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Fecal Microbiota Transplantation and Detection of Prevalence of IgA-Coated Bacteria in the Gut

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Dear Editor,

Based upon the greatly appreciated editors and reviewers' comments received 31 Oct 2019, we have performed additional experiments and added new data into figures. Moreover, we have made revise of our manuscript and submit our manuscript entitled "*Fecal microbiota transplantation and the detection of prevalence of IgA-coated bacteria in the gut*" to the journal of *JoVE*. All the revised contents are marked as red.

We also provide a rebuttal letter to answer the reviewers' comments point by point. We look forward to hearing the positive feedback from you.

Thank you for your consideration.

Sincerely,

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TITLE:**Fecal Microbiota Transplantation and Detection of Prevalence of IgA-Coated Bacteria in the Gut****AUTHORS AND AFFILIATIONS:**

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KEYWORDS:

gut bacterial depletion, fecal microbiota transplantation, quadruple-antibiotic treatment, 16S ribosomal RNA sequencing, immunoglobulin A (IgA)-binding bacteria, flow cytometry

SUMMARY:

We established an efficient way to deplete intestinal bacteria in three days, and subsequently transplant fecal microbiota via gavage of fecal fluid prepared from fresh or frozen intestinal contents in mice. We also present an optimized method to detect the frequency of IgA-coated bacteria in the gut.

ABSTRACT:

Gut microbiota exert pleiotropic roles in human health and disease. Fecal microbiota transplantation (FMT) is an effective method to investigate the biological function of intestinal bacteria as a whole or at the species level. Several different FMT methods have been published. Here, we present an FMT protocol that successfully depletes gut microbiota in a matter of days, followed by transplantation of fecal microbiota from fresh or frozen donor intestinal contents to conventional mice. Real time-PCR is applied to test the efficacy of bacterial depletion. Sequencing of the 16S ribosomal RNA (rRNA) is then applied to test the relative abundance and identity of gut microbiota in recipient mice. We also present a flow cytometry-based detection method of immunoglobulin A (IgA)-coated bacteria in the gut.

INTRODUCTION:

A diverse gut microbiota plays a major role in maintaining host homeostasis. This microbiome aids in various physiological processes ranging from digestion and absorption of nutrients from food, defense against infection of pathogens, regulation of immune system development, and

immune homeostasis¹. Perturbation in gut microbial composition has been linked to many diseases, including cancer², autoimmune diseases³, inflammatory bowel disease⁴, neurological diseases⁵, and metabolic diseases^{6,7}. Germ-free (GF) mice are powerful tools in fecal microbiota transplantation models to study the biological effects of microbiota⁸. However, the GF housing environment is very stringent, and performing fecal microbiota transplantation (FMT) in these mice is expensive. Moreover, GF mice have different barrier and mucosal properties, which regulate bacterial penetration, compared to conventional mice⁹. These factors limit the wide application of GF mice in studies. An alternative to using GF mice is to deplete the microbiota in conventional mice using an antibiotic cocktail followed by FMT. Previously reported FMT methods are not well described and inconsistent; therefore, it is necessary to establish a feasible, efficient, and reproducible protocol to perform FMT using conventional mice.

Several steps are crucial to a successful FMT. The efficiency of microbiota depletion is the first important step. For bacteria depletion, use of a single broad-spectrum antibiotic (e.g., streptomycin¹⁰) or an antibiotic cocktail (triple or quadruple-antibiotic treatment) has been reported^{11,12}. The quadruple-antibiotic treatment including ampicillin, metronidazole, neomycin, and vancomycin, has been found to be the most effective regimen and has been used in several studies¹³⁻¹⁵. In addition to the type of antibiotic used, the route of administration, dosage, and duration of the antibiotic treatment affect the efficacy of bacterial depletion. Some researchers apply antibiotics in the drinking water to eliminate bacteria in the gastrointestinal tract¹⁵. However, it is hard to control the dosage of antibiotics that each mouse receives this way. Therefore, in subsequent studies, researchers have treated mice with antibiotics by oral gavage for 1–2 weeks¹² to achieve satisfactory depletion. However, the long-term use of antibiotics can be problematic, as the antibiotics themselves may affect some diseases in rodent models¹⁶. Therefore, faster and more efficient methods for microbiota depletion are warranted.

Fecal fluid preparation is another key step to ensure successful FMT. In the gastrointestinal tract, pH ranges from 1 in the stomach to 7 in the proximal and distal intestine⁹. The microbiota in the stomach is limited due to high acidity and includes *Helicobacter pylori*¹⁷. The proximal intestine produces bile acid for the liver-gut circulation, and contains microbiota associated with fat, protein, and glucose digestion. The distal intestinal tract contains abundant anaerobic bacteria and exhibits high microbial diversity¹⁸. Given the spatial heterogeneity of gut microbiota, it is imperative to isolate gut contents from different regions of the intestinal tracts for fecal fluid preparation. Additionally, other factors, including the nature of the donor sample (e.g., fresh or frozen sample), transplantation frequency, and duration are crucial when performing FMT. Frozen stool is most commonly used for colonizing conventional mice with human gut microbiota¹⁹. In contrast, FMT using fresh stool from animal donors is more appropriate and commonly used in animal models^{20,21}. FMT frequency and duration vary depending on the experimental design and models. In previous studies, FMT was either performed daily or every second day. The transplantation duration ranged from 3 days²² to 5 weeks²³. In addition to the above factors, maintaining an aseptic surgical environment and the use of sterilized surgical instruments is crucial to avoid unexpected environmental bacterial contamination.

The gut microbiota has the potential to regulate the accumulation of cells that express

Immunoglobulin A (IgA). IgA, a predominant antibody isotype, is critical in protecting the host from infection through neutralization and exclusion. High-affinity IgA is transcytosed into the intestinal lumen and can bind and coat offending pathogens. In contrast, coating with IgA may provide a colonization advantage for bacteria²⁴. In contrast to pathogen-induced IgA, indigenous commensal-induced IgA has lower affinity and specificity²⁵. The proportion of intestinal bacteria coated with IgA is reported to be significantly increased in some diseases^{25,26}. IgA-coated bacteria can initiate a positive feedback loop of IgA production²⁷. Therefore, the relative level of IgA-coated bacteria can predict the magnitude of the inflammatory response in the gut. In fact, this combination can be detected via flow cytometry²⁸. Using IgA-based sorting, Floris et al.²⁷, Palm et al.²⁵, and Andrew et al.²⁹ acquired IgA⁺ and IgA⁻ fecal bacteria from mice and characterized taxa-specific coated-intestinal microbiota via 16S rRNA sequencing.

In this study, we describe an optimized method to efficiently deplete intestinal dominant bacteria and colonize conventional mice with fresh or frozen fecal microbiota isolated from the contents of the ileum and colon. We also demonstrate a method based on flow cytometry to detect IgA-binding bacteria in the gut.

PROTOCOL:

Animal experiments were conducted in accordance with the current ethical regulations for animal care and use in China.

NOTE: Animals were housed in a specific pathogen-free (SPF), controlled environment under 12-hour light and dark cycles at 25 °C. Food was irradiated before being fed to mice. Drinking water and cages were autoclaved before use. Eight-week-old male C57BL/6J mice were used in the study following 1 week of acclimatization. They were divided into several groups based on the experiment design. Each group consisted of at least three mice.

1. Gut microbiota depletion

1.1. Antibiotic cocktail preparation

1.1.1. Prepare an antibiotic solution in sterile phosphate buffered saline (PBS) with 0.5 mg/mL vancomycin hydrochloride, 1 mg/mL metronidazole, 1 mg/mL ampicillin sodium salt, and 1 mg/mL neomycin sulfate.

NOTE: Store the antibiotics at 2–8 °C and avoid direct light. Prepare the antibiotic cocktail solution fresh and use immediately.

1.2. Treatment regimen

1.2.1. For 3 days, orally administer 200 µL of prepared antibiotic cocktail with a #10 needle to a mouse. Hold the mouse vertically in one hand while using the other hand to adjust the angle of the needle to avoid reaching the stomach.

NOTE: The mouse must be handled gently to avoid struggling, because surface damage of the esophagus and stomach may result in inflammation or death.

1.2.2. Add antibiotics to the drinking water at the same concentrations as indicated in step 1.1.1.

1.2.3. Three days later, sacrifice the mouse by CO₂ asphyxiation.

1.2.4. Dissect the abdomen aseptically using sterile instruments. At a distance of 2 cm away from the caecum, cut off a 2 cm tract of the ileum. Using sterile tweezers to clamp off one end of the tract, squeeze the fresh contents out of the tract into pre-weighed tubes.

1.2.5. To collect the contents of the cecum, cut it in half with surgical scissors. Squeeze the contents of each half of the cecum into pre-weighed tubes.

1.3. Evaluate gut microbiota depletion efficacy.

1.3.1. Weigh gut contents isolated from the ileum or cecum from naive mice and antibiotic cocktail treated mice, and extract stool microbiota DNA using a kit according to the manufacturer's instructions. Determine the DNA concentration according to the formula:

$$\text{concentration}_{\text{sample}} (\mu\text{g}/\text{mL}) = \text{OD}_{260} \times 50$$

1.3.2. Construct a standard curve.

1.3.2.1. Amplify *E. Coli* genes with a polymerase chain reaction (PCR) using V3-V4 specific primers. Predenature at 95 °C for 1 min, amplify for 40 cycles of 95 °C for 10 s, 60 °C for 30 s, 72 °C for 30 s.

1.3.2.2. Construct a plasmid by linking the amplified product to a TA vector. Clone the culture with a TA vector kit according to the manufacturer's instructions.

1.3.2.3. Measure the plasmid concentration (ng/μL) based on the OD₂₆₀ value as described in step 1.3.1.

NOTE: The unit for plasmid concentration is different from the unit for DNA concentration.

1.3.2.4. Calculate the copy numbers using the following formula, where MW stands for molecular weight:

$$\text{copies in } 1 \mu\text{L} = \text{concentration (ng}/\mu\text{L}) \times 10^{-9} \times 6.02 \times 10^{23} / (\text{MW}_{\text{plasmid}} \times 660)$$

1.3.2.5. Reconstitute the plasmid with double distilled water to a final concentration of 40 μg/μL. Prepare a 10x gradient dilution series with eight stages. Construct a standard curve by plotting

the C_T value (Y-axis) against $\log(\text{Copies}_{\text{plasmid}})$ (X-axis) after PCR amplification, where C_T stands for threshold cycle for target amplification. Extract the equation from the plot (in this case, it was $y = -3.07x + 45.07$, $R^2 = 0.994$).

1.3.3. Amplify 1 μL of the DNA samples obtained in step 1.3.1 extracted from the ileum or cecum from a naive control group and the antibiotic cocktail treatment group by real-time PCR as described in step 1.3.2.1. Calculate the copy number in 1 μL of the DNA samples based on the standard curve in step 1.3.2.5 and then calculate the total copy number using the following formula:

Total copy number (per mg) in the weighted samples = copy numbers $\times$ total DNA volume/initial weight of the sample

1.4. Analyze the microbiota DNA by sequencing the 16S rRNA V3 and V4 regions.

2. Fecal microbiota transplantation

2.1. Fecal fluid preparation for both fresh and frozen stool samples

NOTE: All instruments are soaked in 75% alcohol prior to usage to avoid preexisting bacterial contamination. It is crucial to avoid contamination when the ileum and colon contents are collected.

2.1.1. Sacrifice 3–5 donor mice by CO_2 asphyxiation.

2.1.2. Collect the contents of the ileum as described in step 1.2.4.

2.1.3. To collect the contents in the colon, make the first incision near the anus and cut the upper 2 cm tract. Extract the contents as explained in step 1.2.4. Collect the samples in 1 min to reduce exposure to air.

2.1.4. For frozen fecal fluid, collect the ileum or colon contents as described in steps 2.1.2 and 2.1.3, and flash freeze the contents in liquid nitrogen.

2.1.5. Store samples in a -80°C freezer until ready for use.

2.2. Pool and weigh the contents, add in fresh sterile tubes with beads. For frozen samples, thaw the fecal pellets on ice before weighing.

2.3. Add sterile PBS into the tube and resuspend the fecal pellets in PBS (1 mL of PBS/0.2 g of fecal pellet) using a 5 mL syringe needle. Homogenize the fecal pellet completely with beads and vortex 3x for 1 min each.

2.4. Centrifuge at $800 \times g$ for 3 min, then filter the supernatants by passing through a $70 \mu\text{m}$ cell

strainer. Collect the filtered fecal fluid in a sterile tube and use for FMT immediately.

3. Fecal microbiota transplantation procedure

3.1. Administer 200 μ L of prepared fecal fluid to the microbiota-depleted mice via oral gavage every second day for 14 days. Gavage control mice with 100 μ L of sterile PBS.

3.2. Sacrifice the mice by CO₂ asphyxiation and harvest the contents from the ileum and colon according to steps 2.1.2 and 2.1.3. Store samples at -80 °C until further processing.

3.3. Extract the microbiota DNA of the ileum and colon contents as described in step 1.3.1. Verify the microbiota composition in the gut of transplanted mice by 16S rRNA sequencing.

4. IgA-coated bacteria measurement

4.1. Sample preparation

4.1.1. Collect 50 mg of fecal pellets from donor mice as described in steps 2.1.2 and 2.1.3, and incubate in 1 mL of sterile PBS at 4 °C for 1 h. Homogenize the pellets using a bead beater for 5 s.

4.1.2. Centrifuge the solution at 300 x *g* for 10 min at 4 °C. Collect supernatant after filtrating through a 70 μ m strainer.

NOTE: Avoid high speed centrifugation.

4.1.3. Add 5 μ L of the supernatant to 1 mL of 1% bovine serum albumin (BSA) in PBS (FACS buffer). Pellet at 8,000 x *g* for 5 min at 4 °C and discard the supernatant.

4.1.4. Resuspend the pellet in 1 mL of FACS buffer, centrifuge at 8,000 x *g* for 5 min at 4 °C, and discard the supernatant.

NOTE: The volume used here may need to be optimized. Too much of the supernatant at this step may mask the positive signal of IgA-coated bacteria.

4.1.5. Resuspend the pellet in 100 μ L of PBS containing 10% goat serum and incubate on ice or at 4 °C for 30 min. Add 1 mL of FACS buffer in the tube and centrifuge at 8,000 x *g* for 5 min at 4 °C to pellet.

4.2. Flow cytometry

4.2.1. Resuspend the pellet obtained in step 4.1.5 with 200 μ L of FACS buffer containing biotin anti-mouse IgA antibody (1:100) and APC-conjugated anti-biotin antibody (1:100) and incubate for 30 min at 4 °C.

4.2.2. Add 1 mL of FACS buffer in the tube and centrifuge at 8,000 x *g* for 5 min at 4 °C. Discard the supernatant.

4.2.3 Stain the pellet from step 4.2.2 by adding 200 µL of FACS buffer containing green fluorescent nucleic acid stain (1:200) and incubate at 4 °C for 5 min.

