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The Effect of Gut Microbiota on Overwintering Success in Mule Deer

Emma Wilcox

A thesis submitted to the faculty of
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Master of Science

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ABSTRACT

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Mule deer are an important rangeland grazer, large prey species, and game animal for the state of Utah, so herd size is monitored and managed actively. A significant cause of population decline is poor overwintering survival, including from the lack of available forage during winter months. Mule deer energy storage is correlated with greater overwintering success, so physical estimates of energy storage including body condition score (BCS), rump fat (RF), and loin thickness (LT), can be used to track and predict a herd's health. Current methods of collecting deer information are costly, time consuming, and cause physical stress to deer, so here we sought to test if a microbiome analysis could be used to predict deer overwintering success. We analyzed nearly 1000 fecal samples collected from deer in Utah over a five-year period. We found that the microbiome composition of these samples shared characteristics with published reports of other reported ruminant species. Also, the location and time when the samples were collected significantly influenced mule deer microbiota composition and abundance. We found that there is a relationship between microbes and health measures (BCS, RF, LT), including some microbial abundances that could predict the health measures of mule deer several months ahead of time. There were also microbial groups whose abundances were significantly correlated with the latitude and elevation of the deer. Finally, a longitudinal analysis on a subset of sampled deer produced slightly different results than the broad analysis of all samples, including suggesting that some of the differences in microbiota composition with time may have been related more to sampling distinct deer at different time points, rather than that the deer microbiota composition changed with time. These results suggest possible candidate microbial taxa for use in developing assays to replace current methods of measuring and tracking deer health.

Keywords: mule deer, microbiota, overwintering success, body condition score, rump fat, loin thickness

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CHAPTER 1

The Effect of Gut Microbiota on Overwintering Success in Mule Deer

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ABSTRACT

Mule deer are an important rangeland grazer, large prey species, and game animal for the state of Utah, so herd size is monitored and managed actively. A significant cause of population decline is poor overwintering survival, including from the lack of available forage during winter months. Mule deer energy storage is correlated with greater overwintering success, so physical estimates of energy storage including body condition score (BCS), rump fat (RF), and loin thickness (LT), can be used to track and predict a herd's health. Current methods of collecting deer information are costly, time consuming, and cause physical stress to deer, so here we sought to test if a microbiome analysis could be used to predict deer overwintering success. We analyzed nearly 1000 fecal samples collected from deer in Utah over a five-year period. We found that the microbiome composition of these samples shared characteristics with published reports of other reported ruminant species. Also, the location and time when the samples were collected significantly influenced mule deer microbiota composition and abundance. We found that there is a relationship between microbes and health measures (BCS, RF, LT), including some microbial abundances that could predict the health measures of mule deer several months ahead of time. There were also microbial groups whose abundances were significantly correlated with the latitude and elevation of the deer. Finally, a longitudinal analysis on a subset of sampled deer produced slightly different results than the broad analysis of all samples, including

suggesting that some of the differences in microbiota composition with time may have been related more to sampling distinct deer at different time points, rather than that the deer microbiota composition changed with time. These results suggest possible candidate microbial taxa for use in developing assays to replace current methods of measuring and tracking deer health.

INTRODUCTION

The mule deer, *Odocoileus hemionus*, is a ruminant native to western North America. It is a species that is conserved for ecological and recreational purposes. In the state of Utah, much of which is part of the animal’s natural range, mule deer are important to the natural ecology as rangeland grazers and prey for native predator species. They are also a popular recreational hunting target in Utah, bringing in money to the state through the sale of hunting tags and licenses.

Due to the ecological and economic importance of mule deer to Utah, millions of dollars and man-hours are spent every year to determine the health of the population and ensure deer herds maintain high population numbers through rangeland improvements, predator control or removal, and supplemental winter non-forage food [1]. Herd survival through winter and health in the spring months has been a particular focus of research. Tracking the average body mass of deer herds before winter is important in keeping population sizes high, as larger maternal body mass leads to decreased fawn mortality [1]. Winter conditions are highly variable in the intermountain west and contribute to herd size decline over time. If a deer’s body mass or body fat stores are low before winter, they are less likely to survive the winter because of a lack of food due to the low quantity and/or quality of plant materials [2] [3]. Habitat improvement and protection efforts, including changes to the available forage in winter ranges, have been insufficient to decrease overwinter mortality. Instead, one of the best solutions to reduce overwinter mortality in deer populations with low body fat stores is for rangeland managers to provide non-forage food for the deer [4] [5] [6].

To determine a deer population's overall health and if supplemental feed is needed, rangeland managers manually capture and estimate body fat stores in representatives of the target population [7]. Deer can be tracked using GPS collar data, captured with helicopter net guns, anesthetized, and examined. Estimated body fat morphometrics such as body condition score, rump fat, and loin thickness can be recorded along with each deer's age, location, gender, weight, etc. [8]. Body condition score (BCS) is a measure of total body fat made using ultrasound at multiple points across the body. Rump fat (RF) is a sub measure of BCS located at the thickest part of the hind quarters. Loin thickness (LT) is a measurement of the loin muscle and predicts protein reserves [8] [9]. Traditional procedures involving helicopters and net guns are costly, time-consuming, and physically risky for the deer. In particular, net-gun capture can be associated with short-term capture-related deer mortality [10].

The microbiota of ruminants, including deer, has been shown to directly impact the health of an individual or herd and to be affected by differences in genotype, geography, age, gender, and diet [11] [12] [13] [14] [15]. There are strong maternal effects in the development of the rumen microbiota. Ruminants are born sterile or mostly sterile, acquiring microbes during birth from the dam's vaginal tract, colostrum, and post-birth environment. The rumen microbiota changes during development, stabilizing after weaning [16]. Up to 70% of all dietary energy is a result of microbial digestion [17]. 95% of the rumen microbiota is made up of bacteria, the majority of which are anaerobes or facultative anaerobes [18]. Some microbes are essential for health and metabolism [19]. Two of the core bacterial phyla found in ruminants are involved in digestion: Firmicutes break down fibers such as cellulose and Bacteroidetes digest proteins and polysaccharides [14]. Ruminants lack several enzymes necessary for digestion and it is believed that gut symbionts perform these functions [16] [20].

