Uncl
Nitrospirae_Thermodesulfovibrionales_Thermodesulfovibrionales_Thermodesulfovibrionaceae
OP10_CH21_Uncl_Uncl
OP10_CL500-48_Uncl_Uncl
Planctomycetes_Planctomycetacia_Planctomycetales_Uncl
Proteobacteria_Alphaproteobacteria_Azospirillaceae_Azospirillaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Bradyrhizobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Hyphomicrobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacteriaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Caedibacteraceae_Caedibacteraceae
Proteobacteria_Alphaproteobacteria_Caulobacterales_Brevundimonas_FM
Proteobacteria_Alphaproteobacteria_Caulobacterales_Uncl
Proteobacteria_Alphaproteobacteria_Rhizobiaceae_Rhizobiaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Hyphomonadaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacter_FM
Proteobacteria_Alphaproteobacteria_Rhodobacterales_S36_FM
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Uncl
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Porphyrobacter_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingobium_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonas_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Uncl
Proteobacteria_Alphaproteobacteria_Uncl_Uncl
Proteobacteria_Deltaproteobacteria_Bdellovibrio_Bdellovibrio_FM
Proteobacteria_Deltaproteobacteria_Desulfovibrio_Desulfovibrio_FM
Proteobacteria_Desulfovibrionales_Desulfovibrionales_Desulfovibrionaceae
Proteobacteria_Epsilonproteobacteria_Hydrogenimonaceae_Hydrogenimonaceae
Proteobacteria_Epsilonproteobacteria_Sulfuricurvales_Sulfuricurvaceae
Proteobacteria_Gammaproteobacteria_Alcaligenaceae_Alcaligenaceae
Proteobacteria_Gammaproteobacteria_Alteromonadales_Rheinheimeraceae
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Ellin339_Uncl
Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacteriales_Enterobacteriaceae
Proteobacteria_Gammaproteobacteria_Legionellales_Legionella_FM
Proteobacteria_Gammaproteobacteria_Legionellales_Uncl
Proteobacteria_Gammaproteobacteria_Pseudomonadaceae_Pseudomonadaceae
Proteobacteria_Gammaproteobacteria_Rhodocyclales_Accumulibacter_FM
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Lysobacter_FM
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Uncl
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Xylella_FM
Proteobacteria_Gammaproteobacteria_ZA3605c_Uncl
Spirochaetes_Treponemaceae_Treponemaceae_Treponemaceae
Thermi_Thermales_Thermales_Thermaceae
TM7_Uncl_Uncl_Uncl
Verrucomicrobia_Pedosphaerae_Uncl_Uncl
VHS-B5-50_Uncl_Uncl_Uncl

Set 1-16

Family (Phy-Subphy-Order-Family) (23 families)

Actinobacteria_Actinobacteridae_Arthrobacter_Arthrobacter_FM
Actinobacteria_Actinobacteridae_Bifidobacteriaceae_Bifidobacteriaceae
Actinobacteria_Actinobacteridae_Propionibacterineae_Propionibacterineae
Bacteroidetes_Flavobacteriales_Flavobacteriales_Flavobacteriaceae
Caldithrix_KSB1_Caldithrixales_Caldithrixales_Uncl
Cyanobacteria_Chloroplasts_Uncl_Uncl
Firmicutes_Clostridia_Catabacter_Catabacter_FM
Firmicutes_Clostridia_Clostridiales_Uncl
Poribacteria_Uncl_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Bradyrhizobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Oleomonas_Oleomonas_FM
Proteobacteria_Alphaproteobacteria_Rickettsiales_Uncl
Proteobacteria_Epsilonproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Moraxellaceae_Moraxellaceae
Proteobacteria_Gammaproteobacteria_Pseudomonadaceae_Pseudomonadaceae
Proteobacteria_Gammaproteobacteria_Ralstoniaceae_Ralstoniaceae
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
Sulfobacilli_Sulfobacillus_Sulfobacillus_Sulfobacillus_FM
WS5_Uncl_Uncl_Uncl

JPL 2-1

Family (Phy-Subphy-Order-Family) (26 families)

Actinobacteria_Actinobacteridae_Gordoniaceae_Gordoniaceae
Actinobacteria_Actinobacteridae_Rhodococcus_Rhodococcus_FM
Actinobacteria_WCHB1-81_Uncl_Uncl
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Firmicutes_Bacilli_Lactobacillales_Streptococcaceae
Poribacteria_Uncl_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Bradyrhizobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Rhodoplanaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Oleomonas_Oleomonas_FM
Proteobacteria_Alphaproteobacteria_Rhizobiaceae_Rhizobiaceae
Proteobacteria_Alphaproteobacteria_Rickettsiales_Uncl
Proteobacteria_Alphaproteobacteria_Schlegelella_Schlegelella_FM
Proteobacteria_Epsilonproteobacteria_Arcobacteraceae_Arcobacteraceae
Proteobacteria_Gammaproteobacteria_Alcaligenaceae_Alcaligenaceae
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacteriales_Enterobacteriaceae
Proteobacteria_Gammaproteobacteria_Legionellales_Uncl
Proteobacteria_Gammaproteobacteria_Sutterellaceae_Sutterellaceae
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Uncl
Sulfobacilli_Sulfobacillus_Sulfobacillus_Sulfobacillus_FM
WS5_Uncl_Uncl_Uncl

JPL 2-3

Family (Phy-Subphy-Order-Family) (30 families)

ABY1_OD1_WCHB1-58_Uncl_Uncl
Actinobacteria_Actinobacteridae_Bifidobacteriaceae_Bifidobacteriaceae
Actinobacteria_Actinobacteridae_Uncl_Uncl
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Bacteroidetes_Saprospirales_Saprospirales_Uncl
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Cyanobacteria_Chloroplasts_Uncl_Uncl
Firmicutes_Bacilli_Halobacillus_Halobacillus_FM
Firmicutes_Bacilli_Lactobacillales_Streptococcaceae
Firmicutes_Clostridia_Peptostreptococcaceae_Peptostreptococcaceae
Poribacteria_Uncl_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Bradyrhizobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Rhodoplanaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Xanthobacteraceae
Proteobacteria_Alphaproteobacteria_Caulobacterales_Brevundimonas_FM
Proteobacteria_Alphaproteobacteria_Oleomonas_Oleomonas_FM
Proteobacteria_Alphaproteobacteria_Rhizobiaceae_Rhizobiaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacter_FM
Proteobacteria_Alphaproteobacteria_Rickettsiales_Uncl
Proteobacteria_Alphaproteobacteria_Uncl_Uncl
Proteobacteria_Deltaproteobacteria_Geobacter_Geobacter_FM
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Legionellales_Uncl
Proteobacteria_Gammaproteobacteria_Ralstoniaceae_Ralstoniaceae
Thermi_Thermales_Thermales_Thermaceae
TM7_Uncl_Uncl_Uncl
WS5_Uncl_Uncl_Uncl

JPL 2-7

Family (Phy-Subphy-Order-Family) (34 families)

Actinobacteria_Actinobacteridae_Leucobacter_Leucobacter_FM
Actinobacteria_Actinobacteridae_Rhodococcus_Rhodococcus_FM
Bacteroidetes_Bacteroidales_Bacteroidales_Uncl
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Cyanobacteria_Chloroplasts_Uncl_Uncl
Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae
Firmicutes_Bacilli_Staphylococcaceae_Staphylococcaceae
Firmicutes_Bacilli_Uncl_Uncl
Firmicutes_Clostridia_Clostridiales_Gracilibacter_FM
Firmicutes_Clostridia_Peptostreptococcaceae_Peptostreptococcaceae
Firmicutes_Desulfotomaculum_Desulfotomaculum_Desulfotomaculum_FM
Firmicutes_Uncl_Uncl_Uncl
Poribacteria_Uncl_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_Acetobacterales_Acetobacteraceae
Proteobacteria_Alphaproteobacteria_Acetobacterales_Roseomonas_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Bradyrhizobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Rhodoplanaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Caulobacterales_Brevundimonas_FM
Proteobacteria_Alphaproteobacteria_Nordella_Nordella_FM
Proteobacteria_Alphaproteobacteria_Oleomonas_Oleomonas_FM
Proteobacteria_Alphaproteobacteria_Rhizobiaceae_Rhizobiaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacter_FM
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodovulum_FM
Proteobacteria_Alphaproteobacteria_Rickettsiales_Uncl
Proteobacteria_Alphaproteobacteria_Schlegelella_Schlegelella_FM
Proteobacteria_Alphaproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Alcaligenaceae_Alcaligenaceae
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacteriales_Enterobacteriaceae
Proteobacteria_Gammaproteobacteria_Legionellales_Uncl
Sulfobacilli_Sulfobacillus_Sulfobacillus_Sulfobacillus_FM

JPL 2-9

Family (Phy-Subphy-Order-Family) (64 families)

Actinobacteria_Acidimicrobidae_Uncl_Uncl
Actinobacteria_Actinobacteridae_Frankineae_Frankineae
Actinobacteria_Actinobacteridae_Gordoniaceae_Gordoniaceae
Actinobacteria_Actinobacteridae_Intrasporangiaceae_Intrasporangiaceae
Actinobacteria_Actinobacteridae_Micromonosporaceae_Micromonosporaceae
Actinobacteria_Actinobacteridae_Propionibacterineae_Propionibacterineae
Actinobacteria_Actinobacteridae_Streptomycineae_Streptomycineae
Actinobacteria_Actinobacteridae_Streptosporangineae_Streptosporangineae
Actinobacteria_Actinobacteridae_Uncl_Uncl
Bacteroidetes_Bacteroidales_Bacteroidales_Uncl
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Chlorobi_Uncl_Uncl_Uncl
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Cyanobacteria_Chloroplasts_Uncl_Uncl
Cyanobacteria_Uncl_Uncl_Uncl
Firmicutes_Bacilli_Bacillus_Bacillus_FM
Firmicutes_Bacilli_Halobacillus_Halobacillus_FM
Firmicutes_Bacilli_Lactobacillales_Aerococcaceae
Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae
Firmicutes_Bacilli_Lactobacillales_Uncl
Firmicutes_Bacilli_Paenibacillaceae_Paenibacillaceae
Firmicutes_Bacilli_Staphylococcaceae_Staphylococcaceae
Firmicutes_Bacilli_Uncl_Uncl
Firmicutes_Clostridia_Clostridiales_Uncl
Firmicutes_Clostridia_Peptostreptococcaceae_Peptostreptococcaceae
Nitrospirae_Nitrospirales_Nitrospirales_Nitrospira_FM
OP10_Uncl_Uncl_Uncl
Planctomycetes_Planctomycetacia_Planctomycetales_Uncl
Poribacteria_Uncl_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_Acetobacterales_Acetobacteraceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Bradyrhizobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Rhodoplanaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Caedibacteraceae_Caedibacteraceae
Proteobacteria_Alphaproteobacteria_Nordella_Nordella_FM
Proteobacteria_Alphaproteobacteria_Pseudochrobactrum_Pseudochrobactrum_FM
Proteobacteria_Alphaproteobacteria_Rhizobiaceae_Rhizobiaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacter_FM
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Uncl
Proteobacteria_Alphaproteobacteria_Rickettsiales_Uncl
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Porphyrobacter_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonas_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Uncl
Proteobacteria_Alphaproteobacteria_Uncl_Uncl
Proteobacteria_Deltaproteobacteria_JG37-AG-2_Uncl
Proteobacteria_Epsilonproteobacteria_Campylobacteraceae_Campylobacteraceae
Proteobacteria_Epsilonproteobacteria_Nautilliales_Nautillaceae
Proteobacteria_Epsilonproteobacteria_Sulfuricurvales_Sulfuricurvaceae
Proteobacteria_Gammaproteobacteria_Alcaligenaceae_Alcaligenaceae
Proteobacteria_Gammaproteobacteria_Alteromonadales_Colwelliaceae
Proteobacteria_Gammaproteobacteria_Alteromonadales_Rheinheimeraceae
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Ellin339_Uncl
Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacteriales_Enterobacteriaceae
Proteobacteria_Gammaproteobacteria_Legionellales_Uncl
Proteobacteria_Gammaproteobacteria_Neisseriales_Uncl
Proteobacteria_Gammaproteobacteria_Pasteurellaceae_Pasteurellaceae
Proteobacteria_Gammaproteobacteria_Pseudomonadaceae_Pseudomonadaceae
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Uncl
SR1_BD2-14_Uncl_Uncl
Sulfobacilli_Sulfobacillus_Sulfobacillus_FM
WCHB1-27_Uncl_Uncl_Uncl

JPL 2-10

Family (Phy-Subphy-Order-Family) (39 families)

ABY1_OD1_WCHB1-58_Uncl_Uncl
Actinobacteria_Actinobacteridae_Actinomycineae_Actinomycineae
Actinobacteria_Actinobacteridae_Frankineae_Frankineae
Actinobacteria_Actinobacteridae_Gordoniaceae_Gordoniaceae
Actinobacteria_Actinobacteridae_Intrasporangiaceae_Intrasporangiaceae
Actinobacteria_Actinobacteridae_Micromonosporaceae_Micromonosporaceae
Actinobacteria_Actinobacteridae_Propionibacterineae_Propionibacterineae
Actinobacteria_Actinobacteridae_Streptomycineae_Streptomycineae
Actinobacteria_Actinobacteridae_Streptosporangineae_Streptosporangineae
Actinobacteria_Actinobacteridae_Uncl_Uncl
Actinobacteria_Rubrobacteridae_Thermoleiphilaceae_Thermoleiphilaceae
Bacteroidetes_E13_Bacteroidales_Uncl
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Chlorobi_Uncl_Uncl_Uncl
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Cyanobacteria_YS2_Uncl_Uncl
Firmicutes_Bacilli_Lactobacillales_Aerococcaceae
Firmicutes_Bacilli_Staphylococcaceae_Staphylococcaceae
Firmicutes_Bacilli_Uncl_Uncl
Firmicutes_Clostridia_Peptostreptococcaceae_Peptostreptococcaceae
Firmicutes_Desulfotomaculum_Desulfotomaculum_Desulfotomaculum_FM
Nitrospirae_Nitrospirales_Nitrospirales_Nitrospira_FM
Planctomycetes_Planctomycetacia_Planctomycetales_Uncl
Proteobacteria_Alphaproteobacteria_Acetobacterales_Acetobacteraceae
Proteobacteria_Alphaproteobacteria_Azospirillaceae_Azospirillaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Hyphomicrobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Rhodoplanaceae
Proteobacteria_Alphaproteobacteria_Rickettsiales_Uncl
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Uncl
Proteobacteria_Alphaproteobacteria_Uncl_Uncl
Proteobacteria_Desulfovibrionales_Desulfovibrionales_Desulfovibrionaceae
Proteobacteria_Gammaproteobacteria_Alteromonadales_Colwelliaceae
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Pasteurellaceae_Pasteurellaceae
Proteobacteria_Gammaproteobacteria_Ralstoniaceae_Ralstoniaceae
Thermi_Thermales_Thermales_Thermaceae
Thermodesulfobacteria_Thermodesulfobacteriaceae_Thermodesulfobacteriaceae_Thermodesulfobacteriaceae
VHS-B5-50_Uncl_Uncl_Uncl

GI-3

Family (Phy-Subphy-Order-Family) (98 families)

ABY1_OD1_WCHB1-58_Uncl_Uncl
Acidobacteria_iii1-15_Uncl_Uncl
Actinobacteria_Acidimicrobidae_Microthrixineae_Microthrixineae
Actinobacteria_Acidimicrobidae_Uncl_Uncl
Actinobacteria_Actinobacteridae_Frankineae_Frankineae
Actinobacteria_Actinobacteridae_Gordoniaceae_Gordoniaceae
Actinobacteria_Actinobacteridae_Micromonosporaceae_Micromonosporaceae
Actinobacteria_Actinobacteridae_Nocardiaceae_Nocardiaceae
Actinobacteria_Actinobacteridae_Propionibacterineae_Propionibacterineae
Actinobacteria_Actinobacteridae_Streptomycineae_Streptomycineae
Actinobacteria_Actinobacteridae_Streptosporangineae_Streptosporangineae
Actinobacteria_Actinobacteridae_Uncl_Uncl
Bacteroidetes_Bacteroidales_Bacteroidales_Bacteroidaceae
Bacteroidetes_Bacteroidales_Bacteroidales_Uncl
Bacteroidetes_Flavobacteriales_Flavobacteriales_Cytophaga_FM
Bacteroidetes_Flavobacteriales_Flavobacteriales_Sporocytophaga_FM
Bacteroidetes_Flexibacterales_Flexibacterales_Roseivirga_FM
Bacteroidetes_FukuN24_Saprospirales_Uncl
Bacteroidetes_PC1-9_Uncl_Uncl
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Bacteroidetes_Saprospirales_Saprospirales_Uncl
Bacteroidetes_Uncl_Uncl_Uncl
Caldithrix_KSB1_Caldithrixales_Caldithrixales_Uncl
Chlorobi_Uncl_Uncl_Uncl
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Cyanobacteria_Calothrix_Calothrix_Calothrix_FM
Cyanobacteria_Chloroplasts_Uncl_Uncl
Cyanobacteria_OS_Type_B_Uncl_Uncl
Cyanobacteria_Stigonematales_Stigonematales_Uncl
Firmicutes_Acidaminococcaceae_Acidaminococcaceae_Acidaminococcaceae
Firmicutes_Bacilli_Halobacillus_Halobacillus_FM
Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae
Firmicutes_Bacilli_Lactobacillales_Leuconostoc_FM
Firmicutes_Bacilli_Lactobacillales_Streptococcaceae
Firmicutes_Bacilli_Lactobacillales_Uncl
Firmicutes_Bacilli_Marinococcus_Marinococcus_FM
Firmicutes_Bacilli_Staphylococcaceae_Staphylococcaceae
Firmicutes_Bacilli_Uncl_Uncl
Firmicutes_Clostridia_Clostridiales_Ruminococcus_FM
Firmicutes_Clostridia_Clostridiales_Uncl
Firmicutes_Mollicutes_Uncl_Uncl
OP10_CH21_Uncl_Uncl
OP10_CL500-48_Uncl_Uncl
OP10_SJA-22_Uncl_Uncl
OP10_Uncl_Uncl_Uncl
Planctomycetes_Planctomycetacia_Gemmatales_Gemmata_FM
Planctomycetes_Planctomycetacia_Planctomycetales_Uncl
Poribacteria_Uncl_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_Acetobacterales_Acetobacteraceae
Proteobacteria_Alphaproteobacteria_Aurantimonadaceae_Aurantimonadaceae
Proteobacteria_Alphaproteobacteria_Azospirillaceae_Azospirillaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Bradyrhizobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Hyphomicrobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Rhodoplanaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Xanthobacteraceae
Proteobacteria_Alphaproteobacteria_Caedibacteraceae_Caedibacteraceae
Proteobacteria_Alphaproteobacteria_Caulobacterales_Brevundimonas_FM
Proteobacteria_Alphaproteobacteria_Caulobacterales_Uncl
Proteobacteria_Alphaproteobacteria_Consistiales_SAR11_FM
Proteobacteria_Alphaproteobacteria_Phyllobacteriaceae_Phyllobacteriaceae
Proteobacteria_Alphaproteobacteria_Rhizobiaceae_Rhizobiaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Hyphomonadaceae
Proteobacteria_Alphaproteobacteria_Rickettsiales_Uncl
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Porphyrobacter_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingobium_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonadaceae
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonas_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Uncl
Proteobacteria_Alphaproteobacteria_Uncl_Uncl
Proteobacteria_Deltaproteobacteria_Desulfobacteraceae_Desulfobacteraceae
Proteobacteria_Deltaproteobacteria_Desulfovibrio_Desulfovibrio_FM
Proteobacteria_Deltaproteobacteria_Geobacter_Geobacter_FM
Proteobacteria_Deltaproteobacteria_Myxococcales_Polyangiaceae
Proteobacteria_Desulfovibrionales_Desulfovibrionales_Desulfovibrionaceae
Proteobacteria_Epsilonproteobacteria_Sulfuricurvales_Sulfuricurvaceae
Proteobacteria_Gammaproteobacteria_Alcaligenaceae_Alcaligenaceae
Proteobacteria_Gammaproteobacteria_Alteromonadales_Rheinheimeraceae
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Ellin339_Uncl
Proteobacteria_Gammaproteobacteria_endosymbiont_RT7_of_Lyrodus_pedicellatus_Uncl
Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacteriales_Enterobacteriaceae
Proteobacteria_Gammaproteobacteria_Legionellales_Legionella_FM
Proteobacteria_Gammaproteobacteria_Legionellales_Uncl
Proteobacteria_Gammaproteobacteria_Marinobacter_Marinobacter_FM
Proteobacteria_Gammaproteobacteria_Moraxellaceae_Moraxellaceae
Proteobacteria_Gammaproteobacteria_Neisseriales_Chromobacterium_FM
Proteobacteria_Gammaproteobacteria_Nitrosomonadales_Uncl
Proteobacteria_Gammaproteobacteria_Pasteurellaceae_Pasteurellaceae
Proteobacteria_Gammaproteobacteria_Pseudomonadaceae_Pseudomonadaceae
Proteobacteria_Gammaproteobacteria_Rhodocyclales_Accumulibacter_FM
Proteobacteria_Gammaproteobacteria_Sutterellaceae_Sutterellaceae
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Lysobacter_FM
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Uncl
Proteobacteria_Gammaproteobacteria_ZA3605c_Uncl
Verrucomicrobia_Pedosphaerae_Uncl_Uncl

GI-4

Family (Phy-Subphy-Order-Family) (116 families)

Acidobacteria_iii1-15_Uncl_Uncl
Actinobacteria_Acidimicrobidae_JTB31_BD2-10_FM
Actinobacteria_Actinobacteridae_Bifidobacteriaceae_Bifidobacteriaceae
Actinobacteria_Actinobacteridae_Frankineae_Frankineae
Actinobacteria_Actinobacteridae_Micromonosporaceae_Micromonosporaceae
Actinobacteria_Actinobacteridae_Propionibacterineae_Propionibacterineae
Actinobacteria_Actinobacteridae_Streptosporangineae_Streptosporangineae
Actinobacteria_Actinobacteridae_Uncl_Uncl
Actinobacteria_Rubrobacteridae_Rubrobacteraceae_Rubrobacteraceae
Bacteroidetes_Bacteroidales_Bacteroidales_Bacteroidaceae
Bacteroidetes_Flavobacteriales_Flavobacteriales_Flavobacteriaceae
Bacteroidetes_Flavobacteriales_Flavobacteriales_Sporocytophaga_FM
Bacteroidetes_Flexibacterales_Flexibacterales_Roseivirga_FM
Bacteroidetes_LD1_Uncl_Uncl
Bacteroidetes_PC1-9_Uncl_Uncl
Bacteroidetes_Pedobacter_Pedobacter_Pedobacter_FM
Bacteroidetes_RF14_Bacteroidales_Uncl
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Bacteroidetes_Saprospirales_Saprospirales_Uncl
Bacteroidetes_Sphingobacteriaceae_Sphingobacteriaceae_Sphingobacteriaceae
Chlorobi_Uncl_Uncl_Uncl
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Chloroflexi_Dehalococcoidetes_Uncl_Uncl
Cyanobacteria_Calothrix_Calothrix_Calothrix_FM
Cyanobacteria_Chloroplasts_Uncl_Uncl
Cyanobacteria_YS2_Uncl_Uncl
Deferribacteres_Uncl_Uncl_Uncl
Elusimicrobia_TG1_Uncl_Uncl_Uncl
Firmicutes_Acidaminococcaceae_Acidaminococcaceae_Acidaminococcaceae
Firmicutes_Bacilli_Bacillus_Bacillus_FM
Firmicutes_Bacilli_Halobacillus_Halobacillus_FM
Firmicutes_Bacilli_Lactobacillales_Aerococcaceae
Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae
Firmicutes_Bacilli_Lactobacillales_Streptococcaceae
Firmicutes_Bacilli_Lactobacillales_Uncl
Firmicutes_Bacilli_Paenibacillaceae_Paenibacillaceae
Firmicutes_Bacilli_Staphylococcaceae_Staphylococcaceae
Firmicutes_Clostridia_Clostridiales_RF6_FM
Firmicutes_Clostridia_Clostridiales_Uncl
Firmicutes_Clostridia_Peptostreptococcaceae_Peptostreptococcaceae
Firmicutes_Desulfotomaculum_Desulfotomaculum_Desulfotomaculum_FM
Firmicutes_Symbiobacteria_Uncl_Uncl
Firmicutes_Syntrophomonadaceae_Syntrophomonadaceae_Syntrophomonadaceae
Fusobacteria_Fusobacteriaceae_Fusobacteriaceae_Fusobacteriaceae
Haloanaerobiales_Halanaerobiaceae_Halanaerobiaceae_Halanaerobiaceae
OP10_CH21_Uncl_Uncl
Planctomycetes_Planctomycetacia_Planctomycetales_Uncl
Planctomycetes_Planctomycetacia_Rhodopirellulaceae_Rhodopirellulaceae
Poribacteria_Uncl_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_Acetobacterales_Acetobacteraceae
Proteobacteria_Alphaproteobacteria_Acetobacterales_Roseomonas_FM
Proteobacteria_Alphaproteobacteria_alpha_proteobacterium_MBIC1474_Uncl
Proteobacteria_Alphaproteobacteria_Azospirillaceae_Azospirillaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Beijerinckiaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Bradyrhizobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacteriaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Rhodoplanaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Xanthobacteraceae
Proteobacteria_Alphaproteobacteria_Caedibacteraceae_Caedibacteraceae
Proteobacteria_Alphaproteobacteria_Caulobacterales_Brevundimonas_FM
Proteobacteria_Alphaproteobacteria_Caulobacterales_Uncl
Proteobacteria_Alphaproteobacteria_Phyllobacteriaceae_Phyllobacteriaceae
Proteobacteria_Alphaproteobacteria_Rhizobiaceae_Rhizobiaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Hyphomonadaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacter_FM
Proteobacteria_Alphaproteobacteria_Rhodobacterales_S36_FM
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Uncl
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Porphyrobacter_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingobium_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonas_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Uncl
Proteobacteria_Alphaproteobacteria_Uncl_Uncl
Proteobacteria_Deltaproteobacteria_Bdellovibrio_Bdellovibrio_FM
Proteobacteria_Deltaproteobacteria_Desulfobacterium_Desulfobacterium_FM
Proteobacteria_Deltaproteobacteria_Desulfovibrio_Desulfovibrio_FM
Proteobacteria_Deltaproteobacteria_Myxococcales_Polyangiaceae
Proteobacteria_Epsilonproteobacteria_Arcobacteraceae_Arcobacteraceae
Proteobacteria_Epsilonproteobacteria_Sulfuricurvales_Sulfuricurvaceae
Proteobacteria_Gammaproteobacteria_Alcaligenaceae_Alcaligenaceae
Proteobacteria_Gammaproteobacteria_Alteromonadales_Colwelliaceae
Proteobacteria_Gammaproteobacteria_Alteromonadales_Rheinheimeraceae
Proteobacteria_Gammaproteobacteria_bacterium_Ellin6067_Uncl
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Ellin339_Uncl
Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacteriales_Enterobacteriaceae
Proteobacteria_Gammaproteobacteria_environmental_sequence_ZA3913c_FM
Proteobacteria_Gammaproteobacteria_Halomonadaceae_Halomonadaceae
Proteobacteria_Gammaproteobacteria_Hydrogenophilales_Petrobacter_FM
Proteobacteria_Gammaproteobacteria_Legionellales_Legionella_FM
Proteobacteria_Gammaproteobacteria_Legionellales_Uncl
Proteobacteria_Gammaproteobacteria_Methylococcaceae_Methylococcaceae
Proteobacteria_Gammaproteobacteria_Methylophaga_Methylophaga_FM
Proteobacteria_Gammaproteobacteria_Methylophilales_Methylophilus_FM
Proteobacteria_Gammaproteobacteria_Methylophilales_Uncl
Proteobacteria_Gammaproteobacteria_Moraxellaceae_Moraxellaceae
Proteobacteria_Gammaproteobacteria_Oceanospirillales_Marinobacterium_FM
Proteobacteria_Gammaproteobacteria_Oceanospirillales_Uncl
Proteobacteria_Gammaproteobacteria_Pasteurellaceae_Pasteurellaceae
Proteobacteria_Gammaproteobacteria_Pseudomonadaceae_Pseudomonadaceae
Proteobacteria_Gammaproteobacteria_SBR1001_Uncl
Proteobacteria_Gammaproteobacteria_Sutterellaceae_Sutterellaceae
Proteobacteria_Gammaproteobacteria_Thiotrichales_Thiothrix_FM
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Vibrionaceae_Vibrionaceae
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Frateuria_FM
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Lysobacter_FM
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Uncl
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Xylella_FM
Proteobacteria_Gammaproteobacteria_ZA3605c_Uncl
Spirochaetes_S_aurantia_Spirochaetales_Uncl
Thermi_Thermales_Thermales_Meiothermaceae
Thermi_Thermales_Thermales_Thermaceae
WS3_Sediment-1_Uncl_Uncl

GI-5

Family (Phy-Subphy-Order-Family) (132 families)

ABY1_OD1_WCHB1-58_Uncl_Uncl
Acidobacteria_Chloracidobacteria_Uncl_Uncl
Acidobacteria_iii1-15_Uncl_Uncl
Acidobacteria_Solibacteres_Solibacteraceae_Solibacteraceae
Acidobacteria_Solibacteres_Uncl_Uncl
Actinobacteria_Acidimicrobidae_JTB31_BD2-10_FM
Actinobacteria_Acidimicrobidae_Uncl_Uncl
Actinobacteria_Actinobacteridae_Bifidobacteriaceae_Bifidobacteriaceae
Actinobacteria_Actinobacteridae_Frankineae_Frankineae
Actinobacteria_Actinobacteridae_Gordoniaceae_Gordoniaceae
Actinobacteria_Actinobacteridae_Micromonosporaceae_Micromonosporaceae
Actinobacteria_Actinobacteridae_Propionibacterineae_Propionibacterineae
Actinobacteria_Actinobacteridae_Streptosporangineae_Streptosporangineae
Actinobacteria_Actinobacteridae_Uncl_Uncl
Actinobacteria_Rubrobacteridae_Rubrobacteraceae_Rubrobacteraceae
Bacteroidetes_Bacteroidales_Bacteroidales_Bacteroidaceae
Bacteroidetes_Bacteroidales_Bacteroidales_Parabacteroidaceae
Bacteroidetes_Bacteroidales_Bacteroidales_Proteophilaceae
Bacteroidetes_Bacteroidales_Bacteroidales_Uncl
Bacteroidetes_Flavobacteriales_Flavobacteriales_Cytophaga_FM
Bacteroidetes_Flavobacteriales_Flavobacteriales_Flavobacteriaceae
Bacteroidetes_Flavobacteriales_Flavobacteriales_Sporocytophaga_FM
Bacteroidetes_Flexibacterales_Flexibacterales_Roseivirga_FM
Bacteroidetes_Hymenobacterales_Hymenobacterales_Hymenobacteraceae
Bacteroidetes_LD1_Uncl_Uncl
Bacteroidetes_Pedobacter_Pedobacter_Pedobacter_FM
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Bacteroidetes_Saprospirales_Saprospirales_Uncl
Bacteroidetes_Uncl_Uncl_Uncl
Caldithrix_KSB1_Caldithrixales_Caldithrixales_Uncl
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Chloroflexi_Chloroflexi-4_Uncl_Uncl
Cyanobacteria_Calothrix_Calothrix_Calothrix_FM
Cyanobacteria_Chloroplasts_Uncl_Uncl
Cyanobacteria_Leptolyngbya_Leptolyngbya_Leptolyngbya_FM
Cyanobacteria_OS_Type_B_Uncl_Uncl
Cyanobacteria_Stigonematales_Stigonematales_Uncl
Cyanobacteria_Uncl_Uncl_Uncl
Deferribacteres_Uncl_Uncl_Uncl
Firmicutes_Bacilli_Halobacillus_Halobacillus_FM
Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae
Firmicutes_Bacilli_Lactobacillales_Leuconostoc_FM
Firmicutes_Bacilli_Lactobacillales_Streptococcaceae
Firmicutes_Bacilli_Lactobacillales_Uncl
Firmicutes_Bacilli_Staphylococcaceae_Staphylococcaceae
Firmicutes_Bacilli_Uncl_Uncl
Firmicutes_Clostridia_Catabacter_Catabacter_FM
Firmicutes_Clostridia_Clostridiales_Anaerofilum_FM
Firmicutes_Clostridia_Clostridiales_Coprococcus_FM
Firmicutes_Clostridia_Clostridiales_RF6_FM
Firmicutes_Clostridia_Clostridiales_rRNA157_FM
Firmicutes_Clostridia_Clostridiales_Uncl
Firmicutes_Clostridia_Peptostreptococcaceae_Peptostreptococcaceae
Firmicutes_Desulfotomaculum_Desulfotomaculum_Desulfotomaculum_FM
Firmicutes_Syntrophomonadaceae_Syntrophomonadaceae_Syntrophomonadaceae
Fusobacteria_Fusobacteriaceae_Fusobacteriaceae_Fusobacteriaceae
Fusobacteria_Leptotrichales_Leptotrichales_Leptotrichiaceae
Haloanaerobiales_Halanaerobiaceae_Halanaerobiaceae_Halanaerobiaceae
Marine_group_AA714017_Uncl_Uncl
OP10_CL500-48_Uncl_Uncl
Planctomycetes_Planctomycetacia_Gemmatales_Gemmata_FM
Planctomycetes_Planctomycetacia_Gemmatales_Uncl
Planctomycetes_Planctomycetacia_Planctomycetales_Uncl
Poribacteria_Uncl_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_Acetobacterales_Acetobacteraceae
Proteobacteria_Alphaproteobacteria_alpha_proteobacterium_MBIC1474_Uncl
Proteobacteria_Alphaproteobacteria_Azospirillaceae_Azospirillaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Beijerinckiaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Bradyrhizobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacteriaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Rhodoplanaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Xanthobacteraceae
Proteobacteria_Alphaproteobacteria_Caedibacteraceae_Caedibacteraceae
Proteobacteria_Alphaproteobacteria_Caulobacterales_Brevundimonas_FM
Proteobacteria_Alphaproteobacteria_Caulobacterales_Uncl
Proteobacteria_Alphaproteobacteria_Consistiales_SAR11_FM
Proteobacteria_Alphaproteobacteria_Phyllobacteriaceae_Phyllobacteriaceae
Proteobacteria_Alphaproteobacteria_Pseudochrobactrum_Pseudochrobactrum_FM
Proteobacteria_Alphaproteobacteria_Rhizobiaceae_Rhizobiaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Hyphomonadaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacter_FM
Proteobacteria_Alphaproteobacteria_Rickettsiales_Uncl
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Porphyrobacter_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingobium_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonas_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingosinicella_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Uncl
Proteobacteria_Alphaproteobacteria_Uncl_Uncl
Proteobacteria_Deltaproteobacteria_Bdellovibrio_Bdellovibrio_FM
Proteobacteria_Deltaproteobacteria_Desulfovibrio_Desulfovibrio_FM
Proteobacteria_Deltaproteobacteria_Myxococcales_Polyangiaceae
Proteobacteria_Epsilonproteobacteria_Arcobacteraceae_Arcobacteraceae
Proteobacteria_Epsilonproteobacteria_Sulfuricurvales_Sulfuricurvaceae
Proteobacteria_Epsilonproteobacteria_Sulfurovumales_Sulfurovumaceae
Proteobacteria_Gammaproteobacteria_Alcaligenaceae_Alcaligenaceae
Proteobacteria_Gammaproteobacteria_Alteromonadales_Rheinheimeraceae
Proteobacteria_Gammaproteobacteria_bacterium_Ellin6067_Uncl
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Chromatiaceae_Chromatiaceae
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Ellin339_Uncl
Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacteriales_Enterobacteriaceae
Proteobacteria_Gammaproteobacteria_environmental_sequence_CHAB-I-7_FM
Proteobacteria_Gammaproteobacteria_Halomonadaceae_Halomonadaceae
Proteobacteria_Gammaproteobacteria_Legionellales_Legionella_FM
Proteobacteria_Gammaproteobacteria_Legionellales_Uncl
Proteobacteria_Gammaproteobacteria_Marinobacter_Marinobacter_FM
Proteobacteria_Gammaproteobacteria_Methylococcaceae_Methylococcaceae

Proteobacteria_Gammaproteobacteria_Methylophilales_Methylophilus_FM
Proteobacteria_Gammaproteobacteria_MND1_GR-WP33-36_FM
Proteobacteria_Gammaproteobacteria_Moraxellaceae_Moraxellaceae
Proteobacteria_Gammaproteobacteria_Neisseriales_Uncl
Proteobacteria_Gammaproteobacteria_Pasteurellaceae_Pasteurellaceae
Proteobacteria_Gammaproteobacteria_Piscirickettsiaceae_Piscirickettsiaceae
Proteobacteria_Gammaproteobacteria_Pseudomonadaceae_Pseudomonadaceae
Proteobacteria_Gammaproteobacteria_Rhodocyclales_Accumulibacter_FM
Proteobacteria_Gammaproteobacteria_SBR1001_Uncl
Proteobacteria_Gammaproteobacteria_Shewanellaceae_Shewanellaceae
Proteobacteria_Gammaproteobacteria_Sutterellaceae_Sutterellaceae
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Vibrionaceae_Vibrionaceae
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Frateuria_FM
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Lysobacter_FM
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Uncl
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Xylella_FM
Proteobacteria_Gammaproteobacteria_ZA3605c_Uncl
Sulfobacilli_Thermaerobacter_Thermaerobacter_Thermaerobacter_FM
Thermi_Thermales_Thermales_Thermaceae
TM6_Uncl_Uncl_Uncl
WS3_Sediment-1_Uncl_Uncl

GI-7A

Family (Phy-Subphy-Order-Family) (74 families)

Acidobacteria_iii1-15_Uncl_Uncl
Actinobacteria_Acidimicrobidae_Microthrixineae_Microthrixineae
Actinobacteria_Actinobacteridae_Actinomycineae_Actinomycineae
Actinobacteria_Actinobacteridae_Frankineae_Frankineae
Actinobacteria_Actinobacteridae_Propionibacterineae_Propionibacterineae
Actinobacteria_Actinobacteridae_Pseudonocardiaceae_Pseudonocardiaceae
Actinobacteria_Actinobacteridae_Streptomycineae_Streptomycineae
Actinobacteria_Actinobacteridae_Streptosporangineae_Streptosporangineae
Actinobacteria_Actinobacteridae_Uncl_Uncl
Actinobacteria_WCHB1-81_Uncl_Uncl
Bacteroidetes_Hymenobacterales_Hymenobacterales_Hymenobacteraceae
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Bacteroidetes_Uncl_Uncl_Uncl
Chlorobi_Uncl_Uncl_Uncl
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Chloroflexi_Dehalococcoidetes_Uncl_Uncl
Cyanobacteria_Chloroplasts_Uncl_Uncl
Cyanobacteria_OS_Type_B_Uncl_Uncl
Cyanobacteria_Uncl_Uncl_Uncl
Cyanobacteria_YS2_Uncl_Uncl
Firmicutes_Bacilli_Halobacillus_Halobacillus_FM
Firmicutes_Bacilli_Lactobacillales_Streptococcaceae
Firmicutes_Bacilli_Staphylococcaceae_Staphylococcaceae
Firmicutes_Bacilli_Uncl_Uncl
Firmicutes_Clostridia_Peptostreptococcaceae_Peptostreptococcaceae
Firmicutes_Syntrophomonadaceae_Syntrophomonadaceae_Syntrophomonadaceae
Haloanaerobiales_Halanaerobiaceae_Halanaerobiaceae_Halanaerobiaceae
Nitrospirae_Thermodesulfovibrionales_Thermodesulfovibrionales_Thermodesulfovibrionaceae
OP10_CH21_Uncl_Uncl
OP10_CL500-48_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_Acetobacterales_Acetobacteraceae
Proteobacteria_Alphaproteobacteria_Acetobacterales_Roseomonas_FM
Proteobacteria_Alphaproteobacteria_Azospirillaceae_Azospirillaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Beijerinckiaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacteriaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Rhodoplanaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Xanthobacteraceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Hyphomonadaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacter_FM
Proteobacteria_Alphaproteobacteria_Rhodobacterales_S36_FM
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Uncl
Proteobacteria_Alphaproteobacteria_Rickettsiales_Uncl
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Porphyrobacter_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingobium_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonas_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Uncl
Proteobacteria_Alphaproteobacteria_Uncl_Uncl
Proteobacteria_Deltaproteobacteria_Geobacter_Geobacter_FM
Proteobacteria_Desulfovibrionales_Desulfovibrionales_Desulfovibrionaceae
Proteobacteria_Epsilonproteobacteria_Arcobacteraceae_Arcobacteraceae
Proteobacteria_Gammaproteobacteria_Alteromonadales_Alteromonas_FM
Proteobacteria_Gammaproteobacteria_bacterium_Ellin6067_Uncl
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacteriales_Enterobacteriaceae
Proteobacteria_Gammaproteobacteria_environmental_sequence_CHAB-I-7_FM
Proteobacteria_Gammaproteobacteria_Halothiobacillaceae_Halothiobacillaceae
Proteobacteria_Gammaproteobacteria_Neisseriales_Chromobacterium_FM
Proteobacteria_Gammaproteobacteria_Pasteurellaceae_Pasteurellaceae
Proteobacteria_Gammaproteobacteria_Ralstoniaceae_Ralstoniaceae
Proteobacteria_Gammaproteobacteria_Rhodocyclales_Accumulibacter_FM
Proteobacteria_Gammaproteobacteria_Rhodocyclales_Thauera_FM
Proteobacteria_Gammaproteobacteria_Spirillaceae_Spirillaceae
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Vibrionaceae_Vibrionaceae
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Uncl
Spirochaetes_Treponemaceae_Treponemaceae_Treponemaceae
Sulfobacilli_Sulfobacillus_Sulfobacillus_Sulfobacillus_FM
Thermi_Thermales_Thermales_Thermaceae
Thermoanaerobacteria_Uncl_Uncl_Uncl
Verrucomicrobia_Pedosphaerae_Uncl_Uncl
Verrucomicrobia_Verrucomicrobiae_Uncl_Uncl

GI-7B

Family (Phy-Subphy-Order-Family) (25 families)

Actinobacteria_Actinobacteridae_Frankineae_Frankineae
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Chlorobi_Uncl_Uncl_Uncl
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Firmicutes_Bacilli_Lactobacillales_Uncl
Firmicutes_Bacilli_Uncl_Uncl
Marine_group_AA714017_Uncl_Uncl
Planctomycetes_Planctomycetacia_Uncl_Uncl
Poribacteria_Uncl_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Oleomonas_Oleomonas_FM
Proteobacteria_Alphaproteobacteria_Rickettsiales_Uncl
Proteobacteria_Deltaproteobacteria_Geobacter_Geobacter_FM
Proteobacteria_Desulfovibrionales_Desulfovibrionales_Desulfovibrionaceae
Proteobacteria_Epsilonproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Alcaligenaceae_Alcaligenaceae
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacteriales_Enterobacteriaceae
Proteobacteria_Gammaproteobacteria_Nitrosomonadales_Uncl
Proteobacteria_Gammaproteobacteria_Ralstoniaceae_Ralstoniaceae
Proteobacteria_Gammaproteobacteria_Spirillaceae_Spirillaceae
Spirochaetes_Spirochaetales_Spirochaetales_Spirochaetaceae
Sulfobacilli_Sulfobacillus_Sulfobacillus_Sulfobacillus_FM

GI-7C

Family (Phy-Subphy-Order-Family) (21 families)

Actinobacteria_Actinobacteridae_Gordoniaceae_Gordoniaceae
Actinobacteria_Actinobacteridae_Rhodococcus_Rhodococcus_FM
Bacteroidetes_Bacteroidales_Bacteroidales_Bacteroidaceae
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Cyanobacteria_Spirulina_Spirulina_Spirulina_FM
Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae
Firmicutes_Clostridia_Catabacter_Catabacter_FM
Firmicutes_Symbiobacteria_Symbiobacterales_Symbiobacterium_FM
Marine_group_AA714017_Uncl_Uncl
Poribacteria_Uncl_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Caulobacterales_Uncl
Proteobacteria_Alphaproteobacteria_Consistiales_SAR11_FM
Proteobacteria_Alphaproteobacteria_Oleomonas_Oleomonas_FM
Proteobacteria_Alphaproteobacteria_Rickettsiales_Uncl
Proteobacteria_Epsilonproteobacteria_Nautilliales_Nautillaceae
Proteobacteria_Epsilonproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
TM7_Uncl_Uncl_Uncl
WS5_Uncl_Uncl_Uncl

GI-7D

Family (Phy-Subphy-Order-Family)

ABY1_OD1_WCHB1-58_Uncl_Uncl
Actinobacteria_Actinobacteridae_Frankineae_Frankineae
Actinobacteria_Actinobacteridae_Gordoniaceae_Gordoniaceae
Actinobacteria_Actinobacteridae_Propionibacterineae_Propionibacterineae
Actinobacteria_Actinobacteridae_Streptomycineae_Streptomycineae
Actinobacteria_Actinobacteridae_Streptosporangineae_Streptosporangineae
Actinobacteria_Actinobacteridae_Uncl_Uncl
Bacteroidetes_RF14_Bacteroidales_Uncl
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Bacteroidetes_Uncl_Uncl_Uncl
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Cyanobacteria_YS2_Uncl_Uncl
Firmicutes_Bacilli_Bacillus_Bacillus_FM
Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae
Firmicutes_Clostridia_Peptostreptococcaceae_Peptostreptococcaceae
Marine_group_AA714017_Uncl_Uncl
Planctomycetes_Planctomycetacia_Planctomycetales_Uncl
Planctomycetes_WPS-1_MB-C2-105_Uncl
Proteobacteria_Alphaproteobacteria_Acetobacterales_Acetobacteraceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacteriaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Rhodoplanaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Xanthobacteraceae
Proteobacteria_Alphaproteobacteria_Caulobacterales_Uncl
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingobium_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonas_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Uncl
Proteobacteria_Alphaproteobacteria_Uncl_Uncl
Proteobacteria_Epsilonproteobacteria_Arcobacteraceae_Arcobacteraceae
Proteobacteria_Epsilonproteobacteria_Sulfuricurvales_Sulfuricurvaceae
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacteriales_Enterobacteriaceae
Proteobacteria_Gammaproteobacteria_Legionellales_Uncl
Proteobacteria_Gammaproteobacteria_Neisseriales_Chromobacterium_FM
Proteobacteria_Gammaproteobacteria_Nitrosomonadales_Uncl
Proteobacteria_Gammaproteobacteria_Pseudomonadaceae_Pseudomonadaceae
Proteobacteria_Gammaproteobacteria_Ralstoniaceae_Ralstoniaceae
Proteobacteria_Gammaproteobacteria_Rhodocyclales_Uncl
Proteobacteria_Gammaproteobacteria_Sutterellaceae_Sutterellaceae
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Uncl
SR1_BD2-14_Uncl_Uncl
Thermi_Thermales_Thermales_Thermaceae
TM7_Uncl_Uncl_Uncl

GI-7F

Family (Phy-Subphy-Order-Family) (36 families)

Actinobacteria_Actinobacteridae_Arthrobacter_Arthrobacter_FM
Actinobacteria_Actinobacteridae_Frankineae_Frankineae
Actinobacteria_Actinobacteridae_Propionibacterineae_Propionibacterineae
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Chlorobi_Uncl_Uncl_Uncl
Cyanobacteria_Calothrix_Calothrix_Calothrix_FM
Firmicutes_Clostridia_Peptostreptococcaceae_Peptostreptococcaceae
Firmicutes_Uncl_Uncl_Uncl
OP10_Uncl_Uncl_Uncl
Planctomycetes_Planctomycetacia_Pirellula_Pirellula_FM
Planctomycetes_Planctomycetacia_Uncl_Uncl
Poribacteria_Uncl_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Beijerinckiaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Rhodoplanaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Xanthobacteraceae
Proteobacteria_Alphaproteobacteria_Caulobacterales_Uncl
Proteobacteria_Alphaproteobacteria_Devosia_Devosia_FM
Proteobacteria_Alphaproteobacteria_Phyllobacteriaceae_Phyllobacteriaceae
Proteobacteria_Alphaproteobacteria_Rhizobiaceae_Rhizobiaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacter_FM
Proteobacteria_Alphaproteobacteria_Uncl_Uncl
Proteobacteria_Epsilonproteobacteria_Arcobacteraceae_Arcobacteraceae
Proteobacteria_Epsilonproteobacteria_Sulfuricurvales_Sulfuricurvaceae
Proteobacteria_Gammaproteobacteria_Alcaligenaceae_Alcaligenaceae
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Legionellales_Uncl
Proteobacteria_Gammaproteobacteria_Moraxellaceae_Moraxellaceae
Proteobacteria_Gammaproteobacteria_Nitrosomonadales_Uncl
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Uncl
Sulfobacilli_Sulfobacillus_Sulfobacillus_Sulfobacillus_FM
Thermi_Thermales_Thermales_Thermaceae
TM7_Uncl_Uncl_Uncl

JPL 8-1

Family (Phy-Subphy-Order-Family) (137 families)

ABY1_OD1_WCHB1-58_Uncl_Uncl
Acidobacteria_iii1-15_Uncl_Uncl
Acidobacteria_iii1-8_Uncl_Uncl
Acidobacteria_Sva0725_Uncl_Uncl
Actinobacteria_Actinobacteridae_Agromyces_Agromyces_FM
Actinobacteria_Actinobacteridae_Brachybacterium_Brachybacterium_FM
Actinobacteria_Actinobacteridae_Brevibacteriaceae_Brevibacteriaceae
Actinobacteria_Actinobacteridae_Curtobacterium_Curtobacterium_FM
Actinobacteria_Actinobacteridae_Frankineae_Frankineae
Actinobacteria_Actinobacteridae_Gordoniaceae_Gordoniaceae
Actinobacteria_Actinobacteridae_Intrasporangiaceae_Intrasporangiaceae
Actinobacteria_Actinobacteridae_Leucobacter_Leucobacter_FM
Actinobacteria_Actinobacteridae_Micromonosporaceae_Micromonosporaceae
Actinobacteria_Actinobacteridae_Propionibacterineae_Propionibacterineae
Actinobacteria_Actinobacteridae_Streptomycineae_Streptomycineae
Actinobacteria_Actinobacteridae_Streptosporangineae_Streptosporangineae
Actinobacteria_Actinobacteridae_Uncl_Uncl
Bacteroidetes_Bacteroidales_Bacteroidales_Bacteroidaceae
Bacteroidetes_Bacteroidales_Bacteroidales_Parabacteroidaceae
Bacteroidetes_Bacteroidales_Bacteroidales_Proteophilaceae
Bacteroidetes_Bacteroidales_Bacteroidales_Uncl
Bacteroidetes_Flavobacteriales_Flavobacteriales_Cytophaga_FM
Bacteroidetes_Flavobacteriales_Flavobacteriales_Flavobacteriaceae
Bacteroidetes_Flavobacteriales_Flavobacteriales_Polaribacter_FM
Bacteroidetes_Flavobacteriales_Flavobacteriales_Sporocytophaga_FM
Bacteroidetes_Hymenobacterales_Hymenobacterales_Hymenobacteraceae
Bacteroidetes_PC1-9_Uncl_Uncl
Bacteroidetes_PHOS-HE21_Flexibacterales_Uncl
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Bacteroidetes_Saprospirales_Saprospirales_Uncl
Bacteroidetes_Sphingobacteriaceae_Sphingobacteriaceae_Sphingobacteriaceae
Bacteroidetes_Uncl_Uncl_Uncl
Caldithrix_KSB1_Caldithrixales_Caldithrixales_Uncl
Chlorobi_Uncl_Uncl_Uncl
Cyanobacteria_Chloroplasts_Uncl_Uncl
Cyanobacteria_Leptolyngbya_Leptolyngbya_Leptolyngbya_FM
Cyanobacteria_OS_Type_B_Uncl_Uncl
Cyanobacteria_Oscillatoriales_Oscillatoriales__Planktothrix_FM
Cyanobacteria_Uncl_Uncl_Uncl
Firmicutes_Acidaminococcaceae_Acidaminococcaceae_Acidaminococcaceae
Firmicutes_Bacilli_Bacillus_Bacillus_FM
Firmicutes_Bacilli_Exiguobacterium_Exiguobacterium_FM
Firmicutes_Bacilli_Halobacillus_Halobacillus_FM
Firmicutes_Bacilli_Lactobacillales_Aerococcaceae
Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae
Firmicutes_Bacilli_Lactobacillales_Leuconostoc_FM
Firmicutes_Bacilli_Lactobacillales_Streptococcaceae
Firmicutes_Bacilli_Lactobacillales_Uncl
Firmicutes_Bacilli_Paenibacillaceae_Paenibacillaceae
Firmicutes_Bacilli_Staphylococcaceae_Staphylococcaceae
Firmicutes_Bacilli_Uncl_Uncl
Firmicutes_Clostridia_Clostridiales_Clostridiaceae
Firmicutes_Clostridia_Clostridiales_Clostridium_FM
Firmicutes_Clostridia_Clostridiales_Eubacterium_FM
Firmicutes_Clostridia_Clostridiales_Faecalibacterium_FM
Firmicutes_Clostridia_Clostridiales_Gracilibacter_FM
Firmicutes_Clostridia_Clostridiales_rRNA157_FM
Firmicutes_Clostridia_Clostridiales_Ruminococcus_FM
Firmicutes_Clostridia_Clostridiales_Uncl
Firmicutes_Clostridia_Peptostreptococcaceae_Peptostreptococcaceae
Firmicutes_Clostridia_Uncl_Uncl
Fusobacteria_Ilyobacter_Ilyobacter_Ilyobacter_FM
Haloanaerobiales_Halanaerobiaceae_Halanaerobiaceae_Halanaerobiaceae
OP10_Uncl_Uncl_Uncl
OP9_JS1_JS1_Uncl_Uncl
Planctomycetes_agg27_ARKCH2Br2-76_Uncl

Planctomycetes_Planctomycetacia_Planctomycetales_Uncl
Poribacteria_Uncl_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_Acetobacterales_Acetobacteraceae
Proteobacteria_Alphaproteobacteria_Acetobacterales_Roseomonas_FM
Proteobacteria_Alphaproteobacteria_Azospirillaceae_Azospirillaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Bradyrhizobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacteriaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Rhodoplanaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Xanthobacteraceae
Proteobacteria_Alphaproteobacteria_Caedibacteraceae_Caedibacteraceae
Proteobacteria_Alphaproteobacteria_Caulobacterales_Uncl
Proteobacteria_Alphaproteobacteria_Devosia_Devosia_FM
Proteobacteria_Alphaproteobacteria_KF-JG30-B3_Uncl
Proteobacteria_Alphaproteobacteria_Oleomonas_Oleomonas_FM
Proteobacteria_Alphaproteobacteria_Phyllobacteriaceae_Phyllobacteriaceae
Proteobacteria_Alphaproteobacteria_Rhizobiaceae_Rhizobiaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Hyphomonadaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacter_FM
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodovulum_FM
Proteobacteria_Alphaproteobacteria_Rhodobacterales_S36_FM
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Uncl
Proteobacteria_Alphaproteobacteria_Schlegelella_Schlegelella_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Porphyrobacter_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingobium_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonas_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingopyxis_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Uncl
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Zymomonas_FM
Proteobacteria_Alphaproteobacteria_Uncl_Uncl
Proteobacteria_Deltaproteobacteria_Desulfobacterium_Desulfobacterium_FM
Proteobacteria_Deltaproteobacteria_Desulfovibrio_Desulfovibrio_FM
Proteobacteria_Desulfovibrionales_Desulfovibrionales_Desulfovibrionaceae
Proteobacteria_Epsilonproteobacteria_Arcobacteraceae_Arcobacteraceae
Proteobacteria_Epsilonproteobacteria_Sulfuricurvales_Sulfuricurvaceae
Proteobacteria_Gammaproteobacteria_Alcaligenaceae_Alcaligenaceae
Proteobacteria_Gammaproteobacteria_Alteromonadales_Rheinheimeraceae
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Ellin339_Uncl
Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacteriales_Enterobacteriaceae
Proteobacteria_Gammaproteobacteria_environmental_sequence_ZA3913c_FM
Proteobacteria_Gammaproteobacteria_Gammaproteobacteria_Uncl
Proteobacteria_Gammaproteobacteria_Halomonadaceae_Halomonadaceae
Proteobacteria_Gammaproteobacteria_Legionellales_Legionella_FM
Proteobacteria_Gammaproteobacteria_Legionellales_Uncl
Proteobacteria_Gammaproteobacteria_Methylophaga_Methylophaga_FM
Proteobacteria_Gammaproteobacteria_Methylophilales_Uncl
Proteobacteria_Gammaproteobacteria_Moraxellaceae_Moraxellaceae
Proteobacteria_Gammaproteobacteria_Nitrosomonadales_Uncl
Proteobacteria_Gammaproteobacteria_Pasteurellaceae_Pasteurellaceae
Proteobacteria_Gammaproteobacteria_Pseudomonadaceae_Pseudomonadaceae
Proteobacteria_Gammaproteobacteria_Ralstoniaceae_Ralstoniaceae
Proteobacteria_Gammaproteobacteria_Rhodocyclales_Accumulibacter_FM
Proteobacteria_Gammaproteobacteria_Rhodocyclales_Azoarcus_FM
Proteobacteria_Gammaproteobacteria_Rhodocyclales_beta_FM
Proteobacteria_Gammaproteobacteria_Rhodocyclales_Uncl
Proteobacteria_Gammaproteobacteria_SBR1001_Uncl
Proteobacteria_Gammaproteobacteria_Shewanellaceae_Shewanellaceae
Proteobacteria_Gammaproteobacteria_Sutterellaceae_Sutterellaceae
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Vibrionaceae_Vibrionaceae
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Lysobacter_FM
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Uncl
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Xylella_FM
Thermi_Thermales_Thermales_Thermaceae
Thermoanaerobacteria_Uncl_Uncl_Uncl
Thermotogae_Fervidobacteriaceae_Fervidobacteriaceae_Fervidobacteriaceae
Verrucomicrobia_Pedosphaerae_Uncl_Uncl
VHS-B5-50_Uncl_Uncl_Uncl

JPL 8-2

Family (Phy-Subphy-Order-Family) (25 families)
Actinobacteria_Actinobacteridae_Arthrobacter_Arthrobacter_FM
Actinobacteria_Actinobacteridae_Rhodococcus_Rhodococcus_FM
Actinobacteria_Rubrobacteridae_Thermoleiphilaceae_Thermoleiphilaceae
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Chloroflexi_Chloroflexi-4_Uncl_Uncl
Cyanobacteria_Chloroplasts_Uncl_Uncl
Firmicutes_Acidaminococcaceae_Acidaminococcaceae_Acidaminococcaceae
Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae
Firmicutes_Bacilli_Lactobacillales_Streptococcaceae
Firmicutes_Bacilli_Uncl_Uncl
Firmicutes_Clostridia_Clostridiales_Uncl
Firmicutes_Clostridia_Peptostreptococcaceae_Peptostreptococcaceae
Firmicutes_Mollicutes_Uncl_Uncl
Nitrospirae_Nitrospirales_Nitrospirales_Uncl
Planctomycetes_Planctomycetacia_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_KF-JG30-B3_Uncl
Proteobacteria_Alphaproteobacteria_Rickettsiales_Uncl
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacteriales_Enterobacteriaceae
Proteobacteria_Gammaproteobacteria_Pseudomonadaceae_Pseudomonadaceae
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
Sulfobacilli_Sulfobacillus_Sulfobacillus_Sulfobacillus_FM
ZB3_Rs-J96_Uncl_Uncl

JPL 8-3

Family (Phy-Subphy-Order-Family) (25 families)

Actinobacteria_Actinobacteridae_Propionibacterineae_Propionibacterineae
Actinobacteria_Rubrobacteridae_Thermoleiphilaceae_Thermoleiphilaceae
Actinobacteria_WCHB1-81_Uncl_Uncl
Chloroflexi_Chloroflexi-4_Uncl_Uncl
Firmicutes_Bacilli_Bacillus_thermocloaceae_Bacillus_thermocloaceae
Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae
Firmicutes_Bacilli_Lactobacillales_Streptococcaceae
Firmicutes_Bacilli_Paenibacillaceae_Paenibacillaceae
Firmicutes_Mollicutes_Uncl_Uncl
Nitrospirae_Nitrospirales_Nitrospirales_Uncl
Planctomycetes_Planctomycetacia_Gemmatales_Gemmata_FM
Planctomycetes_Planctomycetacia_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_Acetobacterales_Acetobacteraceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Defluvicoccus_Defluvicoccus_FM
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacter_FM
Proteobacteria_Alphaproteobacteria_Schlegelella_Schlegelella_FM
Proteobacteria_Deltaproteobacteria_Desulfobacterium_Desulfobacterium_FM
Proteobacteria_Epsilonproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Legionellales_Legionella_FM
Proteobacteria_Gammaproteobacteria_Oxalobacteraceae_Oxalobacteraceae
Sulfobacilli_Sulfobacillus_Sulfobacillus_Sulfobacillus_FM

GI-10

Family (Phy-Subphy-Order-Family) (76 families)

Acidobacteria_Solibacteres_Solibacteraceae_Solibacteraceae
Actinobacteria_Acidimicrobidae_ML316M-15_Uncl
Actinobacteria_Acidimicrobidae_Uncl_Uncl
Actinobacteria_Actinobacteridae_Agromyces_Agromyces_FM
Actinobacteria_Actinobacteridae_Frankineae_Frankineae
Actinobacteria_Actinobacteridae_Gordoniaceae_Gordoniaceae
Actinobacteria_Actinobacteridae_Intrasporangiaceae_Intrasporangiaceae
Actinobacteria_Actinobacteridae_Micromonosporaceae_Micromonosporaceae
Actinobacteria_Actinobacteridae_Propionibacterineae_Propionibacterineae
Actinobacteria_Actinobacteridae_Rhodococcus_Rhodococcus_FM
Actinobacteria_Actinobacteridae_Streptomycineae_Streptomycineae
Actinobacteria_Actinobacteridae_Streptosporangineae_Streptosporangineae
Actinobacteria_Actinobacteridae_Uncl_Uncl
Bacteroidetes_Bacteroidales_Bacteroidales_Bacteroidaceae
Bacteroidetes_Bacteroidales_Bacteroidales_Proteophilaceae
Bacteroidetes_Flavobacteriales_Flavobacteriales_Flavobacteriaceae
Bacteroidetes_Flavobacteriales_Flavobacteriales_Polaribacter_FM
Bacteroidetes_Flavobacteriales_Flavobacteriales_Sporocytophaga_FM
Bacteroidetes_Hymenobacterales_Hymenobacterales_Hymenobacteraceae
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Bacteroidetes_Saprospirales_Saprospirales_Uncl
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Cyanobacteria_Chloroplasts_Uncl_Uncl
Deferribacteres_Uncl_Uncl_Uncl
Firmicutes_Bacilli_Bacillus_Bacillus_FM
Firmicutes_Bacilli_Halobacillus_Halobacillus_FM
Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae
Firmicutes_Bacilli_Lactobacillales_Streptococcaceae
Firmicutes_Bacilli_Lactobacillales_Uncl
Firmicutes_Bacilli_Paenibacillaceae_Paenibacillaceae
Firmicutes_Bacilli_Staphylococcaceae_Staphylococcaceae
Firmicutes_Clostridia_Clostridiales_Anaerofilum_FM
Firmicutes_Clostridia_Clostridiales_Eubacterium_FM
Firmicutes_Clostridia_Clostridiales_Uncl
Firmicutes_Clostridia_Peptostreptococcaceae_Peptostreptococcaceae
Firmicutes_Mollicutes_Acholeplasmatales_Uncl
Firmicutes_Mollicutes_Uncl_Uncl
Marine_group_AA714017_Uncl_Uncl
OP10_CH21_Uncl_Uncl
OP10_Uncl_Uncl_Uncl
Planctomycetes_Planctomycetacia_Planctomycetales_Uncl
Proteobacteria_Alphaproteobacteria_Acetobacterales_Acetobacteraceae
Proteobacteria_Alphaproteobacteria_Aurantimonadaceae_Aurantimonadaceae
Proteobacteria_Alphaproteobacteria_Azospirillaceae_Azospirillaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Bradyrhizobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Rhodoplanaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Caedibacteraceae_Caedibacteraceae
Proteobacteria_Alphaproteobacteria_Rhizobiaceae_Rhizobiaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Hyphomonadaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacter_FM
Proteobacteria_Alphaproteobacteria_Schlegelella_Schlegelella_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonas_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Uncl
Proteobacteria_Alphaproteobacteria_Uncl_Uncl
Proteobacteria_Deltaproteobacteria_JG37-AG-2_Uncl
Proteobacteria_Desulfovibrionales_Desulfovibrionales_Desulfovibrionaceae
Proteobacteria_Epsilonproteobacteria_Sulfuricurvales_Sulfuricurvaceae
Proteobacteria_Epsilonproteobacteria_Sulfurospirillaceae_Sulfurospirillaceae
Proteobacteria_Gammaproteobacteria_Alcaligenaceae_Alcaligenaceae
Proteobacteria_Gammaproteobacteria_Alteromonadales_Rheinheimeraceae
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacteriales_Enterobacteriaceae
Proteobacteria_Gammaproteobacteria_Moraxellaceae_Moraxellaceae
Proteobacteria_Gammaproteobacteria_Nitrosomonadales_Uncl
Proteobacteria_Gammaproteobacteria_Pasteurellaceae_Pasteurellaceae
Proteobacteria_Gammaproteobacteria_Pseudomonadaceae_Pseudomonadaceae
Proteobacteria_Gammaproteobacteria_Rhodocyclales_Accumulibacter_FM
Proteobacteria_Gammaproteobacteria_Sutterellaceae_Sutterellaceae
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Uncl
Spirochaetes_Treponemaceae_Treponemaceae_Treponemaceae
Sulfobacilli_Sulfobacillus_Sulfobacillus_Sulfobacillus_FM
Thermoanaerobacteria_Uncl_Uncl_Uncl

GI-11

Family (Phy-Subphy-Order-Family) (106 families)

Acidobacteria_Chloracidobacteria_Uncl_Uncl
Acidobacteria_Solibacteres_Solibacteraceae_Solibacteraceae
Actinobacteria_Actinobacteridae_Arthrobacter_Arthrobacter_FM
Actinobacteria_Actinobacteridae_Nocardiaceae_Nocardiaceae
Actinobacteria_Actinobacteridae_Propionibacterineae_Propionibacterineae
Actinobacteria_Actinobacteridae_Streptosporangineae_Streptosporangineae
Actinobacteria_Rubrobacteridae_Rubrobacteraceae_Rubrobacteraceae
Bacteroidetes_Bacteroidales_Bacteroidales_Uncl
Bacteroidetes_Flavobacteriales_Flavobacteriales_Sporocytophaga_FM
Bacteroidetes_PC1-9_Uncl_Uncl
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Bacteroidetes_Saprospirales_Saprospirales_Uncl
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Coprothermobacteria_Uncl_Uncl_Uncl
Cyanobacteria_Calothrix_Calothrix_Calothrix_FM
Cyanobacteria_Chloroplasts_Uncl_Uncl
Cyanobacteria_Leptolyngbya_Leptolyngbya_Leptolyngbya_FM
Cyanobacteria_Oscillatoriales_Oscillatoriales__Planktothrix_FM
Cyanobacteria_Oscillatoriales_Oscillatoriales_Uncl
Cyanobacteria_Stigonematales_Stigonematales_Uncl
Cyanobacteria_Uncl_Uncl_Uncl
Deferribacteres_Uncl_Uncl_Uncl
Firmicutes_Bacilli_Ammoniphilus_Ammoniphilus_FM
Firmicutes_Bacilli_Bacillus_Bacillus_FM
Firmicutes_Bacilli_Exiguobacterium_Exiguobacterium_FM
Firmicutes_Bacilli_Halobacillus_Halobacillus_FM
Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae
Firmicutes_Bacilli_Lactobacillales_Leuconostoc_FM
Firmicutes_Bacilli_Lactobacillales_Streptococcaceae
Firmicutes_Bacilli_Lactobacillales_Uncl
Firmicutes_Bacilli_Marinococcus_Marinococcus_FM