4.2.4. Add 1 mL of FACS buffer and centrifuge at 8,000 x *g* for 5 min at 4 °C to pellet.

4.2.5 Resuspend the pellet in 250 µL of FACS buffer before measurement.

4.2.6. Acquire the data using a flow cytometer and analyze it using FlowJo software.

REPRESENTATIVE RESULTS:

The FMT schedule used in this study is outlined in **Figure 1**. After treatment with the antibiotic cocktail, the efficiency of intestinal microbiota depletion was analyzed by sequencing the 16S rRNA region. We detected 196 species in the ileum of naive mice, whereas 3-day antibiotic treatment reduced the bacterial species to 169 (**Figure 2A**). There were eight species detected solely in mice that underwent the antibiotic cocktail treatment (**Figure 2A**). Beta-diversity analysis at the genus level further indicated that the predominant bacteria in the ileum of naive mice, e.g., *Norank_f__Bacteroidales_S24-7_group*, *Desulfovibrio*, *Lactobacillus*, and *Staphylococcus*, were eliminated after antibiotic cocktail treatment. In contrast, *Escherichia-Shigella* accounted for more than 99% of the gut bacteria in the antibiotic-treated mice (**Figure 2B**). Besides the significant reduction of bacterial species, mice receiving the antibiotic cocktail had a dramatic decrease in copy numbers in the equal amount of gut contents in the ileum and cecum compared to naive mice (**Figure 2C**). The efficacy of gut microbiota depletion reached up to 99%.

Firmicutes, *Bacteroidetes*, *Proteobacteria*, *Actinobacteria*, and *Verrucomicrobia* were found to be the most abundant bacteria in donor mice at the phylum level (**Figure 3A**). Mice receiving either fresh or frozen fecal transplantation for 7 days displayed similar predominant bacterial taxa to the naive group. Principal component analysis (PCoA) was performed to identify differences among donor, PBS, fresh, and frozen fecal transplantation groups. By comparison, samples from the fresh fecal transplantation group formed a cluster that was close to the cluster of donor groups in PCoA1 (3.0%) and PCoA2 (6.3%) (**Figure 3B**). Compared to the PBS group, the bacterial cluster formed in the frozen fecal transplantation group was closer to that of control group. While samples from the PBS group were clustered differently from the control group cluster, PCoA1 and PCoA2 accounted for 27.9% and 8.6% of the variance, respectively (**Figure 3B**).

Figure 4 represents a typical flow cytometry plot analysis of IgA-coated bacteria in intestinal contents based on antibody-binding bacterial cell sorting. **Figure 4B** shows the sample without antibody staining. As shown in **Figure 4C**, there was positive APC fluorescence signal in the sample stained with biotin anti-mouse IgA antibody and APC streptavidin. We also detected the positive staining population in the sample stained with only green fluorescent nucleic acid stain

(Figure 4D). Moreover, no fluorescence compensation was observed between APC and bacterial nuclear staining signal channel (Figure 4C,D). IgA-coated bacteria in the contents of the ileum from naive mice were 1.97% based on flow cytometry analysis (Figure 4E).

FIGURE LEGENDS:

Figure 1: Experimental schedule of fecal microbiota transplantation. ATB = antibiotic treatment; FMT = Fecal microbiota transplantation; PBS = phosphate buffer saline.

Figure 2: Gut microbiota community alteration after antibiotic cocktail treatment. (A) Venn diagram displaying the degree of bacterial overlap at the species level between naive and ATBs cocktail treatment groups. (B) The relative abundance of different taxa at the phylum level in mice with or without antibiotic cocktail treatment. (C) Copy numbers in the contents of the ileum and cecum from naive mice or mice treated with the antibiotic cocktail.

Figure 3: Characteristics of gut microbiota in donor mice and mice receiving sterile PBS or fecal fluid prepared from fresh or frozen contents of ileum. (A) Relative abundance of the dominant bacteria at the phylum level in the ileum of donor mice, PBS, fresh, and frozen fecal transplantation groups. (B) Principal coordinate analyses (PCoA) of beta diversity based on binary Jaccard analysis in the gut microbiota of donor mice and mice receiving sterile PBS or fecal fluid prepared from fresh or frozen intestinal contents.

Figure 4: Representative flow cytometry plot of IgA-coating bacteria. (A) FSS versus SSC plot. (B) Blank control. (C) APC-IgA-single staining. (D) Nucleic acid single staining. (E) IgA and nucleic acid double staining population for naive mice.

DISCUSSION:

Antibiotics used in the depletion procedure have different antibacterial properties. Vancomycin is specific for gram-positive bacteria³⁰. Oral doxycycline can induce significant intestinal microbiota composition changes in female C57BL/6NCrI mice³¹. Neomycin is a broad-spectrum antibiotic that targets most gut-resident bacteria³². It does not prevent intestinal inflammation, however. Broad-spectrum antibiotic cocktails are more effective than a single antibiotic^{13,33,34}. One study reported that triple-antibiotic treatment (amoxicillin, fosfomycin, and metronidazole) synergistically depleted the imbalanced gut microbial community in ulcerative colitis¹¹. The quadruple-antibiotic treatment successfully eliminated gut microbiota in an asthma mice model¹³ and a high fat diet mice model¹⁴. In previous studies, microbiota depletion with a single antibiotic dissolved in drinking water required more than a 6 week treatment period¹⁵. With oral gavage, the time for microbiota depletion was reduced to 2 weeks¹². However, 17 days administering an antibiotic cocktail in drinking water can lead to significant weight loss in mice due to the bitter taste of metronidazole and the subsequent decrease of water and food intake⁹. Our method, combining oral gavage and drinking water, was even more efficient in achieving satisfactory bacterial depletion in 3 days. Additionally, our antibiotic treatment regimen can avoid body weight loss in mice caused by extended an antibiotic cocktail treatment.

Avoiding bacterial contamination is an important consideration in our FMT schedule. First, it is

necessary to wipe out bacteria existing in the immediate feeding environment, including cages, water, and food. Second, an aseptic environment must be maintained, including sterile tips, tubes, and surgical instruments. Test tubes and surgical instruments may contain environmental microbiota. The risk of environmental contamination can be reduced by wearing latex gloves, spraying them with 75% alcohol, and washing hands before starting a new procedure. The instruments should also be washed with 75% alcohol to avoid fecal microbiota contamination across individual mice.

Some studies have shown that coprophagic and grooming behaviors can be exploited by transient cohousing of mice, which results in the sharing of microbes across cohabitated individuals. This technique may be the simplest and most convenient method to transplant fecal microbiota³⁵. Cohousing of mice showed similar effects as FMT on body mass³⁶ and in obesity disease³⁷ and tumor models³⁸. However, the impact of cohousing on fecal microbiota is difficult to standardize, especially with F2 littermates³⁵. Moreover, this strategy is not suitable for large numbers of mice and could introduce variability. Furthermore, the time required to transplant fecal microbiota by cohousing was 4 weeks longer than that of FMT³⁹, in which the intake is identical and controllable for all mice.

FMT protocols are not standardized across studies published in the literature. Researchers use different fecal samples such as fresh and frozen stool to prepared fecal fluid and treat recipient mice with different gavage frequency and duration. Technically, fresh stool is the best choice. However, for frozen stool, no significant difference in successful transplantation rate was noted in relation to different storage periods (1 week to 6 months)^{40,41}. A recent study suggested that, although freezing did not significantly affect in vitro fecal bacterial viability, it reduced the colonization ability of the transplanted fecal microbiota⁴². In addition, it is notable that the genetic background⁴³ and age⁴⁴ of the recipient rodents are other important factors that significantly affect engraftment of donor microbiota. Interestingly, Ericsson et al. found that even the richness difference between the donor and the recipient's microbiota impacts the inoculum engraftment³¹. Another study indicated the effect of transplantation frequency on bacterial colonization and community. When human microbiota is transplanted into mice, the increase of transplantation frequency from once a week to twice a week leads to different results. In this study, it was found that FMT once a week appears to be the best compromise, because it supported higher diversity in microbiota engraftment⁴⁵. This opinion was further confirmed by a study by Staley et al.⁴⁶ in which a single gavage treatment of human fecal fluid was able to establish a human microbiota-associated (HMA) animal model. Importantly, they also showed the influence of different antibiotic treatment on the engraftment efficacy of FMT. Although both "systemic" and "non-absorbable" antibiotic cocktails showed comparable effects in disrupting the indigenous microbiota to a level that permitted colonization of abundant HMA taxa, the extended antibiotic course seems more likely to contribute to consistent and extended engraftment⁴⁶. Most researchers administered 200 μ L of fecal suspension (100 mg/mL) to the mice^{23,45}. However, transplantation duration ranged from 3 days²² to 5 weeks²³. In another study, mice receiving fecal microbiota from patients with constipation for 7 and 15 days displayed different defecation parameters⁴⁷. The transplantation duration was variable depending on the study design.

High levels of IgA-coated bacteria play an important role in the pathogenesis of inflammatory bowel disease²⁷ and arthritis²⁶. The method for measuring IgA-coated bacteria consists of pelleting bacteria by centrifugation (10,000 x *g* for 1 min at 24 °C), followed by pellet resuspension in 100 µL of PBS and flow cytometry²⁹. These centrifugation conditions were unsuitable for our method. To avoid loss of bacterial viability, we used a lower speed for centrifugation (800 x *g*). In our experiment, the IgA-coating bacteria population was hardly distinct from the negative population when staining 100 µL of fecal fluid with fluorescence-labeled antibodies for flow cytometry analysis. However, 20x dilution of fecal fluid followed with the same amount of antibody staining was sufficient to resolve this problem.

In conclusion, we established a method for rapid depletion of most dominant gut microbiota in 3 days and a procedure to use fresh or frozen donor samples in FMT. We also presented an optimized method to analyze the proportion of IgA-coated bacteria in the gut. Although our protocols cannot be directly extended to human FMT studies, they can still be helpful for studying the role of gut microbiota in the pathogenesis of many diseases in rodent models.

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DISCLOSURES:

The authors have nothing to disclose.

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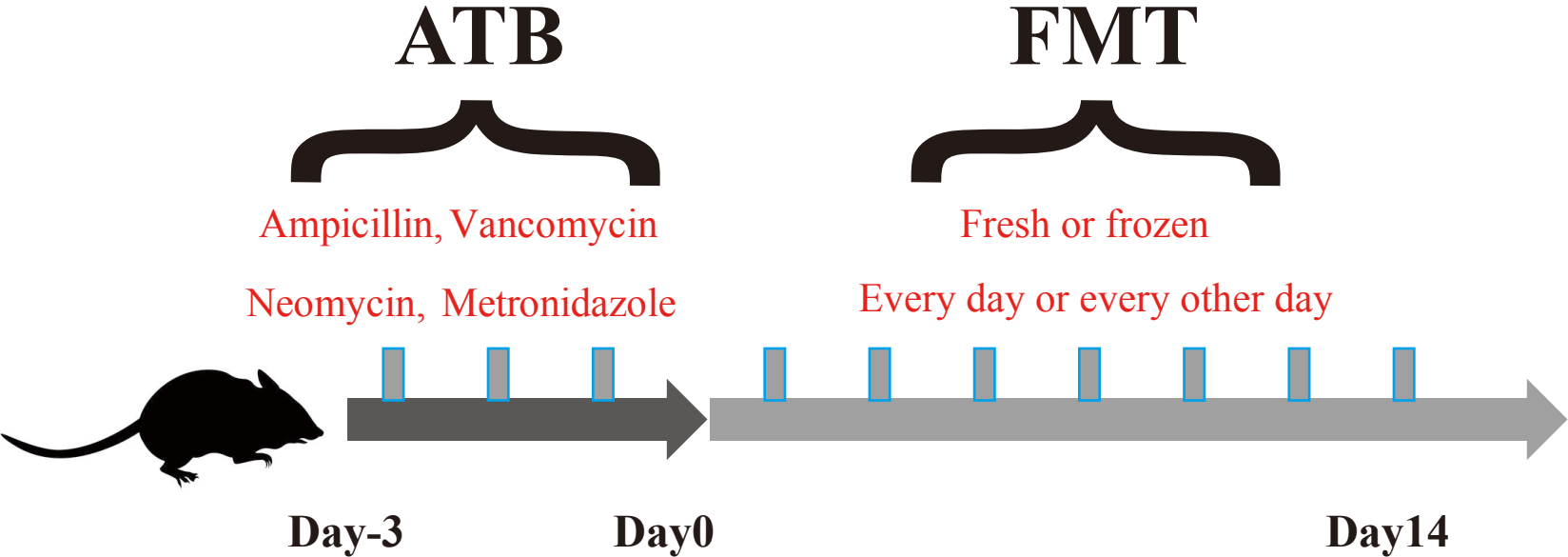
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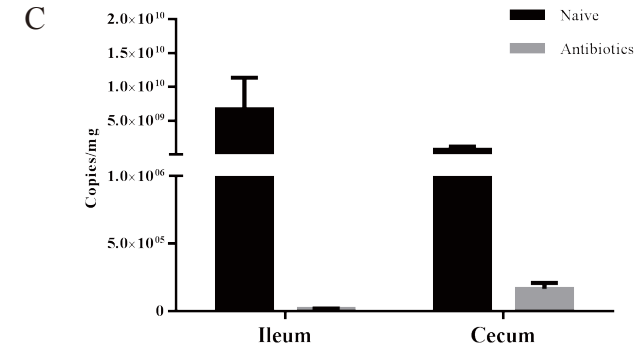
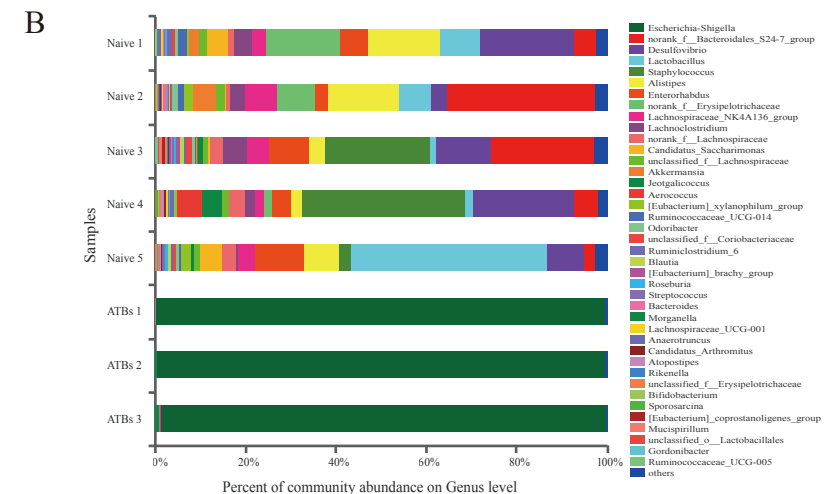
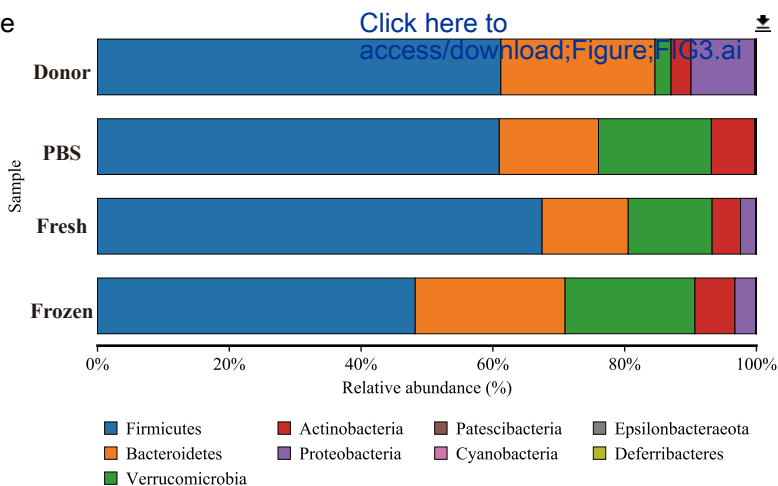
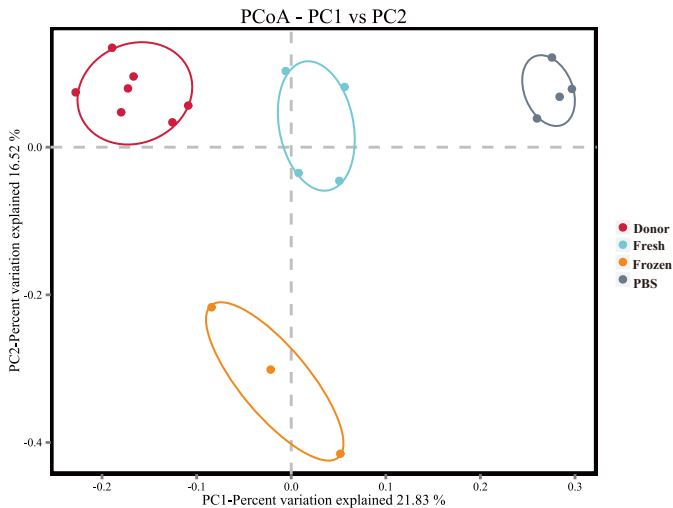