Here we explored if there is a relationship between the gut microbiota of mule deer and traditionally measured health morphometrics. We previously had performed a similar analysis on a cohort of deer from two locations in Utah and had identified candidate bacterial strains associated with near-term deer protein levels and future deer overwintering success [21]. In this work, we expanded the analysis to include samples from 7 sites and 5 years across the state of Utah. We expected that increasing the sampling size of our analysis would be useful to provide insight into if these predictions were restricted to the previously sampled animals, or general across multiple herds and time points. A major motivator for such work is that fecal sample collection and microbiota testing efforts could be used to supplement or replace current deer conservation efforts in a cost-effective way if bioindicator taxa can be identified. For example, collection of fecal samples could replace live-capture of animals for monitoring herd health.

METHODS

Sample Collection

All procedures were carried out in compliance with the requirements of the Institutional Animal Care and Use Committee for Brigham Young University (protocol 150110) and the guidelines for the use of wild mammals in the research of the American Society of Mammologists [22]. To obtain morphometric measurements and fecal samples from deer in the wild, deer were tracked with GPS collar data from a helicopter and caught by net-gun. They were hobbled, blindfolded, and secured in a sling under the helicopter. Deer were then transported to ground crews for measurement. These crews recorded the deer's gender, weight, temperature, age, etc. To estimate the deer's body fat stores the ground crews measured body condition score (BCS), rump fat (RF), and loin thickness (LT), estimates of body mass or stored body fat [23]. They also took blood and fecal samples for further testing. Sampling included two captures a year, in December and March, from 2015 - 2019, and within seven geographical areas across Utah: Cache, Monroe, Oquirrh-Stansbury, Pine Valley, San Juan, South Slope, and Wasatch Manti **(Figure 1)**.

16s Sequencing

Fecal samples from the captured deer were analyzed to determine their microbial composition, and what microbes were present in each sample. DNA fragments were sequenced and matched to known bacterial sequences. DNA was extracted using the Zymo Quick-DNA Fecal/Soil Microbe 96 Kit, and sequencing libraries were preparing using a dual-barcoded PCR-based tagging approach as described previously [24]. Briefly, the V4 region of the 16s rRNA gene was amplified in a one-step PCR reaction, normalized using the SequalPrep Normalization Plate Kit, and sequenced on an Illumina HiSeq using 500-cycle paired-end chemistry. A minor deviation from the published protocol is that we added immersion oil to prevent sample evaporation during PCR.

Data Analysis

To summarize geographical and temporal changes to microbe composition, a table containing amplicon sequence variant (ASV) counts for each fecal sample was created using QIIME2 [25]. DNA sequence files were imported into QIIME2, demultiplexed with the q2-

demux plugin, and denoised with dada2, a program for correcting and quality-checking DNA reads [26]. A counts table was created, containing per-sample counts for each ASV. Phylogenetic trees were also made to determine taxonomic relationships between ASVs, which were assigned using GreenGenes [27] [28] [29] [30]. ASVs were filtered to remove all archaea, Eukaryota, chloroplast, and mitochondria reads. We also used QIIME2 to perform beta diversity analyses using the Bray-Curtis, unweighted Unifrac, and weighted Unifrac distance metrics, after rarefying the data to a read depth of 3000 **(Figure S1)** [31] [32] [33]. Significant differences in total community composition with the different beta-diversity metrics were determined using PERMANOVA [34]. When geographic location of the deer was included as a covariate, latitude and longitude values were rounded to the nearest tenth of a location to avoid over specifying the model. Latitude and elevation values were determined based on the geographic coordinate where the deer fecal sample was collected using GPS Visualizer (https://www.gpsvisualizer.com/elevation). We also commonly used three additional covariates corresponding to the time when samples were collected: the 'season' (either pre-winter (Nov-Jan) or post-winter (Mar-May)), or the 'overwinter' year (i.e., modified from the Gregorian year, we used, e.g., the value 'Overwinter 2015' to bin the pre-winter (December) 2015 and post-winter (March) 2016 samples). The rationale behind distinguishing the overwinter year from the Gregorian year was to connect samples collected from a deer before and after a specific winter season. We used Analysis of Composition of Microbiomes (ANCOM) to identify specific microbial ASVs that varied in abundance with the space and time of the sampled deer feces [35]. Throughout the text we report only the results of grouping reads at the Order- and ASV-levels when performing ANCOM because we found that these were generally a good reflection of the significant variation that as detected at all taxonomic levels, and reporting both provides high-and low-level resolution. Unlike the full text, supplemental tables report the ANCOM results for all taxonomic levels. When we report that reads were grouped for ANCOM or correlation analyses (see next section), we mean that the ASVs were additively grouped together based on the taxonomic assignment made to the ASVs. Finally, a longitudinal analysis of a subset of 31 individual deer from which fecal samples had been collected at least 4 different points in time was performed using the QIIME2 linear mixed-effects modeling plugin [36][37].

To determine the relationship between the deer microbiota and proximate or distal measures of deer health, we tested if microbial ASV abundances were correlated with three health metrics: the body condition score (BCS), rump fat (RF), and loin thickness (LT). For each sample, we performed a Spearman Correlation in R between each ASV and body condition score. We also performed the analyses when reads were grouped at higher taxonomic levels. We use false-discovery rate (FDR) adjustment on p-values to correct for multiple tests [38]. Our correlations compared the abundance of reads in the fecal microbiota and deer health metrics based on two types of comparisons: proximate and future. For “proximate” analyses, we compared microbiota and health measures from the same time point. For “future” analyses, we compared the microbiota of pre-winter animals with their post-winter health measures. In the ‘future’ analyses any individual deer that did not have both a pre-winter microbiota samples and post-winter health measures was omitted from the analysis.