Firmicutes_Bacilli_Paenibacillaceae_Paenibacillaceae
Firmicutes_Bacilli_Staphylococcaceae_Staphylococcaceae
Firmicutes_Bacilli_Uncl_Uncl
Firmicutes_Clostridia_Clostridiales_Clostridiaceae
Firmicutes_Clostridia_Clostridiales_Coprococcus_FM
Firmicutes_Clostridia_Clostridiales_Ruminococcus_FM
Firmicutes_Clostridia_Peptostreptococcaceae_Peptostreptococcaceae
Firmicutes_Mollicutes_Acholeplasmatales_Uncl
Haloanaerobiales_Halanaerobiaceae_Halanaerobiaceae_Halanaerobiaceae
Marine_group_AA714017_Uncl_Uncl
OP10_SJA-22_Uncl_Uncl
OP10_Uncl_Uncl_Uncl
Planctomycetes_Planctomycetacia_Gemmatales_Gemmata_FM
Planctomycetes_Planctomycetacia_Planctomycetales_Uncl
Proteobacteria_Alphaproteobacteria_Acetobacterales_Acetobacteraceae
Proteobacteria_Alphaproteobacteria_Acetobacterales_Roseomonas_FM
Proteobacteria_Alphaproteobacteria_Azospirillaceae_Azospirillaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Bradyrhizobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Hyphomicrobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacteriaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Pleomorphomonas_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Rhodoplanaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Xanthobacteraceae
Proteobacteria_Alphaproteobacteria_Caedibacteraceae_Caedibacteraceae
Proteobacteria_Alphaproteobacteria_Caulobacterales_Brevundimonas_FM
Proteobacteria_Alphaproteobacteria_Caulobacterales_Uncl
Proteobacteria_Alphaproteobacteria_Oleomonas_Oleomonas_FM
Proteobacteria_Alphaproteobacteria_Phyllobacteriaceae_Phyllobacteriaceae
Proteobacteria_Alphaproteobacteria_Rhizobiaceae_Rhizobiaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Hyphomonadaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacter_FM
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Uncl
Proteobacteria_Alphaproteobacteria_Rickettsiales_Uncl
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Porphyrobacter_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingobium_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonas_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Uncl
Proteobacteria_Alphaproteobacteria_Uncl_Uncl
Proteobacteria_Deltaproteobacteria_Desulfovibrio_Desulfovibrio_FM
Proteobacteria_Deltaproteobacteria_Myxococcales_Polyangiaceae
Proteobacteria_Desulfovibrionales_Desulfovibrionales_Desulfovibrionaceae
Proteobacteria_Epsilonproteobacteria_Sulfuricurvales_Sulfuricurvaceae
Proteobacteria_Gammaproteobacteria_Alcaligenaceae_Alcaligenaceae
Proteobacteria_Gammaproteobacteria_Alteromonadales_Alteromonas_FM
Proteobacteria_Gammaproteobacteria_Alteromonadales_Rheinheimeraceae
Proteobacteria_Gammaproteobacteria_bacterium_Ellin6067_Uncl
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Ellin339_Uncl
Proteobacteria_Gammaproteobacteria_endosymbiont_RT7_of_Lyrodus_pedicellatus_Uncl
Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacteriales_Enterobacteriaceae
Proteobacteria_Gammaproteobacteria_Legionellales_Legionella_FM
Proteobacteria_Gammaproteobacteria_Legionellales_Uncl
Proteobacteria_Gammaproteobacteria_Moraxellaceae_Moraxellaceae
Proteobacteria_Gammaproteobacteria_Neisseriales_Chromobacterium_FM
Proteobacteria_Gammaproteobacteria_Neisseriales_Uncl
Proteobacteria_Gammaproteobacteria_Nitrosomonadales_Uncl
Proteobacteria_Gammaproteobacteria_obligately_oligotrophic_bacteria_KI89C_Uncl
Proteobacteria_Gammaproteobacteria_Pasteurellaceae_Pasteurellaceae
Proteobacteria_Gammaproteobacteria_Pseudomonadaceae_Pseudomonadaceae
Proteobacteria_Gammaproteobacteria_Rhodocyclales_Accumulibacter_FM
Proteobacteria_Gammaproteobacteria_Rhodocyclales_beta_FM
Proteobacteria_Gammaproteobacteria_Rhodocyclales_Thauera_FM
Proteobacteria_Gammaproteobacteria_SBR1001_Uncl
Proteobacteria_Gammaproteobacteria_Sutterellaceae_Sutterellaceae
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Lysobacter_FM
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Uncl
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Xylella_FM
Proteobacteria_Gammaproteobacteria_ZA3605c_Uncl
Thermi_Thermales_Thermales_Meiothermaceae
Thermi_Thermales_Thermales_Thermaceae
Verrucomicrobia_Pedosphaerae_Uncl_Uncl

GI-13

Family (Phy-Subphy-Order-Family) (94 families)

Acidobacteria_iii1-15_Uncl_Uncl
Actinobacteria_Actinobacteridae_Frankineae_Frankineae
Actinobacteria_Actinobacteridae_Gordoniaceae_Gordoniaceae
Actinobacteria_Actinobacteridae_Leucobacter_Leucobacter_FM
Actinobacteria_Actinobacteridae_Micromonosporaceae_Micromonosporaceae
Actinobacteria_Actinobacteridae_Propionibacterineae_Propionibacterineae
Actinobacteria_Actinobacteridae_Streptomycineae_Streptomycineae
Bacteroidetes_Bacteroidales_Bacteroidales_Uncl
Bacteroidetes_Flavobacteriales_Flavobacteriales_Flavobacteriaceae
Bacteroidetes_Flavobacteriales_Flavobacteriales_Sporocytophaga_FM
Bacteroidetes_Flexibacterales_Flexibacterales_Algoriphagaceae
Bacteroidetes_Hymenobacterales_Hymenobacterales_Hymenobacteraceae
Bacteroidetes_PC1-9_Uncl_Uncl
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Bacteroidetes_Saprospirales_Saprospirales_Uncl
Bacteroidetes_SHA-94_Bacteroidales_Uncl
Chlorobi_Uncl_Uncl_Uncl
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Cyanobacteria_Chloroplasts_Uncl_Uncl
Cyanobacteria_Uncl_Uncl_Uncl
Firmicutes_Bacilli_Bacillus_Bacillus_FM
Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae
Firmicutes_Bacilli_Lactobacillales_Leuconostoc_FM
Firmicutes_Bacilli_Lactobacillales_Streptococcaceae
Firmicutes_Bacilli_Lactobacillales_Uncl
Firmicutes_Bacilli_Paenibacillaceae_Paenibacillaceae
Firmicutes_Bacilli_Staphylococcaceae_Staphylococcaceae
Firmicutes_Bacilli_Uncl_Uncl
Firmicutes_Clostridia_Clostridiales_Clostridium_FM
Firmicutes_Clostridia_Clostridiales_Uncl
Firmicutes_Clostridia_Peptostreptococcaceae_Peptostreptococcaceae
Firmicutes_Clostridia_Uncl_Uncl
Firmicutes_Mollicutes_Acholeplasmatales_Uncl
Firmicutes_Mollicutes_Uncl_Uncl
Firmicutes_Syntrophomonadaceae_Syntrophomonadaceae_Syntrophomonadaceae
Marine_group_AA714017_Uncl_Uncl
OP10_CL500-48_Uncl_Uncl
OP10_SJA-22_Uncl_Uncl
OP10_Uncl_Uncl_Uncl
OP8_OP8_1_Uncl_Uncl
Planctomycetes_Planctomycetacia_Planctomycetales_Uncl
Planctomycetes_Planctomycetacia_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_alpha_proteobacterium_MBIC1474_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Bradyrhizobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Rhodoplanaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Xanthobacteraceae
Proteobacteria_Alphaproteobacteria_Caulobacterales_Brevundimonas_FM
Proteobacteria_Alphaproteobacteria_Caulobacterales_Uncl
Proteobacteria_Alphaproteobacteria_Labrys_Labrys_FM
Proteobacteria_Alphaproteobacteria_Phyllobacteriaceae_Phyllobacteriaceae
Proteobacteria_Alphaproteobacteria_Rhizobiaceae_Rhizobiaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Hyphomonadaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacter_FM
Proteobacteria_Alphaproteobacteria_Rhodobacterales_S36_FM
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Uncl
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Porphyrobacter_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingobium_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonas_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Uncl
Proteobacteria_Alphaproteobacteria_Uncl_Uncl
Proteobacteria_Deltaproteobacteria_Desulfovibrio_Desulfovibrio_FM
Proteobacteria_Desulfovibrionales_Desulfovibrionales_Desulfovibrionaceae
Proteobacteria_Epsilonproteobacteria_Sulfuricurvales_Sulfuricurvaceae
Proteobacteria_Gammaproteobacteria_Aeromonadaceae_Aeromonadaceae
Proteobacteria_Gammaproteobacteria_Alteromonadales_Rheinheimeraceae
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Ellin339_Uncl
Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacteriales_Enterobacteriaceae
Proteobacteria_Gammaproteobacteria_Halothiobacillaceae_Halothiobacillaceae
Proteobacteria_Gammaproteobacteria_Legionellales_Legionella_FM
Proteobacteria_Gammaproteobacteria_Legionellales_Uncl
Proteobacteria_Gammaproteobacteria_Methylophilales_Methylophilus_FM
Proteobacteria_Gammaproteobacteria_Methylophilales_Uncl
Proteobacteria_Gammaproteobacteria_Moraxellaceae_Moraxellaceae
Proteobacteria_Gammaproteobacteria_Neisseriales_Uncl
Proteobacteria_Gammaproteobacteria_Nitrosomonadales_Uncl
Proteobacteria_Gammaproteobacteria_obligately_oligotrophic_bacteria_KI89C_Uncl
Proteobacteria_Gammaproteobacteria_Oceanospirillales_Oleispira_FM
Proteobacteria_Gammaproteobacteria_Pseudomonadaceae_Pseudomonadaceae
Proteobacteria_Gammaproteobacteria_Rhodocyclales_Uncl
Proteobacteria_Gammaproteobacteria_Sutterellaceae_Sutterellaceae
Proteobacteria_Gammaproteobacteria_Thiotrichales_Thiothrix_FM
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Vibrionaceae_Vibrionaceae
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Lysobacter_FM
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Uncl
Proteobacteria_Gammaproteobacteria_ZA3605c_Uncl
Spirochaetes_Treponemaceae_Treponemaceae_Treponemaceae
Sulfobacilli_Sulfobacillus_Sulfobacillus_Sulfobacillus_FM
Thermi_Thermales_Thermales_Thermaceae
Verrucomicrobia_Pedosphaerae_Uncl_Uncl

GI-14

Family (Phy-Subphy-Order-Family) (81 families)

Acidobacteria_iii1-15_Uncl_Uncl
Actinobacteria_Acidimicrobidae_JTB31_BD2-10_FM
Actinobacteria_Acidimicrobidae_Microthrixineae_Microthrixineae
Actinobacteria_Acidimicrobidae_Uncl_Uncl
Actinobacteria_Actinobacteridae_Actinomycineae_Actinomycineae
Actinobacteria_Actinobacteridae_Agromyces_Agromyces_FM
Actinobacteria_Actinobacteridae_Frankineae_Frankineae
Actinobacteria_Actinobacteridae_Gordoniaceae_Gordoniaceae
Actinobacteria_Actinobacteridae_Intrasporangiaceae_Intrasporangiaceae
Actinobacteria_Actinobacteridae_Micromonosporaceae_Micromonosporaceae
Actinobacteria_Actinobacteridae_Propionibacterineae_Propionibacterineae
Actinobacteria_Actinobacteridae_Pseudonocardiaceae_Pseudonocardiaceae
Actinobacteria_Actinobacteridae_Rhodococcus_Rhodococcus_FM
Actinobacteria_Actinobacteridae_Streptosporangineae_Streptosporangineae
Actinobacteria_Actinobacteridae_Uncl_Uncl
Bacteroidetes_Flexibacterales_Flexibacterales_Roseivirga_FM
Bacteroidetes_Hymenobacterales_Hymenobacterales_Hymenobacteraceae
Bacteroidetes_PC1-9_Uncl_Uncl
Bacteroidetes_Pedobacter_Pedobacter_Pedobacter_FM
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Chloroflexi_Dehalococcoidetes_Uncl_Uncl
Cyanobacteria_Chloroplasts_Uncl_Uncl
Firmicutes_Acidaminococcaceae_Acidaminococcaceae_Acidaminococcaceae
Firmicutes_Bacilli_Bacillus_Bacillus_FM
Firmicutes_Bacilli_Halobacillus_Halobacillus_FM
Firmicutes_Bacilli_Lactobacillales_Aerococcaceae
Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae
Firmicutes_Bacilli_Lactobacillales_Streptococcaceae
Firmicutes_Bacilli_Lactobacillales_Uncl
Firmicutes_Bacilli_Marinococcus_Marinococcus_FM
Firmicutes_Bacilli_Paenibacillaceae_Paenibacillaceae
Firmicutes_Bacilli_Staphylococcaceae_Staphylococcaceae
Firmicutes_Bacilli_Uncl_Uncl
Firmicutes_Clostridia_Clostridiales_Uncl
Firmicutes_Clostridia_Peptostreptococcaceae_Peptostreptococcaceae
Firmicutes_Mollicutes_Clostridium_Clostridium_FM
Firmicutes_Mollicutes_Uncl_Uncl
Firmicutes_Syntrophomonadaceae_Syntrophomonadaceae_Syntrophomonadaceae
Fusobacteria_BU064_Leptotrichales_Uncl
OP10_SJA-22_Uncl_Uncl
OP10_Uncl_Uncl_Uncl
Poribacteria_Uncl_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_Azospirillaceae_Azospirillaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Bradyrhizobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Hyphomicrobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Rhodoplanaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Caedibacteraceae_Caedibacteraceae
Proteobacteria_Alphaproteobacteria_Oleomonas_Oleomonas_FM
Proteobacteria_Alphaproteobacteria_Phyllobacteriaceae_Phyllobacteriaceae
Proteobacteria_Alphaproteobacteria_Rhizobiaceae_Rhizobiaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Hyphomonadaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacter_FM
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodovulum_FM
Proteobacteria_Alphaproteobacteria_Schlegelella_Schlegelella_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Porphyrobacter_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingobium_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Uncl
Proteobacteria_Alphaproteobacteria_Uncl_Uncl
Proteobacteria_Deltaproteobacteria_Myxococcales_Uncl
Proteobacteria_Desulfovibrionales_Desulfovibrionales_Desulfovibrionaceae
Proteobacteria_Epsilonproteobacteria_Arcobacteraceae_Arcobacteraceae
Proteobacteria_Epsilonproteobacteria_Sulfuricurvales_Sulfuricurvaceae
Proteobacteria_Gammaproteobacteria_Alteromonadales_Rheinheimeraceae
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_endosymbiont_RT7_of_Lyrodus_pedicellatus_Uncl
Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacteriales_Enterobacteriaceae
Proteobacteria_Gammaproteobacteria_Legionellales_Legionella_FM
Proteobacteria_Gammaproteobacteria_Legionellales_Uncl
Proteobacteria_Gammaproteobacteria_Moraxellaceae_Moraxellaceae
Proteobacteria_Gammaproteobacteria_Nitrosomonadales_Uncl
Proteobacteria_Gammaproteobacteria_Pasteurellaceae_Pasteurellaceae
Proteobacteria_Gammaproteobacteria_Rhodocyclales_Accumulibacter_FM
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Uncl
Proteobacteria_Gammaproteobacteria_ZA3605c_Uncl
Spirochaetes_Treponemaceae_Treponemaceae_Treponemaceae
Verrucomicrobia_Pedosphaerae_Uncl_Uncl

1P Pooled

Family (Phy-Subphy-Order-Family) (170 families)
ABY1_OD1_WCHB1-58_Uncl_Uncl
Acidobacteria_Chloracidobacteria_Uncl_Uncl
Acidobacteria_iii1-15_Uncl_Uncl
Acidobacteria_Solibacteres_Uncl_Uncl
Actinobacteria_Acidimicrobidae_JTB31_BD2-10_FM
Actinobacteria_Acidimicrobidae_Microthrixineae_Microthrixineae
Actinobacteria_Acidimicrobidae_Uncl_Uncl
Actinobacteria_Actinobacteridae_Agromyces_Agromyces_FM
Actinobacteria_Actinobacteridae_Bifidobacteriaceae_Bifidobacteriaceae
Actinobacteria_Actinobacteridae_Curtobacterium_Curtobacterium_FM
Actinobacteria_Actinobacteridae_Frankineae_Frankineae
Actinobacteria_Actinobacteridae_Gordoniaceae_Gordoniaceae
Actinobacteria_Actinobacteridae_Intrasporangiaceae_Intrasporangiaceae
Actinobacteria_Actinobacteridae_Micromonosporaceae_Micromonosporaceae
Actinobacteria_Actinobacteridae_Nocardiaceae_Nocardiaceae
Actinobacteria_Actinobacteridae_Propionibacterineae_Propionibacterineae
Actinobacteria_Actinobacteridae_Pseudonocardiaceae_Pseudonocardiaceae
Actinobacteria_Actinobacteridae_Rhodococcus_Rhodococcus_FM
Actinobacteria_Actinobacteridae_Streptosporangineae_Streptosporangineae
Actinobacteria_Actinobacteridae_Uncl_Uncl
Actinobacteria_Rubrobacteridae_Rubrobacteraceae_Rubrobacteraceae
Actinobacteria_WCHB1-81_Uncl_Uncl
Aquificae_Desulfurobacteria_Uncl_Uncl
Bacteroidetes_Bacteroidales_Bacteroidales_Bacteroidaceae
Bacteroidetes_Bacteroidales_Bacteroidales_Parabacteroidaceae
Bacteroidetes_Bacteroidales_Bacteroidales_Tannerellaceae
Bacteroidetes_Bacteroidales_Bacteroidales_Uncl
Bacteroidetes_Flavobacteriales_Flavobacteriales_Cytophaga_FM
Bacteroidetes_Flavobacteriales_Flavobacteriales_Flavobacteriaceae
Bacteroidetes_Flavobacteriales_Flavobacteriales_Polaribacter_FM
Bacteroidetes_Flavobacteriales_Flavobacteriales_Sporocytophaga_FM
Bacteroidetes_Flexibacterales_Flexibacterales_Algoriphagaceae
Bacteroidetes_Flexibacterales_Flexibacterales_Roseivirga_FM
Bacteroidetes_Hymenobacterales_Hymenobacterales_Hymenobacteraceae
Bacteroidetes_PC1-9_Uncl_Uncl
Bacteroidetes_Pedobacter_Pedobacter_Pedobacter_FM
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Bacteroidetes_Saprospirales_Saprospirales_Uncl
Bacteroidetes_SHA-107_Bacteroidales_Uncl
Bacteroidetes_Sphingobacteriaceae_Sphingobacteriaceae_Sphingobacteriaceae
Bacteroidetes_Uncl_Uncl_Uncl
Caldithrix_KSB1_Caldithrixales_Caldithrixales_Uncl
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Cyanobacteria_Calothrix_Calothrix_Calothrix_FM
Cyanobacteria_Chloroplasts_Uncl_Uncl
Cyanobacteria_Leptolyngbya_Leptolyngbya_Leptolyngbya_FM
Cyanobacteria_OS_Type_B_Uncl_Uncl
Cyanobacteria_Oscillatoriales_Oscillatoriales_Uncl
Cyanobacteria_Symploca_Symploca_Symploca_FM
Cyanobacteria_Synechococcus_Synechococcus_Synechococcus_FM
Cyanobacteria_Uncl_Uncl_Uncl
Elusimicrobia_TG1_Elusimicrobiales_Elusimicrobiales__Elusimicrobiaceae
Firmicutes_Acidaminococcaceae_Acidaminococcaceae_Acidaminococcaceae
Firmicutes_Alicyclobacillus_Alicyclobacillus_Alicyclobacillus_FM
Firmicutes_Bacilli_Ammoniphilus_Ammoniphilus_FM
Firmicutes_Bacilli_Bacillus_Bacillus_FM
Firmicutes_Bacilli_Halobacillus_Halobacillus_FM
Firmicutes_Bacilli_Lactobacillales_Aerococcaceae
Firmicutes_Bacilli_Lactobacillales_Carnobacteriaceae
Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae
Firmicutes_Bacilli_Lactobacillales_Leuconostoc_FM
Firmicutes_Bacilli_Lactobacillales_Streptococcaceae
Firmicutes_Bacilli_Lactobacillales_Uncl
Firmicutes_Bacilli_Marinococcus_Marinococcus_FM
Firmicutes_Bacilli_Paenibacillaceae_Paenibacillaceae
Firmicutes_Bacilli_Staphylococcaceae_Staphylococcaceae
Firmicutes_Bacilli_Uncl_Uncl
Firmicutes_Clostridia_Clostridiales_adhufec405_FM
Firmicutes_Clostridia_Clostridiales_Clostridiaceae
Firmicutes_Clostridia_Clostridiales_Clostridium_FM
Firmicutes_Clostridia_Clostridiales_Eubacterium_FM
Firmicutes_Clostridia_Clostridiales_Gracilibacter_FM
Firmicutes_Clostridia_Clostridiales_Johnsonella_FM
Firmicutes_Clostridia_Clostridiales_RF6_FM
Firmicutes_Clostridia_Clostridiales_Uncl
Firmicutes_Clostridia_Peptostreptococcaceae_Peptostreptococcaceae
Firmicutes_Desulfotomaculum_Desulfotomaculum_Desulfotomaculum_FM
Firmicutes_Mollicutes_Acholeplasmatales_Uncl
Firmicutes_Syntrophomonadaceae_Syntrophomonadaceae_Syntrophomonadaceae
Firmicutes_Uncl_Uncl_Uncl
Haloanaerobiales_Halanaerobiaceae_Halanaerobiaceae_Halanaerobiaceae
Marine_group_AA714017_Uncl_Uncl
OP10_CH21_Uncl_Uncl
OP10_SJA-22_Uncl_Uncl
OP10_Uncl_Uncl_Uncl
Planctomycetes_Planctomycetacia_Gemmatales_Gemmata_FM
Planctomycetes_Planctomycetacia_Isosphaerales_Isosphaeraceae
Planctomycetes_Planctomycetacia_Isosphaerales_Isospheraceae
Planctomycetes_Planctomycetacia_PRR-7_BCf2-25_FM
Planctomycetes_Planctomycetacia_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_Acetobacterales_Acetobacteraceae
Proteobacteria_Alphaproteobacteria_Acetobacterales_Roseomonas_FM
Proteobacteria_Alphaproteobacteria_Acetobacterales_Uncl
Proteobacteria_Alphaproteobacteria_alpha_proteobacterium_MBIC1474_Uncl
Proteobacteria_Alphaproteobacteria_Azospirillaceae_Azospirillaceae
Proteobacteria_Alphaproteobacteria_Azospirillales_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Beijerinckiaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Bradyrhizobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Hyphomicrobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacteriaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Pleomorphomonas_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Rhodoplanaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Xanthobacteraceae
Proteobacteria_Alphaproteobacteria_Caedibacteraceae_Caedibacteraceae
Proteobacteria_Alphaproteobacteria_Caulobacterales_Brevundimonas_FM
Proteobacteria_Alphaproteobacteria_Phyllobacteriaceae_Phyllobacteriaceae
Proteobacteria_Alphaproteobacteria_Rhizobiaceae_Rhizobiaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Hyphomonadaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacter_FM

Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodovulum_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Porphyrobacter_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingobium_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonas_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Uncl
Proteobacteria_Alphaproteobacteria_Stappia_Stappia_FM
Proteobacteria_Alphaproteobacteria_Uncl_Uncl
Proteobacteria_Deltaproteobacteria_Desulfobacteraceae_Desulfobacteraceae
Proteobacteria_Deltaproteobacteria_Desulfobacterium_Desulfobacterium_FM
Proteobacteria_Deltaproteobacteria_Desulfovibrio_Desulfovibrio_FM
Proteobacteria_Deltaproteobacteria_Myxococcales_Polyangiaceae
Proteobacteria_Desulfovibrionales_Desulfovibrionales_Desulfovibrionaceae
Proteobacteria_Epsilonproteobacteria_Arcobacteraceae_Arcobacteraceae
Proteobacteria_Epsilonproteobacteria_Sulfuricurvales_Sulfuricurvaceae
Proteobacteria_Gammaproteobacteria_Alcaligenaceae_Alcaligenaceae
Proteobacteria_Gammaproteobacteria_Alteromonadales_Alteromonas_FM
Proteobacteria_Gammaproteobacteria_Alteromonadales_Pseudoalteromonadaceae
Proteobacteria_Gammaproteobacteria_Alteromonadales_Rheinheimeraceae
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Chromatiaceae_Chromatiaceae
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Ellin339_Uncl
Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacteriales_Enterobacteriaceae
Proteobacteria_Gammaproteobacteria_Halomonadaceae_Halomonadaceae
Proteobacteria_Gammaproteobacteria_HalOR_hodoSP_ira_HalOR_hodoSP_ira_FM
Proteobacteria_Gammaproteobacteria_Hydrogenophilales_Petrobacter_FM
Proteobacteria_Gammaproteobacteria_Legionellales_Legionella_FM
Proteobacteria_Gammaproteobacteria_Legionellales_Uncl
Proteobacteria_Gammaproteobacteria_Marinobacter_Marinobacter_FM
Proteobacteria_Gammaproteobacteria_Methylococcaceae_Methylococcaceae
Proteobacteria_Gammaproteobacteria_MND1_GR-WP33-36_FM
Proteobacteria_Gammaproteobacteria_Moraxellaceae_Moraxellaceae
Proteobacteria_Gammaproteobacteria_Neisseriales_Chromobacterium_FM
Proteobacteria_Gammaproteobacteria_Neisseriales_Uncl
Proteobacteria_Gammaproteobacteria_Nevskiaceae_Nevskiaceae
Proteobacteria_Gammaproteobacteria_Pasteurellaceae_Pasteurellaceae
Proteobacteria_Gammaproteobacteria_Pseudomonadaceae_Pseudomonadaceae
Proteobacteria_Gammaproteobacteria_Rhodocyclales_Accumulibacter_FM
Proteobacteria_Gammaproteobacteria_Rhodocyclales_Azoarcus_FM
Proteobacteria_Gammaproteobacteria_Rhodocyclales_beta_FM
Proteobacteria_Gammaproteobacteria_Rhodocyclales_Thauera_FM
Proteobacteria_Gammaproteobacteria_Rhodocyclales_Uncl
Proteobacteria_Gammaproteobacteria_SBR1001_Uncl
Proteobacteria_Gammaproteobacteria_Sutterellaceae_Sutterellaceae
Proteobacteria_Gammaproteobacteria_Thiotrichaceae_Thiotrichaceae
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Vibrionaceae_Vibrionaceae
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Lysobacter_FM
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Uncl
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Xylella_FM
Proteobacteria_Gammaproteobacteria_ZA3605c_Uncl
Proteobacteria_Zetaproteobacteria_Uncl_Uncl
Spirochaetes_S_aurantia_Spirochaetales_Uncl
Spirochaetes_WWE1_SHA-4_Uncl
Synergistetes_Aminanaerobia_Thermovirga_Thermovirga_Thermovirga_FM
Thermi_Thermales_Thermales_Meiothermaceae
Thermi_Thermales_Thermales_Thermaceae
TM7_TM7-3_Uncl_Uncl
Verrucomicrobia_Opitutae_Opitutaceae_Opitutaceae

2P Pooled

Family (Phy-Subphy-Order-Family) (103 families)

Acidobacteria_Chloracidobacteria_Uncl_Uncl
Acidobacteria_iii1-15_Uncl_Uncl
Actinobacteria_Acidimicrobidae_Uncl_Uncl
Actinobacteria_Actinobacteridae_Actinomycineae_Actinomycineae
Actinobacteria_Actinobacteridae_Agromyces_Agromyces_FM
Actinobacteria_Actinobacteridae_Bifidobacteriaceae_Bifidobacteriaceae
Actinobacteria_Actinobacteridae_Curtobacterium_Curtobacterium_FM
Actinobacteria_Actinobacteridae_Frankineae_Frankineae
Actinobacteria_Actinobacteridae_Gordoniaceae_Gordoniaceae
Actinobacteria_Actinobacteridae_Micromonosporaceae_Micromonosporaceae
Actinobacteria_Actinobacteridae_Propionibacterineae_Propionibacterineae
Actinobacteria_Actinobacteridae_Streptomycineae_Streptomycineae
Actinobacteria_Actinobacteridae_Streptosporangineae_Streptosporangineae
Actinobacteria_Actinobacteridae_Uncl_Uncl
Actinobacteria_WCHB1-81_Uncl_Uncl
Bacteroidetes_Bacteroidales_Bacteroidales_Bacteroidaceae
Bacteroidetes_Flavobacteriales_Flavobacteriales_Flavobacteriaceae
Bacteroidetes_Flavobacteriales_Flavobacteriales_Sporocytophaga_FM
Bacteroidetes_Flexibacterales_Flexibacterales_Roseivirga_FM
Bacteroidetes_LD1_Uncl_Uncl
Bacteroidetes_Pedobacter_Pedobacter_Pedobacter_FM
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Chlorobi_Uncl_Uncl_Uncl
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Cyanobacteria_Chloroplasts_Uncl_Uncl
Cyanobacteria_Uncl_Uncl_Uncl
Deferribacteres_Uncl_Uncl_Uncl
Elusimicrobia_TG1_Elusimicrobiales_Elusimicrobiales__Elusimicrobiaceae
Firmicutes_Bacilli_Bacillus_Bacillus_FM
Firmicutes_Bacilli_Halobacillus_Halobacillus_FM
Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae
Firmicutes_Bacilli_Lactobacillales_Streptococcaceae
Firmicutes_Bacilli_Paenibacillaceae_Paenibacillaceae
Firmicutes_Bacilli_Staphylococcaceae_Staphylococcaceae
Firmicutes_Bacilli_Uncl_Uncl
Firmicutes_Clostridia_Clostridiales_Eubacterium_FM
Firmicutes_Clostridia_Clostridiales_Uncl
Firmicutes_Clostridia_Peptostreptococcaceae_Peptostreptococcaceae
Firmicutes_Mollicutes_Uncl_Uncl
Firmicutes_Syntrophomonadaceae_Syntrophomonadaceae_Syntrophomonadaceae
Haloanaerobiales_Halanaerobiaceae_Halanaerobiaceae_Halanaerobiaceae
Marine_group_AA714017_Uncl_Uncl
OP10_CH21_Uncl_Uncl
OP10_CL500-48_Uncl_Uncl
Planctomycetes_Planctomycetacia_Isosphaerales_Isosphaeraceae
Planctomycetes_Planctomycetacia_Planctomycetales_Uncl
Poribacteria_Uncl_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_Acetobacterales_Acetobacteraceae
Proteobacteria_Alphaproteobacteria_Acetobacterales_Roseomonas_FM
Proteobacteria_Alphaproteobacteria_alpha_proteobacterium_MBIC1474_Uncl
Proteobacteria_Alphaproteobacteria_Azospirillaceae_Azospirillaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Bradyrhizobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacteriaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Rhodoplanaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Xanthobacteraceae
Proteobacteria_Alphaproteobacteria_Caedibacteraceae_Caedibacteraceae
Proteobacteria_Alphaproteobacteria_Caulobacterales_Brevundimonas_FM
Proteobacteria_Alphaproteobacteria_Caulobacterales_Uncl
Proteobacteria_Alphaproteobacteria_H29_Uncl
Proteobacteria_Alphaproteobacteria_Rhizobiaceae_Rhizobiaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Hyphomonadaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacter_FM
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Uncl
Proteobacteria_Alphaproteobacteria_Rickettsiales_Uncl
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Porphyrobacter_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingobium_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonas_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Uncl
Proteobacteria_Alphaproteobacteria_Uncl_Uncl
Proteobacteria_Deltaproteobacteria_Desulfovibrio_Desulfovibrio_FM
Proteobacteria_Deltaproteobacteria_Myxococcales_Polyangiaceae
Proteobacteria_Epsilonproteobacteria_Arcobacteraceae_Arcobacteraceae
Proteobacteria_Epsilonproteobacteria_Sulfuricurvales_Sulfuricurvaceae
Proteobacteria_Gammaproteobacteria_Alcaligenaceae_Alcaligenaceae
Proteobacteria_Gammaproteobacteria_Alteromonadales_Rheinheimeraceae
Proteobacteria_Gammaproteobacteria_bacterium_Ellin6067_Uncl
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Ellin339_Uncl
Proteobacteria_Gammaproteobacteria_endosymbiont_RT7_of_Lyrodus_pedicellatus_Uncl
Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacteriales_Enterobacteriaceae
Proteobacteria_Gammaproteobacteria_Hydrogenophilales_Petrobacter_FM
Proteobacteria_Gammaproteobacteria_Legionellales_Legionella_FM
Proteobacteria_Gammaproteobacteria_Legionellales_Uncl
Proteobacteria_Gammaproteobacteria_Marinobacter_Marinobacter_FM
Proteobacteria_Gammaproteobacteria_Methylococcaceae_Methylococcaceae
Proteobacteria_Gammaproteobacteria_Methylophilales_Methylophilus_FM
Proteobacteria_Gammaproteobacteria_MND1_GR-WP33-36_FM
Proteobacteria_Gammaproteobacteria_Moraxellaceae_Moraxellaceae
Proteobacteria_Gammaproteobacteria_Neisseriales_Chromobacterium_FM
Proteobacteria_Gammaproteobacteria_Pasteurellaceae_Pasteurellaceae
Proteobacteria_Gammaproteobacteria_Pseudomonadaceae_Pseudomonadaceae
Proteobacteria_Gammaproteobacteria_Shewanellaceae_Shewanellaceae
Proteobacteria_Gammaproteobacteria_Sutterellaceae_Sutterellaceae
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Vibrionaceae_Vibrionaceae
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Lysobacter_FM
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Uncl
Proteobacteria_Gammaproteobacteria_ZA3605c_Uncl
Thermi_Thermales_Thermales_Thermaceae
Thermotogae_A2_Uncl_Uncl

3P Pooled

Family (Phy-Subphy-Order-Family) (151 families)

ABY1_OD1_WCHB1-58_Uncl_Uncl
Acidobacteria_Chloracidobacteria_Uncl_Uncl
Acidobacteria_iii1-15_Uncl_Uncl
Acidobacteria_Solibacteres_Solibacteraceae_Solibacteraceae
Actinobacteria_Acidimicrobidae_Microthrixineae_Microthrixineae
Actinobacteria_Acidimicrobidae_Uncl_Uncl
Actinobacteria_Actinobacteridae_Agromyces_Agromyces_FM
Actinobacteria_Actinobacteridae_Bifidobacteriaceae_Bifidobacteriaceae
Actinobacteria_Actinobacteridae_Frankineae_Frankineae
Actinobacteria_Actinobacteridae_Gordoniaceae_Gordoniaceae
Actinobacteria_Actinobacteridae_Intrasporangiaceae_Intrasporangiaceae
Actinobacteria_Actinobacteridae_Micromonosporaceae_Micromonosporaceae
Actinobacteria_Actinobacteridae_Propionibacterineae_Propionibacterineae
Actinobacteria_Actinobacteridae_Streptosporangineae_Streptosporangineae
Actinobacteria_Actinobacteridae_Uncl_Uncl
Actinobacteria_WCHB1-81_Uncl_Uncl
Bacteroidetes_Bacteroidales_Bacteroidales_Parabacteroidaceae
Bacteroidetes_Bacteroidales_Bacteroidales_Proteophilaceae
Bacteroidetes_Bacteroidales_Bacteroidales_Uncl
Bacteroidetes_F1CA7_Flavobacteriales_Uncl
Bacteroidetes_Flavobacteriales_Flavobacteriales_Cytophaga_FM
Bacteroidetes_Flavobacteriales_Flavobacteriales_Flavobacteriaceae
Bacteroidetes_Flavobacteriales_Flavobacteriales_Polaribacter_FM
Bacteroidetes_Flavobacteriales_Flavobacteriales_Sporocytophaga_FM
Bacteroidetes_Flavobacteriales_Flavobacteriales_Uncl
Bacteroidetes_FukuN24_Saprospirales_Uncl
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Bacteroidetes_Saprospirales_Saprospirales_Uncl
Bacteroidetes_Sphingobacteriaceae_Sphingobacteriaceae_Sphingobacteriaceae
Bacteroidetes_Uncl_Uncl_Uncl
Caldithrix_KSB1_Caldithrixales_Caldithrixales_Uncl
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Cyanobacteria_Chloroplasts_Uncl_Uncl
Cyanobacteria_Stigonematales_Stigonematales_Uncl
Cyanobacteria_Synechococcus_Synechococcus_Synechococcus_FM
Cyanobacteria_Uncl_Uncl_Uncl
Deferribacteres_Uncl_Uncl_Uncl
Elusimicrobia_TG1_Elusimicrobiales_Elusimicrobiales__Elusimicrobiaceae
Firmicutes_Alicyclobacillus_Alicyclobacillus_Alicyclobacillus_FM
Firmicutes_Bacilli_Ammoniphilus_Ammoniphilus_FM
Firmicutes_Bacilli_Bacillus_Bacillus_FM
Firmicutes_Bacilli_Exiguobacterium_Exiguobacterium_FM
Firmicutes_Bacilli_Geobacillus_Geobacillus_FM
Firmicutes_Bacilli_Halobacillus_Halobacillus_FM
Firmicutes_Bacilli_Lactobacillales_Aerococcaceae
Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae
Firmicutes_Bacilli_Lactobacillales_Leuconostoc_FM
Firmicutes_Bacilli_Lactobacillales_Streptococcaceae
Firmicutes_Bacilli_Lactobacillales_Uncl
Firmicutes_Bacilli_Paenibacillaceae_Paenibacillaceae
Firmicutes_Bacilli_Staphylococcaceae_Staphylococcaceae
Firmicutes_Bacilli_Uncl_Uncl
Firmicutes_Clostridia_Clostridiales_adhufec405_FM
Firmicutes_Clostridia_Clostridiales_RF6_FM
Firmicutes_Clostridia_Clostridiales_Uncl
Firmicutes_Clostridia_Peptostreptococcaceae_Peptostreptococcaceae
Firmicutes_Desulfotomaculum_Desulfotomaculum_Desulfotomaculum_FM
Firmicutes_Mollicutes_Acholeplasmatales_Uncl
Firmicutes_Mollicutes_Clostridium_Clostridium_FM
Firmicutes_Symbiobacteria_Uncl_Uncl
Firmicutes_Uncl_Uncl_Uncl
Fusobacteria_Fusobacteriaceae_Fusobacteriaceae_Fusobacteriaceae
Haloanaerobiales_Halanaerobiaceae_Halanaerobiaceae_Halanaerobiaceae
Marine_group_AA714017_Uncl_Uncl
OP10_CH21_Uncl_Uncl
OP10_CL500-48_Uncl_Uncl
Planctomycetes_Planctomycetacia_Gemmatales_Gemmata_FM
Planctomycetes_Planctomycetacia_Gemmatales_Uncl
Planctomycetes_Planctomycetacia_Planctomycetales_Uncl
Planctomycetes_Planctomycetacia_PRR-7_BCf2-25_FM
Poribacteria_Uncl_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_Acetobacterales_Acetobacteraceae
Proteobacteria_Alphaproteobacteria_Acetobacterales_Roseomonas_FM
Proteobacteria_Alphaproteobacteria_alpha_proteobacterium_MBIC1474_Uncl
Proteobacteria_Alphaproteobacteria_Azospirillaceae_Azospirillaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Beijerinckiaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Bradyrhizobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Hyphomicrobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacteriaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Rhodoplanaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Xanthobacteraceae
Proteobacteria_Alphaproteobacteria_Brucellaceae_Brucellaceae
Proteobacteria_Alphaproteobacteria_Caedibacteraceae_Caedibacteraceae
Proteobacteria_Alphaproteobacteria_Caulobacterales_Brevundimonas_FM
Proteobacteria_Alphaproteobacteria_Caulobacterales_Uncl
Proteobacteria_Alphaproteobacteria_Rhizobiaceae_Rhizobiaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Hyphomonadaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacter_FM
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Uncl
Proteobacteria_Alphaproteobacteria_Rickettsiales_Uncl
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Porphyrobacter_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingobium_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonas_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingosinicella_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Uncl
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Zymomonas_FM
Proteobacteria_Alphaproteobacteria_Uncl_Uncl
Proteobacteria_Deltaproteobacteria_Bacteriovorax_Bacteriovorax_FM
Proteobacteria_Deltaproteobacteria_Desulfobacterium_Desulfobacterium_FM
Proteobacteria_Deltaproteobacteria_Desulfovibrio_Desulfovibrio_FM
Proteobacteria_Deltaproteobacteria_Myxococcales_Anaeromyxobacter_FM
Proteobacteria_Deltaproteobacteria_Myxococcales_Polyangiaceae
Proteobacteria_Deltaproteobacteria_Syntrophobacteraceae_Syntrophobacteraceae
Proteobacteria_Epsilonproteobacteria_Arcobacteraceae_Arcobacteraceae
Proteobacteria_Epsilonproteobacteria_LKC3_15615_Uncl
Proteobacteria_Epsilonproteobacteria_Nautilliales_Nautillaceae
Proteobacteria_Epsilonproteobacteria_Sulfuricurvales_Sulfuricurvaceae
Proteobacteria_Epsilonproteobacteria_Sulfurospirillaceae_Sulfurospirillaceae
Proteobacteria_Gammaproteobacteria_Alcaligenaceae_Alcaligenaceae

Proteobacteria_Gammaproteobacteria_Alteromonadales_Pseudoalteromonadaceae
Proteobacteria_Gammaproteobacteria_Alteromonadales_Rheinheimeraceae
Proteobacteria_Gammaproteobacteria_Alteromonadales_Uncl
Proteobacteria_Gammaproteobacteria_bacterium_Ellin6067_Uncl
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Ellin339_Uncl
Proteobacteria_Gammaproteobacteria_endosymbiont_RT7_of_Lyrodus_pedicellatus_Uncl
Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacteriales_Enterobacteriaceae
Proteobacteria_Gammaproteobacteria_Halomonadaceae_Halomonadaceae
Proteobacteria_Gammaproteobacteria_HalOR_hodoSP_ira_HalOR_hodoSP_ira_FM
Proteobacteria_Gammaproteobacteria_Hydrogenophilales_Petrobacter_FM
Proteobacteria_Gammaproteobacteria_Legionellales_Legionella_FM
Proteobacteria_Gammaproteobacteria_Legionellales_Uncl
Proteobacteria_Gammaproteobacteria_Marinobacter_Marinobacter_FM
Proteobacteria_Gammaproteobacteria_Methylococcaceae_Methylococcaceae
Proteobacteria_Gammaproteobacteria_Methylophilales_Methylophilus_FM
Proteobacteria_Gammaproteobacteria_Methylophilales_Uncl
Proteobacteria_Gammaproteobacteria_Moraxellaceae_Moraxellaceae
Proteobacteria_Gammaproteobacteria_Neisseriales_Chromobacterium_FM
Proteobacteria_Gammaproteobacteria_Pasteurellaceae_Pasteurellaceae
Proteobacteria_Gammaproteobacteria_Pseudomonadaceae_Pseudomonadaceae
Proteobacteria_Gammaproteobacteria_Rhodocyclales_Accumulibacter_FM
Proteobacteria_Gammaproteobacteria_Rhodocyclales_Thauera_FM
Proteobacteria_Gammaproteobacteria_Rhodocyclales_Uncl
Proteobacteria_Gammaproteobacteria_Sutterellaceae_Sutterellaceae
Proteobacteria_Gammaproteobacteria_Thiotrichaceae_Thiotrichaceae
Proteobacteria_Gammaproteobacteria_Thiotrichales_Thiothrix_FM
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Vibrionaceae_Vibrionaceae
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Lysobacter_FM
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Uncl
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Xylella_FM
Proteobacteria_Gammaproteobacteria_ZA3605c_Uncl
Spirochaetes_S_aurantia_Spirochaetales_Uncl
Sulfobacilli_Thermaerobacter_Thermaerobacter_Thermaerobacter_FM
Thermi_Thermales_Thermales_Meiothermaceae
Thermi_Thermales_Thermales_Thermaceae
Thermotogae_A2_Uncl_Uncl
Verrucomicrobia_Opitutae_Opitutaceae_Opitutaceae
Verrucomicrobia_Verrucomicrobiae_Uncl_Uncl

JPL Sample 1

Family (Phy-Subphy-Order-Family) (43 families)

Acidobacteria_iii1-15_Uncl_Uncl
Actinobacteria_Actinobacteridae_Bifidobacteriaceae_Bifidobacteriaceae
Actinobacteria_Actinobacteridae_Gordoniaceae_Gordoniaceae
Actinobacteria_Actinobacteridae_Intrasporangiaceae_Intrasporangiaceae
Actinobacteria_Actinobacteridae_Micromonosporaceae_Micromonosporaceae
Actinobacteria_Actinobacteridae_Propionibacterineae_Propionibacterineae
Actinobacteria_Actinobacteridae_Streptomycineae_Streptomycineae
Actinobacteria_Actinobacteridae_Streptosporangineae_Streptosporangineae
Actinobacteria_Actinobacteridae_Uncl_Uncl
Chloroflexi_Chloroflexi-4_Uncl_Uncl
Cyanobacteria_Uncl_Uncl_Uncl
Deferribacteres_Uncl_Uncl_Uncl
Firmicutes_Bacilli_Bacillus_Bacillus_FM
Firmicutes_Bacilli_Bacillus_thermocloaceae_Bacillus_thermocloaceae
Firmicutes_Bacilli_Lactobacillales_Aerococcaceae
Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae
Firmicutes_Bacilli_Lactobacillales_Streptococcaceae
Firmicutes_Bacilli_Lactobacillales_Uncl
Firmicutes_Bacilli_Paenibacillaceae_Paenibacillaceae
Firmicutes_Bacilli_Uncl_Uncl
Firmicutes_Clostridia_Clostridiales_Uncl
Firmicutes_Clostridia_Peptostreptococcaceae_Peptostreptococcaceae
Firmicutes_Mollicutes_Uncl_Uncl
Gemmatimonadetes_Gemm-1c_Uncl_Uncl
Marine_group_AA714017_Uncl_Uncl
OP10_CL500-48_Uncl_Uncl
Planctomycetes_Planctomycetacia_Planctomycetales_Uncl
Planctomycetes_Planctomycetacia_Uncl_Uncl
Poribacteria_Uncl_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Bradyrhizobium_FM
Proteobacteria_Alphaproteobacteria_Caedibacteraceae_Caedibacteraceae
Proteobacteria_Alphaproteobacteria_Oleomonas_Oleomonas_FM
Proteobacteria_Alphaproteobacteria_Rickettsiales_Uncl
Proteobacteria_Deltaproteobacteria_Geobacter_Geobacter_FM
Proteobacteria_Deltaproteobacteria_Myxococcales_Polyangiaceae
Proteobacteria_Epsilonproteobacteria_Arcobacteraceae_Arcobacteraceae
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacteriales_Enterobacteriaceae
Spirochaetes_WWE1_SHA-4_GZKB57_FM
Thermi_Thermales_Thermales_Thermaceae
Thermodesulfobacteria_Thermodesulfobacteriaceae_Thermodesulfobacteriaceae_Thermodesulfobacteriaceae
Uncl_Uncl_Uncl_Uncl
WCHB1-27_Uncl_Uncl_Uncl

JPL Sample 2

Family (Phy-Subphy-Order-Family) (41 families)

Acidobacteria_iii1-15_Uncl_Uncl
Actinobacteria_Actinobacteridae_Arthrobacter_Arthrobacter_FM
Actinobacteria_Actinobacteridae_Bifidobacteriaceae_Bifidobacteriaceae
Actinobacteria_Actinobacteridae_Brachybacterium_Brachybacterium_FM
Actinobacteria_Actinobacteridae_Intrasporangiaceae_Intrasporangiaceae
Actinobacteria_Actinobacteridae_Micromonosporaceae_Micromonosporaceae
Actinobacteria_Actinobacteridae_Propionibacterineae_Propionibacterineae
Actinobacteria_Actinobacteridae_Streptomycineae_Streptomycineae
Actinobacteria_Actinobacteridae_Streptosporangineae_Streptosporangineae
Actinobacteria_Actinobacteridae_Uncl_Uncl
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Coprothermobacteria_Uncl_Uncl_Uncl
Firmicutes_Bacilli_Bacillus_Bacillus_FM
Firmicutes_Bacilli_Bacillus_thermocloaceae_Bacillus_thermocloaceae
Firmicutes_Bacilli_Lactobacillales_Aerococcaceae
Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae
Firmicutes_Bacilli_Lactobacillales_Leuconostoc_FM
Firmicutes_Bacilli_Lactobacillales_Uncl
Firmicutes_Bacilli_Paenibacillaceae_Paenibacillaceae
Firmicutes_Bacilli_Planococcaceae_Planococcaceae
Firmicutes_Bacilli_Uncl_Uncl
Firmicutes_Clostridia_Clostridiales_Clostridiaceae
Firmicutes_Clostridia_Clostridiales_Uncl
Firmicutes_Clostridia_Uncl_Uncl
Firmicutes_Mollicutes_Uncl_Uncl
Nitrospirae_Thermodesulfovibrionales_Thermodesulfovibrionales_Thermodesulfovibrionaceae
OP11_Uncl_Uncl_Uncl
Planctomycetes_Planctomycetacia_Planctomycetales_Uncl
Planctomycetes_Planctomycetacia_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_Acetobacterales_Acetobacteraceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Beijerinckiaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Consistiales_Surf113_FM
Proteobacteria_Gammaproteobacteria_Nitrosomonadales_Uncl
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Uncl
Spirochaetes_WWE1_SHA-4_GZKB57_FM
Thermi_Thermales_Thermales_Thermaceae
Thermodesulfobacteria_Thermodesulfobacteriaceae_Thermodesulfobacteriaceae_Thermodesulfobacteriaceae
Verrucomicrobia_Pedosphaerae_Uncl_Uncl

JPL Sample 3

Family (Phy-Subphy-Order-Family) (36 families)

ABY1_OD1_WCHB1-58_Uncl_Uncl
Actinobacteria_Actinobacteridae_Agromyces_Agromyces_FM
Actinobacteria_Actinobacteridae_Frankineae_Frankineae
Actinobacteria_Actinobacteridae_Intrasporangiaceae_Intrasporangiaceae
Actinobacteria_Actinobacteridae_Micromonosporaceae_Micromonosporaceae
Actinobacteria_Actinobacteridae_Propionibacterineae_Propionibacterineae
Actinobacteria_Actinobacteridae_Pseudonocardiaceae_Pseudonocardiaceae
Actinobacteria_Actinobacteridae_Streptosporangineae_Streptosporangineae
Actinobacteria_Actinobacteridae_Uncl_Uncl
Bacteroidetes_Flexibacterales_Flexibacterales_Uncl
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Cyanobacteria_Uncl_Uncl_Uncl
Firmicutes_Bacilli_Bacillus_Bacillus_FM
Firmicutes_Bacilli_Halobacillus_Halobacillus_FM
Firmicutes_Bacilli_Lactobacillales_Aerococcaceae
Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae
Firmicutes_Bacilli_Lactobacillales_Leuconostoc_FM
Firmicutes_Bacilli_Staphylococcaceae_Staphylococcaceae
Firmicutes_Bacilli_Uncl_Uncl
Firmicutes_Clostridia_Peptostreptococcaceae_Peptostreptococcaceae
Firmicutes_Mollicutes_Uncl_Uncl
Marine_group_AA714017_Uncl_Uncl
Planctomycetes_Planctomycetacia_Planctomycetales_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Rickettsiales_Uncl
Proteobacteria_Alphaproteobacteria_Schlegelella_Schlegelella_FM
Proteobacteria_Deltaproteobacteria_NB1-i_Uncl
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacteriales_Enterobacteriaceae
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Uncl
Spirochaetes_Spirochaetales_Spirochaetales_Spirochaetaceae
Thermi_Thermales_Thermales_Meiothermaceae
Thermi_Thermales_Thermales_Thermaceae
Verrucomicrobia_Pedosphaerae_Uncl_Uncl
WCHB1-27_Uncl_Uncl_Uncl

JPL Sample 4

Family (Phy-Subphy-Order-Family) (72 families)

Acidobacteria_Chloracidobacteria_Uncl_Uncl
Acidobacteria_iii1-15_RB40_Uncl
Acidobacteria_OS-K_Uncl_Uncl
Actinobacteria_Acidimicrobidae_Microthrixineae_Microthrixineae
Actinobacteria_Acidimicrobidae_Uncl_Uncl
Actinobacteria_Actinobacteridae_Actinomycineae_Actinomycineae
Actinobacteria_Actinobacteridae_Agromyces_Agromyces_FM
Actinobacteria_Actinobacteridae_Arthrobacter_Arthrobacter_FM
Actinobacteria_Actinobacteridae_Brachybacterium_Brachybacterium_FM
Actinobacteria_Actinobacteridae_Frankineae_Frankineae
Actinobacteria_Actinobacteridae_Gordoniaceae_Gordoniaceae
Actinobacteria_Actinobacteridae_Intrasporangiaceae_Intrasporangiaceae
Actinobacteria_Actinobacteridae_Kineosporiaceae_Kineosporiaceae
Actinobacteria_Actinobacteridae_Leucobacter_Leucobacter_FM
Actinobacteria_Actinobacteridae_Micromonosporaceae_Micromonosporaceae
Actinobacteria_Actinobacteridae_Propionibacterineae_Propionibacterineae
Actinobacteria_Actinobacteridae_Rhodococcus_Rhodococcus_FM
Actinobacteria_Actinobacteridae_Streptosporangineae_Streptosporangineae
Actinobacteria_Actinobacteridae_Uncl_Uncl
Actinobacteria_Rubrobacteridae_Thermoleiphilaceae_Thermoleiphilaceae
Actinobacteria_WCHB1-81_Uncl_Uncl
Bacteroidetes_Bacteroidales_Bacteroidales_Proteophilaceae
Bacteroidetes_Flexibacterales_Flexibacterales_Roseivirga_FM
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Chlorobi_Chlorobiales_Chlorobiales_Chlorobaculum_FM
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Cyanobacteria_Chloroplasts_Uncl_Uncl
Cyanobacteria_Uncl_Uncl_Uncl
Cyanobacteria_YS2_Uncl_Uncl
Deferribacteres_Uncl_Uncl_Uncl
Firmicutes_Alicyclobacillus_Alicyclobacillus_Alicyclobacillus_FM
Firmicutes_Bacilli_Bacillus_Bacillus_FM
Firmicutes_Bacilli_Bacillus_thermocloaceae_Bacillus_thermocloaceae
Firmicutes_Bacilli_Geobacillus_Geobacillus_FM
Firmicutes_Bacilli_Halobacillus_Halobacillus_FM
Firmicutes_Bacilli_Lactobacillales_Aerococcaceae
Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae
Firmicutes_Bacilli_Lactobacillales_Leuconostoc_FM
Firmicutes_Bacilli_Lactobacillales_Streptococcaceae
Firmicutes_Bacilli_Lactobacillales_Uncl
Firmicutes_Bacilli_Paenibacillaceae_Paenibacillaceae
Firmicutes_Bacilli_Staphylococcaceae_Staphylococcaceae
Firmicutes_Bacilli_Uncl_Uncl
Firmicutes_Clostridia_Clostridiales_Clostridium_FM
Firmicutes_Clostridia_Clostridiales_Uncl
Firmicutes_Clostridia_Peptostreptococcaceae_Peptostreptococcaceae
Firmicutes_Mollicutes_Clostridium_Clostridium_FM
Firmicutes_Mollicutes_Uncl_Uncl
Nitrospirae_Nitrospirales_Nitrospirales_Uncl
OP10_Uncl_Uncl_Uncl
Planctomycetes_Planctomycetacia_Planctomycetales_Uncl
Planctomycetes_Planctomycetacia_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Rhodoplanaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Caulobacterales_Uncl
Proteobacteria_Alphaproteobacteria_Rhizobiaceae_Rhizobiaceae
Proteobacteria_Alphaproteobacteria_Rickettsiales_Uncl
Proteobacteria_Alphaproteobacteria_Uncl_Uncl
Proteobacteria_Deltaproteobacteria_Desulfobacteraceae_Desulfobacteraceae
Proteobacteria_Epsilonproteobacteria_Sulfurospirillaceae_Sulfurospirillaceae
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacteriales_Enterobacteriaceae
Proteobacteria_Gammaproteobacteria_Moraxellaceae_Moraxellaceae
Proteobacteria_Gammaproteobacteria_Nitrosomonadales_Uncl
Proteobacteria_Gammaproteobacteria_Pseudomonadaceae_Pseudomonadaceae
Proteobacteria_Gammaproteobacteria_Rhodocyclales_Azoarcus_FM
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Uncl
Spirochaetes_Treponemaceae_Treponemaceae_Treponemaceae
Thermi_Thermales_Thermales_Thermaceae
Thermodesulfobacteria_Thermodesulfobacteriaceae_Thermodesulfobacteriaceae_Thermodesulfobacteriaceae
TM6_Uncl_Uncl_Uncl

Set 1 PCR neg conc

Family (Phy-Subphy-Order-Family) (30 families)

Actinobacteria_Actinobacteridae_Propionibacterineae_Propionibacterineae
Actinobacteria_Actinobacteridae_Streptomycineae_Streptomycineae
Actinobacteria_Actinobacteridae_Uncl_Uncl
Actinobacteria_WCHB1-81_Uncl_Uncl
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Firmicutes_Bacilli_Lactobacillales_Streptococcaceae
Firmicutes_Bacilli_Paenibacillaceae_Paenibacillaceae
Firmicutes_Clostridia_Peptostreptococcaceae_Peptostreptococcaceae
Firmicutes_Mollicutes_Uncl_Uncl
OP10_CL500-48_Uncl_Uncl
OP10_Uncl_Uncl_Uncl
Planctomycetes_Planctomycetacia_Planctomycetales_Uncl
Planctomycetes_Planctomycetacia_Uncl_Uncl
Poribacteria_Uncl_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_Azospirillaceae_Azospirillaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Hyphomicrobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Schlegelella_Schlegelella_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Uncl
Proteobacteria_Epsilonproteobacteria_Nautilliales_Nautillaceae
Proteobacteria_Epsilonproteobacteria_Sulfuricurvales_Sulfuricurvaceae
Proteobacteria_Gammaproteobacteria_Alteromonadales_Alteromonas_FM
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Legionellales_Aquicella_FM
Proteobacteria_Gammaproteobacteria_Legionellales_Uncl
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
TM7_TM7-3_Uncl_Uncl

Set 1 PCR neg

Family (Phy-Subphy-Order-Family) (6 families)

Acidobacteria_iii1-8_Uncl_Uncl
Firmicutes_Mollicutes_Acholeplasmatales_Uncl
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Ralstoniaceae_Ralstoniaceae
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
Thermotogae_Thermotogaceae_Thermotogaceae_Thermotogaceae

JPL 2-1 Blank

Family (Phy-Subphy-Order-Family) (36 families)

Actinobacteria_Actinobacteridae_Bifidobacteriaceae_Bifidobacteriaceae
Actinobacteria_Actinobacteridae_Rhodococcus_Rhodococcus_FM
Bacteroidetes_Bacteroidales_Bacteroidales_Parabacteroidaceae
Bacteroidetes_Bacteroidetes__bacterium_PPf50E2_Bacteroidales_BA017_FM
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Chloroflexi_Roseiflexales_Roseiflexales_Kouleothrix_FM
Cyanobacteria_Chloroplasts_Uncl_Uncl
Cyanobacteria_YS2_Uncl_Uncl
Firmicutes_Bacilli_Uncl_Uncl
Firmicutes_Clostridia_Clostridiales_Uncl
Firmicutes_Clostridia_Peptostreptococcaceae_Peptostreptococcaceae
Firmicutes_Mollicutes_Acholeplasmatales_Uncl
Planctomycetes_Planctomycetacia_Planctomycetales_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Bradyrhizobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Rhodoplanaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Caulobacterales_Brevundimonas_FM
Proteobacteria_Alphaproteobacteria_Nordella_Nordella_FM
Proteobacteria_Alphaproteobacteria_Oleomonas_Oleomonas_FM
Proteobacteria_Alphaproteobacteria_Rhizobiaceae_Rhizobiaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Hyphomonadaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacter_FM
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodovulum_FM
Proteobacteria_Alphaproteobacteria_Roseospira_Roseospira_FM
Proteobacteria_Alphaproteobacteria_Schlegelella_Schlegelella_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Porphyrobacter_FM
Proteobacteria_Alphaproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Alteromonadales_Uncl
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Legionellales_Uncl
Sulfobacilli_Sulfobacillus_Sulfobacillus_Sulfobacillus_FM
Thermi_Thermales_Thermales_Thermaceae
Thermodesulfobacteria_Thermodesulfobacteriaceae_Thermodesulfobacteriaceae_Thermodesulfobacteriaceae
VHS-B5-50_Uncl_Uncl_Uncl

JPL 2-3 Blank

Family (Phy-Subphy-Order-Family) (58 families)

Actinobacteria_Acidimicrobidae_JTB31_BD2-10_FM
Actinobacteria_Actinobacteridae_Bifidobacteriaceae_Bifidobacteriaceae
Actinobacteria_Actinobacteridae_Brachybacterium_Brachybacterium_FM
Actinobacteria_Actinobacteridae_Gordoniaceae_Gordoniaceae
Actinobacteria_Actinobacteridae_Intrasporangiaceae_Intrasporangiaceae
Actinobacteria_Actinobacteridae_Micromonosporaceae_Micromonosporaceae
Actinobacteria_Actinobacteridae_Propionibacterineae_Propionibacterineae
Actinobacteria_Actinobacteridae_Streptosporangineae_Streptosporangineae
Bacteroidetes_Bacteroidales_Bacteroidales_Bacteroidaceae
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Bacteroidetes_SHA-94_Bacteroidales_Uncl
Bacteroidetes_Uncl_Uncl_Uncl
Chlorobi_Uncl_Uncl_Uncl
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Cyanobacteria_Chloroplasts_Uncl_Uncl
Cyanobacteria_Uncl_Uncl_Uncl
Firmicutes_Acidaminococcaceae_Acidaminococcaceae_Acidaminococcaceae
Firmicutes_Bacilli_Lactobacillales_Aerococcaceae
Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae
Firmicutes_Bacilli_Lactobacillales_Streptococcaceae
Firmicutes_Bacilli_Paenibacillaceae_Paenibacillaceae
Firmicutes_Bacilli_Staphylococcaceae_Staphylococcaceae
Firmicutes_Bacilli_Uncl_Uncl
Firmicutes_Clostridia_Clostridiales_Acetivibrio_FM
Firmicutes_Clostridia_Clostridiales_Uncl
Firmicutes_Mollicutes_Acholeplasmatales_Uncl
Firmicutes_Mollicutes_Uncl_Uncl
Planctomycetes_Planctomycetacia_Isosphaerales_Isosphaeraceae
Planctomycetes_Planctomycetacia_Uncl_Uncl
Poribacteria_Uncl_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_Acetobacterales_Roseomonas_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Bradyrhizobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Rhodoplanaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Consistiales_SAR11_FM
Proteobacteria_Alphaproteobacteria_Nordella_Nordella_FM
Proteobacteria_Alphaproteobacteria_Pseudochrobactrum_Pseudochrobactrum_FM
Proteobacteria_Alphaproteobacteria_Rhizobiaceae_Rhizobiaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacter_FM
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodovulum_FM
Proteobacteria_Alphaproteobacteria_Schlegelella_Schlegelella_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Porphyrobacter_FM
Proteobacteria_Alphaproteobacteria_Uncl_Uncl
Proteobacteria_Epsilonproteobacteria_Nautilliales_Nautillaceae
Proteobacteria_Gammaproteobacteria_Alcaligenaceae_Alcaligenaceae
Proteobacteria_Gammaproteobacteria_Alteromonadales_Rheinheimeraceae
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacteriales_Enterobacteriaceae
Proteobacteria_Gammaproteobacteria_Hydrogenophilales_Petrobacter_FM
Proteobacteria_Gammaproteobacteria_Pseudomonadaceae_Pseudomonadaceae
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Stenotrophomonas_FM
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Uncl
Spirochaetes_Treponemaceae_Treponemaceae_Treponemaceae
Sulfobacilli_Sulfobacillus_Sulfobacillus_Sulfobacillus_FM
Thermi_Thermales_Thermales_Thermaceae
Verrucomicrobia_Pedosphaerae_Uncl_Uncl

JPL 2-7 Blank

Family (Phy-Subphy-Order-Family) (48 families)

ABY1_OD1_WCHB1-58_Uncl_Uncl
Actinobacteria_Actinobacteridae_Micromonosporaceae_Micromonosporaceae
Actinobacteria_Actinobacteridae_Propionibacterineae_Propionibacterineae
Bacteroidetes_Flexibacterales_Flexibacterales_Roseivirga_FM
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Bacteroidetes_Saprospirales_Saprospirales_Uncl
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Cyanobacteria_Chloroplasts_Uncl_Uncl
Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae
Firmicutes_Bacilli_Lactobacillales_Leuconostoc_FM
Firmicutes_Bacilli_Lactobacillales_Streptococcaceae
Firmicutes_Bacilli_Paenibacillaceae_Paenibacillaceae
Firmicutes_Bacilli_Uncl_Uncl
Firmicutes_Clostridia_Clostridiales_Clostridium_FM
Firmicutes_Clostridia_Peptostreptococcaceae_Peptostreptococcaceae
Firmicutes_Mollicutes_Uncl_Uncl
Planctomycetes_Planctomycetacia_Planctomycetales_Uncl
Poribacteria_Uncl_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Bradyrhizobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Rhodoplanaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Defluvicoccus_Defluvicoccus_FM
Proteobacteria_Alphaproteobacteria_Oleomonas_Oleomonas_FM
Proteobacteria_Alphaproteobacteria_Phyllobacteriaceae_Phyllobacteriaceae
Proteobacteria_Alphaproteobacteria_Rhizobiaceae_Rhizobiaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacter_FM
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodovulum_FM
Proteobacteria_Alphaproteobacteria_Roseospira_Roseospira_FM
Proteobacteria_Alphaproteobacteria_Schlegelella_Schlegelella_FM
Proteobacteria_Alphaproteobacteria_Uncl_Uncl
Proteobacteria_Deltaproteobacteria_JG37-AG-2_Uncl
Proteobacteria_Deltaproteobacteria_NB1-i_Uncl
Proteobacteria_Epsilonproteobacteria_Arcobacteraceae_Arcobacteraceae
Proteobacteria_Gammaproteobacteria_Alteromonadales_Uncl
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacteriales_Enterobacteriaceae
Proteobacteria_Gammaproteobacteria_Legionellales_Legionella_FM
Proteobacteria_Gammaproteobacteria_Legionellales_Uncl
Proteobacteria_Gammaproteobacteria_Moraxellaceae_Moraxellaceae
Proteobacteria_Gammaproteobacteria_Nitrosomonadales_Uncl
Proteobacteria_Gammaproteobacteria_Pasteurellaceae_Pasteurellaceae
Proteobacteria_Gammaproteobacteria_Pseudomonadaceae_Pseudomonadaceae
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Uncl
Sulfobacilli_Sulfobacillus_Sulfobacillus_Sulfobacillus_FM
Thermi_Thermales_Thermales_Thermaceae
VHS-B5-50_Uncl_Uncl_Uncl

JPL 2-9 Blank

Family (Phy-Subphy-Order-Family) (46 families)

Acidobacteria_iii1-15_Uncl_Uncl
Actinobacteria_Acidimicrobidae_Acidimicrobineae_Acidimicrobineae
Actinobacteria_Acidimicrobidae_JTB31_BD2-10_FM
Actinobacteria_Actinobacteridae_Intrasporangiaceae_Intrasporangiaceae
Actinobacteria_Actinobacteridae_Micromonosporaceae_Micromonosporaceae
Actinobacteria_Actinobacteridae_Propionibacterineae_Propionibacterineae
Actinobacteria_WCHB1-81_Uncl_Uncl
Bacteroidetes_Bacteroidales_Bacteroidales_Bacteroidaceae
Bacteroidetes_Flexibacterales_Flexibacterales_Roseivirga_FM
Bacteroidetes_FukuN24_Saprospirales_Uncl
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Firmicutes_Bacilli_Bacillus_Bacillus_FM
Firmicutes_Bacilli_Lactobacillales_Streptococcaceae
Firmicutes_Bacilli_Uncl_Uncl
Firmicutes_Clostridia_Clostridiales_Clostridiaceae
Firmicutes_Clostridia_Clostridiales_Ruminococcus_FM
Firmicutes_Clostridia_Clostridiales_Uncl
Firmicutes_Desulfotomaculum_Desulfotomaculum_Desulfotomaculum_FM
Planctomycetes_Planctomycetacia_Gemmatales_Gemmata_FM
Poribacteria_Uncl_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Beijerinckiaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Bradyrhizobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Caulobacterales_Uncl
Proteobacteria_Alphaproteobacteria_Defluvicoccus_Defluvicoccus_FM
Proteobacteria_Alphaproteobacteria_Oleomonas_Oleomonas_FM
Proteobacteria_Alphaproteobacteria_Rhizobiaceae_Rhizobiaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Hyphomonadaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacter_FM
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodovulum_FM
Proteobacteria_Alphaproteobacteria_Schlegelella_Schlegelella_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingobium_FM
Proteobacteria_Alphaproteobacteria_Uncl_Uncl
Proteobacteria_Deltaproteobacteria_JG37-AG-2_Uncl
Proteobacteria_Epsilonproteobacteria_Hydrogenimonaceae_Hydrogenimonaceae
Proteobacteria_Gammaproteobacteria_Alteromonadales_Alteromonas_FM
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Legionellales_Legionella_FM
Proteobacteria_Gammaproteobacteria_Legionellales_Uncl
Proteobacteria_Gammaproteobacteria_Pseudomonadaceae_Pseudomonadaceae
Proteobacteria_Gammaproteobacteria_Symbionts_Uncl
Sulfobacilli_Sulfobacillus_Sulfobacillus_Sulfobacillus_FM
Thermi_Thermales_Thermales_Thermaceae
Thermodesulfobacteria_Thermodesulfobacteriaceae_Thermodesulfobacteriaceae_Thermodesulfobacteriaceae