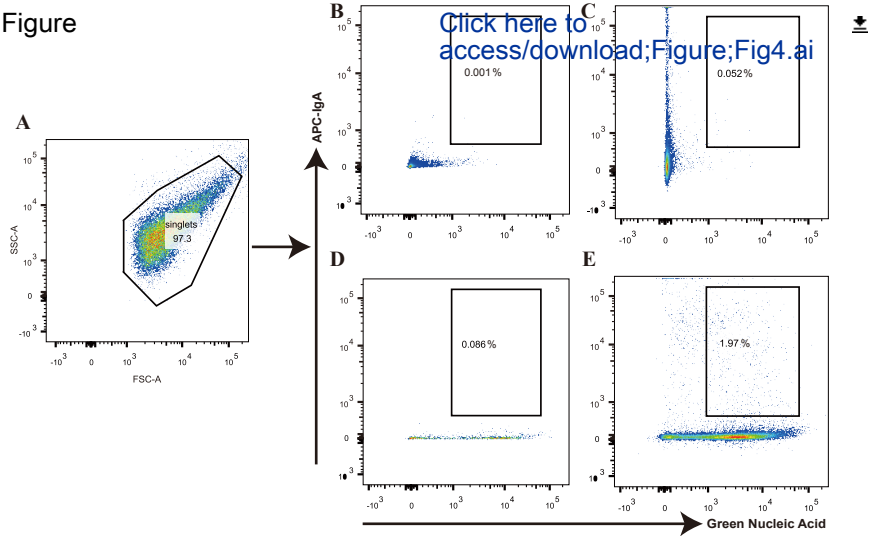
Figure A



B



Figure



Name	Company	Catalog
5 mL syringe needle	Sheng guang biotech	5mL
70 µm cell strainer	BD biosciences	352350
Ampicillin sodium salt	AMERESCO	0339
APC Streptavidin	BD biosciences	554067
Biotin anti-mouse IgA antibody	Biolegend	407003
Bovine serum albumin (BSA)	Sigma	B2064-50G
C57BL/6J mice	Chengdu Dashuo	
CO ₂	Xiyuan biotech	
<i>E.Coil</i> genome DNA	TsingKe	
Eppendorf tubes	Axygen	MCT150-C
Fast DNA stool mini Handbook	QIAGEN	51604
Metronidazole	Shyuanye	S17079-5g
Neomycin sulfate	SIGMA	N-1876
Oral gavage needle	Yuke biotech	10#
pClone007 Versatile simple TA vector kit	TsingKe	007VS
Phosphate Buffer Saline (PBS)	Hyclone	SH30256
Precellys lysing kit	Precellys	KT03961-1-001
RT PCR SYBR MIX	Vazyme	Q411-01
SYTO BC green Fluorescent Nucleic Acid Stain	Thermo fisher scientific	S34855
V338 F primer	TsingKe	
V806 R primer	TsingKe	
Vancomycin hydrochloride	Sigma	V2002

Equipments

BD FACSCalibur flow cytometer	BD biosciences
Bead beater vortex	Scilogex
BIORAD CFX Connect	BIORAD
Centrifuge machine	Eppendorf
Illumina MiSeq	Illumina
Nanodrop nucleic acid measurements machine	Thermo fisher scientific
Surgical instruments	Yuke biotech

Software

Adobe Illustrator CC 2015	Version 2015
BIORAD CFX qPCR SOFTWARE	
FlowJo software	
Graphpad prism 7	

Database

Silva (SSU132) 16S rRNA database

1.2

ACTCCTACGGGAGGCAGCAG
GGACTACHVGGGTWTCTAAT

software

FlowJo software

BIORADQPCR SOFTWARE

Graphpad prism 7

AI

Dear Dr. Luo,

Your manuscript, JoVE60772 "Fecal microbiota transplantation and the detection of prevalence of IgA-coated bacteria in the gut," has been editorially and peer reviewed, and the following comments need to be addressed. Note that editorial comments address both requirements for video production and formatting of the article for publication. Please track the changes within the manuscript to identify all of the edits.

After revising and uploading your submission, please also upload a separate rebuttal document that addresses each of the editorial and peer review comments individually. Please submit each figure as a vector image file to ensure high resolution throughout production: (.psd, ai, .eps., .svg). Please ensure that the image is 1920 x 1080 pixels or 300 dpi. Additionally, please upload tables as .xlsx files.

Your revision is due by Nov 13, 2019.

To submit a revision, go to the JoVE submission site and log in as an author. You will find your submission under the heading "Submission Needing Revision". Please note that the corresponding author in Editorial Manager refers to the point of contact during the review and production of the video article.

Best,

Peer Review,

Peer Review

JoVE

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About JoVE

Editorial comments:

1. Please take this opportunity to thoroughly proofread the manuscript to ensure that there are no spelling or grammar issues. The JoVE editor will not copy-edit your manuscript and any errors in the submitted revision may be present in the published version.

[Response: Thanks for the editors' suggestion. We have checked the manuscript thoroughly before submission.](#)

2. Authors and affiliations: Please provide an email address for each author in the manuscript.

[Response: As required by editors, we have provided a file with an email address for each author.](#)

3. Keywords: Please provide at least 6 keywords or phrases.

[Response: As required by editors, we have provided 6 keywords in the manuscript.](#)

4. JoVE cannot publish manuscripts containing commercial language. This includes trademark symbols (™), registered symbols (®), and company names before an instrument or reagent. Please remove all commercial language from your manuscript and use generic terms instead. All commercial products should be sufficiently referenced in the Table of Materials. You may use the generic term followed by "(Table of Materials)" to draw the readers' attention to specific commercial names. Examples of commercial sounding language in your manuscript are: eBioscience, SYTOTM, Thermo Fisher Scientific, BD FACSCalibur, BD Biosciences, etc.

[Response: As required by editors, we have removed the above information in the manuscript and provided commercial products information in Table of Materials.](#)

5. Please revise the Protocol to contain only action items that direct the reader to do something (e.g., “Do this,” “Ensure that,” etc.). The actions should be described in the imperative tense in complete sentences wherever possible. Avoid usage of phrases such as “could be,” “should be,” and “would be” throughout the Protocol. Any text that cannot be written in the imperative tense may be added as a “NOTE.” Please include all safety procedures and use of hoods, etc. However, notes should be used sparingly and actions should be described in the imperative tense wherever possible. Please move the discussion about the protocol to the Discussion.
6. The Protocol should be made up almost entirely of discrete steps without large paragraphs of text between sections. Please simplify the Protocol so that individual steps contain only 2-3 actions per step and a maximum of 4 sentences per step. Use sub-steps as necessary.
7. For each protocol step, please ensure you answer the “how” question, i.e., how is the step performed? Alternatively, add references to published material specifying how to perform the protocol action.

Response: As required by editors for comments 5, 6 and 7, we have revised Protocol section in the manuscript.

8. Figure 4: Please replace SYTO with a generic term.

Response: We have replaced SYTO with “Green Fluorescent Nucleic Acid Stain” in the manuscript.

9. Table of Materials: Please provide company and catalog number for all relevant supplies, reagents, equipment and software used, especially those mentioned in the Protocol. Please sort the materials alphabetically by material name.

Response: We have provided commercial products information in Table of Materials.

10. References: Please do not abbreviate journal titles; use full journal name.

Response: We have used full journal name in the manuscript.

Reviewers' comments:

Reviewer #1:

Manuscript Summary:

Antibiotics treatment, FMT, and IgA flow are all important procedures that are of broad interest in the microbiome field. The article covers these well and provides clear guidelines.

Major Concerns:

1. The total bacterial load is not assessed in any experiments, either by culturable colonies on nonselective media, or qPCR of all bacterial 16S. This is an important point for assessing the effectiveness of the antibiotics as well as comparing the different methods of FMT. Either qPCR or plating could be used to account for this.

Response: As suggested by the reviewer, we used RT-PCR to test the efficacy of bacteria depletion. The copy numbers in 1 mg gut contents is significantly reduced in the cecum and ileum in mice receiving antibiotics cocktail. The depletion efficacy is over 99%. Data were showed in Fig 2C.

2. Figure 4 is less convincing without including a FACS plot of bacteria stained with only SYTO-BC (and not anti IgA PE), which would make the rationale for the IgA+ gate more clear. The alternative would be staining with both colors but using a RAG KO mouse or other mouse that lacks IgA.

Response: We replaced PE-conjugated IgA antibody with biotin anti-IgA and APC-conjugated

biotin antibody for IgA staining. The FACS plots for single staining and double staining were added in Fig4.

Reviewer #2:

This manuscript is presenting an efficient way of fecal microbiota transplantation (FMT) from fresh or frozen donor intestinal contents to conventional mice and a flow cytometry-based method for detection of immunoglobulin A (IgA)-coating bacteria in the gut. Generally, the manuscript is well-written and provide a reproducible method in experimental study.

My major concern is that the method for FMT and detection of IgA-coating bacteria have been described in various literatures, could the authors describe the method for IgA-coating bacteria sorting using FACS-based method? In addition, if the authors transplant IgA+ and IgA- bacteria to recipients, what will be the difference of composition of bacteria in the recipient mice?

Response: Thanks for the reviewer's suggestion. However, we never sorted IgA-coating bacteria in our previous study. The reviewer can find the IgA-coating bacteria sorting, culture and transplantation details in the paper published by Palm et al (Immunoglobulin A Coating Identifies Colitogenic Bacteria in Inflammatory Bowel Disease. *Cell*, 2014, 158, 1000-1010).

Reviewer #3:

Manuscript Summary:

The authors address a very relevant question to the field of host-microbiota interactions. Indeed, a consensus on the best protocol to perform FMT in rodents would be very useful. However, the authors do not demonstrate that their protocol more efficient than other protocols or even just efficient. For that, they should 1) demonstrate the efficacy of the

microbiota depletion, and 2) explain figure 3 in a way that allow the reader to decipher if the recipient mice have an intestinal microbiota composition close to the inoculum composition. The following point should be addressed.

Major Concerns:

1. Several key publications documenting the impact of FMT protocols on the establishment of the inoculated microbiota should be mentioned and more importantly discussed, in particular:

a. Staley et al., 2017 about the efficacy of different antibiotics combinations to deplete the gut microbiota.

b. Wos-Oxley et al., 2012 about the impact of the recipient species (rat/mouse) on the quality of the transfer.

c. Ericsson et al., 2017 about the impact of the richness of the donors and recipients microbiota on the FMT, even after antibiotics-induced microbiota depletion.

d. Le Roy et al., 2019 about the impact of the age of the recipients and the necessity to remove antibiotics with laxatives before performing the FMT.

[Response: As suggested by the reviewer, we have incited these references and discussed in details in the discussion section.](#)

2. The authors indicate the difficulty to control the antibiotics dose when antibiotics are administered in the drinking water, however in my experience and as documented in the literature by others (Reikvam et al., 2011) the major pitfall of administering the antibiotics in drinking water is the extremely bitter taste of metronidazole that lead to a massive decrease of water and food intake and thus a significant weight loss. The authors should mention this limitation and indicate the water and food consumption along with the body

weight of the mice during the experiment. The authors also should explain why they decided to administer the antibiotics both by gavage and in the drinking water. Moreover, the choice of using the same concentrations of antibiotics in the drinking water and for the force-feeding is odd. Indeed, mice usually drink 3 to 5 ml per day, thus administering 200 µl by force feeding once a day should not dramatically increase the amount of antibiotics the mice receive per day.

Response: Thanks for the reviewer's suggestion. We have mentioned the limitation of administering antibiotics in drinking water as well as the weight loss problem in mice in the Discussion section. In our system, we orally gavage mice with antibiotics cocktails to make sure that mice receiving enough antibiotics dosage to deplete microbiota. In fact, others reported to deplete gut microbiota by oral gavage for 12 h, 24 h or 72 h although they did not show the depletion efficacy. The reason why we also administrated antibiotics in drinking water is : 1. to avoid bacteria contamination from the environment; 2. to ensure depletion efficacy.

3. Lines 78-85. I agree with the authors that different bacterial population are found in the different regions of the gastrointestinal tract, however I fail to understand what the authors mean by « it is imperative to isolate relevant gut contents for fecal fluid preparation » and what is the connection with the previous statements.

Response: We have revised this sentence to make it clear in the introduction section.