RESULTS

The Microbiota Composition of Adult Deer Feces Varies in Space and Time

Fecal samples from wild mule deer were collected and sequenced across the 16S rRNA V4 region to test the relationship between variation in microbiota composition and multiple variables, including deer age, ‘geography’, ‘overwinter’, and ‘season’. Together with controls and primer blanks, sequencing the 16S rRNA V4 region yielded 43,162,774 reads from 1,536 deer fecal samples (mean 28,100 reads per sample) that were assigned to 17,185 features (mean 2,512 reads per feature). We rarefied the data to 3000 reads per sample and filtered out samples with insufficient metadata, retaining data for 989 deer samples (156 newborns (0-0.5 years old), 68 yearlings (0.5-2.5 years old), and 765 adults (2.5+ years old)) and 2,967,000 total reads. Several of the most abundant bacterial orders across these samples match previously identified dominant rumen bacterial phyla (Bacteroidales, Clostridiales, Coriobacteriales), while others had been detected in relatively low abundance in previous analyses (Selenomonadales, and Verrucomicrobiales) (**Figure 2**) [39] [15]. Permutational analysis of variance (PERMANOVA) using three different beta-diversity metrics revealed that the microbiota composition of all deer sampled varied in time and space with each of our four primary variables of interest: deer age (ranging from 0.5 to 12.5 years), geography (one of seven locations: Cache, Monroe, Oquirrh Stansbury, Wasatch-Manti, San Juan, Pine Valley, South Slope, overwintering year (each of 2015-2019), and season of year (either pre-winter or post-winter) (**Table S1**). Because deer age was a significant covariate and most of our samples came from adult deer (765 samples ages 2.5+), we focused first on the relationship between time, geography, and changes in the microbiota composition of adult deer. When adult deer samples were analyzed separately from samples collected from younger deer, the geography, overwinter, and season variables, and their interaction terms, varied significantly, and geography explained the most variation in microbiota composition (**Figure 3, Table 1**). Also, the most abundant bacterial orders in the adult deer are common in ruminants [39][15]. Therefore, variation in time and space are both important in determining differences in the microbiota in these wild, adult deer.

To better understand the relationship between time, geography, and the adult deer microbiota, we examined the effects of each of these variables within subsets of the other. When we tested if microbiota composition varied in each specific geography, overwinter, and season subset, we continued to detect significant variation in the remaining covariates, suggesting that the significant effects in the entire dataset were not driven by outlier trends in one or a few geographies or at only a subset of the tested time points (**Table S2, S3, S4**). Together, these findings suggest strong, systematic variations in the microbiota composition of 7 Utah deer herds with geography, overwinter, and season.

We identified which bacterial reads were driving the differences in microbial community composition using ANCOM. ANCOM was performed on reads grouped at all taxonomic levels (**Table S5, S6, S7**), and we focus our text on ANCOM results when reads were grouped at the order-level or had not post-hoc grouping assigned (i.e., ASVs), since these provide a high- and low-taxonomic view of the results. Reads assigned to six bacterial orders varied significantly in abundance in all adult deer samples with geography, overwintering year, or season. Read abundances assigned to five orders varied significantly with geography: Bacteroidales, Coriobacteriales, Desulfovibrionales, Pirellulales, and Spirochaetales **(Figure 4, Table S5)**. Also, the abundance of 53 ASVs varied significantly with geography (**Table S5**). All 53 of these ASVs belong to one of the five most abundant bacterial orders found in the adult deer samples. Turning to the remaining covariates, 2 orders and 8 ASVs varied significantly with the overwinter variable (**Table S6**), and 2 orders and 16 ASVs varied with season (**Table S7**). Of these only 2 ASVs (and 2 orders) were not from one of the five most abundant bacterial orders, and these belonged to the order Pirellulales and Enterobacteriales. These results show that in most cases, microbes that varied significantly in abundance by geography, overwinter, or season generally were from or belonged to the most abundant orders in ruminants, suggesting that the microbes that are the most abundant also drive the geographic and temporal shifts in the deer microbiota.

Microbiota Composition and Abundance Vary Across Age Groups

To investigate the microbiota composition of younger deer, we analyzed samples from newborns (< 6 months old, N = 156) and yearlings (6 to 30 months old, N = 68) (**Table 2**). As in adults, the microbiota composition of newborns and yearlings varied significantly with geography and space, though not with the overwintering variable (**Table 3**). ANCOM analyses also identified a relatively small number of read groupings that varied in abundance with geography, season (yearling deer only), and year. Deer are only classified as newborns for 6 months, so newborn samples only occurred in March and have no corresponding overwinter variable; therefore, we analyzed them using a 'year', rather than an 'overwinter' variable. In yearlings, one and four ASVs varied with geography and season, respectively; no orders varied significantly with these or any other tested variables (**Figure 5, Table S8)**. In newborn deer, Coriobacteriales reads (grouped at the order level) varied significantly in abundance with geography and overwinter year **(Table S9)**; and the abundance of four ASVs varied significantly with geography **(Table S9)**. Several of the microbial groups that varied in younger deer also varied in adults, together suggesting that at least some of the trends in microbial abundance that we observed are general and are not restricted to specific deer ages.

Microbes are Correlated to Health Measures

To identify microbes that might impact mule deer health, we calculated correlations between microbial abundances and adult deer health measures. The health measures used in this study are estimates of body fat: BCS, RF, and LT. In adult deer, four bacterial orders were significantly correlated with at least one of the health measures: the Bacteroidales, Rhizobiales, Rhodospirillales, and Spirochaetales (**Figure 2**). When we calculated the same correlations at the ASV level we detected generally similar trends. Of 11102 ASVs, the abundances of 73 were significantly correlated with one or more health measures, and 11 of these fell into one of the significantly variable orders (ASV Table Supplemental; 10 Bacteroidales, 1 Spirochaetales; **Table S10**). Of the remaining 62 ASV level correlations, 58 were Clostridiales, and most were positively associated with mule deer health **(Table S10)**. Finally, 16 ASVs were negatively associated with mule deer health, including 14 Clostridiales ASVs and 1 Mollicutes ASV which was significantly negatively correlated with all three health measures. Taken together, these analyses reveal microbes whose abundances are positively and negatively associated with changes in deer health measure, identifying candidate strains that have impacts on or respond to changes in the health of their animal host.