JPL 2-10 Blank

Family (Phy-Subphy-Order-Family) (35 families)

Acidobacteria_Solibacteres_Uncl_Uncl
Actinobacteria_Actinobacteridae_Propionibacterineae_Propionibacterineae
Actinobacteria_Actinobacteridae_Rhodococcus_Rhodococcus_FM
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Bacteroidetes_Saprospirales_Saprospirales_Uncl
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Firmicutes_Clostridia_Peptostreptococcaceae_Peptostreptococcaceae
Firmicutes_Mollicutes_Acholeplasmatales_Uncl
Nitrospirae_Nitrospirales_Nitrospirales_Uncl
OP10_CL500-48_Uncl_Uncl
OP11_Uncl_Uncl_Uncl
Poribacteria_Uncl_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Beijerinckiaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Bradyrhizobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Rhodoplanaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Caedibacteraceae_Caedibacteraceae
Proteobacteria_Alphaproteobacteria_Caulobacterales_Uncl
Proteobacteria_Alphaproteobacteria_Defluvicoccus_Defluvicoccus_FM
Proteobacteria_Alphaproteobacteria_Nordella_Nordella_FM
Proteobacteria_Alphaproteobacteria_Rhizobiaceae_Rhizobiaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacter_FM
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodovulum_FM
Proteobacteria_Alphaproteobacteria_Rickettsiales_Uncl
Proteobacteria_Alphaproteobacteria_Schlegelella_Schlegelella_FM
Proteobacteria_Alphaproteobacteria_Uncl_Uncl
Proteobacteria_Deltaproteobacteria_Syntrophobacteraceae_Syntrophobacteraceae
Proteobacteria_Epsilonproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Legionellales_Uncl
Proteobacteria_Gammaproteobacteria_Nitrosomonadales_Uncl
Sulfobacilli_Sulfobacillus_Sulfobacillus_Sulfobacillus_FM
Thermi_Thermales_Thermales_Thermaceae
Thermodesulfobacteria_Thermodesulfobacteriaceae_Thermodesulfobacteriaceae_Thermodesulfobacteriaceae

JPL Set 3 PCR neg

Family (Phy-Subphy-Order-Family) (26 families)

Actinobacteria_Actinobacteridae_Rhodococcus_Rhodococcus_FM
Bacteroidetes_Flavobacteriales_Flavobacteriales_Cytophaga_FM
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Coprothermobacteria_Uncl_Uncl_Uncl
Cyanobacteria_YS2_Uncl_Uncl
Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae
Firmicutes_Bacilli_Lactobacillales_Streptococcaceae
Firmicutes_Bacilli_Paenibacillaceae_Paenibacillaceae
Firmicutes_Clostridia_Peptostreptococcaceae_Peptostreptococcaceae
Firmicutes_Mollicutes_Uncl_Uncl
Nitrospirae_Nitrospirales_Nitrospirales_Uncl
Planctomycetes_WPS-1_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_Oleomonas_Oleomonas_FM
Proteobacteria_Alphaproteobacteria_Phyllobacteriaceae_Phyllobacteriaceae
Proteobacteria_Epsilonproteobacteria_Sulfuricurvales_Sulfuricurvaceae
Proteobacteria_Gammaproteobacteria_Alcaligenaceae_Alcaligenaceae
Proteobacteria_Gammaproteobacteria_Alteromonadales_Alteromonas_FM
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Pseudomonadaceae_Pseudomonadaceae
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
Sulfobacilli_Sulfobacillus_Sulfobacillus_Sulfobacillus_FM
Synergistetes_Aminanaerobia_Synergistes_Synergistes_Synergistes_FM
Thermi_Thermales_Thermales_Thermaceae
WS5_Uncl_Uncl_Uncl

PCR NEG CONT

Family (Phy-Subphy-Order-Family) (34 families)

Actinobacteria_Acidimicrobidae_Acidimicrobidae_bacterium_Ellin7143_Uncl
Actinobacteria_Actinobacteridae_Arthrobacter_Arthrobacter_FM
Actinobacteria_Actinobacteridae_Propionibacterineae_Propionibacterineae
Actinobacteria_Actinobacteridae_Rhodococcus_Rhodococcus_FM
Bacteroidetes_Flexibacterales_Flexibacterales_Roseivirga_FM
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Bacteroidetes_Uncl_Uncl_Uncl
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Cyanobacteria_Chloroplasts_Uncl_Uncl
Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae
Firmicutes_Bacilli_Lactobacillales_Leuconostoc_FM
Firmicutes_Bacilli_Paenibacillaceae_Paenibacillaceae
OP10_Uncl_Uncl_Uncl
Planctomycetes_Planctomycetacia_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Labrys_Labrys_FM
Proteobacteria_Alphaproteobacteria_Oleomonas_Oleomonas_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Uncl
Proteobacteria_Alphaproteobacteria_Uncl_Uncl
Proteobacteria_Epsilonproteobacteria_Sulfuricurvales_Sulfuricurvaceae
Proteobacteria_Epsilonproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Alcaligenaceae_Alcaligenaceae
Proteobacteria_Gammaproteobacteria_Alteromonadales_Uncl
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Gammaproteobacteria_Uncl
Proteobacteria_Gammaproteobacteria_Legionellales_Uncl
Proteobacteria_Gammaproteobacteria_Pseudomonadaceae_Pseudomonadaceae
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Uncl
Sulfobacilli_Sulfobacillus_Sulfobacillus_Sulfobacillus_FM
Verrucomicrobia_Spartobacteria_Uncl_Uncl
Verrucomicrobia_Verrucomicrobiae_Prosthecobacter_Prosthecobacter_FM
ZB3_Rs-J96_Uncl_Uncl

GI-3 BIG

Family (Phy-Subphy-Order-Family) (19 families)

Acidobacteria_iii1-15_Uncl_Uncl
Actinobacteria_Uncl_Uncl_Uncl
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Caldithrix_KSB1_Caldithrixales_Caldithrixales_Uncl
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Chloroflexi_Chloroflexi-4_Uncl_Uncl
Firmicutes_Clostridia_Catabacter_Catabacter_FM
Firmicutes_Desulfotomaculum_Desulfotomaculum_Desulfotomaculum_FM
Planctomycetes_Planctomycetacia_Gemmatales_Gemmata_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Bradyrhizobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Rhodoplanaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Oleomonas_Oleomonas_FM
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Hyphomonadaceae
Proteobacteria_Alphaproteobacteria_Schlegelella_Schlegelella_FM
Proteobacteria_Gammaproteobacteria_Pseudomonadaceae_Pseudomonadaceae
Spirochaetes_Leptospirales_Leptospirales_Leptonemaceae
Synergistetes_Aminanaerobia_Anaerobaculum_Anaerobaculum_Anaerobaculum_FM

GI-3 Blank

Family (Phy-Subphy-Order-Family) (24 families)

Actinobacteria_Actinobacteridae_Gordoniaceae_Gordoniaceae
Actinobacteria_Actinobacteridae_Propionibacterineae_Propionibacterineae
Actinobacteria_Actinobacteridae_Streptosporangineae_Streptosporangineae
Actinobacteria_Coriobacteridae_Coriobacteriales_Collinsella_FM
Bacteroidetes_Flavobacteriales_Flavobacteriales_Flavobacteriaceae
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Chlorobi_Uncl_Uncl_Uncl
Firmicutes_Bacilli_Uncl_Uncl
Firmicutes_Clostridia_Clostridiales_Uncl
Firmicutes_Uncl_Uncl_Uncl
Marine_group_AA714017_Uncl_Uncl
OP10_CH21_Uncl_Uncl
Planctomycetes_Planctomycetacia_Planctomycetales_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Hyphomonadaceae
Proteobacteria_Alphaproteobacteria_Rickettsiales_Uncl
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacteriales_Enterobacteriaceae
Proteobacteria_Gammaproteobacteria_Moraxellaceae_Moraxellaceae
Proteobacteria_Gammaproteobacteria_Neisseriales_Chromobacterium_FM
Proteobacteria_Gammaproteobacteria_Nitrosomonadales_Uncl
Proteobacteria_Gammaproteobacteria_Ralstoniaceae_Ralstoniaceae
WS5_Uncl_Uncl_Uncl

GI-3 FC

Family (Phy-Subphy-Order-Family) (71 families)

Acidobacteria_iii1-15_Uncl_Uncl
Acidobacteria_Solibacteres_Solibacteraceae_Solibacteraceae
Actinobacteria_Acidimicrobidae_JTB31_BD2-10_FM
Actinobacteria_Acidimicrobidae_Microthrixineae_Microthrixineae
Actinobacteria_Actinobacteridae_Frankineae_Frankineae
Actinobacteria_Actinobacteridae_Gordoniaceae_Gordoniaceae
Actinobacteria_Actinobacteridae_Micromonosporaceae_Micromonosporaceae
Actinobacteria_Actinobacteridae_Propionibacterineae_Propionibacterineae
Actinobacteria_Actinobacteridae_Pseudonocardiaceae_Pseudonocardiaceae
Actinobacteria_Actinobacteridae_Streptomycineae_Streptomycineae
Actinobacteria_Actinobacteridae_Streptosporangineae_Streptosporangineae
Actinobacteria_Actinobacteridae_Uncl_Uncl
Actinobacteria_Rubrobacteridae_Uncl_Uncl
Bacteroidetes_Bacteroidales_Bacteroidales_Bacteroidaceae
Bacteroidetes_Bacteroidales_Bacteroidales_Uncl
Bacteroidetes_Flexibacterales_Flexibacterales_Roseivirga_FM
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Bacteroidetes_Saprospirales_Saprospirales_Uncl
Bacteroidetes_SHA-94_Bacteroidales_Uncl
Chlorobi_Uncl_Uncl_Uncl
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Cyanobacteria_YS2_Uncl_Uncl
Firmicutes_Bacilli_Bacillus_Bacillus_FM
Firmicutes_Bacilli_Exiguobacterium_Exiguobacterium_FM
Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae
Firmicutes_Bacilli_Planococcaceae_Planococcaceae
Firmicutes_Bacilli_Staphylococcaceae_Staphylococcaceae
Firmicutes_Bacilli_Uncl_Uncl
Firmicutes_Clostridia_Peptostreptococcaceae_Peptostreptococcaceae
Firmicutes_Syntrophomonadaceae_Syntrophomonadaceae_Syntrophomonadaceae
Nitrospirae_Thermodesulfovibrionales_Thermodesulfovibrionales_Thermodesulfovibrionaceae
OP10_CH21_Uncl_Uncl
OP10_Uncl_Uncl_Uncl
Planctomycetes_Planctomycetacia_Planctomycetales_Uncl
Planctomycetes_Planctomycetacia_Uncl_Uncl
Poribacteria_Uncl_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_alpha_proteobacterium_MBIC1474_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Rhodoplanaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Xanthobacteraceae
Proteobacteria_Alphaproteobacteria_Caedibacteraceae_Caedibacteraceae
Proteobacteria_Alphaproteobacteria_Caulobacterales_Uncl
Proteobacteria_Alphaproteobacteria_Nordella_Nordella_FM
Proteobacteria_Alphaproteobacteria_Rhizobiaceae_Rhizobiaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Hyphomonadaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacter_FM
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodovulum_FM

Proteobacteria_Alphaproteobacteria_Rhodobacterales_S36_FM
Proteobacteria_Alphaproteobacteria_Rickettsiales_Uncl
Proteobacteria_Alphaproteobacteria_Schlegelella_Schlegelella_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Porphyrobacter_FM
Proteobacteria_Alphaproteobacteria_Uncl_Uncl
Proteobacteria_Deltaproteobacteria_Syntrophaceae_Syntrophaceae
Proteobacteria_Desulfovibrionales_Desulfovibrionales_Desulfovibrionaceae
Proteobacteria_Gammaproteobacteria_Alcaligenaceae_Alcaligenaceae
Proteobacteria_Gammaproteobacteria_Alteromonadales_Alteromonas_FM
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacteriales_Enterobacteriaceae
Proteobacteria_Gammaproteobacteria_Legionellales_Legionella_FM
Proteobacteria_Gammaproteobacteria_Legionellales_Uncl
Proteobacteria_Gammaproteobacteria_Moraxellaceae_Moraxellaceae
Proteobacteria_Gammaproteobacteria_Neisseriales_Chromobacterium_FM
Proteobacteria_Gammaproteobacteria_Nitrosomonadales_Uncl
Proteobacteria_Gammaproteobacteria_Pseudomonadaceae_Pseudomonadaceae
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Vibrionaceae_Vibrionaceae
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Uncl
Spirochaetes_Spirochaetales_Spirochaetales_Spirochaetaceae
Thermi_Thermales_Thermales_Meiothermaceae
Thermi_Thermales_Thermales_Thermaceae

GI-4 BIG

Family (Phy-Subphy-Order-Family) (10 families)
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Caldithrix_KSB1_Caldithrixales_Caldithrixales_Uncl
Chlorobi_BSV19_Uncl_Uncl
Planctomycetes_Planctomycetacia_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Bradyrhizobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Consistiales_Uncl
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
TM6_Uncl_Uncl_Uncl
TM7_TM7-1_Uncl_Uncl

GI-4 Blank

Family (Phy-Subphy-Order-Family) (61 families)
Actinobacteria_Actinobacteridae_Frankineae_Frankineae
Actinobacteria_Actinobacteridae_Gordoniaceae_Gordoniaceae
Actinobacteria_Actinobacteridae_Propionibacterineae_Propionibacterineae
Actinobacteria_Actinobacteridae_Pseudonocardiaceae_Pseudonocardiaceae
Actinobacteria_Actinobacteridae_Streptomycineae_Streptomycineae
Actinobacteria_Actinobacteridae_Uncl_Uncl
Bacteroidetes_FukuN24_Saprospirales_Uncl
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Chlorobi_Uncl_Uncl_Uncl
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae
Firmicutes_Bacilli_Lactobacillales_Leuconostoc_FM
Firmicutes_Bacilli_Staphylococcaceae_Staphylococcaceae
Firmicutes_Bacilli_Uncl_Uncl
Firmicutes_Clostridia_Clostridiales_Uncl
Firmicutes_Clostridia_Peptostreptococcaceae_Peptostreptococcaceae
Firmicutes_Mollicutes_Uncl_Uncl
Firmicutes_Syntrophomonadaceae_Syntrophomonadaceae_Syntrophomonadaceae
Firmicutes_Uncl_Uncl_Uncl
Nitrospirae_Nitrospirales_Nitrospirales_Nitrospira_FM
Nitrospirae_Nitrospirales_Nitrospirales_Uncl
OP10_CH21_Uncl_Uncl
Planctomycetes_Planctomycetacia_Isosphaerales_Isosphaeraceae
Planctomycetes_Planctomycetacia_Planctomycetales_Uncl
Poribacteria_Uncl_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_alpha_proteobacterium_MBIC1474_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Beijerinckiaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Rhodoplanaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Caedibacteraceae_Caedibacteraceae
Proteobacteria_Alphaproteobacteria_Nordella_Nordella_FM
Proteobacteria_Alphaproteobacteria_Rhizobiaceae_Rhizobiaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacter_FM
Proteobacteria_Alphaproteobacteria_Rhodobacterales_S36_FM
Proteobacteria_Alphaproteobacteria_Rickettsiales_Uncl
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Porphyrobacter_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonas_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Uncl
Proteobacteria_Alphaproteobacteria_Uncl_Uncl
Proteobacteria_Deltaproteobacteria_JG37-AG-2_Uncl
Proteobacteria_Deltaproteobacteria_Syntrophaceae_Syntrophaceae
Proteobacteria_Deltaproteobacteria_Uncl_Uncl
Proteobacteria_Desulfovibrionales_Desulfovibrionales_Desulfovibrionaceae
Proteobacteria_Epsilonproteobacteria_Arcobacteraceae_Arcobacteraceae
Proteobacteria_Epsilonproteobacteria_Sulfurovumales_Sulfurovumaceae
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacteriales_Enterobacteriaceae
Proteobacteria_Gammaproteobacteria_Legionellales_Uncl
Proteobacteria_Gammaproteobacteria_Neisseriales_Chromobacterium_FM
Proteobacteria_Gammaproteobacteria_Neisseriales_Uncl
Proteobacteria_Gammaproteobacteria_Nitrosomonadales_Uncl
Proteobacteria_Gammaproteobacteria_Ralstoniaceae_Ralstoniaceae
Proteobacteria_Gammaproteobacteria_Rhodocyclales_Uncl
Proteobacteria_Gammaproteobacteria_Shewanellaceae_Shewanellaceae
Proteobacteria_Gammaproteobacteria_Sutterellaceae_Sutterellaceae
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Vibrionaceae_Vibrionaceae
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Uncl
SR1_BD2-14_Uncl_Uncl

GI-7A Blank

Family (Phy-Subphy-Order-Family) (21 families)

Actinobacteria_Actinobacteridae_Rhodococcus_Rhodococcus_FM
Bacteroidetes_E13_Bacteroidales_Uncl
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Bacteroidetes_SHA-94_Bacteroidales_Uncl
Bacteroidetes_Uncl_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_Acetobacterales_Roseomonas_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Bradyrhizobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Rhodoplanaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Uncl
Proteobacteria_Deltaproteobacteria_Myxococcales_Polyangiaceae
Proteobacteria_Epsilonproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_MND1_mle1-7_FM
Proteobacteria_Gammaproteobacteria_Ralstoniaceae_Ralstoniaceae
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
Thermi_Thermales_Thermales_Thermaceae
Uncl_Uncl_Uncl_Uncl
WCHB1-27_Uncl_Uncl_Uncl
WPS-2_Uncl_Uncl_Uncl

GI-7B Blankhaha

Family (Phy-Subphy-Order-Family) (33 families)

Actinobacteria_Actinobacteridae_Micromonosporaceae_Micromonosporaceae
Actinobacteria_Actinobacteridae_Propionibacterineae_Propionibacterineae
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Bacteroidetes_Uncl_Uncl_Uncl
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Firmicutes_Clostridia_Clostridiales_Clostridiaceae
Firmicutes_Clostridia_Peptostreptococcaceae_Peptostreptococcaceae
Firmicutes_Clostridia_Uncl_Uncl
Firmicutes_Mollicutes_Uncl_Uncl
OP10_Uncl_Uncl_Uncl
Poribacteria_Uncl_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_alpha_proteobacterium_MBIC1474_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Oleomonas_Oleomonas_FM
Proteobacteria_Alphaproteobacteria_Phyllobacteriaceae_Phyllobacteriaceae
Proteobacteria_Alphaproteobacteria_Rickettsiales_Uncl
Proteobacteria_Alphaproteobacteria_Schlegelella_Schlegelella_FM
Proteobacteria_Alphaproteobacteria_Uncl_Uncl
Proteobacteria_Desulfovibrionales_Desulfovibrionales_Desulfovibrionaceae
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacteriales_Enterobacteriaceae
Proteobacteria_Gammaproteobacteria_Legionellales_Uncl
Proteobacteria_Gammaproteobacteria_Moraxellaceae_Moraxellaceae
Proteobacteria_Gammaproteobacteria_Nitrosomonadales_Uncl
Proteobacteria_Gammaproteobacteria_Pasteurellaceae_Pasteurellaceae
Proteobacteria_Gammaproteobacteria_Pseudomonadaceae_Pseudomonadaceae
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Vibrionaceae_Vibrionaceae
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Uncl
Spirochaetes_Leptospirales_Leptospirales_Leptonemaceae
SR1_BD2-14_Uncl_Uncl
Sulfobacilli_Sulfobacillus_Sulfobacillus_Sulfobacillus_FM

GI-7C Blank

Family (Phy-Subphy-Order-Family) (49 families)
Actinobacteria_Acidimicrobidae_Uncl_Uncl
Actinobacteria_Actinobacteridae_Micromonosporaceae_Micromonosporaceae
Actinobacteria_Actinobacteridae_Propionibacterineae_Propionibacterineae
Actinobacteria_Actinobacteridae_Streptomycineae_Streptomycineae
Actinobacteria_Actinobacteridae_Streptosporangineae_Streptosporangineae
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Cyanobacteria_Chloroplasts_Uncl_Uncl
Elusimicrobia_TG1_Uncl_Uncl_Uncl
Firmicutes_Clostridia_Clostridiales_Ruminococcus_FM
Firmicutes_Clostridia_Clostridiales_Uncl
Firmicutes_Clostridia_Peptostreptococcaceae_Peptostreptococcaceae
OP10_Uncl_Uncl_Uncl
Planctomycetes_agg27_ARKCH2Br2-76_Uncl
Planctomycetes_Planctomycetacia_Planctomycetales_Uncl
Poribacteria_Uncl_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_Uncl_Uncl
Proteobacteria_Deltaproteobacteria_Geobacter_Geobacter_FM
Proteobacteria_Deltaproteobacteria_Syntrophobacteraceae_Syntrophobacteraceae
Proteobacteria_Desulfovibrionales_Desulfovibrionales_Desulfovibrionaceae
Proteobacteria_Epsilonproteobacteria_Hydrogenimonaceae_Hydrogenimonaceae
Proteobacteria_Epsilonproteobacteria_Sulfurovumales_Sulfurovumaceae
Proteobacteria_Gammaproteobacteria_Alcaligenaceae_Alcaligenaceae
Proteobacteria_Gammaproteobacteria_Alteromonadales_Rheinheimeraceae
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Bradyrhizobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Hyphomicrobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacteriaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Rhodoplanaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Xanthobacteraceae
Proteobacteria_Alphaproteobacteria_Caulobacterales_Brevundimonas_FM
Proteobacteria_Alphaproteobacteria_Consistiales_SAR11_FM
Proteobacteria_Alphaproteobacteria_Oleomonas_Oleomonas_FM
Proteobacteria_Alphaproteobacteria_Pseudochrobactrum_Pseudochrobactrum_FM
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Hyphomonadaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacter_FM
Proteobacteria_Alphaproteobacteria_Rhodobacterales_S36_FM
Proteobacteria_Alphaproteobacteria_Schlegelella_Schlegelella_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Uncl
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacteriales_Enterobacteriaceae
Proteobacteria_Gammaproteobacteria_Legionellales_Uncl
Proteobacteria_Gammaproteobacteria_Nitrosomonadales_Uncl
Proteobacteria_Gammaproteobacteria_Pseudomonadaceae_Pseudomonadaceae
Proteobacteria_Gammaproteobacteria_Sutterellaceae_Sutterellaceae
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
Sulfobacilli_Sulfobacillus_Sulfobacillus_Sulfobacillus_FM
Thermi_Thermales_Thermales_Thermaceae

GI-7D Blank

Family (Phy-Subphy-Order-Family) (51 families)
Actinobacteria_Actinobacteridae_Agromyces_Agromyces_FM
Actinobacteria_Actinobacteridae_Frankineae_Frankineae
Actinobacteria_Actinobacteridae_Intrasporangiaceae_Intrasporangiaceae
Actinobacteria_Actinobacteridae_Micromonosporaceae_Micromonosporaceae
Actinobacteria_Actinobacteridae_Propionibacterineae_Propionibacterineae
Actinobacteria_Actinobacteridae_Pseudonocardiaceae_Pseudonocardiaceae
Actinobacteria_Actinobacteridae_Rhodococcus_Rhodococcus_FM
Actinobacteria_Actinobacteridae_Streptomycineae_Streptomycineae
Actinobacteria_Actinobacteridae_Streptosporangineae_Streptosporangineae
Actinobacteria_Actinobacteridae_Uncl_Uncl
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Cyanobacteria_YS2_Uncl_Uncl
Elusimicrobia_TG1_Elusimicrobiales_Elusimicrobiales__Elusimicrobiaceae
Firmicutes_Acidaminococcaceae_Acidaminococcaceae_Acidaminococcaceae
Firmicutes_Bacilli_Bacillus_Bacillus_FM
Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae
Firmicutes_Bacilli_Paenibacillaceae_Paenibacillaceae
Firmicutes_Bacilli_Staphylococcaceae_Staphylococcaceae
Firmicutes_Clostridia_Clostridiales_Ruminococcus_FM
Firmicutes_Clostridia_Peptostreptococcaceae_Peptostreptococcaceae
Firmicutes_Desulfotomaculum_Desulfotomaculum_Desulfotomaculum_FM
OP10_Uncl_Uncl_Uncl
OP9_JS1_JS1_Uncl_Uncl
Planctomycetes_Planctomycetacia_Planctomycetales_Uncl
Poribacteria_Uncl_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_Anderseniella_Anderseniella_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Bradyrhizobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Rhodoplanaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Xanthobacteraceae
Proteobacteria_Alphaproteobacteria_Caulobacterales_Brevundimonas_FM
Proteobacteria_Alphaproteobacteria_Oleomonas_Oleomonas_FM
Proteobacteria_Alphaproteobacteria_Phyllobacteriaceae_Phyllobacteriaceae
Proteobacteria_Alphaproteobacteria_Rickettsiales_Uncl
Proteobacteria_Alphaproteobacteria_Schlegelella_Schlegelella_FM
Proteobacteria_Alphaproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Alcaligenaceae_Alcaligenaceae
Proteobacteria_Gammaproteobacteria_Alteromonadales_Uncl
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacteriales_Enterobacteriaceae
Proteobacteria_Gammaproteobacteria_Legionellales_Uncl
Proteobacteria_Gammaproteobacteria_Nitrosomonadales_Uncl
Proteobacteria_Gammaproteobacteria_Pseudomonadaceae_Pseudomonadaceae
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
Spirochaetes_Treponemaceae_Treponemaceae_Treponemaceae
SR1_BD2-14_Uncl_Uncl
Sulfobacilli_Sulfobacillus_Sulfobacillus_Sulfobacillus_FM
Thermi_Thermales_Thermales_Thermaceae

GI-10 Blank

Family (Phy-Subphy-Order-Family) (41 families)

Acidobacteria_Solibacteres_Solibacteraceae_Solibacteraceae
Actinobacteria_Actinobacteridae_Streptomycineae_Streptomycineae
Bacteroidetes_Bacteroidales_Bacteroidales_Proteophilaceae
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Cyanobacteria_Chloroplasts_Uncl_Uncl
Firmicutes_Acidaminococcaceae_Acidaminococcaceae_Acidaminococcaceae
Firmicutes_Bacilli_Bacillus_Bacillus_FM
Firmicutes_Bacilli_Lactobacillales_Streptococcaceae
Firmicutes_Bacilli_Paenibacillaceae_Paenibacillaceae
Firmicutes_Bacilli_Uncl_Uncl
Firmicutes_Clostridia_Peptostreptococcaceae_Peptostreptococcaceae
Firmicutes_Mollicutes_Uncl_Uncl
Haloanaerobiales_Halanaerobiaceae_Halanaerobiaceae_Halanaerobiaceae
Marine_group_AA714017_Uncl_Uncl
NC10_Uncl_Uncl_Uncl
Planctomycetes_Planctomycetacia_Planctomycetales_Uncl
Planctomycetes_Planctomycetacia_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_Acetobacterales_Roseomonas_FM
Proteobacteria_Alphaproteobacteria_Aurantimonadaceae_Aurantimonadaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Pleomorphomonas_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Rhodoplanaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Rhodobacterales_S36_FM
Proteobacteria_Alphaproteobacteria_Rickettsiales_Uncl
Proteobacteria_Alphaproteobacteria_Schlegelella_Schlegelella_FM
Proteobacteria_Alphaproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_bacterium_Ellin6067_Uncl
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacteriales_Enterobacteriaceae
Proteobacteria_Gammaproteobacteria_Gammaproteobacteria_Uncl
Proteobacteria_Gammaproteobacteria_Moraxellaceae_Moraxellaceae
Proteobacteria_Gammaproteobacteria_Neisseriales_Chromobacterium_FM
Proteobacteria_Gammaproteobacteria_Nitrosomonadales_Uncl
Proteobacteria_Gammaproteobacteria_Pseudomonadaceae_Pseudomonadaceae
Proteobacteria_Gammaproteobacteria_Sutterellaceae_Sutterellaceae
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Uncl
Sulfobacilli_Sulfobacillus_Sulfobacillus_Sulfobacillus_FM
Thermi_Thermales_Thermales_Thermaceae
Thermodesulfobacteria_Thermodesulfobacteriaceae_Thermodesulfobacteriaceae_Thermodesulfobacteriaceae

GI-10 Neg

Family (Phy-Subphy-Order-Family) (15 families)

Actinobacteria_Actinobacteridae_Streptosporangineae_Streptosporangineae
Actinobacteria_Uncl_Uncl_Uncl
Actinobacteria_WCHB1-81_Uncl_Uncl
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Chloroflexi_Dehalococcoidetes_Uncl_Uncl
Firmicutes_Clostridia_Clostridiales_Uncl
Proteobacteria_Alphaproteobacteria_Phyllobacteriaceae_Phyllobacteriaceae
Proteobacteria_Alphaproteobacteria_Rickettsiales_Uncl
Proteobacteria_Gammaproteobacteria_Alteromonadales_Colwelliaceae
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacteriales_Enterobacteriaceae
Proteobacteria_Gammaproteobacteria_Legionellales_Uncl
Proteobacteria_Gammaproteobacteria_Moraxellaceae_Moraxellaceae
Proteobacteria_Gammaproteobacteria_Pasteurellaceae_Pasteurellaceae
Proteobacteria_Gammaproteobacteria_Pseudomonadaceae_Pseudomonadaceae

GI-11 Blank

Family (Phy-Subphy-Order-Family) (75 families)
Actinobacteria_Actinobacteridae_Bifidobacteriaceae_Bifidobacteriaceae
Actinobacteria_Actinobacteridae_Brachybacterium_Brachybacterium_FM
Bacteroidetes_Bacteroidales_Bacteroidales_Uncl
Bacteroidetes_Flavobacteriales_Flavobacteriales_Cytophaga_FM
Bacteroidetes_Flavobacteriales_Flavobacteriales_Sporocytophaga_FM
Bacteroidetes_Flexibacterales_Flexibacterales_Roseivirga_FM
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Bacteroidetes_Saprospirales_Saprospirales_Uncl
Bacteroidetes_SHA-94_Bacteroidales_Uncl
Bacteroidetes_Uncl_Uncl_Uncl
Chlorobi_Uncl_Uncl_Uncl
Chloroflexi_Anaerolineae_Anaerolineae_Anaerolineae
Cyanobacteria_Chloroplasts_Uncl_Uncl
Cyanobacteria_Uncl_Uncl_Uncl
Elusimicrobia_TG1_Uncl_Uncl_Uncl
Firmicutes_Bacilli_Halobacillus_Halobacillus_FM
Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae
Firmicutes_Bacilli_Paenibacillaceae_Paenibacillaceae
Firmicutes_Bacilli_Staphylococcaceae_Staphylococcaceae
Firmicutes_Bacilli_Uncl_Uncl
Firmicutes_Clostridia_Clostridiales_Clostridiaceae
Firmicutes_Clostridia_Clostridiales_Uncl
Firmicutes_Clostridia_Peptostreptococcaceae_Peptostreptococcaceae
Firmicutes_Clostridia_Uncl_Uncl
Firmicutes_Mollicutes_Uncl_Uncl
Haloanaerobiales_Halanaerobiaceae_Halanaerobiaceae_Halanaerobiaceae
Marine_group_AA714017_Uncl_Uncl
OP10_Uncl_Uncl_Uncl
Planctomycetes_Planctomycetacia_Planctomycetales_Uncl
Poribacteria_Uncl_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_Azospirillaceae_Azospirillaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Bradyrhizobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Hyphomicrobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacteriaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Rhodoplanaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Caedibacteraceae_Caedibacteraceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacter_FM
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodovulum_FM
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Uncl
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingobium_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Sphingomonas_FM
Proteobacteria_Alphaproteobacteria_Sphingomonadales_Uncl
Proteobacteria_Alphaproteobacteria_Uncl_Uncl
Proteobacteria_Deltaproteobacteria_Desulfovibrio_Desulfovibrio_FM
Proteobacteria_Deltaproteobacteria_Geobacter_Geobacter_FM
Proteobacteria_Desulfovibrionales_Desulfovibrionales_Desulfovibrionaceae
Proteobacteria_Epsilonproteobacteria_Arcobacteraceae_Arcobacteraceae
Proteobacteria_Epsilonproteobacteria_Sulfuricurvales_Sulfuricurvaceae
Proteobacteria_Epsilonproteobacteria_Sulfurospirillaceae_Sulfurospirillaceae
Proteobacteria_Gammaproteobacteria_Alcaligenaceae_Alcaligenaceae
Proteobacteria_Gammaproteobacteria_Alteromonadaceae_Alteromonadaceae
Proteobacteria_Gammaproteobacteria_Alteromonadales_Alteromonas_FM
Proteobacteria_Gammaproteobacteria_Alteromonadales_Rheinheimeraceae
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Enterobacteriales_Enterobacteriaceae_Enterobacteriales_Enterobacteriaceae
Proteobacteria_Gammaproteobacteria_Hydrogenophilales_Petrobacter_FM
Proteobacteria_Gammaproteobacteria_Legionellales_Uncl
Proteobacteria_Gammaproteobacteria_Marinobacter_Marinobacter_FM
Proteobacteria_Gammaproteobacteria_Moraxellaceae_Moraxellaceae
Proteobacteria_Gammaproteobacteria_Neisseriales_Chromobacterium_FM
Proteobacteria_Gammaproteobacteria_Neisseriales_Uncl
Proteobacteria_Gammaproteobacteria_Pasteurellaceae_Pasteurellaceae
Proteobacteria_Gammaproteobacteria_Pseudomonadaceae_Pseudomonadaceae
Proteobacteria_Gammaproteobacteria_Rhodocyclales_Uncl
Proteobacteria_Gammaproteobacteria_SBR1001_Uncl
Proteobacteria_Gammaproteobacteria_Sutterellaceae_Sutterellaceae
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
Spirochaetes_Treponemaceae_Treponemaceae_Treponemaceae
Thermi_Thermales_Thermales_Meiothermaceae
Thermi_Thermales_Thermales_Thermaceae
Thermoanaerobacteria_Uncl_Uncl_Uncl
Thermotogae_Geotogaceae_Geotogaceae_Geotogaceae

GI-11 Neg

Family (Phy-Subphy-Order-Family) (28 families)
Actinobacteria_Actinobacteridae_Brachybacterium_Brachybacterium_FM
Actinobacteria_Actinobacteridae_Gordoniaceae_Gordoniaceae
Actinobacteria_Actinobacteridae_Propionibacterineae_Propionibacterineae
Actinobacteria_Actinobacteridae_Streptomycineae_Streptomycineae
Bacteroidetes_Flavobacteriales_Flavobacteriales_Flavobacteriaceae
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Bacteroidetes_Saprospirales_Saprospirales_Uncl
Cyanobacteria_Oscillatoria_Oscillatoria_Oscillatoria_FM
Elusimicrobia_TG1_Uncl_Uncl_Uncl
Firmicutes_Acidaminococcaceae_Acidaminococcaceae_Acidaminococcaceae
Firmicutes_Clostridia_Clostridiales_Clostridiaceae
Firmicutes_Clostridia_Clostridiales_Uncl
Firmicutes_Clostridia_Peptostreptococcaceae_Peptostreptococcaceae
Firmicutes_Mollicutes_Uncl_Uncl
OP10_Uncl_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Rhodoplanaceae
Proteobacteria_Alphaproteobacteria_Phyllobacteriaceae_Phyllobacteriaceae
Proteobacteria_Alphaproteobacteria_Uncl_Uncl
Proteobacteria_Deltaproteobacteria_JG37-AG-2_Uncl
Proteobacteria_Gammaproteobacteria_Alteromonadales_Alteromonas_FM
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Legionellales_Uncl
Proteobacteria_Gammaproteobacteria_Moraxellaceae_Moraxellaceae
Proteobacteria_Gammaproteobacteria_obligately_oligotrophic_bacteria_KI89C_Uncl
Proteobacteria_Gammaproteobacteria_Pseudomonadaceae_Pseudomonadaceae
Proteobacteria_Gammaproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Xanthomonadales_Uncl

GI-13 BIG

Family (Phy-Subphy-Order-Family) (17 families)

Actinobacteria_Actinobacteridae_Propionibacterineae_Propionibacterineae
Actinobacteria_Actinobacteridae_Rhodococcus_Rhodococcus_FM
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Caldithrix_KSB1_Caldithrixales_Caldithrixales_Uncl
Firmicutes_Mollicutes_Clostridium_Clostridium_FM
Poribacteria_Uncl_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Oleomonas_Oleomonas_FM
Proteobacteria_Alphaproteobacteria_Rickettsiales_Uncl
Proteobacteria_Gammaproteobacteria_Alcaligenaceae_Alcaligenaceae
Proteobacteria_Gammaproteobacteria_Alteromonadales_Idiomarinaceae
Proteobacteria_Gammaproteobacteria_Burkholderiaceae_Burkholderiaceae
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Pseudomonadaceae_Pseudomonadaceae
Spirochaetes_Leptospirales_Leptospirales_Leptonemaceae
TM7_TM7-3_Uncl_Uncl

GI-13 Blank

Family (Phy-Subphy-Order-Family) (16 families)

ABY1_OD1_WCHB1-58_Uncl_Uncl
Caldithrix_KSB1_Caldithrixales_Caldithrixales_Uncl
Chlorobi_SJA-28_Uncl_Uncl
Chloroflexi_Ktedonobacteria_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Bradyrhizobium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Caulobacterales_Uncl
Proteobacteria_Alphaproteobacteria_Consistiales_Uncl
Proteobacteria_Alphaproteobacteria_Devosia_Devosia_FM
Proteobacteria_Alphaproteobacteria_Oleomonas_Oleomonas_FM
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Hyphomonadaceae
Proteobacteria_Epsilonproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_MND1_LO131_FM
Proteobacteria_Gammaproteobacteria_Pseudomonadaceae_Pseudomonadaceae

GI-14 Blank

Family (Phy-Subphy-Order-Family) (27 families)

Actinobacteria_Actinobacteridae_Propionibacterineae_Propionibacterineae
Actinobacteria_Actinobacteridae_Rhodococcus_Rhodococcus_FM
Actinobacteria_Actinobacteridae_Uncl_Uncl
Bacteroidetes_Saprospirales_Saprospirales_Saprospiraceae
Chloroflexi_Roseiflexales_Roseiflexales_Kouleothrix_FM
Cyanobacteria_Chloroplasts_Uncl_Uncl
Firmicutes_Bacilli_Lactobacillales_Streptococcaceae
Firmicutes_Clostridia_Clostridiales_Clostridiaceae
OP10_Uncl_Uncl_Uncl
Poribacteria_Uncl_Uncl_Uncl
Proteobacteria_Alphaproteobacteria_Azospirillaceae_Azospirillaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Methylobacterium_FM
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Rhodoplanaceae
Proteobacteria_Alphaproteobacteria_Bradyrhizobiales_Uncl
Proteobacteria_Alphaproteobacteria_Caulobacterales_Brevundimonas_FM
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Hyphomonadaceae
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodobacter_FM
Proteobacteria_Alphaproteobacteria_Rhodobacterales_Rhodovulum_FM
Proteobacteria_Alphaproteobacteria_Schlegelella_Schlegelella_FM
Proteobacteria_Alphaproteobacteria_Uncl_Uncl
Proteobacteria_Deltaproteobacteria_JG37-AG-2_Uncl
Proteobacteria_Epsilonproteobacteria_Uncl_Uncl
Proteobacteria_Gammaproteobacteria_Alcaligenaceae_Alcaligenaceae
Proteobacteria_Gammaproteobacteria_Comamonadaceae_Comamonadaceae
Proteobacteria_Gammaproteobacteria_Pseudomonadaceae_Pseudomonadaceae
Spirochaetes_Leptospirales_Leptospirales_Leptonemaceae
Synergistetes_Aminanaerobia_TTA_B6_Uncl_Uncl

E.2.2 Generation 3 (G3) PhyloChip

E.2.2.1 Amount of PCR Product Loaded onto PhyloChips (G3) (ng)

Sample Name	Amount of PCR product loaded onto PhyloChips (G3)	(ng)
G3 PhyloChips		
GI_15		350
GI_16	N	
GI_17		350
GI_18	N	
GI_19		350
GI_20		128
GI_21		350
GI_22	N	
GI_23		350
GI_24		350
GI_25		140
GI_26		350
GI_27		92
GI_28		70
GI_29		280
GI_30	N	
GI_32	N	
GI_36-3		450
GI_36-4		400
GI_38	N	
GI_39	N	
GI_40	N	
GI_41	N	
	N = no measureable 16S rRNA gene band	
Blanks		
GIB_15–28	N	
18B	N	
19B	N	
20B		72
GI_Blank-Set 29–43	N	
GI_38b	N	

E.2.2.2 Sample Data

GI-15

Phylum/Class; Genus (80)
Actinobacteria; Acidimicrobium
Actinobacteria; Arthrobacter
Actinobacteria; Corynebacterium
Actinobacteria; Saccharomonospora
Actinobacteria; Streptomyces
Actinobacteria; Uncl_Corynebacteriaceae
Alphaproteobacteria; Bradyrhizobium
Alphaproteobacteria; Novosphingobium
Alphaproteobacteria; Ochrobactrum
Alphaproteobacteria; Sphingobium
Alphaproteobacteria; Uncl_Holosporaceae
Alphaproteobacteria; Uncl_Rhodobacteraceae
Alphaproteobacteria; Uncl_Rhodospirillaceae
Bacteroidetes; Chryseobacterium
Bacteroidetes; Flavobacterium
Bacteroidetes; Salinibacter
Bacteroidetes; Sphingobacterium
Bacteroidetes; Uncl_Corymorphaceae
Bacteroidetes; Uncl_Flavobacteriaceae
Bacteroidetes; Uncl_RikenellaceaeII
Bacteroidetes; Uncl_Sphingobacteriaceae
Betaproteobacteria; Achromobacter
Betaproteobacteria; Acidovorax
Betaproteobacteria; Aquabacterium
Betaproteobacteria; Burkholderia
Betaproteobacteria; Comamonas
Betaproteobacteria; Delftia
Betaproteobacteria; Diaphorobacter
Betaproteobacteria; Herbaspirillum
Betaproteobacteria; Massilia
Betaproteobacteria; Methyloversatilis
Betaproteobacteria; Rhodocyclus
Betaproteobacteria; Roseateles
Betaproteobacteria; Thiobacillus
Betaproteobacteria; Thiomonas
Betaproteobacteria; Uncl_Alcaligenaceae
Betaproteobacteria; Uncl_Comamonadaceae
Betaproteobacteria; Uncl_Methylophilaceae
Betaproteobacteria; Uncl_Nitrosomonadaceae
Betaproteobacteria; Uncl_Oxalobacteraceae
Chloroflexi; A4b
Chloroflexi; Uncl_Caldilineaceae
Cyanobacteria; Leptolyngbya
Cyanobacteria; Nostoc
Deltaproteobacteria; Desulfovibrio
Deltaproteobacteria; Uncl_Syntrophaceae
Firmicutes; Bacillus
Firmicutes; Clostridium
Firmicutes; Coprococcus
Firmicutes; Lactobacillus
Firmicutes; Staphylococcus
Firmicutes; Streptococcus
Firmicutes; Trichococcus
Firmicutes; Uncl_Lachnospiraceae
Firmicutes; Uncl_Planococcaceae
Firmicutes; Uncl_Ruminococcaceae
Gammaproteobacteria; Acinetobacter
Gammaproteobacteria; Congregibacter
Gammaproteobacteria; Halomonas
Gammaproteobacteria; Klebsiella
Gammaproteobacteria; Methylomonas
Gammaproteobacteria; Pantoea
Gammaproteobacteria; Pseudoalteromonas
Gammaproteobacteria; Pseudomonas
Gammaproteobacteria; Salmonella
Gammaproteobacteria; Shewanella
Gammaproteobacteria; Succinivibrio
Gammaproteobacteria; Uncl_Coxiellaceae
Gammaproteobacteria; Uncl_Enterobacteriaceae
Gammaproteobacteria; Uncl_Halothiobacillaceae
Gammaproteobacteria; Uncl_HTCC2188
Gammaproteobacteria; Uncl_Methylococcaceae
Gammaproteobacteria; Uncl_Pseudomonadaceae
Gammaproteobacteria; Vibrio
Gemmatimonadetes; sfA
Planctomycetes; Uncl_Planctomycetaceae
Spirochaetes; Brachyspira
Tenericutes; Mycoplasma
Tenericutes; Ureaplasma
Thermi; Deinococcus

GI-16

Phylum/Class; Genus (16)
Actinobacteria; Corynebacterium
Actinobacteria; unclassified Corynebacteriaceae
Alphaproteobacteria; Bartonella
Alphaproteobacteria; Mycoplana
Alphaproteobacteria; Paracoccus
Bacteroidetes; unclassified Flavobacteriaceae
Betaproteobacteria; Aquabacterium
CD12; unclassified
Firmicutes; Bacillus
Firmicutes; Staphylococcus
Firmicutes; Streptococcus
Firmicutes; unclassified Ruminococcaceae
Gammaproteobacteria; Actinobacillus
Gammaproteobacteria; Haemophilus
Gammaproteobacteria; unclassified Moraxellaceae
Gemmatimonadetes; unclassified Gemmatimonadetes

GI-17

Phylum/Class; Genus (142)

Acidobacteria; Candidatus Solibacter
Acidobacteria; unclassified Chloracidobacteria
Acidobacteria; unclassified Sva0725
Actinobacteria; Acidimicrobium
Actinobacteria; Brevibacterium
Actinobacteria; Collinsella
Actinobacteria; Corynebacterium
Actinobacteria; Nonomuraea
Actinobacteria; Propionibacterium
Actinobacteria; Saccharomonospora
Actinobacteria; Streptomyces
Actinobacteria; unclassified Coriobacteriaceae
Actinobacteria; unclassified Corynebacteriaceae
Actinobacteria; unclassified EB1017
Actinobacteria; unclassified MC47
Alphaproteobacteria; Agrobacterium
Alphaproteobacteria; Bosea
Alphaproteobacteria; Bradyrhizobium
Alphaproteobacteria; Brevundimonas
Alphaproteobacteria; Erythrobacter
Alphaproteobacteria; Methylobacterium
Alphaproteobacteria; Novosphingobium
Alphaproteobacteria; Paracoccus
Alphaproteobacteria; Rhodobacter
Alphaproteobacteria; Shinella
Alphaproteobacteria; Sphingobium
Alphaproteobacteria; Sphingomonas
Alphaproteobacteria; Sphingopyxis
Alphaproteobacteria; unclassified Caulobacteraceae
Alphaproteobacteria; unclassified Erythrobacteraceae
Alphaproteobacteria; unclassified Rhizobiales
Alphaproteobacteria; unclassified Rhodobacteraceae
Alphaproteobacteria; unclassified Rhodospirillaceae
Bacteroidetes; Algoriphagus
Bacteroidetes; Candidatus Amoebophilus
Bacteroidetes; unclassified Chitinophagaceae
Bacteroidetes; unclassified Corymorphaceae
Bacteroidetes; unclassified Flavobacteriaceae
Bacteroidetes; unclassified Flexibacteraceae
Bacteroidetes; unclassified RikenellaceaeII
Betaproteobacteria; Achromobacter
Betaproteobacteria; Acidovorax
Betaproteobacteria; Aquabacterium
Betaproteobacteria; Brachymonas
Betaproteobacteria; Burkholderia
Betaproteobacteria; Comamonas
Betaproteobacteria; Cupriavidus
Betaproteobacteria; Dechloromonas
Betaproteobacteria; Delftia
Betaproteobacteria; Diaphorobacter
Betaproteobacteria; Herbaspirillum
Betaproteobacteria; Massilia
Betaproteobacteria; Methylobacillus
Betaproteobacteria; Methyloversatilis
Betaproteobacteria; Procabacter
Betaproteobacteria; Ralstonia
Betaproteobacteria; Ramlibacter
Betaproteobacteria; Rhodocyclus
Betaproteobacteria; Rhodoferax
Betaproteobacteria; Simplicispira
Betaproteobacteria; Tepidimonas
Betaproteobacteria; Thiomonas
Betaproteobacteria; unclassified Alcaligenaceae
Betaproteobacteria; unclassified Burkholderiaceae
Betaproteobacteria; unclassified Comamonadaceae
Betaproteobacteria; unclassified Methylophilaceae
Betaproteobacteria; unclassified Neisseriaceae
Betaproteobacteria; unclassified Nitrosomonadaceae
Betaproteobacteria; unclassified Oxalobacteraceae
Betaproteobacteria; unclassified Rhodocyclaceae
Betaproteobacteria; unclassified Rhodocyclales
Betaproteobacteria; Vitreoscilla
Betaproteobacteria; Zoogloea
Chlamydiae; Parachlamydia
Chloroflexi; unclassified
Chloroflexi; unclassified A4b
Chloroflexi; unclassified S0208
Cyanobacteria; Chlorophyta
Cyanobacteria; Euglenozoa
Cyanobacteria; Streptophyta
Deltaproteobacteria; Desulfomicrobium
Deltaproteobacteria; Desulfovibrio
Deltaproteobacteria; Myxococcus
Deltaproteobacteria; unclassified Desulfobacteraceae
Deltaproteobacteria; unclassified Nitrospinaceae
Deltaproteobacteria; unclassified Syntrophaceae
Epsilonproteobacteria; Arcobacter
Fibrobacteres; Fibrobacter
Firmicutes; Alicyclobacillus
Firmicutes; Bacillus
Firmicutes; Blautia
Firmicutes; Clostridium
Firmicutes; Faecalibacterium
Firmicutes; Lactobacillus
Firmicutes; Lactococcus
Firmicutes; Listeria
Firmicutes; Moorella
Firmicutes; Paenibacillus
Firmicutes; Pediococcus
Firmicutes; Roseburia
Firmicutes; Staphylococcus
Firmicutes; Streptococcus
Firmicutes; unclassified Clostridiales Family XIII. Incertae Sedis
Firmicutes; unclassified Lachnospiraceae
Firmicutes; unclassified Planococcaceae
Firmicutes; unclassified Ruminococcaceae
Gammaproteobacteria; Acinetobacter
Gammaproteobacteria; Aeromonas
Gammaproteobacteria; Candidatus Portiera
Gammaproteobacteria; Chromatium
Gammaproteobacteria; Citrobacter
Gammaproteobacteria; Dyella
Gammaproteobacteria; Klebsiella
Gammaproteobacteria; Legionella
Gammaproteobacteria; Leucothrix
Gammaproteobacteria; Lysobacter
Gammaproteobacteria; Pantoea
Gammaproteobacteria; Pseudoalteromonas
Gammaproteobacteria; Pseudomonas
Gammaproteobacteria; Pseudoxanthomonas
Gammaproteobacteria; Salmonella
Gammaproteobacteria; unclassified Enterobacteriaceae
Gammaproteobacteria; unclassified Pseudomonadaceae
Gammaproteobacteria; unclassified Sinobacteraceae
Gammaproteobacteria; unclassified SUP05
Gammaproteobacteria; unclassified Xanthomonadaceae
Gammaproteobacteria; Vibrio
Gammaproteobacteria; Xanthomonas
Gemmatimonadetes; Gemmatimonadetes
Gemmatimonadetes; unclassified Gemmatimonadaceae
Gemmatimonadetes; unclassified Gemmatimonadetes
GN04; unclassified
HDBW-WB69; unclassified
OP3; unclassified
Planctomycetes; Planctomyces
SAR406; unclassified ZA3312c
Spirochaetes; Brachyspira
Spirochaetes; unclassified Zplanct13
Tenericutes; Catenibacterium
Tenericutes; Mycoplasma
Tenericutes; unclassified RF39
ZB2; unclassified

GI-18

Phylum/Class; Genus (4)
Actinobacteria; Corynebacterium
Actinobacteria; Propionibacterium
Betaproteobacteria; Diaphorobacter
Betaproteobacteria; Ralstonia

GI-19

Phylum/Class; Genus (102)
Acidobacteria; unclassified Acidobacteriaceae
Acidobacteria; unclassified Chloracidobacteria
Actinobacteria; Arthrobacter
Actinobacteria; Corynebacterium
Actinobacteria; Kocuria
Actinobacteria; Microbacterium
Actinobacteria; Nocardioides
Actinobacteria; Propionibacterium
Actinobacteria; Scardovia
Actinobacteria; Streptomyces
Actinobacteria; unclassified ACK-M1
Actinobacteria; unclassified Coriobacteriaceae
Actinobacteria; unclassified Corynebacteriaceae
Alphaproteobacteria; Bosea
Alphaproteobacteria; Novosphingobium
Alphaproteobacteria; Rhodobaca
Alphaproteobacteria; Rhodobacter
Alphaproteobacteria; Sphingobium
Alphaproteobacteria; unclassified Caulobacteraceae
Alphaproteobacteria; unclassified Hyphomicrobiaceae
Alphaproteobacteria; unclassified Rhodobacteraceae
Alphaproteobacteria; unclassified Rhodospirillaceae
Bacteroidetes; unclassified Corymorphaceae
Bacteroidetes; unclassified Flavobacteriaceae
Bacteroidetes; unclassified Flexibacteraceae
Bacteroidetes; unclassified RikenellaceaeII
Betaproteobacteria; Achromobacter
Betaproteobacteria; Acidovorax
Betaproteobacteria; Aquabacterium
Betaproteobacteria; Brachymonas
Betaproteobacteria; Burkholderia
Betaproteobacteria; Comamonas
Betaproteobacteria; Cupriavidus
Betaproteobacteria; Diaphorobacter
Betaproteobacteria; Herbaspirillum
Betaproteobacteria; Hydrogenophilus
Betaproteobacteria; Massilia
Betaproteobacteria; Oxalobacter
Betaproteobacteria; Procabacter
Betaproteobacteria; Ralstonia
Betaproteobacteria; Rhodocyclus
Betaproteobacteria; Rhodoferax
Betaproteobacteria; Simplicispira
Betaproteobacteria; Tepidimonas
Betaproteobacteria; Thauera
Betaproteobacteria; Thiomonas
Betaproteobacteria; unclassified
Betaproteobacteria; unclassified Alcaligenaceae
Betaproteobacteria; unclassified Comamonadaceae
Betaproteobacteria; unclassified Nitrosomonadaceae
Betaproteobacteria; unclassified Oxalobacteraceae
Betaproteobacteria; unclassified Rhodocyclaceae
Betaproteobacteria; unclassified Rhodocyclales
Betaproteobacteria; Verminephrobacter
Betaproteobacteria; Vitreoscilla
Chloroflexi; unclassified A4b
Chloroflexi; unclassified H39
Chloroflexi; unclassified T78
Deltaproteobacteria; Desulfovibrio
Deltaproteobacteria; unclassified
Deltaproteobacteria; unclassified Syntrophaceae
Firmicutes; Alicyclobacillus
Firmicutes; Anaerococcus
Firmicutes; Bacillus
Firmicutes; Blautia
Firmicutes; Brochothrix
Firmicutes; Clostridium
Firmicutes; Faecalibacterium
Firmicutes; Finegoldia
Firmicutes; Geobacillus
Firmicutes; Lactobacillus
Firmicutes; Lactococcus
Firmicutes; Leuconostoc
Firmicutes; Paenibacillus
Firmicutes; Roseburia
Firmicutes; Sporosarcina
Firmicutes; Staphylococcus
Firmicutes; Streptococcus
Firmicutes; Trichococcus
Firmicutes; unclassified Clostridiales Family XI. Incertae Sedis
Firmicutes; unclassified Lachnospiraceae
Firmicutes; unclassified Planococcaceae
Firmicutes; unclassified Ruminococcaceae
Gammaproteobacteria; Acinetobacter
Gammaproteobacteria; Escherichia
Gammaproteobacteria; Pseudomonas
Gammaproteobacteria; Pseudoxanthomonas
Gammaproteobacteria; Sedimenticola
Gammaproteobacteria; Stenotrophomonas
Gammaproteobacteria; Thiomicrospira
Gammaproteobacteria; unclassified Enterobacteriaceae
Gammaproteobacteria; unclassified Pseudomonadaceae
Gammaproteobacteria; unclassified Sinobacteraceae
Gemmatimonadetes; Gemmatimonadetes
Gemmatimonadetes; unclassified Gemmatimonadetes
GN04; unclassified
OP8; unclassified HMMVPog-54
Planctomycetes; unclassified Planctomycetaceae
SAR406; unclassified ZA3312c
Spirochaetes; Leptospira
Tenericutes; Mycoplasma
Verrucomicrobia; unclassified Verrucomicrobiaceae

GI-20

Phylum/Class; Genus (90)

Acidobacteria; unclassified Acidobacteriaceae
Acidobacteria; unclassified Chloracidobacteria
Actinobacteria; Acidimicrobium
Actinobacteria; Arthrobacter
Actinobacteria; Brevibacterium
Actinobacteria; Collinsella
Actinobacteria; Corynebacterium
Actinobacteria; Propionibacterium
Actinobacteria; Rhodococcus
Actinobacteria; Streptomyces
Actinobacteria; unclassified 0319-7L14
Actinobacteria; unclassified Acidimicrobiaceae
Actinobacteria; unclassified ACK-M1
Actinobacteria; unclassified Corynebacteriaceae
Actinobacteria; unclassified Microbacteriaceae
Actinobacteria; unclassified Microthrixaceae
Actinobacteria; Virgisporangium
Alphaproteobacteria; Amaricoccus
Alphaproteobacteria; Bartonella
Alphaproteobacteria; Bosea
Alphaproteobacteria; Bradyrhizobium
Alphaproteobacteria; Brevundimonas
Alphaproteobacteria; Novosphingobium
Alphaproteobacteria; Sphingobium
Alphaproteobacteria; Sphingomonas
Alphaproteobacteria; unclassified Caulobacteraceae
Alphaproteobacteria; unclassified Erythrobacteraceae
Alphaproteobacteria; unclassified Rhodospirillaceae
Bacteroidetes; Flavobacterium
Bacteroidetes; unclassified Flavobacteriaceae
Bacteroidetes; unclassified RikenellaceaeII
Betaproteobacteria; Acidovorax
Betaproteobacteria; Aquabacterium
Betaproteobacteria; Burkholderia
Betaproteobacteria; Comamonas
Betaproteobacteria; Cupriavidus
Betaproteobacteria; Delftia
Betaproteobacteria; Diaphorobacter
Betaproteobacteria; Hydrogenophilus
Betaproteobacteria; Massilia
Betaproteobacteria; Methyloversatilis
Betaproteobacteria; Rhodocyclus
Betaproteobacteria; Rubrivivax
Betaproteobacteria; Simplicispira
Betaproteobacteria; Thiomonas
Betaproteobacteria; unclassified Comamonadaceae
Betaproteobacteria; unclassified Methylophilaceae
Betaproteobacteria; unclassified Nitrosomonadaceae
Betaproteobacteria; unclassified Oxalobacteraceae
Betaproteobacteria; unclassified Rhodocyclaceae
Chloroflexi; unclassified A4b
Cyanobacteria; Microcystis
Cyanobacteria; Streptophyta
Deltaproteobacteria; Geobacter
Deltaproteobacteria; unclassified
Deltaproteobacteria; unclassified Desulfobacteraceae
Deltaproteobacteria; unclassified Syntrophaceae
Firmicutes; Alicyclobacillus
Firmicutes; Anoxybacillus
Firmicutes; Bacillus
Firmicutes; Blautia
Firmicutes; Clostridium
Firmicutes; Enterococcus
Firmicutes; Faecalibacterium
Firmicutes; Lactobacillus
Firmicutes; Ruminococcus
Firmicutes; Staphylococcus
Firmicutes; Streptococcus
Firmicutes; unclassified Lachnospiraceae
Firmicutes; unclassified Ruminococcaceae
GAL15; unclassified
Gammaproteobacteria; Acinetobacter
Gammaproteobacteria; Escherichia
Gammaproteobacteria; Pantoea
Gammaproteobacteria; Pseudomonas
Gammaproteobacteria; Pseudoxanthomonas
Gammaproteobacteria; Sedimenticola
Gammaproteobacteria; unclassified Coxiellaceae
Gammaproteobacteria; unclassified Enterobacteriaceae
Gammaproteobacteria; unclassified Halothiobacillaceae
Gammaproteobacteria; unclassified Xanthomonadaceae
Nitrospirae; Leptospirillum
Nitrospirae; Nitrospira
OP9; unclassified SHA-1
Planctomycetes; unclassified Planctomycetaceae
Spirochaetes; Leptospira
SR1; unclassified
Tenericutes; Allobaculum
Tenericutes; Mycoplasma
Tenericutes; Spiroplasma

GI-21

Phylum/Class; Genus (146)

Acidobacteria; unclassified Acidobacteriaceae
Acidobacteria; unclassified RB25
Acidobacteria; unclassified Sva0725
Actinobacteria; Arthrobacter
Actinobacteria; Corynebacterium
Actinobacteria; Cryobacterium
Actinobacteria; Frankia
Actinobacteria; Kocuria
Actinobacteria; Microbacterium
Actinobacteria; Mycobacterium
Actinobacteria; Propionibacterium
Actinobacteria; Pseudonocardia
Actinobacteria; Rhodococcus
Actinobacteria; Saccharomonospora
Actinobacteria; Streptomyces
Actinobacteria; unclassified ACK-M1
Actinobacteria; unclassified CL500-29
Actinobacteria; unclassified Corynebacteriaceae
Actinobacteria; unclassified Cryptosporangiaceae
Actinobacteria; unclassified Kineosporiaceae
Actinobacteria; unclassified koll13
Alphaproteobacteria; Azospirillum
Alphaproteobacteria; Bartonella
Alphaproteobacteria; Bosea
Alphaproteobacteria; Bradyrhizobium
Alphaproteobacteria; Brevundimonas
Alphaproteobacteria; Candidatus Pelagibacter
Alphaproteobacteria; Caulobacter
Alphaproteobacteria; Methylobacterium
Alphaproteobacteria; Novosphingobium
Alphaproteobacteria; Paracoccus
Alphaproteobacteria; Rhizobium
Alphaproteobacteria; Rhodobacter
Alphaproteobacteria; Rhodopseudomonas
Alphaproteobacteria; Roseivivax
Alphaproteobacteria; Roseobacter
Alphaproteobacteria; Roseomonas
Alphaproteobacteria; Rubellimicrobium
Alphaproteobacteria; Skermanella
Alphaproteobacteria; Sphingobium
Alphaproteobacteria; Sphingomonas
Alphaproteobacteria; unclassified Phyllobacteriaceae
Alphaproteobacteria; unclassified Rhizobiales
Alphaproteobacteria; unclassified Rhodobacteraceae
Alphaproteobacteria; unclassified Rhodospirillaceae
Armatimonadetes; unclassified Armatimonadaceae
Bacteroidetes; Flavobacterium
Bacteroidetes; Porphyromonas
Bacteroidetes; Prevotella
Bacteroidetes; unclassified Chitinophagaceae
Bacteroidetes; unclassified Flavobacteriaceae
Bacteroidetes; unclassified Flexibacteraceae
Bacteroidetes; unclassified RikenellaceaeII
Betaproteobacteria; Achromobacter
Betaproteobacteria; Aquabacterium
Betaproteobacteria; Bordetella
Betaproteobacteria; Brachymonas
Betaproteobacteria; Burkholderia
Betaproteobacteria; Comamonas
Betaproteobacteria; Cupriavidus
Betaproteobacteria; Delftia
Betaproteobacteria; Diaphorobacter
Betaproteobacteria; Herbaspirillum
Betaproteobacteria; Hydrogenophilus
Betaproteobacteria; Methylibium
Betaproteobacteria; Methylotenera
Betaproteobacteria; Nitrosomonas
Betaproteobacteria; Oxalobacter
Betaproteobacteria; Polaromonas
Betaproteobacteria; Procabacter
Betaproteobacteria; Rhodocyclus
Betaproteobacteria; Rhodoferax
Betaproteobacteria; Simplicispira
Betaproteobacteria; Tepidimonas
Betaproteobacteria; Thauera
Betaproteobacteria; Thiomonas
Betaproteobacteria; unclassified Alcaligenaceae
Betaproteobacteria; unclassified Comamonadaceae
Betaproteobacteria; unclassified Methylophilaceae
Betaproteobacteria; unclassified Nitrosomonadaceae
Betaproteobacteria; unclassified Oxalobacteraceae
Betaproteobacteria; unclassified Rhodocyclales
Betaproteobacteria; Zoogloea
Chlamydiae; Parachlamydia
Chloroflexi; unclassified A4b
Chloroflexi; unclassified OPB11
Cyanobacteria; Leptolyngbya
Cyanobacteria; Nostoc
Cyanobacteria; Prochlorococcus
Cyanobacteria; Streptophyta
Cyanobacteria; Synechococcus
Deltaproteobacteria; Desulfovibrio
Deltaproteobacteria; Desulfurella
Deltaproteobacteria; unclassified
Deltaproteobacteria; unclassified Syntrophaceae
Fibrobacteres; Fibrobacter
Firmicutes; Anaerococcus
Firmicutes; Bacillus
Firmicutes; Blautia
Firmicutes; Clostridium
Firmicutes; Coprococcus
Firmicutes; Desemzia
Firmicutes; Enterococcus
Firmicutes; Eubacterium
Firmicutes; Faecalibacterium
Firmicutes; Geobacillus
Firmicutes; Lactobacillus
Firmicutes; Lysinibacillus
Firmicutes; Oscillospira
Firmicutes; Paenibacillus
Firmicutes; Roseburia
Firmicutes; Ruminococcus
Firmicutes; Solibacillus
Firmicutes; Staphylococcus
Firmicutes; Streptococcus
Firmicutes; unclassified Clostridiales Family XI. Incertae Sedis
Firmicutes; unclassified Halanaerobiaceae
Firmicutes; unclassified Lachnospiraceae
Firmicutes; unclassified Planococcaceae
Firmicutes; unclassified Ruminococcaceae
Firmicutes; unclassified Veillonellaceae
Gammaproteobacteria; Acinetobacter
Gammaproteobacteria; Brenneria
Gammaproteobacteria; Methylomonas
Gammaproteobacteria; Nitrosococcus
Gammaproteobacteria; Pantoea
Gammaproteobacteria; Pseudoalteromonas
Gammaproteobacteria; Pseudomonas
Gammaproteobacteria; Pseudoxanthomonas
Gammaproteobacteria; Salinisphaera
Gammaproteobacteria; Salmonella
Gammaproteobacteria; Serratia
Gammaproteobacteria; unclassified
Gammaproteobacteria; unclassified Chromatiaceae
Gammaproteobacteria; unclassified Coxiellaceae
Gammaproteobacteria; unclassified Ectothiorhodospiraceae
Gammaproteobacteria; unclassified Enterobacteriaceae
Gammaproteobacteria; unclassified Halothiobacillaceae
Gammaproteobacteria; unclassified OM60
Gammaproteobacteria; unclassified Pseudomonadaceae
Gemmatimonadetes; unclassified Gemmatimonadetes
Planctomycetes; Planctomyces
Planctomycetes; unclassified Planctomycetaceae
Spirochaetes; Leptospira
TG3; unclassified M2PB4-14
Verrucomicrobia; Akkermansia

GI-22

Phylum/Class; Genus (69)

Acidobacteria; unclassified Acidobacteriaceae
Acidobacteria; unclassified Chloracidobacteria
Actinobacteria; Arthrobacter
Actinobacteria; Corynebacterium
Actinobacteria; Microbacterium
Actinobacteria; Micromonospora
Actinobacteria; Propionibacterium
Actinobacteria; Rhodococcus
Actinobacteria; Streptomyces
Actinobacteria; unclassified Iamiaceae
Actinobacteria; unclassified MC47
Actinobacteria; unclassified ZA3409c
Alphaproteobacteria; Novosphingobium
Alphaproteobacteria; Sphingobium
Alphaproteobacteria; unclassified Rhodospirillaceae
Bacteroidetes; Prevotella
Bacteroidetes; unclassified Flavobacteriaceae
Bacteroidetes; unclassified RikenellaceaeII
Betaproteobacteria; Achromobacter
Betaproteobacteria; Acidovorax
Betaproteobacteria; Aquabacterium
Betaproteobacteria; Comamonas
Betaproteobacteria; Cupriavidus
Betaproteobacteria; Delftia
Betaproteobacteria; Diaphorobacter
Betaproteobacteria; Hydrogenophilus
Betaproteobacteria; Malikia
Betaproteobacteria; Methylibium
Betaproteobacteria; Pandoraea
Betaproteobacteria; Polaromonas
Betaproteobacteria; Procabacter
Betaproteobacteria; Ralstonia
Betaproteobacteria; Rhodocyclus
Betaproteobacteria; Rhodoferax
Betaproteobacteria; Rubrivivax
Betaproteobacteria; Simplicispira
Betaproteobacteria; Thauera
Betaproteobacteria; Thiomonas
Betaproteobacteria; unclassified Comamonadaceae
Betaproteobacteria; unclassified Nitrosomonadaceae
Betaproteobacteria; unclassified Oxalobacteraceae
Betaproteobacteria; unclassified Rhodocyclaceae
CD12; unclassified
Chloroflexi; unclassified A4b
Deltaproteobacteria; unclassified Syntrophobacteraceae
Firmicutes; Alicyclobacillus
Firmicutes; Bacillus
Firmicutes; Blautia
Firmicutes; Clostridium
Firmicutes; Faecalibacterium
Firmicutes; Lactobacillus
Firmicutes; Oscillospira
Firmicutes; Roseburia
Firmicutes; Staphylococcus
Firmicutes; Streptococcus
Firmicutes; unclassified Clostridiales Family XI. Incertae Sedis
Firmicutes; unclassified Lachnospiraceae
Firmicutes; unclassified Ruminococcaceae
Gammaproteobacteria; Acidithiobacillus
Gammaproteobacteria; Pseudoalteromonas
Gammaproteobacteria; Pseudomonas
Gammaproteobacteria; unclassified
Gammaproteobacteria; unclassified Enterobacteriaceae
Gammaproteobacteria; unclassified Sinobacteraceae
Gammaproteobacteria; Vibrio
Tenericutes; Allobaculum
Tenericutes; Spiroplasma
Thermi; Deinococcus
Zetaproteobacteria; Mariprofundus