4. The authors should distinguish between human to human FMT for therapeutics purposes and human/mice to mice FMT for research purposes. The conclusions from one approach can not be extended to the other.

Response: The reviewer is right. We have modified the conclusion in the end of manuscript.

5. It is imperative that the authors explain how the fecal microbiota of the recipients mice was analyzed. In particular,

- a. the method of DNA extraction
- b. the sequencing primers sequences
- c. the initial number of sequences per sample
- d. the number of sequences after quality filtering
- e. the number of sequences of the smallest samples, in other words, what was the number of sequences used to compensate for differential sequencing depth between samples create normalized counts? Did the authors filter very low abundance sequences? This is generally highly recommended to filter sequences that represent less than 0.005% of the whole dataset.
- f. the software used to perform clustering
- g. the database used to assign a taxonomy to the OTUs

Response: Thanks for the reviewer's comment. We extracted DNA using QIAamp DNA Stool mini kit. The V3-V4 hypervariable regions of the bacteria 16S rRNA gene were amplified with primers 338F (5'- ACTCCTACGGGAGGCAGCAG-3') and 806R (5'-GGACTACHVGGGTWTCTAAT-3'). The taxonomy of each 16S rRNA gene sequence was analyzed against the Silva (SSU132) 16S rRNA database using a confidence threshold of 70%.

In this paper, we emphasize on the methods of microbiota depletion, FMT and IgA-coating bacteria measurement instead of data analysis. We have provided a material table and original sequencing table for microbiota depletion method. For FMT data, we include the sequencing and data analysis details in another article we will submit to a journal soon. Therefore, we only show the representative graphs as Figure 4 in this article.

6. Did the authors take care to avoid oxygen exposure during inocula preparations ? Did the authors eliminated the antibiotics from the gastrointestinal tract before performing the FMT ? If not, what was the time period between the last antibiotics administration and the first inoculum administration ? These points can be critical to ensure the success of the FMT.

Response: The points the reviewer brings up are very critical to the success of the FMT. In fact, In order to reduce the oxygen exposure time, we perform the gut contents collection and weighting steps as fast as possible (within 2-3 min). We did not eliminate the antibiotics before performing FMT. We perform FMT 24 h after the last antibiotics administration.

7. The efficacy of the microbiota depletion is not demonstrated. For that the authors should perform quantitative qPCR on total bacteria and/or bacterial cultivation.

Response: As suggested by the reviewer, we used RT-PCR to test the efficacy of bacteria depletion. The copy numbers in 1 mg of gut contents is significantly reduced in the cecum and ileum in mice receiving antibiotics cocktail. The depletion efficacy is over 99% based on the copy numbers. Data are shown in Fig 2C.

8. I fail to understand what results are presented in figure 3A. Are the results the fecal microbiota of the recipient mice ? the ileal microbiota of recipient mice ? Are these the results of recipient mice colonized with the ileal or the colonic content of donor mice ? The inocula composition?

Response: We are sorry for the unclear information for figure 3. We have modified the figure legends for Fig 3.

9. The connection between the FMT protocol and the IgA coated bacteria detection protocol is not clear.

Response: The microbiota shapes host immunity, the immune system shapes the gut microbiota as well through the secretion of IgA and antimicrobial peptides. It would be interesting to detect IgA-coating bacteria before and after FMT. However, since we always focus on IgA-coated bacteria alteration in the mice without FMT, in this study, we present FMT protocol and IgA-coating bacteria detection method separately in the manuscript.

Minor Concerns:

1. Please indicate the supplier and the reference number of the products in the table of materials.

Response: We have provided a Table of Materials with the supplier and reference number of the products.

2. It is indicated that the mice were sacrificed « humanely » but has the experiment been approved by an ethics committee and performed in accordance with the country laws ?

Response: Yes, we have an approval of Animal Ethical and Welfare in West China Hospital, Chengdu, China (Approval No: 2019248A).

3. Line 46 : document, present, detail... seems better word choice than « demonstrate ».

Response: We have changed to “demonstrate” in the manuscript.

4. Lines 54-55 : metabolic diseases are also largely affected by the composition of the microbiota, I suggest to the authors to add this point and one relevant reference.

Response: Thanks for the reviewer’s suggestion. We have added 2 references in the introduction section.

5. Lines 59-60: the reference 7 refers to the pulmonary mucosa, I suggest to the authors to replace it by a reference documenting the intestinal mucosa properties of germ-free mice, for example (Johansson et al., 2015; Reikvam et al., 2011; Smith et al., 2007).

Response: Thanks for the reviewer’s comment. We have replaced the reference 7 with paper published by Reikvam et al. 2011.

Line 63: did the authors mean « not consistant » or « inconsistant » instead of « not inconsistant » ?

Response: Sorry about the mistake. We have corrected it in the manuscript.

6. Please check the numbers of the references, I think that lines 80-81 refer to reference 14 instead of reference 15.

Response: We have checked the reference the reviewer mentioned and corrected it in the manuscript.

7. The amount of antibiotics given by oral gavage should be expressed as mg or g of antibiotics per kg.

Response: The reviewer is right. Sorry about the mistake. We have corrected it in the protocol.

8. Line 129: typo on the size of the force-feeding needle.

Response: We have added the size of the force-feeding needle in the manuscript.

9. Figure 2A, please indicate the unit of the Y axis.

Response: We have indicated the unit of the Y axis in Fig 2 as required by the reviewer.

Domain	Kingdom	Phylum	Class	Order	Family	Genus
d__Bacteri	k__norank	p__Firmicu	c__Clostrid	o__Clostric	f__Rumino	g__Ruminococcaceae_UCG-014
d__Bacteri	k__norank	p__Firmicu	c__Clostrid	o__Clostric	f__Rumino	g__Ruminococcus_1
d__Bacteri	k__norank	p__Proteol	c__Gamma	o__Enterol	f__Enterob	g__Escherichia-Shigella
d__Bacteri	k__norank	p__Firmicu	c__Erysipel	o__Erysipe	f__Erysipel	g__unclassified_f__Erysipelotrichaceae
d__Bacteri	k__norank	p__Firmicu	c__Clostrid	o__Clostric	f__Christer	g__Christensenellaceae_R-7_group
d__Bacteri	k__norank	p__Teneric	c__Mollicu	o__Mycopl	f__Mycopl	g__Mycoplasma
d__Bacteri	k__norank	p__Firmicu	c__Erysipel	o__Erysipe	f__Erysipel	g__Erysipelatoclostridium
d__Bacteri	k__norank	p__Firmicu	c__Clostrid	o__Clostric	f__Rumino	g__Subdoligranulum
d__Bacteri	k__norank	p__Proteol	c__Gamma	o__Pseudo	f__Pseudo	g__Pseudomonas
d__Bacteri	k__norank	p__Teneric	c__Mollicu	o__Mollicu	f__norank	g__norank_o__Mollicutes_RF9
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d__Bacteri	k__norank	p__Firmicu	c__Clostrid	o__Clostric	f__unclassi	g__unclassified_o__Clostridiales
d__Bacteri	k__norank	p__Teneric	c__Mollicu	o__Mollicu	f__norank	g__norank_o__Mollicutes_RF9
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d__Bacteri	k__norank	p__Proteol	c__Gamma	o__Pseudo	f__Moraxe	g__Acinetobacter
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d__Bacteri	k__norank	p__Teneric	c__Mollicu	o__Mollicu	f__norank	g__norank_o__Mollicutes_RF9
d__Bacteri	k__norank	p__Firmicu	c__Clostrid	o__Clostric	f__Rumino	g__Ruminococcaceae_UCG-013
d__Bacteri	k__norank	p__Proteol	c__Gamma	o__Pasteur	f__Pasteur	g__Pasteurella
d__Bacteri	k__norank	p__Proteol	c__Alphap	o__Rickett	f__Mitoch	g__norank_f__Mitochondria
d__Bacteri	k__norank	p__Firmicu	c__Clostrid	o__Clostric	f__Lachnos	g__Lachnospiraceae_UCG-006

d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Clostrid g__norank f__Clostridiales_vadinBB60_g
d__Bacteri.k__norank p__Teneric c__Mollicu o__Mollicu f__norank g__norank o__Mollicutes_RF9
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Ruminococcaceae_UCG-010
d__Bacteri.k__norank p__Teneric c__Mollicu o__Mollicu f__norank g__norank o__Mollicutes_RF9
d__Bacteri.k__norank p__Proteol c__Gamma o__Pasteur f__Pasteur g__Pasteurella
d__Bacteri.k__norank p__Actinot c__Actinob o__Coryne f__Corynet g__Corynebacterium
d__Bacteri.k__norank p__Proteol c__Alphapri o__Rhodos f__Rhodosi g__Reyranella
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__Marvinbryantia
d__Bacteri.k__norank p__Proteol c__Gamma o__Enterot f__Enterob g__Morganella
d__Bacteri.k__norank p__Teneric c__Mollicu o__Mollicu f__norank g__norank o__Mollicutes_RF9
d__Bacteri.k__norank p__Teneric c__Mollicu o__Mollicu f__norank g__norank o__Mollicutes_RF9
d__Bacteri.k__norank p__Firmicu c__Erysipel o__Erysipe f__Erysipel g__unclassified_f__Erysipelotrichaceae
d__Bacteri.k__norank p__Actinot c__Actinob o__Corioba f__Corioba g__Enterorhabdus
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__Lachnospiraceae_UCG-001
d__Bacteri.k__norank p__Proteol c__Alphapri o__Rhizobi f__Phyllobi g__Mesorhizobium
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__unclassified_f__Lachnospiraceae
d__Bacteri.k__norank p__Firmicu c__Bacilli o__Bacillat f__Bacillat g__Bacillus
d__Bacteri.k__norank p__Firmicu c__Bacilli o__Bacillat f__Family g__Exiguobacterium
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Ruminococcaceae_UCG-014
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__Lachnoclostridium
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Ruminococcus_1
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__unclassified_f__Lachnospiraceae
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__unclassified_f__Lachnospiraceae
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__norank_f__Ruminococcaceae
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Ruminiclostridium_5
d__Bacteri.k__norank p__Proteol c__Gamma o__Enterot f__Enterob g__Proteus
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Rikenell g__Alistipes
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__Lachnospiraceae_NK4A136_group
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__norank_f__Lachnospiraceae
d__Bacteri.k__norank p__Firmicu c__unclassi o__unclass f__unclassi g__unclassified_p__Firmicutes
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__norank_f__Lachnospiraceae
d__Bacteri.k__norank p__Actinot c__Actinob o__Corioba f__Corioba g__unclassified_f__Coriobacteriaceae
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__[Eubacterium]_coprostanoligenes_grc
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Christer g__Christensenellaceae_R-7_group
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__Lachnospiraceae_NK4A136_group
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Ruminiclostridium_6
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__unclassified_f__Lachnospiraceae
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__unclassified_f__Lachnospiraceae
d__Bacteri.k__norank p__Actinot c__Actinob o__Corioba f__Corioba g__Collinsella
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Prevote g__Prevotellaceae_UCG-001
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__Lachnospiraceae_UCG-006
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__unclassified_f__Lachnospiraceae
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Rikenell g__Alistipes
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__unclassified_f__Lachnospiraceae
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Family g__Family_XIII_AD3011_group
d__Bacteri.k__norank p__Firmicu c__Erysipel o__Erysipe f__Erysipel g__Allobaculum
d__Bacteri.k__norank p__Firmicu c__Erysipel o__Erysipe f__Erysipel g__norank_f__Erysipelotrichaceae

d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Anaerotruncus
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Ruminococcaceae_UCG-014
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Ruminococcaceae_UCG-014
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__norank_f__Lachnospiraceae
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__unclassified_f__Lachnospiraceae
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Ruminiclostridium_5
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Ruminococcaceae_UCG-010
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__Lachnoclostridium
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__unclassified_f__Lachnospiraceae
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__Anaerostipes
d__Bacteri.k__norank p__Cyanobc__Cyanob o__Gastrar f__norank_g__norank_o__Gastranaerophilales
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__Lachnospiraceae_FCS020_group
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Ruminococcaceae_UCG-014
d__Bacteri.k__norank p__Proteol c__Epsilon o__Campyl f__Helicob;g__Helicobacter
d__Bacteri.k__norank p__Teneric c__Mollicu o__Mollicu f__norank_g__norank_o__Mollicutes_RF9
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Ruminococcaceae_UCG-014
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__norank_f__Lachnospiraceae
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Peptocc g__norank_f__Peptococcaceae
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Ruminococcaceae_UCG-014
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Ruminococcaceae_UCG-009
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Peptocc g__norank_f__Peptococcaceae
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__unclassified_f__Lachnospiraceae
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__unclassi g__unclassified_o__Bacteroidales
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__unclassified_f__Lachnospiraceae
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__Roseburia
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Rikenell g__Alistipes
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__Blautia
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Christer g__norank_f__Christensenellaceae
d__Bacteri.k__norank p__Firmicu c__Erysipel o__Erysipe f__Erysipel g__unclassified_f__Erysipelotrichaceae
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Peptocc g__norank_f__Peptococcaceae
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Ruminococcaceae_UCG-014
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__unclassified_f__Lachnospiraceae
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__norank_f__Lachnospiraceae
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__unclassified_f__Lachnospiraceae
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Ruminiclostridium_9
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__unclassified_f__Ruminococcaceae
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__norank_f__Ruminococcaceae
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Anaerotruncus
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Ruminococcus_1
d__Bacteri.k__norank p__Teneric c__Mollicu o__Mollicu f__norank_g__norank_o__Mollicutes_RF9
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__Lachnospiraceae_NK4A136_group
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Bactero g__norank_f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__unclassified_f__Ruminococcaceae
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Bactero g__norank_f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Faecalibacterium
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Ruminococcaceae_UCG-014
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Anaerotruncus