Microbes Can Predict Overwinter Success

To investigate if fecal sequencing data can predict deer health, we tested if microbial abundances in fecal samples collected from deer in December could predict adult deer health outcomes at the end of the winter. We reasoned that microbial presence before overwintering could either be a bioindicator of current deer health, which can predict overwintering outcomes or could reflect the digestive capacity of the deer which would directly influence their physiology in ensuing months. When we analyzed the data at the ASV level, we identified the 2 ASVs whose relative abundance in deer in December was significantly correlated with at least one health measure in the same deer in March (**Figure 6, Table S11**). Both ASVs were members of the family Ruminococcaceae in the order Clostridiales; one was positively correlated with future loin thickness and had a relative abundance of >1.5%, and the other was negatively correlated with future rump fat but did not have a relative abundance of >1.5% (**Figure 6**). These findings suggest that some microbes are bioindicators of a deer's overwinter health and may directly influence survival.

There were other microbes that did not significantly predict overwintering outcomes in all adult deer samples but did predict outcomes specific to deer from specific geographic locations or dates. When we tested for significant correlations at the ASV level in each geography and time subset of adult samples and found that for all comparisons the abundances of 25 total ASVs were significantly correlated with at least one March health measure (**Table S11**). Of the geography and time subset groups with more than 5 samples, the maximum R^2 value was 0.7974 for BCS, 1 for Rump Fat, and 0.8425 for Loin Thickness. The much higher R^2 value when analyzing subsets of data may suggest microbes have more predictive potential within geographic or temporal groups than across years and most of the state of Utah, although some may also be due to a small sample size. When we performed the same analyses on reads grouped at higher taxonomic levels, no overwintering outcomes were predicted in the set of all adult deer; however, some order-level groupings did predict deer health when samples were filtered to include only a specific geographic location, season, or overwintering categories (**Table S11**). When looking at samples from a specific geographical location, winter, or season there are different microbes that are significantly correlated with March health. This suggests there are more localized trends in the microbiota than is clear in all adult deer for all geographical locations, winters, and seasons together. In summary, we identified ASVs in pre-winter deer feces that can predict poster-winter deer health across samples collected over five years and in eight geographic locations, but geography-specific analyses had more precise predictive power.

Microbes are Correlated to Latitude and Elevation

Due to previously reported effects that latitude and elevation have on the microbiota of ruminants, and the fact that our samples were collected from wild animals across latitudinal and elevational gradients, we investigated correlations between microbes and latitude and elevation in our adult deer samples [40] [41] (**Figure 2**). Reads from 3 order-level groupings and 111 ungrouped ASVs had abundances that significantly differed with latitude; of these, the positive correlations represented 2 of the order-level and 67 of the ASV-level groupings, most of which were ASVs in the orders Bacteroidales and Clostridiales **(Table S12)**. No order-level grouping and 40 ASVs were significantly correlated with elevation of the sample collection site, including 15 ASVs that were positively correlated with elevation, all but 3 of which also belong to Bacteroidales or Clostridiales **(Table S13)**. Nine ASVs were significantly correlated with both latitude and elevation, two of which positively correlated with both measures. Taken together, these results identify specific microbial taxa that are likely to vary with two key parameters that can reflect disparate environmental conditions.

A Longitudinal Analysis of Mule Deer Across Utah

From our sequencing data, 31 adult deer were sampled 4-7 (mean 4.65) times over the length of the study, representing 146 total samples. The samples span all sampling seasons and 6 of the 7 geographies, and each deer was only sampled in one geography. This subset of samples was used to study longitudinal trends in deer with repeated samples. As with the entire dataset of adult samples, a PERMANOVA showed that time and geography significantly affect microbial variation; geography had the largest effect, explaining 34.6% of the microbial variation (**Figure 7, Table 4**). In a longitudinal mixed-effects analysis, deer sampling season did not significantly affect microbial variation over time in deer with repeated measures: there was no change in microbial variation in deer with either the season or overwintering variables (**Table 5**). The non-significant effect of season contrasts with the results of a PERMANOVA on the same samples and may suggest that much of the variation in time that we observed in the analyses presented above may be more attributable to the sampling of different individuals than to the season-dependent variation in the fecal microbiota composition.

DISCUSSION

We set out to test if there are microbes present in the stool of wild mule deer that are associated with measured estimates of body fat storage. In this work, fecal microbiota data from wild mule deer in Utah, collected between 2014 and 2019, showed geographic and temporal variation in microbial composition. Additionally, specific microbes varied in relative abundance with space, time, and deer age in these deer. All microbes that represented at least 1.5% total relative abundance in our dataset have been previously reported as abundant in other ruminants. We successfully identified microbes that are correlated with and predictive of future deer health. Finally, our analysis of a subset of deer that had been sampled at least four different times over the five-year period of our study suggested that repeated sampling measures can provide insights that are not revealed by analyzing pools of different animals over time.

The composition and abundance of microbes changed by geography, overwinter, and season. geography, overwinter, and season had significant effects on what microbes were present in the fecal samples of adult mule deer. There were also microbes at both the order and ASV levels that varied significantly in abundance by geography, overwinter, and season. Because the microbiota of mule deer is affected by geography, overwinter, and season these are important covariates to explore when evaluating similar data sets. At the order level, Bacteroidales, Clostridiales, Coriobacteriales, Selenomonadales, and Verrucomicrobiales were microbes that were at least 1.5% abundant in all adult deer. These taxa have been previously reported as abundant in other species of deer and other ruminants, in many locations across the world. This shows that the microbiota of our wild mule deer samples were broadly typical of known ruminant microbiota.