GI-23

Phylum/Class; Genus (75)

Actinobacteria; Corynebacterium
Actinobacteria; Propionibacterium
Actinobacteria; Streptomyces
Actinobacteria; Uncl_Corynebacteriaceae
Alphaproteobacteria; Balneimonas
Alphaproteobacteria; Bartonella
Alphaproteobacteria; Bosea
Alphaproteobacteria; Bradyrhizobium
Alphaproteobacteria; Candidatus Pelagibacter
Alphaproteobacteria; Gluconobacter
Alphaproteobacteria; Methylobacterium
Alphaproteobacteria; Novosphingobium
Alphaproteobacteria; Phyllobacterium
Alphaproteobacteria; Rhizobium
Alphaproteobacteria; Rhodoplanes
Alphaproteobacteria; Rhodopseudomonas
Alphaproteobacteria; Sphingobium
Alphaproteobacteria; Sphingomonas
Alphaproteobacteria; Uncl_Bradyrhizobiaceae
Alphaproteobacteria; Uncl_Brucellaceae
Alphaproteobacteria; Uncl_Erythrobacteraceae
Alphaproteobacteria; Uncl_Rhizobiaceae
Alphaproteobacteria; Uncl_Rhodobacteraceae
Alphaproteobacteria; Uncl_Rhodospirillaceae
Alphaproteobacteria; Uncl_Sphingomonadaceae
Bacteroidetes; Uncl_Corymorphaceae
Bacteroidetes; Uncl_Flavobacteriaceae
Bacteroidetes; Uncl_RikenellaceaeII
Betaproteobacteria; Acidovorax
Betaproteobacteria; Aquabacterium
Betaproteobacteria; Comamonas
Betaproteobacteria; Delftia
Betaproteobacteria; Diaphorobacter
Betaproteobacteria; Massilia
Betaproteobacteria; Methyloversatilis
Betaproteobacteria; Pandoraea
Betaproteobacteria; Rhodocyclus
Betaproteobacteria; Simplicispira
Betaproteobacteria; Thiomonas
Betaproteobacteria; Uncl_Alcaligenaceae
Betaproteobacteria; Uncl_Comamonadaceae
Betaproteobacteria; Uncl_Nitrosomonadaceae
Betaproteobacteria; Uncl_Rhodocyclaceae
Betaproteobacteria; Zoogloea
Chloroflexi; HN1-15
Chloroflexi; Ktedonobacter
Cyanobacteria; Leptolyngbya
Deltaproteobacteria; Uncl_Syntrophobacteraceae
Epsilonproteobacteria; Arcobacter
Firmicutes; Alicyclobacillus
Firmicutes; Bacillus
Firmicutes; Coprococcus
Firmicutes; Enterococcus
Firmicutes; Faecalibacterium
Firmicutes; Lactobacillus
Firmicutes; Staphylococcus
Firmicutes; Uncl_Lachnospiraceae
Firmicutes; Uncl_Ruminococcaceae
Gammaproteobacteria; Acinetobacter
Gammaproteobacteria; Aeromonas
Gammaproteobacteria; Escherichia
Gammaproteobacteria; Halomonas
Gammaproteobacteria; Pantoea
Gammaproteobacteria; Pseudomonas
Gammaproteobacteria; Rhodanobacter
Gammaproteobacteria; Thiomicrospira
Gammaproteobacteria; Uncl_Enterobacteriaceae
Gammaproteobacteria; Uncl_Pseudomonadaceae
Gammaproteobacteria; Uncl_Sinobacteraceae
Gammaproteobacteria; Vibrio
Gemmatimonadetes; sfA
OP11; sfB
OP9; sfA
Planctomycetes; Uncl_Planctomycetaceae
Thermi; Deinococcus

GI-24

Phylum; Genus; 124 unique genera

Acidobacteria; unclassified Acidobacteriaceae
Actinobacteria; Acidimicrobium
Actinobacteria; Brevibacterium
Actinobacteria; Collinsella
Actinobacteria; Corynebacterium
Actinobacteria; Lentzea
Actinobacteria; Microbacterium
Actinobacteria; Nocardia
Actinobacteria; Propionibacterium
Actinobacteria; Rubrobacter
Actinobacteria; Streptomyces
Actinobacteria; unclassified Actinobacteria
Actinobacteria; unclassified CL500-29
Actinobacteria; unclassified Corynebacteriaceae
Actinobacteria; unclassified Solirubrobacteraceae
Alphaproteobacteria; Azospirillum
Alphaproteobacteria; Bartonella
Alphaproteobacteria; Bosea
Alphaproteobacteria; Brevundimonas
Alphaproteobacteria; Candidatus Odyssella
Alphaproteobacteria; Inquilinus
Alphaproteobacteria; Novosphingobium
Alphaproteobacteria; Paracoccus
Alphaproteobacteria; Porphyrobacter
Alphaproteobacteria; Rhodobaca
Alphaproteobacteria; Rhodopseudomonas
Alphaproteobacteria; Roseobacter
Alphaproteobacteria; Roseomonas
Alphaproteobacteria; Roseospira
Alphaproteobacteria; Skermanella
Alphaproteobacteria; Sphingobium
Alphaproteobacteria; Sphingomonas
Alphaproteobacteria; Sphingopyxis
Alphaproteobacteria; unclassified Bradyrhizobiaceae
Alphaproteobacteria; unclassified Erythrobacteraceae
Alphaproteobacteria; unclassified Hyphomicrobiaceae
Alphaproteobacteria; unclassified Phyllobacteriaceae
Alphaproteobacteria; unclassified Rhizobiales
Alphaproteobacteria; unclassified Rhodobacteraceae
Alphaproteobacteria; unclassified Rhodospirillaceae
Alphaproteobacteria; unclassified Sphingomonadaceae
Bacteroidetes; Flavobacterium
Bacteroidetes; Leeuwenhoekiella
Bacteroidetes; Prevotella
Bacteroidetes; unclassified Flavobacteriaceae
Bacteroidetes; unclassified RikenellaceaeII
Betaproteobacteria; Achromobacter
Betaproteobacteria; Aquabacterium
Betaproteobacteria; Burkholderia
Betaproteobacteria; Chromobacterium
Betaproteobacteria; Comamonas
Betaproteobacteria; Cupriavidus
Betaproteobacteria; Delftia
Betaproteobacteria; Diaphorobacter
Betaproteobacteria; Hydrogenophilus
Betaproteobacteria; Massilia
Betaproteobacteria; Ralstonia
Betaproteobacteria; Rhodocyclus
Betaproteobacteria; Rhodoferax
Betaproteobacteria; Simplicispira
Betaproteobacteria; Thiobacillus
Betaproteobacteria; Thiomonas
Betaproteobacteria; unclassified Comamonadaceae
Betaproteobacteria; unclassified Methylophilaceae
Betaproteobacteria; unclassified Neisseriaceae
Betaproteobacteria; unclassified Nitrosomonadaceae
Betaproteobacteria; unclassified Oxalobacteraceae
Betaproteobacteria; unclassified Rhodocyclaceae
Betaproteobacteria; Verminephrobacter
Betaproteobacteria; Zoogloea
Chlamydiae; Parachlamydia
Chloroflexi; unclassified A4b
Cyanobacteria; Microcystis
Cyanobacteria; Spirulina
Cyanobacteria; Streptophyta
Deltaproteobacteria; Desulfomicrobium
Deltaproteobacteria; Desulfurella
Deltaproteobacteria; unclassified Syntrophaceae
Firmicutes; Bacillus
Firmicutes; Clostridium
Firmicutes; Faecalibacterium
Firmicutes; Geobacillus
Firmicutes; Lactobacillus
Firmicutes; Leuconostoc
Firmicutes; Roseburia
Firmicutes; Ruminococcus
Firmicutes; Staphylococcus
Firmicutes; Streptococcus
Firmicutes; unclassified Lachnospiraceae
Firmicutes; unclassified Ruminococcaceae
Gammaproteobacteria; Acinetobacter
Gammaproteobacteria; Halomonas
Gammaproteobacteria; Leucothrix
Gammaproteobacteria; Moraxella
Gammaproteobacteria; Pantoea
Gammaproteobacteria; Pseudoalteromonas
Gammaproteobacteria; Pseudomonas
Gammaproteobacteria; Pseudoxanthomonas
Gammaproteobacteria; Serratia
Gammaproteobacteria; Stenotrophomonas
Gammaproteobacteria; Thiomicrospira
Gammaproteobacteria; unclassified
Gammaproteobacteria; unclassified Chromatiaceae
Gammaproteobacteria; unclassified Enterobacteriaceae
Gammaproteobacteria; unclassified Francisellaceae
Gammaproteobacteria; unclassified Halothiobacillaceae
Gammaproteobacteria; unclassified Methylococcaceae
Gammaproteobacteria; unclassified Pseudomonadaceae
Gammaproteobacteria; unclassified SUP05
Gammaproteobacteria; unclassified Xanthomonadaceae
Gammaproteobacteria; Vibrio
GN04; unclassified
Lentisphaerae; unclassified Victivallaceae
Planctomycetes; Gemmata
Planctomycetes; unclassified Planctomycetaceae
SAR406; unclassified ZA3312c
SC4; unclassified
Spirochaetes; Leptospira
Synergistetes; unclassified TG5
Tenericutes; Candidatus Phytoplasma
Tenericutes; Mycoplasma
Verrucomicrobia; Akkermansia
Verrucomicrobia; unclassified R76-B18
WS3; unclassified GN03

GI-25

Phylum; Genus; 40 unique genera

Actinobacteria; Corynebacterium
Actinobacteria; unclassified Corynebacteriaceae
Alphaproteobacteria; Azospirillum
Alphaproteobacteria; Candidatus Pelagibacter
Alphaproteobacteria; Devosia
Alphaproteobacteria; Mesorhizobium
Alphaproteobacteria; Phenylobacterium
Alphaproteobacteria; unclassified Caulobacteraceae
Armatimonadetes; unclassified CH21
Bacteroidetes; Prevotella
Bacteroidetes; Sediminibacterium
Bacteroidetes; unclassified Chitinophagaceae
Bacteroidetes; unclassified RikenellaceaeII
Betaproteobacteria; Acidovorax
Betaproteobacteria; Aquabacterium
Betaproteobacteria; Burkholderia
Betaproteobacteria; Delftia
Betaproteobacteria; Diaphorobacter
Betaproteobacteria; Methylobacillus
Betaproteobacteria; Methylotenera
Betaproteobacteria; Methyloversatilis
Betaproteobacteria; Pandoraea
Betaproteobacteria; Ralstonia
Betaproteobacteria; Thiomonas
Betaproteobacteria; unclassified Comamonadaceae
Chloroflexi; unclassified A4b
Deltaproteobacteria; Desulfomicrobium
Deltaproteobacteria; unclassified Bdellovibrionaceae
Deltaproteobacteria; unclassified Haliangiaceae
Deltaproteobacteria; unclassified Myxococcales
Firmicutes; Bacillus
Firmicutes; Faecalibacterium
Firmicutes; Streptococcus
Gammaproteobacteria; Enterobacter
Gammaproteobacteria; Klebsiella
Gammaproteobacteria; Pseudomonas
Gammaproteobacteria; unclassified Enterobacteriaceae
Gemmatimonadetes; Gemmatimonadetes
KSB1; unclassified
Verrucomicrobia; unclassified LP2A

GI-26

Phylum; Genus; 82 unique genera

Acidobacteria; unclassified Acidobacteriaceae
Acidobacteria; unclassified Chloracidobacteria
Actinobacteria; Brevibacterium
Actinobacteria; Collinsella
Actinobacteria; Corynebacterium
Actinobacteria; Gordonia
Actinobacteria; Microbacterium
Actinobacteria; Modestobacter
Actinobacteria; Mycobacterium
Actinobacteria; Nocardioides
Actinobacteria; Propionibacterium
Actinobacteria; Rhodococcus
Actinobacteria; Scardovia
Actinobacteria; unclassified Corynebacteriaceae
Actinobacteria; unclassified koll13
Alphaproteobacteria; Novosphingobium
Alphaproteobacteria; Sphingomonas
Alphaproteobacteria; unclassified Rhodospirillaceae
Bacteroidetes; Flavobacterium
Bacteroidetes; unclassified Flavobacteriaceae
Bacteroidetes; unclassified Flexibacteraceae
Bacteroidetes; unclassified RikenellaceaeII
Betaproteobacteria; Acidovorax
Betaproteobacteria; Aquabacterium
Betaproteobacteria; Burkholderia
Betaproteobacteria; Comamonas
Betaproteobacteria; Cupriavidus
Betaproteobacteria; Delftia
Betaproteobacteria; Diaphorobacter
Betaproteobacteria; Hydrogenophilus
Betaproteobacteria; Hylemonella
Betaproteobacteria; Methylibium
Betaproteobacteria; Methyloversatilis
Betaproteobacteria; Rhodocyclus
Betaproteobacteria; Roseateles
Betaproteobacteria; Rubrivivax
Betaproteobacteria; Simplicispira
Betaproteobacteria; Thiomonas
Betaproteobacteria; unclassified Comamonadaceae
Betaproteobacteria; unclassified Nitrosomonadaceae
Betaproteobacteria; unclassified Oxalobacteraceae
Betaproteobacteria; unclassified Rhodocyclaceae
Betaproteobacteria; unclassified Rhodocyclales
Betaproteobacteria; Vitreoscilla
Chloroflexi; unclassified A4b
Deltaproteobacteria; unclassified Desulfuromonadaceae
Firmicutes; Alicyclobacillus
Firmicutes; Bacillus
Firmicutes; Blautia
Firmicutes; Caloramator
Firmicutes; Carnobacterium
Firmicutes; Coprococcus
Firmicutes; Enterococcus
Firmicutes; Faecalibacterium
Firmicutes; Geobacillus
Firmicutes; Lactobacillus
Firmicutes; Planococcus
Firmicutes; Salinicoccus
Firmicutes; Staphylococcus
Firmicutes; Streptococcus
Firmicutes; Tetragenococcus
Firmicutes; Trichococcus
Firmicutes; unclassified Clostridiaceae
Firmicutes; unclassified Clostridiales Family XIII. Incertae Sedis
Firmicutes; unclassified Lachnospiraceae
Firmicutes; unclassified Planococcaceae
Firmicutes; unclassified Ruminococcaceae
Gammaproteobacteria; Acinetobacter
Gammaproteobacteria; Candidatus Portiera
Gammaproteobacteria; Pseudomonas
Gammaproteobacteria; unclassified
Gammaproteobacteria; unclassified Enterobacteriaceae
Gammaproteobacteria; unclassified Pseudomonadaceae
GN04; unclassified
OP9; unclassified SHA-1
Planctomycetes; Planctomyces
Planctomycetes; unclassified Planctomycetaceae
SAR406; unclassified ZA3312c
SAR406; unlcassified SHAG537
Tenericutes; Allobaculum
Tenericutes; Mycoplasma
Tenericutes; Spiroplasma

GI-27

Phylum; Genus; 24 unique genera
Actinobacteria; Corynebacterium
Actinobacteria; unclassified Corynebacteriaceae
Actinobacteria; unclassified koll13
Bacteroidetes; unclassified RikenellaceaeII
Betaproteobacteria; Aquabacterium
Betaproteobacteria; Burkholderia
Betaproteobacteria; Diaphorobacter
Betaproteobacteria; Ralstonia
Betaproteobacteria; Thiomonas
Betaproteobacteria; Zoogloea
Chloroflexi; unclassified A4b
Cyanobacteria; Streptophyta
Firmicutes; Bacillus
Firmicutes; Clostridium
Firmicutes; Desulfosporosinus
Firmicutes; Staphylococcus
Firmicutes; Streptococcus
Firmicutes; unclassified Lachnospiraceae
Firmicutes; unclassified Ruminococcaceae
Gammaproteobacteria; Aeromonas
Gammaproteobacteria; Pseudomonas
Gammaproteobacteria; unclassified Enterobacteriaceae
OP9; unclassified SHA-1
Verrucomicrobia; unclassified LP2A

GI-28

Phylum; Genus; 24 unique genera
Actinobacteria; Corynebacterium
Actinobacteria; Propionibacterium
Actinobacteria; Streptomyces
Actinobacteria; unclassified Corynebacteriaceae
Actinobacteria; unclassified Microbacteriaceae
Betaproteobacteria; Aquabacterium
Betaproteobacteria; Cupriavidus
Betaproteobacteria; Delftia
Betaproteobacteria; Diaphorobacter
Betaproteobacteria; Ralstonia
Betaproteobacteria; Thiomonas
Betaproteobacteria; unclassified Comamonadaceae
Betaproteobacteria; Zoogloea
Epsilonproteobacteria; Campylobacter
Firmicutes; Alicyclobacillus
Firmicutes; Bacillus
Firmicutes; Staphylococcus
Gammaproteobacteria; Acinetobacter
Gammaproteobacteria; Escherichia
Gammaproteobacteria; Pseudomonas
Gammaproteobacteria; Rhodanobacter
Gammaproteobacteria; Stenotrophomonas
Gemmatimonadetes; Gemmatimonadetes
OP9; unclassified SHA-1

GI-29

Phylum; Genus; 109 unique genera
Acidobacteria; Candidatus Solibacter
Acidobacteria; unclassified Acidobacteriaceae
Actinobacteria; Brevibacterium
Actinobacteria; Collinsella
Actinobacteria; Corynebacterium
Actinobacteria; Propionibacterium
Actinobacteria; Saccharomonospora
Actinobacteria; Streptomyces
Actinobacteria; unclassified Corynebacteriaceae
Alphaproteobacteria; Afipia
Alphaproteobacteria; Bartonella
Alphaproteobacteria; Bradyrhizobium
Alphaproteobacteria; Brevundimonas
Alphaproteobacteria; Candidatus Pelagibacter
Alphaproteobacteria; Methylobacterium
Alphaproteobacteria; Methylosinus
Alphaproteobacteria; Rhizobium
Alphaproteobacteria; Rhodobacter
Alphaproteobacteria; Rhodoplanes
Alphaproteobacteria; Rhodopseudomonas
Alphaproteobacteria; Sphingobium
Alphaproteobacteria; Sphingomonas
Alphaproteobacteria; Thioclava
Alphaproteobacteria; unclassified Caulobacteraceae
Alphaproteobacteria; unclassified Phyllobacteriaceae
Alphaproteobacteria; unclassified Rhizobiales
Alphaproteobacteria; unclassified Rhodobacteraceae
Alphaproteobacteria; unclassified Rhodospirillaceae
Bacteroidetes; Candidatus Sulcia
Bacteroidetes; Flavisolibacter
Bacteroidetes; Prevotella
Bacteroidetes; Sediminibacterium
Bacteroidetes; unclassified Chitinophagaceae
Bacteroidetes; unclassified Corymorphaceae
Bacteroidetes; unclassified Flavobacteriaceae
Bacteroidetes; unclassified RikenellaceaeII
Betaproteobacteria; Achromobacter
Betaproteobacteria; Aquabacterium
Betaproteobacteria; Burkholderia
Betaproteobacteria; Comamonas
Betaproteobacteria; Diaphorobacter
Betaproteobacteria; Janthinobacterium
Betaproteobacteria; Pandoraea
Betaproteobacteria; Rhodocyclus
Betaproteobacteria; Roseateles
Betaproteobacteria; Simplicispira
Betaproteobacteria; unclassified Alcaligenaceae
Betaproteobacteria; unclassified Comamonadaceae
Betaproteobacteria; unclassified Methylophilaceae
Betaproteobacteria; unclassified Neisseriaceae
Betaproteobacteria; unclassified Nitrosomonadaceae
Betaproteobacteria; unclassified Oxalobacteraceae
Betaproteobacteria; unclassified Rhodocyclales
Betaproteobacteria; Variovorax
Betaproteobacteria; Verminephrobacter
Chlamydiae; Parachlamydia
Chloroflexi; unclassified
Chloroflexi; unclassified A4b
Cyanobacteria; Streptophyta
Cyanobacteria; Synechococcus
Cyanobacteria; unclassified Pseudanabaenaceae
Cyanobacteria; unclassified Ulvophyceae
Deltaproteobacteria; Desulfomicrobium
Deltaproteobacteria; unclassified Desulfuromonadaceae
Deltaproteobacteria; unclassified Haliangiaceae
Deltaproteobacteria; unclassified Syntrophaceae
Firmicutes; Alicyclobacillus
Firmicutes; Bacillus
Firmicutes; Clostridium
Firmicutes; Enterococcus
Firmicutes; Faecalibacterium
Firmicutes; Lactobacillus
Firmicutes; Planococcus
Firmicutes; Pseudobutyrivibrio
Firmicutes; Staphylococcus
Firmicutes; Streptococcus
Firmicutes; unclassified Bacillaceae
Firmicutes; unclassified Lachnospiraceae
Firmicutes; unclassified Ruminococcaceae
Firmicutes; unclassified Veillonellaceae
Gammaproteobacteria; Acinetobacter
Gammaproteobacteria; Chelonobacter
Gammaproteobacteria; Erwinia
Gammaproteobacteria; Klebsiella
Gammaproteobacteria; Pantoea
Gammaproteobacteria; Pseudomonas
Gammaproteobacteria; Thiomicrospira
Gammaproteobacteria; unclassified Chromatiaceae
Gammaproteobacteria; unclassified Coxiellaceae
Gammaproteobacteria; unclassified Enterobacteriaceae

Gammaproteobacteria; unclassified FCPT525
Gammaproteobacteria; unclassified Halothiobacillaceae
Gammaproteobacteria; unclassified Pseudomonadaceae
Gammaproteobacteria; unclassified Sinobacteraceae
Gammaproteobacteria; unclassified SUP05
Gammaproteobacteria; Vibrio
Gemmatimonadetes; unclassified Gemmatimonadetes
Nitrospirae; Leptospirillum
Nitrospirae; unclassified GOUTA19
Planctomycetes; Planctomyces
Planctomycetes; unclassified Isosphaeraceae
Planctomycetes; unclassified Planctomycetaceae
SAR406; unclassified ZA3312c
Spirochaetes; Leptospira
Synergistetes; unclassified TG5
Tenericutes; Candidatus Phytoplasma
TM6; unclassified
Verrucomicrobia; unclassified MC18
Zetaproteobacteria; Mariprofundus

GI-30

Phylum; Genus; 15 unique genera
Actinobacteria; Corynebacterium
Actinobacteria; Kytococcus
Actinobacteria; Propionibacterium
Actinobacteria; Streptomyces
Actinobacteria; unclassified Corynebacteriaceae
Alphaproteobacteria; Bradyrhizobium
Alphaproteobacteria; Methylobacterium
Betaproteobacteria; unclassified Neisseriaceae
Betaproteobacteria; Zoogloea
Firmicutes; Bacillus
Firmicutes; Caldanaerobacter
Firmicutes; Enterococcus
Gammaproteobacteria; Pseudomonas
Gammaproteobacteria; unclassified Enterobacteriaceae
Verrucomicrobia; unclassified LP2A

GI-32

Phylum; Genus; 9 unique genera
Actinobacteria; Corynebacterium
Actinobacteria; unclassified Corynebacteriaceae
Alphaproteobacteria; Ochrobactrum
Chloroflexi; unclassified A4b
Firmicutes; Bacillus
Firmicutes; Lysinibacillus
Firmicutes; Streptococcus
Gammaproteobacteria; Pseudomonas
Tenericutes; Allobaculum

GI-36-3

Phylum; Genus; 278 unique genera
ABY1_OD1; unclassified
Acidobacteria; Candidatus Solibacter
Acidobacteria; Edaphobacter
Acidobacteria; unclassified Acidobacteriaceae
Acidobacteria; unclassified Chloracidobacteria
Actinobacteria; Actinomyces
Actinobacteria; Actinoplanes
Actinobacteria; Adlercreutzia
Actinobacteria; Arthrobacter
Actinobacteria; Bifidobacterium
Actinobacteria; Corynebacterium
Actinobacteria; Cryobacterium
Actinobacteria; Dactylosporangium
Actinobacteria; Geodermatophilus
Actinobacteria; Janibacter
Actinobacteria; Kocuria
Actinobacteria; Micrococcus
Actinobacteria; Mycobacterium
Actinobacteria; Phycicoccus
Actinobacteria; Propionibacterium
Actinobacteria; Propionicimonas
Actinobacteria; Rhodococcus
Actinobacteria; Rothia
Actinobacteria; Rubrobacter
Actinobacteria; Streptomyces
Actinobacteria; unclassified 0319-7L14
Actinobacteria; unclassified Acidimicrobiaceae
Actinobacteria; unclassified Actinobacteria
Actinobacteria; unclassified Cellulomonadaceae
Actinobacteria; unclassified CL500-29
Actinobacteria; unclassified Conexibacteraceae
Actinobacteria; unclassified Coriobacteriaceae
Actinobacteria; unclassified Corynebacteriaceae
Actinobacteria; unclassified Frankiaceae
Actinobacteria; unclassified koll13
Actinobacteria; unclassified MC47
Actinobacteria; unclassified Microbacteriaceae
Actinobacteria; unclassified Nocardioidaceae
Actinobacteria; unclassified Patulibacteraceae
Alphaproteobacteria; Acidisphaera
Alphaproteobacteria; Agrobacterium
Alphaproteobacteria; Amaricoccus
Alphaproteobacteria; Azospirillum
Alphaproteobacteria; Balneimonas
Alphaproteobacteria; Bosea
Alphaproteobacteria; Bradyrhizobium
Alphaproteobacteria; Brevundimonas
Alphaproteobacteria; Candidatus Pelagibacter
Alphaproteobacteria; Devosia
Alphaproteobacteria; Hyphomicrobium
Alphaproteobacteria; Kaistobacter
Alphaproteobacteria; Kiloniella
Alphaproteobacteria; Lutibacterium
Alphaproteobacteria; Magnetococcus
Alphaproteobacteria; Mesorhizobium
Alphaproteobacteria; Methylobacterium
Alphaproteobacteria; Novosphingobium
Alphaproteobacteria; Paracoccus
Alphaproteobacteria; Pedomicrobium
Alphaproteobacteria; Phaeospirillum
Alphaproteobacteria; Phenylobacterium
Alphaproteobacteria; Rhizobium
Alphaproteobacteria; Rhodobacter
Alphaproteobacteria; Rhodoplanes
Alphaproteobacteria; Rhodopseudomonas
Alphaproteobacteria; Roseomonas
Alphaproteobacteria; Rubellimicrobium
Alphaproteobacteria; Ruegeria
Alphaproteobacteria; Skermanella
Alphaproteobacteria; Sphingobium
Alphaproteobacteria; Sphingomonas
Alphaproteobacteria; Sphingopyxis
Alphaproteobacteria; Thioclava
Alphaproteobacteria; unclassified
Alphaproteobacteria; unclassified Acetobacteraceae
Alphaproteobacteria; unclassified Bradyrhizobiaceae
Alphaproteobacteria; unclassified Caulobacteraceae
Alphaproteobacteria; unclassified Erythrobacteraceae
Alphaproteobacteria; unclassified Hyphomicrobiaceae
Alphaproteobacteria; unclassified Hyphomonadaceae
Alphaproteobacteria; unclassified Phyllobacteriaceae
Alphaproteobacteria; unclassified Rhizobiaceae
Alphaproteobacteria; unclassified Rhizobiales
Alphaproteobacteria; unclassified Rhodobacteraceae
Alphaproteobacteria; unclassified Rhodospirillaceae
Aquificae; Hydrogenobaculum
Bacteroidetes; Alistipes
Bacteroidetes; Bacteroides
Bacteroidetes; Capnocytophaga
Bacteroidetes; Chitinophaga

Bacteroidetes; Chryseobacterium
Bacteroidetes; Dyadobacter
Bacteroidetes; Flavisolibacter
Bacteroidetes; Flavobacterium
Bacteroidetes; Hymenobacter
Bacteroidetes; Pedobacter
Bacteroidetes; Pontibacter
Bacteroidetes; Prevotella
Bacteroidetes; Segetibacter
Bacteroidetes; Sphingobacterium
Bacteroidetes; unclassified Chitinophagaceae
Bacteroidetes; unclassified Corymorphaceae
Bacteroidetes; unclassified Flavobacteriaceae
Bacteroidetes; unclassified Flexibacteraceae
Bacteroidetes; unclassified Marinilabiaceae
Bacteroidetes; unclassified RikenellaceaeII
Bacteroidetes; unclassified Saprospiraceae
Bacteroidetes; unclassified Sphingobacteriaceae
Betaproteobacteria; Achromobacter
Betaproteobacteria; Aquabacterium
Betaproteobacteria; Azoarcus
Betaproteobacteria; Burkholderia
Betaproteobacteria; Comamonas
Betaproteobacteria; Cupriavidus
Betaproteobacteria; Diaphorobacter
Betaproteobacteria; Massilia
Betaproteobacteria; Methylibium
Betaproteobacteria; Methylotenera
Betaproteobacteria; Methyloversatilis
Betaproteobacteria; Oxalobacter
Betaproteobacteria; Polaromonas
Betaproteobacteria; Ralstonia
Betaproteobacteria; Rhodocyclus
Betaproteobacteria; Simplicispira
Betaproteobacteria; Stenoxybacter
Betaproteobacteria; Sutterella
Betaproteobacteria; Tepidimonas
Betaproteobacteria; Thiomonas
Betaproteobacteria; unclassified
Betaproteobacteria; unclassified Burkholderiaceae
Betaproteobacteria; unclassified Comamonadaceae
Betaproteobacteria; unclassified Hydrogenophilaceae
Betaproteobacteria; unclassified Methylophilaceae
Betaproteobacteria; unclassified Neisseriaceae
Betaproteobacteria; unclassified Nitrosomonadaceae
Betaproteobacteria; unclassified Oxalobacteraceae
Betaproteobacteria; unclassified Rhodocyclales
Chlorobi; unclassified SJA-28
Chloroflexi; Ktedonobacter
Chloroflexi; unclassified
Chloroflexi; unclassified A4b
Chloroflexi; unclassified Dehalococcoidaceae
Chloroflexi; unclassified HN1-15
Cyanobacteria; Chroococcidiopsis
Cyanobacteria; Leptolyngbya
Cyanobacteria; Rhodophyta
Cyanobacteria; Stramenopiles
Cyanobacteria; Streptophyta
Cyanobacteria; Synechococcus
Cyanobacteria; unclassified Ulvophyceae
Deltaproteobacteria; Bdellovibrio
Deltaproteobacteria; Corallococcus
Deltaproteobacteria; Desulfofrigus
Deltaproteobacteria; unclassified
Deltaproteobacteria; unclassified Desulfobulbaceae
Deltaproteobacteria; unclassified Haliangiaceae
Deltaproteobacteria; unclassified Myxococcales
Deltaproteobacteria; unclassified Syntrophaceae
Deltaproteobacteria; unclassified Syntrophobacteraceae
Epsilonproteobacteria; Arcobacter
Epsilonproteobacteria; Campylobacter
Fibrobacteres; Fibrobacter
Firmicutes; Aerococcus
Firmicutes; Alicyclobacillus
Firmicutes; Anaerococcus
Firmicutes; Aneurinibacillus
Firmicutes; Bacillus
Firmicutes; Blautia
Firmicutes; Butyrivibrio
Firmicutes; Clostridium
Firmicutes; Coprococcus
Firmicutes; Desemzia
Firmicutes; Desulfosporomusa
Firmicutes; Desulfotomaculum
Firmicutes; Enterococcus
Firmicutes; Eubacterium
Firmicutes; Faecalibacterium
Firmicutes; Finegoldia
Firmicutes; Geobacillus
Firmicutes; Helcococcus
Firmicutes; Lactobacillus
Firmicutes; Lysinibacillus
Firmicutes; Oribacterium
Firmicutes; Oscillospira
Firmicutes; Paenibacillus
Firmicutes; Peptoniphilus
Firmicutes; Planomicrobium
Firmicutes; Pseudobutyrivibrio
Firmicutes; Roseburia
Firmicutes; Ruminococcus
Firmicutes; Selenomonas
Firmicutes; Staphylococcus
Firmicutes; Streptococcus
Firmicutes; Trichococcus
Firmicutes; unclassified 1B07
Firmicutes; unclassified Aerococcaceae
Firmicutes; unclassified Bacillaceae
Firmicutes; unclassified Bacillales
Firmicutes; unclassified Catabacteriaceae
Firmicutes; unclassified Clostridiales Family XI. Incertae Sedis
Firmicutes; unclassified Lachnospiraceae
Firmicutes; unclassified ML1228J-1
Firmicutes; unclassified OPB54
Firmicutes; unclassified Planococcaceae
Firmicutes; unclassified Ruminococcaceae
Firmicutes; unclassified Thermoanaerobacterales
Firmicutes; unclassified Turicibacteraceae
Firmicutes; unclassified Veillonellaceae
Firmicutes; unclassified YNPFFP6
Firmicutes; Veillonella
Fusobacteria; Cetobacterium
Fusobacteria; Leptotrichia
Gammaproteobacteria; Acinetobacter
Gammaproteobacteria; Aeromonas
Gammaproteobacteria; Aggregatibacter
Gammaproteobacteria; Allochromatium
Gammaproteobacteria; Anaerobiospirillum
Gammaproteobacteria; Candidatus Portiera
Gammaproteobacteria; Enterobacter
Gammaproteobacteria; Erwinia
Gammaproteobacteria; Halomonas
Gammaproteobacteria; Klebsiella
Gammaproteobacteria; Leclercia
Gammaproteobacteria; Lysobacter
Gammaproteobacteria; Marinobacter
Gammaproteobacteria; Marinobacterium
Gammaproteobacteria; Nevskia
Gammaproteobacteria; Nitrosococcus
Gammaproteobacteria; Pantoea
Gammaproteobacteria; Pseudoalteromonas
Gammaproteobacteria; Pseudomonas
Gammaproteobacteria; Pseudoxanthomonas
Gammaproteobacteria; Psychrobacter
Gammaproteobacteria; Salmonella
Gammaproteobacteria; Serratia
Gammaproteobacteria; Shewanella
Gammaproteobacteria; Shigella
Gammaproteobacteria; Stenotrophomonas
Gammaproteobacteria; Succinivibrio
Gammaproteobacteria; unclassified
Gammaproteobacteria; unclassified Chromatiaceae
Gammaproteobacteria; unclassified Coxiellaceae
Gammaproteobacteria; unclassified Ectothiorhodospiraceae
Gammaproteobacteria; unclassified Enterobacteriaceae
Gammaproteobacteria; unclassified FCPT525
Gammaproteobacteria; unclassified Halomonadaceae
Gammaproteobacteria; unclassified OM60
Gammaproteobacteria; unclassified Pasteurellaceae
Gammaproteobacteria; unclassified Sinobacteraceae
Gammaproteobacteria; unclassified Xanthomonadaceae
Gammaproteobacteria; unclassified ZA3412c
Gammaproteobacteria; Vibrio
Gammaproteobacteria; Xylella
Gemmatimonadetes; unclassified Gemmatimonadaceae
Gemmatimonadetes; unclassified Gemmatimonadetes
LCP-89; unclassified
NC10; Candidatus Methylomirabilis
Nitrospirae; Leptospirillum
Nitrospirae; Nitrospira
OP3; unclassified
Planctomycetes; Rhodopirellula
Planctomycetes; unclassified Isosphaeraceae
Planctomycetes; unclassified Planctomycetaceae
SAR406; unclassified ZA3312c

SC4; unclassified
SC4; unclassified KD3-113
SPAM; unclassified 0319-6G9
Spirochaetes; unclassified Zplanct13
SR1; unclassified
Thermi; Deinococcus
TK-SH1; unclassified
TM7; unclassified
Verrucomicrobia; Akkermansia
Verrucomicrobia; unclassified MC18
Verrucomicrobia; unclassified R76-B18
Verrucomicrobia; unclassified RFP12
Verrucomicrobia; unclassified Verrucomicrobiales
ZB2; unclassified

GI-36-4

Phylum; Genus;134 unique genera
Acidobacteria; Candidatus Solibacter
Acidobacteria; unclassified Acidobacteriaceae
Actinobacteria; Arthrobacter
Actinobacteria; Brevibacterium
Actinobacteria; Corynebacterium
Actinobacteria; Cryobacterium
Actinobacteria; Dactylosporangium
Actinobacteria; Friedmanniella
Actinobacteria; Gordonia
Actinobacteria; Kocuria
Actinobacteria; Mycobacterium
Actinobacteria; Nocardioides
Actinobacteria; Propionibacterium
Actinobacteria; Propionicimonas
Actinobacteria; Rhodococcus
Actinobacteria; Saccharomonospora
Actinobacteria; Tessaracoccus
Actinobacteria; unclassified Cellulomonadaceae
Actinobacteria; unclassified Corynebacteriaceae
Actinobacteria; unclassified Euzebiaceae
Actinobacteria; unclassified Geodermatophilaceae
Actinobacteria; unclassified Microbacteriaceae
Actinobacteria; Yaniella
Alphaproteobacteria; Azospirillum
Alphaproteobacteria; Bradyrhizobium
Alphaproteobacteria; Brevundimonas
Alphaproteobacteria; Candidatus Pelagibacter
Alphaproteobacteria; Methylobacterium
Alphaproteobacteria; Mycoplana
Alphaproteobacteria; Novosphingobium
Alphaproteobacteria; Paracoccus
Alphaproteobacteria; Rhizobium
Alphaproteobacteria; Shinella
Alphaproteobacteria; Skermanella
Alphaproteobacteria; Sphingobium
Alphaproteobacteria; Sphingomonas
Alphaproteobacteria; unclassified Acetobacteraceae
Alphaproteobacteria; unclassified Bradyrhizobiaceae
Alphaproteobacteria; unclassified Caulobacteraceae
Alphaproteobacteria; unclassified Erythrobacteraceae
Alphaproteobacteria; unclassified Holosporaceae
Alphaproteobacteria; unclassified Phyllobacteriaceae
Alphaproteobacteria; unclassified Rhodospirillaceae
Alphaproteobacteria; Wolbachia
Bacteroidetes; Bacteroides
Bacteroidetes; Hymenobacter
Bacteroidetes; Prevotella
Bacteroidetes; unclassified Chitinophagaceae
Bacteroidetes; unclassified Flavobacteriaceae
Bacteroidetes; unclassified Flexibacteraceae
Bacteroidetes; unclassified RikenellaceaeII
Betaproteobacteria; Achromobacter
Betaproteobacteria; Aquabacterium
Betaproteobacteria; Burkholderia
Betaproteobacteria; Delftia
Betaproteobacteria; Diaphorobacter
Betaproteobacteria; Hydrogenophilus
Betaproteobacteria; Massilia
Betaproteobacteria; Methylibium
Betaproteobacteria; Ralstonia
Betaproteobacteria; Rhodocyclus
Betaproteobacteria; Roseateles
Betaproteobacteria; Rubrivivax
Betaproteobacteria; Simplicispira
Betaproteobacteria; Thiomonas
Betaproteobacteria; unclassified Alcaligenaceae
Betaproteobacteria; unclassified Comamonadaceae
Betaproteobacteria; unclassified Neisseriaceae
Betaproteobacteria; unclassified Nitrosomonadaceae
Betaproteobacteria; unclassified Oxalobacteraceae
Chloroflexi; unclassified
Chloroflexi; unclassified A4b
Cyanobacteria; Microcystis
Cyanobacteria; Prochlorococcus
Cyanobacteria; Streptophyta
Cyanobacteria; Synechococcus
Cyanobacteria; unclassified Gomontiellaceae
Cyanobacteria; unclassified mle1-12
Deltaproteobacteria; Desulfomicrobium
Deltaproteobacteria; unclassified
Deltaproteobacteria; unclassified Desulfuromonadaceae
Deltaproteobacteria; unclassified Haliangiaceae
Deltaproteobacteria; unclassified Syntrophaceae
Epsilonproteobacteria; Arcobacter
Fibrobacteres; Fibrobacter
Firmicutes; Anaerococcus
Firmicutes; Bacillus
Firmicutes; Blautia
Firmicutes; Butyrivibrio
Firmicutes; Clostridium
Firmicutes; Enterococcus
Firmicutes; Faecalibacterium
Firmicutes; Lactobacillus
Firmicutes; Lactococcus
Firmicutes; Listeria
Firmicutes; Marinilactibacillus
Firmicutes; Paenibacillus
Firmicutes; Planococcus
Firmicutes; Pseudobutyrivibrio
Firmicutes; Roseburia
Firmicutes; Ruminococcus
Firmicutes; Staphylococcus
Firmicutes; Streptococcus
Firmicutes; unclassified Carnobacteriaceae
Firmicutes; unclassified Clostridiaceae
Firmicutes; unclassified Lachnospiraceae
Firmicutes; unclassified Ruminococcaceae
Firmicutes; unclassified Thermoanaerobacterales
Firmicutes; Weissella
Gammaproteobacteria; Acinetobacter
Gammaproteobacteria; Citrobacter
Gammaproteobacteria; Pantoea
Gammaproteobacteria; Pseudoalteromonas
Gammaproteobacteria; Pseudomonas
Gammaproteobacteria; Succinivibrio
Gammaproteobacteria; unclassified Enterobacteriaceae
Gammaproteobacteria; unclassified Pseudomonadaceae
Gammaproteobacteria; unclassified SUP05
Gammaproteobacteria; unlcassified Thiotrichales
GN04; unclassified
KSB1; unclassified
Nitrospirae; Leptospirillum
OP3; unclassified
Planctomycetes; unclassified Isosphaeraceae
Planctomycetes; unclassified Planctomycetaceae
SAR406; unclassified SHAS460
SBR1093; unclassified
Spirochaetes; Leptospira
Synergistetes; unclassified TG5
Tenericutes; Candidatus Phytoplasma
Tenericutes; Mycoplasma
Tenericutes; unclassified EMP_E11
TM7; unclassified
TM7; unclassified EW055

GI-38

Phylum; Genus; 13 unique genera

Actinobacteria; Corynebacterium
Actinobacteria; Propionibacterium
Alphaproteobacteria; Candidatus Pelagibacter
Betaproteobacteria; Aquabacterium
Deltaproteobacteria; Nannocystis
Deltaproteobacteria; unclassified Haliangiaceae
Firmicutes; Bacillus
Firmicutes; Enterococcus
Firmicutes; Geobacillus
Firmicutes; Marinibacillus
Firmicutes; Staphylococcus
Firmicutes; Streptococcus
Gammaproteobacteria; Pseudomonas

GI-39

Phylum; Genus; 0 unique genera

GI-40

Phylum; Genus; 9 unique genera

Actinobacteria; Corynebacterium
Actinobacteria; Promicromonospora
Actinobacteria; Propionibacterium
Alphaproteobacteria; Mesorhizobium
Alphaproteobacteria; unclassified Brucellaceae
Alphaproteobacteria; unclassified Phyllobacteriaceae
Firmicutes; Bacillus
Gammaproteobacteria; Pantoea
WS3; unclassified CV106

GI-41

Phylum; Genus; 20 unique genera

Actinobacteria; Corynebacterium
Actinobacteria; unclassified Corynebacteriaceae
Alphaproteobacteria; Bradyrhizobium
Alphaproteobacteria; Ochrobactrum
Alphaproteobacteria; Sphingobium
Alphaproteobacteria; Sphingomonas
Betaproteobacteria; Aquabacterium
Betaproteobacteria; Diaphorobacter
Deltaproteobacteria; Myxococcus
Deltaproteobacteria; unclassified Myxococcales
Firmicutes; Bacillus
Firmicutes; Enterococcus
Firmicutes; Geobacillus
Firmicutes; Salinicoccus
Firmicutes; Staphylococcus
Firmicutes; unclassified Bacillaceae
Firmicutes; unclassified Lachnospiraceae
Gammaproteobacteria; Pseudomonas
Gammaproteobacteria; unclassified Moraxellaceae
Tenericutes; Allobaculum

GIB-15-28

Phylum/Class; Genus (19)

Firmicutes; Bacillus
Firmicutes; Staphylococcus
Actinobacteria; Corynebacterium
Actinobacteria; Uncl_Corynebacteriaceae
Alphaproteobacteria; Roseobacter
Alphaproteobacteria; Sphingobium
Alphaproteobacteria; Uncl_Caulobacteraceae
Bacteroidetes; Uncl_Chitinophagaceae
Betaproteobacteria; Aquabacterium
Betaproteobacteria; Diaphorobacter
Betaproteobacteria; Polynucleobacter
Betaproteobacteria; Ralstonia
Betaproteobacteria; Thiomonas
Betaproteobacteria; Zoogloea
Chloroflexi; A4b
Firmicutes; Enterococcus
Gammaproteobacteria; Pseudomonas
Gammaproteobacteria; Uncl_Chromatiaceae
Gammaproteobacteria; Uncl_Enterobacteriaceae

GI-18B

Phylum/Class; Genus (10)

Actinobacteria; Corynebacterium
Bacteroidetes; Uncl_Flavobacteriaceae
Bacteroidetes; Uncl_Rhodothermaceae
Firmicutes; Enterococcus
Firmicutes; Paenibacillus
Firmicutes; Streptococcus
Gammaproteobacteria; Haemophilus
Gammaproteobacteria; Pseudomonas
Gammaproteobacteria; Raoultella
Gammaproteobacteria; Uncl_Enterobacteriaceae

GI-19B

Phylum/Class; Genus (41)
Actinobacteria; Corynebacterium
Actinobacteria; Microbacterium
Actinobacteria; Uncl_Microbacteriaceae
Bacteroidetes; Uncl_Rhodothermaceae
Betaproteobacteria; Acidovorax
Betaproteobacteria; Aquabacterium
Betaproteobacteria; Burkholderia
Betaproteobacteria; Delftia
Betaproteobacteria; Diaphorobacter
Betaproteobacteria; Limnohabitans
Betaproteobacteria; Pandoraea
Betaproteobacteria; Ralstonia
Betaproteobacteria; Rhodocyclus
Betaproteobacteria; Simplicispira
Betaproteobacteria; Sphaerotilus
Betaproteobacteria; Thiomonas
Betaproteobacteria; Uncl_Comamonadaceae
Betaproteobacteria; Uncl_Nitrosomonadaceae
Betaproteobacteria; Verminephrobacter
Betaproteobacteria; Zoogloea
Chloroflexi; A4b
Deltaproteobacteria; Uncl_Haliangiaceae
Firmicutes; Bacillus
Firmicutes; Coprococcus
Firmicutes; Enterococcus
Firmicutes; Geobacillus
Firmicutes; Paenibacillus
Firmicutes; Staphylococcus
Firmicutes; Streptococcus
Firmicutes; Uncl_Lachnospiraceae
Firmicutes; Uncl_Ruminococcaceae
Gammaproteobacteria; Acinetobacter
Gammaproteobacteria; Chelonobacter
Gammaproteobacteria; Klebsiella
Gammaproteobacteria; Pseudomonas
Gammaproteobacteria; Rhodanobacter
Gammaproteobacteria; Serratia
KSB1; sfA
Planctomycetes; Uncl_Planctomycetaceae
Tenericutes; Ureaplasma
Verrucomicrobia; LP2A

GI-20B

Phylum/Class; Genus (25)
Actinobacteria; Corynebacterium
Actinobacteria; Streptomyces
Actinobacteria; Uncl_Corynebacteriaceae
Betaproteobacteria; Acidovorax
Betaproteobacteria; Aquabacterium
Betaproteobacteria; Comamonas
Betaproteobacteria; Delftia
Betaproteobacteria; Diaphorobacter
Betaproteobacteria; Pandoraea
Betaproteobacteria; Rhodocyclus
Betaproteobacteria; Roseateles
Betaproteobacteria; Thiomonas
Betaproteobacteria; Uncl_Comamonadaceae
Betaproteobacteria; Uncl_Neisseriaceae
Betaproteobacteria; Uncl_Nitrosomonadaceae
Betaproteobacteria; Uncl_Oxalobacteraceae
Betaproteobacteria; Zoogloea
Chloroflexi; A4b
Firmicutes; Bacillus
Firmicutes; Uncl_Ruminococcaceae
Gammaproteobacteria; Acinetobacter
Gammaproteobacteria; Pseudomonas
Gammaproteobacteria; Uncl_Enterobacteriaceae
Gemmatimonadetes; sfM
Verrucomicrobia; LP2A

GI-Blank-Set 29-43

Phylum/Class; Genus (7)
Actinobacteria; Corynebacterium
Betaproteobacteria; Aquabacterium
Gammaproteobacteria; Klebsiella
Gammaproteobacteria; Pantoea
Gammaproteobacteria; Pseudomonas
Gammaproteobacteria; sfD
Gammaproteobacteria; Vibrio

GI-38B

Phylum/Class; Genus (17)
Actinobacteria; Corynebacterium
Actinobacteria; Uncl_Corynebacteriaceae
Alphaproteobacteria; Bartonella
Alphaproteobacteria; Bradyrhizobium
Bacteroidetes; Uncl; Flavobacteriaceae
Bacteroidetes; Uncl; RikenellaceaeII
Betaproteobacteria; Achromobacter
Betaproteobacteria; Aquabacterium
Betaproteobacteria; Thiomonas
Firmicutes; Bacillus
Firmicutes; Lactobacillus
Firmicutes; Staphylococcus
Gammaproteobacteria; Pseudomonas
Gammaproteobacteria; sfA
Gammaproteobacteria; Uncl_Enterobacteriaceae
Tenericutes; Ureaplasma
Verrucomicrobia; LP2A

E.3 454 Tag-Encoded Pyrosequencing: Metadata

Table E.3-1. Sample characteristics of various spacecraft and associated surfaces.

Sample	Sample ID	Sampling Devices	Sample Type	Area (m^2)	Mission	Cleanroom Type	Description
Group I: Cleanroom types (33 m^2)							
GI-37	150	BisKit	Floor-70A	10	None	Non-NASA Cleanroom	LBNL Cleanroom (70A)
GI-35-4	141	BisKit	Shoe Cleaner	1	None	Ordinary room	Ordinary room adjacent to JPL-SAF
GI-35-5	142	BisKit	ARD	1	None	Ordinary room	Ordinary room adjacent to JPL-SAF
GI-35-6	143	BisKit	Entrance floor	1	None	Ordinary room	Ordinary room adjacent to JPL-SAF
GI-35-7	144	BisKit	Floor 1	1	None	Ordinary room	Ordinary room adjacent to JPL-SAF
GI-35-8	145	BisKit	Floor 2	1	None	Ordinary room	Ordinary room adjacent to JPL-SAF
GI-36-3	146	BisKit	GSE	9	Mars	Class 100K	During spacecraft assembly (JPL-SAF)
GI-36-4	148	BisKit	Floor	9	Mars	Class 100K	During spacecraft assembly (JPL-SAF)
Group II: Cleaning vs. precleaning (38 m^2)							
GI-42-1	155	BisKit	Floor	9	None	Class 100K	Bldg 144 cleanroom prior to cleaning
GI-42-2	157	BisKit	GSE	9	None	Class 100K	Bldg 144 cleanroom prior to cleaning
GI-43-1	159	Polyester wipe	Floor	10	Mars	Class 100K	Bldg 144 cleanroom after cleaning
GI-43-2	161	Polyester wipe	GSE	10	Mars	Class 100K	Bldg 144 cleanroom after cleaning
Group III: Spacecraft surfaces (spore count-based determination) (110 m^2)							
GI-16	124	Polyester wipe	Spacecraft	6	Mars	Class 100K	No spore count
GI-17	125	Polyester wipe	Spacecraft	10	Mars	Class 100K	No spore count
GI-25	133	Polyester wipe	Spacecraft	8	Mars	Class 100K	No spore count
GI-26	134	Polyester wipe	Spacecraft	7	Mars	Class 100K	No spore count
GI-27	135	Polyester wipe	Spacecraft	4	Mars	Class 100K	No spore count
GI-28	136	Polyester wipe	Spacecraft	6	Mars	Class 100K	No spore count
GI-29	137	Polyester wipe	Spacecraft	18	Mars	Class 100K	No spore count
GI-18	126	Polyester wipe	Spacecraft	10	Mars	Class 100K	1 to 5 spore per m^2
GI-19	127	Polyester wipe	Spacecraft	14	Mars	Class 100K	1 to 5 spore per m^2
GI-20	128	Polyester wipe	Spacecraft	5	Mars	Class 100K	1 to 5 spore per m^2
GI-21	129	Polyester wipe	Spacecraft	4	Mars	Class 100K	1 to 5 spore per m^2
GI-22	130	Polyester wipe	Spacecraft	1	Mars	Class 100K	1 to 5 spore per m^2
GI-30	138	Polyester wipe	Spacecraft	13	Mars	Class 100K	1 to 5 spore per m^2
GI-32	140	Polyester wipe	Spacecraft	3	Mars	Class 100K	5 to 10 spore per m^2
GI-24	132	Polyester wipe	Spacecraft	1	Mars	Class 100K	300 spores per m^2
Group IV: Spacecraft surfaces (mission component-based determinations) (52 m^2)							
GI-38	151	Polyester wipe	Spacecraft	26	Mars	Class 100K	Cruise stage (0.2 spores per m^2)
GI-39	152	Polyester wipe	Spacecraft	9	Mars	Class 100K	Descent stage (0.4 spores per m^2)
GI-40	153	Polyester wipe	Spacecraft	16	Mars	Class 100K	Rover (0.3 spores per m^2)
GI-41	154	Polyester wipe	Spacecraft	1	None	Class 100K	Non-flight samples (14 spores per m^2)

Note: LBNL: Lawrence Berkeley National Laboratories; JPL-SAF, Jet Propulsion Laboratory Spacecraft Assembly Facility.

Table E.3-2. Bacterial sequences retrieved from various spacecraft and associated surfaces.

Bacterial Taxa	Group I								Group II				Group III															Group IV			
	150	141	142	143	144	145	146	148	155	157	159	161	124	125	133	134	135	136	137	126	127	128	129	130	138	140	132	151	152	153	154
	Floor-70A	Shoe Cleaner	Air lock	Entrance floor	Floor 1	Floor 2	GSE	Floor	Floor	GSE	Floor	GSE	Spacecraft	Spacecraft	Spacecraft	Spacecraft	Spacecraft	Spacecraft	Spacecraft	Spacecraft	Spacecraft	Spacecraft	Spacecraft	Spacecraft	Spacecraft	Spacecraft	Spacecraft	Spacecraft	Spacecraft	Spacecraft	Spacecraft
Actinobacteria	81	315	222	798	279	106	1764	55	88	618	8	120			1	76		3	1		49	60	105			79	7	5			
Armatimonadetes	1	6		21	7				6	1					27																
Bacteroidetes	7	101	62	252	64	104	214	108	2477	436	59	97						4				18					47				
Chlorobi										3																					
Verrucomicrobia				1					8		5																				
Chloroflexi	1	15	5	10	7	17	26	4		27													25								
Deinococcus-Thermus	3	1		6	7	2	26		7	41		11											1								
Acidobacteria	4	10	1	23	11	16	113	350	1	37		11			3																
Firmicutes	13	186	17	322	174	15	383	157	17	157		8				33					2		19		3	60					
Fusobacteria		10		67	17	6	1	1		2													25								
Gemmatimonadetes	1	4		13			17		3	2		2																			
Nitrospirae									1	1																					
Planctomycetes		2	3	11			1		2	4		3																			
Proteobacteria																															
Alpha	5776	693	196	2465	1065	785	1120	606	7495	2517	692	73		1	23	22						26	129		15		127		54		
Beta	1478	215	104	431	154	215	523	100	1031	565	291	271	9	2	42	101	33	139		32	77	139	329	26	3		103	37	2	5	
Delta		3		3	2		5	36	6	7					12																
Gamma	1211	962	100	3374	1165	796	251	357	4833	1127	456	250			3	43	30	25		27	91	96	36	7			175	15	36	74	15
Unidentified		6	7	13	24	12			104	13			4																		
Spirochaetes								1																							
Tenericutes	2	1																													
Unidentified division																															
SC4							24			6																					
TM7		3		6			3																					12			
WPS-2				14					2																						
Unclassified bacteria	20	89	78	277	61	10	224	8	159	384		737			1								29								
Total # of sequences	**8598**	**2622**	**795**	**8107**	**3037**	**2084**	**4695**	**1783**	**16240**	**5948**	**1511**	**1583**	**13**	**3**	**112**	**275**	**63**	**171**	**1**	**59**	**219**	**339**	**698**	**33**	**21**	**139**	**459**	**69**	**92**	**79**	**15**

Note: Taxa in bold are relevant to Planetary Protection.

Table E.3-3. Taxonomic affiliation of OTUs observed using next generation 454 FLX tag-encoded pyrosequencing. Numbers of sequences belonging to each OTU are also mentioned for respective samples.

OTU	Sample ID																			
No.	123	131	139	141	142	143	144	145	150	155	157	159	161	Kingdom	Phylum	Class	Order	Family	Genus	Species
1	3332			5	10	19			54	3	1		125	Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Pseudomonas_veronii
2	426			2					264	5	21			Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
3	36	241		136	25	458	15	4	1021	255	82	54	5	Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Unclassified
4	58	16		5	8	6			3	64	21	12		Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Delftia	Unclassified
5	16									2				Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
6	18													Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Chryseobacterium	Unclassified
7	11			6					2					Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
8	7													Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Unclassified	Unclassified
9	5									2				Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
10	2													Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Unclassified
11	3							6	10					Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Unclassified	Unclassified
12	1													Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Flavobacterium	Unclassified
13	3					3				76	21	1		Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Roseomonas	Unclassified
14	1													Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
15	1													Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Spirosoma	Unclassified
16	2													Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
17	1													Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Sphingobacteriaceae	Unclassified	Unclassified
18	1													Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Unclassified	Unclassified
19	1													Bacteria	Proteobacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
20	1													Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Unclassified
21	1													Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Sphingobacteriaceae	Unclassified	Unclassified
22	1			6		5			1	1	6		17	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
23	1													Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Chryseobacterium	Unclassified
24														Bacteria	Proteobacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
25					13		10	5						Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Acidovorax	Acidovorax_caeni
26											3	3		Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Aquabacteriaceae	Aquabacterium	Unclassified
27														Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	Burkholderia	Burkholderia_vietnamiensis
28				21	29	49	87	43	1		2		5	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	Blastobacter	Bradyrhizobium_sp._BTAi1
29					1									Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Pelomonas	Pelomonas_puraquae
30				43		355	4	8	2	15	46		1	Bacteria	Proteobacteria	Gamma-proteobacteria	Xanthomonadales	Xanthomonadaceae	Stenotrophomonas	Pseudomonas_geniculata
31						2			4					Bacteria	Proteobacteria	Gamma-proteobacteria	Enterobacteriales	Enterobacteriaceae	Unclassified	Unclassified
32														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Mycobacteriaceae	Mycobacterium	Mycobacterium_chelonae