d__Bacteri.k__norank p__Firmicu.c__Erysipel.o__Erysipe.f__Erysipel.g__Erysipelatoclostridium
d__Bacteri.k__norank p__Firmicu.c__Bacilli.o__Lactoba.f__Enteroc.g__Enterococcus
d__Bacteri.k__norank p__Bacterc.c__Bacterc.o__Bacterc.f__Bactero.g__norank.f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Rumino.g__Ruminococcaceae_UCG-010
d__Bacteri.k__norank p__Firmicu.c__unclassi.o__unclass.f__unclassi.g__unclassified_p__Firmicutes
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__Lachnospiraceae_NK4A136_group
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__Lachnospiraceae_NK4A136_group
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__Lachnospiraceae_UCG-001
d__Bacteri.k__norank p__Actinot.c__Actinob.o__Corioba.f__Corioba.g__Enterorhabdus
d__Bacteri.k__norank p__Bacterc.c__Bacterc.o__Bacterc.f__Bactero.g__norank.f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Teneric.c__Mollicu.o__Mollicu.f__norank.g__norank.o__Mollicutes_RF9
d__Bacteri.k__norank p__Bacterc.c__Bacterc.o__Bacterc.f__Rikenell.g__Alistipes
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Rumino.g__Ruminiclostridium_9
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Clostrid.g__norank.f__Clostridiales_vadinBB60_g
d__Bacteri.k__norank p__Bacterc.c__Bacterc.o__Bacterc.f__Bactero.g__norank.f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Bacterc.c__Bacterc.o__Bacterc.f__Bactero.g__norank.f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Sacchar.c__Unknov.o__Unknov.f__Unknov.g__Candidatus_Saccharimonas
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__unclassified.f__Lachnospiraceae
d__Bacteri.k__norank p__Bacterc.c__Bacterc.o__Bacterc.f__Bactero.g__norank.f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Rumino.g__Ruminococcaceae_UCG-014
d__Bacteri.k__norank p__Bacterc.c__Bacterc.o__Bacterc.f__Bactero.g__norank.f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Rumino.g__Ruminococcaceae_UCG-014
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Rumino.g__Ruminococcaceae_UCG-013
d__Bacteri.k__norank p__Firmicu.c__Bacilli.o__Lactoba.f__Lactoba.g__Lactobacillus
d__Bacteri.k__norank p__Firmicu.c__Bacilli.o__unclass.f__unclassi.g__unclassified_c__Bacilli
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Rumino.g__Ruminococcaceae_UCG-014
d__Bacteri.k__norank p__Bacterc.c__Bacterc.o__Bacterc.f__Bactero.g__norank.f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Clostrid.g__norank.f__Clostridiales_vadinBB60_g
d__Bacteri.k__norank p__Bacterc.c__Bacterc.o__Bacterc.f__Prevote.g__Paraprevotella
d__Bacteri.k__norank p__Teneric.c__Mollicu.o__Mollicu.f__norank.g__norank.o__Mollicutes_RF9
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__unclassified.f__Lachnospiraceae
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Rumino.g__Anaerotruncus
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Rumino.g__Ruminococcaceae_UCG-014
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__unclassified.f__Lachnospiraceae
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__norank.f__Lachnospiraceae
d__Bacteri.k__norank p__Bacterc.c__Bacterc.o__Bacterc.f__Bactero.g__norank.f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Rumino.g__Anaerotruncus
d__Bacteri.k__norank p__Proteol.c__Deltapr.o__Desulfc.f__Desulfo.g__Bilophila
d__Bacteri.k__norank p__Bacterc.c__Bacterc.o__Bacterc.f__Prevote.g__Prevotellaceae_UCG-001
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Rumino.g__Ruminococcaceae_UCG-014
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__norank.f__Lachnospiraceae
d__Bacteri.k__norank p__Actinot.c__Actinob.o__Corioba.f__Corioba.g__unclassified.f__Coriobacteriaceae
d__Bacteri.k__norank p__Firmicu.c__Bacilli.o__Lactoba.f__Lactoba.g__Lactobacillus
d__Bacteri.k__norank p__Bacterc.c__Bacterc.o__Bacterc.f__Bactero.g__norank.f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Firmicu.c__Bacilli.o__Lactoba.f__Lactoba.g__Lactobacillus
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Rumino.g__Anaerotruncus
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Family.g__Family_XIII_AD3011_group

d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Clostrid g__norank f__Clostridiales_vadinBB60_g
d__Bacteri.k__norank p__Teneric c__Mollicu o__Mollicu f__norank g__norank o__Mollicutes_RF9
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Bactero g__norank f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Family_g__Family_XIII_AD3011_group
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Ruminococcaceae_UCG-013
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Ruminococcaceae_UCG-014
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__norank f__Lachnospiraceae
d__Bacteri.k__norank p__Firmicu c__Erysipel o__Erysipe f__Erysipel g__unclassified_f__Erysipelotrichaceae
d__Bacteri.k__norank p__Teneric c__Mollicu o__Mollicu f__norank g__norank o__Mollicutes_RF9
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Bactero g__norank f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Anaerotruncus
d__Bacteri.k__norank p__Teneric c__Mollicu o__Mollicu f__norank g__norank o__Mollicutes_RF9
d__Bacteri.k__norank p__Teneric c__Mollicu o__Mollicu f__norank g__norank o__Mollicutes_RF9
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Bactero g__norank f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Rikenell g__Rikenellaceae_RC9_gut_group
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Bactero g__norank f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Teneric c__Mollicu o__Mollicu f__norank g__norank o__Mollicutes_RF9
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Oscillibacter
d__Bacteri.k__norank p__Teneric c__Mollicu o__Mollicu f__norank g__norank o__Mollicutes_RF9
d__Bacteri.k__norank p__Firmicu c__Bacilli o__Lactoba f__Lactoba g__Lactobacillus
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Oscillibacter
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Bactero g__norank f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Anaerotruncus
d__Bacteri.k__norank p__Teneric c__Mollicu o__Anaero f__Anaero g__Anaeroplasma
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Anaerotruncus
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__Tyzzerella
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Anaerotruncus
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Bactero g__norank f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Firmicu c__unclassi o__unclass f__unclassi g__unclassified_p__Firmicutes
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__Blautia
d__Bacteri.k__norank p__Firmicu c__Bacilli o__Lactoba f__unclassi g__unclassified_o__Lactobacillales
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__[Eubacterium]_ventriosum_group
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Oscillibacter
d__Bacteri.k__norank p__Actinot c__Actinob o__Bifidob f__Bifidoba g__Bifidobacterium
d__Bacteri.k__norank p__Teneric c__Mollicu o__Mollicu f__norank g__norank o__Mollicutes_RF9
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__norank f__Lachnospiraceae
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Butyricicoccus
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__unclassi g__unclassified_o__Bacteroidales
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__Lachnospiraceae_NK4A136_group
d__Bacteri.k__norank p__Teneric c__Mollicu o__Mollicu f__norank g__norank o__Mollicutes_RF9
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__Lachnospiraceae_NK4A136_group
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Bactero g__norank f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Bactero g__norank f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Actinot c__Actinob o__Corioba f__Corioba g__Enterorhabdus
d__Bacteri.k__norank p__Teneric c__Mollicu o__Mollicu f__norank g__norank o__Mollicutes_RF9
d__Bacteri.k__norank p__Cyanob c__Cyanob o__Gastrar f__norank g__norank o__Gastranaerophilales
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Clostrid g__norank f__Clostridiales_vadinBB60_g

d__Bacteri.k__norank p__Actinot.c__Actinob.o__Corioba.f__Corioba.g__Coriobacteriaceae_UCG-002
d__Bacteri.k__norank p__Bacterc.c__Bacterc.o__Bacterc.f__Bactero.g__norank.f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Bacterc.c__Bacterc.o__Bacterc.f__Bactero.g__norank.f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Clostrid.g__norank.f__Clostridiales_vadinBB60_g
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Rumino.g__Ruminococcaceae_UCG-014
d__Bacteri.k__norank p__Teneric.c__Mollicu.o__Mollicu.f__norank.g__norank.o__Mollicutes_RF9
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Clostrid.g__norank.f__Clostridiales_vadinBB60_g
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Rumino.g__Ruminiclostridium
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Rumino.g__Subdoligranulum
d__Bacteri.k__norank p__Firmicu.c__Erysipel.o__Erysipe.f__Erysipel.g__Catenibacterium
d__Bacteri.k__norank p__Proteol.c__Gamma.o__Pasteur.f__Pasteur.g__Haemophilus
d__Bacteri.k__norank p__Actinot.c__Actinob.o__Corioba.f__Corioba.g__Parvibacter
d__Bacteri.k__norank p__Teneric.c__Mollicu.o__Mollicu.f__norank.g__norank.o__Mollicutes_RF9
d__Bacteri.k__norank p__Bacterc.c__Bacterc.o__Bacterc.f__Bactero.g__norank.f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Cyanob.c__Cyanob.o__Gastrar.f__norank.g__norank.o__Gastranaerophilales
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Rumino.g__Ruminococcaceae_UCG-014
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Rumino.g__Ruminococcaceae_UCG-014
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Rumino.g__unclassified.f__Ruminococcaceae
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__unclassified.f__Lachnospiraceae
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Rumino.g__Candidatus_Soleaferrea
d__Bacteri.k__norank p__Bacterc.c__Bacterc.o__Bacterc.f__Bactero.g__norank.f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Verrucc.c__Verrucc.o__Verrucc.f__Verruco.g__Akkermansia
d__Bacteri.k__norank p__Bacterc.c__Bacterc.o__Bacterc.f__Bactero.g__norank.f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__norank.f__Lachnospiraceae
d__Bacteri.k__norank p__Firmicu.c__Erysipel.o__Erysipe.f__Erysipel.g__Allobaculum
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__unclassified.f__Lachnospiraceae
d__Bacteri.k__norank p__Bacterc.c__Bacterc.o__Bacterc.f__Rikenell.g__Alistipes
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Rumino.g__Anaerotruncus
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__Lachnospiraceae_NK4A136_group
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__norank.f__Lachnospiraceae
d__Bacteri.k__norank p__Actinot.c__Actinob.o__Corioba.f__Corioba.g__Enterorhabdus
d__Bacteri.k__norank p__Teneric.c__Mollicu.o__Mollicu.f__norank.g__norank.o__Mollicutes_RF9
d__Bacteri.k__norank p__Bacterc.c__Bacterc.o__Bacterc.f__Bactero.g__norank.f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Family.g__[Eubacterium]_brachy_group
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__unclassified.f__Lachnospiraceae
d__Bacteri.k__norank p__Bacterc.c__Bacterc.o__Bacterc.f__Porphyrg__Parabacteroides
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__unclassified.f__Lachnospiraceae
d__Bacteri.k__norank p__Actinot.c__Actinob.o__Coryne.f__Corynet.g__unclassified.f__Corynebacteriaceae
d__Bacteri.k__norank p__Firmicu.c__unclassi.o__unclass.f__unclassi.g__unclassified.p__Firmicutes
d__Bacteri.k__norank p__Proteol.c__Alphapri.o__Rhodos.f__Rhodos.g__norank.f__Rhodospirillaceae
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__Lachnospiraceae_NK4A136_group
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__Lachnospiraceae_NK4A136_group
d__Bacteri.k__norank p__Bacterc.c__Bacterc.o__Bacterc.f__Bactero.g__norank.f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Firmicu.c__Erysipel.o__Erysipe.f__Erysipel.g__Solobacterium
d__Bacteri.k__norank p__Bacterc.c__Bacterc.o__Bacterc.f__unclassi.g__unclassified.o__Bacteroidales
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__Lachnospiraceae_NK4A136_group
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__unclassified.f__Lachnospiraceae

d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Clostrid g__norank_f__Clostridiales_vadinBB60_g
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__unclassified_f__Ruminococcaceae
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Anaerotruncus
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Bactero g__norank_f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Bactero g__norank_f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Rikenell g__Alistipes
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Clostrid g__norank_f__Clostridiales_vadinBB60_g
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Bactero g__norank_f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__norank_f__Lachnospiraceae
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Clostrid g__norank_f__Clostridiales_vadinBB60_g
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Bactero g__Bacteroides
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__unclassified_f__Ruminococcaceae
d__Bacteri.k__norank p__Actinot c__Actinob o__Corioba f__Corioba g__Enterorhabdus
d__Bacteri.k__norank p__Proteol c__Deltapr o__Desulfc f__Desulfo g__Desulfovibrio
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Bactero g__norank_f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Proteol c__Deltapr o__Desulfc f__Desulfo g__Desulfovibrio
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Porphyrg__Odoribacter
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Clostrid g__norank_f__Clostridiales_vadinBB60_g
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Bactero g__norank_f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Christer g__norank_f__Christensenellaceae
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Bactero g__norank_f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Proteol c__Betaprc o__Burkho f__Alcalige g__Parasutterella
d__Bacteri.k__norank p__Firmicu c__Bacilli o__Bacillal f__Bacillaci g__unclassified_f__Bacillaceae
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Bactero g__norank_f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Rikenell g__Alistipes
d__Bacteri.k__norank p__Actinot c__Actinob o__Corioba f__Corioba g__norank_f__Coriobacteriaceae
d__Bacteri.k__norank p__Proteol c__Betaprc o__Burkho f__Alcalige g__Paenalcaligenes
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__Lachnospiraceae_NK4A136_group
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Bactero g__Bacteroides
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Clostrid g__norank_f__Clostridiales_vadinBB60_g
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__Lachnospiraceae_NK4A136_group
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__unclassified_f__Lachnospiraceae
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Ruminiclostridium_5
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Eubacte g__Anaerofustis
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Ruminiclostridium
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Ruminococcaceae_UCG-014
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__norank_f__Lachnospiraceae
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__unclassified_f__Lachnospiraceae
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__Blautia
d__Bacteri.k__norank p__Proteol c__Gamma o__Enterof f__Enterob g__Providencia
d__Bacteri.k__norank p__Firmicu c__Bacilli o__Lactob f__Lactoba g__Lactobacillus
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__[Eubacterium]_xylanophilum_group
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Ruminococcaceae_UCG-013
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Ruminococcaceae_UCG-010
d__Bacteri.k__norank p__Firmicu c__Erysipel o__Erysipe f__Erysipel g__Candidatus_Stoquefichus
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__unclassified_f__Ruminococcaceae
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Bactero g__norank_f__Bacteroidales_S24-7_grou

d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Bactero g__norank_f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__unclassi g__unclassified_o__Bacteroidales
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__unclassified_f__Lachnospiraceae
d__Bacteri.k__norank p__Actinot c__Actinob o__Corioba f__Corioba g__Enterorhabdus
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Bactero g__norank_f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Bactero g__norank_f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Deferril c__Deferril o__Deferril f__Deferril g__Mucispirillum
d__Bacteri.k__norank p__Teneric c__Mollicu o__Mollicu f__norank_g__norank_o__Mollicutes_RF9
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Bactero g__norank_f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Bactero g__norank_f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Firmicu c__Erysipel o__Erysipe f__Erysipel g__norank_f__Erysipelotrichaceae
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Anaerotruncus
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Clostrid g__norank_f__Clostridiales_vadinBB60_g
d__Bacteri.k__norank p__Firmicu c__Erysipel o__Erysipe f__Erysipel g__unclassified_f__Erysipelotrichaceae
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Bactero g__norank_f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__unclassified_f__Ruminococcaceae
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Ruminococcaceae_UCG-014
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__unclassified_f__Lachnospiraceae
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Ruminococcaceae_UCG-014
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Prevote g__Alloprevotella
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__unclassified_f__Lachnospiraceae
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__norank_f__Lachnospiraceae
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Bactero g__norank_f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Proteol c__Gamma o__Pseudo f__Moraxe g__Psychrobacter
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Bactero g__norank_f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__Roseburia
d__Bacteri.k__norank p__Firmicu c__unclassi o__unclass f__unclassi g__unclassified_p__Firmicutes
d__Bacteri.k__norank p__Proteol c__Deltapr o__Desulfc f__Desulfo g__Desulfovibrio
d__Bacteri.k__norank p__Firmicu c__Erysipel o__Erysipe f__Erysipel g__Erysipelatoclostridium
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Anaerotruncus
d__Bacteri.k__norank p__Proteol c__Betaprc o__Burkho f__Comam g__Comamonas
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Bactero g__Bacteroides
d__Bacteri.k__norank p__Actinot c__Actinob o__Microc f__Microcc g__Glutamicibacter
d__Bacteri.k__norank p__unclass c__unclassi o__unclass f__unclassi g__unclassified_k__norank
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Ruminiclostridium_9
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Christer g__norank_f__Christensenellaceae
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Ruminiclostridium_5
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Bactero g__norank_f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Bactero g__norank_f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Proteol c__Gamma o__Xantho f__Xanthor g__Stenotrophomonas
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Clostrid g__Candidatus_Arthromitus
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Rikenell g__Alistipes
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Family_g__[Eubacterium]_nodatum_group
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__Marvinbryantia
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Bactero g__norank_f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Bacterc c__Sphingc o__Sphingc f__Sphingo g__Sphingobacterium
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__norank_f__Lachnospiraceae