We found ASVs in deer samples in December that predicted (i.e. are significantly correlated with) the health measures of the same deer several months later. Two ASVs of Clostridiales were correlated with positive March health measures, one of which had greater than 1.5% abundance in adult deer samples. Therefore, the abundance of this ASV, which belongs to the family Ruminococcaceae, could be used to predict a deer or herd's overwintering health. Some Ruminococcaceae are involved in the microbial biohydrogenation of dietary polyunsaturated fatty acids, which could hint to a possible explanation why this ASV's abundance is positively associated with overwintering: higher levels of the ASV in December may be related to a greater capacity for fat metabolism that liberates fat stores throughout the winter. Further experiments are necessary to test this hypothesis. We also found higher R^2 values for the correlation tests could be higher when the deer from different geographies were tested only with other deer from the same geography, rather than with all deer across the state of Utah, possibly suggesting that focusing on correlations within a herd may be a better predictor of overwintering success than looking for a universal predictive microbe. For example, at the ASV level, Clostridiales ASVs made up the majority of significant ASVs in 5 of 7 geographies and the majority overall. However, the two ASVs that were significant in adult samples were not significant in any specific geographies. Consistent with the idea that predictive signals are strongest on a per-location basis, a previous analysis of Utah deer in Monroe and Cache Valleys (only Cache is represented in our current dataset) identified that the abundance of ASVs assigned to an unassigned *Collinsella* species designation were positively associated with deer overwintering in those areas; but our analysis did not identify any *Collinsella* – ASVs that were correlated with overwintering success. Therefore, while a geography-agnostic diagnostic ASV represents a desirable end goal, it may be more realistic to identify ASVs that predict overwintering success in only a specific area.

Future efforts could focus on the microbes that we found that were related to deer health to determine the extent of their impact, rather than simply their possible use as a diagnostic tool.. For example, we have established a correlation between microbes and health. To establish a causative relationship these deer herds could be followed for several more years, collecting fecal samples and health measurements, to see if the same patterns are observed. Then, we could test if deer overwinter health can be improved by adding beneficial microbes to supplemental feed or if feed should be tested to make sure harmful microbes aren't present. Alternatively, since probiotic dosing may not lead to long-term changes in the ruminant fecal microbiota, it might make more sense to try to find prebiotic feeds that increase the abundance of health-promoting microbes. However, we note that our longitudinal analysis of a subset of deer that we sampled may suggest the fecal microbiota of individuals is relatively resilient to changes in diet (see below). Taken together, these represent some possible ideas for future investigations.

Our study revealed that time significantly impacts the deer fecal microbiota composition, but a longitudinal analysis on a subset of the samples from deer that had been sampled at least four times each raised questions about the importance of time as a determinant of change in the microbiota. Certainly, one key difference between the dataset on which most of our analyses focused, and the longitudinal analysis, is the number of individuals sampled (fewer in the longitudinal analysis). However, it seems unlikely to us that the sampling N alone can explain why time was a significant covariate in the entire dataset, but not in the subset of longitudinally sampled deer, including because a PERMANOVA analysis of the subset of deer also revealed that time was a significant covariate. Instead, it suggests that analyses that lack repeated sampling measures may be unable to distinguish between variation in individuals and variation in time. At least one reason why it is surprising that the fecal microbiota does not vary with time in the longitudinal analysis is because the diet of the deer is so different between December and March, our two main sampling times; diet is a major determinant of microbiota composition. Together, these findings highlight the importance of repeated sampling and of the individual, which can be a challenge in studies of animals in the wild but was made possible by our analyses of animals that were geo-tagged by radio collars.

We have shown a relationship between microbes and health and how prewinter microbiota data may be able to be used to predict post winter deer health. After further experimentation, replicating these methods could reduce the deer captures needed to evaluate if supplemental feed is needed to ensure herd overwinter survival. However, we have not investigated the correlation between microbes and other measurements needed by rangeland managers such as age, gender, if pregnant or lactating, etc. that need net-gun capture to record. More research should be done to see if there is a way to replace these other measures, taken during routine captures, to eliminate or reduce capture and physical measures in the future. Reducing the need for netgun capture and physical measurements will limit the stress and negative health effects of net-gun captures on wild deer.

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FIGURES

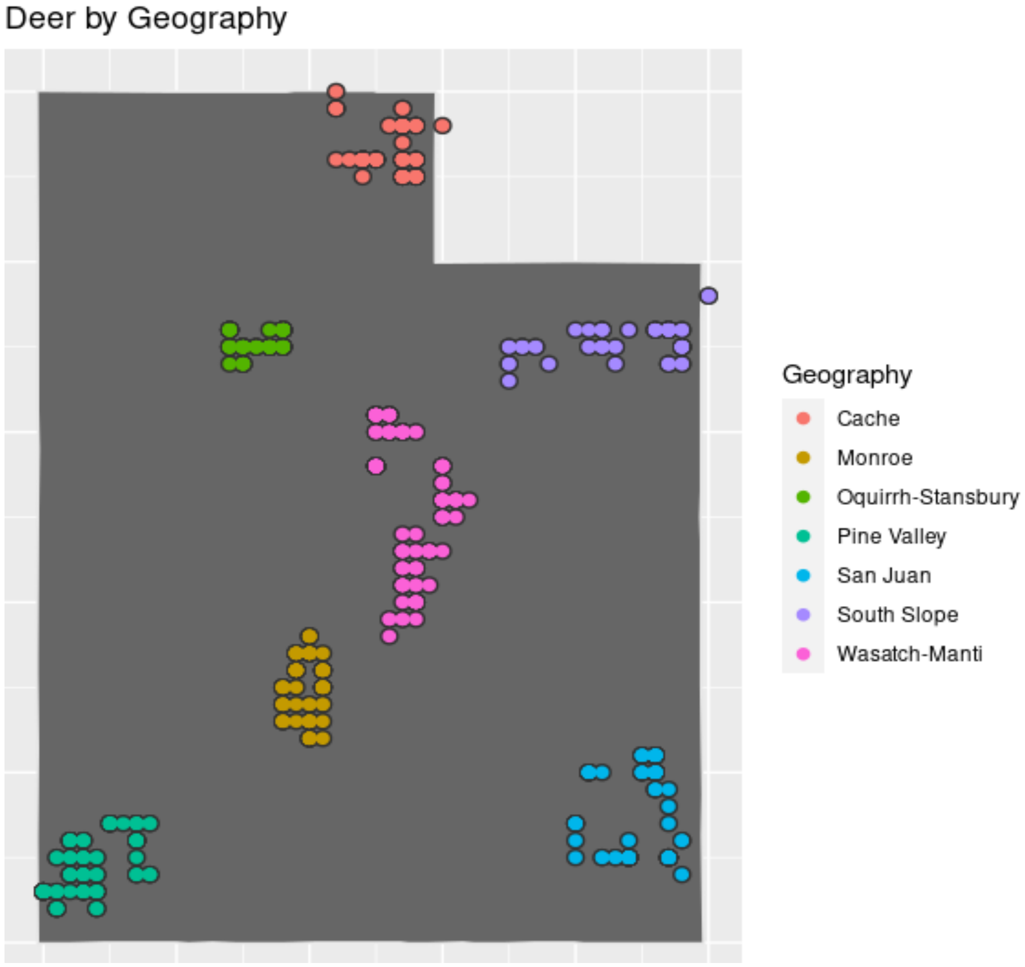


Figure 1. A map of deer sampling location in Utah. Each point on the graph is the location of each deer at capture, color-coded by geographical location, with latitude and longitude values rounded to 0.1.