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
33				1						1				Bacteria	Proteobacteria	Gamma-proteobacteria	Xanthomonadales	Xanthomonadaceae	Stenotrophomonas	Unclassified
34														Bacteria	Proteobacteria	Gamma-proteobacteria	Xanthomonadales	Xanthomonadaceae	Stenotrophomonas	Unclassified
35		2		2		1	8	4	81			29		Bacteria	Proteobacteria	Gamma-proteobacteria	Enterobacteriales	Enterobacteriaceae	Escherichia	Escherichia_fergusonii
36														Bacteria	Firmicutes	Bacilli	Bacillales	Alicyclobacillaceae	Alicyclobacillus	Unclassified
37														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified(93)	Unclassified	Unclassified
38				155	14	491	455	304		1313	407	118	1	Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Acinetobacter_johnsonii
39				303	10	1359	78	7		21	15		52	Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Acinetobacter_lwoffii
40														Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Flavobacterium	Unclassified
41				50		314	5	5		225	52	109		Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Agrobacterium	Rhizobium_sp._IRBG_74
42				2		11	1	2		355	50	34		Bacteria	Proteobacteria	Gamma-proteobacteria	Alteromonadales	Unclassified(95)	Unclassified	Unclassified
43				14	1	34	71	26	30	13	38	2	4	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Propionibacteriaceae	Propionibacterium	Propionibacterium_acnes
44										5				Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Novosphingobium	Unclassified
45														Bacteria	Actinobacteria	Actinobacteria	Solirubrobacterales	Conexibacteraceae	Unclassified	Unclassified
46														Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Unclassified	Unclassified
47														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Okibacterium	Okibacterium_fritillariae
48												1		Bacteria	Proteobacteria	Gamma-proteobacteria	Enterobacteriales	Enterobacteriaceae	Unclassified	Unclassified
49				1		3					10		10	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophilaceae	Unclassified	Unclassified
50						1	26	16		13	6			Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Unclassified
51					7						3			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophilaceae	Modestobacter	Unclassified
52														Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Agrobacterium	Unclassified
53														Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Agrobacterium	Rhizobium_sp._IRBG_74
54														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophilaceae	Unclassified	Unclassified
55														Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Flavobacterium	Unclassified
56				3		5	19	26		1	5			Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Unclassified	Unclassified
57				3	7	12	10		7	3	22		6	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium	Corynebacterium_tuberculostearicum
58														Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
59												1		Bacteria	Proteobacteria	Gamma-proteobacteria	Enterobacteriales	Enterobacteriaceae	Unclassified	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
60				14	7	30	2			2	23			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophila-ceae	Modestobacter	Unclassified
61							12				2			Bacteria	Fusobacteria	Fusobacteria	Fusobacteriales	Fusobacteriaceae	Fusobacterium	Unclassified
62														Bacteria	Chloroflexi	SOGA31	Unclassified	Unclassified	Unclassified	Unclassified
63		23083		3	10	16			9	11	32		1	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Methylobacterium _adhaesivum
64											1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Curtobacterium	Unclassified
65							9							Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Kocuria	Kocuria_rosea
66														Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	Bacillus_soli
67				7		49	65		3	6				Bacteria	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Staphylococcus	Staphylococcus_ hominis
68		3		13		26	1	1	81	105	24	42		Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Acidovorax	Unclassified
69												17		Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Roseateles	Unclassified
70										1	1			Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Skermanella	Unclassified
71				1			1			539	77	177		Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Comamonas	Comamonas_ aquatica
72														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae	Actinomyces	Unclassified
73														Bacteria	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolinaceae	DRC31	Unclassified
74				34	16	81	4			5	8			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Agrococcus	Agrococcus_ jenensis
75						3	25			4	28		1	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rubellimicrobium	Unclassified
76				16		105					2			Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Pseudomonas_ stutzeri
77														Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rubellimicrobium	Unclassified
78		10		2		1	5	25	146	114	17			Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Unclassified
79								1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophila-ceae	Blastococcus	Blastococcus_ aggregatus
80														Bacteria	Firmicutes	Bacilli	Lactobacillales	Aerococcaceae	Unclassified	Unclassified
81				14	2	55	75	1	4	2	7			Bacteria	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Staphylococcus	Staphylococcus_ epidermidis
82						2								Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Unclassified	Unclassified
83														Bacteria	Actinobacteria	Actinobacteria	MC47	Unclassified	Unclassified	Unclassified
84														unknown (200)	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
85														Bacteria	Proteobacteria	Gamma-proteobacteria	Xanthomonadales	Xanthomonadaceae	Stenotrophomo-nas	Unclassified
86														Bacteria	Thermi	Deinococci	Deinococcales	Deinococcaceae	Deinococcus	Deinococcus_ radiodurans
87														Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Unclassified	Unclassified	Unclassified
88						10								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Marmoricola	Unclassified
89														Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
90		1971			29	2			13	1				Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Sphingomonas_ melonis
91		10		31	19	26	43	67						Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Hyphomicrobium	Hyphomicrobium _facile
92		1		1			2							Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Unclassified	Unclassified
93		2		1										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
94		2												Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Unclassified
95		1												Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Unclassified
96		1												Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Methylobacterium _adhaesivum
97		1												Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Unclassified
98														Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Flavobacterium	Unclassified
99				2		6			8	151	34	15		Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Novosphingobi-um	Unclassified
100				1		6		4	2	45	8	27	5	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
101				6										Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
102				1	2	6	118	45		129	108			Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Unclassified	Unclassified
103								1		23	15			Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Unclassified	Unclassified
104				17	7	83	36	26	1	3576	673	263		Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Brevundimonas	Brevundimonas_ mediterranea
105										1	1			Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Skermanella	Unclassified
106										25		117		Bacteria	Proteobacteria	Gamma-proteobacteria	Xanthomonadales	Xanthomonadaceae	Pseudoxantho-monas	Pseudoxantho-monas_mexicana
107			1	104	2	58	273	166		2063	26	2		Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Acinetobacter_ johnsonii
108														Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
109														Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Unclassified
110														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium	Corynebacterium _efficiens
111				15		17				62	43			Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
112														Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Flavobacterium	Unclassified
113							1			146	38	10		Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
114														Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Unclassified	Unclassified
115														Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
116										1582	181	10		Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Flavobacterium	Unclassified
117				1				8			1			Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Methylibiaceae(96)	Methylibium	Unclassified
118														Bacteria	Armatimona-detes	CH21	Unclassified	Unclassified	Unclassified	Unclassified
119														Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	Haliangiaceae	Unclassified	Unclassified
120														Bacteria	Acidobacteria	Solibacteres	Solibacterales	Solibacteraceae	Candidatus_ Solibacter	Unclassified
121				8		3	2	2			2			Bacteria	Proteobacteria	Alphaproteobacteria	Unclassified	Unclassified	Unclassified	Unclassified
122														Bacteria	Acidobacteria	Solibacteres	Solibacterales	Solibacteraceae	Candidatus_ Solibacter	Unclassified
123														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Dietziaceae	Dietzia	Unclassified
124														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Brevibacteriaceae	Brevibacterium	Unclassified
125														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Unclassified	Unclassified
126						1								Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
127						3	1				1			Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Unclassified	Unclassified
128				5		2			4	4	13			Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Unclassified	Unclassified
129						1					1			Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Roseomonas	Unclassified
130					13	3				4	5		1	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Arthrobacter	Unclassified
131														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Intrasporangiaceae	Unclassified	Unclassified
132														Bacteria	Actinobacteria	Actinobacteria	Solirubrobacterales	Solirubrobactera-ceae	Unclassified	Unclassified
133														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Brevibacteriaceae	Brevibacterium	Unclassified
134														Bacteria	Proteobacteria	Gamma-proteobacteria	Xanthomonadales	Xanthomonadaceae	Stenotrophomo-nas	Unclassified
135														Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Unclassified	Unclassified
136				1										Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
137			7	1		6			35	3				Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae	Achromobacter	Unclassified
138														Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Flavobacterium	Unclassified
139				2		15				2	6	11		Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Methylobacterium _adhaesivum
140														Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Schlegelella	Schlegelella_ther-modepolymerans
141														Bacteria	Firmicutes	Bacilli	Lactobacillales	Carnobacteriaceae	Unclassified	Unclassified
142			1											Bacteria	Firmicutes	Bacilli	Lactobacillales	Carnobacteriaceae	Unclassified	Unclassified
143											10			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium	Corynebacterium _aurimucosum
144														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae	Mobiluncus	Mobiluncus_ curtisii
145							1							Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium	Corynebacterium _freneyi
146														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium	Unclassified
147				60	22	402	516	295	1	518	119	51		Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Mycoplana	Unclassified
148				93		167	8	1		1	5			Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Acinetobacter_ haemolyticus
149				56		402	4			4	20		5	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Unclassified	Unclassified
150				85		303	5	1	1	14	21			Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingobium	Sphingobium_ yanoikuyae
151				39		122								Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Roseomonas	Roseomonas_ mucosa
152				28		60	24	11			2			Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Paracoccus	Paracoccus_yeei
153				34		3					7			Bacteria	Proteobacteria	Betaproteobacteria	Neisseriales	Neisseriaceae	Neisseria	Neisseria_sub-flava
154				25		86								Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylocystaceae	Methylopila	Unclassified
155				21	15	9					1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Arthrobacter	Unclassified
156				23		48								Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Agrobacterium	Agrobacterium_ larrymoorei
157				16		2								Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Unclassified	Unclassified
158				15		22								Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Flavobacterium	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
159				21	3	10					1		2	Bacteria	Proteobacteria	Gamma-proteobacteria	Pasteurellales	Pasteurellaceae	Haemophilus	Haemophilus_parainfluenzae
160				11	5	60	4				3		2	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Arthrobacter	Arthrobacter_agilis
161				9		12	4	10						Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium	Clostridium_hiranonis
162				17	1	5	11	4						Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	Burkholderia	Burkholderia_heleia
163				7										Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	Unclassified
164				7					2		15			Bacteria	Firmicutes	Bacilli	Gemellales	Gemellaceae	Gemella	Unclassified
165				8		19								Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Unclassified	Unclassified
166				7										Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Rhodoplanes	Unclassified
167				9						1				Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Intrasporangiaceae	Unclassified	Unclassified
168				57										Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Lactococcus	Lactococcus_lactis
169				6										Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	Unclassified
170				7		9				1	1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Kineosporiaceae(97)	Kineococcus	Unclassified
171				11		19	17	38						Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	Burkholderia	Unclassified
172				7		1				35	50			Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Novosphingobium	Novosphingobium_resinovorum
173				13	1	78	214	196		37	6			Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Acinetobacter_johnsonii
174				5										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Marmoricola	Unclassified
175				5										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
176				5			1							Bacteria	Proteobacteria	Gamma-proteobacteria	Legionellales	Legionellaceae	Unclassified	Unclassified
177				6						5				Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Comamonas	Unclassified
178				5	16	12	33	16			4			Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Unclassified	Unclassified
179				8		15				3	1			Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Phenylobacterium	Unclassified
180				7		5								Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Unclassified	Unclassified
181				5	2	3	6	12						Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	Xanthobacter	Xanthobacter_flavus
182				6			1			15	1			Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Shinella	Unclassified
183				10										Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
184				4										Bacteria	Firmicutes	Clostridia	Clostridiales	Unclassified	Unclassified	Unclassified
185				4			1			29	5			Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Unclassified
186				4		19		9			2		8	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
187				10		46	6	1	1	11	62		43	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
188				5		14					2			Bacteria	Unclassified(96)	Unclassified(96)	Unclassified(96)	Unclassified(96)	Unclassified	Unclassified
189				4										Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Segetibacter	Unclassified
190				5		1								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
191				4		2								Bacteria	Firmicutes(67)	Clostridia(67)	Clostridiales(67)	Ruminococcaceae(67)	Unclassified	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
192				5										Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Unclassified
193				4					2	3	1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium	Unclassified
194				4										Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
195				8		2								Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae(70)	Unclassified	Unclassified
196				4										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Propionicimonas	Unclassified
197				3										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Kocuria	Kocuria_rhizo-phila
198				8			1							Bacteria	Firmicutes	Bacilli	Gemellales	Gemellaceae	Gemella	Gemella_san-guinis
199				3			1							Bacteria	Proteobacteria	Gamma-proteobacteria	Xanthomonadales	Xanthomonadaceae	Unclassified	Unclassified
200				3	4	8	2	8	3	7	17		23	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Roseomonas	Unclassified
201				8										Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium	Unclassified
202				5		17	18							Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Unclassified
203				4										Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Unclassified	Unclassified
204				4							1			Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Ideonellaceae(80)	Ideonella	Unclassified
205				3										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
206				7		7	20			1	11		4	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	Balneimonas	Unclassified
207				9	5	23	3	1	1	2	4			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Kocuria	Kocuria_rosea
208				4										Bacteria	Firmicutes	Bacilli	Bacillales	Planococcaceae	Planomicrobium	Unclassified
209				4		8								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Dermacoccaceae	Kytococcus	Kytococcus_ schroeteri
210				5		3					11			Bacteria	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Staphylococcus	Staphylococcus_ equorum
211				9										Bacteria	Chloroflexi	SOGA31	Unclassified	Unclassified	Unclassified	Unclassified
212				4										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Micrococcus	Micrococcus_ lylae
213				3						1				Bacteria	Acidobacteria	Acidobacteria	Acidobacteriales	Acidobacteriaceae	Unclassified	Unclassified
214				3		1								Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
215				3		13								Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
216				13	13	30	11	21						Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	Burkholderia	Unclassified
217				3							1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Nocardioides	Nocardioides_ oleivorans
218				5		2				8	1			Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Aurantimonadaceae	Aurantimonas	Aurantimonas_ altamirensis
219				4	9		10						9	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
220				8		57	1							Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Enhydrobacter	Enhydrobacter_ aerosaccus
221				9		7		15		48	223	8	25	Bacteria	Proteobacteria	Gamma-proteobacteria	Legionellales	Coxiellaceae	Rickettsiella	Rickettsiella_grylli
222				4										Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
223				6		53		6						Bacteria	Fusobacteria	Fusobacteria	Fusobacteriales	Fusobacteriaceae	Sneathia	Leptotrichia_ amnionii
224				3							11			Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
225				3					5					Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Sphingomonas_ asaccharolytica
226				6										Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Methylibiaceae	Methylibium	Unclassified
227				5		9								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Intrasporangiaceae	Unclassified	Unclassified
228				6		1					12		2	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nakamurellaceae	Unclassified	Unclassified
229				3										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Arthrobacter	Arthrobacter_ bergerei
230				2	2				1	1	6		2	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Friedmanniella	Unclassified
231				5		21								Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Cytophaga	Cytophaga_ hutchinsonii
232				2		4			1	989	410	42		Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Paracoccus	Paracoccus_ marcusii
233				2		3			2		2			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium	Unclassified
234				15		28	11	3	3	13	34		48	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Unclassified	Unclassified
235				2										Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Unclassified	Unclassified
236				2										Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	Unclassified
237				5		9			1					Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Nocardioides	Nocardioides_ oleivorans
238				3										Bacteria	Actinobacteria	Actinobacteria	Solirubrobacterales	Conexibacteraceae	Unclassified	Unclassified
239				4		9								Bacteria	Proteobacteria	Gamma-proteobacteria	Xanthomonadales	Xanthomonadaceae	Lysobacter	Unclassified
240				4							1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
241				2										Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Bacteroides	Bacteroides_ capillosus
242				3										Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Sarcina	Unclassified
243				2		1								Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Unclassified	Unclassified
244				3		9					7			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Micrococcus	Unclassified
245				2										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Cellulomonadaceae	Cellulomonas	Cellulomonas_ uda
246				2										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Kocuria	Unclassified
247				3										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium	Corynebacterium _kroppenstedtii
248				4										Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Wautersiella	Unclassified
249				3										Bacteria	Armatimonadete s	Armatimonadia	Armatimonadales	Armatimonadaceae	Unclassified	Unclassified
250				2							3			Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Methylibiaceae	Methylibium	Unclassified
251				7	5	57	11	26		6	42		81	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
252				4										Bacteria	Proteobacteria	Gamma-proteobacteria	Xanthomonadales	Xanthomonadaceae	Lysobacter	Unclassified
253				2										Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium	Faecalibacterium _prausnitzii
254				2							5			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophila-ceae	Unclassified	Unclassified
255				3		4					4			Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Roseomonas	Unclassified
256				3										Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
257				2										Bacteria	Proteobacteria	Betaproteobacteria	Unclassified	Unclassified	Unclassified	Unclassified
258				3										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Streptomycetaceae	Streptomyces	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
259				3										Bacteria	Bacteroidetes	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
260				3				3						Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Sphingomonas_ asaccharolytica
261				4							8			Bacteria	Proteobacteria	Gamma-proteobacteria	Pasteurellales	Pasteurellaceae	Unclassified	Unclassified
262				7										Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingobium	Unclassified
263				2			11	3						Bacteria	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Staphylococcus	Unclassified
264				5										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Brevibacteriaceae	Brevibacterium	Unclassified
265				2										Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
266				2									2	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
267				3										Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Unclassified	Unclassified
268				4		1								Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Unclassified	Unclassified
269				2				4			3			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Friedmanniella	Unclassified
270				3							5			Bacteria	Firmicutes	Bacilli	Turicibacterales	Turicibacteraceae	Turicibacter	Unclassified
271				2										Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	Bacillus_longi-quaesitum
272				3		11								Bacteria	Proteobacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
273				2										Bacteria	Acidobacteria	Acidobacteria	Acidobacteriales	Acidobacteriaceae	Unclassified	Unclassified
274				3										Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
275				2										Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Unclassified	Unclassified
276				4										Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
277				10		17	1		1	33	12		2	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Skermanella	Unclassified
278				2	4	7	7			17	7	2	2	Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Pseudomonas_ stutzeri
279				7		11				14	71			Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Caulobacter	Caulobacter_ vibrioides
280				2										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
281				2										Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
282				2										Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Flavobacterium	Unclassified
283				2		3	7			41	9			Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rhodobacter	Rhodobacter_ azotoformans
284				2										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Unclassified	Unclassified
285				2		4								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Curtobacterium	Curtobacterium_ flaccumfaciens
286				3										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardiaceae	Rhodococcus	Unclassified
287				2										Bacteria	Planctomycetes	Planctomycea	Gemmatales	Gemmataceae	Gemmata	Unclassified
288				4		14								Bacteria	Fusobacteria	Fusobacteria	Fusobacteriales	Fusobacteriaceae	Sneathia	Unclassified
289				2										Bacteria	Chloroflexi	Thermomicrobia	Sphaerobacterales	Sphaerobacterineae	HN1-15	Unclassified
290				2										Bacteria	Firmicutes	Clostridia	Clostridiales	Veillonellaceae	Veillonella	Veillonella_ratti
291				2										Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Amaricoccus	Unclassified
292				2										Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Unclassified	Unclassified
293				2										Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Pseudomonas_ entomophila

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
294				3										Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Epulopiscium	Unclassified
295				3										Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Chryseobacteri-um	Unclassified
296				2		2				6	4			Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Unclassified	Unclassified
297				5										Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Flavobacterium	Flavobacterium_ gelidilacus
298				5		1		11			12			Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
299				2										Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Flavobacterium	Unclassified
300				3		6	3		1					Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Unclassified	Unclassified
301				1										Bacteria	Thermi	Deinococci	Deinococcales	Deinococcaceae	Deinococcus	Unclassified
302				1							1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Kocuria	Unclassified
303				2										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Nocardioides	Unclassified
304				2										Bacteria	Actinobacteria	Actinobacteria	Solirubrobacterales	Unclassified	Unclassified	Unclassified
305				1										Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
306				1		7		11						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nakamurellaceae	Unclassified	Unclassified
307				1										Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Unclassified	Unclassified
308				1										Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
309				1			1	11						Bacteria	Proteobacteria	Gamma-proteobacteria	Xanthomonadales	Xanthomonadaceae	Rhodanobacter	Rhodanobacter_ lindaniclasticus
310				1										Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rubellimicrobium	Unclassified
311				1		2	6						11	Bacteria	Acidobacteria	Chloracidobacteria	Unclassified	Unclassified	Unclassified	Unclassified
312				2										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Pseudonocardiaceae	Actinomyceto-spora	Unclassified
313				1		3								Bacteria	Proteobacteria	Alphaproteobacteria	Unclassified	Unclassified	Unclassified	Unclassified
314				1				9						Bacteria	Proteobacteria	Gamma-proteobacteria	Unclassified	Unclassified	Unclassified	Unclassified
315				3						15	7	5		Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	Bosea	Unclassified
316				1										Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Unclassified	Unclassified
317				1										Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Ramlibacter	Unclassified
318				1										Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Unclassified	Unclassified
319				1										Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Erythrobacteraceae	Unclassified	Unclassified
320				2		1		1						Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
321				3	1	2					1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophila-ceae	Geodermatoph-ilus	Blastococcus_ saxobsidens
322				1		6					2			Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	Bacillus_ anthracis
323				1						1				Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Spirosoma	Unclassified
324				1										Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira	Unclassified
325				1		4								Bacteria	Firmicutes(80)	Clostridia(80)	Clostridiales(80)	Lachnospiraceae(80)	Unclassified	Unclassified
326				1										Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
327				1										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Dietziaceae	Dietzia	Dietzia_maris
328				2										Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
329				1										Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Thioclava	Unclassified
330				3			1	3						Bacteria	Proteobacteria	Gamma-proteobacteria	Unclassified	Unclassified	Unclassified	Unclassified
331				2			1		1		1			Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rubellimicrobium	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
332				4						1	7			Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
333				2		43	3			438	147	42	6	Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Acinetobacter_johnsonii
334				2		8								Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	RikenellaceaeII	Unclassified	Unclassified
335				1										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Bogoriellaceae	Georgenia	Unclassified
336				1										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Unclassified	Unclassified
337				1										Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Lactococcus	Lactococcus_lactis
338				2	3	3	4	5						Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Phyllobacteriaceae	Mesorhizobium	Unclassified
339				1										Bacteria	Acidobacteria	iii1-8	DS-18	Unclassified	Unclassified	Unclassified
340				1		4								Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Flavobacterium	Unclassified
341				2		2				1				Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Kocuria	Kocuria_palustris
342				1										Bacteria	Tenericutes	Erysipelotrichi	Erysipelotrichales	Erysipelotrichaceae	Coprobacillus	Unclassified
343				2		5								Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Flavobacterium	Unclassified
344				1										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium	Corynebacterium_auriscanis
345				2	11	15		1	1	2	9			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophila-ceae	Blastococcus	Blastococcus_aggregatus
346				1										Bacteria	Proteobacteria	Alphaproteobacteria	Unclassified	Unclassified	Unclassified	Unclassified
347				1										unknown(200)	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
348				1										Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
349				1										Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Unclassified
350				1										Bacteria	Acidobacteria	Acidobacteria	Acidobacteriales	Acidobacteriaceae	Unclassified	Unclassified
351				2						2	1		1	Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Flavisolibacter	Unclassified
352				1										Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
353				1		2			1	1	6			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Rathayibacter	Unclassified
354				1							5			Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
355				1						1				Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Frigoribacterium	Unclassified
356				2										Bacteria	Firmicutes	Bacilli	Bacillales	Planococcaceae	Planomicrobium	Planomicrobium_koreense
357				1										Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Unclassified	Unclassified
358				1										Bacteria	Gemmatimona-detes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadacea e	Unclassified	Unclassified
359				1		4								Bacteria	Proteobacteria	Gamma-proteobacteria	Enterobacteriales	Enterobacteriaceae	Klebsiella	Klebsiella_oxytoca
360				1										Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Unclassified	Unclassified	Unclassified
361				1										Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Sphingobacteriaceae	Pedobacter	Unclassified
362				1						1			17	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardiaceae	Rhodococcus	Rhodococcus_fascians
363				1										Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Unclassified	Unclassified
364				2										Bacteria	Gemmatimona-detes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadacea e	Unclassified	Unclassified
365				2										Bacteria	Actinobacteria	Actinobacteria	Acidimicrobiales	Unclassified	Unclassified	Unclassified
366				1		4							3	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
367				1			3							Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Unclassified	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
368				2										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Kineosporiaceae	Kineococcus	Unclassified
369				1										Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
370				2										Bacteria	Firmicutes	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
371				1		3								Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Adlercreutzia	Unclassified
372				4	21	24				54	20			Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
373				1										Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Adhaeribacter	Unclassified
374				1		1								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Propionibacteriaceae	Microlunatus	Unclassified
375				2										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
376				2										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nakamurellaceae	Unclassified	Unclassified
377				1		5								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium	Unclassified
378				2		2					8			Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Ramlibacter	Unclassified
379				1										Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	Bacillus_clausii
380				1										Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Unclassified	Unclassified
381				2		3				29	3			Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingopyxis	Unclassified
382				1										Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Erythrobacteraceae	Unclassified	Unclassified
383				1			2	2						Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Sediminibacteri-um	Unclassified
384				2		16								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Brevibacteriaceae	Brevibacterium	Brevibacterium_ sanguinis
385				1										Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Unclassified	Unclassified
386				1										Bacteria	Gemmatimona-detes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadacea e	Gemmatimonas	Unclassified
387				1		3								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Arthrobacter	Unclassified
388				1	2						2			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Nocardioides	Unclassified
389				1										Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
390				2									2	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Friedmanniella	Unclassified
391				1										Bacteria	Proteobacteria	Gamma-proteobacteria	Xanthomonadales	Xanthomonadaceae	Unclassified	Unclassified
392				1		1							3	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Pseudonocardiaceae (80)	Pseudonocardia	Unclassified
393				1		4					1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Arthrobacter	Unclassified
394				1										Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Unclassified	Unclassified
395				1		31								Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium	Unclassified
396				2										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
397				1										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Pseudonocardiaceae	Pseudonocardia	Unclassified
398				2		7								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Friedmanniella	Unclassified
399				1										Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Unclassified	Unclassified
400				1										Bacteria	Acidobacteria	Solibacteres	Solibacterales	Solibacteraceae	Candidatus_ Solibacter	Unclassified
401				1										Bacteria	Proteobacteria	Gamma-proteobacteria	Xanthomonadales	Xanthomonadaceae	Unclassified	Unclassified
402				1										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Microbacterium	Unclassified
403				1										Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Unclassified	Unclassified
404				2		6								Bacteria	Proteobacteria	Alphaproteobacteria	Unclassified	Unclassified	Unclassified	Unclassified
405				2		1								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
406				1		2				2	4			Bacteria	Proteobacteria	Gamma-proteobacteria	Enterobacteriales	Enterobacteriaceae	Pantoea	Pantoea_anana-tis
407				1	1						8			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium	Unclassified
408				1										Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
409				2			39	17						Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Unclassified	Unclassified
410				1										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Intrasporangiaceae	Unclassified	Unclassified
411				2										Bacteria	Proteobacteria	Betaproteobacteria	Neisseriales	Neisseriaceae	Neisseria	Neisseria_elon-gata
412				1		15	3				1			Bacteria	Firmicutes	Bacilli	Lactobacillales	Carnobacteriaceae	Desemzia	Desemzia_ incerta
413				1				3						Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Methyloversatilis	Unclassified
414				1							1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium	Unclassified
415				2										Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rubellimicrobium	Unclassified
416				1							1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Microbacterium	Microbacterium_ esteraromaticum
417				1										Bacteria	Chloroflexi	Dehalococcoidetes	TK17	S085	Unclassified	Unclassified
418				1										Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Amaricoccus	Unclassified
419				1										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Arthrobacter	Unclassified
420				2										Bacteria	Armatimona-detes	Armatimonadia	Armatimonadales	Armatimonadaceae	Unclassified	Unclassified
421				2										Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Methyloversatilis	Methyloversatilis_ universalis
422				1										Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Skermanella	Unclassified
423				1		1								Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Chryseobacteri-um	Unclassified
424				2	3									Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Intrasporangiaceae	Janibacter	Unclassified
425				1		8	1							Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
426				1										Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Unclassified	Unclassified
427				1										Bacteria	Bacteroidetes	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
428				1						2	13			Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Skermanella	Unclassified
429				1										Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	Unclassified
430				1						109	25	12		Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Agrobacterium	Unclassified
431				1		1								Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Polaromonas	Unclassified
432				1										Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rubellimicrobium	Unclassified
433				2										Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Flavobacterium	Unclassified
434				1						1				Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophila-ceae	Geodermatoph-ilus	Geodermatophi-lus_obscurus
435				1										Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Skermanella	Unclassified
436				3		1			143	3	11			Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Methylobacterium _radiotolerans
437				2						52	19			Bacteria	Proteobacteria	Alphaproteobacteria	Unclassified	Unclassified	Unclassified	Unclassified
438				1		4								Bacteria	Unclassified(80)	Unclassified(80)	Unclassified(80)	Unclassified(80)	Unclassified	Unclassified
439				1				1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Intrasporangiaceae	Arsenicicoccus	Unclassified
440				1										Bacteria	Acidobacteria	Chloracidobacteria	Unclassified	Unclassified	Unclassified	Unclassified
441				1										Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Unclassified	Unclassified
442				2		8								Bacteria	Firmicutes(61)	Clostridia(61)	Clostridiales(61)	Ruminococcaceae (61)	Unclassified	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
443				1										Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Unclassified	Unclassified
444				1		9								Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
445				1										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Nocardioides	Unclassified
446				1										Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Unclassified	Unclassified
447				1	1	7					13		3	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
448				1										Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
449				1										Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
450				1										Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Unclassified	Unclassified
451				1										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Intrasporangiaceae	Knoellia	Unclassified
452				1										Bacteria	Chloroflexi	SOGA31	Unclassified	Unclassified	Unclassified	Unclassified
453				1		1								Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	Burkholderia	Unclassified
454				1		23				1	15			Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
455				1										Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Unclassified	Unclassified
456				1										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Leucobacter	Unclassified
457				1										Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	Unclassified	Unclassified	Unclassified
458				2										Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Geobacillus	Unclassified
459				2	13	1					2			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Marmoricola	Unclassified
460				1										Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Unclassified	Unclassified
461				1										Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Roseomonas	Unclassified
462				1										Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Unclassified	Unclassified
463				1										Bacteria	Actinobacteria	Actinobacteria	Solirubrobacterales	Solirubrobactera-ceae	Unclassified	Unclassified
464				1										Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rubellimicrobium	Unclassified
465				1										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Intrasporangiaceae	Janibacter	Janibacter_ limosus
466				1						1				Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Kaistobacter	Unclassified
467				1										Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
468				1										Bacteria	Armatimona-detes	CH21	Unclassified	Unclassified	Unclassified	Unclassified
469				1				2						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium	Corynebacterium _amycolatum
470				1					1					Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rubellimicrobium	Unclassified
471				1										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
472				1		6				1	1			Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Comamonas	Unclassified
473				1										Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	Unclassified
474				1										Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Unclassified	Unclassified
475				1		2								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
476				1										Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
477				1										Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
478				1			5	10						Bacteria	Proteobacteria	Gamma-proteobacteria	Xanthomonadales	Xanthomonadaceae	Stenotrophomo-nas	Unclassified
479				1										Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Erythrobacteraceae	Unclassified	Unclassified
480				1										Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
481				3										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Gordoniaceae	Gordonia	Gordonia_terrae
482				1										Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
483				1										Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Methylobacterium _brachiatum
484				1										Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
485				1										Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
486				2										Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
487				1		1				1	8			Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Erythrobacteraceae	Unclassified	Unclassified
488				1										Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
489				1										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophila-ceae	Modestobacter	Unclassified
490				1										Bacteria	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophobactera-ceae	Unclassified	Unclassified
491				1										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Unclassified	Unclassified
492				1										Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
493				1										Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_Family _XI._Incertae_Sedis	Peptoniphilus	Unclassified
494				1		2								Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Sphingobacteriaceae	Pedobacter	Unclassified
495				1										Bacteria	Proteobacteria	Gamma-proteobacteria	Pasteurellales	Pasteurellaceae	Aggregatibacter	Aggregatibacter_ segnis
496				1										Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
497				1										Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
498				1										Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Unclassified	Unclassified	Unclassified
499				1										Bacteria	Proteobacteria	Deltaproteobacteria	MIZ46	Unclassified	Unclassified	Unclassified
500				1		1								Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingobium	Sphingomonas_ sp._SKA58
501				1										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Unclassified	Unclassified
502				1		1								Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
503				1		15								Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Flavobacterium	Unclassified
504				1										Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	Ancylobacter	Unclassified
505				1		2				1	1			Bacteria	Proteobacteria	Gamma-proteobacteria	Xanthomonadales	Xanthomonadaceae	Lysobacter	Unclassified
506				1										Bacteria	Bacteroidetes	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
507				1						1				Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Unclassified	Unclassified
508				1										Bacteria	Chloroflexi	Dehalococcoidetes	TK17	S085	Unclassified	Unclassified
509				1										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Propionibacteriaceae	Tessaracoccus	Unclassified
510				1	1	5								Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Acinetobacter_ gyllenbergii
511				1		7		3						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Rothia	Rothia_mucilagi-nosa
512				1		1	1			2				Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Unclassified
513				1										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Brevibacteriaceae	Brevibacterium	Brevibacterium_ aureum
514				2		5				3				Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Roseomonas	Roseomonas_ cervicalis
515				1										Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Unclassified	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
516				1										Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Unclassified	Unclassified
517				1										Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
518				1										Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
519				1										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
520				1										Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Caulobacter	Caulobacter_ vibrioides
521				1		6	1			3	3			Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Sphingomonas_ asaccharolytica
522				1							8			Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rubellimicrobium	Unclassified
523				1		5								Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium	Unclassified
524				1										Bacteria	Actinobacteria	Actinobacteria	Acidimicrobiales	CL500-29	Unclassified	Unclassified
525				1										Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Unclassified
526				2										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Aeromicrobium	Aeromicrobium_ fastidiosum
527				1		4		1						Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Shuttleworthia	Unclassified
528				1										Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
529				1										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Marmoricola	Unclassified
530				1										Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
531				1										Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Unclassified	Unclassified
532				1		2					3			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardiaceae	Unclassified	Unclassified
533				1		9					1			Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Segetibacter	Unclassified
534				1										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Arthrobacter	Arthrobacter_ crystallopoietes
535				1										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Unclassified	Unclassified
536				1										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Arthrobacter	Unclassified
537				1										Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Unclassified	Unclassified
538				1										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Dermabacteraceae	Brachybacterium	Brachybacterium _conglomeratum
539				1		5								Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Flavobacterium	Unclassified
540				1										Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Caulobacter	Unclassified
541				1		1					1			Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Acinetobacter_ schindleri
542				1									3	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Dermabacteraceae	Dermabacter	Unclassified
543				1										Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Phyllobacteriaceae	Unclassified	Unclassified
544				1		37				5				Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Brucellaceae	Pseudochrobac-trum	Pseudochrobac-trum_saccharoly-ticum
545				1	2	2					1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Arthrobacter	Unclassified
546				1		1								Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Roseomonas	Unclassified
547				1										Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rubellimicrobium	Unclassified
548				1							3			Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Adhaeribacter	Unclassified
549				1										Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
550				1										Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
551				1										Bacteria	TM7	TM7-3	EW055	Unclassified	Unclassified	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
552				1										Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_Family _XI._Incertae_Sedis	Parvimonas	Parvimonas_ micra
553				1										Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophila-ceae	Geodermatoph-ilus	Unclassified
554				1			1			461	20	24		Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Sphingobacteriaceae	Pedobacter	Unclassified
555				1										Bacteria	TM7	TM7-3	EW055	Unclassified	Unclassified	Unclassified
556				1										Bacteria	Chloroflexi	Thermomicrobia	Sphaerobacterales	Sphaerobacterineae	HN1-15	Unclassified
557				1		1								Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Unclassified	Unclassified
558				1										unknown (200)	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
559				1										Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
560					20									Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Segetibacter	Unclassified
561					13	9				1	2		14	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Unclassified	Unclassified
562					15									Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Unclassified	Unclassified
563					13	3								Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
564					10									Bacteria	Firmicutes	Bacilli	Lactobacillales	Unclassified	Unclassified	Unclassified
565					10						2			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardiaceae	Rhodococcus	Rhodococcus_ fascians
566					14									Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Acinetobacter_ rhizosphaerae
567					8	1								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Nocardioides	Nocardioides_ oleivorans
568					11									Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Unclassified	Unclassified
569					8	10		4			2			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Unclassified	Unclassified
570					12				1					Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nakamurellaceae	Unclassified	Unclassified
571					9									Bacteria	Actinobacteria	Actinobacteria	Acidimicrobiales(89)	Unclassified(78)	Unclassified	Unclassified
572					13	18					1		1	Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
573					5				1					Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Erythrobacteraceae	Unclassified	Unclassified
574					8									Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
575					7									Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
576					5									Bacteria	Proteobacteria	Gamma-proteobacteria	Xanthomonadales	Xanthomonadaceae	Lysobacter	Unclassified
577					7									Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales (72)	Unclassified(72)	Unclassified	Unclassified
578					5	4					3		1	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
579					5									Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	Unclassified
580					5									Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Dermabacteraceae	Brachybacterium	Unclassified
581					5									Bacteria	Proteobacteria	Gamma-proteobacteria	Enterobacteriales	Enterobacteriaceae	Unclassified	Unclassified
582					3	2								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Sanguibacteraceae	Sanguibacter	Unclassified
583					3									Bacteria	Proteobacteria	Gamma-proteobacteria	Xanthomonadales	Xanthomonadaceae	Lysobacter	Unclassified
584					5									Bacteria	Chloroflexi	Thermomicrobia	Sphaerobacterales	Sphaerobacterineae	HN1-15	Unclassified
585					5									Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Friedmanniella	Unclassified
586					4	10								Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Segetibacter	Unclassified
587					3	2					1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophila-ceae	Unclassified	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
588					2						1			Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Unclassified
589					5									Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Sejongia	Unclassified
590					2									unknown (150)	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
591					2									Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Pseudonocardiaceae	Pseudonocardia	Unclassified
592					2									Bacteria	Planctomycetes	Planctomycea	Gemmatales	Gemmataceae	Unclassified	Unclassified
593					2									Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Propionibacteriaceae	Microlunatus	Microlunatus_ phosphovorus
594					5									Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
595					4	1								Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Sphingobacteriaceae	Pedobacter	Pedobacter_ cryoconitis
596					4									Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
597					2									Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
598					7									Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Devosia	Unclassified
599					1									Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Arthrobacter	Unclassified
600					2									Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Microbacterium	Unclassified
601					1									Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
602					1									unknown (200)	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
603					5									Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Unclassified	Unclassified
604					4									Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
605					1									Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Unclassified	Unclassified	Unclassified
606					1						4			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
607					1	1					2			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Unclassified	Unclassified
608					2									Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Unclassified	Unclassified
609					2		5	2		1	1		1	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Arthrobacter	Unclassified
610					2									Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Pseudonocardiaceae	Pseudonocardia	Pseudonocardia_ yunnanensis
611					1									Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Williamsiaceae	Williamsia	Williamsia_ muralis
612					1						2		5	Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Spirosoma	Unclassified
613					1									Bacteria	Actinobacteria	Actinobacteria	MC47	Unclassified	Unclassified	Unclassified
614					1									Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Unclassified	Unclassified
615					1		10				1			Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Roseococcus	Unclassified
616					1									Bacteria	Planctomycetes	Planctomycea	Gemmatales	Isosphaeraceae	Unclassified	Unclassified
617					1									Bacteria	Proteobacteria	Gamma-proteobacteria	Enterobacteriales	Enterobacteriaceae	Buchnera	Unclassified
618					1									Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	Burkholderia	Unclassified
619					3						1			Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Unclassified	Unclassified
620					1									Bacteria	Acidobacteria	Acidobacteria	Acidobacteriales	Acidobacteriaceae	Unclassified	Unclassified
621					2		37	15		13				Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Phenylobacteri-um	Unclassified
622					1									Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
623					1									Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Nesterenkonia	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
624					1									Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
625					4									Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
626					1						2			Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
627					1									unknown (200)	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
628					3									Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Devosia	Unclassified
629					2									Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
630					1		1							Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales	Holosporaceae	Unclassified	Unclassified
631					1	5					4			Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
632					1	2					4		2	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Arthrobacter	Unclassified
633					1									Bacteria	Proteobacteria	Gamma-proteobacteria	Enterobacteriales	Enterobacteriaceae	Erwinia	Erwinia_rhapon-tici
634					1									Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
635					4									Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
636					1	2					4			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
637					1									Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Skermanella	Unclassified
638					1	2								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Tsukamurellaceae	Tsukamurella	Unclassified
639					1									Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Unclassified
640					1									Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
641					1									Bacteria	Actinobacteria	Actinobacteria	Acidimicrobiales	Acidimicrobiaceae	Unclassified	Unclassified
642					1									Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Unclassified	Unclassified
643					1	1				1	1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified(75)	Unclassified	Unclassified
644					1	2								Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
645						24								Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Atopobium	Atopobium_ vaginae
646						36								Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylocystaceae	Methylopila	Unclassified
647						21								Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
648						20								Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Moraxella	Moraxella_ nonliquefaciens
649						17								Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Flavisolibacter	Unclassified
650						14			1					Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Marmoricola	Unclassified
651						12								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
652						14								Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
653						12								Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Unclassified	Unclassified
654						14								Bacteria	Actinobacteria	Actinobacteria	Solirubrobacterales	Solirubrobactera-ceae	Unclassified	Unclassified
655						15		1						Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Atopobium	Atopobium_ vaginae
656						20								Bacteria	Actinobacteria	Actinobacteria	Acidimicrobiales	Unclassified	Unclassified	Unclassified
657						18					4			Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
658						18								Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
659						13				1				Bacteria	WPS-2	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
660						11								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
661						29					3			Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Shuttleworthia	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
662						9								Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Unclassified	Unclassified
663						10								Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Rhodoplanes	Unclassified
664						16				5				Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Acinetobacter_johnsonii
665						11								Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
666						13								Bacteria	Firmicutes	Bacilli	Bacillales	Planococcaceae	Planomicrobium	Unclassified
667						10	13	17	7	31	40		3	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
668						14								Bacteria	Acidobacteria	Acidobacteria	Acidobacteriales	Acidobacteriaceae	Edaphobacter	Unclassified
669						10								Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Methylobacterium_adhaesivum
670						11								Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Segetibacter	Unclassified
671						10				1	5			Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
672						8								Bacteria	Armatimonadetes	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
673						7								Bacteria	Proteobacteria	Betaproteobacteria	Neisseriales	Neisseriaceae	Unclassified	Unclassified
674						8				1	1			Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Erythrobacteraceae	Lutibacterium	Unclassified
675						8	4							Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Arthrobacter	Unclassified
676						8								Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia	Ruminococcus_obeum
677						6								Bacteria	Actinobacteria	Actinobacteria	Solirubrobacterales	Conexibacteraceae	Unclassified	Unclassified
678						8								Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Rhodoplanes	Unclassified
679						9		2	136					Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Erythrobacteraceae	Porphyrobacter	Porphyrobacter_donghaensis
680						8			1					Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Unclassified	Unclassified
681						8								Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	Rhodopseudo-monas	Unclassified
682						6								Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella	Unclassified
683						13								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
684						5								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Nocardioides	Nocardioides_oleivorans
685						5								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Friedmanniella	Unclassified
686						10								Bacteria	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonada-ceae	Unclassified	Unclassified
687						6								Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Amaricoccus	Unclassified
688						6								Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
689						5								Bacteria	TM7	TM7-1	Unclassified	Unclassified	Unclassified	Unclassified
690						4								Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Flavisolibacter	Unclassified
691						5								Bacteria	Armatimonadetes	CH21	Unclassified	Unclassified	Unclassified	Unclassified
692						6								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
693						4	11							Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	Ralstonia	Ralstonia_mannitolilytica
694						6					19			Bacteria	Firmicutes	Bacilli	Bacillales	Planococcaceae	Planomicrobium	Unclassified
695						10			1	2				Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Skermanella	Unclassified
696						4								Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Unclassified	Unclassified
697						9								Bacteria	Actinobacteria	Actinobacteria	Solirubrobacterales	Conexibacteraceae	Unclassified	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
698						4					28		14	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Micrococcus	Micrococcus_ luteus
699						7								Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	Ruminococcus_ flavefaciens
700						8								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Pseudonocardiaceae	Actinomyceto-spora	Unclassified
701						4								Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Unclassified	Unclassified
702						6					16			Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
703						10								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Aeromicrobium	Unclassified
704						4								Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium	Unclassified
705						7								Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Unclassified	Unclassified
706						4				1	1			Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae	Unclassified	Unclassified
707						5								Bacteria	Proteobacteria	Gamma-proteobacteria	Legionellales	Legionellaceae	Unclassified	Unclassified
708						4								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Nocardioides	Nocardioides_ oleivorans
709						4								Bacteria	Actinobacteria	Actinobacteria	Acidimicrobiales	Microthrixaceae	Unclassified	Unclassified
710						6								Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella	Unclassified
711						6								Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Unclassified	Unclassified
712						4								Bacteria	Proteobacteria	Betaproteobacteria	Unclassified	Unclassified	Unclassified	Unclassified
713						3								Bacteria	Chloroflexi	Thermomicrobia	Sphaerobacterales	Sphaerobacterineae	HN1-15	Unclassified
714						12								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
715						4								Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Unclassified	Unclassified
716						5								Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Janthinobacteri-um	Janthinobacteri-um_lividum
717						4								Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	Unclassified
718						4								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Cellulomonadaceae	Demequina	Unclassified
719						3								Bacteria	Proteobacteria	Gamma-proteobacteria	Xanthomonadales	Xanthomonadaceae	Rhodanobacter	Rhodanobacter_ lindaniclasticus
720						4				26				Bacteria	Proteobacteria(74)	Unclassified(74)	Unclassified(74)	Unclassified(74)	Unclassified	Unclassified
721						5								Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
722						3				2				Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Unclassified(61)	Unclassified	Unclassified
723						3								Bacteria	Proteobacteria	Gamma-proteobacteria	Oceanospirillales	Halomonadaceae	Halomonas	Unclassified
724						9	1			1	1			Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Devosia	Unclassified
725						3								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Pseudonocardiaceae	Pseudonocardia	Unclassified
726						3								Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
727						4								Bacteria	Proteobacteria	Betaproteobacteria	Neisseriales	Neisseriaceae	Neisseria	Neisseria_ weaveri
728						3		8						Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
729						6			2					Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nakamurellaceae	Unclassified	Unclassified
730						5								Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Atopobium	Atopobium_ vaginae
731						5								Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
732						6								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
733						4								Bacteria	Planctomycetes	Planctomycea	Planctomycetales	Planctomycetaceae	Unclassified	Unclassified
734						5				88	25			Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingobium	Unclassified
735						6								Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Unclassified	Unclassified
736						3								Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Unclassified	Unclassified
737						4					8			Bacteria	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Staphylococcus	Staphylococcus_ aureus
738						5	14	37		53	16	33		Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Acidovorax	Unclassified
739						3								Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Sphingomonas_ wittichii
740						3								Bacteria	Planctomycetes	Planctomycea	Gemmatales	Isosphaeraceae	Unclassified	Unclassified
741						4								Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingopyxis	Sphingopyxis_ panaciterrae
742						3								Bacteria	Acidobacteria	Chloracidobacteria	Unclassified	Unclassified	Unclassified	Unclassified
743						3								Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Thioclava	Unclassified
744						3								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Intrasporangiaceae	Phycicoccus	Unclassified
745						2								Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Methylibiaceae	Methylibium	Unclassified
746						2	3	5						Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales	Holosporaceae	Unclassified	Unclassified
747						5			2	3	9			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Friedmanniella	Unclassified
748						2								Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
749						5					1			Bacteria	Proteobacteria	Gamma-proteobacteria	Enterobacteriales	Enterobacteriaceae	Buchnera	Unclassified
750						2								Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
751						7								Bacteria	Actinobacteria	Actinobacteria	Solirubrobacterales	Conexibacteraceae	Unclassified	Unclassified
752						2								Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Shinella	Shinella_ zoogloeoides
753						3								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Pseudonocardiaceae	Thermobispora	Thermobispora_ bispora
754						5								Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
755						3								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
756						2								Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Variovorax	Variovorax_ paradoxus
757						2								Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Cytophaga	Unclassified
758						2								Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
759						2								Bacteria	Thermi	Deinococci	Deinococcales	Deinococcaceae	Deinococcus	Unclassified
760						3								Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium	Unclassified
761						3								Bacteria	Proteobacteria	Gamma-proteobacteria	Xanthomonadales	Xanthomonadaceae	Lysobacter	Unclassified
762						6								Bacteria	Armatimona-detes (84)	Unclassified(84)	Unclassified(84)	Unclassified(84)	Unclassified	Unclassified
763						4								Bacteria	Firmicutes	Bacilli	Bacillales	Planococcaceae	Planomicrobium	Unclassified
764						3								Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Alkanindiges	Unclassified
765						2								Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Flavisolibacter	Unclassified
766						2								Bacteria	Actinobacteria	Actinobacteria	Solirubrobacterales	Conexibacteraceae	Unclassified	Unclassified
767						2								Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
768						2								Bacteria	Proteobacteria	Gamma-proteobacteria	Chromatiales	Sinobacteraceae	Unclassified	Unclassified
769						3								Bacteria	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolinaceae	T78	Unclassified
770						2								Bacteria	Acidobacteria	Chloracidobacteria	Unclassified	Unclassified	Unclassified	Unclassified
771						3								Bacteria	Chloroflexi	Caldilineae	Caldilineales	Caldilineaceae	Caldilinea	Unclassified
772						3								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Unclassified	Unclassified
773						2		13	1					Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Sphingomonas_ asaccharolytica
774						3								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Streptomycetaceae	Streptomyces	Unclassified
775						3								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
776						2								Bacteria	Proteobacteria	Betaproteobacteria	Hydrogenophilales	Hydrogenophilaceae	Unclassified	Unclassified
777						2								Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
778						9				2	5			Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Unclassified	Unclassified
779						4								Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Methylibiaceae	Methylibium	Unclassified
780						3								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Microbacterium	Unclassified
781						4								Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Unclassified	Unclassified
782						2								Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Unclassified	Unclassified
783						3			3		29			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium	Unclassified
784						3				9				Bacteria	Proteobacteria	Alphaproteobacteria	Unclassified	Unclassified	Unclassified	Unclassified
785						3					2		6	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium	Faecalibacterium _prausnitzii
786						4							5	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Propionibacteriaceae	Microlunatus	Unclassified
787						3								Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Roseomonas	Unclassified
788						2								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Friedmanniella	Unclassified
789						2								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
790						4								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Dermabacteraceae	Brachybacterium	Unclassified
791						3								Bacteria	Gemmatimona-detes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonada-ceae	Unclassified	Unclassified
792						2								Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
793						3								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Microbacterium	Unclassified
794						2				1				Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae	Pigmentiphaga	Unclassified
795						6								Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Amaricoccus	Unclassified
796						2				3				Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Caldimonas	Unclassified
797						3								Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	Unclassified	Unclassified
798						3								Bacteria	Planctomycetes	Planctomycea	Planctomycetales	Planctomycetaceae	Pirellula	Unclassified
799						3								Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Unclassified	Unclassified
800						4								Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
801						5								Bacteria	Proteobacteria	Gamma-proteobacteria	Enterobacteriales	Enterobacteriaceae	Buchnera	Unclassified
802						3								Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Segetibacter	Unclassified
803						3								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
804						2								Bacteria	Armatimona-detes	Chthonomonadetes	Chthonomonadales	Chthonomonada-ceae	Unclassified	Unclassified
805						3								Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Collinsella	Collinsella_ stercoris

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
806						2								Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingobium	Unclassified
807						2								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
808						3					3			Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Unclassified	Unclassified
809						2								Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
810						3					1			Bacteria	Actinobacteria	Actinobacteria	Solirubrobacterales	Solirubrobactera-ceae	Unclassified	Unclassified
811						2								Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
812						4					2			Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Segetibacter	Unclassified
813						1								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micromonospora-ceae	Unclassified	Unclassified
814						2								Bacteria	Firmicutes	Bacilli	Bacillales	Planococcaceae	Planomicrobium	Unclassified
815						2								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Nocardioides	Unclassified
816						2								Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Unclassified	Unclassified	Unclassified
817						1								Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
818						1								Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
819						1								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
820						2								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Pseudoclavibac-ter	Pseudoclavibac-ter_helvolus
821						1								Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Unclassified
822						1								Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	Unclassified
823						2								Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rubellimicrobium	Unclassified
824						1								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Brevibacteriaceae	Brevibacterium	Brevibacterium_ sanguinis
825						2								Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Cytophaga	Unclassified
826						2								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae	Actinomyces	Actinomyces_oris
827						2				1				Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
828						4								Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Flavisolibacter	Unclassified
829						3								Bacteria	Firmicutes	Bacilli	Bacillales	Planococcaceae	Planomicrobium	Unclassified
830						2		1						Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
831						3								Bacteria	Proteobacteria (67)	Unclassified(67)	Unclassified(67)	Unclassified(67)	Unclassified	Unclassified
832						2								Bacteria	Proteobacteria	Gamma-proteobacteria	Xanthomonadales	Xanthomonadaceae	Unclassified	Unclassified
833						1								unknown (200)	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
834						3								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Pseudoclavibac-ter	Zimmermannella _bifida
835						1								Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Rhodoplanes	Unclassified
836						1	1			1				Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Psychrobacter	Unclassified
837						2								Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Unclassified	Unclassified
838						1								Bacteria	Proteobacteria	Alphaproteobacteria	Unclassified	Unclassified	Unclassified	Unclassified
839						3								Bacteria	Proteobacteria	Gamma-proteobacteria	Legionellales	Legionellaceae	Legionella	Unclassified
840						1								Bacteria	Proteobacteria	Deltaproteobacteria	CTD005-82B-02	Unclassified	Unclassified	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
841						2								Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Unclassified	Unclassified
842						1								Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Unclassified	Unclassified
843						1								Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Niabella	Unclassified
844						1								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Intrasporangiaceae	Knoellia	Knoellia_ subterranea
845						2								Bacteria	Thermi	Deinococci	Deinococcales	Deinococcaceae	Deinococcus	Unclassified
846						1								Bacteria	Proteobacteria	Betaproteobacteria	Unclassified	Unclassified	Unclassified	Unclassified
847						1								Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	Unclassified
848						1								Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
849						2								Bacteria	Proteobacteria	Gamma-proteobacteria	Xanthomonadales	Xanthomonadaceae	Unclassified	Unclassified
850						2								Bacteria	Actinobacteria	Actinobacteria	MC47	Unclassified	Unclassified	Unclassified
851						2								Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
852						1		1		1				Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
853						2								Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Unclassified	Unclassified
854						1								Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Atopobium	Atopobium_ vaginae
855						1								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophila-ceae	Geodermatoph-ilus	Unclassified
856						3				1				Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Propionibacteriaceae	Microlunatus	Unclassified
857						1								Bacteria	Verrucomicrobia	Opitutae	Opitutales	Opitutaceae	Unclassified	Unclassified
858						1								Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Unclassified	Unclassified
859						2	7							Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Nocardioides	Unclassified
860						2								Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Acinetobacter_ guillouiae
861						3								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Marmoricola	Unclassified
862						1								Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella	Prevotella_copri
863						1								Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Unclassified
864						1								Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Agrobacterium	Unclassified
865						1								Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Unclassified
866						2								Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Caulobacter	Caulobacter_ henricii
867						1								Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
868						1								Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Unclassified	Unclassified
869						1								Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Unclassified
870						1								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
871						1								Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Unclassified
872						1								Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
873						1		1						Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	Burkholderia	Unclassified
874						1								Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
875						1								Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Unclassified	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
876						1					7			Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Flavobacterium	Flavobacterium_ succinicans
877						1								Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
878						1								Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
879						1				1				Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Kocuria	Kocuria_palustris
880						3								Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	RikenellaceaeII	Unclassified	Unclassified
881						5								Bacteria	Proteobacteria	Gamma-proteobacteria	Chromatiales	Sinobacteraceae	Unclassified	Unclassified
882						3					13			Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Unclassified	Unclassified
883						1								Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Acinetobacter_ lwoffii
884						1								Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Unclassified	Unclassified
885						1								Bacteria	Actinobacteria	Actinobacteria	Acidimicrobiales	Acidimicrobiaceae	Unclassified	Unclassified
886						2								Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
887						1								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Bogoriellaceae	Georgenia	Unclassified
888						1								Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Caulobacter	Unclassified
889						1								Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylocystaceae	Methylopila	Unclassified
890						1								Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
891						1								Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Unclassified	Unclassified
892						2								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Nocardioides	Nocardioides_ oleivorans
893						2								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Unclassified	Unclassified
894						2		1						Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
895						3								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Unclassified	Unclassified
896						1								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Arthrobacter	Arthrobacter_ agilis
897						2								Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Unclassified	Unclassified
898						1								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Agromyces	Unclassified
899						1								Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Unclassified	Unclassified
900						1								Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Acinetobacter_ schindleri
901						1								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Microbacterium	Microbacterium_ flavescens
902						2								Bacteria	Actinobacteria	Actinobacteria	Solirubrobacterales	Conexibacteraceae	Unclassified	Unclassified
903						1								Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Agrobacterium	Unclassified
904						2		1						Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
905						1			2	3	4			Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Roseomonas	Unclassified
906						1				15				Bacteria	Proteobacteria	Gamma-proteobacteria	Enterobacteriales	Enterobacteriaceae	Unclassified	Unclassified
907						3								Bacteria	Actinobacteria	Actinobacteria	Solirubrobacterales	Conexibacteraceae	Unclassified	Unclassified
908						1								Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rubellimicrobium	Unclassified
909						2								Bacteria	Actinobacteria	Actinobacteria	Solirubrobacterales	Patulibacteraceae	Unclassified	Unclassified
910						1								Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Acinetobacter_ lwoffii
911						1		1						Bacteria	Proteobacteria	Gamma-proteobacteria	Oceanospirillales	Alteromonadaceae	Cellvibrio	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
912						3								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Bogoriellaceae	Georgenia	Unclassified
913						2								Bacteria	Proteobacteria	Gamma-proteobacteria	Chromatiales	Sinobacteraceae	Unclassified	Unclassified
914						1								Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Sphingomonas_ asaccharolytica
915						1								Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Unclassified	Unclassified
916						2	3							Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
917						1								Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	Bacillus_funiculus
918						1								Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
919						1								Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
920						2								Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
921						1								Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Novosphingobi-um	Novosphingobi-um_resinovorum
922						1								Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales	Rickettsiaceae	Rickettsia	Unclassified
923						1								Bacteria	Proteobacteria	Betaproteobacteria	Unclassified	Unclassified	Unclassified	Unclassified
924						3								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Nocardioides	Unclassified
925						1								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Microbacterium	Unclassified
926						1								Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Unclassified	Unclassified
927						1								Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Unclassified	Unclassified
928						1				1				Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Unclassified	Unclassified
929						1		10						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Beutenbergiaceae	Unclassified	Unclassified
930						1								Bacteria	Proteobacteria	Deltaproteobacteria	CTD005-82B-02	Unclassified	Unclassified	Unclassified
931						1								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Beutenbergiaceae	Unclassified	Unclassified
932						1								Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Skermanella	Unclassified
933						2				1				Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Phenylobacteri-um	Unclassified
934						1					1			Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	Bacillus_ foraminis
935						1								Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Phenylobacteri-um	Unclassified
936						1								Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Collinsella	Collinsella_ stercoris
937						3								Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
938						1								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophila-ceae	Geodermatoph-ilus	Unclassified
939						1								Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
940						3								Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified(67)	Unclassified	Unclassified
941						2								Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Agrobacterium	Unclassified
942						2								Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium	Faecalibacterium _prausnitzii
943						1								Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingobium	Sphingobium_ yanoikuyae
944						1								Bacteria	Actinobacteria	Actinobacteria	Unclassified	Unclassified	Unclassified	Unclassified
945						1								Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Unclassified	Unclassified
946						1	3							Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_Family _XI._Incertae_Sedis	Peptoniphilus	Peptoniphilus_ asaccharolyticus
947						1								Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
948						2								Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Unclassified	Unclassified
949						1								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Clavibacter	Clavibacter_ michiganensis
950						1								Bacteria	Proteobacteria	Gamma-proteobacteria	Xanthomonadales	Xanthomonadaceae	Unclassified	Unclassified
951						1								Bacteria	Proteobacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
952						1								Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Skermanella	Unclassified
953						1								Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingobium	Unclassified
954						1								Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Sphingomonas_ asaccharolytica
955						2								Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	Bacillus_badius
956						1								unknown (200)	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
957						1								Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Unclassified	Unclassified
958						2								Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Unclassified	Unclassified
959						1		1						Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Adlercreutzia	Unclassified
960						1								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
961						1								Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	Balneimonas	Unclassified
962						2	3				1			Bacteria	Proteobacteria	Gamma-proteobacteria	Enterobacteriales	Enterobacteriaceae	Unclassified	Unclassified
963						1								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
964						1								Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Flavobacterium	Unclassified
965						2								Bacteria	Thermi	Deinococci	Deinococcales	Deinococcaceae	Deinococcus	Unclassified
966						1								Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Amaricoccus	Unclassified
967						1								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Pseudoclavibac-ter	Zimmermannella _bifida
968						1								Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Erythrobacteraceae	Unclassified	Unclassified
969						1								Bacteria	WPS-2	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
970						1				1				Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Agrobacterium	Rhizobium_sp._ IRBG_74
971						1								Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
972						1								Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Roseomonas	Unclassified
973						1								Bacteria	Proteobacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
974						1								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophila-ceae	Geodermatoph-ilus	Unclassified
975						1								Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Unclassified	Unclassified
976						1								Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Unclassified	Unclassified
977						1								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Pseudonocardiaceae	Pseudonocardia	Unclassified
978						1								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Brevibacteriaceae	Brevibacterium	Brevibacterium_ paucivorans
979						1								Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Unclassified	Unclassified
980						1								Bacteria	Proteobacteria	Gamma-proteobacteria	Xanthomonadales	Xanthomonadaceae	Stenotrophomo-nas	Unclassified
981						1								Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
982						1							2	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium	Unclassified
983						1								Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
984						2								Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Phenylobacteri-um	Unclassified
985						1								Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Unclassified	Unclassified
986						1								Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
987						1								Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
988						1					5			Bacteria	Proteobacteria	Gamma-proteobacteria	Xanthomonadales	Xanthomonadaceae	Xanthomonas	Xanthomonas_ oryzae
989						1								Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
990						1								Bacteria	Cyanobacteria	S15B-MN24	Unclassified	Unclassified	Unclassified	Unclassified
991						1								Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rhodobacter	Unclassified
992						1								Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Unclassified	Unclassified	Unclassified
993						1								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Pseudonocardiaceae	Actinomyceto-spora	Unclassified
994						1								Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Unclassified	Unclassified
995						1								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
996						1								Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Unclassified	Unclassified
997						1								Bacteria	Chloroflexi	SOGA31	Unclassified	Unclassified	Unclassified	Unclassified
998						4								Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Phenylobacteri-um	Unclassified
999						1								Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Unclassified
1000						1								Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1001						1								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Arthrobacter	Arthrobacter_psy-chrolactophilus
1002						1								Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Skermanella	Unclassified
1003						1								Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	Burkholderia	Burkholderia_ heleia
1004						1								Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
1005						1								Bacteria	Proteobacteria	Alphaproteobacteria	Unclassified	Unclassified	Unclassified	Unclassified
1006						1								Bacteria	Proteobacteria	Deltaproteobacteria	CTD005-82B-02	Unclassified	Unclassified	Unclassified
1007						1								Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rubellimicrobium	Unclassified
1008						1								Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingobium	Unclassified
1009						1								Bacteria	Armatimona-detes	Armatimonadia	Armatimonadales	Unclassified	Unclassified	Unclassified
1010						1								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Rothia	Unclassified
1011						1								Bacteria	Actinobacteria	Actinobacteria	Coriobacteriales	Coriobacteriaceae	Collinsella	Unclassified
1012						1					2			Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	Bacteroides_ stercoris
1013						1								Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1014						1								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1015						1								Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1016						1								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Intrasporangiaceae	Terracoccus	Unclassified
1017						1								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1018						1								Bacteria	Actinobacteria	Actinobacteria	MC47	Unclassified	Unclassified	Unclassified
1019						1								Bacteria	Planctomycetes	Planctomycea	Planctomycetales	Planctomycetaceae	Unclassified	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
1020						1								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Cellulomonadaceae	Actinotalea	Actinotalea_ fermentans
1021						1								Bacteria	TM7	TM7-3	EW055	Unclassified	Unclassified	Unclassified
1022						1								Bacteria	Acidobacteria	Solibacteres	Solibacterales	Solibacteraceae	Candidatus_ Solibacter	Unclassified
1023						1								Bacteria	Acidobacteria	Acidobacteria	Acidobacteriales	Acidobacteriaceae	Unclassified	Unclassified
1024						1				19	9			Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
1025						1								unknown (200)	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1026						1								Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Acinetobacter_ lwoffii
1027						1								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Leucobacter	Leucobacter_ komagatae
1028							41							Bacteria	Actinobacteria	Actinobacteria	MC47	Unclassified	Unclassified	Unclassified
1029							15							Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Propionibacteriaceae	Microlunatus	Unclassified
1030							15							Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium	Unclassified
1031							18							Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Moraxella	Unclassified
1032							6							unknown (117)	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1033							14							Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Rhodoplanes	Unclassified
1034							8							Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Unclassified	Unclassified
1035							12							Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1036							10							Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micromonospora-ceae	Actinoplanes	Unclassified
1037							7							Bacteria	Armatimona-detes	CH21	Unclassified	Unclassified	Unclassified	Unclassified
1038							5							Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
1039							4							Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Streptomycetaceae	Streptomyces	Unclassified
1040							6							Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1041							6							Bacteria	Chloroflexi	Thermomicrobia	Sphaerobacterales	Sphaerobacterineae	Unclassified	Unclassified
1042							4							Bacteria	Proteobacteria	Gamma-proteobacteria	Alteromonadales	Chromatiaceae	Rheinheimera	Rheinheimera_ aquimaris
1043							4							Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Segetibacter	Unclassified
1044							5							Bacteria	Fusobacteria	Fusobacteria	Fusobacteriales	Fusobacteriaceae	Fusobacterium	Unclassified
1045							3							Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Sphingomonas_ yabuuchiae
1046							3							Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Dermabacteraceae	Brachybacterium	Unclassified
1047							4							Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Unclassified	Unclassified
1048							3							Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1049							5							Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Roseomonas	Unclassified
1050							5							Bacteria	Acidobacteria	Chloracidobacteria	Unclassified	Unclassified	Unclassified	Unclassified
1051							3							Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1052							5							Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Pseudonocardiaceae	Pseudonocardia	Unclassified
1053							5							Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Ramlibacter	Unclassified
1054							5							Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Unclassified	Unclassified
1055							5							Bacteria	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Jeotgalicoccus	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
1056							4		3		6			Bacteria	Thermi	Deinococci	Deinococcales	Deinococcaceae	Deinococcus	Unclassified
1057							2							unknown (150)	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1058							5				2			Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rhodobacter	Rhodobacter_ capsulatus
1059							3							Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Segetibacter	Unclassified
1060							2							Bacteria	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophobacterace ae	Unclassified	Unclassified
1061							2							Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1062							3							Bacteria	Proteobacteria	Deltaproteobacteria(67)	Unclassified(67)	Unclassified(67)	Unclassified	Unclassified
1063							4							Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1064							2							Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Pseudonocardiaceae	Unclassified	Unclassified
1065							2							Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium	Unclassified
1066							4							Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Marmoricola	Unclassified
1067							2							Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Unclassified	Unclassified
1068							2			11				Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada- ceae	Sphingomonas	Sphingomonas_ asaccharolytica
1069							2							Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophila- ceae	Geodermatoph- ilus	Unclassified
1070							1							Bacteria	Proteobacteria	Gamma- proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Acinetobacter_ johnsonii
1071							3							Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae	Actinomyces	Actinomyces_oris
1072							1	6						Bacteria	Proteobacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1073							1							Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Arthrobacter	Unclassified
1074							2							Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Unclassified	Unclassified	Unclassified
1075							2							Bacteria	Proteobacteria	Gamma- proteobacteria	Pseudomonadales	Moraxellaceae	Alkanindiges	Unclassified
1076							1							Bacteria	Chloroflexi	Caldilineae	Caldilineales	Caldilineaceae	Caldilinea	Unclassified
1077							3							Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
1078							4			3				Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
1079							2							Bacteria	Actinobacteria	Actinobacteria	MC47	Unclassified	Unclassified	Unclassified
1080							1							Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Unclassified	Unclassified
1081							2							Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophila- ceae	Geodermatoph- ilus	Geodermatoph- ilus_obscurus
1082							2							Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Pseudonocardiaceae	Pseudonocardia	Pseudonocardia_ zijingensis
1083							2				13			Bacteria	Proteobacteria	Gamma- proteobacteria	Enterobacteriales	Enterobacteriaceae	Buchnera	Unclassified
1084							1							Bacteria	Proteobacteria	Gamma- proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Unclassified
1085							1							Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Propionibacteriaceae	Microlunatus	Unclassified
1086							1			1				Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium	Faecalibacterium _prausnitzii
1087							3							Bacteria	Proteobacteria	Gamma- proteobacteria	Pseudomonadales	Moraxellaceae	Psychrobacter	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
1088							2			1				Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophila-ceae	Unclassified	Unclassified
1089							1		2					Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	Lautropia	Unclassified
1090							5	3						Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Chryseobacteri-um	Unclassified
1091							1							Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rubellimicrobium	Unclassified
1092							1							Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Acinetobacter_johnsonii
1093							1							Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1094							4							Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Nocardioides	Unclassified
1095							1							Bacteria	Thermi	Deinococci	Deinococcales	Deinococcaceae	Deinococcus	Deinococcus_hohokamensis
1096							2							Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
1097							1							Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
1098							1							Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophila-ceae	Modestobacter	Unclassified
1099							2							Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
1100							3							Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Intrasporangiaceae (67)	Unclassified	Unclassified
1101							1							Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Roseococcus	Unclassified
1102							1							Bacteria	Firmicutes	Bacilli	Bacillales	Planococcaceae	Planomicrobium	Unclassified
1103							1							Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Unclassified
1104							1			13	5			Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	Bosea	Afipia_genosp._9
1105							2				2			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Arthrobacter	Unclassified
1106							1			1				Bacteria	Firmicutes	Bacilli	Bacillales	Planococcaceae	Planomicrobium	Unclassified
1107							1							Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Unclassified
1108							2							Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	Bacillus_selena-tarsenatis
1109							2							Bacteria	Thermi	Deinococci	Deinococcales	Deinococcaceae	Deinococcus	Unclassified
1110							1							Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1111							1	13	1422					Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
1112							1							Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Unclassified	Unclassified
1113							1							Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Unclassified
1114							1							Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Acinetobacter_schindleri
1115							1							Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Unclassified
1116							1							Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Unclassified
1117							1							Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Nocardioides	Unclassified
1118							1							Bacteria	Proteobacteria	Gamma-proteobacteria	Xanthomonadales	Xanthomonadaceae	Unclassified	Unclassified
1119							1							Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Mycoplana	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
1120								23						Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Unclassified	Unclassified
1121								20		1				Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
1122								29			3			Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Flavobacterium	Unclassified
1123								16						Bacteria	Acidobacteria	Acidobacteria	Acidobacteriales	Acidobacteriaceae	Unclassified	Unclassified
1124								16						Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Novosphingobi-um	Unclassified
1125								12		1	10			Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Unclassified	Unclassified
1126								9						Bacteria	Proteobacteria	Gamma-proteobacteria	Xanthomonadales	Xanthomonadaceae	Unclassified	Unclassified
1127								12						Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Unclassified
1128								8						Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Roseococcus	Unclassified
1129								11			4			Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
1130								9			11			Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Erythrobacteraceae	Unclassified	Unclassified
1131								10						Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Unclassified	Unclassified
1132								20						Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
1133								12						Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
1134								7						Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1135								10						Bacteria	Chloroflexi(90)	Bljii12(90)	Unclassified(90)	Unclassified(90)	Unclassified	Unclassified
1136								4						Bacteria	Proteobacteria	Gamma-proteobacteria	Enterobacteriales	Enterobacteriaceae	Buchnera	Unclassified
1137								6						Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Segetibacter	Unclassified
1138								6						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Mycobacteriaceae	Mycobacterium	Unclassified
1139								7						Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Chryseobacteri-um	Unclassified
1140								16						Bacteria	Proteobacteria	Gamma-proteobacteria	Enterobacteriales	Enterobacteriaceae	Buchnera	Unclassified
1141								4						Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
1142								6						Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
1143								3						Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Paracoccus	Unclassified
1144								3						Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Unclassified	Unclassified
1145								3						Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Flavobacterium	Unclassified
1146								7						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Intrasporangiaceae	Janibacter	Janibacter_ melonis
1147								5						Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
1148								2		1	4			Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rubellimicrobium	Unclassified
1149								5						Bacteria	Actinobacteria	Actinobacteria	Rubrobacterales	Rubrobacteraceae	Rubrobacter	Unclassified
1150								3						Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingobium	Unclassified
1151								4	1		2			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium	Corynebacterium _simulans
1152								4			10			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Curtobacterium	Curtobacterium_ flaccumfaciens
1153								1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Dermacoccaceae	Dermacoccus	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
1154								1						Bacteria	Proteobacteria	Gamma-proteobacteria	Enterobacteriales	Enterobacteriaceae	Buchnera	Buchnera_sp.
1155								1						Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Unclassified	Unclassified
1156								3						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1157								2						Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1158								1						Bacteria	Proteobacteria	Gamma-proteobacteria	Xanthomonadales	Xanthomonadaceae	Stenotroph-omonas	Unclassified
1159								2						Bacteria	Proteobacteria	Gamma-proteobacteria	Enterobacteriales	Enterobacteriaceae	Buchnera	Unclassified
1160								2						Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Unclassified
1161								2						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Dermacoccaceae	Dermacoccus	Unclassified
1162								1		33	25	5		Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Agrobacterium	Agrobacterium_ larrymoorei
1163								2						unknown (150)	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1164								3	1					Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
1165								2						Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Sejongia	Unclassified
1166								1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Nocardioides	Unclassified
1167								1						Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
1168								1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Friedmanniella	Unclassified
1169								1		1				Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Unclassified	Unclassified
1170								1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1171								1			3			Bacteria	Thermi	Deinococci	Deinococcales	Deinococcaceae	Deinococcus	Unclassified
1172								1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Pseudonocardiaceae	Pseudonocardia	Unclassified
1173								1						Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Agrobacterium	Agrobacterium_ larrymoorei
1174								1						Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Unclassified	Unclassified
1175								1						Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
1176								1			1			Bacteria	Thermi	Deinococci	Deinococcales	Deinococcaceae	Deinococcus	Unclassified
1177								1						Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingobium	Sphingobium_ herbicidovorans
1178								1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Marmoricola	Unclassified
1179								1						Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Unclassified	Unclassified
1180								3						Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Roseomonas	Unclassified
1181								2						Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Flavobacterium	Flavobacterium_ succinicans
1182								1						Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Unclassified
1183								1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Mycobacteriaceae	Mycobacterium	Unclassified
1184								1						Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
1185											28			Bacteria	Acidobacteria	Acidobacteria	Acidobacteriales	Acidobacteriaceae	Edaphobacter	Edaphobacter_ modestus

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
1186													10	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Methylobacterium _komagatae
1187									381					Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
1188														Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus	Lactobacillus_ aviarius
1189														Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Unclassified	Unclassified
1190														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Marmoricola	Unclassified
1191														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1192														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Mycobacteriaceae	Mycobacterium	Unclassified
1193														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Intrasporangiaceae	Unclassified	Unclassified
1194														Bacteria	Actinobacteria	Actinobacteria	Solirubrobacterales	Solirubrobactera-ceae	Unclassified	Unclassified
1195														Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1196														Bacteria	Actinobacteria	Actinobacteria	Solirubrobacterales	Conexibacteraceae	Unclassified	Unclassified
1197														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Arthrobacter	Unclassified
1198											4			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified(97)	Unclassified	Unclassified
1199														Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Unclassified	Unclassified
1200														Bacteria	Firmicutes	Bacilli	Bacillales	Planococcaceae	Planomicrobium	Unclassified
1201														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1202														Bacteria	Chloroflexi	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1203										1				Bacteria	Proteobacteria	Gamma-proteobacteria	Legionellales	Coxiellaceae	Rickettsiella	Unclassified
1204														Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
1205														Bacteria	Firmicutes	Bacilli	Bacillales	Planococcaceae	Solibacillus	Unclassified
1206														Bacteria	SC4	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1207									66					Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Unclassified
1208														Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
1209														Bacteria	Actinobacteria	Actinobacteria	Solirubrobacterales	Solirubrobactera-ceae	Solirubrobacter	Unclassified
1210														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1211														Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified(89)	Unclassified	Unclassified
1212														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Streptomycetaceae	Streptomyces	Unclassified
1213														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Unclassified	Unclassified
1214														Bacteria	Actinobacteria	Actinobacteria	Solirubrobacterales	Conexibacteraceae	Unclassified	Unclassified
1215														Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Unclassified	Unclassified
1216													10	Bacteria	Proteobacteria	Gamma-proteobacteria	Xanthomonadales	Xanthomonadaceae	Thermomonas	Unclassified
1217														Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1218											1		2	Bacteria	Proteobacteria	Gamma-proteobacteria	Unclassified	Unclassified	Unclassified	Unclassified
1219														Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Roseomonas	Unclassified
1220														Bacteria	Planctomycetes (92)	Unclassified(92)	Unclassified(92)	Unclassified(92)	Unclassified	Unclassified
1221														Bacteria	Chloroflexi	Chloroflexi	Chloroflexales	Unclassified(93)	Unclassified	Unclassified
1222										1	2		1	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
1223														Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Unclassified	Unclassified
1224														Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Unclassified	Unclassified	Unclassified
1225											2			Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rubellimicrobium	Unclassified
1226														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium	Unclassified
1227														Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Roseomonas	Unclassified
1228														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1229														Bacteria	Proteobacteria	Gamma-proteobacteria	Chromatiales	Unclassified	Unclassified	Unclassified
1230														Bacteria	Actinobacteria	Actinobacteria	Solirubrobacterales	Conexibacteraceae	Unclassified	Unclassified
1231											1			Bacteria	Proteobacteria	Gamma-proteobacteria	Enterobacteriales	Enterobacteriaceae	Unclassified	Unclassified
1232														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Friedmanniella	Unclassified
1233														Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Acidisoma	Unclassified
1234														Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	RikenellaceaeII	Unclassified	Unclassified
1235														Bacteria	Proteobacteria	Gamma-proteobacteria	Pasteurellales	Pasteurellaceae	Actinobacillus	Haemophilus_ parahaemolyticus
1236														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Yonghaparkia	Unclassified
1237											1			Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
1238														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Nocardioides	Unclassified
1239														Bacteria	Proteobacteria	Betaproteobacteria	Neisseriales	Neisseriaceae	Unclassified	Unclassified
1240														Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Segetibacter	Unclassified
1241														Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	Bacillus_thermo-amylovorans
1242											9		3	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Rothia	Rothia_aeria
1243														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1244														Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	Bacillus_ foraminis
1245														Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Unclassified	Unclassified
1246														Bacteria	Actinobacteria	Actinobacteria	Acidimicrobiales	Iamiaceae	Unclassified	Unclassified
1247														Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1248														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Unclassified	Unclassified
1249														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1250														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Unclassified	Unclassified
1251														Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1252											13		1	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rubellimicrobium	Unclassified
1253														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Unclassified	Unclassified
1254														Bacteria	Thermi	Deinococci	Deinococcales	Deinococcaceae	Deinococcus	Unclassified
1255														Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Flavisolibacter	Unclassified
1256														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Unclassified	Unclassified
1257														Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Unclassified	Unclassified
1258														Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
1259														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Unclassified	Unclassified
1260														Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Variovorax	Variovorax_ paradoxus