d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__unclassified.f__Lachnospiraceae
d__Bacteri.k__norank p__Bacterc.c__Bacterc.o__Bacterc.f__Bactero.g__norank.f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Firmicu.c__Bacilli.o__Lactob.f__Strepto.g__Lactococcus
d__Bacteri.k__norank p__unclass.c__unclass.o__unclass.f__unclassi.g__unclassified.k__norank
d__Bacteri.k__norank p__Deferril.c__Deferril.o__Deferril.f__Deferril.g__Mucispirillum
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Rumino.g__Ruminococcaceae_UCG-014
d__Bacteri.k__norank p__Firmicu.c__Erysipel.o__Erysipe.f__Erysipel.g__norank.f__Erysipelotrichaceae
d__Bacteri.k__norank p__Bacterc.c__Bacterc.o__Bacterc.f__Rikenell.g__Alistipes
d__Bacteri.k__norank p__Bacterc.c__Bacterc.o__Bacterc.f__Rikenell.g__Alistipes
d__Bacteri.k__norank p__Proteol.c__Deltapr.o__Desulfc.f__Desulfo.g__Desulfovibrio
d__Bacteri.k__norank p__Firmicu.c__Negativ.o__Seleno.f__Veillone.g__Megamonas
d__Bacteri.k__norank p__Proteol.c__Alphapr.o__Caulob.f__Cauloba.g__Brevundimonas
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Clostrid.g__norank.f__Clostridiales_vadinBB60_g
d__Bacteri.k__norank p__Firmicu.c__Bacilli.o__Lactob.f__Carnob.f__Trichococcus
d__Bacteri.k__norank p__Bacterc.c__Bacterc.o__Bacterc.f__Bactero.g__Bacteroides
d__Bacteri.k__norank p__Actinot.c__Actinob.o__Coryne.f__Corynet.g__Corynebacterium_1
d__Bacteri.k__norank p__Bacterc.c__Sphingc.o__Sphingc.f__Sphingo.g__Sphingobacterium
d__Bacteri.k__norank p__Firmicu.c__Bacilli.o__Bacillal.f__Planoco.g__Solibacillus
d__Bacteri.k__norank p__Actinot.c__Actinob.o__Microc.f__Microcc.g__Enteractinococcus
d__Bacteri.k__norank p__Firmicu.c__Bacilli.o__Lactob.f__Aerococ.g__Facklamia
d__Bacteri.k__norank p__Firmicu.c__Bacilli.o__Lactob.f__Carnob.f__Atopostipes
d__Bacteri.k__norank p__Firmicu.c__Bacilli.o__Lactob.f__Carnob.f__Atopostipes
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Rumino.g__Anaerotruncus
d__Bacteri.k__norank p__Firmicu.c__Bacilli.o__Bacillal.f__Staphyl.g__Staphylococcus
d__Bacteri.k__norank p__Bacterc.c__Bacterc.o__Bacterc.f__Bactero.g__norank.f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Proteol.c__Gamma.o__Aerom.f__Aeromo.g__Aeromonas
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__Roseburia
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__Coprococcus_2
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Clostrid.g__norank.f__Clostridiales_vadinBB60_g
d__Bacteri.k__norank p__Firmicu.c__Bacilli.o__Lactob.f__Lactoba.g__Lactobacillus
d__Bacteri.k__norank p__Firmicu.c__Bacilli.o__Lactob.f__Strepto.g__Streptococcus
d__Bacteri.k__norank p__Actinot.c__Actinob.o__Coriob.f__Corioba.g__Gordonibacter
d__Bacteri.k__norank p__Firmicu.c__Bacilli.o__Bacillal.f__Planoco.g__Lysinibacillus
d__Bacteri.k__norank p__Firmicu.c__unclass.o__unclass.f__unclassi.g__unclassified.p__Firmicutes
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Rumino.g__Ruminococcaceae_UCG-014
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__norank.f__Lachnospiraceae
d__Bacteri.k__norank p__Firmicu.c__Bacilli.o__Lactob.f__Lactoba.g__Lactobacillus
d__Bacteri.k__norank p__Bacterc.c__Bacterc.o__Bacterc.f__Bactero.g__norank.f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Actinot.c__Actinob.o__Microc.f__Dermab.g__Brachybacterium
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__unclassified.f__Lachnospiraceae
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Rumino.g__Ruminiclostridium
d__Bacteri.k__norank p__Actinot.c__Actinob.o__Pseudo.f__Pseudor.g__Saccharopolyspora
d__Bacteri.k__norank p__Teneric.c__Mollicu.o__Mollicu.f__norank.g__norank.o__Mollicutes_RF9
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Rumino.g__Ruminococcus_2
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__Lachnospiraceae_NK4A136_group
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Family.g__[Eubacterium]_brachy_group
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Rumino.g__Ruminococcaceae_UCG-014

d__Bacteri.k__norank p__Teneric.c__Mollicu.o__Mollicu.f__norank.g__norank.o__Mollicutes_RF9
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Rumino.g__Ruminococcaceae_UCG-013
d__Bacteri.k__norank p__Teneric.c__Mollicu.o__Mollicu.f__norank.g__norank.o__Mollicutes_RF9
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Rumino.g__Ruminococcaceae_UCG-014
d__Bacteri.k__norank p__Bacterc.c__Bacterc.o__Bacterc.f__Bactero.g__norank.f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Peptost.g__Paraclostridium
d__Bacteri.k__norank p__Actinot.c__Actinob.o__Microc.f__Breviba.g__Brevibacterium
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__norank.f__Lachnospiraceae
d__Bacteri.k__norank p__Bacterc.c__Bacterc.o__Bacterc.f__Prevote.g__Prevotella_9
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Rumino.g__Anaerotruncus
d__Bacteri.k__norank p__Bacterc.c__Bacterc.o__Bacterc.f__Bactero.g__Bacteroides
d__Bacteri.k__norank p__Firmicu.c__Bacilli.o__Lactob.f__Lactoba.g__Lactobacillus
d__Bacteri.k__norank p__Firmicu.c__Negativ.o__Selenof__Veillone.g__Dialister
d__Bacteri.k__norank p__Bacterc.c__Bacterc.o__Bacterc.f__Bactero.g__Bacteroides
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__norank.f__Lachnospiraceae
d__Bacteri.k__norank p__Firmicu.c__Bacilli.o__Lactob.f__Aerococ.g__Faeklamia
d__Bacteri.k__norank p__Bacterc.c__Bacterc.o__Bacterc.f__Bactero.g__Bacteroides
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__unclassified.f__Lachnospiraceae
d__Bacteri.k__norank p__Proteol.c__Gamma.o__Pseudo.f__Moraxe.g__Acinetobacter
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__norank.f__Lachnospiraceae
d__Bacteri.k__norank p__Proteol.c__Gamma.o__Enterof__Enterob.g__Citrobacter
d__Bacteri.k__norank p__Firmicu.c__Bacilli.o__Lactob.f__Lactoba.g__Lactobacillus
d__Bacteri.k__norank p__Teneric.c__Mollicu.o__Mollicu.f__norank.g__norank.o__Mollicutes_RF9
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__unclassified.f__Lachnospiraceae
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Rumino.g__Ruminococcaceae_UCG-002
d__Bacteri.k__norank p__Firmicu.c__Negativ.o__Selenof__Acidamig__Phascolarctobacterium
d__Bacteri.k__norank p__Actinot.c__Actinob.o__Microc.f__Microb.g__Curtobacterium
d__Bacteri.k__norank p__Firmicu.c__Erysipel.o__Erysipe.f__Erysipel.g__Faecalibaculum
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Rumino.g__unclassified.f__Ruminococcaceae
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__unclassified.f__Lachnospiraceae
d__Bacteri.k__norank p__Actinot.c__Actinob.o__Coriob.f__Corioba.g__Enterorhabdus
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__Roseburia
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Rumino.g__Anaerotruncus
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__unclassified.f__Lachnospiraceae
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Rumino.g__Ruminococcaceae_UCG-014
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__unclassified.f__Lachnospiraceae
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__unclassified.f__Lachnospiraceae
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__Lachnospiraceae_NK4A136_group
d__Bacteri.k__norank p__Actinot.c__Actinob.o__Coryne.f__Nocardi.g__Rhodococcus
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Rumino.g__Anaerotruncus
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__Lachnoclostridium
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__norank.f__Lachnospiraceae
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__norank.f__Lachnospiraceae
d__Bacteri.k__norank p__Bacterc.c__Bacterc.o__Bacterc.f__Bactero.g__norank.f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__norank.f__Lachnospiraceae
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__unclassified.f__Lachnospiraceae
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__Blautia

d__Bacteri.k__norank p__Firmicu.c__Bacilli o__Lactoba.f__Lactoba.g__Lactobacillus
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Rumino.g__Anaerotruncus
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Rumino.g__Ruminiclostridium_9
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__Lachnospiraceae_UCG-001
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__Tyzzerella_3
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Rumino.g__Ruminococcaceae_NK4A214_group
d__Bacteri.k__norank p__Bacterc.c__Bacterc.o__Bacterc.f__Porphyrg__Parabacteroides
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Clostrid.g__norank.f__Clostridiales_vadinBB60_g
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__unclassified.f__Lachnospiraceae
d__Bacteri.k__norank p__Bacterc.c__Bacterc.o__Bacterc.f__Bacterog__norank.f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__unclassified.g__unclassified.o__Clostridiales
d__Bacteri.k__norank p__Bacterc.c__Bacterc.o__Bacterc.f__Bacterog__norank.f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Teneric.c__Mollicu.o__Mollicu.f__norank.g__norank.o__Mollicutes_RF9
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__Lachnospiraceae_NK4A136_group
d__Bacteri.k__norank p__Bacterc.c__Bacterc.o__Bacterc.f__Porphyrg__Odoribacter
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__norank.f__Lachnospiraceae
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Rumino.g__Anaerotruncus
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__Roseburia
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Rumino.g__norank.f__Ruminococcaceae
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__Blautia
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Rumino.g__Anaerotruncus
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Rumino.g__Ruminococcaceae_UCG-004
d__Bacteri.k__norank p__Firmicu.c__Erysipel.o__Erysipe.f__Erysipel.g__norank.f__Erysipelotrichaceae
d__Bacteri.k__norank p__Teneric.c__Mollicu.o__Mollicu.f__norank.g__norank.o__Mollicutes_RF9
d__Bacteri.k__norank p__Bacterc.c__Bacterc.o__Bacterc.f__Bacterog__norank.f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__norank.f__Lachnospiraceae
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__Lachnospiraceae_UCG-001
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Rumino.g__Ruminiclostridium_5
d__Bacteri.k__norank p__Bacterc.c__Bacterc.o__Bacterc.f__Rikenell.g__Alistipes
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__Lachnospiraceae_UCG-001
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Clostrid.g__norank.f__Clostridiales_vadinBB60_g
d__Bacteri.k__norank p__Cyanobc__Cyanob.o__norank.f__norank.g__norank.c__Cyanobacteria
d__Bacteri.k__norank p__Bacterc.c__Bacterc.o__Bacterc.f__Bacterog__norank.f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__Roseburia
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__norank.f__Lachnospiraceae
d__Bacteri.k__norank p__Firmicu.c__Bacilli o__Lactoba.f__Lactoba.g__Lactobacillus
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__norank.f__Lachnospiraceae
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__unclassified.f__Lachnospiraceae
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Clostrid.g__norank.f__Clostridiales_vadinBB60_g
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Lachnos.g__Lachnospiraceae_UCG-001
d__Bacteri.k__norank p__Firmicu.c__Bacilli o__Lactoba.f__Enteroc.g__Enterococcus
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Rumino.g__[Eubacterium]_coprostanoligenes_grc
d__Bacteri.k__norank p__Bacterc.c__Bacterc.o__Bacterc.f__Bacterog__norank.f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Bacterc.c__Bacterc.o__Bacterc.f__Rikenell.g__Rikenella
d__Bacteri.k__norank p__Firmicu.c__Bacilli o__Lactoba.f__Strepto.g__Streptococcus
d__Bacteri.k__norank p__Firmicu.c__Clostrid.o__Clostric.f__Rumino.g__Ruminiclostridium
d__Bacteri.k__norank p__Bacterc.c__Bacterc.o__Bacterc.f__Bacterog__norank.f__Bacteroidales_S24-7_grou