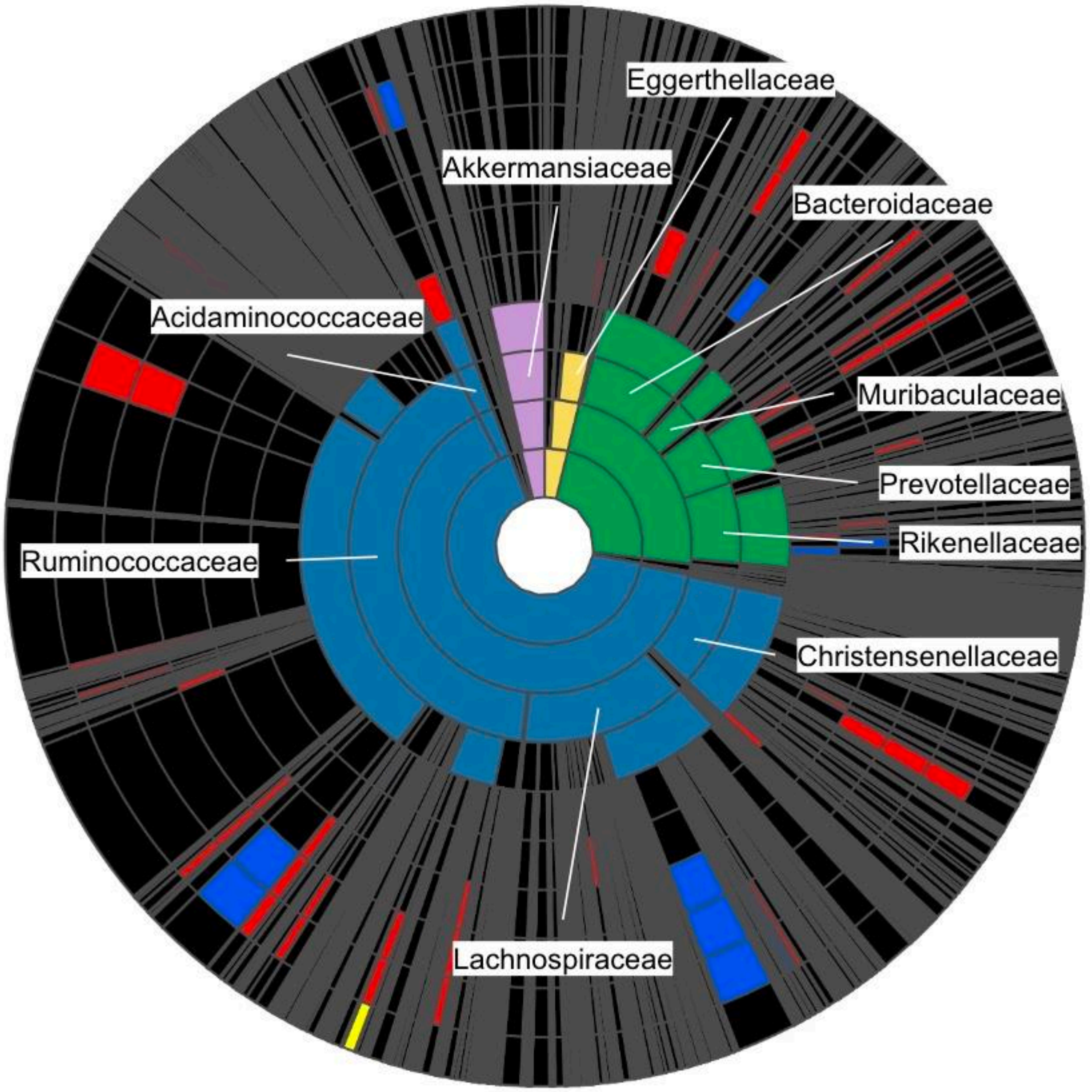


Figure 2. KRONA chart of the relative abundance of microbes in adult deer feces. Each ring represents a taxonomic level, and the width of each segment represents the relative abundance of the reads classified at that taxonomic level. Colored segments represent the four dominant taxonomic groups: Clostridiales (blue), Bacteroidales (green), Verrucomicrobiales (purple), Coriobacteriales (yellow), any classification with < 1.5 % relative abundance (black). Gray lines separate taxonomic designations. From the inside, the rings show the following taxonomic groupings of reads: Phylum, Order, Family, Genus. The outer 6 rings show ASV-level designations and are color-coded to show ASVs that were positively (red) or negatively (blue) associated with a change in deer (ring 6) Latitude, (ring 7) Elevation, (ring 8) LT in the proximate analysis, (ring 9) BCS in the proximate analysis, (ring 8) RF in the proximate analysis, (ring 10) LT in the future analysis. The yellow bar in ring 10 represents an ASV correlated to LT in the future analysis (Figure 6).