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
1261													2	Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Segetibacter	Unclassified
1262														Bacteria	Chloroflexi	Thermomicrobia	Sphaerobacterales	Sphaerobacterineae	HN1-15	Unclassified
1263														Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1264														Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Unclassified	Unclassified
1265														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1266											2			Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Erythrobacteraceae	Unclassified	Unclassified
1267														Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	Unclassified	Unclassified	Unclassified
1268											6			Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Unclassified
1269														Bacteria	Thermi	Deinococci	Deinococcales	Deinococcaceae	Deinococcus	Unclassified
1270										8				Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Roseomonas	Unclassified
1271														Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1272														Bacteria	Acidobacteria	Acidobacteria	Acidobacteriales	Acidobacteriaceae	Unclassified	Unclassified
1273									1					Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
1274											1			Bacteria	Gemmatimona-detes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonada-ceae	Unclassified	Unclassified
1275														Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Unclassified	Unclassified
1276														Bacteria	Acidobacteria	Acidobacteria	Acidobacteriales	Acidobacteriaceae	Unclassified	Unclassified
1277										2	3			Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
1278														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1279														Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Nordellaceae	Nordella	Unclassified
1280														Bacteria	TM7	TM7-1	Unclassified	Unclassified	Unclassified	Unclassified
1281														Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Saprospiraceae	Unclassified	Unclassified
1282														Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Salinimicrobium	Unclassified
1283														Bacteria	Proteobacteria	Alphaproteobacteria	Unclassified	Unclassified	Unclassified	Unclassified
1284														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Propionibacteriaceae	Propionibacteri-um	Propionibacteri-um_granulosum
1285														Bacteria	Chloroflexi	Chloroflexi	Chloroflexales	Unclassified	Unclassified	Unclassified
1286														Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1287											4			Bacteria	Proteobacteria	Gamma-proteobacteria	Enterobacteriales	Enterobacteriaceae	Unclassified	Unclassified
1288														Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1289														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Microbacterium	Unclassified
1290														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Intrasporangiaceae	Terracoccus	Unclassified
1291											1			Bacteria	SC4	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1292														Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Roseomonas	Unclassified
1293														Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Sphingomonas_ asaccharolytica
1294														Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
1295														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Dermabacteraceae	Brachybacterium	Brachybacterium _fresconis
1296														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium	Corynebacterium _riegelii
1297														Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Devosia	Unclassified
1298											8			Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
1299														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Intrasporangiaceae	Tetrasphaera	Tetrasphaera_ australiensis
1300														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Unclassified	Unclassified
1301														Bacteria	Proteobacteria (75)	Deltaproteobacteria(75)	Unclassified(75)	Unclassified(75)	Unclassified	Unclassified
1302														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Cellulomonadaceae	Unclassified	Unclassified
1303											1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae	Actinomyces	Actinomyces_oris
1304														Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Unclassified	Unclassified
1305														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Williamsiaceae	Williamsia	Williamsia_ muralis
1306														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophila-ceae	Unclassified	Unclassified
1307														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae(61)	Unclassified	Unclassified
1308														Bacteria	Actinobacteria	Actinobacteria	Unclassified	Unclassified	Unclassified	Unclassified
1309														Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Unclassified	Unclassified
1310														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Citricoccus	Unclassified
1311														Bacteria	Actinobacteria	Actinobacteria	Acidimicrobiales	CL500-29	Unclassified	Unclassified
1312														Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1313														Bacteria	Proteobacteria	Gamma-proteobacteria	Unclassified	Unclassified	Unclassified	Unclassified
1314														Bacteria	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Salinicoccus	Unclassified
1315														Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	Unclassified
1316													6	Bacteria	Proteobacteria	Betaproteobacteria	Neisseriales	Neisseriaceae	Stenoxybacter	Unclassified
1317														Bacteria	Actinobacteria	Actinobacteria	MC47	Unclassified	Unclassified	Unclassified
1318														Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Unclassified	Unclassified
1319														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1320														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nakamurellaceae	Unclassified	Unclassified
1321														Bacteria	Gemmatimona-detes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonada-ceae	Unclassified	Unclassified
1322														Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium	Unclassified
1323														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Bogoriellaceae	Georgenia	Unclassified
1324														Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
1325														Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
1326														Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
1327														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Arthrobacter	Arthrobacter_ agilis
1328										1	3			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophila-ceae	Geodermatoph-ilus	Geodermatoph-ilus_obscurus
1329										1				Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Propionibacteriaceae	Propionibacteri-um	Propionibacteri-um_acnes
1330											4			Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	Burkholderia	Burkholderia_ fungorum
1331														Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
1332														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Unclassified	Unclassified
1333														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1334														Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1335														Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Unclassified	Unclassified
1336														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium	Unclassified
1337														Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
1338														Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Roseomonas	Unclassified
1339														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1340														Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Devosia	Unclassified
1341														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micromonospora-ceae	Actinoplanes	Actinoplanes_ ferrugineus
1342														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophila-ceae	Unclassified	Unclassified
1343														Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Cyclobacteriaceae	Unclassified	Unclassified
1344														Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
1345														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nakamurellaceae	Unclassified	Unclassified
1346														Bacteria	Cyanobacteria	Chloroplast	Chlorophyta	Unclassified	Unclassified	Unclassified
1347														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1348														Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Phenylobacteri-um	Unclassified
1349														Bacteria	Actinobacteria	Actinobacteria	Acidimicrobiales	AKIW874	Unclassified	Unclassified
1350														Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
1351														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1352														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1353														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Arthrobacter	Unclassified
1354														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Marmoricola	Unclassified
1355														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micromonospora-ceae	Unclassified	Unclassified
1356														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Propionibacteriaceae	Propionibacteri-um	Propionibacteri-um_acnes
1357														Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Unclassified	Unclassified
1358														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1359														Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Unclassified	Unclassified
1360														Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1361														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1362														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1363														Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1364														unknown (200)	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1365														Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
1366														Bacteria	Proteobacteria	Gamma-proteobacteria	Aeromonadales	Aeromonadaceae	Aeromonas	Unclassified
1367														Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1368														Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1369														unknown (200)	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
1370														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micromonospora-ceae	Unclassified	Unclassified
1371														Bacteria	Proteobacteria	Gamma-proteobacteria	Enterobacteriales	Enterobacteriaceae	Unclassified	Unclassified
1372														Bacteria	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolinaceae	A4b	Unclassified
1373														Bacteria	Thermi	Deinococci	Deinococcales	Deinococcaceae	Deinococcus	Unclassified
1374														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1375														Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Moraxella	Unclassified
1376														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1377														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1378														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophila-ceae	Unclassified	Unclassified
1379														Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Roseomonas	Unclassified
1380											1			Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	Unclassified
1381														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Sanguibacteraceae	Sanguibacter	Sanguibacter_ inulinus
1382														Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1383														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1384														Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Sphingomonas_ asaccharolytica
1385														Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1386														Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
1387														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae	Actinomyces	Actinomyces_ odontolyticus
1388														Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1389														Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
1390														Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
1391														Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
1392														Bacteria	Actinobacteria	Actinobacteria	Acidimicrobiales	CL500-29	Unclassified	Unclassified
1393														Bacteria	Actinobacteria	Actinobacteria	Solirubrobacterales	Solirubrobactera-ceae	Unclassified	Unclassified
1394														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Intrasporangiaceae	Unclassified	Unclassified
1395														Bacteria	Firmicutes	Bacilli	Lactobacillales	Carnobacteriaceae	Trichococcus	Unclassified
1396														Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Unclassified	Unclassified
1397														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Friedmanniella	Unclassified
1398										2	8			Bacteria	Thermi	Deinococci	Deinococcales	Deinococcaceae	Deinococcus	Unclassified
1399														Bacteria	Proteobacteria	Betaproteobacteria	Neisseriales	Neisseriaceae	Stenoxybacter	Unclassified
1400														Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Gillisia	Unclassified
1401														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Arthrobacter	Unclassified
1402														Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Unclassified	Unclassified
1403														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Unclassified	Unclassified
1404														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Unclassified	Unclassified
1405														Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Unclassified
1406														Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
1407														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
1408														Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Sphingomonas_ asaccharolytica
1409														Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	Bacillus_ foraminis
1410										1				Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Unclassified	Unclassified
1411									2		2			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae (61)	Unclassified	Unclassified
1412														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Kocuria	Kocuria_rosea
1413														Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Unclassified	Unclassified
1414														Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Unclassified	Unclassified
1415														Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Methylocella	Unclassified
1416										1				Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Intrasporangiaceae	Phycicoccus	Unclassified
1417														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophila-ceae	Unclassified	Unclassified
1418														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophila-ceae	Unclassified	Unclassified
1419														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophila-ceae	Modestobacter	Unclassified
1420														Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	Unclassified	Unclassified
1421														Bacteria	Firmicutes	Bacilli	Bacillales	Unclassified	Unclassified	Unclassified
1422														Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
1423														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1424														Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Unclassified	Unclassified
1425														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Arthrobacter	Unclassified
1426														Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Unclassified	Unclassified
1427														Bacteria	Actinobacteria	Actinobacteria	Solirubrobacterales	Conexibacteraceae	Unclassified	Unclassified
1428														Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Roseomonas	Unclassified
1429														Bacteria	Actinobacteria	Actinobacteria	Solirubrobacterales	Conexibacteraceae	Unclassified	Unclassified
1430														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1431														Bacteria	Gemmatimona-detes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonada-ceae	Unclassified	Unclassified
1432														Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	Bacillus_safensis
1433														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Friedmanniella	Unclassified
1434														Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Unclassified	Unclassified	Unclassified
1435														Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
1436														Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Roseomonas	Unclassified
1437														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1438														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1439														Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Unclassified	Unclassified
1440														Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
1441														Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Skermanella	Unclassified
1442														Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Roseomonas	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
1443														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Friedmanniella	Unclassified
1444														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophila-ceae	Unclassified	Unclassified
1445														Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Unclassified	Unclassified
1446										3	5			unknown (112)	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1447														Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Methylobacterium _adhaesivum
1448									1		2			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Microbacterium	Unclassified
1449														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Arthrobacter	Unclassified
1450														Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
1451														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Kocuria	Kocuria_rosea
1452														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Arthrobacter	Unclassified
1453														Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Unclassified	Unclassified
1454														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1455														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Sanguibacteraceae	Sanguibacter	Sanguibacter_ inulinus
1456														Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	Bacillus_novalis
1457											3			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Friedmanniella	Unclassified
1458														Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rubellimicrobium	Unclassified
1459														Bacteria	Planctomycetes	Planctomycea	Gemmatales	Isosphaeraceae	Unclassified	Unclassified
1460														Bacteria	SC4	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1461														Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rubellimicrobium	Unclassified
1462														Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
1463														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Arthrobacter	Arthrobacter_ albus
1464														Bacteria	Actinobacteria	Actinobacteria	Acidimicrobiales	Unclassified	Unclassified	Unclassified
1465														Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1466														Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1467														Bacteria	Proteobacteria	Alphaproteobacteria	Unclassified(63)	Unclassified(63)	Unclassified	Unclassified
1468														Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1469														Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	Unclassified
1470														Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	Unclassified	Unclassified
1471														Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Roseomonas	Unclassified
1472											1			Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
1473										200	59			Bacteria	Proteobacteria	Alphaproteobacteria	Unclassified	Unclassified	Unclassified	Unclassified
1474											3			Bacteria	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Staphylococcus	Staphylococcus_ lugdunensis
1475										167	67	37		Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingobium	Sphingobium_ xenophagum
1476									1724		5			Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Methylobacterium _aquaticum
1477									732					Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Dechloromonas	Unclassified
1478									327		5			Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Methylobacterium _aquaticum
1479									221					Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
1480									240					Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Unclassified
1481									210					Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Hydrogenophaga	Hydrogenophaga _palleronii
1482									97	5				Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Unclassified	Unclassified
1483									157	1				Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
1484									106	1	24			Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
1485									80					Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Novosphingobi-um	Unclassified
1486									132					Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Unclassified
1487									71					Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Methylobacterium _hispanicum
1488									55					Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
1489									45					Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Unclassified	Unclassified	Unclassified
1490									43					Bacteria	Proteobacteria	Gamma-proteobacteria	Xanthomonadales	Xanthomonadaceae	Lysobacter	Unclassified
1491									41					Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingobium	Sphingomonas_ sp._SKA58
1492									31					Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
1493									54					Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae	Cupriavidus	Unclassified
1494									24					Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Unclassified
1495									41					Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Unclassified
1496									9					Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Unclassified	Unclassified
1497									6					Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Unclassified
1498									11					Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
1499									4					Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1500									3					Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Mycobacteriaceae	Mycobacterium	Unclassified
1501									3					Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Methylobacterium _zatmanii
1502									3					Bacteria	Actinobacteria	Actinobacteria	Solirubrobacterales	Unclassified	Unclassified	Unclassified
1503									3	13		12		Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingobium	Sphingomonas_ sp._SKA58
1504									3					unknown (134)	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1505									3					Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
1506									2					Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Unclassified	Unclassified
1507									5					Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Unclassified	Unclassified	Unclassified
1508									2					Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Unclassified	Unclassified
1509									4	4				Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	Rhodopseudo-monas	Unclassified
1510									2					Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Unclassified	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
1511									2					Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1512									2					Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
1513									2					Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rubellimicrobium	Unclassified
1514									3		11			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium	Corynebacterium _jeikeium
1515									3					Bacteria	Acidobacteria	Acidobacteria	Acidobacteriales	Acidobacteriaceae	Terriglobus	Unclassified
1516									5					Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified(80)	Unclassified	Unclassified
1517									1					Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
1518									1					Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Variovorax	Variovorax_ paradoxus
1519									1					Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
1520									1		6			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium	Unclassified
1521									1					Bacteria	Gemmatimona-detes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonada-ceae	Unclassified	Unclassified
1522									1					Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Methylobacterium _aquaticum
1523									1					Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Thioclava	Unclassified
1524									1					Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Unclassified
1525									1					Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	Bacteroides_ ovatus
1526									1					Bacteria	Cyanobacteria	Chloroplast	Unclassified	Unclassified	Unclassified	Unclassified
1527									1					Bacteria	Proteobacteria	Betaproteobacteria	Unclassified	Unclassified	Unclassified	Unclassified
1528									4					Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae	Pigmentiphaga	Unclassified
1529									1					Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia	Unclassified
1530									1					Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Pelomonas	Unclassified
1531									1					Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Unclassified	Unclassified
1532									1					Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Propionibacteriaceae	Propionibacteri-um	Propionibacteri-um_acnes
1533									1					Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Unclassified	Unclassified
1534									1					Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Unclassified
1535									1					Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1536									1					Bacteria	Proteobacteria	Alphaproteobacteria	Unclassified	Unclassified	Unclassified	Unclassified
1537									1					Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Brevundimonas	Brevundimonas_ mediterranea
1538									1					Bacteria	Chloroflexi	Thermomicrobia	Sphaerobacterales	Sphaerobacterineae	HN1-15	Unclassified
1539									1					Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Unclassified
1540									1					Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Methylobacterium _aquaticum
1541									1					Bacteria	Armatimona-detes	Armatimonadia	Armatimonadales	WD294	Unclassified	Unclassified
1542									1					Bacteria	Actinobacteria	Actinobacteria	Acidimicrobiales	Unclassified	Unclassified	Unclassified
1543									1					Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
1544									1					Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Unclassified	Unclassified	Unclassified
1545									1					Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Sphingomonas_ yabuuchiae
1546									1					Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Propionibacteriaceae	Propionibacteri-um	Propionibacteri-um_acnes
1547									1					Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Unclassified
1548									1					Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Methylobacterium _aquaticum
1549									1					Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1550									1					Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1551									1					Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Unclassified	Unclassified
1552									1					Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Unclassified
1553									1					Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Sphingobacteriaceae	Unclassified	Unclassified
1554									1					Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Unclassified
1555									1					Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1556									1					Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Nordellaceae	Nordella	Unclassified
1557									1					Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Pseudonocardiaceae	Actinomyceto-spora	Unclassified
1558									1					Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
1559									1					Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1560									1					Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Unclassified
1561									1					Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia	Unclassified
1562									1					Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
1563									1					Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Unclassified	Unclassified
1564									2					Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Unclassified
1565									1					Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Unclassified
1566									1					Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Unclassified	Unclassified
1567									1					Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales	Rickettsiaceae	Wolbachia	Unclassified
1568									1					Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Unclassified
1569									1					Bacteria	Proteobacteria	Gamma-proteobacteria	Xanthomonadales	Xanthomonadaceae	Lysobacter	Unclassified
1570									1					Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Unclassified	Unclassified
1571									1					Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Unclassified
1572									1					Bacteria	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	Spiroplasma	Spiroplasma_sp.
1573									1					Bacteria	Proteobacteria	Betaproteobacteria	Neisseriales	Neisseriaceae	Unclassified	Unclassified
1574									1					Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Unclassified	Unclassified
1575									1					Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1576									1					Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Unclassified	Unclassified
1577									1					Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Unclassified
1578									1					Bacteria	Tenericutes	Mollicutes	Entomoplasmatales	Spiroplasmataceae	Spiroplasma	Unclassified
1579									1					Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Methylobacterium _aquaticum
1580									1					Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
1581									1					Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
1582									1					Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia	Unclassified
1583									1		7			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1584									1					Bacteria	Proteobacteria	Gamma-proteobacteria	Enterobacteriales	Enterobacteriaceae	Buchnera	Unclassified
1585									1					Bacteria	Proteobacteria	Gamma-proteobacteria	Enterobacteriales	Enterobacteriaceae	Unclassified	Unclassified
1586									1					Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
1587									1					Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Unclassified
1588									1					Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Salinimicrobium	Unclassified
1589									1					Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Amaricoccus	Unclassified
1590									1					Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Unclassified
1591									1					Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Nocardioides	Nocardioides_ sp._JS614
1592									1					Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Unclassified
1593									1					Bacteria	Acidobacteria	Chloracidobacteria	Unclassified	Unclassified	Unclassified	Unclassified
1594									1					Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Methylobacterium _aquaticum
1595									1					Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Unclassified	Unclassified
1596									1					Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1597									1					Bacteria	Proteobacteria	Gamma-proteobacteria	Enterobacteriales	Enterobacteriaceae	Unclassified	Unclassified
1598														Bacteria	TM7	TM7-3	EW055	Unclassified	Unclassified	Unclassified
1599														Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Pseudomonas_ balearica
1600										327	44	21		Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Chryseobacteri-um	Unclassified
1601										90	1			Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1602										89	9	54		Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae(97)	Unclassified	Unclassified
1603										68	7			Bacteria	Proteobacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1604										46	28	46		Bacteria	Proteobacteria	Gamma-proteobacteria	Xanthomonadales	Xanthomonadaceae	Lysobacter	Unclassified
1605										49	8			Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Chryseobacteri-um	Unclassified
1606										51				Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Comamonas	Comamonas_ denitrificans
1607										29	4			Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Unclassified	Unclassified
1608										30	4			Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1609										38	6			Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified(96)	Unclassified	Unclassified
1610										38				Bacteria	Proteobacteria	Gamma-proteobacteria	Enterobacteriales	Enterobacteriaceae	Unclassified	Unclassified
1611										24	35		6	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
1612										12		6		Bacteria	Proteobacteria	Alphaproteobacteria	Unclassified	Unclassified	Unclassified	Unclassified
1613										14	4			Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Phenylobacteri-um	Unclassified
1614										10				Bacteria	Proteobacteria	Alphaproteobacteria	Unclassified	Unclassified	Unclassified	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
1615										20				Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Unclassified	Unclassified
1616										10				Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Unclassified
1617										14	8			Bacteria	Proteobacteria	Gamma-proteobacteria	Legionellales	Legionellaceae	Legionella	Unclassified
1618										9				Bacteria	Proteobacteria	Gamma-proteobacteria	Legionellales	Legionellaceae	Unclassified	Unclassified
1619										10				Bacteria	Proteobacteria	Gamma-proteobacteria	Enterobacteriales	Enterobacteriaceae	Unclassified	Unclassified
1620										5				Bacteria	Actinobacteria	Actinobacteria	Euzebiales	Euzebiaceae	Unclassified	Unclassified
1621										7				Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
1622										5	10			Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
1623										9				Bacteria	Proteobacteria	Alpha-proteobacteria(89)	Rhodospirillales(89)	Acetobacteraceae (89)	Unclassified	Unclassified
1624										4				Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Flavobacterium	Unclassified
1625										4				Bacteria	Verrucomicrobia	Opitutae	Opitutales	Opitutaceae	Unclassified	Unclassified
1626										5				Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Flavobacterium	Flavobacterium_ succinicans
1627										4				Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Unclassified
1628										4				Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
1629										3				Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Streptomycetaceae	Streptomyces	Unclassified
1630										4				Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Unclassified	Unclassified
1631										3				Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Flavobacterium	Flavobacterium_ succinicans
1632										4				Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified(75)	Unclassified	Unclassified
1633										4	1			Bacteria	Proteobacteria	Gamma-proteobacteria	Aeromonadales	Aeromonadaceae	Aeromonas	Unclassified
1634										3				Bacteria	Proteobacteria	Deltaproteobacteria	CTD005-82B-02	Unclassified	Unclassified	Unclassified
1635										7				Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	Unclassified	Unclassified
1636										2				Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Roseomonas	Unclassified
1637										2	1			Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
1638										2	5			Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Unclassified
1639										4				Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae	Actinomyces	Unclassified
1640										4				Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
1641										2				Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Erythrobacteraceae	Unclassified	Unclassified
1642										8				Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Erythrobacteraceae	Erythromicrobium	Erythromicrobium _ramosum
1643										2				Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Acinetobacter_ radioresistens
1644										3				Bacteria	Proteobacteria	Gamma-proteobacteria	Enterobacteriales	Enterobacteriaceae	Providencia	Providencia_ alcalifaciens

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
1645										2				Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
1646										4		7		Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Unclassified	Unclassified	Unclassified
1647										2				Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
1648										2				Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Agrobacterium	Unclassified
1649										2				Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Unclassified	Unclassified
1650										4				Bacteria	Armatimona-detes	CH21	Unclassified	Unclassified	Unclassified	Unclassified
1651										2				Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Agrobacterium	Unclassified
1652										5				Bacteria	Proteobacteria	Alphaproteobacteria	Unclassified	Unclassified	Unclassified	Unclassified
1653										4				Bacteria	Proteobacteria	Alphaproteobacteria	Unclassified	Unclassified	Unclassified	Unclassified
1654										3				Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
1655										5	7			Bacteria	Proteobacteria	Alphaproteobacteria	Unclassified	Unclassified	Unclassified	Unclassified
1656										2				Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Unclassified
1657										2				Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
1658										2				Bacteria	Proteobacteria	Deltaproteobacteria	MIZ46	Unclassified	Unclassified	Unclassified
1659										1				Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium	Corynebacterium _glucuronoly-ticum
1660										1				Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rubellimicrobium	Unclassified
1661										1				Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1662										1				Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Paracoccus	Paracoccus_ marcusii
1663										1				Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Unclassified	Unclassified	Unclassified
1664										2				Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Novosphingobi-um	Unclassified
1665										4				Bacteria	Proteobacteria	Gamma-proteobacteria	Enterobacteriales	Enterobacteriaceae	Unclassified	Unclassified
1666										1				Bacteria	Proteobacteria	Betaproteobacteria	Unclassified	Unclassified	Unclassified	Unclassified
1667										1				Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1668										1	10			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Cellulomonadaceae	Oerskovia	Unclassified
1669										2				Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Acinetobacter_ johnsonii
1670										1				Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Kaistia	Unclassified
1671										3		5		Bacteria	Verrucomicrobia	Opitutae	Opitutales	Opitutaceae	Unclassified	Unclassified
1672										1				Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Novosphingobi-um	Unclassified
1673										1				Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Unclassified	Unclassified
1674										1	1			Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
1675										1	1	2		Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
1676										1				Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Thioclava	Unclassified
1677										1				Bacteria	Proteobacteria	Gamma-proteobacteria	Legionellales	Legionellaceae	Legionella	Unclassified
1678										1	5		4	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
1679										1				Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Sphingobacteriaceae	Pedobacter	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
1680										4		2		Bacteria	Proteobacteria	Gamma-proteobacteria	Xanthomonadales	Xanthomonadaceae	Unclassified	Unclassified
1681										3	2	1		Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
1682										1				Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Kineosporiaceae	Kineococcus	Kineococcus_radiotolerans
1683										3				Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Unclassified	Unclassified
1684										1				Bacteria	Actinobacteria	Actinobacteria	Solirubrobacterales	Solirubrobactera-ceae	Unclassified	Unclassified
1685										1				Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1686										1	2			Bacteria	Thermi	Deinococci	Deinococcales	Deinococcaceae	Deinococcus	Unclassified
1687										1				Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae	Unclassified	Unclassified
1688										2				Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Comamonas	Comamonas_aquatica
1689										2				Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
1690										3				Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
1691										4			2	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Unclassified	Unclassified
1692										1				Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Acinetobacter_johnsonii
1693										2				Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Agrobacterium	Rhizobium_sp._IRBG_74
1694										1				Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Unclassified	Unclassified	Unclassified
1695										2				Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Segetibacter	Unclassified
1696										2	1			Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified(67)	Unclassified	Unclassified
1697										1				Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Roseomonas	Unclassified
1698										2				Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
1699										1				Bacteria	Proteobacteria	Betaproteobacteria	Unclassified	Unclassified	Unclassified	Unclassified
1700										1				Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Unclassified
1701										1				Bacteria	Actinobacteria	Actinobacteria	Solirubrobacterales	Conexibacteraceae	Unclassified	Unclassified
1702										1				Bacteria	Actinobacteria	Actinobacteria	Solirubrobacterales	Solirubrobactera-ceae	Unclassified	Unclassified
1703										1				Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Unclassified
1704										1				Bacteria	Chloroflexi	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1705										2				Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Brevundimonas	Brevundimonas_mediterranea
1706										1	1			Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Diaphorobacter	Unclassified
1707										1	4			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nakamurellaceae	Unclassified	Unclassified
1708										5			2	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
1709										1				Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	Unclassified	Unclassified	Unclassified
1710										3				Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Brevundimonas	Brevundimonas_mediterranea
1711										1				Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Shinella	Unclassified
1712										1				Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Friedmanniella	Unclassified
1713										3				Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Unclassified	Unclassified
1714										2				Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
1715										2				Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Segetibacter	Unclassified
1716										1				Bacteria	Firmicutes	Bacilli	Bacillales	Thermoactinomyce-taceae	Unclassified	Unclassified
1717										1				Bacteria	Proteobacteria	Gamma-proteobacteria	Aeromonadales	Aeromonadaceae	Aeromonas	Unclassified
1718										1	1			Bacteria	Nitrospirae	Nitrospira	Nitrospirales	Nitrospiraceae	Nitrospira	Unclassified
1719										1				Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1720										2				Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Agrobacterium	Rhizobium_sp._IRBG_74
1721										1				Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Chryseobacteri-um	Unclassified
1722										1				Bacteria	Proteobacteria	Alphaproteobacteria	Unclassified	Unclassified	Unclassified	Unclassified
1723										1				Bacteria	Proteobacteria	Alphaproteobacteria	Unclassified	Unclassified	Unclassified	Unclassified
1724										1				Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Rhizobium	Rhizobium_galegae
1725										1				Bacteria	Armatimona-detes	Armatimonadia	Armatimonadales	Armatimonadaceae	Unclassified	Unclassified
1726										1				Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Adhaeribacter	Unclassified
1727										1				Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Agrobacterium	Unclassified
1728										1				Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Unclassified	Unclassified
1729										1				Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1730										1				Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Devosia	Unclassified
1731										1				Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Agrobacterium	Unclassified
1732										1	1			Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
1733										1				Bacteria	Gemmatimona-detes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonada-ceae	Unclassified	Unclassified
1734										1				Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Unclassified	Unclassified
1735										1				Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Adhaeribacter	Unclassified
1736										3				Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
1737										1				Bacteria	Gemmatimona-detes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonada-ceae	Unclassified	Unclassified
1738										2				Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Unclassified	Unclassified
1739										1				Bacteria	Proteobacteria	Gamma-proteobacteria	Alteromonadales	Alteromonadaceae	Alishewanella	Unclassified
1740										1				Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Unclassified	Unclassified
1741										1				Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Unclassified	Unclassified
1742										1				Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Agrobacterium	Rhizobium_sp._IRBG_74
1743										1				Bacteria	Planctomycetes	Planctomycea	Gemmatales	Isosphaeraceae	Unclassified	Unclassified
1744										1				Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Brevundimonas	Brevundimonas_mediterranea
1745										1				Bacteria	Thermi	Deinococci	Deinococcales	Deinococcaceae	Deinococcus	Unclassified
1746										1				Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Brevundimonas	Brevundimonas_mediterranea

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
1747										1				Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Paracoccus	Paracoccus_ solventivorans
1748										1				Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Brevundimonas	Brevundimonas_ mediterranea
1749										1				Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Unclassified
1750										1				Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Unclassified	Unclassified
1751										1				Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Unclassified
1752										1				Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1753										1				Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
1754										1				Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Unclassified	Unclassified
1755										1				Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Unclassified	Unclassified
1756										1				Bacteria	WPS-2	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1757										1				Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Agrobacterium	Agrobacterium_ larrymoorei
1758										2				Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Unclassified
1759										2				Bacteria	Proteobacteria	Gamma-proteobacteria	Xanthomonadales	Xanthomonadaceae	Stenotrophomo-nas	Stenotrophomo-nas_nitritiredu-cens
1760										1				Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Aurantimonadaceae	Aurantimonas	Unclassified
1761										1				Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Chryseobacteri-um	Unclassified
1762										1				Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Unclassified	Unclassified
1763										2				Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Unclassified	Unclassified	Unclassified
1764										1				Bacteria	Proteobacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1765										2				Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Agrococcus	Agrococcus_ jenensis
1766										1				Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Flavobacterium	Unclassified
1767										7	2	1		Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Brevundimonas	Brevundimonas_ mediterranea
1768										1		2		Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Chryseobacteri-um	Unclassified
1769										1	1			Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Unclassified	Unclassified
1770										1				Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Unclassified	Unclassified
1771										1				Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1772										1				Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
1773										1				Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Brevundimonas	Brevundimonas_ mediterranea
1774										1				Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Unclassified
1775										1	3			Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Unclassified	Unclassified
1776										1				Bacteria	Thermi	Deinococci	Deinococcales	Deinococcaceae	Deinococcus	Unclassified
1777										2				Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Unclassified	Unclassified
1778										2				Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Flavobacterium	Unclassified
1779										1				Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
1780										1				Bacteria	Actinobacteria	Actinobacteria	Acidimicrobiales	CL500-29	Unclassified	Unclassified
1781										1				Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1782										1			2	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Agromyces	Unclassified
1783										1	1			Bacteria	Gemmatimona-detes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonada-ceae	Unclassified	Unclassified
1784										1				Bacteria	Proteobacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1785										1				Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
1786										1				Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
1787										1				Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Wautersiella	Wautersiella_ falsenii
1788										1				Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Unclassified
1789										1				Bacteria	Firmicutes	Bacilli	Bacillales	Unclassified	Unclassified	Unclassified
1790										1				Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Agrobacterium	Unclassified
1791										1				Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1792										1				Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Unclassified	Unclassified
1793										2				Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Skermanella	Unclassified
1794										1				Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Unclassified	Unclassified
1795										1				Bacteria	Proteobacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1796										1				Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Novosphingobi-um	Unclassified
1797										1				Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium	Unclassified
1798										1				Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Sphingomonas_ wittichii
1799										1				Bacteria	Proteobacteria	Alphaproteobacteria	Unclassified	Unclassified	Unclassified	Unclassified
1800										1				Bacteria	Proteobacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1801										1				Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Unclassified	Unclassified	Unclassified
1802										1				Bacteria	Proteobacteria	Gamma-proteobacteria	Enterobacteriales	Enterobacteriaceae	Unclassified	Unclassified
1803										1				Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Nocardioides	Nocardioides_ oleivorans
1804										1				Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Unclassified
1805										1				Bacteria	Proteobacteria	Gamma-proteobacteria	Unclassified	Unclassified	Unclassified	Unclassified
1806										1	2			Bacteria	Actinobacteria	Actinobacteria	Solirubrobacterales	Conexibacteraceae	Unclassified	Unclassified
1807										1				Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Unclassified	Unclassified
1808										1				Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1809										1				Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingobium	Unclassified
1810										1				Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Rhodoplanes	Unclassified
1811										1				Bacteria	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobia-ceae	Haloferula	Unclassified
1812										1				Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium	Unclassified
1813										1				Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium	Unclassified
1814										1				Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Brevundimonas	Brevundimonas_ mediterranea

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
1815										1				Bacteria	Proteobacteria	Alphaproteobacteria	Unclassified	Unclassified	Unclassified	Unclassified
1816										1				Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Paracoccus	Unclassified
1817										1				Bacteria	Thermi	Deinococci	Deinococcales	Deinococcaceae	Deinococcus	Unclassified
1818										1				Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Unclassified	Unclassified
1819										1				Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Unclassified
1820										1				Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Roseomonas	Unclassified
1821										1				Bacteria	Bacteroidetes	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1822										2	1			Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Agrobacterium	Unclassified
1823										1				Bacteria	Proteobacteria	Gamma-proteobacteria	Xanthomonadales	Xanthomonadaceae	Stenotrophomo-nas	Unclassified
1824										1	2			Bacteria	Proteobacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1825										1				Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Brevundimonas	Brevundimonas_ mediterranea
1826										1				Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Unclassified
1827										1				Bacteria	Proteobacteria	Gamma-proteobacteria	Xanthomonadales	Xanthomonadaceae	Stenotrophomo-nas	Xanthomonas_ retroflexus
1828										1	1	1		Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Agrobacterium	Rhizobium_sp._ IRBG_74
1829										1				Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Chryseobacteri-um	Unclassified
1830										1				Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Unclassified	Unclassified
1831										1				Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Unclassified	Unclassified
1832										1				Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Roseomonas	Unclassified
1833										1				Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Skermanella	Unclassified
1834										1				Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Brevundimonas	Brevundimonas_ mediterranea
1835										1				Bacteria	Thermi	Deinococci	Deinococcales	Deinococcaceae	Deinococcus	Unclassified
1836										1				Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1837										2				Bacteria	Proteobacteria	Gamma-proteobacteria	Enterobacteriales	Enterobacteriaceae	Enterobacter	Enterobacter_ sp._638
1838										1				Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Acinetobacter_ johnsonii
1839										1				Bacteria	Firmicutes	Bacilli	Unclassified	Unclassified	Unclassified	Unclassified
1840										1				Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Pontibacter	Pontibacter_ korlensis
1841										1				Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardiopsaceae	Nocardiopsis	Unclassified
1842										1				Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Unclassified	Unclassified
1843										1				Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
1844										1				Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Roseomonas	Unclassified
1845										1				Bacteria	Proteobacteria	Alphaproteobacteria	Unclassified	Unclassified	Unclassified	Unclassified
1846										1				Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Unclassified	Unclassified
1847										1				Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1848										1				Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
1849										1				Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Methyloversatilis	Methyloversatilis_ universalis
1850										1				Bacteria	Planctomycetes	Planctomycea	Gemmatales	Gemmataceae	Gemmata	Unclassified
1851										1				Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Adhaeribacter	Unclassified
1852										1				Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Roseomonas	Unclassified
1853										1	2			Bacteria	Proteobacteria	Gamma-proteobacteria	Xanthomonadales	Solimonaceae	Solimonas	Unclassified
1854										2				Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Unclassified	Unclassified
1855										1				Bacteria	Armatimona-detes	Armatimonadia	Armatimonadales	Armatimonadaceae	Unclassified	Unclassified
1856										1				Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Unclassified	Unclassified
1857										1				Bacteria	Proteobacteria	Gamma-proteobacteria	Alteromonadales	Unclassified	Unclassified	Unclassified
1858										1				Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Brevundimonas	Brevundimonas_ mediterranea
1859										1				Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Thioclava	Unclassified
1860										1				Bacteria	Firmicutes	Bacilli	Lactobacillales	Aerococcaceae	Unclassified	Unclassified
1861										1				Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	Balneimonas	Unclassified
1862										1				Bacteria	Proteobacteria	Gamma-proteobacteria	Xanthomonadales	Xanthomonadaceae	Stenotrophomo-nas	Xanthomonas_ retroflexus
1863										1				Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1864										1				Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1865										1				Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Brevundimonas	Brevundimonas_ mediterranea
1866										1				Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Unclassified	Unclassified
1867										1				Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Unclassified	Unclassified
1868										1				Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1869										1				Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Unclassified	Unclassified
1870										1				Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Agrobacterium	Unclassified
1871										1				Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1872										1	1		2	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1873										1				Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales	Caedibacteraceae	Caedibacter	Unclassified
1874										1			1	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
1875										1				Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Unclassified
1876										1				Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Unclassified
1877											19			Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Unclassified	Unclassified
1878											23			Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Unclassified	Unclassified
1879											16			Bacteria	Firmicutes	Bacilli	Bacillales	Unclassified	Unclassified	Unclassified
1880											16			Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Geobacillus	Geobacillus_ther-modenitrificans
1881											15			Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
1882											11			Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Unclassified	Unclassified
1883											11			Bacteria	Chloroflexi	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1884											9			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae	Actinomyces	Unclassified
1885											13			Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Segetibacter	Unclassified
1886											8			Bacteria	Thermi	Deinococci	Deinococcales	Deinococcaceae	Deinococcus	Unclassified
1887											10			Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1888											11			Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Unclassified	Unclassified
1889											8			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Kineosporiaceae	Kineococcus	Kineococcus_ radiotolerans
1890											10			Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Erythrobacteraceae	Unclassified	Unclassified
1891											8			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Unclassified	Unclassified
1892											9		5	Bacteria	Thermi	Deinococci	Deinococcales	Deinococcaceae	Deinococcus	Unclassified
1893											7			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Streptomycetaceae	Streptomyces	Unclassified
1894											10			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Nocardioides	Nocardioides_ oleivorans
1895											7			Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Flavobacterium	Flavobacterium_ succinicans
1896											7			Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Unclassified	Unclassified
1897											9			Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
1898											7			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Unclassified	Unclassified
1899											6			Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
1900											6		8	Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Spirosoma	Unclassified
1901											6			Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Unclassified	Unclassified	Unclassified
1902											6			Bacteria	Actinobacteria	Actinobacteria	Solirubrobacterales	Conexibacteraceae	Unclassified	Unclassified
1903											5			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1904											7			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1905											7			Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1906											10			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Aeromicrobium	Unclassified
1907											5			Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Pseudomonas_ mosselii
1908											4			Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Flavisolibacter	Unclassified
1909											8			Bacteria	Firmicutes	Bacilli	Bacillales	Paenibacillaceae	Brevibacillus	Brevibacillus_ levickii
1910											4			Bacteria	Firmicutes	Bacilli	Bacillales	Planococcaceae	Solibacillus	Unclassified
1911											4			Bacteria	Actinobacteria	Actinobacteria	Solirubrobacterales	Solirubrobactera-ceae	Unclassified	Unclassified
1912											6			Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
1913											4			Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Unclassified	Unclassified
1914											4			Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Flavobacterium	Unclassified
1915											6			Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Unclassified	Unclassified
1916											5			Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Adhaeribacter	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
1917											4			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micromonospora-ceae	Unclassified	Unclassified
1918											5			Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rhodobacter	Rhodobacter_ capsulatus
1919											4			Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1920											7			Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
1921											4			Bacteria	Acidobacteria	Acidobacteria	Acidobacteriales	Acidobacteriaceae	Unclassified	Unclassified
1922											4			Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Segetibacter	Unclassified
1923											7			Bacteria	Chloroflexi	Thermomicrobia	Sphaerobacterales	Sphaerobacterineae	HN1-15	Unclassified
1924											3			Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium	Unclassified
1925											3			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micromonospora-ceae	Actinoplanes	Unclassified
1926											6			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1927											5			Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	Bacteroides_ uniformis
1928											3			Bacteria	Chloroflexi	Thermomicrobia	Sphaerobacterales	Sphaerobacterineae	HN1-15	Unclassified
1929											5			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Intrasporangiaceae	Unclassified	Unclassified
1930											3			Bacteria	Actinobacteria	Actinobacteria	Solirubrobacterales	Solirubrobactera-ceae	Unclassified	Unclassified
1931											6			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Curtobacterium	Unclassified
1932											12			Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rubellimicrobium	Unclassified
1933											4			Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Rhodoferax	Unclassified
1934											6			Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	Bacillus_ trypoxylicola
1935											3			Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Unclassified	Unclassified
1936											3			Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Flavisolibacter	Unclassified
1937											6			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1938											3			Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Flavobacterium	Unclassified
1939											5			Bacteria	Firmicutes	Bacilli	Bacillales	Planococcaceae	Planomicrobium	Unclassified
1940											3			Bacteria	Chlorobi	Chlorobia	Chlorobiales	OPB56/SM1B09	Unclassified	Unclassified
1941											3			Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
1942											4			Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1943											2			Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Skermanella	Unclassified
1944											3			Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Unclassified	Unclassified
1945											2			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Propionibacteriaceae	Tessaracoccus	Unclassified
1946											2			Bacteria	Firmicutes	Bacilli	Bacillales	Planococcaceae	Planomicrobium	Unclassified
1947											2			Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
1948											2			Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Erythrobacteraceae	Unclassified	Unclassified
1949											3			Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingobium	Unclassified
1950											2			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Nocardioides	Unclassified
1951											3			Bacteria	Proteobacteria	Betaproteobacteria	Methylophilales	Methylophilaceae	Methylotenera	Unclassified
1952											2			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Nocardioides	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
1953											2			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Nocardioides	Nocardioides_ oleivorans
1954											2			Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
1955											3			Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Unclassified	Unclassified
1956											5			Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales	Rickettsiaceae	Wolbachia	Unclassified
1957											3			Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1958											3			Bacteria	Proteobacteria	Alpha-proteobacteria(67)	Unclassified(67)	Unclassified(67)	Unclassified	Unclassified
1959											3			Bacteria	Firmicutes	Bacilli	Bacillales	Planococcaceae	Unclassified	Unclassified
1960											3			Bacteria	SC4	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1961											2			unknown (150)	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1962											2			Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Unclassified
1963											2			Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Unclassified	Unclassified
1964											3			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Arthrobacter	Unclassified
1965											6			Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Ideonellaceae	Ideonella	Unclassified
1966											2			Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Unclassified	Unclassified
1967											2			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1968											2			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Pseudonocardiaceae	Pseudonocardia	Unclassified
1969											3			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Intrasporangiaceae	Terracoccus	Unclassified
1970											3			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Gordoniaceae	Gordonia	Unclassified
1971											3			Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
1972											4			Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Unclassified	Unclassified	Unclassified
1973											2			Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Capnocytophaga	Capnocytophaga _sputigena
1974											3			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1975											5			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Unclassified	Unclassified
1976											2			Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1977											3			Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Unclassified	Unclassified
1978											4			Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Adhaeribacter	Unclassified
1979											2			Bacteria	Firmicutes	Bacilli	Bacillales	Paenibacillaceae	Paenibacillus	Unclassified
1980											5			Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Sphingomonas_ yabuuchiae
1981											2			Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Unclassified	Unclassified	Unclassified
1982											2			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Nocardioides	Unclassified
1983											3			Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Flavisolibacter	Unclassified
1984											5			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Intrasporangiaceae	Unclassified	Unclassified
1985											2			unknown (150)	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
1986											3			Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium	Clostridium_ sordellii
1987											3			Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	Polyangiaceae	Chondromyces	Chondromyces_ robustus

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
1988											2			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophila-ceae	Geodermatoph-ilus	Unclassified
1989											1			Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Unclassified	Unclassified
1990											1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Curtobacterium	Unclassified
1991											1			Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Unclassified	Unclassified
1992											1			Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Mycoplana	Unclassified
1993											3			Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella	Unclassified
1994											1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Cellulomonadaceae	Actinotalea	Actinotalea_ fermentans
1995											3			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium	Corynebacterium _matruchotii
1996											1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
1997											1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micromonospora-ceae	Actinoplanes	Unclassified
1998											1			Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Flavobacterium	Unclassified
1999											2			Bacteria	Chloroflexi	Thermomicrobia	Sphaerobacterales	Sphaerobacterineae	HN1-15	Unclassified
2000											1			Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Segetibacter	Unclassified
2001											1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Propionibacteriaceae	Luteococcus	Unclassified
2002											1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Unclassified	Unclassified
2003											1			Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	Bacillus_ trypoxylicola
2004											2			Bacteria	Proteobacteria	Deltaproteobacteria	Unclassified	Unclassified	Unclassified	Unclassified
2005											1			Bacteria	Armatimona-detes	S1a-1H	Unclassified	Unclassified	Unclassified	Unclassified
2006											2			Bacteria	Acidobacteria	Acidobacteria	Acidobacteriales	Acidobacteriaceae	Unclassified	Unclassified
2007											3			Bacteria	Planctomycetes	Planctomycea	Gemmatales	Isosphaeraceae	Unclassified	Unclassified
2008											1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
2009											4			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
2010											2			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Nocardioides	Nocardioides_ sp._JS614
2011											1			Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Segetibacter	Unclassified
2012											4			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium	Unclassified
2013											1			Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingobium	Unclassified
2014											1			Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Unclassified	Unclassified
2015											2			Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Devosia	Unclassified
2016											2			Bacteria	Proteobacteria	Gamma-proteobacteria	Enterobacteriales	Enterobacteriaceae	Unclassified	Unclassified
2017											1			Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
2018											3			Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
2019											1			Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
2020											1			Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Flavobacterium	Unclassified
2021											1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Unclassified	Unclassified
2022											1			Bacteria	Thermi	Deinococci	Deinococcales	Deinococcaceae	Deinococcus	Unclassified
2023											2			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
2024											1			Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
2025											2			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Unclassified	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
2026											4			Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Agrobacterium	Unclassified
2027											2			Bacteria	Proteobacteria	Deltaproteobacteria	Bdellovibrionales	Bdellovibrionaceae	Bdellovibrio	Unclassified
2028											1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
2029											2			Bacteria	Actinobacteria	Actinobacteria	MC47	Unclassified	Unclassified	Unclassified
2030											1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Propionibacteriaceae	Microlunatus	Unclassified
2031											1			Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
2032											1			Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
2033											2			Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
2034											2			Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rubellimicrobium	Unclassified
2035											1			Bacteria	Thermi	Deinococci	Deinococcales	Deinococcaceae	Deinococcus	Unclassified
2036											2			Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Unclassified	Unclassified
2037											3			Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	Unclassified
2038											1			Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Capnocytophaga	Capnocytophaga _ochracea
2039											1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium	Unclassified
2040											1			Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Roseomonas	Unclassified
2041											1			Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
2042											1			unknown (200)	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
2043											2			Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Flavobacterium	Flavobacterium_ succinicans
2044											1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Arthrobacter	Unclassified
2045											3			Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
2046											1			Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
2047											1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
2048											1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
2049											1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
2050											1			Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae	Pigmentiphaga	Unclassified
2051											1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Pseudoclavibac-ter	Zimmermannella _bifida
2052											1			Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Acinetobacter_jo hnsonii
2053											2			Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Amaricoccus	Unclassified
2054											1			Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Caulobacter	Unclassified
2055											1			Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Agrobacterium	Rhizobium_sp._ IRBG_74
2056											2			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
2057											1			Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Caulobacter	Caulobacter_ vibrioides
2058											1			Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Brevundimonas	Unclassified
2059											2			Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
2060											1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Plantibacter	Unclassified
2061											1			Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Unclassified	Unclassified
2062											1			Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Methylobacterium _aquaticum
2063											2			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Marmoricola	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
2064											1			Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Unclassified	Unclassified
2065											1			Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
2066											1			Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
2067											1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Unclassified	Unclassified
2068											2			Bacteria	Proteobacteria	Gamma-proteobacteria	Chromatiales	Sinobacteraceae	Unclassified	Unclassified
2069											1			Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
2070											2			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
2071											1			Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
2072											1			Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Unclassified	Unclassified
2073											1			Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	Unclassified
2074											1			Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
2075											1			Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rubellimicrobium	Unclassified
2076											1			Bacteria	Actinobacteria	Actinobacteria	Solirubrobacterales	Conexibacteraceae	Unclassified	Unclassified
2077											1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Arthrobacter	Unclassified
2078											1			Bacteria	Actinobacteria	Actinobacteria	Unclassified	Unclassified	Unclassified	Unclassified
2079											1			Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Unclassified	Unclassified
2080											1			Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Roseomonas	Unclassified
2081											1			Bacteria	Acidobacteria	Chloracidobacteria	Unclassified	Unclassified	Unclassified	Unclassified
2082											2			Bacteria	Thermi	Deinococci	Deinococcales	Deinococcaceae	Deinococcus	Unclassified
2083											2			Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Unclassified	Unclassified	Unclassified
2084											1			Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
2085											1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Nocardioides	Unclassified
2086											1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
2087											1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Mycobacteriaceae	Mycobacterium	Unclassified
2088											1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
2089											1			Bacteria	Cyanobacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
2090											2			Bacteria	Acidobacteria	Solibacteres	Solibacterales	Solibacteraceae	Candidatus_ Solibacter	Unclassified
2091											1			Bacteria	Proteobacteria	Alphaproteobacteria	Unclassified	Unclassified	Unclassified	Unclassified
2092											1			Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	Unclassified	Unclassified
2093											1			Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
2094											1			Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	Unclassified
2095											2			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Microbacterium	Unclassified
2096											3			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified(67)	Unclassified	Unclassified
2097											3			Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Unclassified	Unclassified
2098											3			Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
2099											1			Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Roseomonas	Unclassified
2100											1			Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
2101											1			Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Phenylobacteri-um	Unclassified
2102											1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
2103											1			Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Dyadobacter	Unclassified
2104											2			Bacteria	Chloroflexi	Chloroflexi	Chloroflexales	Unclassified	Unclassified	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
2105											3			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium	Unclassified
2106											1			Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
2107											1			Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Unclassified	Unclassified	Unclassified
2108											1			Bacteria	Planctomycetes	Planctomycea	Gemmatales	Isosphaeraceae	Unclassified	Unclassified
2109											1		22	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Mycobacteriaceae	Mycobacterium	Mycobacterium_ neoaurum
2110											2			Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Segetibacter	Unclassified
2111											1			Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Roseomonas	Unclassified
2112											1			Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
2113											2			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
2114											3			Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Unclassified	Unclassified
2115											2			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Dermabacteraceae	Brachybacterium	Unclassified
2116											1			Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
2117											2			Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
2118											1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Propionibacteriaceae	Tessaracoccus	Unclassified
2119											1			Bacteria	Proteobacteria	Alphaproteobacteria	Unclassified	Unclassified	Unclassified	Unclassified
2120											2			Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Acidisoma	Unclassified
2121											1			Bacteria	Actinobacteria	Actinobacteria	Solirubrobacterales	Solirubrobactera-ceae	Unclassified	Unclassified
2122											1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Arthrobacter	Arthrobacter_ pascens
2123											1			Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Amaricoccus	Unclassified
2124											1			Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
2125											3			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Arthrobacter	Unclassified
2126											2			Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
2127											1			Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Brevundimonas	Brevundimonas_ mediterranea
2128											1		3	Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Unclassified
2129											1			Bacteria	Actinobacteria	Actinobacteria	Acidimicrobiales	Iamiaceae	Unclassified	Unclassified
2130											1			Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Salinimicrobium	Unclassified
2131											1			Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
2132											2			Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Brevundimonas	Brevundimonas_ mediterranea
2133											1			Bacteria	Proteobacteria	Gamma-proteobacteria	Chromatiales	Sinobacteraceae	Unclassified	Unclassified
2134											1		2	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
2135											1			Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Unclassified	Unclassified
2136											1			Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Unclassified	Unclassified
2137											2			Bacteria	SC4	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
2138											1			Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	RikenellaceaeII	Unclassified	Unclassified
2139											2			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
2140											1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Propionibacteriaceae	Propionibacteri-um	Propionibacteri-um_acnes
2141											1			Bacteria	Chloroflexi	SOGA31	Unclassified	Unclassified	Unclassified	Unclassified
2142											1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Microbacterium	Microbacterium_ paraoxydans

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
2143											1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium	Unclassified
2144											1			Bacteria	Firmicutes	Bacilli	Lactobacillales	Unclassified	Unclassified	Unclassified
2145											1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Actinosynnemata-ceae	Saccharothrix	Saccharothrix_ xinjiangensis
2146											1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Aeromicrobium	Unclassified
2147											1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Cellulomonadaceae	Actinotalea	Actinotalea_ fermentans
2148											1			Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
2149											1			Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
2150											1			Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Agrobacterium	Unclassified
2151											1			Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
2152											1			Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rubellimicrobium	Unclassified
2153											1			Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	Unclassified
2154											1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Citricoccus	Unclassified
2155											1			Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Methylibiaceae	Methylibium	Unclassified
2156											1			Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Unclassified	Unclassified
2157											1			Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
2158											1			Bacteria	Actinobacteria	Actinobacteria	Solirubrobacterales	Conexibacteraceae	Unclassified	Unclassified
2159											1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Streptomycetaceae	Streptomyces	Streptomyces_ chrestomyceticus
2160											1			Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Sphingobacteriaceae	Pedobacter	Unclassified
2161											1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
2162											1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Streptomycetaceae	Streptomyces	Streptomyces_ armeniacus
2163											1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae	Actinomyces	Actinomyces_ odontolyticus
2164											1			Bacteria	Firmicutes	Bacilli	Bacillales	Planococcaceae	Bacillus	Unclassified
2165											1			Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
2166											1			Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Segetibacter	Unclassified
2167											1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Pseudonocardiaceae	Pseudonocardia	Unclassified
2168											1			Bacteria	Chloroflexi	Thermomicrobia	Sphaerobacterales	Sphaerobacterineae	HN1-15	Unclassified
2169											1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micromonospora-ceae	Unclassified	Unclassified
2170											2			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Unclassified	Unclassified
2171											1			Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Unclassified	Unclassified
2172											1			Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Flavobacterium	Unclassified
2173											1			Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
2174											1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Streptomycetaceae	Streptomyces	Unclassified
2175											1			Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Unclassified	Unclassified
2176											1			Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Unclassified	Unclassified
2177											1			Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Brevundimonas	Brevundimonas_ mediterranea
2178											1			Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Pseudonocardiaceae	Unclassified	Unclassified
2179											1			Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Unclassified	Unclassified
2180											1			Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Clostridium	Unclassified
2181											1			Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
2182														Bacteria	Acidobacteria	Acidobacteria	Acidobacteriales	Acidobacteriaceae	Unclassified	Unclassified
2183														Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
2184														Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	Unclassified
2185														Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Unclassified
2186														Bacteria	Armatimona-detes	Armatimonadia	Armatimonadales	Armatimonadaceae	Unclassified	Unclassified
2187														Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Unclassified	Unclassified
2188														Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
2189														Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
2190														Bacteria	Gemmatimona-detes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonada-ceae	Unclassified	Unclassified
2191														Bacteria	Proteobacteria (67)	Alpha-proteobacteria(67)	Rhodospirillales(67)	Acetobacteraceae (67)	Unclassified	Unclassified
2192														Bacteria	Acidobacteria	Acidobacteria	Acidobacteriales	Acidobacteriaceae	Unclassified	Unclassified
2193														Bacteria	Actinobacteria	Actinobacteria	Acidimicrobiales	Unclassified	Unclassified	Unclassified
2194														Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Unclassified	Unclassified
2195														Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
2196														Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
2197														Bacteria	Armatimona-detes	S1a-1H	Unclassified	Unclassified	Unclassified	Unclassified
2198														Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
2199												11		Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales	Rickettsiaceae	Rickettsia	Unclassified
2200												11		Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Unclassified	Unclassified
2201												6		Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophila-ceae	Geodermatoph-ilus	Unclassified
2202												2		Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Sphingobacteriaceae	Pedobacter	Unclassified
2203												1		Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingobium	Sphingobium_ xenophagum
2204												1		Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Unclassified	Unclassified
2205												1		Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingobium	Sphingobium_ xenophagum
2206												1		Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Agrobacterium	Rhizobium_sp._ IRBG_74
2207												1		Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Agrobacterium	Unclassified
2208														Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingobium	Sphingobium_ xenophagum
2209														Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Agrobacterium	Unclassified
2210														Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Unclassified	Unclassified
2211														Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
2212														Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Agrobacterium	Rhizobium_sp._ IRBG_74
2213													26	Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Salinimicrobium	Unclassified
2214													20	Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Unclassified	Unclassified
2215													14	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Unclassified	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
2216													10	Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
2217													6	Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Segetibacter	Unclassified
2218													7	Bacteria	Proteobacteria	Gamma-proteobacteria	Enterobacteriales	Enterobacteriaceae	Unclassified	Unclassified
2219													4	Bacteria	Actinobacteria	Actinobacteria	Acidimicrobiales	Acidimicrobiaceae	Unclassified	Unclassified
2220													4	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Unclassified	Unclassified
2221													8	Bacteria	Proteobacteria	Gamma-proteobacteria	Xanthomonadales	Xanthomonadaceae	Lysobacter	Lysobacter_ taiwanensis
2222													4	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	Bacteroides_ eggerthii
2223													2	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bartonellaceae	Bartonella	Unclassified
2224													3	Bacteria	Planctomycetes	Planctomycea	Gemmatales	Isosphaeraceae	Unclassified	Unclassified
2225													2	Bacteria	Proteobacteria	Betaproteobacteria	Unclassified	Unclassified	Unclassified	Unclassified
2226													4	Bacteria	Thermi	Deinococci	Deinococcales	Deinococcaceae	Deinococcus	Unclassified
2227													2	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Unclassified	Unclassified
2228													3	Bacteria	Bacteroidetes	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
2229													1	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
2230													2	Bacteria	Gemmatimona-detes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonada-ceae	Unclassified	Unclassified
2231													2	Bacteria	Thermi	Deinococci	Deinococcales	Deinococcaceae	Deinococcus	Unclassified
2232													4	Bacteria	Bacteroidetes (75)	Unclassified(75)	Unclassified(75)	Unclassified(75)	Unclassified	Unclassified
2233													1	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Arthrobacter	Unclassified
2234													1	Bacteria	Proteobacteria	Gamma-proteobacteria	Chromatiales	Unclassified	Unclassified	Unclassified
2235													2	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micromonospora-ceae	Unclassified	Unclassified
2236													1	Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
2237													2	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella	Unclassified
2238													1	Bacteria	Proteobacteria	Betaproteobacteria	Neisseriales	Neisseriaceae	Stenoxybacter	Unclassified
2239													1	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
2240													1	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Unclassified	Unclassified
2241													1	unknown (200)	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
2242													2	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Microbacterium	Unclassified
2243													2	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Phyllobacteriaceae	Aminobacter	Unclassified
2244													2	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massilia_timonae
2245													1	Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Unclassified	Unclassified
2246													1	Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Flavobacterium	Flavobacterium_ succinicans
2247													2	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophila-ceae	Geodermatoph-ilus	Unclassified
2248													1	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	Balneimonas	Unclassified
2249													1	Bacteria	Cyanobacteria	Chloroplast	Streptophyta	Unclassified	Unclassified	Unclassified
2250													1	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Roseomonas	Unclassified
2251													1	Bacteria	Proteobacteria	Alphaproteobacteria	Unclassified	Unclassified	Unclassified	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
2252													1	Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Segetibacter	Unclassified
2253													1	Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Cyclobacteriaceae	Unclassified	Unclassified
2254													2	Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Unclassified	Unclassified
2255													1	unknown (200)	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
2256													1	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Acetobacteraceae	Roseomonas	Unclassified
2257													1	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	Unclassified	Unclassified
2258														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Arthrobacter	Arthrobacter_ woluwensis
2259														Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Segetibacter	Unclassified
2260														Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Unclassified	Unclassified
2261														Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae	Unclassified	Unclassified
2262														Bacteria	Proteobacteria	Deltaproteobacteria	Unclassified(95)	Unclassified(95)	Unclassified	Unclassified
2263														Bacteria	Actinobacteria	Actinobacteria	Acidimicrobiales	EB1017	Unclassified	Unclassified
2264														Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium	Unclassified
2265														Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	Rhodopseudo-monas	Unclassified
2266														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
2267														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Streptomycetaceae	Streptomyces	Unclassified
2268														Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Unclassified	Unclassified
2269														Bacteria	Proteobacteria	Alphaproteobacteria	Rickettsiales	Rickettsiaceae	Wolbachia	Unclassified
2270														Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Salinimicrobium	Unclassified
2271														unknown (121)	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
2272														Bacteria	Proteobacteria	Gamma-proteobacteria	Legionellales	Coxiellaceae	Rickettsiella	Unclassified
2273														Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	Bacillus_ sonorensis
2274														Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
2275														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Marmoricola	Unclassified
2276														Bacteria	Chloroflexi	Caldilineae	Caldilineales	Caldilineaceae	Caldilinea	Unclassified
2277														Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
2278														Bacteria	Actinobacteria	Actinobacteria	Solirubrobacterales	Conexibacteraceae	Unclassified	Unclassified
2279														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
2280														Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Unclassified	Unclassified	Unclassified
2281														Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Brevundimonas	Unclassified
2282														Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Unclassified	Unclassified
2283														unknown (200)	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
2284														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Brevibacteriaceae	Brevibacterium	Unclassified
2285														Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium	Unclassified
2286														Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Acinetobacter_ lwoffii
2287														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophila-ceae	Modestobacter	Unclassified
2288														Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	Unclassified	Unclassified

OTU No.	Sample ID													Kingdom	Phylum	Class	Order	Family	Genus	Species
	123	131	139	141	142	143	144	145	150	155	157	159	161							
2289														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Propionibacteriaceae	Propionibacteri-um	Propionibacteri-um_acnes
2290														Bacteria	Proteobacteria	Gamma-proteobacteria	Enterobacteriales	Enterobacteriaceae	Buchnera	Unclassified
2291														unknown (200)	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
2292														Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Unclassified
2293														Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	Unclassified
2294														Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Propionibacteriaceae	Propionibacteri-um	Propionibacteri-um_acnes
2295														Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Acinetobacter_ johnsonii
2296														Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Kaistobacter	Unclassified
2297														Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium	Unclassified
2298														Bacteria	Spirochaetes	Leptospirae	Leptospirales	Leptospiraceae	Leptospira	Leptospira_ biflexa
2299														Bacteria	Proteobacteria	Gamma-proteobacteria	Enterobacteriales	Enterobacteriaceae	Unclassified	Unclassified
2300														Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonada-ceae	Sphingomonas	Sphingomonas_ asaccharolytica
2301														Bacteria	Actinobacteria	Actinobacteria	Acidimicrobiales	EB1017	Unclassified	Unclassified
2302														Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Acinetobacter_ lwoffii
2303														Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Flavobacterium	Unclassified
2304														Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	Unclassified	Unclassified
2305														Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Unclassified	Unclassified
2306														Bacteria	Fusobacteria	Fusobacteria	Fusobacteriales	Fusobacteriaceae	Unclassified	Unclassified
2307														Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Paracoccus	Unclassified

Table E.3-4. Taxonomic affiliation of OTUs observed using next-generation 454 FLX tag-encoded pyrosequencing. Numbers of sequences belonging to each OTU are also mentioned for respective samples.