d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Bactero g__norank_f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Clostrid g__norank_f__Clostridiales_vadinBB60_g
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Ruminococcaceae_UCG-005
d__Bacteri.k__norank p__Firmicu c__Bacilli o__Bacillal f__Bacillac g__Bacillus
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Porphyrg__Odoribacter
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Bactero g__norank_f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Clostrid g__norank_f__Clostridiales_vadinBB60_g
d__Bacteri.k__norank p__Proteol c__Betaprc o__Burkho f__Alcalige g__Bordetella
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__Lachnospiraceae_NK4A136_group
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Bactero g__Bacteroides
d__Bacteri.k__norank p__Firmicu c__unclassi o__unclass f__unclassi g__unclassified_p__Firmicutes
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Ruminococcaceae_UCG-005
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__Lachnospiraceae_NK4A136_group
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__norank_f__Lachnospiraceae
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__norank_f__Lachnospiraceae
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__unclassified_f__Lachnospiraceae
d__Bacteri.k__norank p__Firmicu c__Bacilli o__Bacillal f__Staphyl g__Jeotgalicoccus
d__Bacteri.k__norank p__Firmicu c__Bacilli o__Lactob f__Lactoba g__Lactobacillus
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__Lachnoclostridium
d__Bacteri.k__norank p__Actinot c__Actinob o__Coriob f__Corioba g__Enterorhabdus
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Family_g__Family_XIII_UCG-001
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Butyricicoccus
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Ruminococcaceae_UCG-010
d__Bacteri.k__norank p__Firmicu c__Bacilli o__Bacillal f__Bacillac g__Bacillus
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__unclassified_f__Ruminococcaceae
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Bactero g__norank_f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Proteol c__Gamma o__Pseudo f__Moraxe g__Psychrobacter
d__Bacteri.k__norank p__Firmicu c__Bacilli o__Bacillal f__Staphyl g__Staphylococcus
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Rikenell g__Alistipes
d__Bacteri.k__norank p__Firmicu c__Bacilli o__Bacillal f__Staphyl g__Staphylococcus
d__Bacteri.k__norank p__Firmicu c__Bacilli o__Bacillal f__Planoco g__Sporosarcina
d__Bacteri.k__norank p__Proteol c__Gamma o__Pseudo f__Moraxe g__Acinetobacter
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Rikenell g__Alistipes
d__Bacteri.k__norank p__Firmicu c__Bacilli o__Bacillal f__Staphyl g__Jeotgalicoccus
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__[Eubacterium]_coprostanoligenes_grc
d__Bacteri.k__norank p__Firmicu c__Bacilli o__Bacillal f__Planoco g__Sporosarcina
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__Lachnospiraceae_NK4A136_group
d__Bacteri.k__norank p__Firmicu c__Negativ o__Selenor f__Veillone g__Dialister
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__norank_f__Lachnospiraceae
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__Roseburia
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Clostrid g__norank_f__Clostridiales_vadinBB60_g
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__Anaerotruncus
d__Bacteri.k__norank p__Actinot c__Actinob o__Bifidob f__Bifidob g__Bifidobacterium
d__Bacteri.k__norank p__Firmicu c__Erysipel o__Erysipe f__Erysipel g__Faecalitalea
d__Bacteri.k__norank p__Firmicu c__Bacilli o__Bacillal f__Staphyl g__Staphylococcus
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Rumino g__unclassified_f__Ruminococcaceae
d__Bacteri.k__norank p__Firmicu c__Bacilli o__Bacillal f__Planoco g__Sporosarcina

d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Bactero g__norank f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Firmicu c__Bacilli o__Lactobꜛ f__Carnobꜛ g__Atopostipes
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Porphy r g__Parabacteroides
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__Lachnospiraceae_NK4A136_group
d__Bacteri.k__norank p__Teneric c__Mollicu o__Mollicu f__norank g__norank o__Mollicutes_RF9
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__norank f__Lachnospiraceae
d__Bacteri.k__norank p__Firmicu c__Erysipel o__Erysipe f__Erysipel g__norank f__Erysipelotrichaceae
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Bactero g__Bacteroides
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__[Eubacterium]_xylanophilum_group
d__Bacteri.k__norank p__Bacterc c__Bacterc o__Bacterc f__Bactero g__norank f__Bacteroidales_S24-7_grou
d__Bacteri.k__norank p__Firmicu c__Bacilli o__Lactobꜛ f__Carnobꜛ g__Atopostipes
d__Bacteri.k__norank p__Firmicu c__Bacilli o__Lactobꜛ f__Aerococ g__Aerococcus
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__norank f__Lachnospiraceae
d__Bacteri.k__norank p__Firmicu c__Bacilli o__Lactobꜛ f__unclassi g__unclassified_o__Lactobacillales
d__Bacteri.k__norank p__Firmicu c__Clostrid o__Clostric f__Lachnos g__Lachnospiraceae_NK4A136_group
d__Bacteri.k__norank p__Firmicu c__Erysipel o__Erysipe f__Erysipel g__unclassified_f__Erysipelotrichaceae
d__Bacteri.k__norank p__Firmicu c__Erysipel o__Erysipe f__Erysipel g__unclassified_f__Erysipelotrichaceae
d__Bacteri.k__norank p__Firmicu c__Bacilli o__Lactobꜛ f__Lactoba g__Lactobacillus
d__Bacteri.k__norank p__Firmicu c__Bacilli o__unclass f__unclassi g__unclassified_c__Bacilli

Species	OTU	AD1	AD2	AD3	h1M	h2M	h3M	h4M
s__unident	OTU19	0	0	0	0	0	0	0
s__uncultu	OTU35	0	0	0	0	0	0	0
s__unclassi	OTU5	37499	38032	41555	1	1	0	2
s__unclassi	OTU26	0	0	0	7	3	26	0
s__uncultu	OTU33	0	0	0	0	0	0	0
s__Mycopl	OTU2	100	8	0	0	0	0	0
s__unclassi	OTU11	0	0	0	0	0	0	0
s__uncultu	OTU1	3	2	0	1	3	4	0
s__unclassi	OTU4	10	0	12	0	0	0	0
s__uncultu	OTU21	0	0	0	0	0	0	0
s__uncultu	OTU17	0	0	0	0	0	0	0
s__uncultu	OTU24	0	0	0	0	0	0	0
s__uncultu	OTU16	0	0	0	0	4	0	0
s__unclassi	OTU7	0	0	0	0	0	0	0
s__unclassi	OTU23	0	0	0	0	0	0	0
s__uncultu	OTU6	0	0	0	0	0	0	0
s__[Clostri	OTU20	0	0	0	8	4	18	1
s__Acineto	OTU46	0	0	0	0	0	0	0
s__unclassi	OTU53	0	0	0	0	0	0	0
s__unclassi	OTU55	0	0	1	281	361	220	0
s__Clostrid	OTU57	0	0	0	6	0	0	0
s__uncultu	OTU48	0	0	0	18	0	1	0
s__uncultu	OTU40	0	0	0	71	50	10	0
s__unclassi	OTU8	0	0	0	2	1	3	0
s__unclassi	OTU9	0	0	0	0	0	0	0
s__unclassi	OTU18	0	0	1	3	15	2	0
s__uncultu	OTU28	0	0	0	0	0	0	0
s__unclassi	OTU49	0	0	0	3	0	4	1
s__unclassi	OTU51	0	0	0	3	0	0	0
s__unclassi	OTU30	0	0	0	0	1	0	0
s__unclassi	OTU38	0	0	0	0	0	0	0
s__unclassi	OTU39	0	0	0	5	47	9	8
s__uncultu	OTU52	0	0	0	0	0	0	0
s__uncultu	OTU58	0	0	0	102	100	141	51
s__uncultu	OTU14	0	0	0	0	0	0	0
s__unclassi	OTU41	0	0	0	1	0	0	0
s__unclassi	OTU25	0	0	0	21	8	0	10
s__uncultu	OTU47	0	0	0	1	1	0	0
s__unclassi	OTU32	0	0	0	3	11	0	0
s__uncultu	OTU37	0	0	0	274	21	45	334
s__unclassi	OTU45	0	0	0	1	3	0	0
s__unclassi	OTU12	0	0	0	4	3	0	0
s__unclassi	OTU36	0	0	0	2	8	0	0
s__[Pasteu	OTU62	0	0	0	0	0	0	0
s__unclassi	OTU43	0	0	0	0	0	1	0
s__uncultu	OTU61	0	0	0	43	4	2	57

s__uncultu OTU29	0	0	0	0	0	0	0
s__uncultu OTU15	0	0	0	10	1	0	0
s__unclassi OTU31	0	0	0	1	0	3	0
s__unclassi OTU22	0	0	1	0	0	0	0
s__[Pasteu OTU56	0	0	0	0	0	0	0
s__Corynel OTU34	0	0	1	6	0	5	2
s__unclassi OTU44	0	0	0	0	0	0	0
s__uncultu OTU63	0	0	0	24	1	0	6
s__Morgan OTU3	37	116	412	0	0	0	0
s__uncultu OTU10	0	0	0	0	1	0	0
s__unclassi OTU13	0	0	0	11	0	2	0
s__unclassi OTU27	0	0	1	8	1	7	0
s__mouse_ OTU42	0	0	0	93	84	348	84
s__unclassi OTU50	0	0	0	81	8	0	18
s__unclassi OTU59	0	0	0	0	0	0	0
s__unclassi OTU54	0	0	0	2	0	0	0
s__unclassi OTU64	0	0	0	0	0	0	0
s__Exiguob OTU60	0	0	0	0	0	0	0
s__unclassi OTU90	0	0	0	0	0	0	0
s__unclassi OTU75	0	0	3	423	485	658	647
s__unclassi OTU86	0	0	0	0	1	10	0
s__unclassi OTU82	0	0	0	6	6	1	0
s__unclassi OTU66	0	0	0	5	1	0	0
s__unclassi OTU72	0	0	0	0	1	0	0
s__uncultu OTU73	0	0	0	3	5	1	0
s__unclassi OTU65	0	0	0	0	0	2	0
s__unclassi OTU71	0	0	0	0	1	0	0
s__unclassi OTU68	0	0	1	0	1044	147	0
s__uncultu OTU89	0	0	0	0	3	8	0
s__unclassi OTU85	0	0	0	0	0	0	0
s__unclassi OTU100	0	0	0	0	0	0	1
s__unclassi OTU70	0	0	1	181	43	595	8
s__uncultu OTU76	0	0	0	0	0	0	0
s__unclassi OTU79	0	0	0	0	5	2	0
s__uncultu OTU67	0	0	2	147	6	17	2
s__uncultu OTU80	0	0	0	4	1	28	0
s__unclassi OTU109	0	0	0	0	0	0	0
s__unclassi OTU110	0	0	0	0	0	0	0
s__Collinse OTU126	0	1	0	0	0	0	0
s__uncultu OTU96	0	0	0	0	0	0	0
s__uncultu OTU101	0	0	0	6	37	50	14
s__unclassi OTU102	0	0	0	0	0	0	0
s__uncultu OTU116	0	0	0	0	1	0	0
s__unclassi OTU118	0	0	0	0	0	0	0
s__unclassi OTU111	0	0	0	0	0	0	0
s__uncultu OTU121	0	0	0	0	0	0	0
s__uncultu OTU124	0	0	2	7161	3127	2	706

s__uncultu OTU74	0	0	0	0	0	0	0
s__unclassi OTU84	0	0	0	0	3	0	0
s__unclassi OTU87	0	0	0	0	0	0	0
s__unclassi OTU94	0	0	0	1	2	1	0
s__unclassi OTU114	0	0	0	0	0	1	0
s__uncultu OTU117	0	0	0	5	12	20	1
s__uncultu OTU127	0	0	0	1	2	0	0
s__uncultu OTU77	0	0	0	219	181	74	6
s__unclassi OTU103	0	0	0	0	0	0	0
s__unclassi OTU112	0	0	0	0	0	0	0
s__unclassi OTU120	0	0	0	0	0	0	0
s__unclassi OTU78	0	0	0	1	0	0	0
s__unclassi OTU98	0	0	0	0	7	0	0
s__Helicob OTU99	0	0	0	0	4	1	1
s__uncultu OTU115	0	0	0	6	0	0	0
s__unclassi OTU93	0	0	0	0	3	0	0
s__unclassi OTU113	0	0	0	47	9	43	3
s__unclassi OTU122	0	0	0	8	13	1	2
s__unclassi OTU88	0	0	0	173	90	3	0
s__unclassi OTU95	0	0	0	3	0	0	0
s__uncultu OTU119	0	0	0	7	6	1	0
s__unclassi OTU91	0	0	0	8	2	0	0
s__unclassi OTU92	0	0	0	0	0	0	0
s__unclassi OTU107	0	0	0	0	0	0	0
s__uncultu OTU108	0	0	0	0	0	0	0
s__uncultu OTU125	0	0	0	10	12	3	0
s__Rumino OTU69	0	0	0	4	1	3	3
s__uncultu OTU97	0	0	0	0	10	5	0
s__unclassi OTU123	0	0	0	1	1	145	23
s__unclassi OTU128	0	0	0	2	27	3	0
s__uncultu OTU81	0	0	0	0	0	0	0
s__unclassi OTU83	0	0	0	0	8	7	1
s__Lachno: OTU104	0	0	0	5	2	7	6
s__unclassi OTU105	0	0	0	0	0	0	0
s__unclassi OTU106	0	0	0	1	2	13	0
s__unclassi OTU151	0	0	0	0	0	1	0
s__unclassi OTU149	0	0	0	0	0	0	0
s__uncultu OTU148	0	0	0	10	0	0	0
s__unclassi OTU139	0	0	0	62	3	0	0
s__uncultu OTU132	0	0	0	2	0	0	0
s__uncultu OTU129	0	0	0	238	4	22	4
s__unclassi OTU134	0	0	0	2	16	274	0
s__unclassi OTU138	0	0	0	0	0	0	0
s__uncultu OTU133	0	0	0	3	44	180	11
s__unclassi OTU137	16	8	2	17	13	5	15
s__unclassi OTU155	0	0	0	1	45	0	0
s__uncultu OTU131	0	0	0	1	0	0	2

s__unclassi OTU142	0	0	0	0	1	0	0
s__unclassi OTU171	0	0	1	0	0	0	0
s__uncultu OTU141	0	0	0	5	7	71	2
s__unclassi OTU130	0	0	0	0	0	0	0
s__unclassi OTU176	0	0	0	0	0	0	0
s__uncultu OTU186	0	0	0	84	4	17	2
s__uncultu OTU177	0	0	0	1	3	3	0
s__unclassi OTU182	0	0	0	0	12	0	20
s__uncultu OTU156	0	0	0	5	2	15	3
s__uncultu OTU144	0	0	0	1	8	16	0
s__unclassi OTU175	0	0	0	0	0	0	0
s__uncultu OTU185	0	0	0	2	10	0	0
s__unclassi OTU190	0	0	0	25	31	28	1
s__unclassi OTU145	0	0	0	1	0	0	0
s__unclassi OTU150	0	0	0	2	10	0	0
s__unclassi OTU163	0	0	0	0	15	6	0
s__uncultu OTU191	0	0	0	1972	118	38	8
s__unclassi OTU135	0	0	0	10	2	2	1
s__uncultu OTU157	0	0	0	0	0	0	0
s__unclassi OTU167	0	0	0	0	0	0	0
s__uncultu OTU147	0	0	0	10	655	70	13
s__unclassi OTU159	0	0	0	0	2	0	0
s__unclassi OTU168	0	0	0	5	0	45	2
s__uncultu OTU174	0	0	0	31	27	2	0
s__unclassi OTU180	0	0	0	0	0	3	0
s__unclassi OTU188	0	0	0	18	20	0	0
s__uncultu OTU143	0	0	6	1587	6333	1907	748
s__uncultu OTU153	0	0	0	0	0	0	0
s__gut_me OTU164	0	0	1	0	0	0	0
s__uncultu OTU169	0	0	0	0	0	0	0
s__unclassi OTU136	0	0	0	0	0	0	0
s__uncultu OTU160	0	0	0	0	0	0	6
s__unclassi OTU165	0	0	1	251	142	75	23
s__unclassi OTU178	0	0	1	16	384	218	4
s__uncultu OTU140	0	0	0	0	0	4	0
s__uncultu OTU146	0	0	0	66	933	559	7
s__[Clostridi OTU161	0	0	0	8	6	1	1
s__uncultu OTU179	0	0	0	0	2	7	1
s__uncultu OTU187	0	0	0	4	54	61	0
s__unclassi OTU166	0	0	0	78	13	3	0
s__unclassi OTU173	0	0	0	0	0	0	0
s__unclassi OTU152	0	0	0	136	10	13	0
s__unclassi OTU158	0	0	0	37	31	1	0
s__uncultu OTU162	0	0	0	0	6	86	3
s__unclassi OTU172	0	0	0	7	0	0	0
s__Anaerotr OTU181	0	0	0	4	0	0	1
s__unclassi OTU154	0	0	0	0	2	0	0