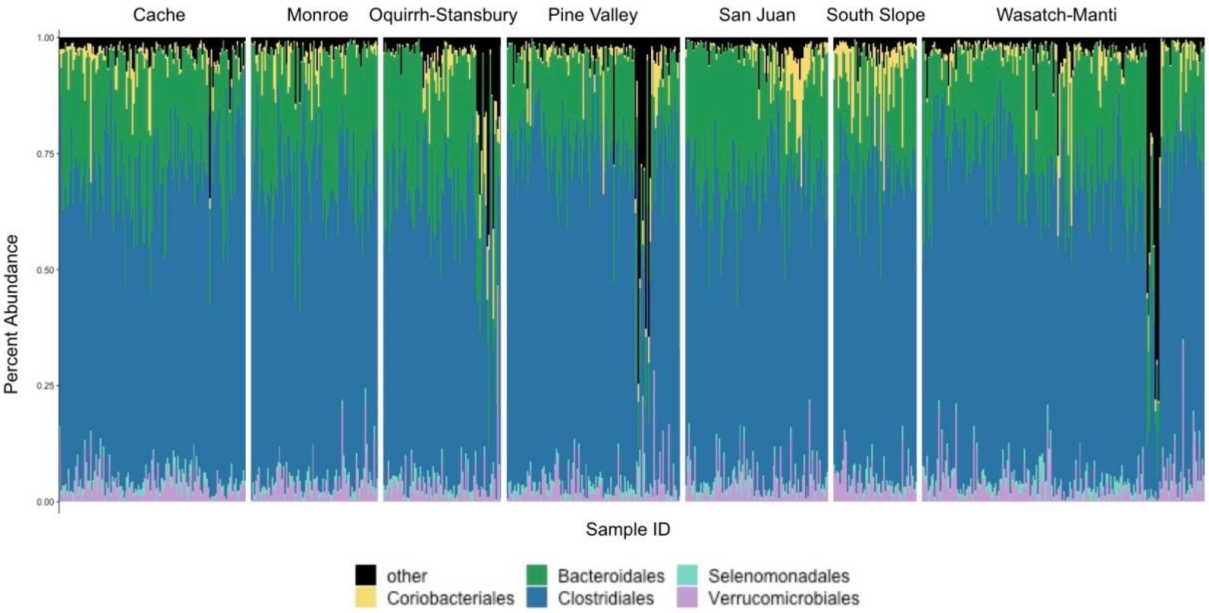


Figure 3. Microbial communities of wild adult deer feces**.** The relative abundance of common bacterial orders in each adult deer fecal sample is shown, grouped by the geographic sampling location.

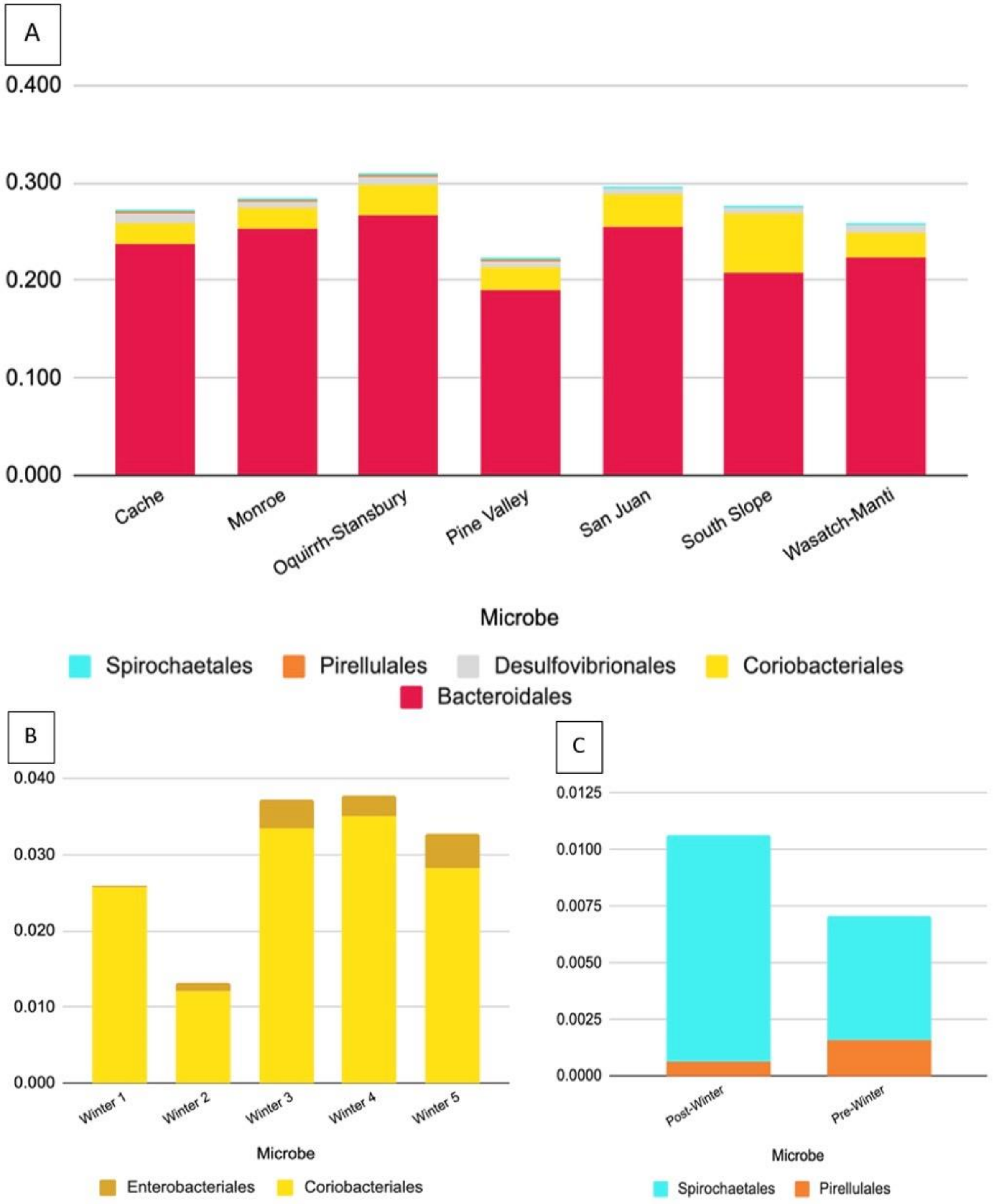


Figure 4. An order-level ANCOM analysis of Adult deer a) by geography, b) by overwinter, c) by season.