OTU	Sample ID																												
No.	124	125	126	127	128	129	130	132	133	134	135	136	137	138	140	146	148	151	152	153	154	Kingdom	Phylum	Class	Order	Family	Genus	Species
1																1	2					Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudo-monadales	Pseudo-monadaceae	Pseudomonas	Pseudo-monasveroni
2	2							82								17						Bacteria	Proteobacteria	Beta-proteobacteria	Burkholderiales	Oxalobactera-ceae	Massilia	Massiliatimona
3				47	9	3										5						Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudo-monadales	Pseudo-monadaceae	Pseudomonas	Unclassified
4	4																					Bacteria	Proteobacteria	Beta-proteobacteria	Unclassified	Unclassified	Unclassified	Unclassified
5	4																					Bacteria	Proteobacteria	Beta-proteobacteria	Burkholderiales	Comamonada-ceae	Acidovorax	Acidovoraxcaen
6	3																			5		Bacteria	Proteobacteria	Beta-proteobacteria	Burkholderiales	Unclassified	Unclassified	Unclassified
7		2					3															Bacteria	Proteobacteria	Beta-proteobacteria	Burkholderiales	Burkholderia-ceae	Burkholderia	Burkholderia-gladiol
8		1				1										96	47					Bacteria	Proteobacteria	Alpha-proteobacteria	Rhizobiales	Bradyrhizobi-aceae	Unclassified	Unclassified
9			32		48					11		43				16		37				Bacteria	Proteobacteria	Beta-proteobacteria	Burkholderiales	Comamonada-ceae	Pelomonas	Unclassified
10			26		5				1	31	25						1	2	11	74	1	Bacteria	Proteobacteria	Gamma-proteobacteria	Xanthomona-dales	Xanthomona-daceae	Stenotroph-omonas	Pseudo-monasgeniculat
11			1						2		1	19							7			Bacteria	Proteobacteria	Gamma-proteobacteria	Enterobacteri-ales	Enterobacteri-aceae	Escherichia	Unclassified
12				77	91	309	23		27	76		96										Bacteria	Proteobacteria	Beta-proteobacteria	Burkholderiales	Comamonada-ceae	Delftia	Unclassified
13				49																		Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Mycobacteria-ceae	Mycobacterium	Mycobacteri-umchelona
14				42																		Bacteria	Proteobacteria	Gamma-proteobacteria	Xanthomona-dales	Xanthomona-daceae	Stenotroph-omonas	Unclassified
15				1																		Bacteria	Proteobacteria	Gamma-proteobacteria	Xanthomona-dales	Xanthomona-daceae	Stenotroph-omonas	Unclassified
16				1	9	6	5			7		6				3	4		14		9	Bacteria	Proteobacteria	Gamma-proteobacteria	Enterobacteri-ales	Enterobacteri-aceae	Unclassified	Unclassified
17				2																		Bacteria	Firmicutes	Bacilli	Bacillales	Alicyclobacil-laceae	Alicyclobacillus	Unclassified
18					28																	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
19					32			18								1	45					Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudo-monadales	Moraxellaceae	Acinetobacter	Acinetobacter-johnsoni
20					30			140								2	179					Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudo-monadales	Moraxellaceae	Acinetobacter	Acinetobacter-lwoffi
21					17			8														Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteri-aceae	Flavobacterium	Unclassified
22					15																	Bacteria	Proteobacteria	Alpha-proteobacteria	Rhizobiales	Rhizobiaceae	Agrobacterium	Unclassified
23					8			5								15	2					Bacteria	Proteobacteria	Gamma-proteobacteria	Alteromona-dales	Alteromona-daceae	Alishewanella	Unclassified
24					8	15				1		3	1		64	317	218	5				Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Propionibacteri-aceae	Propionibac-terium	Propionibac-teriumacne
25					5																	Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomona-dales	Sphingomona-daceae	Novosphin-gobium	Unclassified
26					13																	Bacteria	Actinobacteria	Actinobacteria	Solirubrobac-terales	Unclassified	Unclassified	Unclassified

OTU No.	Sample ID																						Kingdom	Phylum	Class	Order	Family	Genus	Species
	124	125	126	127	128	129	130	132	133	134	135	136	137	138	140	146	148	151	152	153	154								
27					4																		Bacteria	Proteobacteria	Alpha-proteobacteria	Rhodobacterales	Rhodobacteraceae	Unclassified	Unclassified
28					4																		Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Okibacterium	Okibacterium-fritillaria
29					2	2	2			1													Bacteria	Proteobacteria	Gamma-proteobacteria	Enterobacteriales	Enterobacteriaceae	Escherichia	Unclassified
30					4	6										6							Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophilaceae	Unclassified	Unclassified
31					1			1									1						Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Acinetobacterhaemolyticu
32					2																		Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophilaceae	Modestobacter	Unclassified
33					1																		Bacteria	Proteobacteria	Alpha-proteobacteria	Rhizobiales	Rhizobiaceae	Agrobacterium	Unclassified
34					1																		Bacteria	Proteobacteria	Alpha-proteobacteria	Rhizobiales	Rhizobiaceae	Agrobacterium	Unclassified
35					1																		Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophilaceae	Unclassified	Unclassified
36					1																		Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Flavobacterium	Flavobacterium-gelidilacu
37						91										9	7						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhodobacterales	Rhodobacteraceae	Unclassified	Unclassified
38						26										11	1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium	Unclassified
39						27																	Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
40						17				3	4					3		13	4				Bacteria	Proteobacteria	Gamma-proteobacteria	Enterobacteriales	Enterobacteriaceae	Unclassified	Unclassified
41						14										76	4						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophilaceae	Modestobacter	Unclassified
42						25																	Bacteria	Fusobacteria	Fusobacteria	Fusobacteriales	Fusobacteriaceae	Fusobacterium	Unclassified
43						20																	Bacteria	Chloroflexi	SOGA31	Unclassified	Unclassified	Unclassified	Unclassified
44						20								5		83	1						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Methylobacteriumadhaesivu
45						13																	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Curtobacterium	Unclassified
46						9																	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Kocuria	Kocuriarose
47						7																	Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	Unclassified
48						5										34	64						Bacteria	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Staphylococcus	Staphylococcushomini
49						6													2				Bacteria	Proteobacteria	Beta-proteobacteria	Burkholderiales	Comamonadaceae	Acidovorax	Unclassified
50						7		12			28												Bacteria	Proteobacteria	Beta-proteobacteria	Burkholderiales	Comamonadaceae	Pelomonas	Unclassified
51						6																	Bacteria	Proteobacteria	Alpha-proteobacteria	Rhodospirillales	Rhodospirillaceae	Skermanella	Unclassified
52						6																	Bacteria	Proteobacteria	Beta-proteobacteria	Burkholderiales	Comamonadaceae	Comamonas	Unclassified
53						5																	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae	Actinomyces	Unclassified
54						5																	Bacteria	Chloroflexi	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
55						9																	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Agrococcus	Agrococcusjenensi

OTU No.	Sample ID																					Kingdom	Phylum	Class	Order	Family	Genus	Species
	124	125	126	127	128	129	130	132	133	134	135	136	137	138	140	146	148	151	152	153	154							
56						3										39	22					Bacteria	Proteobacteria	Alpha-proteobacteria	Rhodobacterales	Rhodobacteraceae	Rubellimicrobium	Unclassified
57						7																Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Pseudomonasstutzer
58						4																Bacteria	Proteobacteria	Alpha-proteobacteria	Rhodobacterales	Rhodobacteraceae	Rubellimicrobium	Unclassified
59						2		6								29	9					Bacteria	Proteobacteria	Alpha-proteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Unclassified
60						6											2					Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophilaceae	Unclassified	Unclassified
61						2																Bacteria	Firmicutes	Bacilli	Lactobacillales	Aerococcaceae	Unclassified	Unclassified
62						5									60	89	39					Bacteria	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Staphylococcus	Staphylococcusepidermidi
63						2										7						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhodobacterales	Rhodobacteraceae	Unclassified	Unclassified
64						1																Bacteria	Actinobacteria	Actinobacteria	MC47	Unclassified	Unclassified	Unclassified
65						1																Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
66						1																Bacteria	Proteobacteria	Gamma-proteobacteria	Xanthomonadales	Xanthomonadaceae	Stenotrophomonas	Pseudomonasgeniculat
67						1																Bacteria	Thermi	Deinococci	Deinococcales	Deinococcaceae	Deinococcus	Deinococcusradioduran
68						1																Bacteria	Proteobacteria	Beta-proteobacteria	Burkholderiales	Unclassified	Unclassified	Unclassified
69						1																Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Marmoricola	Unclassified
70						1																Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
71									18													Bacteria	Proteobacteria	Alpha-proteobacteria	Rhizobiales	Hyphomicrobiaceae	Hyphomicrobium	Unclassified
72								36														Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Flavobacterium	Unclassified
73								32								1						Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomonadales	Sphingomonadaceae	Novosphingobium	Unclassified
74								29								53						Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	Sphingomonasasaccharolytic
75								9														Bacteria	Proteobacteria	Alpha-proteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
76								13														Bacteria	Proteobacteria	Alpha-proteobacteria	Rhodobacterales	Rhodobacteraceae	Unclassified	Unclassified
77								14									3					Bacteria	Proteobacteria	Alpha-proteobacteria	Caulobacterales	Caulobacteraceae	Unclassified	(89); Unclassified
78								9								10	72					Bacteria	Proteobacteria	Alpha-proteobacteria	Caulobacterales	Caulobacteraceae	Brevundimonas	Brevundimonasmediterrane
79								8														Bacteria	Proteobacteria	Beta-proteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massiliatimona
80								3								13						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhodospirillales	Rhodospirillaceae	Skermanella	Unclassified
81								3														Bacteria	Proteobacteria	Gamma-proteobacteria	Xanthomonadales	Xanthomonadaceae	Pseudoxanthomonas	Pseudoxanthomonasmexican
82								4														Bacteria	Proteobacteria	Alpha-proteobacteria	Rhodobacterales	Rhodobacteraceae	Unclassified	Unclassified
83								8								7	45					Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Acinetobacterjohnsoni

OTU No.	Sample ID																					Kingdom	Phylum	Class	Order	Family	Genus	Species
	124	125	126	127	128	129	130	132	133	134	135	136	137	138	140	146	148	151	152	153	154							
84								2														Bacteria	Proteobacteria	Alpha-proteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
85								7								4						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteri-aceae	Corynebacteri-um	Corynebacteri-umefficien
86								3														Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomona-dales	Sphingomona-daceae	Sphingomonas	Unclassified
87								1														Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteri-aceae	Flavobacterium	Flavobacterium-gelidilacu
88								1								2	10					Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomona-dales	Sphingomona-daceae	Sphingomonas	Sphingomona-sasaccharolytic
89								2														Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomona-dales	Sphingomona-daceae	Unclassified	Unclassified
90								1														Bacteria	Proteobacteria	Beta-proteobacteria	Burkholderiales	Comamonada-ceae	Acidovorax	Acidovorax-delafieldi
91								1														Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteri-aceae	Flavobacterium	Unclassified
92									15													Bacteria	Proteobacteria	Beta-proteobacteria	Burkholderiales	Unclassified	Unclassified	Unclassified
93									27													Bacteria	Armatimona-detes	CH21	Unclassified	Unclassified	Unclassified	Unclassified
94									12													Bacteria	Proteobacteria	Delta-proteobacteria	Myxococcales	Haliangiaceae	Unclassified	Unclassified
95									2													Bacteria	Acidobacteria	Solibacteres	Solibacterales	Solibacteraceae	Candidatus-Solibacter	Unclassified
96									4							4	9					Bacteria	Proteobacteria	Alpha-proteobacteria	Unclassified	Unclassified	Unclassified	Unclassified
97									1													Bacteria	Acidobacteria	Solibacteres	Solibacterales	Solibacteraceae	Candidatus-Solibacter	Unclassified
98									1							92			54			Bacteria	Proteobacteria	Alpha-proteobacteria	Rhizobiales	Bradyrhizobi-aceae	Unclassified	(99); Unclassified
99									1													Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Dietziaceae	Dietzia	Dietziamari
100										34												Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Brevibacteria-ceae	Brevibacterium	Unclassified
101										33												Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteria-ceae	Unclassified	Unclassified
102										33						10						Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	Unclassified
103										18												Bacteria	Proteobacteria	Alpha-proteobacteria	Rhodobac-terales	Rhodobactera-ceae	Unclassified	Unclassified
104										13												Bacteria	Proteobacteria	Beta-proteobacteria	Burkholderiales	Oxalobactera-ceae	Unclassified	Unclassified
105										3												Bacteria	Proteobacteria	Alpha-proteobacteria	Rhodospirillales	Acetobactera-ceae	Roseomonas	Unclassified
106										2						38	3					Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Arthrobacter	Unclassified
107										2						27						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Intrasporangia-ceae	Arsenicicoccus	Unclassified
108										3												Bacteria	Actinobacteria	Actinobacteria	Solirubrobac-terales	Solirubrobacter-aceae	Unclassified	Unclassified
109										1												Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Brevibacteria-ceae	Brevibacterium	Unclassified
110										1												Bacteria	Proteobacteria	Gamma-proteobacteria	Xanthomona-dales	Xanthomona-daceae	Stenotroph-omonas	Pseudo-monasgeniculat
111										1												Bacteria	Proteobacteria	Alpha-proteobacteria	Rhodobac-terales	Rhodobactera-ceae	Unclassified	Unclassified

OTU No.	Sample ID																						Kingdom	Phylum	Class	Order	Family	Genus	Species
	124	125	126	127	128	129	130	132	133	134	135	136	137	138	140	146	148	151	152	153	154								
112										1													Bacteria	Proteobacteria	Beta-proteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massiliatimona
113											5												Bacteria	Proteobacteria	Beta-proteobacteria	Burkholderiales	Alcaligenaceae	Achromobacter	Unclassified
114												4											Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Flavobacterium	Unclassified
115														10									Bacteria	Proteobacteria	Alpha-proteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Methylobacteriumadhaesivu
116														3									Bacteria	Proteobacteria	Beta-proteobacteria	Burkholderiales	Comamonadaceae	Schlegelella	Unclassified
117														2									Bacteria	Firmicutes	Bacilli	Lactobacillales	Carnobacteriaceae	Unclassified	Unclassified
118														1									Bacteria	Firmicutes	Bacilli	Lactobacillales	Carnobacteriaceae	Unclassified	Unclassified
119															6								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium	Corynebacteriumaurimucosu
120															6								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae	Mobiluncus	Mobiluncuscurtisi
121															2								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium	Corynebacteriumfreney
122															1								Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium	Corynebacteriumaurimucosu
123																20							Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Arthrobacter	Arthrobacteragili
124																67							Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Kineosporiaceae	(99);Kineococcus	(99);Kineococcusradiotoleran
125																55							Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Kocuria	Kocuriarose
126																1							Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	Unclassified
127																17							Bacteria	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Staphylococcus	Unclassified
128																7							Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Curtobacterium	Curtobacteriumflaccumfacien
129																77							Bacteria	Proteobacteria	Beta-proteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	(77);Massiliatimona
130																116							Bacteria	Proteobacteria	Beta-proteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massiliatimona
131																7							Bacteria	Proteobacteria	Beta-proteobacteria	Burkholderiales	Comamonadaceae	Unclassified	Unclassified
132																2							Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Dermabacteraceae	Brachybacterium	Unclassified
133																4							Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
134																7							Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Unclassified	Unclassified
135																66							Bacteria	Proteobacteria	Alpha-proteobacteria	Rhodospirillales	Acetobacteraceae	Roseomonas	Unclassified
136																8							Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Friedmanniella	Unclassified
137																11							Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Nocardioides	Nocardioidesoleivoran
138																2							Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomonadales	Sphingomonadaceae	Unclassified	Unclassified
139																58							Bacteria	Proteobacteria	Gamma-proteobacteria	Legionellales	Coxiellaceae	Rickettsiella	Rickettsiellagryll

OTU No.	Sample ID																					Kingdom	Phylum	Class	Order	Family	Genus	Species
	124	125	126	127	128	129	130	132	133	134	135	136	137	138	140	146	148	151	152	153	154							
140																13						Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteri-ales	Flexibactera-ceae	Hymenobacter	Unclassified
141																38						Bacteria	Proteobacteria	Beta-proteobacteria	Burkholderiales	Oxalobactera-ceae	Massilia	Massiliatimona
142																10	20					Bacteria	Proteobacteria	Alpha-proteobacteria	Rhodobac-terales	Rhodobactera-ceae	Paracoccus	Paracoccus-marcusi
143																30						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioida-ceae	Aeromicrobium	Unclassified
144																4						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
145																28						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatoph-ilaceae	Geodermatoph-ilus	Blastococcus-saxobsiden
146																5	15					Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteri-ales	Unclassified	Unclassified	Unclassified
147																27	4					Bacteria	Proteobacteria	Alpha-proteobacteria	Rhizobiales	Methylobacteri-aceae	Methylobacteri-um	Methylobacteri-umradiotoleran
148																4						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardiaceae	Rhodococcus	Unclassified
149																12						Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomona-dales	Sphingomona-daceae	Sphingomonas	Sphingomon-asyabuuchia
150																78						Bacteria	Proteobacteria	Beta-proteobacteria	Burkholderiales	Oxalobactera-ceae	Unclassified	(83); Unclassified
151																14						Bacteria	Proteobacteria	Beta-proteobacteria	Burkholderiales	Oxalobactera-ceae	Massilia	Massiliatimona
152																93	55					Bacteria	Acidobacteria	Acidobacteria	Acidobacteri-ales	Acidobacteri-aceae	Edaphobacter	Edaphobacter-modestu
153																63						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteri-aceae	Corynebacteri-um	Corynebacteri-umkroppen-stedti
154																77						Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium	Unclassified
155																45						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhizobiales	Methylobacteri-aceae	Methylobacteri-um	Unclassified
156																39						Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomona-dales	Sphingomona-daceae	Sphingomonas	Unclassified
157																36						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Williamsiaceae	Williamsia	Williamsiamurali
158																44						Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacilla-ceae	Lactobacillus	Lactobacillus-aviariu
159																68	46					Bacteria	Proteobacteria	Beta-proteobacteria	Burkholderiales	Oxalobactera-ceae	Unclassified	Unclassified
160																39						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioida-ceae	Marmoricola	Unclassified
161																47						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Propionibacteri-aceae	Microlunatus	Unclassified
162																30	10					Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteri-aceae	Corynebacteri-um	Unclassified
163																35						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
164																30						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhizobiales	Bradyrhizobi-aceae	Balneimonas	Unclassified
165																29						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Mycobacteria-ceae	Mycobacterium	Unclassified
166																31						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Intrasporangia-ceae	Unclassified	Unclassified
167																30						Bacteria	Actinobacteria	Actinobacteria	Solirubrobac-terales	Solirubrobacter-aceae	Unclassified	Unclassified
168																28						Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified

OTU No.	Sample ID																					Kingdom	Phylum	Class	Order	Family	Genus	Species
	124	125	126	127	128	129	130	132	133	134	135	136	137	138	140	146	148	151	152	153	154							
169																23						Bacteria	Actinobacteria	Actinobacteria	Solirubrobac-terales	Unclassified	Unclassified	Unclassified
170																24						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Arthrobacter	Unclassified
171																25						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Intrasporangia-ceae	Unclassified	Unclassified
172																23						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatoph-ilaceae	Blastococcus	(96); Unclassified
173																21						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioida-ceae	Marmoricola	Unclassified
174																28						Bacteria	Bacteroidetes	Sphingobacteria	(90);Sphingoba cteriales	(90); Unclassified	(90); Unclassified	(90); Unclassified
175																20						Bacteria	Firmicutes	Bacilli	Bacillales	Planococca-ceae	Planomicrobium	Unclassified
176																22						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
177																20						Bacteria	Chloroflexi	Chloroflexi	Chloroflexales	Unclassified	Unclassified	Unclassified
178																20						Bacteria	Proteobacteria	Gamma-proteobacteria	Legionellales	Coxiellaceae	Rickettsiella	Unclassified
179																20						Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomona-dales	Sphingomona-daceae	Sphingomonas	Unclassified
180																19						Bacteria	Firmicutes	Bacilli	Bacillales	Planococca-ceae	Solibacillus	Unclassified
181																19						Bacteria	SC4	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
182																24						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhizobiales	Methylobacteri-aceae	(96);Methylo-bacterium	(96); Unclassified
183																26						Bacteria	Proteobacteria	Gamma-proteobacteria	Enterobacteri-ales	Enterobacteri-aceae	Unclassified	Unclassified
184																21						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
185																21						Bacteria	Proteobacteria	Beta-proteobacteria	Burkholderiales	Comamonada-ceae	Ramlibacter	Unclassified
186																21						Bacteria	Actinobacteria	Actinobacteria	Solirubrobacter-ales	Solirubrobacter-aceae	Solirubrobacter	Unclassified
187																24						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhizobiales	Bradyrhizobi-aceae	Bosea	Unclassified
188																21						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
189																18						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
190																21						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhizobiales	Hyphomicrobi-aceae	Devosia	Unclassified
191																18						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhodobac-terales	Rhodobactera-ceae	Rubellimicro-bium	Unclassified
192																20						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Streptomyceta-ceae	Streptomyces	Unclassified
193																14						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioida-ceae	Unclassified	Unclassified
194																19	26					Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudo-monadales	Pseudo-monadaceae	Pseudomonas	Pseudomonas-mendocin
195																14						Bacteria	Actinobacteria	Actinobacteria	Solirubrobacter-ales	Unclassified	Unclassified	Unclassified
196																24						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioida-ceae	Nocardioides	Nocardioides-oleivoran
197																28						Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteri-ales	Unclassified	Unclassified	Unclassified

OTU No.	Sample ID																					Kingdom	Phylum	Class	Order	Family	Genus	Species
	124	125	126	127	128	129	130	132	133	134	135	136	137	138	140	146	148	151	152	153	154							
198																16						Bacteria	Proteobacteria	Gamma-proteobacteria	Xanthomonadales	Xanthomonadaceae	Thermomonas	Unclassified
199																18	6					Bacteria	Proteobacteria	Alpha-proteobacteria	Rhodospirillales	Acetobacteraceae	Roseomonas	Unclassified
200																14						Bacteria	Firmicutes	Bacilli	Bacillales	Unclassified	Unclassified	Unclassified
201																15						Bacteria	Proteobacteria	Gamma-proteobacteria	Unclassified	Unclassified	Unclassified	Unclassified
202																17	4					Bacteria	Proteobacteria	Beta-proteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massiliatimona
203																12						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhodospirillales	Acetobacteraceae	Roseomonas	Unclassified
204																12						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Nocardioides	Nocardioides-oleivoran
205																12						Bacteria	Planctomycetes	Phycisphaerae	Unclassified	Unclassified	Unclassified	Unclassified
206																13						Bacteria	Chloroflexi	Chloroflexi	Chloroflexales	Unclassified	Unclassified	Unclassified
207																14						Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomonadales	Sphingomonadaceae	Novosphingobium	Novosphingobiumresinovoru
208																31	19					Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
209																18						Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomonadales	Sphingomonadaceae	Unclassified	Unclassified
210																25						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophilaceae	Blastococcus	Unclassified
211																12						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Intrasporangiaceae	Arsenicicoccus	Unclassified
212																12						Bacteria	Acidobacteria	Chloracidobacteria	Unclassified	Unclassified	Unclassified	Unclassified
213																14						Bacteria	Bacteroidetes	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
214																14						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhizobiales	Bradyrhizobiaceae	Unclassified	Unclassified
215																10						Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Adhaeribacter	Unclassified
216																10						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhodobacterales	Rhodobacteraceae	Rubellimicrobium	Unclassified
217																12						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium	Unclassified
218																13						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhodospirillales	Acetobacteraceae	Roseomonas	(93); Unclassified
219																8						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
220																9						Bacteria	Proteobacteria	Gamma-proteobacteria	Chromatiales	Unclassified	(89);Unclassified	(89); Unclassified
221																7						Bacteria	Actinobacteria	Actinobacteria	Solirubrobacterales	Unclassified	Unclassified	Unclassified
222																10						Bacteria	Proteobacteria	Gamma-proteobacteria	Enterobacteriales	Enterobacteriaceae	Ewingella	Ewingella-american
223																8	11					Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Micrococcus	Micrococcus-luteu
224																8						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Friedmanniella	Unclassified
225																8						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhodospirillales	Acetobacteraceae	Unclassified	Unclassified
226																8						Bacteria	Bacteroidetes	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified

OTU No.	Sample ID																						Kingdom	Phylum	Class	Order	Family	Genus	Species
	124	125	126	127	128	129	130	132	133	134	135	136	137	138	140	146	148	151	152	153	154								
227																8						Bacteria	Proteobacteria	Gamma-proteobacteria	Pasteurellales	Pasteurellaceae	Actinobacillus	Haemophilus-parahaemoly-ticu
228																10						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhodobac-terales	Rhodobactera-ceae	Unclassified	Unclassified
229																10						Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteri-ales	Flexibactera-ceae	Hymenobacter	Unclassified
230																8						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteria-ceae	Unclassified	Unclassified
231																11						Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomona-dales	Sphingomona-daceae	Unclassified	Unclassified
232																6						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioida-ceae	Nocardioides	Unclassified
233																9						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Arthrobacter	Arthrobacteragili
234																10						Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomona-dales	Sphingomona-daceae	Sphingomonas	Unclassified
235																7						Bacteria	Proteobacteria	Beta-proteobacteria	Neisseriales	Neisseriaceae	Unclassified	Unclassified
236																7						Bacteria	Proteobacteria	Beta-proteobacteria	Burkholderiales	Oxalobactera-ceae	Massilia	Massiliatimona
237																8						Bacteria	Bacteroidetes	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
238																8						Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	Unclassified
239																9						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Rothia	Rothiaaeri
240																11						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
241																11						Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	Unclassified
242																5						Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteri-ales	Unclassified	Unclassified	Unclassified
243																6						Bacteria	Actinobacteria	Actinobacteria	Acidimicrobiales	Iamiaceae	Unclassified	Unclassified
244																5						Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
245																16	5					Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteria-ceae	Rathayibacter	Unclassified
246																5						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteria-ceae	Unclassified	Unclassified
247																11						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatoph-ilaceae	Unclassified	Unclassified
248																6						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
249																6						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioida-ceae	Unclassified	Unclassified
250																6						Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	Unclassified
251																9						Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
252																9						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhodobac-terales	Rhodobactera-ceae	Rubellimicro-bium	Unclassified
253																8						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteria-ceae	Microbacterium	Unclassified
254																6						Bacteria	Thermi	Deinococci	Deinococcales	Deinococca-ceae	Deinococcus	Unclassified
255																4						Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteri-ales	Unclassified	Unclassified	Unclassified
256																5						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhizobiales	Methylobacteri-aceae	Methylobacteri-um	Methylobacteri-umadhaesivu
257																4						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioida-ceae	Unclassified	Unclassified
258																6						Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteri-ales	Flexibactera-ceae	Unclassified	Unclassified

OTU No.	Sample ID																						Kingdom	Phylum	Class	Order	Family	Genus	Species
	124	125	126	127	128	129	130	132	133	134	135	136	137	138	140	146	148	151	152	153	154								
259																6						Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomonadales	Sphingomonadaceae	Unclassified	Unclassified
260																9						Bacteria	Bacteroidetes	Sphingobacteria	(56);Sphingobacteriales	(56);Unclassified	(56);Unclassified	Unclassified
261																4						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Unclassified	Unclassified
262																6						Bacteria	Proteobacteria	Beta-proteobacteria	Burkholderiales	Comamonadaceae	Variovorax	Variovorax-paradoxu
263																6						Bacteria	Firmicutes	Bacilli	Bacillales	Planococcaceae	Planomicrobium	Unclassified
264																5						Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Unclassified	Unclassified	Unclassified
265																6						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhodospirillales	Acetobacteraceae	Roseococcus	(84);Unclassified
266																5						Bacteria	Chloroflexi	Thermomicrobia	HN1-15	Unclassified	Unclassified	Unclassified
267																4						Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
268																4						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhizobiales	Rhizobiaceae	Unclassified	Unclassified
269																13						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Friedmanniella	Unclassified
270																8						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
271																18						Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomonadales	Erythrobacteraceae	Unclassified	Unclassified
272																5						Bacteria	Proteobacteria	Delta-proteobacteria	Myxococcales	Unclassified	Unclassified	Unclassified
273																5						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Unclassified
274																6						Bacteria	Thermi	Deinococci	Deinococcales	Deinococcaceae	Deinococcus	Unclassified
275																4						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhodospirillales	Acetobacteraceae	Roseomonas	Unclassified
276																4						Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
277																3						Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingobium	Unclassified
278																9						Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Sphingobacteriaceae	Pedobacter	Unclassified
279																3						Bacteria	Acidobacteria	Acidobacteria	Acidobacteriales	Unclassified	Unclassified	Unclassified
280																7						Bacteria	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Staphylococcus	Staphylococcusaureu
281																4						Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	Unclassified
282																12	6					Bacteria	Proteobacteria	Gamma-proteobacteria	Enterobacteriales	Enterobacteriaceae	Pantoea	Pantoeaananati
283																10						Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
284																9	7					Bacteria	Proteobacteria	Alpha-proteobacteria	Caulobacterales	Caulobacteraceae	Unclassified	Unclassified
285																6						Bacteria	Bacteroidetes	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
286																5						Bacteria	Acidobacteria	Acidobacteria	Acidobacteriales	Unclassified	Unclassified	Unclassified
287																5						Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
288																5						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
289																5						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified

OTU No.	Sample ID																						Kingdom	Phylum	Class	Order	Family	Genus	Species
	124	125	126	127	128	129	130	132	133	134	135	136	137	138	140	146	148	151	152	153	154								
290																4						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
291																3						Bacteria	TM7	TM7-1	Unclassified	Unclassified	Unclassified	Unclassified
292																5						Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteri-ales	Saprospiraceae	Unclassified	Unclassified
293																3						Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteri-aceae	Salinimicrobium	Unclassified
294																3						Bacteria	Proteobacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
295																3	2					Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Propionibacteri-aceae	Propionibac-terium	Propionibac-teriumgranulosu
296																4						Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudo-monadales	Moraxellaceae	Enhydrobacter	Enhydrobac-teraerosaccu
297																4						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardiaceae	Rhodococcus	Rhodococcus-fascian
298																3						Bacteria	Chloroflexi	Chloroflexi	Unclassified	Unclassified	Unclassified	Unclassified
299																5						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioida-ceae	Friedmanniella	Unclassified
300																3						Bacteria	Proteobacteria	Beta-proteobacteria	Burkholderiales	Oxalobactera-ceae	Unclassified	Unclassified
301																3						Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
302																4						Bacteria	Proteobacteria	Gamma-proteobacteria	Enterobacteri-ales	Enterobacteri-aceae	Arsenophonus	Unclassified
303																4						Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
304																5						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteria-ceae	Microbacterium	Unclassified
305																5						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Intrasporangia-ceae	Terracoccus	Unclassified
306																4						Bacteria	SC4	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
307																4						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhodospirillales	Acetobactera-ceae	Roseomonas	Unclassified
308																4	108					Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomona-dales	Sphingomona-daceae	Sphingomonas	Sphingomona-sasaccharolytic
309																2						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
310																2						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Dermabactera-ceae	Brachybacteri-um	Brachybacteri-umfresconi
311																2						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhizobiales	Bradyrhizobi-aceae	Balneimonas	Unclassified
312																2						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteri-aceae	Corynebacteri-um	Corynebacteri-umriegeli
313																8						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhizobiales	Hyphomicrobi-aceae	Devosia	Unclassified
314																8						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
315																3						Bacteria	Thermi	Deinococci	Deinococcales	Deinococca-ceae	Deinococcus	Unclassified
316																2						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Intrasporangia-ceae	Tetrasphaera	Tetrasphaera-australiensi
317																3						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteria-ceae	Unclassified	Unclassified
318																8						Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
319																3						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Cellulomonada-ceae	Unclassified	Unclassified

OTU No.	Sample ID																						Kingdom	Phylum	Class	Order	Family	Genus	Species
	124	125	126	127	128	129	130	132	133	134	135	136	137	138	140	146	148	151	152	153	154								
320																2						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Actinomyceta-ceae	Actinomyces	Actinomycesori
321																4	9					Bacteria	Proteobacteria	Beta-proteobacteria	Burkholderiales	Oxalobactera-ceae	Massilia	Massiliatimona
322																4						Bacteria	Proteobacteria	Beta-proteobacteria	Burkholderiales	Oxalobactera-ceae	Herbaspirillum	Unclassified
323																2						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Williamsiaceae	Williamsia	Williamsiamurali
324																5						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Arthrobacter	Unclassified
325																2						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatoph-ilaceae	Unclassified	Unclassified
326																3						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhodobac-terales	Rhodobactera-ceae	Rubellimicro-bium	Unclassified
327																6						Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteri-ales	Flexibactera-ceae	Hymenobacter	Unclassified
328																5						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
329																4						Bacteria	Proteobacteria	Gamma-proteobacteria	Enterobacteri-ales	Enterobacteri-aceae	Unclassified	Unclassified
330																6						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioida-ceae	Unclassified	Unclassified
331																2						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
332																3						Bacteria	Proteobacteria	Beta-proteobacteria	Neisseriales	Neisseriaceae	Neisseria	Unclassified
333																2						Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomona-dales	Sphingomona-daceae	Unclassified	Unclassified
334																2						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioida-ceae	Marmoricola	Unclassified
335																2						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Citricoccus	Unclassified
336																2						Bacteria	Actinobacteria	Actinobacteria	Acidimicrobiales	CL500-29	Unclassified	Unclassified
337																2						Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
338																3						Bacteria	Proteobacteria	Gamma-proteobacteria	Unclassified	Unclassified	Unclassified	Unclassified
339																4						Bacteria	Firmicutes	Bacilli	Bacillales	Staphylococ-caceae	Salinicoccus	Unclassified
340																4						Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	Unclassified
341																3						Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomona-dales	Unclassified	Unclassified	Unclassified
342																8						Bacteria	Proteobacteria	Beta-proteobacteria	Neisseriales	Neisseriaceae	Stenoxybacter	Unclassified
343																3						Bacteria	Actinobacteria	Actinobacteria	MC47	Unclassified	Unclassified	Unclassified
344																2						Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomona-dales	Sphingomona-daceae	Unclassified	Unclassified
345																5						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
346																2						Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomona-dales	Sphingomona-daceae	Kaistobacter	Unclassified
347																5						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nakamurella-ceae	Unclassified	Unclassified
348																5						Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
349																3						Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium	Unclassified
350																2						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Bogoriellaceae	Georgenia	Unclassified
351																3						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
352																2						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteria-ceae	Microbacterium	Unclassified

OTU No.	Sample ID																						Kingdom	Phylum	Class	Order	Family	Genus	Species
	124	125	126	127	128	129	130	132	133	134	135	136	137	138	140	146	148	151	152	153	154								
353																2						Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	Unclassified
354																6						Bacteria	Thermi	Deinococci	Deinococcales	Deinococcaceae	Deinococcus	Unclassified
355																2						Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	Unclassified
356																1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Arthrobacter	Unclassified
357																2						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophilaceae	Geodermatophilus	Geodermatophilusobscuru
358																1	4					Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Propionibacteriaceae	Propionibacterium	Propionibacteriumacne
359																3						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nakamurellaceae	Unclassified	Unclassified
360																1						Bacteria	Proteobacteria	Beta-proteobacteria	Burkholderiales	Burkholderiaceae	Burkholderia	Unclassified
361																2						Bacteria	Proteobacteria	Beta-proteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massiliatimona
362																1						Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
363																1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Unclassified	Unclassified
364																1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
365																2						Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
366																1						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhodospirillales	Acetobacteraceae	Unclassified	Unclassified
367																2						Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Unclassified	Unclassified	Unclassified
368																1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium	Unclassified
369																3						Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
370																1						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhodospirillales	Acetobacteraceae	Roseomonas	Unclassified
371																1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
372																4						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Curtobacterium	Curtobacteriumflaccumfacien
373																1						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhizobiales	Hyphomicrobiaceae	Devosia	Unclassified
374																2						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micromonosporaceae	Actinoplanes	Actinoplanesferrugineu
375																3						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophilaceae	Unclassified	(67); Unclassified
376																2						Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
377																1						Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
378																3						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nakamurellaceae	Unclassified	Unclassified
379																1						Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
380																1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
381																2						Bacteria	Proteobacteria	Alpha-proteobacteria	Caulobacterales	Caulobacteraceae	Phenylobacterium	Unclassified
382																1						Bacteria	Actinobacteria	Actinobacteria	Acidimicrobiales	AKIW874	Unclassified	Unclassified
383																2						Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified

OTU No.	Sample ID																					Kingdom	Phylum	Class	Order	Family	Genus	Species
	124	125	126	127	128	129	130	132	133	134	135	136	137	138	140	146	148	151	152	153	154							
384																3						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
385																1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
386																1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Arthrobacter	Unclassified
387																1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioida-ceae	Marmoricola	Unclassified
388																1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micromono-sporaceae	Unclassified	Unclassified
389																1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Propionibacteri-aceae	Propionibac-terium	Propionibac-teriumacne
390																3						Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteri-ales	Unclassified	Unclassified	Unclassified
391																1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
392																2						Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomona-dales	Sphingomona-daceae	Unclassified	Unclassified
393																1						Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
394																1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
395																1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
396																2						Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
397																1						Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
398																1						Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteri-ales	Flexibactera-ceae	Hymenobacter	Unclassified
399																1						Bacteria	Proteobacteria	Gamma-proteobacteria	Aeromonadales	Aeromonada-ceae	Aeromonas	Unclassified
400																1						Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
401																1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatoph-ilaceae	Geodermatoph-ilus	Blastococcus-saxobsiden
402																1						Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
403																1						Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
404																3						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micromono-sporaceae	Unclassified	Unclassified
405																1						Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococca-ceae	Lactococcus	Lactococcus-lacti
406																1						Bacteria	Proteobacteria	Gamma-proteobacteria	Enterobacteri-ales	Enterobacteri-aceae	Unclassified	Unclassified
407																2						Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
408																1						Bacteria	Thermi	Deinococci	Deinococcales	Deinococca-ceae	Deinococcus	Unclassified
409																2						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
410																3						Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudo-monadales	Moraxellaceae	Moraxella	Unclassified
411																1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
412																1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
413																3						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatoph-ilaceae	Unclassified	Unclassified
414																3						Bacteria	Thermi	Deinococci	Deinococcales	Deinococca-ceae	Deinococcus	Unclassified
415																1						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhodospirillales	Acetobactera-ceae	Roseomonas	Unclassified
416																1						Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	Bacillusnealsoni
417																1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Sanguibactera-ceae	Sanguibacter	Sanguibacteri-nulinu
418																1	1					Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatoph-ilaceae	Modestobacter	Unclassified
419																2						Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified

OTU No.	Sample ID																					Kingdom	Phylum	Class	Order	Family	Genus	Species
	124	125	126	127	128	129	130	132	133	134	135	136	137	138	140	146	148	151	152	153	154							
420																5						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
421																1						Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomona-dales	Sphingomona-daceae	Sphingomonas	Sphingomona-sasaccharolytic
422																1						Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
423																1						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhizobiales	Rhizobiaceae	Unclassified	Unclassified
424																1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Actinomyceta-ceae	Actinomyces	Actinomyceso-dontolyticu
425																2						Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
426																1						Bacteria	Proteobacteria	Beta-proteobacteria	Burkholderiales	Oxalobactera-ceae	Massilia	Massiliatimona
427																1						Bacteria	Proteobacteria	Beta-proteobacteria	Burkholderiales	Oxalobactera-ceae	Massilia	Massiliatimona
428																2						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
429																1						Bacteria	Actinobacteria	Actinobacteria	Acidimicrobiales	CL500-29	Unclassified	Unclassified
430																2						Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomona-dales	Sphingomona-daceae	Unclassified	Unclassified
431																3						Bacteria	Actinobacteria	Actinobacteria	Solirubrobacter-ales	Solirubrobacter-aceae	Unclassified	Unclassified
432																1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Intrasporangia-ceae	Unclassified	Unclassified
433																2						Bacteria	Firmicutes	Bacilli	Lactobacillales	Carnobacteri-aceae	Trichococcus	Unclassified
434																2						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatoph-ilaceae	Unclassified	Unclassified
435																2						Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteri-ales	Unclassified	Unclassified	Unclassified
436																1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioida-ceae	Friedmanniella	Unclassified
437																1						Bacteria	Thermi	Deinococci	Deinococcales	Deinococca-ceae	Deinococcus	Unclassified
438																1						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhodospirillales	Acetobactera-ceae	Roseomonas	Unclassified
439																2						Bacteria	Proteobacteria	Beta-proteobacteria	Neisseriales	Neisseriaceae	Stenoxybacter	Unclassified
440																2						Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteri-aceae	Gillisia	Unclassified
441																1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Arthrobacter	Unclassified
442																1						Bacteria	Bacteroidetes	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
443																1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteria-ceae	Unclassified	Unclassified
444																2						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteria-ceae	Unclassified	Unclassified
445																1						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhizobiales	Methylobacteri-aceae	Methylobacteri-um	Unclassified
446																1						Bacteria	Proteobacteria	Beta-proteobacteria	Burkholderiales	Oxalobactera-ceae	Massilia	Massiliatimona
447																1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
448																1						Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomona-dales	Sphingomona-daceae	Sphingomonas	Sphingomona-sasaccharolytic
449																1						Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	Unclassified
450																1						Bacteria	Fusobacteria	Fusobacteria	Fusobacteriales	Fusobacteria-ceae	Fusobacterium	Unclassified

OTU No.	Sample ID																					Kingdom	Phylum	Class	Order	Family	Genus	Species
	124	125	126	127	128	129	130	132	133	134	135	136	137	138	140	146	148	151	152	153	154							
451																3						Bacteria	Chloroflexi	Thermomicrobia	HN1-15	Unclassified	Unclassified	Unclassified
452																1						Bacteria	Proteobacteria	Beta-proteobacteria	Burkholderiales	Oxalobactera-ceae	Massilia	Massiliatimona
453																1						Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomona-dales	Sphingomona-daceae	Unclassified	Unclassified
454																1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteria-ceae	Unclassified	Unclassified
455																3						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Kocuria	Kocuriarose
456																2						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhodobac-terales	Rhodobactera-ceae	Unclassified	Unclassified
457																1						Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteri-ales	Unclassified	Unclassified	Unclassified
458																2						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
459																2						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Intrasporangia-ceae	Phycicoccus	Unclassified
460																1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatoph-ilaceae	Unclassified	Unclassified
461																1						Bacteria	Proteobacteria	Beta-proteobacteria	Burkholderiales	Oxalobactera-ceae	Massilia	Massiliatimona
462																2						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatoph-ilaceae	Unclassified	Unclassified
463																1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatoph-ilaceae	Modestobacter	Unclassified
464																1						Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomona-dales	Sphingomona-daceae	Unclassified	Unclassified
465																1						Bacteria	Firmicutes	Bacilli	Bacillales	Staphylococ-caceae	Staphylococcus	Staphylococ-cussuccinu
466																1						Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudo-monadales	Pseudo-monadaceae	Pseudomonas	Unclassified
467																2						Bacteria	Firmicutes	Bacilli	Bacillales	Unclassified	Unclassified	Unclassified
468																1						Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomona-dales	Sphingomona-daceae	Sphingomonas	Unclassified
469																1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
470																1						Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomona-dales	Sphingomona-daceae	Unclassified	Unclassified
471																1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Arthrobacter	Unclassified
472																2						Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomona-dales	Sphingomona-daceae	Unclassified	Unclassified
473																1						Bacteria	Actinobacteria	Actinobacteria	Solirubrobacter-ales	Unclassified	Unclassified	Unclassified
474																2						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhodospirillales	Acetobactera-ceae	Roseomonas	Unclassified
475																1						Bacteria	Actinobacteria	Actinobacteria	Unclassified	Unclassified	Unclassified	Unclassified
476																1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
477																2						Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
478																1						Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	Unclassified
479																1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
480																1						Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteri-ales	Unclassified	Unclassified	Unclassified
481																1						Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteri-ales	Flexibactera-ceae	Hymenobacter	Unclassified
482																1						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhodospirillales	Acetobactera-ceae	Roseomonas	Unclassified

OTU No.	Sample ID																					Kingdom	Phylum	Class	Order	Family	Genus	Species
	124	125	126	127	128	129	130	132	133	134	135	136	137	138	140	146	148	151	152	153	154							
483																1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
484																2						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
485																1						Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomonadales	Sphingomonadaceae	Unclassified	Unclassified
486																1						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhizobiales	Unclassified	Unclassified	Unclassified
487																1						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhodospirillales	Rhodospirillaceae	Skermanella	Unclassified
488																1						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhodospirillales	Acetobacteraceae	Roseomonas	Unclassified
489																1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium	Corynebacteriumamycolatu
490																1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
491																1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophilaceae	Unclassified	Unclassified
492																2						Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Unclassified	Unclassified	Unclassified
493																1						Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
494																1						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Methylobacteriumadhaesivu
495																1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	Microbacterium	Unclassified
496																1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Arthrobacter	Unclassified
497																1						Bacteria	Proteobacteria	Beta-proteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massiliatimona
498																1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophilaceae	Geodermatophilus	Blastococcussaxobsiden
499																1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Kocuria	Kocuriarose
500																1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Arthrobacter	Unclassified
501																1						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhodospirillales	Acetobacteraceae	Unclassified	Unclassified
502																2						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
503																1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Sanguibacteraceae	Sanguibacter	Sanguibacterinulinu
504																1						Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	Unclassified
505																1						Bacteria	Proteobacteria	Beta-proteobacteria	Burkholderiales	Oxalobacteraceae	Massilia	Massiliatimona
506																1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Friedmanniella	Unclassified
507																1						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhodobacterales	Rhodobacteraceae	Rubellimicrobium	Unclassified
508																1						Bacteria	Planctomycetes	Planctomycea	Gemmatales	Isosphaeraceae	Unclassified	Unclassified
509																1						Bacteria	SC4	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
510																1						Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomonadales	Erythrobacteraceae	Unclassified	Unclassified
511																1						Bacteria	Proteobacteria	Alpha-proteobacteria	Rhodobacterales	Rhodobacteraceae	Rubellimicrobium	Unclassified
512																1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Pseudonocardiaceae	Pseudonocardia	Unclassified
513																1						Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
514																1						Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
515																1						Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Arthrobacter	Arthrobacteralbu

OTU No.	Sample ID																					Kingdom	Phylum	Class	Order	Family	Genus	Species
	124	125	126	127	128	129	130	132	133	134	135	136	137	138	140	146	148	151	152	153	154							
516																1						Bacteria	Actinobacteria	Actinobacteria	Acidimicrobiales	Unclassified	Unclassified	Unclassified
517																1						Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
518																		12				Bacteria	TM7	TM7-3	EW055	Unclassified	Unclassified	Unclassified
519																					5	Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudo-monadales	Pseudo-monadaceae	Pseudomonas	Pseudomonas-balearic
520																	37					Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteri-ales	Unclassified	Unclassified	Unclassified
521																	46					Bacteria	Proteobacteria	Alpha-proteobacteria	Caulobacterales	Caulobacter-aceae	Caulobacter	Caulobacter-vibrioide
522																	35					Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomona-dales	Sphingomona-daceae	Sphingomonas	Sphingomonas-meloni
523																	40					Bacteria	Proteobacteria	Alpha-proteobacteria	Unclassified	Unclassified	Unclassified	Unclassified
524																	31					Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteri-ales	Unclassified	Unclassified	Unclassified
525																	36					Bacteria	Proteobacteria	Delta-proteobacteria	Myxococcales	Unclassified	Unclassified	Unclassified
526																	45					Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomona-dales	Erythrobacter-aceae	Erythromicro-bium	Erythromicrobi-umramosu
527																	23					Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomona-dales	Sphingomona-daceae	Sphingobium	Sphingobium-yanoikuya
528																	21					Bacteria	Proteobacteria	Beta-proteobacteria	Burkholderiales	Comamonada-ceae	Unclassified	Unclassified
529																	18					Bacteria	Actinobacteria	Actinobacteria	Acidimicrobiales	EB1017	Unclassified	Unclassified
530																	24					Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium	Unclassified
531																	15					Bacteria	Proteobacteria	Alpha-proteobacteria	Rhizobiales	Bradyrhizobi-aceae	Rhodopseu-domonas	Unclassified
532																	12					Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomona-dales	Sphingomona-daceae	Sphingomonas	Unclassified
533																	15					Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteri-aceae	Corynebacteri-um	Corynebacteri-umjeikeiu
534																	12					Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomona-dales	Sphingomona-daceae	Sphingomonas	Unclassified
535																	12					Bacteria	Proteobacteria	Gamma-proteobacteria	Pasteurellales	Pasteurellaceae	Haemophilus	Haemophilus-parainfluenza
536																	9					Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomona-dales	Sphingomona-daceae	Sphingobium	Unclassified
537																	8					Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
538																	14					Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Streptomyceta-ceae	Streptomyces	Unclassified
539																	10					Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteri-ales	Flexibactera-ceae	Unclassified	Unclassified
540																	7					Bacteria	Firmicutes	Bacilli	Bacillales	Staphylococ-caceae	Staphylococcus	Staphylococ-cuslugdunensi
541																	17					Bacteria	Proteobacteria	Alpha-proteobacteria	Rickettsiales	Rickettsiaceae	Wolbachia	Unclassified
542																	7					Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteri-aceae	Salinimicrobium	Unclassified
543																	5					Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
544																	13					Bacteria	Proteobacteria	Gamma-proteobacteria	Legionellales	Coxiellaceae	Rickettsiella	Unclassified
545																	7					Bacteria	Proteobacteria	Beta-proteobacteria	Burkholderiales	Oxalobactera-ceae	Massilia	Massiliatimona
546																	11					Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	Unclassified

OTU No.	Sample ID																					Kingdom	Phylum	Class	Order	Family	Genus	Species
	124	125	126	127	128	129	130	132	133	134	135	136	137	138	140	146	148	151	152	153	154							
547																	9					Bacteria	Proteobacteria	Beta-proteobacteria	Burkholderiales	Alcaligenaceae	Azohydromonas	Unclassified
548																	5					Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	Unclassified
549																	4					Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae	Marmoricola	Unclassified
550																	4					Bacteria	Chloroflexi	Anaerolineae	Caldilineales	Caldilineaceae	Caldilinea	Unclassified
551																	3					Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Flexibacteraceae	Hymenobacter	Unclassified
552																	6					Bacteria	Firmicutes	Bacilli	Turicibacterales	Turicibacteraceae	Unclassified	Unclassified
553																	3					Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	Flavobacterium	Unclassified
554																	2					Bacteria	Actinobacteria	Actinobacteria	Solirubrobacterales	Unclassified	Unclassified	Unclassified
555																	3					Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
556																	6					Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Acinetobacter-johnsoni
557																	2					Bacteria	Proteobacteria	Beta-proteobacteria	Unclassified	Unclassified	Unclassified	Unclassified
558																	4					Bacteria	Proteobacteria	Alpha-proteobacteria	Rhodospirillales	Rhodospirillaceae	Skermanella	Unclassified
559																	3					Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Acinetobacter-johnsoni
560																	5					Bacteria	Proteobacteria	Gamma-proteobacteria	Pasteurellales	Pasteurellaceae	Unclassified	Unclassified
561																	1					Bacteria	Proteobacteria	Alpha-proteobacteria	Caulobacterales	Caulobacteraceae	Brevundimonas	Unclassified
562																	1					Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unclassified	Unclassified	Unclassified
563																	1					Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Unclassified	Unclassified
564																	1					Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
565																	1					Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Acinetobacter-lwoffi
566																	2					Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Brevibacteriaceae	Brevibacterium	Unclassified
567																	1					Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium	Unclassified
568																	1					Bacteria	Proteobacteria	Beta-proteobacteria	Burkholderiales	Burkholderiaceae	Burkholderia	Burkholderia-fungoru
569																	1					Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	Acinetobacter-lwoffi
570																	1					Bacteria	Proteobacteria	Alpha-proteobacteria	Caulobacterales	Caulobacteraceae	Caulobacter	Unclassified
571																	1					Bacteria	Proteobacteria	Beta-proteobacteria	Burkholderiales	Oxalobacteraceae	Unclassified	Unclassified
572																	1					Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Propionibacteriaceae	Propionibacterium	Propionibacteriumacne
573																	1					Bacteria	Proteobacteria	Gamma-proteobacteria	Enterobacteriales	Enterobacteriaceae	Buchnera	Unclassified
574																	1					Bacteria	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified
575																	1					Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	Unclassified
576																	1					Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	Unclassified

OTU No.	Sample ID																					Kingdom	Phylum	Class	Order	Family	Genus	Species
	124	125	126	127	128	129	130	132	133	134	135	136	137	138	140	146	148	151	152	153	154							
577																	1					Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Propionibacteri-aceae	Propionibac-terium	Propionibac-teriumacne
578																	1					Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomona-dales	Sphingomona-daceae	Sphingobium	Sphingobium-xenophagu
579																	1					Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudo-monadales	Moraxellaceae	Acinetobacter	Unclassified
580																	1					Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomona-dales	Sphingomona-daceae	Kaistobacter	Unclassified
581																	2					Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium	Unclassified
582																	1					Bacteria	Proteobacteria	Alpha-proteobacteria	Caulobacterales	Caulobacter-aceae	Caulobacter	Caulobacter-vibrioide
583																	1					Bacteria	Spirochaetes	Leptospirae	Leptospirales	Leptospiraceae	Leptospira	Leptospirabiflex
584																	1					Bacteria	Proteobacteria	Gamma-proteobacteria	Enterobacteri-ales	Enterobacteri-aceae	Unclassified	Unclassified
585																	1					Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudo-monadales	Pseudo-monadaceae	Pseudomonas	Pseudomonas-umsongensi
586																	1					Bacteria	Actinobacteria	Actinobacteria	Acidimicrobiales	EB1017	Unclassified	Unclassified
587																	1					Bacteria	Proteobacteria	Alpha-proteobacteria	Sphingomona-dales	Sphingomona-daceae	Sphingomonas	Sphingomonas-yabuuchia
588																	1					Bacteria	Proteobacteria	Gamma-proteobacteria	Pseudo-monadales	Moraxellaceae	Acinetobacter	Acinetobacter-lwoffi
589																	2					Bacteria	Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteri-aceae	Flavobacterium	Unclassified
590																	1					Bacteria	Proteobacteria	Alpha-proteobacteria	Rhizobiales	Rhizobiaceae	Agrobacterium	Agrobacterium-larrymoore
591																	1					Bacteria	Proteobacteria	Alpha-proteobacteria	Rhizobiales	Bradyrhizobi-aceae	Unclassified	Unclassified
592																	1					Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospira-ceae	Unclassified	Unclassified
593																	1					Bacteria	Fusobacteria	Fusobacteria	Fusobacteriales	Fusobacteria-ceae	Unclassified	Unclassified
594																	1					Bacteria	Proteobacteria	Alpha-proteobacteria	Rhodobac-terales	Rhodobactera-ceae	Paracoccus	Unclassified

APPENDIX F: GENETIC INVENTORY WORKSHOP REPORTS

The Mars Exploration Program made its initial choices defining scope and expectations based on a workshop of independent experts held in 2006. The workshop findings included advice to develop a qualitative inventory capability (versus quantitative or a capability to do both) and to identify both live and dead organisms (versus live only). These choices, and others to follow, were influenced by practical considerations of time, funding, and the anticipated requirements of upcoming missions. There were modifications over the course of the task, but these initial choices remained valid, as endorsed by a second workshop held in 2009.

The reports contained in this appendix document the results of these two workshops.

Report of the Mars Genetic Inventory of Spacecraft

Workshop held at

California Institute of Technology

on

February 28th and March 1st 2006

Publication Date: April 30, 2006
Editors: J. Andy Spry, K. (Venkat) Venkateswaran, Dave A. Newcombe (JPL)

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2. Opening information about team and citation instructions

This workshop was hosted by JPL's Mars Exploration Directorate, with participants invited from a diverse range of fields related to genetic diversity and planetary protection, with the aim of achieving a balanced and objective discussion.

Participant	Affiliation	Specialism
Anderson, Gary	Lawrence Berkeley National Laboratory, Berkeley CA	Genechip technology
Bartlett, Douglas	Scripps Institute, San Diego CA	Extremophiles
Buxbaum, Karen	Jet Propulsion Laboratory, Pasadena CA	Mars Exploration Directorate
Carlson, Craig	Univ. of California at Santa Barbara	Marine microbiology
Chang, Cathy	Diversa Corp., San Diego CA	Molecular microbiology
Crawford, Ronald	Univ. of Idaho, Moscow ID	Microbial physiology
Fox, George	Univ. Houston, TX	Molecular microbiology
Kastner, Jason	Jet Propulsion Laboratory, Pasadena CA	Planetary protection
McKernan, Kevin	Agencourt Inc., Beverly MA	DNA sequencing
Mills, Aaron	University of Virginia, Charlottesville VA	Microbial ecology
Newcombe, David	Jet Propulsion Laboratory, Pasadena CA	Planetary protection
Oliver, James	University of North Carolina at Charlotte	Viable but non-culturable organisms
Spry, Andy	Jet Propulsion Laboratory, Pasadena CA	Planetary protection
Stahl, David	University of Washington, Seattle WA	Molecular microbial ecology
Torok, Tamas	Lawrence Berkeley National Laboratory, Berkeley CA	Mycology
Venkateswaran, Kasthuri	Jet Propulsion Laboratory, Pasadena CA	Planetary protection
Williamson, Shannon	Craig Venter Institute, Rockville MD	Virology

The report was reviewed by David Stahl (UWash) from within the attendees, as he was unable to attend the sub-group discussions, and Eric Mathur (formerly of Diversa and Member of the NRC-PREVCOM Committee which produced the recommendations which were the spur to holding this Workshop).

This report can be cited as JPL Document D-35346, Report of the Mars Genetic Inventory of Spacecraft Workshop (2006), Jet Propulsion Laboratory, Pasadena CA.

3. Executive Summary and Key Findings

This report presents the findings of a workshop held across two days involving invited science and technology experts from industry, academia and government to discuss and recommend the appropriate way forward to implement a genetic inventory for Mars spacecraft.

As input, the group heard a series of presentations encompassing the state-of-the-art in respect of existing molecular technologies which could be applied to creating a genetic inventory. The group also noted the situation in regard to current planetary protection implementation and the recommendation of the NRC Committee on Preventing the Forward Contamination of Mars (27) to NASA in respect of missions in 2016 and beyond.

The group found that maturity of existing molecular analysis technology is sufficient to permit the development of a genetic inventory for future missions. However, the group noted that current sampling methodologies for low biomass samples may not be adequate and need further development.

The group recommends that NASA should fund the development of a DNA-based genetic inventory, based on detection of known prokaryotic genetic markers. It is the opinion of the group that it is adequate for the technology used to be qualitative (rather than quantitative), as this is sufficient for the requirement and offers the low risk route to successful deployment within the anticipated cost and schedule window.

The group further recommends that NASA should fund a parallel study of methodologies for the detection, isolation and archiving of low abundance genetic material from spacecraft and spacecraft assembly environments.

The authors estimate that it will require funds of the order $5M to achieve a fully validated methodology for the collection, storage and DNA-based analysis of the complete and unbiased genetic inventory of spacecraft and spacecraft assembly facilities, at the level of sophistication envisioned by the group.

4. Introduction

In 2005, the National Research Council's Space Studies Board task force presented its draft advice to NASA in Preventing the Forward Contamination of Mars (PREVCOM) (27). The NRC-PREVCOM report, among a series of 17 recommendations, embraced the concept of updating the technological approach to the study of organisms on spacecraft to include newer technologies than are in current use for planetary protection. Specifically in the context of this workshop's task, recommendation 5 stated that:

> *"NASA should require the routine collection of phylogenetic data to a statistically appropriate level to ensure that the microbial diversity of assembly, test, and launch operations (ATLO) environments, and of all of NASA spacecraft to be sent to Mars, is reliably assessed. NASA should also require the systematic archiving of environmental samples for ATLO environments and for all spacecraft to be sent to Mars"*

The Mars Genetic Inventory of Spacecraft (MARGINS) Workshop was hosted at CalTech by JPL's Mars Exploration Directorate as part of an impact assessment of the output from NRC-PREVCOM. The assembled group of invited scientists was tasked with discussing and recommending the appropriate way forward for implementing a genetic inventory for Mars spacecraft.

4a. Assumptions for this study

At the outset of the study, the analysis group was provided by the NASA Planetary Protection Officer with a list of parameters and concerns to be used for bounding the scope of the discussion and as starting points for analysis, and worked with that list throughout the workshop (See Appendix A).

4b. Intended use of this document

To fulfill its objectives, this document will be delivered to the Mars Exploration Directorate at JPL and made available to NASA and the wider scientific community for the purpose of program planning, proposal generation and evaluation, and planetary protection policy support. Ultimately, it is the intention of the workshop that the information and opinions expressed herein should lead to the commencement of a structured approach to the genetic analysis of spacecraft diversity and archiving.

5. Planetary Protection - The Current Approach for Mars

Planetary protection approaches for current missions are largely based on the heritage from the significant body of data arising from studies supporting the Viking missions in the early 1970s. Scientists of this era determined that the risk of terrestrial microorganisms surviving the journey to Mars and propagating when they got there would be constrained by their hardiness with respect to the environments they encountered. For this reason, NASA selected aerobic, heterotrophic mesophilic spore-forming organisms as the standard organism type against which the microbial cleanliness of spacecraft would be measured. Specifically, enumeration of cultivable spores at the time of launch was undertaken against a maximum limit. The mission-specific limit was derived from a combination of the mission purpose, the target body (in this case always Mars) and a measure of risk that any organism transferred to Mars will result in "harmful contamination" (1) of the planet.

Over time, and with new scientific data, this approach has developed to become the basis for both the current NASA and COSPAR policies (2, 4, 25) where four categories exist for missions to Mars:

Category III. Mars orbiters will be required to meet orbital lifetime requirements[1] or achieve bioburden levels equivalent to the *Viking* lander pre-sterilization total bioburden.(9)

Category IVa. Lander systems not carrying instruments for investigations of extant martian life are restricted to a biological burden no greater than the average Viking lander pre-sterilization surface bioburden levels ($3x10^5$ spores).

Category IVb. For lander systems designed to investigate extant martian life, all of the requirements of Category IVa apply, along with the following requirement:

> *The entire landed system must be sterilized at least to Viking post-sterilization biological burden levels (30 spores), or to levels of biological burden reduction driven by the nature and sensitivity of the particular life-detection experiments, whichever are more stringent*
>
> **OR**
>
> *The subsystems which are involved in the acquisition, delivery, and analysis of samples used for life detection must be sterilized to these levels, and a method of preventing recontamination of the sterilized subsystems and the contamination of the material to be analyzed is in place.*

Category IVc. For missions which investigate martian special regions (definition included in main COSPAR policy), even if they do not include life detection experiments, all of the requirements of Category IVa apply, along with the following requirement:

---

[1] Defined as 20 years after launch at greater than or equal to 99% probability, and 50 years after launch at greater than or equal to 95% probability.

<u>Case 1.</u> If the landing site is within the special region, the entire landed system shall be sterilized at least to the Viking post-sterilization biological burden levels.

<u>Case 2.</u> If the special region is accessed though horizontal or vertical mobility, either i) the entire landed system shall be sterilized to the Viking post-sterilization biological burden levels,

OR

ii) the subsystems which directly contact the special region shall be sterilized to these levels, and a method of preventing their recontamination prior to accessing the special region shall be provided.

It is worth noting that the NRC-PREVCOM committee also commented at length on Mars special regions. A parallel activity to this workshop, under the auspices of MEPAG (Mars Exploration Program Analysis Group), has studied and reported on the definition and interpretation of what constitutes a special region on Mars (2).

6. NRC-PREVCOM and the Potential Role of Molecular Technologies in Planetary Protection

It is widely accepted that perhaps only ~1% of the microorganisms present in an environment have been cultured, so if we are to gain a better understanding of the role that microbes play in any given environment, molecular methods of investigation will need to be developed and put into practice. For example, since the Viking period, a whole new domain of life, the archaea, has been added to the previously identified bacteria and eucarya, and with them the identification of a plethora of previously unknown metabolic pathways (42). For decades microbiologists and ecologists alike have battled with ''the great plate count anomaly,'' that is, how to go about culturing microbes from the environment while minimizing the inherent bias associated with using any one particular approach.

Molecular detection methods have revealed the presence of microbes on spacecraft and in associated environments that are (so far) not cultivable, confirming that the approaches taken to cultivate microbes from these samples were estimating only 10% of the real microbial diversity. Cloning based methods have shown more diverse populations in samples from both the spacecraft and facility than culture- dependent methods. This is reasonable since recovery of DNA fragments yields information from the total microbial population present, dead or alive, unlike culturing microorganisms that requires species-specific conditions for growth of only viable organisms. It has been shown that Q-PCR approaches can be used to detect and quantify "difficult to grow" microbial species once the organism is identified by use of molecular microbial diversity approaches (36). Thus molecular technologies can, theoretically at least, tell of the presence of any and all contaminating microbes, regardless of growth requirement, nutrient availability, syntrophy, or cellular health. These assays are particularly applicable for monitoring samples from environments with extremely low microbial burden.

The definition of what constitutes a habitable environment is therefore under continual review as microorganisms are found to be prospering in environments in which all previously known terrestrial organisms (including humans!) cannot survive. Thermophiles, psychrophiles, halophiles, acidophiles, alkalophiles and barophiles are representatives of such "extremophile" organisms. Thermophiles that can grow at a temperature above 110 °C have been discovered, psychrophiles that can grow at temperatures below freezing point, halophiles that can grow at a sodium chloride concentration above 30%, acidophiles that can grow at a pH below 1, and alkalophiles that can grow at a pH above 13 have been isolated, to name but a few (3, 13, 14, 22, 35). Lithotrophic microorganisms were detected in the deep subsurface of the Columbia River Basalts without any dependence on the surface biosphere (38). These "extreme" microorganisms grow in the deep subsurface of the earth, or in the craters of submarine volcanoes, or in ice cores, or in oil fields, or in deep mines. Some of them may even be able to make a living in an extra-terrestrial environment.

From a planetary protection perspective however, it is significant that these organisms are present not only in exotic locations, but that once their DNA sequences are isolated, they can be detected in environmental samples from diverse sources, sometimes including spacecraft assembly environments as in a recent study by Dekas & Venkateswaran (6). Here, microorganisms were collected from clean room surfaces at the Jet Propulsion

Laboratory, Kennedy Spaceflight Center, Lockheed Martin Astronautics, and Johnson Space Center. The approach used was to use an environmental selective pressure to select for the particular groups of organisms in the samples. One of either: UV-C irradiation, 5% hydrogen peroxide, heat shock (85ºC; 15 minutes), acidic (pH 3.0), alkaline (pH 11.0) or saline (25% sodium chloride) conditions were used, together with variation of incubation temperature (from 4ºC to 65ºC). Individual microbes capable of surviving each of these stresses were isolated and identified via 16S rDNA sequencing. Although previous studies (16, 17, 26) indicate that heat-shocked samples from spacecraft assembly facilities are dominated by species of *Bacillus*, this approach yielded a greater variety of microorganisms. Under non-selecting conditions these additional organisms are masked by more abundant variants. In the Dekas study, only 40% of the total microbes isolated were *Bacillus*. Additionally, the *Bacillaceae* retrieved were more physiologically diverse than those isolated in previous studies. They included thermophiles (*Geobacillus*), anaerobes (*Paenibacillus*), and a halotolerant, alkalophilic species (*Oceanobacillus*). Non-spore-forming microbes (α-, β-proteobacteria, actinobacteria) that showed tolerance to the selected stresses were also isolated and identified.

A further twist, as described by Moissl & Venkateswaran (24), is that the communities in different spacecraft environments were significantly different from each other, revealing only a small subset of microorganisms common to all locations (e.g. *Sphingomonas*, *Staphylococcus*). The JSC samples showed the highest diversity of microbes (esp. within the α-, γ- proteobacteria and Actinomycetes). The KSC community structure revealed a high presence of α-, γ- proteobacteria and Firmicutes, while the JPL sample showed a predominance of Firmicutes.

Phenomena of this type were recognized by the NRC-PREVCOM committee, and highlighted in their recommendations that newer technologies should be used to determine the "real" bioburden on a spacecraft. The use of a surrogate for the organisms most resistant to the sterilization processes for the spacecraft and the expected environmental conditions of the mission is no longer considered to be sufficient.

However, to implement a molecular-based assay technology for a 2016 mission (the NRC-PREVCOM target) will require a working assay system to be in place for a spacecraft build in the 2012 timeframe. Given that this will be a multi-year effort, there are only 5 years left (at the time of writing) until the validation needs to be completed. To give maximum opportunity of getting a working assay in time, the approach needs to be constrained to use existing available knowledge and technology.

7. The Current Knowledge and Technology Environment (2/28/06)

A series of presentations were received from among the participants to explore the spectrum of available technologies for application into the field of planetary protection:

7a. Cultivating the "uncultured" (Cathy Chang – Diversa Corp., San Diego, CA)
Diversa's technology platform draws on the combined advantages of natural and laboratory evolution to deliver innovative products to a number of markets. Through its proprietary integrated technology, Diversa taps into the largest genetic resource on the planet: microbial genomes. Through the use of patented DNA extraction and screening techniques, Diversa is able to access genetic material from uncultured microbes that account for over 99% of the Earth's untapped biodiversity.

Diversa's discovery program begins with access to biodiversity. Biodiversity can be defined as the total variety of life on earth, including genes, species, ecosystems and the complex interactions between them. Diversa collects small environmental samples containing heterogeneous populations of uncultured microbes from diverse ecosystems and extracts the genetic material from these organisms, eliminating the need to grow and maintain the organisms in cultures in the laboratory. Since small samples yield sufficient DNA, the impact on sensitive environments is minimized. The company has obtained samples from virtually all ecosystems represented on earth including such environments as: geothermal and hydrothermal vents, acidic soils and boiling mud pots, alkaline springs, marine and freshwater sediments, marine symbionts, manure piles, contaminated industrial sites, arctic tundra, dry Antarctic valleys, super cooled sea ice, microbial mats, bacterial communities associated with insects and nematodes, fungi and other plant endosymbionts.

Diversa has also developed a novel cultivation technology that combines encapsulation of cells in gel microdroplets for massively parallel microbial cultivation under low nutrient flux conditions, followed by flow cytometry to detect microdroplets containing microcolonies. Diversa'a technology to grow and study previously uncultured organisms in pure culture, as well as its metagenomics analysis and gene evolution tools can be applied in measuring the microbial diversity of oligotrophic environments such as spacecraft and its associated facilities.

7b. Environmental Metagenomics: Taking the Extreme out of the Environment
(Shannon Williamson – Craig Venter Res. Inst., Rockville, MD)
Diverse communities of Bacteria, Archaea, and eukaryotic protists account for more than 98 percent of the ocean's biomass. These microscopic factories - both aerobic and anaerobic - are the essential drivers for all of the chemical reactions within the biogeochemical cycles on Earth. Genomic tools have the potential to make significant impacts in the area of environmental monitoring; helping us to

better understand complex ecosystems as well as facilitating basic science discovery of new species in our oceans, soil and air.

In March 2004 the publication of a scientific paper in the journal Science detailed the results from genomic sequencing and analysis of samples collected from surface waters from the Sargasso Sea off the island of Bermuda (41). Using whole genome shotgun sequencing and high performance computational approaches developed to sequence the human genome; Venter researchers discovered at least 1,800 new species and more than 1.2 million new genes from the Sargasso Sea. The group continues to analyze the data collected as part of the Sorcerer II Global Ocean Sampling Expedition from over 100 sites around the globe.

Some of the technologies adapted by this institute are given below.

1. *Metagenomics*: the application of modern genomics techniques to the study of communities of microbial organisms directly in their natural environments, bypassing the need for isolation and lab cultivation of individual species.
2. *Large insert clone libraries:* Direct sequencing of Bacterial Artificial Chromosomes (BAC) and Fosmid clone libraries which can accommodate naked DNA approximately 100-300 kb and 40 kb in size respectively.
3. *Whole genome shotgun sequencing (small insert libraries):* Extracted DNA from environmental samples is sheared into small pieces (~2kb) prior to cloning. For low copy number samples, the starting material can be amplifed after a linker molecule is added to repaired ends prior to PCR amplification and gel purification (Linker Amplified Shotgun Libraries).
4. *Clone independent technology (454 sequencing):* This is the newest clone-independent technology in which the whole genomic DNA or fragments are immobilized onto beads and amplified in individual pico-titer plate wells. Sequencing is conducted on a Genome sequencer 20 instrument (454 Life Sciences; http://www.454.com/) and the reaction results in chemiluminescent signal detected by CCD camera. The advantage of this technology is that no cloning is needed to get about 20 million bases in 5 hours. However, the disadvantage is that it requires lots (relative to a spacecraft clean room) of DNA, typically 10μg.

7c. Using Microarrays to Explore Microbial Diversity (Gary Anderson – Department of Ecology, Lawrence Berkeley National Laboratory)
Molecular approaches aimed at broad microbial environmental detection routinely rely upon classifying heterogeneous nucleic acids amplified by universal 16S rDNA PCR. Cloning-and-sequencing the PCR products has been the general method of sampling DNA types but it does not scale well for large studies. Instead, hybridizing PCR products to a universal 16S rDNA microarray allows a more rapid evaluation. LBNL has developed a high-density microarray system to accurately measure the key microbial components in air, water, and soil environments. Unique regions of DNA within gene sequences of 16S small subunit of bacterial and archaeal ribosomes are used to identify specific

organisms. A minimum of 11 oligonucleotide probes (25-mers) are used in combination to identify, in parallel, any of over 9,000 distinctive species or taxa on a 500,000 probe, high-density microarray. The combinatorial approach of multiple probes has clear advantages over a single probe for the identification of a target sequence. Broad-range bacterial and archaeal 16S primers that target conserved areas at the 5' and 3' ends of the 16S rRNA gene are used to amplify 1400 – 1500bp (base pair) fragments for analysis.

This 16S microarray system was used to measure the microbial diversity of aerosols collected from a biosurveillance network, subsurface sediment contaminated with uranium, and deep subsurface water from a South African gold mine. In all cases, microbial diversity was greater than when measured by 16S rRNA gene clone library sequencing. As an example, the majority of sub-families documented by cloning aerosol amplicons were also detected in 4 of 4 replicate microarray hybridizations. Conversely, the array detected over double the number of sub-families than did the clone library. The phyla *Nitrospira* and *Spirochaetes* were uniquely detected by the array and were verified with specific PCR primers and subsequent amplicon sequencing. Changes in hybridization intensity of specific probe-sets in 17 consecutive weekly aerosol samples correlated well with quantitative (Q)-PCR results. Compared with sequencing a 16S rDNA clone library, the microarray was unable to recognize novel prokaryotic families but could identify greater diversity from organisms with similarity to existing sequence. Furthermore, the microarray allowed samples to be rapidly evaluated with replication.

7d. SOLiD Sequencing: A Gigabase per day tool for single molecule amplification and sequencing (Kevin McKernan – Agencourt Inc.)
Ligases have evolved as a pivotal DNA repair component performing discrete base excision repair operations (BER) in DNA repair pathways. This evolved behavior of Ligases has several significant distinctions from their nearest polymerase cousins. Ligases interrogate an 8bp region of DNA fidelity near the DNA junction (3bp on the 5' end and 5bp on the 3' end). Polymerases deploy extraordinary fidelity for a 1-4bp pocket at the active site which is 5' justified.

Polymerases also have evolved to perform multiple incorporations per locus whereas ligases perform a single operation per locus. These distinctions of ligases make them ideal candidates for novel reversible terminators, which can be utilized for massively parallel DNA or RNA sequencing. Agencourt has developed a ligation based DNA sequencing system capable of sequencing hundreds of millions of 20bp reads. The technique relies on the use of novel cleavable phosphorothiolate oligonucleotides, which can be utilized for highly accurate ligation and cleavage of DNA. To date, over 1 billion bases have been sequenced utilizing the technique and Agencourt are looking to improve the throughput to 1 - 4 billion bases per run in the next year. The benefit of this technique to metagenomics, chip on chip, gene expression, SNP typing and whole genome associations were described.