s__uncultu OTU183	0	0	0	0	1	0	0
s__uncultu OTU170	0	0	0	2	1	0	1
s__unclassi OTU192	0	0	0	0	0	3	1
s__uncultu OTU184	0	0	0	2	9	6	0
s__unclassi OTU189	0	0	0	0	2	0	0
s__unclassi OTU200	0	0	0	0	0	0	0
s__uncultu OTU214	0	0	0	5	4	1	0
s__unclassi OTU204	0	0	0	0	1	5	0
s__uncultu OTU196	0	0	0	0	0	0	0
s__uncultu OTU253	1	0	1	3	8	93	0
s__unclassi OTU206	0	0	0	0	0	0	0
s__uncultu OTU212	0	0	0	0	0	0	0
s__unclassi OTU197	0	0	0	0	0	0	0
s__uncultu OTU195	0	0	0	77	106	154	93
s__uncultu OTU205	0	0	0	0	0	0	0
s__uncultu OTU193	0	0	0	0	0	0	0
s__unclassi OTU210	0	0	0	1	0	0	0
s__unclassi OTU207	0	0	0	0	11	3	1
s__uncultu OTU194	0	0	0	6	1	0	0
s__Lactoba OTU211	0	0	0	3	0	0	0
s__unclassi OTU220	0	0	0	1	0	0	0
s__unclassi OTU209	0	0	0	1	10	5	0
s__unclassi OTU226	0	0	0	0	0	0	0
s__uncultu OTU227	0	0	0	0	0	0	2
s__uncultu OTU231	0	0	0	3	0	8	0
s__uncultu OTU234	0	0	0	0	0	1	1
s__unclassi OTU237	0	0	0	0	1	0	1
s__uncultu OTU248	0	0	0	0	24	60	3
s__unclassi OTU221	0	0	0	2	3	0	0
s__Lachno: OTU232	0	0	0	21	1	0	5
s__unclassi OTU240	0	0	0	0	1	0	0
s__uncultu OTU216	0	0	0	0	1	0	0
s__[Clostri: OTU230	0	0	0	7	1	1	15
s__unclassi OTU255	0	0	0	160	123	0	1
s__unclassi OTU219	0	0	0	0	0	0	0
s__uncultu OTU203	0	0	0	23	20	34	0
s__uncultu OTU228	0	0	0	1	0	0	0
s__unclassi OTU245	0	0	0	0	0	0	0
s__uncultu OTU215	0	0	0	0	10	2	0
s__uncultu OTU222	0	0	0	7	0	0	0
s__uncultu OTU229	0	0	0	3	44	56	11
s__uncultu OTU249	0	0	0	0	11	2	0
s__uncultu OTU251	1	0	1	5	275	49	1
s__uncultu OTU198	0	0	0	5	4	0	0
s__unclassi OTU201	0	0	0	2	0	0	0
s__unclassi OTU199	0	0	0	0	0	0	0
s__uncultu OTU213	0	0	0	0	0	0	0

s__uncultu OTU243	0	0	0	0	0	0	0
s__uncultu OTU244	0	0	0	0	1	1	0
s__uncultu OTU252	0	0	0	3	29	74	5
s__uncultu OTU208	0	0	0	6	2	0	0
s__unclassi OTU217	0	0	0	0	0	0	0
s__uncultu OTU223	0	0	0	3	0	0	0
s__uncultu OTU236	0	0	0	0	0	1	0
s__uncultu OTU246	0	0	0	9	1	6	4
s__unclassi OTU202	2	0	0	5	0	1	0
s__uncultu OTU239	0	0	0	7	0	0	0
s__Haemoj OTU225	0	0	0	0	0	0	0
s__uncultu OTU233	0	0	0	51	28	14	24
s__unclassi OTU235	0	0	0	0	0	0	0
s__unclassi OTU256	0	0	0	0	0	0	0
s__uncultu OTU218	0	0	0	0	0	0	0
s__unclassi OTU224	0	0	0	0	5	0	0
s__unclassi OTU238	0	0	0	3	2	1	0
s__unclassi OTU241	0	0	0	1	0	0	2
s__unclassi OTU242	0	0	0	7	0	3	0
s__Rumino OTU250	0	0	0	0	0	0	0
s__uncultu OTU247	0	0	0	4	7	57	11
s__Akkerm OTU254	0	1	0	956	1968	0	0
s__uncultu OTU257	0	0	0	0	2	3	0
s__uncultu OTU271	0	0	0	12	0	14	0
s__uncultu OTU259	0	0	1	0	0	0	0
s__unclassi OTU273	0	0	0	0	1	0	0
s__uncultu OTU299	0	0	3	2196	4604	1105	536
s__uncultu OTU284	0	0	0	11	47	30	13
s__uncultu OTU264	0	0	0	4	0	0	0
s__uncultu OTU308	0	0	0	5	0	0	0
s__uncultu OTU270	0	0	0	413	20	1450	120
s__unclassi OTU306	0	0	0	0	0	0	0
s__uncultu OTU261	0	0	0	0	0	0	0
s__uncultu OTU272	0	0	1	129	148	305	35
s__unclassi OTU267	0	0	0	60	8	2	2
s__uncultu OTU269	0	0	1	0	2	1	0
s__unclassi OTU281	0	0	0	0	3	0	0
s__unclassi OTU266	0	0	0	0	0	0	0
s__unclassi OTU258	0	0	0	0	0	0	0
s__uncultu OTU260	0	0	0	0	0	0	0
s__uncultu OTU262	0	0	0	0	0	0	0
s__uncultu OTU265	0	0	0	3	0	0	0
s__uncultu OTU275	0	0	0	15	127	19	1
s__unclassi OTU277	0	0	0	0	0	0	0
s__unclassi OTU327	0	0	0	4	4	0	0
s__unclassi OTU342	0	0	0	417	290	299	149
s__unclassi OTU371	0	0	0	0	0	0	0

s__uncultu OTU377	0	0	1	0	0	0	0
s__unclassi OTU291	0	0	0	0	0	1	0
s__uncultu OTU300	0	0	0	5	7	20	8
s__uncultu OTU319	0	0	0	2	42	17	3
s__unclassi OTU320	0	0	0	5	34	33	17
s__uncultu OTU328	0	0	5	4717	1035	328	499
s__uncultu OTU370	0	0	0	1	0	0	0
s__uncultu OTU379	0	0	0	0	10	76	2
s__uncultu OTU305	0	0	3	242	253	43	462
s__uncultu OTU309	0	0	0	2	4	18	20
s__Bactero OTU318	0	0	0	1	190	48	2
s__unclassi OTU333	0	0	0	0	3	1	0
s__uncultu OTU353	0	0	0	20	17	119	59
s__unclassi OTU335	0	1	2	9045	1209	5153	8885
s__uncultu OTU343	0	0	0	29	125	117	23
s__Desulfo OTU365	0	0	0	2	48	102	12
s__uncultu OTU372	0	0	0	183	144	113	27
s__unclassi OTU274	0	0	0	0	0	0	0
s__uncultu OTU298	0	0	0	0	9	3	1
s__uncultu OTU332	0	0	0	3	7	38	4
s__uncultu OTU347	0	0	0	0	0	0	0
s__uncultu OTU364	0	0	0	28	40	28	3
s__unclassi OTU375	0	0	0	0	0	0	0
s__uncultu OTU380	0	0	0	0	3	8	1
s__uncultu OTU381	0	0	0	2	58	11	0
s__uncultu OTU282	0	0	0	45	17	116	22
s__Paenalc OTU304	0	0	0	0	0	0	0
s__uncultu OTU307	0	0	0	0	0	0	0
s__Bactero OTU312	1	0	0	0	67	13	6
s__uncultu OTU314	0	0	0	9	1	27	0
s__Lachno: OTU322	0	0	0	1	5	1	0
s__unclassi OTU355	0	0	0	182	30	19	77
s__unclassi OTU285	0	0	0	4	7	42	10
s__unclassi OTU286	0	0	0	20	6	35	3
s__uncultu OTU324	0	0	0	4	9	13	2
s__unclassi OTU341	0	0	0	0	8	0	0
s__unclassi OTU346	0	0	0	20	7	45	22
s__unclassi OTU359	0	0	0	2	2	3	0
s__Blautia_ OTU362	0	0	0	2	2	25	0
s__Provide OTU384	0	0	0	0	0	0	0
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s__uncultu OTU292	0	0	1	189	702	4	77
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s__uncultu OTU376	0	0	0	3	24	11	0
s__uncultu OTU331	0	0	0	0	0	0	0
s__unclassi OTU339	0	0	0	1	3	4	2
s__uncultu OTU348	0	0	0	0	6	18	4

s__uncultu OTU373	0	0	0	45	199	2439	316
s__unclassi OTU374	0	0	1	3	18	17	15
s__unclassi OTU283	0	0	0	17	32	31	29
s__uncultu OTU302	0	0	0	80	66	71	345
s__unclassi OTU317	0	0	0	0	0	0	0
s__uncultu OTU325	0	0	0	5	172	67	8
s__uncultu OTU334	0	0	0	2	1	80	0
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s__uncultu OTU352	0	0	0	2	1	9	4
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s__uncultu OTU278	0	0	0	5	17	2	0
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s__unclassi OTU290	0	0	1	187	52	134	60
s__Clostrid OTU293	0	0	0	0	0	0	0
s__unclassi OTU303	0	0	0	0	5	12	2
s__unclassi OTU340	0	0	0	0	0	0	0
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s__uncultu OTU369	0	0	0	5	39	122	15
s__Anaeroi OTU382	0	0	0	9	7	14	9
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s__uncultu OTU263	0	0	0	0	0	0	0
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s__uncultu OTU301	0	0	0	23	279	343	20
s__Stenotr OTU313	0	0	0	0	0	0	0
s__Candida OTU336	0	27	0	0	72	117	122
s__uncultu OTU345	0	0	0	29	85	37	17
s__unclassi OTU276	0	0	0	1	3	7	1
s__Clostrid OTU287	0	0	0	1	1	27	3
s__uncultu OTU296	0	0	0	0	1	1	0
s__Sphingc OTU295	0	0	0	0	0	0	0
s__uncultu OTU310	0	0	0	10	3	1	0

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s__Corynel OTU385	13	3	0	0	0	75	22
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s__unclassi OTU443	0	0	1	509	56	76	36
s__Strepto OTU424	0	0	0	158	57	149	76
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s__uncultu OTU447	0	0	0	5	21	0	53
s__Lactoba OTU400	0	0	0	0	0	0	0
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s__Brachyk OTU416	0	1	0	0	0	0	1
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s__uncultu OTU421	0	0	0	2	1	1	0
s__unclassi OTU418	0	0	0	0	0	0	0
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s__Lachno: OTU407	0	0	0	35	336	892	355
s__uncultu OTU423	0	0	0	10	1	22	12
s__uncultu OTU434	0	0	0	42	67	0	6

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s__unclassi OTU406	0	0	0	2	1	9	5
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s__Breviba OTU431	0	0	0	0	0	0	1
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s__gut_me OTU420	0	16	8	0	0	13	0
s__Bactero OTU395	2	0	2	0	11	3	0
s__uncultu OTU419	0	0	0	3	0	0	3
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s__Bactero OTU426	0	15	2	0	0	0	0
s__unclassi OTU448	0	0	0	12	4	54	0
s__unclassi OTU401	0	0	0	0	0	36	79
s__unclassi OTU412	0	0	0	1	0	13	0
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s__unclassi OTU487	0	0	0	0	1	1	1
s__uncultu OTU459	0	0	0	9	1	0	0
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s__unclassi OTU511	0	0	0	1	2	5	0
s__unclassi OTU465	0	0	0	44	5	20	10
s__unclassi OTU468	0	0	0	3	2	0	0
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s__Parabac OTU500	1	0	1	0	3	2	0
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s__unclassi OTU480	0	0	0	14	8	2	4
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s__Lachno: OTU461	0	0	0	10	0	208	30
s__[Clostri: OTU470	0	0	0	0	1	7	0
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s__uncultu OTU478	0	0	0	4	1	1	3
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s__Clostrid OTU483	0	0	0	2	1	9	1
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s__unclassi OTU499	0	0	0	24	7	10	23
s__gut_me OTU512	0	0	0	5	0	17	2
s__unclassi OTU502	0	0	0	0	4	1	0
s__uncultu OTU526	0	0	0	171	129	78	20
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s__unclassi OTU540	0	0	0	13	37	10	4
s__unclassi OTU535	0	0	0	72	1609	1495	166

s__uncultu OTU525	0	0	0	65	148	718	538
s__unclassi OTU520	0	0	0	0	7	8	0
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s__uncultu OTU516	0	0	0	163	346	147	31
s__uncultu OTU524	0	1	0	26	115	212	1
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s__unclassi OTU548	0	0	0	1	0	2	3
s__uncultu OTU533	0	0	0	1	3	12	0
s__Bactero OTU527	0	0	0	13	0	10	0
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s__unclassi OTU539	0	2	0	938	427	1693	609
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s__Psychro OTU550	0	0	0	0	0	5	58
s__Staphyl OTU551	0	0	0	0	0	163	402
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s__Acineto OTU564	0	0	0	0	0	5	36
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s__gut_me OTU546	0	0	0	1	16	270	7
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s__Lachno: OTU574	0	0	0	2	2	2	0
s__Dialiste OTU547	0	0	0	0	2	0	18
s__Lachno: OTU570	0	0	0	6	0	2	5
s__Clostrid OTU572	0	0	0	0	0	0	0
s__uncultu OTU521	0	0	0	2	0	1	2
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s__Bifidob: OTU557	0	1	0	1	7	2	42
s__[Eubact OTU573	0	0	0	0	2	3	2
s__Staphyl OTU555	9	2	5	5	1	25	60
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s__Parabac OTU528	0	0	0	0	0	2	0
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s__Lachno: OTU582	0	0	0	7	76	247	95
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40517	