7e. Microbial Identification by Mass Cataloging (George Fox – Univ. Houston)
The large and ever-increasing 16S ribosomal RNA (rRNA) sequence data set from various bacteria has resulted in the widespread use of this molecule in molecular approaches to microbial identification and/or phylogenetic characterization. However, detection of a microorganism by one or more hybridization probes targeting unique 16S rRNA subsequences requires *a priori* knowledge of what one is seeking to find and therefore is limited in generality when assaying an unknown sample. To this end, researchers at the Univ. of Houston are developing an alternative approach based on the Matrix Assisted Laser Desorption/Ionization- Time Of Flight (MALDI-TOF) mass spectrometry. The essence of the idea is to digest a target nucleic acid such as a cloned 16S rRNA from an organism of interest with a nuclease of known specificity and then catalog all the mass peaks produced. A pair-wise comparison of the mass catalog of the unknown isolate with all members of an appropriate library of mass catalogs will allow construction of a distance or similarity matrix that can be used to determine the genetic affinity of the unknown. Like direct sequencing, mass catalogs are cumulative in that all previously determined catalogs can be used in the comparison step. In addition, the catalogs can be generated from known complete sequences without experimentation so the needed library is immediately available.

The approach has two apparent problems that must be addressed. First, because fragments that would be produced by RNAse T_1 digestion such as CCCCAG and CACCCG have the same composition, they by necessity have the same mass. There is therefore an inherent loss of information in the method. Investigators have conducted statistical studies of *in silico* digestions on known 16S rRNA sequences and determined that in the case of RNAse T_1 digestion, any fragment of length six or more is nevertheless informative. Sufficient numbers of fragments of length six and longer are produced by a 16S rRNA digestion that a proper identification can be obtained (44). The second difficulty stems from the fact that cytosine and uracil have nearly identical mass. Thus, RNAse T_1 fragments such as CCUCAG and CCCCAG would not be readily distinguished in a routine analysis. Therefore the Houston group has developed an experimental protocol in which one of the bases, e.g. uracil is replaced with an analog of different mass. In initial experimental studies, cloned 16S rRNAs from five phylogenetically distinct bacteria were analyzed and the organisms were in each case successfully identified. Ongoing work will be focused on improving the protocols and increasing the throughput rate.

It is expected that in the near future, if total 16S rRNA from a sample of interest is cloned, high throughput characterization of multiple samples (greater than 100 samples in parallel) will be feasible in less than 3 hours (less than 2 minutes per sample) using widely available instrumentation. However, the approach is not restricted to 16S rRNA as any cloned mRNA could be used. In addition, unlike sequencing, mass spectrometry has frequently been used in space. Miniaturized

MALDI-TOF instruments that might be used on the ISS or the moon are in fact currently under development by others. Finally, although not yet studied, it may be possible to use the approach to look for specific organisms of interest in a complex sample.

7f. The Viable but Nonculturable State in Bacteria and its Implications for Planetary Contamination (Jim Oliver – UNC at Charlotte)
Bacteria in the viable but nonculturable (VBNC) state fail to grow on the routine bacteriological media on which they would normally grow and develop into colonies, but are alive and capable of renewed metabolic activity. Cells in the VBNC state typically demonstrate very low levels of metabolic activity, but on resuscitation are again culturable. Since the original description of this phenomenon in 1982, over 400 papers have described various aspects of the phenomenon. A great many pathogens, as well as non-pathogens, are now known to enter this dormancy state. Its significance in medicine, bioremediation, the use of bacteria as fecal indicators, and indeed in most microbiological studies where culturability is employed as the (often sole) indicator of viability, is becoming increasingly evident.

Cells enter the VBNC state as a response to some form of natural stress, such as starvation, incubation outside the temperature range of growth, elevated osmotic concentrations (e.g. seawater), oxygen concentration, or exposure to white light. These typically are environmental stresses that might be lethal if the cells did not enter this dormancy state. Indeed, a number of studies have found that processes which are normally assumed to be bacteriocidal for bacteria may instead result in cells which reside in the VBNC state. These include such processes as pasteurization of milk and chlorination of wastewater.

Cells entering the VBNC state often exhibit dwarfing, and during this period a number of major metabolic changes occur, including reductions in nutrient transport, respiration rates, and macromolecular synthesis. Protein synthesis does not cease, however, and during this period novel starvation and cold shock proteins are formed. ATP levels, which decline rapidly in dead and moribund cells, have been found to remain high in VBNC cells. Further, recent studies have demonstrated continued gene expression by cells in the VBNC state. Extensive modifications in cytoplasmic membrane fatty acid composition that appear to be essential for entry into this state have been described, and these are likely necessary for the continued membrane potential which these cells exhibit. In what might be characteristic biochemical changes in the cell walls of VBNC cells, increases in cross-linking and unusual DAP-DAP cross-linking, an increase in muropeptides bearing covalently bound lipoprotein, and a shortening of the average length of glycan strands in comparison to exponentially growing cells have been documented. Genomic changes have also been suggested in several studies.

The reasons why cells enter this dormancy state are only now being elucidated. In the case of *Vibrio vulnificus*, low temperature results in a loss of catalase expression, which is essential for growth on routine microbiology media which contain significant levels of hydrogen peroxide. Several recent reviews from UNC discuss these and other aspects of the VBNC state (28-32). An interesting point for speculation is whether or not those bacteria which are routinely encountered in natural environments, and which have never been cultured, may in fact simply be VBNC cells for which resuscitation conditions have not yet been developed. As has been well documented by JPL scientists (16-18), such cells, which generally comprise 99+% of bacteria in the environment, also comprise the bulk of the organisms present on spacecraft hardware and assembly facility environments.

8. Sub-group Discussions (3/1/06)

a. Introduction

The participants were split into sub-groups to consider two approaches to microbial diversity measurements: live vs live/dead detection and qualitative vs quantitative measurement. The basis for these discussion topics was the trade between technical difficulty (which boils down to a cost differential) and the adequacy of a given approach to the planetary protection task.

In considering the first trade, it is generally the case that planetary protection is interested principally in organisms which can propagate on extra-terrestrial solar system bodies, and in the case of NRC PREVCOM, only the forward contamination of Mars. However, discrimination of DNA from live (potentially problematic) organisms from that of dead (inert) organisms is technically challenging.

In considering the second trade, historically planetary protection has concerned itself with a quantitative microbiology method as the gold standard (viable spores/unit area). However, is the total number of an organism present the best indicator of contamination risk? From a technology perspective, the quantitative approach is more challenging than qualitative presence/absence methods.

The discussions were constrained by the following additional guidelines provided by Dr Spry who acted as moderator:

- The sub-groups limited their discussion to nucleic acid-based technologies, since by comparison, available alternatives currently do not have either the same level of discrimination or technical maturity.
- The sub-groups were encouraged to consider only Bacteria and Archaea as targets, since these are the long-standing problem organisms in terms of likelihood of surviving interplanetary transfer. It is accepted that there are organisms such as black yeast (17) which could be problematic in a PP context.[2]
- The discussions were constrained to exclude viruses, because in theoretical terms viruses without hosts (which should be excluded from interplanetary transfer by PP interventions) do not replicate, and in practical terms because it is difficult to discriminate between viral nucleic acid from virus particles and from host cells with latent/inactive viral DNA present.

The intent here was to facilitate the sub-group groups to be productive in a limited time, rather than to stifle debate. Given more opportunity for discussion, additional recommendations for new work may have been forthcoming, though the cost of implementation will be correspondingly increased.

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[2]*Post-meeting note: In subsequent discussions with the NASA PPO, it was considered that a "full" genomic inventory of spacecraft should include a eukaryotic analysis*

b. Sub-group 1: Live vs Dead Approaches

Sub-group 1 was comprised of Dr. Tamas Torok (LBNL, Chair), Dr. Doug Bartlett (Scripps Inst. San Diego), Dr. Craig Carlson (UC Santa Barbara), Dr. Kevin McKernan (Agencourt Inc.), Dr Jim Oliver (UNC at Charlotte) and Dr. Kasthuri Venkateswaran (JPL). The goal of this group was to examine and prioritize approaches for the characterization of microbial communities of spacecraft and spacecraft assembly facilities in the context of the need or lack of need for live vs dead analyses.

There was an immediate consensus among the group members that no matter what approach NASA ultimately adopts, the genetic inventory must **include live and dead analysis of microorganisms**. Chemical analytical techniques are today already sensitive enough to detect nucleic acid or other biopolymer signals even at low levels. It is likely that technologies will advance in sensitivity and accuracy by the time NASA considers scientific methodologies to be employed during extraterrestrial sample return missions of the future.

Sub-group 1 members emphasized the paramount importance of **sampling** and indicated that developing novel sampling methods that enable the acquisition of more representative samples was the primary area of NASA's research needs. The current swab technique may only capture about 10% of the microorganisms from a sampled surface (and these are not necessarily representative of the total). Future sampling techniques not only have to be able to capture the microbial community structure at a reasonably higher fidelity but also cope with complicated architecture of the vehicles and the materials used. Microorganisms have an innate ability to persist in microscopic surface imperfections (37) and the group pointed out that sampling technologies should attempt to address this complication. While exposed spacecraft surfaces may experience very high temperatures and/or radiation during a mission, the shielded internal spaces along with mounting materials, greases, and lubricants represent habitats where microorganisms may be more protected from sterilizing conditions. Furthermore these internal or lubricated areas of the spacecraft are the most difficult to sample. Future sampling protocols also have to account for dead microorganisms, sub-cellular structures, and major polymers and macromolecules (*i.e.,* carbohydrates, lipids, nucleic acids, and proteins) whose signals may contribute to misinterpretations in NASA's search for extraterrestrial life.

Current planetary protection protocols for **bioburden determination** are based on international (COSPAR) guidelines and NASA policy. The methods currently employed are cultivation-based and determine the number of bacterial endospores present on a unit surface area. This type of bioburden determination has successfully reflected the change in the number of endospores in the samples following application of sterilization treatments and even allowed for the detection of novel radiation-resistant endospore-forming bacteria. However, these methods cannot account for the **actual bioburden present** and are certainly insufficient to provide the information needed for the proposed genetic inventory. In addition, they cannot efficiently resolve problems that arise from low microbial load samples.

Implementation of the proposed **genetic inventory** has a multitude of challenges.

- Sampling has already been mentioned above as being NASA's primary R&D need. Here the Sub-group 1 added the emphasis on **representative sample** collection in very **low biomass environments**. The main potential pitfall is a false positive signal from biopolymers of dead microorganisms. The group suggested that NASA may benefit from pharmaceutical and semiconductor industry experiences, which also had to face similar challenges.
- NASA spacecraft are being assembled in many facilities, and Sub-group 1 noted that it was important **to start the genetic inventory as early in the process as possible** integrating it into any quality assurance/quality control effort with respect to spacecraft materials, facilities, and people as they work in the facilities. Preliminary molecular-level investigation has shown that most of the detectible microbial signals collected in a Class 1000 assembly facility were of human origin.
- **Long-term studies** will be needed to asses the individual bioburden contribution of each component and determine how the oligotrophic environment of spacecraft assembly facilities exerts selective pressure on the microbial community.
- Given the increasingly complex architecture of spacecraft, it was recommended that placing and collecting **witness plates** in parallel with the entire spacecraft assembly process could provide a robust solution to bioburden prediction. It was also considered that mock spacecraft should be sampled and possibly sacrificed for proper bioburden estimation.
- There is no shortage of **nucleic acid extraction protocols** in the published literature. Nonetheless, there is no good method that is unbiased to the frequency of microbial species occurrence, lyse equally all types of cells, and **sensitive enough at the sub-picogram level.**
- Additional research is needed to determine the **survival of nucleic acids and other biopolymers** in the low nutrient, highly desiccated, spacecraft assembly environment given that the current sterilization measures are not designed to remove these molecules and thus false "life indicators" may persist.
- The genetic inventory program has to **archive** all samples efficiently and reproducibly whether the sample is comprised of nucleic acids, other biopolymers, or witness plates.

The predictably low biomass samples that will be collected for the genetic inventory need to be treated in a way that leads to a **representative and unbiased amplification of the genomic DNA** material prior to a high-throughput array analysis. Recently, a **phi29 DNA polymerase**-based amplification method that allows direct amplification of entire genomic DNA by isothermal multiple strand displacement (IMDA) has been described (5, 8, 19). Phi29 DNA polymerase is a highly processive enzyme that incorporates at least 70,000 nucleotides in one binding event and performs efficient strand displacement synthesis at a rate of 25 to 50 nucleotides/second with an error rate of 3×10^{-6}, which allows for high fidelity DNA replication. These two properties, strand displacement and processivity, allow phi29 DNA polymerase to be used in novel isothermal amplification strategies to amplify nanograms of genomic DNA into several micrograms. This method

holds promise for amplification of whole genomic DNA from samples as small as a single cell.

Although direct sequencing of environmental samples has provided valuable insight into the metabolic capabilities of uncultured organisms occupying various environmental niches, sequencing of individual large-insert bacterial artificial chromosome (BAC) clones or small-insert libraries made directly from environmental DNA has been challenging. Saturation, the necessary and sufficient number of clones to be sequenced to characterize a given microbial community, has been a problem. On the other hand, high-throughput shotgun sequencing environmental samples have recently provided global views of those communities not obtainable from 16S rRNA or BAC clone–sequencing surveys. Genome assembly also poses challenges. Complex communities demand enormous sequencing expenditure for the assembly of even the most predominant members. Additionally, recent comparisons have shown that DNA array analysis can detect more phylotypes or operational taxonomic units (OTU) (Gary Andersen, personal communication). Therefore, Sub-group 1 recommended that following genomic DNA extraction or whole genome amplification and target gene(s) amplification, **high-throughput DNA array analysis** could provide the microbial community structure information at the lowest cost. Several highly **conserved genes need to be considered** and targeted during the genetic inventory. Limiting this effort to the small subunit ribosomal RNA genes only would ultimately lack resolution power in spite of the wide availability of over 200,000 sequences already collected in public databases. To begin, a good example is a **custom designed Affymetrix microarray** which currently detects around 9,000 bacterial and archaeal OTU-specific sequences (7), and improvements in the algorithm could lead to the detection unidentified sequences. A combination of phi29 whole genome amplification and highly multiplexed single nucleotide polymorphism **BeadArray™ genotyping** was reported to have improved the feasibility and efficiency of mapping common disease susceptibility genes in humans (33). Certainly the latter technique could be employed to low biomass spacecraft surface and assembly facility samples. Sub-group 1 also discussed the possibility of using *RT-PCR* before the microarrays or **applying RNA directly** to the microarrays to avoid the strongly biasing step of PCR. As a further alternative, **determining the proteins encoded by a community**, rather than the types of organisms producing them could be considered to distinguish samples on the basis of the functions selected for by the local environment. This method has successfully revealed insights into features of several disparate microbial communities (39).

Sub-group 1 underlined that the proposed genetic inventory must not discourage simultaneous efforts to improve **microbial isolation and culturing** techniques. Experience teaches that functional genomics also result in more specific isolation and culturing efforts. Learning and understanding the genetic makeup of microorganisms often lead to designing more specific gene probes and novel media and cultivation conditions. Studies with “viable-but-not-culturable” (VBNC) organisms have revealed that culturing techniques can be improved. Once scientists grasp how microbial communities function and apply fewer artificial constraining conditions in the laboratory, the number of cultured microorganisms will most likely increase significantly. **Diversa’s**

approach to high-throughput culturing of a representative microbial community should be adapted to low nutrient conditions of the spacecraft assembly facilities. Culturing these representative species present on spacecraft surfaces and related materials, as well as in the assembly facilities is the prerequisite for survival studies and **true bioburden estimation**. Once "problematic" microorganisms are cultured, their microbial load reduction **treatment tolerance/resistance** can be determined. Furthermore, these same microorganisms can be tested in **mock experiments simulating Martian conditions** to determine if they present any real danger of surviving on Mars and contaminating the planet with terrestrial microorganisms. Sub-group 1 encouraged mutually beneficial collaboration with other disciplines at NASA so that the planetary protection researchers become familiar with the most recent scholarly knowledge about Mars and can adjust accordingly their model experiments. Culturing "problematic" organisms also opens the door to further experiments, such as to various imaging techniques, immunomagnetic separation, etc., to name a few, which one day may become novel tools of target microbe discrimination.

The organizers of the **MARGINS workshop** invited a well-balanced selection of academic and industrial researchers, who in turn reported on the **state-of-the-art of microbial community characterization**. The discussion pointed out many shortcomings, needs, and gaps in knowledge. There was complete agreement among the participants about the importance of MARGINS and the notion that a **minimalist approach must account for live and dead microorganisms**. Ultimately, the knowledge gained by MARGINS will ensure compliance with NASA's planetary protection goals both in designing the microbial load reduction treatments by knowing the most problematic microorganisms and in detecting, recording, and archiving the true bioburden. The participants agreed that **NASA's priority need is in sampling techniques/technologies**. As long as the current sampling method accounts for only approximately 10% of the microorganisms potentially present, without knowing the true bioburden and how it is represented in the collected sample, it is not practical to discuss the costs and benefits of an 80, 90, or 95% fidelity sampling. There was further agreement that **MARGINS and novel isolation and cultivation techniques are interdependent**. Their cross-fertilizing relationship is the second major area of NASA's R&D needs given the uniquely low biomass samples the program has to handle. It was suggested that some of the R&D be better accomplished in-house, such as sampling, phi29 whole genome amplification, archiving, etc., while other activities, such as basic research on problematic microorganisms originating from spacecraft and assembly facility environments should be opened up for academic and private industry competition.

c. Sub-group 2: Qualitative vs Quantitative Approaches

Sub-group 2 was comprised of Dr. Ronald Crawford (University of Idaho, Chair), Dr. Cathy Chang (Diversa), Dr. George Fox (University of Houston), Dr. Aaron Mills (University of Virginia), Dr. Shannon Williamson (Venter Institute), and Dr. David Newcombe (JPL). The goal of this group was to examine and prioritize approaches for characterizing microbial communities of spacecraft and spacecraft assembly facilities in the context of the need or lack of need for qualitative versus quantitative approaches. Qualitative approaches would involve characterizing the phylogenetic compositions of the communities, without determining the number of representatives within each operational taxonomic unit (OTU) observed. Quantitative approaches would both characterize the community composition and determine the numbers (percentage of total population) of cells of each OTU present. Both approaches would require that the total bioburden of the spacecraft or assembly facility be determined or estimated.

In addition to the task described above, Sub-group 2 also examined two scenarios. The first would be a minimal approach to address the goals of protection of Mars from contamination by terrestrial microorganisms (Method 1). The second was an approach that would be more robust than the minimal scenario, irrespective of cost, and provide more information for in depth scientific inquiry (Method 2).

CONCLUSIONS

The conclusions of Sub-group 2, described as Methods 1 and 2, are as follows.

Qualitative versus Quantitative: The group first concluded that **qualitative approaches will be sufficient** for the goals of protection of Mars from forward contamination by spacecraft-associated microorganisms, while decreasing costs and increasing the ability to automate characterization methods. The logic behind this recommendation is that the dominant organisms present on a spacecraft may not be the ones that have the highest likelihood of surviving or proliferating in the martian environment. Low-abundance members of the spacecraft microbiota are also candidates as “problem” microbes. Since one or a few cells have the potential for being detected by life-detection experiments aboard a lander and also would have the potential for growth if landed in a hospitable environment, absolute numbers of each OTU present would not be crucial knowledge for protection of Mars from forward contamination.

Bioburden Determinations: Sub-group 2 recognized that it **may always be necessary to determine or accurately estimate the total bioburden on spacecraft** prior to launch, since this is a COSPAR planetary protection requirement. It was recommended that this be accomplished by use of sacrificial **witness plates and/or mock spacecraft** located at all spacecraft assembly facilities. The use of mock spacecraft will allow the determination of bioburden associated with inaccessible areas that could not be sampled by standard swabbing techniques. Also, use of witness plates will allow more rigorous sampling protocols (e.g., extraction of cells or biomolecules with methodologies not

acceptable to spacecraft engineers for flight hardware, for example strong bases or detergents). NASA needs to support research on and validation of biomarker analysis techniques that might be used with these sacrificial substrates. Such methods could include the use of biomolecular markers (e.g., ATP, LPS, or nucleic acids; (16, 40) or collection and concentration of cells for counting by direct microscopic methods or automated methods such as flow cytometry (15, 20).

Method 1 (minimal): *PCR-based Amplification of Microbial Biomarkers of Community Composition and Diversity* (16S RNA genes, 23S RNA genes, ITS, *rec*A, possibly others). Within this method there would be options for different levels of fidelity (completeness of the inventory of OTUs present) of characterization of the microbiota. The minimally acceptable level of fidelity (~80% of total taxa identified) would be attainable through characterization of 16S rRNA gene libraries using a sequence similarity of 97% homology as the definition of an OTU (5). The acknowledged limitations and biases of PCR in the generation of these libraries would need to be addressed and minimized (12). A second, more desirable level of fidelity (~90% of taxa identified) would be accomplished by the use of additional phylogenetic markers (16S, 23S, ITS, *rec*A, etc) while employing multiple primers sets for each (11). The ultimate goal would be near complete fidelity (>90% taxa identified) and might be accomplished by using in combination with the molecular methods discussed above new, high-throughput cultivation techniques (10, 43) and improved sampling methods to allow observation of representatives of low-frequency taxa that might be missed by molecular methods. Ideally, all three fidelity-level options would be compared to each other to determine which approach is most satisfactory for purposes of planetary protection. As a high priority, NASA should support research and validation of PCR-based amplification of microbial biomarkers of community composition and novel high-throughput cultivation techniques as a means to determine with high fidelity and with rigorously statistically analyzed data (e.g., rarefaction) the diversity of microorganisms on spacecraft and within spacecraft assembly facilities.

Method 2 (optimal): *Metagenomic Approach in Combination with Whole Genome Amplification (WGA) to Asses both Phylogenetic and Functional Genetic Markers.* Here the "metagenome" is defined as DNA obtained from the whole microbial community of a spacecraft or areas within a spacecraft assembly facility, using (as described above) sacrificial witness plates and/or mock spacecraft located at all spacecraft assembly facilities as sources of DNA. WGA is a technique that allows the amplification of DNA using phi29 polymerase in conjunction with exonuclease-resistant random hexamer primers to isothermally amplify DNA 10^4 to 10^6-fold with minimal bias from low-biomass communities such as those found on spacecraft or within spacecraft assembly facilities (21). The metagenomic approach would be of very high fidelity, since essentially all of the DNA obtained in samples could be examined. The level of fidelity in assessing the overall diversity of the communities being examined would increase with the depth of sequencing of the metagenome. The depth of sequencing would need to increase with the diversity observed. It is conceivable that with the rapidly improving capabilities in high-throughput sequencing of DNA at the level of billions of base pairs in a few hours (23), that the sequencing of metagenomic DNA by 2016 may be less

expensive than the traditional community characterization methods described in Method 1. NASA should support research and validation of metagenomic-based approaches for analysis of diversity of microorganisms on spacecraft and within spacecraft assembly facilities.

RECOMMENDATIONS

- **Qualitative approaches will be sufficient** for the goal of establishing a genetic inventory of terrestrial DNA on Mars from forward contamination by spacecraft-associated microorganisms.

- NASA should support research on and validation of biomarker analysis techniques to be used with sacrificial substrates to **characterize the total bioburden** on spacecraft and in spacecraft assembly facilities.

- NASA should support **research and validation of PCR-based amplification** of microbial biomarkers of community composition (16S RNA genes, 23S RNA genes, ITS, *rec*A, possibly others) and novel high-throughput cultivation techniques as a means to determine with high fidelity and with statistic rigor the diversity of microorganisms on spacecraft and within spacecraft assembly facilities.

- NASA should support **research and validation of metagenomic-based approaches** for analysis of diversity of microorganisms on spacecraft and within spacecraft assembly facilities.

9. Conclusions and Recommendations

At the highest level, the group concurred with the NRC-PREVCOM recommendation that use of molecular markers to obtain information about the genetic diversity of a spacecraft was appropriate in the context of planetary protection. Further, it was also agreed that the use of molecular biology techniques was appropriate and that the maturity of technologies such as DNA sequencing and polymerase-based amplification would realistically permit development of an assay system at reasonable cost in the timeframe to 2016 (the target date identified by NRC-PREVCOM).

As described, two areas of discussion were specifically highlighted to examine different technology options. In each case, the choice was presented as being between an expensive, complex, risky, but "ideal" solution, compared to a less risky approach of lower but adequate technical merit.

In the first case, DNA sampling (live + dead) was compared to RNA sampling (live only, since RNA from dead cells is quickly degraded). The fragility of RNA makes it much more challenging to work with, though in the context of planetary protection, only live organisms are a problem from the perspective of proliferation risk. However, the group reasoned that just because an organism in the sample is dead, it does not mean that the same organism may not occur (live) elsewhere on the spacecraft. Conservatively, if the DNA from an organism is detected, then that organism can be presumed to be present on the spacecraft. It is not necessary to prove whether the one in the sample is alive or not.

In the second case, PCR of DNA samples (qualitative) was compared to QPCR (Quantitative PCR) of DNA samples (quantitative, since the amount of nucleic acid is proportional to the number of cells present). QPCR is well known to be a "temperamental" technology, though in a planetary protection context, knowledge of the number of each type of organism present would be the ideal situation. However, the group reasoned that abundance is not the only indicator of risk in this assay – it is the ability of each type of organisms to survive in the target environment that is the problem from the perspective of proliferation risk. Additionally, in the DNA-based approach proposed below, relative abundance of sequences will be an indicator of relative (rather than absolute) abundance of each species, and hence the method can be made to be semi-quantitative in any case.

From all these discussions, the following recommendation arises:

A nucleic acid-based assay system, which includes effective removal of biomarker from surfaces, enabling amplification and analysis of the targeted molecule is recommended for the genomic inventory of Mars spacecraft by MARGINS workgroup.

Details of proposed research to achieve this are given below:

- **Selection of suitable sampling technology:**
  - Should extract nucleic acid but accommodate dead microbes, sub-cellular structures, major polymers and macromolecules (i.e., carbohydrates, lipids, and proteins) as contaminants in the sample
  - Should exploit the existing technology/protocols in semi-conductor, pharmaceutical and other industries, if available
  - Must support the use of witness plates along the entire spacecraft assembly process to collect representative materials
  - Must allow reliable, reproducible collection of representative samples containing sub-picogram levels of DNA

- **Sample preparation and processing:**
  - Optimize nucleic acids extraction procedure that is reliable, reproducible and sensitive enough at the sub-picogram level
  - Develop automated extraction protocol using available technology to avoid operator variability
  - Use one of: *phi*29 DNA polymerase-based amplification to achieve representative and unbiased amplification of the genomic DNA material prior to a high-throughput array analysis, OR RT-PCR before the microarrays OR applying RNA directly to the microarrays to avoid the strongly biasing step of PCR

- **Archiving:**
  - Identification, adoption and appropriate optimization of protocols to preserve nucleic acids, other biopolymers, and/or intact "witness plate" materials

- **Genomic inventory assays:**
  - *Conventional cloning and sequencing*: PCR-based amplification targeting 16S RNA genes to measure the microbial diversity
  - *Metagenomics:* The *phi*29 amplification followed by BAC cloning, and probing for phylogenetic (16S rRNA) and functional genomic markers (problematic microbes; target specific genes such as sporulation, resistance to sterilization regime, survival under oligotrophy, etc.)
  - *DNA microarray*: Custom designed Affymetrix-type microarray described by DeSantis et al. (7) configured specifically for PP, based on the outputs of conventional 16S work and the broader metagenomic work

- **Other genomic inventory assays:**

The following yet-to-be proven assays can be considered when technological maturity and scientific need can be justified.

  - *Whole genome shotgun sequencing (small insert libraries):* Extracted DNA from environmental samples is sheared into small pieces (~2kb)

prior to cloning. For low copy number samples, the starting material can be amplified after a linker molecule is added to repaired ends prior to PCR amplification and gel purification (Linker Amplified Shotgun Libraries; (34).

- *BeadArray™ genotyping*: Combination of *phi*29 whole genome amplification and highly multiplexed single nucleotide polymorphism *BeadArray™ genotyping* described by Pask et al. (33) and at http://www.illumina.com/General/pdf/BEADREADER_DATASHEET_FINAL_0304.pdf

- **Microbial isolation and culturing techniques for subsequent analysis:**
  - *Diversa's approach* to culture so far uncultured [or similar] should be utilized for cultivation and characterization of "problematic" organisms (organisms [if found] showing multi-resistant characteristics) using imaging techniques, immunomagnetic separation, etc.

It is expected that some of the R&D tasks are best accomplished with strong NASA involvement (with appropriate partnering) to allow access to samples, in particular the spacecraft hardware sampling itself, resulting phi29 whole genome amplification and the archiving elements.
However, fundamental research on problematic microorganisms originating from spacecraft and spacecraft assembly facilities should be opened up for academic and private industry to bid for funding.

From these needs and approaches, the Roadmap below (Fig 9.1) is proposed by the authors as an appropriate way forward in the scope of the discussions held:

Figure 9.1:

MARGINS Roadmap: Genetic Inventory of Microbes from the Spacecraft and Associated Environments based on 16S rDNA and other Markers

Tasks	FY07	FY08	FY09	FY10	FY11	FY12
Collection of Samples	←	—	—	—	—	→
Develop sampling methodology for spacecraft and associated surfaces						
Develop sampling methodology for spacecraft assembly facilities						
Introducing established preservation technologies for DNA samples						
Sampling several NASA spacecraft assembly facilities & environs						
Sampling spacecraft sub-assembly systems						
Sampling spacecraft mission hardware (Phoenix, MSL, Scout 11, MSO)						
Cataloguing microbial diversity using conventional cloning and sequencing	←	—	—	—	—	→
Prokaryotic diversity 16S(bacteria and archaea)						
Spore-forming microbes 16S(aerobic and anaerobic)						
Non spore-forming microbes 16S(aerobic and anaerobic)						
Expansion to other Markers						
Characterization of non-cultivable microbial diversity		←	—	—	—	→
PCR -unbiased approach						
Viable but non-cultivable microbes						
Microbial diversity of "problematic" microbes that could thrive under specific conditions						

10. Appendix A: Pre-Workshop Genetic Inventory guidance from the NASA PPO (a telecon with Dr Spry)

1 JAS: What's your view on whether we should look at Live vs Live+Dead (is the purpose for historical record or as an indicator of risk)
JR: 1st step is to look for what is represented. Ideal is to look at what is live, and therefore a risk, but the technology may mean that has to come after.

2 JAS: What's your view on whether we should look at Quantitative vs Qualitative (do we only need to know what is there, or how many there are of them as well).
JR: We should endeavor to do both. We need to know what is there, although how much is there (and whether it is alive) could be measured by different methods – i.e. not nucleic acid based methods.

3 JAS: Do you have any preferred technology approach (analysis based on DNA/RNA/other, which target gene - related to 1 and 2 above)
JR: Nucleic acids are the obvious choice. Other methods e.g. White's membrane based technology can't really compete yet.

4 Statistical discussion
JAS: Should we be looking at spacecraft hardware only or choosing and analvzing representative environments (cleanroom, witness plates)?
What is the level of sampling anticipated (cf NHB5340-like approaches)?
What is an acceptable % of population present to be detected for an approach to be considered useful?
JR: Guide should be "When does increased effort in sampling stop paying off?" Compare to Cindy van Dover's work on ecology of thermal vents – when does an extra sample not give you any new bugs?
The ideal is to understand the spacecraft. Even then, the spacecraft itself might have different populations on different areas. There may be a limitation to how much of the spacecraft can be sampled. If the spacecraft is so well sampled that all the organisms are removed, that would be good, but unlikely. Therefore need to understand the relationship between the spacecraft and the environment around the spacecraft.

5 JAS: Is there a notional cost cap, which will make certain approaches off-limits (*more is in vain when less will serve*)? Should we be driven by 1 thru 4 at this stage?
JR: There is not a cost cap. There is a degree of overspecification that will not be funded.

11. Abbreviations and acronyms

ATLO	Assembly test and launch operations
ATP	Adenosine triphosphate
BAC	Bacterial artificial chromosome
BER	Base excision repair
bp	Base pair (of nucleic acid)
COSPAR	Committee of Space Research
DNA	Deoxyribonucleic acid
IMDA	Isothermal multiple strand displacement
ISS	International Space Station
ITS	Internal transcribed spacer
JPL	Jet Propulsion Laboratory
JSC	Johnson Space Center
KSC	Kennedy Space Center
LBNL	Lawrence Berkeley National Laboratory
MALDI-TOF	Matrix assisted laser desorbtion/ionization – time of flight (mass spectrometry)
MARGINS	Mars Genetic Inventory of Spacecraft
MEPAG	Mars Exploration Program Analysis Group
mRNA	Messenger ribonucleic acid
NASA	National Aeronautics and Space Administration
NRC	National Research Councils
OTU	Operational taxonomic unit
PCR	Polymerase chain reaction
PP	Planetary protection
PPO	Planetary Protection Officer (NASA)
PREVCOM	Prevention of the Forward Contamination of Mars (NRC sub-committee)
QPCR	Quantitative PCR
rDNA	Ribosomal deoxyribonucleic acid
rRNA	Ribosomal ribonucleic acid
RT-PCR	Reverse transcriptase PCR
SNP	Single nucleotide polymorphism
VBNC	Viable but non-culturable
WGA	Whole genome amplification

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1. Title Page

Report of the Genetic Inventory of Spacecraft and Associated Environments

Workshop held at

Jet Propulsion Laboratory

on

September 30th and Oct 1st 2009

Publication Date: April 30, 2010

Editors: Myron T. La Duc, J. Andy Spry, and Kasthuri Venkateswaran

2. Opening information about team and citation instructions

This workshop was hosted by JPL's Mars Program Office, with participants invited from a broad spectrum of fields related to genetic diversity and planetary protection, with the aim of achieving a balanced and objective discussion.

Participant	Affiliation	Specialty
Gary Andersen	LBNL	Biogeomicrobiology/Technology
Todd DeSantis	LBNL	Bioinformatics
Mitch Sogin	MBL	Microbial diversity/Deep Sea Biology
Sue Huse	MBL	Bioinformatics
Cassie Conley	HQ	Planetary Protection
Mary Voytek	HQ	Astrobiology
Tamas Torok	LNBL	Mycology
Ron Crawford	Univ. of Idaho	Microbial Physiology/Bioremediation
George Fox	Univ. Houston	Microbial Identification by Mass Cataloging
Pat Schloss	UMass-Amherst	Bioinformatics
Joseph Petrosino	Baylor College of Medicine	Human Genome Sequencing
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This report can be cited as JPL Document D-65828, Report of the Mars Genetic Inventory of Spacecraft Workshop (2010), Jet Propulsion Laboratory, Pasadena CA.

3. Executive Summary and Key Findings

This report presents the findings of a workshop held over two days in which invited science and technology experts from industry, academia and government laboratories met to hear an update on progress since the first Genetic Inventory workshop in 2006. Recommendations in regards to the correct way in which proceed in implementing a genetic inventory for Mars spacecraft were voiced and openly discussed. The goal of this workshop was to assess whether or not the JPL Genetic Inventory research team has acquired enough of the necessary capabilities over the past few years to deliver an end-to-end analysis process. And if not, the workshop had a second goal of identifying other sufficiently mature technologies that could be considered to elucidate the microbial diversity of spacecraft and associated environments.

Overall, there was a general consensus that target molecules (e.g., 16S rRNA gene) are not being collected in great enough abundance to render much of the downstream molecular processing and analysis significant and/or reproducible. Experts agreed that efforts should be made to concentrate samples since PCR-dependent techniques generally require ca. 10^3 initial copies of the target per reaction to reproducibly assess microbial diversity. Although theoretical calculations posit the need for as low as one copy of a given target molecule, signal to noise ratios demand that target molecules exist in excess of 10^3 copy numbers (due to indigenous DNA in reagents and sampling materials). Ultimately, the workshop committee agreed that optimizing sample collection is critical and hasn't received enough attention. Up until now the GI-team has focused their efforts and energies on the analysis aspect of this project. The team has now been advised to shift emphasis towards sample collection and processing.

A majority of the workshop participants endorsed the PhyloChip technology as being the best available technology for planetary protection research and implementation needs, while 454-Tag sequencing may require significant optimization to circumvent a great deal of noise when working with low-biomass samples. However, experts versed in the practices of the Human Microbiome Project, whose samples are always extremely rich in target molecules, lent support to 454-Tag sequencing and suggested that this technology is evolving rapidly and may be closer to being able to fulfill PP needs than was once thought.

4. Introduction

Planetary protection efforts work towards protecting a) solar system bodies from contamination by terrestrial biological material (forward contamination), thus preserving opportunities for future scientific investigation, and b) the Earth from harmful contamination by materials returned from outer space (back contamination) (COSPAR, 2002). These COSPAR recommended efforts apply directly to the control and eradication of microorganisms present on the surfaces of spacecraft intended to land, orbit, fly-by, or be in the vicinity of extraterrestrial bodies. Consequently, current planetary protection policies require that most planetary spacecraft be assembled and readied for launch in controlled cleanroom environments. Much like facilities in the medical, pharmaceutical, and semiconductor sectors, NASA spacecraft assembly cleanrooms (SAC) are kept extremely clean and are maintained to the relevant industry standards (ISO). Filtered air circulation, controlled temperature and humidity, routine exposure to disinfectants and surfactants, and nutrient-limiting, oligotrophic conditions make it very challenging for microorganisms to persist in such environments, but do not eradicate biological contaminants entirely (La Duc, Dekas, Osman *et al.*, 2007). Several investigations, both culture based and culture independent, have demonstrated that a variety of bacterial taxa are repeatedly isolated under cleanroom conditions (La Duc, Dekas, Osman, Moissl, Newcombe & Venkateswaran, 2007, Moissl, Bruckner & Venkateswaran, 2008, Moissl, La Duc, Osman *et al.*, 2007, Vaishampayan, Osman, Andersen *et al.*, 2009). However, despite a growing understanding of the diverse microbial populations present in SAC, predicting the true risk of any such microbes compromising the findings of extraterrestrial life-detection efforts remains a significant challenge (Rummel, 2001). A better understanding of the distribution and frequency at which contaminant microbes are encountered on spacecraft surfaces would significantly aid in assessing the threat of forward contamination (Space Science Board & National Research Council, 1992).

In 2005, the National Research Council's Space Studies Board task force presented its draft advice to NASA in Preventing the Forward Contamination of Mars (PREVCOM) (NRC, 2006). The NRC-PREVCOM report, which included 17 recommendations, embraced the concept of updating the technological approach to the study of organisms on spacecraft to include newer technologies than are in current use for planetary protection. Specifically relevant to this workshop's task, recommendation 5 stated that:

> *"NASA should require the routine collection of phylogenetic data to a statistically appropriate level to ensure that the microbial diversity of assembly, test, and launch operations (ATLO) environments, and of all of NASA spacecraft to be sent to Mars, is reliably assessed. NASA should also require the systematic archiving of environmental samples for ATLO environments and for all spacecraft to be sent to Mars"*

Intended use of this document

To fulfill its objectives, this document will be delivered to the Mars Program Office at JPL and made available for the purpose of program planning, proposal generation and evaluation, and planetary protection policy support. Ultimately, it is the intention of the workshop organizers that the information and opinions expressed herein should lead to either an endorsement or redirection of the present Mars Program-funded Genetic Inventory task.

History of the "Genetic Inventory" Project

In Spring of 2005 the Mars Program Office at JPL held informal discussions with the NASA-PPO about the value of creating a capability to inventory spacecraft contaminants via a genetics-based approach. Subsequently, the MPO studied options to create such a capability and in March 2006

held the first workshop regarding this venture (JPL-D-35346, 2006). At the first workshop, experts from industry, academia, and national laboratories worked with the MPO to evaluate the options for a genetics-based approach. They endorsed the importance of developing a means of elucidating the complete spectrum of microbial diversity associated with spacecraft and associated surfaces and provided their recommendations. In June of 2006 further discussions with the NASA PPO and Dr. J. Joyce reflected on the workshop recommendations and refined ideas for how to proceed, leading to the eventual onset of the Genetic Inventory Task (October 2006).

Minutes of Workshop-1 (MarGInS):

At the first workshop it was imperative to chart a straightforward course with input from a broad group of experts. Much of the planning hinged on the response of the panel to two essential queries: 1) Should researchers work to detect both live & dead microbes, or live only, and 2) should approaches work towards a qualitative result, or quantitative as well? It was recommended that the GI project focus its efforts on a complete inventory of microbes, both living and dead. Such an approach would make the inventory conservative, having a much more tractable outcome (implicit conclusion—DNA analysis is good enough; more challenging RNA approaches are not needed). Furthermore, it was decided that while a quantitative inventory would be ideal, a qualitative inventory would be sufficient.

Plans for the Genetic Inventory study since FY'06

The initial plan for this work consisted of a 5-year period of performance having a final "delivery" of a capability to thoroughly elucidate the genetic inventory of microbes on spacecraft and associated surfaces by Fall, 2011. However, the future mission set changed and the available budget provided was less than anticipated. This meant the research activity was extended, but the goals and objectives remained relevant for future missions. At the time of the second workshop, the Genetic Inventory project wasessentially at the halfway point, and discussions held at this second workshop once again attempted to answer two key questions: 1) what technologies are required to ensure the characterization of the widest possible spectrum of terrestrial microflora, and 2) how can we best deal with challenges resulting from the gaps in current technologies?

GI-task progress since FY'06:

Key results of the GI-project have been published in two peer-reviewed publications (see Appendix). Topics covered in these communications include the efficiency and efficacy of varying sample processing technologies, and the use of the state-of-the art molecular technologies to analyze low biomass samples.

The purification of nucleic acids, subsequent PCR amplification, and transfer of 16S ribosomal "fingerprint" genes from non-cultivable microorganisms into genetically amenable lab strains of *E. coli* has evolved into a "gold standard" molecular means of elucidating the microbial diversity in a given sample. This is commonly referred to as cloning. In theory, the cloning and sequencing of 16S ribosomal genes from each and every cell present, regardless of cultivability and inclusive of novel taxa, would result in a comprehensive survey of microbial communities about the surfaces of SAC and co-located spacecraft (Moissl, Bruckner & Venkateswaran, 2008, Moissl, La Duc, Osman, Dekas & Venkateswaran, 2007). Unfortunately, full length sequencing of all 16S rRNA genes from environmental samples would be prohibitively expensive, making the approach unfeasible for generating comprehensive phylogenetic profiles of complex microbial communities.

Attempting to infer population membership from clone libraries limited to hundreds or thousands of sequences has proven to be insufficient for detecting low abundance organisms. Recent analyses of

phylogenetic DNA extracted from soil, water and air revealed that clone libraries severely under-represent complex bacterial communities when compared to very rapid (i.e., hours) DNA microarray approaches (Bergogne-Berezin & Joly-Guillou, 1985, Cruz-Martinez, Suttle, Brodie *et al.*, 2009, Flanagan, Brodie, Weng *et al.*, 2007, Ludwig, Strunk, Westram *et al.*, 2004, Yergeau, Schoondermark-Stolk, Brodie *et al.*, 2009). One of the reasons for this is the high sensitivity of PhyloChip methodologies, which are able to detect organisms present in amounts below 10^{-4} abundance of the total sample (Fodor, Read, Pirrung *et al.*, 1991). Numerous validation experiments using sequence-specific PCR have confirmed that taxa identified by the microarray were indeed present in the original environmental samples, despite their absence in corresponding clone libraries (Brodie, DeSantis, Parker *et al.*, 2007). This highlights the utility of the method compared to classical cloning. While each sample analysis by the PhyloChip provides detailed information on microbial composition, the highly parallel and reproducible nature of this array also allows tracking community dynamics over time and treatment. With no prior knowledge, specific microbial interactions may be identified that are key to particular changing environments.

A comprehensive census of the microbial communities present on the surfaces of three NASA SAC supporting two different flight missions was conducted. To ensure that the maximum diversity of resident microbiota was uncovered, subsamples from each cleanroom surface sampling were subjected to both DNA microarray protocols and conventional cloning and sequencing of 16S rRNA genes. This study, to our knowledge the first of its kind, focused on comparing the microbial diversity profiles resulting from DNA microarray analyses and conventional cloning and sequencing of 16S rRNA genes arising from a variety of low biomass surfaces.

In October of 2009 a second workshop was convened to assess the progress of the Genetic Inventory effort to date and to take stock of new perspectives and current and future direction options. That workshop is documented in this report.

Goal of Workshop-2: The goal of this workshop was to assess whether or not the JPL Genetic Inventory research team has acquired enough of the necessary capabilities over the past few years to adequately address an end-to-end analysis process. If not, it was a further goal to identify any candidate technologies mature enough to be used to appropriately elucidate the microbial diversity of spacecraft and associated environments.

Technology gaps identified/discussed:

Sampling. There was a general consensus that efforts should be made to enhance the recovery of target molecules (e.g., 16S rRNA gene). There are significant losses observed in extracting these molecules from samples, and PCR-dependent techniques require 10^3 copies of target molecules to yield reproducible measures of microbial diversity. Furthermore, signal to noise ratios preclude the detection of target molecules below a threshold of 10^3 copy numbers (due to indigenous DNA in reagents and sampling materials). The committee agreed that optimizing sample collection is critical and hasn't received enough attention. Notwithstanding the recommendations stemming from the first workshop, the GI-team was encouraged to focus their efforts and energies on the analysis aspect of this project. The team has now been encouraged to shift its emphasis towards sample collection and processing.

Pooling of samples. The pooling of multiple samples was discouraged by some participants because pooling obscures the patchy distribution of biomatter in a given environment.

However, such a concern is only relevant when and if the GI-team is indeed interested in the heterogeneity of distribution of microbial diversity on a given surface or in a given environment.

Sample consistency and proportion. It was recommended that the GI-team make every effort to keep samples proportionate to one another in every way possible (surface area sampled, sample volume, etc.), to allow direct comparison.

Collection and incorporation of metadata. It was advised that the GI-team collect as much metadata as possible whenever samples are collected. The development of a user-friendly, queriable database to facilitate this need is important.

Sampling instrumentation. There are no recommended specific sampling devices to fill the gaps that persist. However, the recovery of the target molecules from surfaces, as well as the loss of DNA associated with adherence to sampling materials need to be investigated in greater depth.

Collection of samples. Other approaches to sampling should be investigated alongside direct abrasive methods. HEPA filters and/or vacuum filters should be tested and evaluated as sources. In addition, samples collected with air sampling devices such as the Evogen Omni 3000 should be analyzed. Whole genome approaches should also be tested, and their ability to produce an unbiased increase of initial target molecules should be assessed.

ESA. Flocked-nylon swabs are preferred to cotton or polyester swabs by ESA for surface sampling. NASA will test these materials and compare recovery efficiencies.

Sample processing.

The GI-team was advised to continue its current practice of washing the BiSKit sampling kits three times to increase the recovery of target biomolecules. Hence, the team will continue to wash each sampling module three times and subsequently concentrate the product.

Concentration of samples. The committee endorsed the GI team's current method of liquid samples of large volumes with 50-KDa molecular weight cut-off Amicon filters (~500 uL). This facilitates the removal of most DNases and other enzymes capable of degrading target nucleic acids. Whenever possible, DNA extraction should be conducted immediately following the concentration of target molecules. When this is not feasible, concentration should be employed prior to freezing to remove extracellular enzymes.

Bead-beating. Apparently, using various speeds of bead-beating increases the ability to extract the maximum possible diversity, as was expressed by expert workshop participants The GI team agreed to consider how to make use of this knowledge. For very low-biomass samples, additional partitioning and bead-beating conditions may in fact be counterproductive if additional DNA loss would occur as a side effect. In a previous research communication, the GI-team demonstrated the retrieval of differential microbial diversity with and without bead-beating. For now, the GI-team will preface the Maxwell automated DNA extraction step with a single bead-beating regime (La Duc, Osman & Venkateswaran, 2009).

220 **DNA extraction**. Pat Schloss recommended that the GI-team avoid using kits that employ filters
221 since nucleic acids easily adhere to the filters, thus rendering the recovery of these biomolecules
222 extremely cumbersome. The automated method currently employed was endorsed, and the
223 committee cautioned the GI team to avoid dependence on a single manufacturer and/or
224 supplier of consumables whenever possible. The GI-team was advised to discontinue using the
225 nanodrop instrument to assess DNA concentrations (pre- and post-extraction), and the superior,
226 fluorescent-based Qubit instrument was suggested instead.

227 **PCR**. Current levels of lab-cleaning and maintenance practices were considered to be
228 appropriate and must continue to be employed. This includes the use of biohoods, UV lights
229 prior to hood usage, and dedicated bench space for PCR work up. The use of respiratory masks
230 was also recommended. The GI-team is not currently using masks, but will evaluate the "pros-
231 and cons" of these as an additional contamination control option. The GI/BPPG team has
232 already initiated dialogue with JPL facilities personnel to construct an enclosed and controlled
233 "semi-clean room" to this effect. The committee stressed the importance of negative and
234 positive controls, and a constant monitoring of signal to noise ratios.

235 **PCR-bias**. The committee agreed that PCR is an unavoidable necessity as samples are so
236 extremely limited in biomatter. Care should be taken to minimize and understand PCR-related
237 biases. Options to reduce PCR bias include conducting PCR reactions at nanoliter scales, using
238 high fidelity DNA polymerases, when possible employing emulsion PCR, minimizing the amount
239 of Taq polymerase used, and so on. An approach that eliminates PCR and its inherent biases
240 would be ideal, but no such capability exists.

241 **Sample analysis**. Prof. R. Crawford of the Univ of Idaho vocalized that the "PhyloChip is the best
242 available technology for planetary protection issues," and several participants thought that 454-Tag
243 sequencing was not mature and was overly expensive. Based on results stemming from the Human
244 Microbiome Project being conducted at the Baylor College of Medicine, Dr. J. Petrosino said that 454-
245 Tag sequencing is closer to being mature enough for PP needs than many think, and was very optimistic
246 about the emerging titanium technology which generates ~400-bp reads. Dr. M. Sogin reiterated his
247 support for this technology, and stated that his lab is in the process of acquiring the titanium technology
248 to read more basepairs (from 100-bp to 250-bp). Dr. George Fox recommended other emerging mass-
249 parallel sequencing technologies for consideration (see below).

250 **Cloning-Sequencing**. While this approach is powerful and extremely enlightening in its ability to
251 yield rarefaction curves to estimate the percent coverage in microbial diversity estimates, the
252 cloning of 1.5-kb DNA fragments is not all-inclusive, ignores "the rare biosphere," and is highly
253 biased towards abundant organisms. A shorter fragment cloning approach will not yield "semi-
254 quantitative" microbial diversity estimations either. A previously published peer-reviewed
255 manuscript authored by members of the GI-team (and many of the workshop attendees agreed)
256 advocated that this expensive, labor-intensive, and inconclusive approach should be
257 discontinued from use in the GI task. Cloning remains useful in attempts to describe archaeal

and/or eukaryotic diversity as pointed out by Dr. Tamas Torok, or for attempts to confirm presence of organisms detected by other methodologies.

PhyloChip. There was a general consensus that the PhyloChip is a valid means of discerning bacterial diversity from low biomass samples. The use of the PhyloChip for conducting censuses of archaeal signatures should be explored. It was also suggested that the GI-team explore the beta version of the MycoChip in elucidating eukaryotic diversity. Phylochip technology is limited in its ability to uncover novel "microbial" lineages, however, it was argued that if the information needed is at or above the "sub-family" level, the PhyloChip will be able to unambiguously detect such a presence. Finally, it was agreed that a common taxonomy must be agreed to compare between the PhyloChip and Tag-sequencing data.

454-sequencing. Due to significant levels of "noise", and the maturity level of 454-tag sequencing, a significant amount of future work and further optimization will be required in order for this technology to be suitable for PP efforts. There is a significant risk of sequencing errors and hence the committee recommended that the GI-team push for high quality sequences and reproducibility of technology used. The committee agreed that at least 250bp reads are required to decipher family level diversity – above the level used in the earlier V6 GI work, but within the capability of the Titanium 454 technology.

Other sequencing technologies. The GI-team was encouraged to explore other emerging mass-parallel sequencing technologies (i.e. Illumina, HELICOS), and was informed by the experts that SOLID and SOLEXA platforms are not suitable for the needs of the GI-task.

False-Positive Database The development of a planetary protection in-house negative-control/false-positive database was highly recommended.

Outcome of workshop-2:

- **Key question #1:** What technologies are required to ensure the characterization of the widest possible spectrum of terrestrial microflora?

Possible solution: The workshop adjourned without having come to a complete consensus on what, if any, technology can meet the current needs of the GI task. However, several participants felt strongly about the continued use of Phylochip DNA microarrays for the purposes of the GI task in the near future. There was general agreement that superior technologies to accomplish efficient sampling and sample processing were in great demand.

- **Key question #2:** how can we best deal with challenges resulting from the gaps in current technologies?
    - **Recommendation:** There were no clear-cut solutions presented. However, the approach taken by the Genetic Inventory Task team at JPL was commended. The gaps in the current technologies being employed, primarily those associated with PhyloChip Microarray and 454-mass parallel DNA sequencing methods, were identified and the majority of the workshop attendees agreed it best to continue employing PhyloChip-based analyses for the immediate future. The **challenges posed** by PCR-bias, sample

concentration, and other sample handling techniques were discussed, and certain recommendations were put forth (as detailed above), but here again no simple solutions were devised. There was a general consensus that target molecules (e.g., 16S rRNA gene) are not being collected in great enough abundance to render much of the downstream molecular analyses significant and/or reproducible. A major shift in emphasis away from analytical practices and towards the development of superior means of sample collection, sample recovery from sampling matrices, and sample handling/processing was strongly recommended by the collective voice of the committee.

APPENDIX-1 AGENDA

Workshop on Genetic Inventory of Spacecraft and Associated Surfaces

Jet Propulsion Laboratory, Pasadena, CA; Room: 301-370S

Sept. 30th 2009 [Wednesday]

8:00 AM	Check in at Visitors center	Venkateswaran, Spry, others Cell #: Venkat (818) 653-8170
8:30 AM	Workshop overview	Karen Buxbaum
9:00 AM	PP overview	Cassie Conley
9:30 AM	Summary of Genomic Inventory task	Kasthuri Venkateswaran
10:30 AM to 10:45 AM		***Coffee break***
10:45 PM	Task review on DNA microarray	Gary Andersen
11:45 PM		***Lunch at JPL Café (167)***
12:45 AM	Task review on 454-technology	Mitch Sogin
1:45 PM	Toward a Census of Bacteria in Soil, Ocean, & Air	Pat Schloss
2:45 AM	Human Microbiome (Sampling & Identification)	Joe Petrosino
3:45 PM to 4:00 PM		***Coffee break***
4:00 PM	WG topics-I (Technology: Microarray or 454 or what?)	Leader: Spry
4:45 PM	WG topics-II (Analysis: Good for low biomass?)	Leader: Venkateswaran
5:30 PM		***Adjourn Day 1***

Oct 1st 2009 [Thursday]

8:00 AM	Check in at Visitors center	Venkateswaran, Spry, others Cell #: Venkat (818) 653-8170
8:30 AM	Summary of WG-I topics	J. Nick Benardini
9:00 AM	Summary of WG-II topics	Myron LaDuc
9:30 AM	Discussion	All
10:00 AM to 10:15 AM		***Coffee break***
10:15 AM	Where do we go from here/Are we doing the right thing?	Karen Buxbaum
11:15 AM	Way forward discussion and recommendation capture	Spry and Venkat
12 noon	JPL Lab tour (optional)	

Direct feedback from attendees is given below without editing:

Dr. Ron Crawford, Univ. Idaho:

The focus of discussion within the workshop appeared to me to be centered on the question of which of the available technologies to "inventory" the microorganisms associated with spacecraft and spacecraft assembly facilities is best suited in the near term (next 1-3 years) for use by NASA's Planetary Protection Office in developing new standard protocols for monitoring microbial communities on spacecraft-associated surfaces. The workshop panel appeared to agree that (a) characterization of qualitative 16S RNA gene inventories remains the method of choice, (b) the inventory method chosen must be able to detect "rare" members of the community since these may represent organisms capable of surviving in some extraterrestrial environments, (c) the ultimate protocol developed to access community composition must be readily adapted to use in multiple NASA facilities, (d) the adopted method must be usable by professional staff who are not necessarily expert in the science underlying the method (e.g., phylogenetic clustering algorithms), and (e) the adopted method optimally should be able to describe detected Operational Taxonomic Units (OTUs) at the genus level. The primary contenders for use as a new standard microbial inventory method are (a) 16S RNA gene clone libraries, (b) microarray-based techniques (e.g., "PhyloChip"), and (c) high-throughput DNA sequencing methods (454 bar-coded 16S RNA gene tags).

A general consensus of the panel appeared to be that 16S RNA gene clone libraries are not an acceptable route to a new standard protocol. This technique is too laborious and expensive, and is not robust enough without excessive effort (many clones) to detect rare member of the microbial community. Having eliminated clone libraries as an acceptable approach, the remaining discussion centered on microarray and next-generation sequencing techniques. There was not a consensus on which of these alternatives might be the better choice for development into a standard NASA protocol. It is my opinion that of the two technologies remaining, microarray-based techniques should be the method of choice carried forward. There are many reasons this makes sense. In favor of the "PhyloChip" approach are the following observations.

- The PhyloChip approach uses terminology and methods already well-known and largely accepted by the microbial ecology research community.
- It employs replicated "probes" representing all regions of all known high-quality 16S RNA gene sequences in the available public databases.
- It has been tested in many natural environments, including low-biomass systems, and validated in the peer-reviewed literature.
- OTUs identified after hybridization can be reasonably well assigned to phyla at the level of genus.
- The method is very robust and able to detect even very rare members of a microbial community. This can be done even with pooled samples where a few strains may dominate.
- The method can easily be kept updated when new sequences are added to databases by adding new probes to the array. New arrays can hold more than a million probes and thus are easily expanded as needed.
- Though presently employing a proprietary format, similar microarrays can be converted to other formats (printed slide arrays, electrosense arrays) if desired.
- The technique works well with low biomass samples.
- It can easily be expanded to the detection of Eukaryotes and Archaea, as needed.
- The technique can be easily applied to multiple NASA locations.

- The PhyloChip format makes it easy to monitor environments repeatedly over time for changes in microbial community compositions, at reasonable cost.
- The technique can be applied to examination of RNA via use of cDNA.

Though potentially very powerful, 454 sequencing techniques appear not to be ready for immediate development into a standard protocol, for the following reason.

- Due to the very large number of sequence reads obtained in a 16S RNA gene bar-coded 454 run, background noise from sequencing errors requires the development of filtering algorithms to remove this noise. Though several such algorithms are under development, there is no consensus yet as to which algorithms will work best, certainly not within a standard protocol. These filtering methods remain to be fully validated by peer-review and reproduction in numerous laboratories. This process is very complex and will likely require several years to be accomplished.
- The 454 technology thus far has be "validated" using "mock communities" of about 20 pure cultures. The results thus far have been unsatisfying as compared to microarray methods; unless very sophisticated filtering techniques are applied to the data (see above). It is not at all clear that such validation methods will perform similarly on real, highly diverse communities. This work remains to be done.
- Important decisions regarding which "V regions" of the 16S RNA gene are appropriate for amplification and 454 sequencing still have not been made. It is likely that the same regions will not be appropriate for all taxa. Though it may be possible to develop approaches to simultaneously amplify and the sequence multiple V regions and thus overcome this taxa-specificity problem, the work in this regard has only just started and there is no censuses among investigators how this should be done. This will require significant time in the form of additional research and cross-lab validation.
- So-called new-generation sequencing techniques are in a rapidly changing developmental environment. Alternatives to 454-based methods are being developed by many companies and within several academic institutions. It is not clear that 454 methods will still be the approach of choice even within the next 1-2 years. In this sense 454 might not be a good technology for development of a standard NASA protocol as it may not be state-of-the-art even in the very near future.
- The investment of funds in 454 methods is very high. The equipment is very expensive. Individual 454 runs are expensive. The bioinformatics stage of analysis requires special expertise and super-computer level processing of data. These are not issues with competing technologies such as microarrays.
- The power of 454 technologies is best used in the framework of basic research, rather than for design of standard protocols. For example, 454 sequencing of metagenomic DNA can provide invaluable information about functional genes in low-biomass environments. This is the area of most promise for this method.

Other issue discussed included (a) the need to monitor developing methods in DNA extraction for low-biomass samples (e.g., monitor the literature), (b) concentrate significant effort in obtaining negative results from PCR controls, (c) keep a database of inventories of microbes seen in negative controls, (d) record as much metadata as possible during archiving of experimental results, (e) pool samples when possible (e.g., for total inventory assessments), but not always (e.g., when looking at patchiness in microbial distributions), and (e) look into the possible uses of "witness plates" to collect deposited microbes in some regions of spacecraft assembly facilities.. There was general consensus among members of the panel regarding the needs for additional research in these areas.

In summary, it appears to me that of the technologies discussed within the workshop, only microarray methods are “ready for prime time” in the development of a standard NASA protocol for assessing inventories of microbes on spacecraft-associated surfaces and materials. Once methods such as standard DNA extraction protocols and use of data from PCR controls are formalized, microarray techniques such as PhyloChip should be useful as the basis for development of a standardized bio-inventory protocol for application by NASA to spacecraft and their environs in the near future.

Dr. George E. Fox, John and Rebecca Moores Professor,
Dept. Biology and Biochemistry, University of Houston

I realized/remembered at the end of the meeting that the real problem with 16S V6 approach (of V3 + V6; etc) is that you can't reliably place deep branching things and probably can't actually distinguish them from rapidly changing (in V areas) things. So it is likely better to actually sequence sections of 250 plus positions so that you get "clocks" of all speeds.

I think the problem with arrays is perhaps lack of sequencing documentation. The array says X is present and the array is usually right, so we believe it but what exactly is the version of X that is present? Maybe the solution is to find major taxons by arrays and then go look for them with organism specific primers as you started to do for different reasons. That is-not to verify presence, but rather to get sequence information. One of the current goals in planetary protection is apparently to obtain a library of clean room sequences that can subsequently be matched against anything found on Mars and obviously you can't do that with chip data. Personally, I don't see any problem with the "RDP" database of everything being matched against something isolated on Mars in order to demonstrate forward contamination. However, the inventory does have the advantage of potentially providing a direct link between spacecraft assembly and any forward contamination found. In the absence of such a direct link, one could I suppose argue that the forward contamination reached Mars in the form of a meteor from Earth or another country's exploration efforts.

I don't see any immediate need of further clone sequencing at this stage but do see value in culturing and characterizing wherever possible. In particular, if the survey is consistently picking up a particular taxon/(or group of taxons) in high amounts you probably should try to get a genome sequence if one is not available for that group.

I have attached the Helicos paper. Their technology apparently can use extremely small samples and is not bothered by PCR bias (no PCR step). However, the bad news is that reads are very short. You probably can't use- it but it wouldn't do any harm to talk to them as maybe there is a way.

I have little expertise with the sampling issues, but as you know the goal should be to increase recovery levels with less contamination.

Dr. Joseph F. Petrosino
Department of Molecular Virology and Microbiology
Human Genome Sequencing Center
Baylor College of Medicine, Room 239C

Thank you so much again for the opportunity to come out and learn more about your program and to offer our insights on metagenomic sequencing and population characterization. Here are some of my thoughts on the two working group topics: Emerging Technologies and Sample Collection and Amplification

With respect to the goal of characterizing the widest possible spectrum of microbes carried by spacecraft (at low densities), I think it's still best to cast a broad net, in terms of technologies used to gather more data about what method(s) may be best in the long run. I think the methods that should be used at this point are:

1. 454 Titanium 16S PCR amplicon sequencing,
2. Illumina WGS sequencing, and
3. Phylochip (latest generation)

Both 454 and Phylochip are capable of characterizing complex communities, but there are advantages and disadvantages to each that I think warrants the need for further studies with both platforms. Phylochip appears able to generate high-quality, comparative data with great sensitivity, but may be somewhat limited in areas of identifying new organisms from previously uncharacterized taxa and also may not be as reliable for quantification of the organisms it detects. Meanwhile, unlike the Phylochip, 454 titanium currently relies on subdomains of the 16S gene for phylogentic determination. This works well, but an informed approach to read filtering and OTU determination/clustering, as presented at the meeting, is necessary for optimal results. Efforts by the Sogin group (as well as others, including Pat Schloss) and the HMP consortia have advanced 454 metagenomic analyses greatly over the past year. In addition, we at BCM are able to achieve >450 base read length averages for Titanium amplicon runs using the standard Roche reagents (given their funding and high-throughput, genome sequencing centers traditionally push platform developers in terms of reagent and software advancements). The longer reads provided by Titanium will be helpful in that they capture more information about a particular 16S gene, by definition, as compared to shorter reads. The Titanium platform is ready, as is (i.e. Even without the further advancements that are sure to come in upcoming months), for metagenomic population analysis. We would be happy to help JPL/NASA implement the Titanium platform for this purpose, and would be happy/excited to work with others involved in this project to assist in benchmarking 454 Titanium the various technologies associated with the project. Samples, including those from clean room sites and from well-constructed mock communities would be ideal targets for additional studies.

Whole Genome Shotgun (WGS) sequencing on Solexa is a fast advancing area of metagenomic analysis. The ability to identify the antibiotic resistance and/or metabolic potential of a given population (two examples raised during the meeting) is not readily achieved by 16S sequencing but can be revealed when the genetic content of an entire sample is defined. Given the low abundance of organisms and DNA, a fraction of a Solexa run should be enough to query the genes of a given population at a coverage level of at least 1X. (Initial HMP studies suggest that a full Solexa run (~10-30 gigabases of sequence) is enough to sample the genes of a stool microbiome at ~1X coverage. Given the relative complexity, a clean room microbiome should take many fewer reads (hence the estimate). Actual identification of the organisms present in a given sample is also possible with WGS data through a variety of analysis

methods, but given the likely need for whole genome amplification (WGA) in order to have enough DNA for a WGS library, a WGS study should be accompanied by a concurrent Titanium or Phylochip 16S analysis and proper template free controls. Currently, Solexa libraries can be made with <100 ng of input DNA. We anticipate that this amount will become much smaller over the next couple of months and would be of great value for the spacecraft genetic inventory program.

Acknowledging that amplification of some sort is needed to augment the DNA amounts that are being studied, I think some effort is needed in two areas:

1. identifying the v-region(s) of the 16S gene that best suit your needs for the populations being examined and/or anticipated (or simply which v-regions best define the broadest number of taxa at the level desired (family, genus, etc)). This can probably be achieved in silico with minimal effort (and actually has been done for various environments through efforts by the HMP consortia and others, including the Sogin group). The question is, do you want more resolution of species you know are in the clean rooms, or do you want to leave the window open to better approximate the identities of new organisms that are found. Or, as I would imagine to be the case, both—in which case multiple v-regions can be sequenced to get resolution of families/species of interest (when possible by 16S) and to identify a broad range of organisms overall....
2. More effort will be needed in optimizing whole-genome amplification (WGA/MDA) methods to increase the amount of DNA you have access to while introducing as little bias or contamination as possible. There are/have been studies to optimize this, and we have done some initial work in this area as well (including large-scale sequencing runs to identify contaminant reads/organisms), but the lab actually doing the amplification will have to perfect these technical skills as even the slightest variation in protocol can dramatically impact the results.

Other notes:
16S Sanger data of clean room microbiota is still a necessary item as these data will help populate databases that are used for querying purposes. The data one gets from a metagenomic analysis is only as good as the databases being used for the analysis. Therefore, some investment in shoring up the data on organisms relevant to clean room contamination would be most beneficial. (For example, complete sequencing of ALL 16S genes of various species known to exist in clean rooms. Don't rely on Genbank sequences unless it is KNOWN that the 16S genes in the database were actually isolated and sequenced....Many groups plug in stuffer 16S genes in their whole genome sequencing projects...)

Mock communities (both DNA and cell, and perhaps 16S amplicon/gene communities) should be normalized by Petroff-Hauser counts and 16S rRNA gene content rather than by CFU and genome MW to provide the best population for extraction and sequencing benchmarking at a quantitative level...

Extraction methodologies should be vetted/benchmarked at multiple levels...Not only in terms of DNA quality and quantity, but also in terms of its utility in downstream sequencing and/or amplification protocols.

I would always welcome discussing these, and other aspects, of the spacecraft genetic inventory program. We would be happy to work toward furthering studies in all of these areas including processing of samples and analyzing/benchmarking the data coming from these samples. We have a significant amount of expertise in this area stemming from our work in the Human Microbiome Project, and our sequencing center has plenty of capacity to handle such efforts. (e.g. We process ~20-30 Titanium sequencing runs per week, and can increase throughput as necessary....)

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