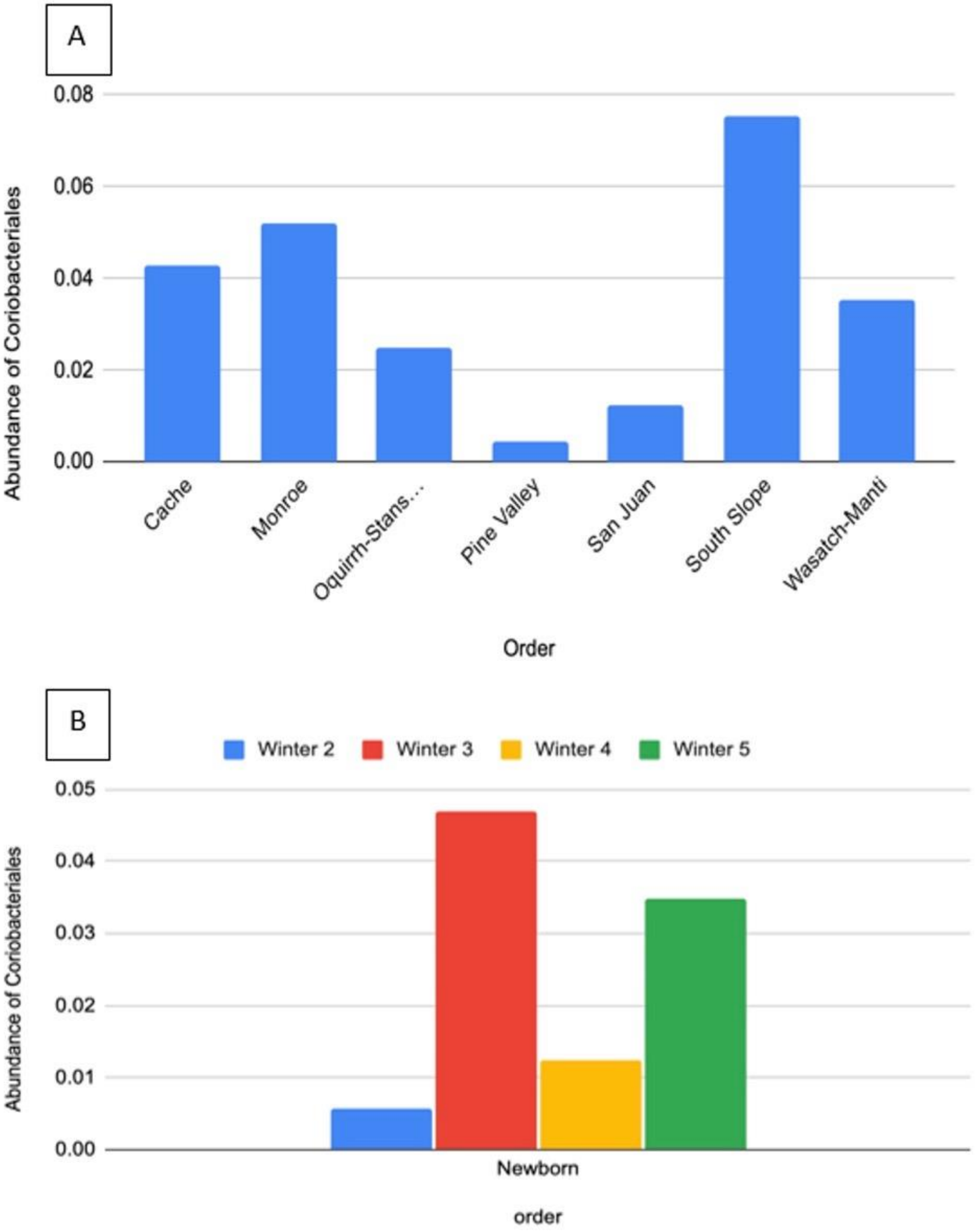
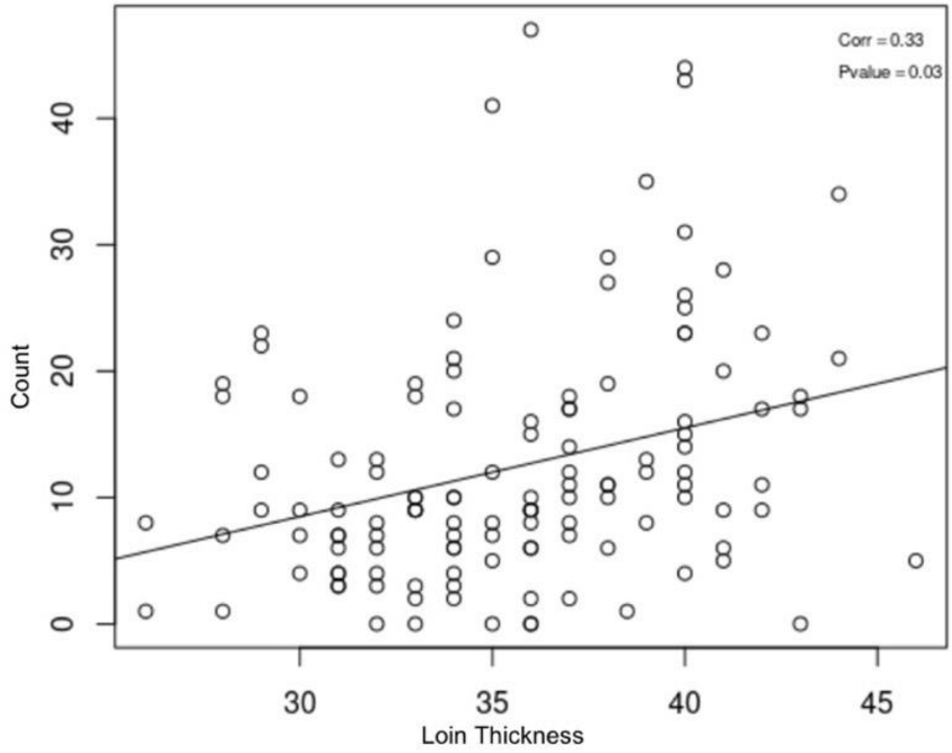


Figure 5. An order-level ANCOM analysis of newborn deer by a) geography and b) the overwinter variable.

A


Corr = 0.33
Pvalue = 0.03
Count
0
10
20
30
40
30
35
40
45
Loin Thickness

B

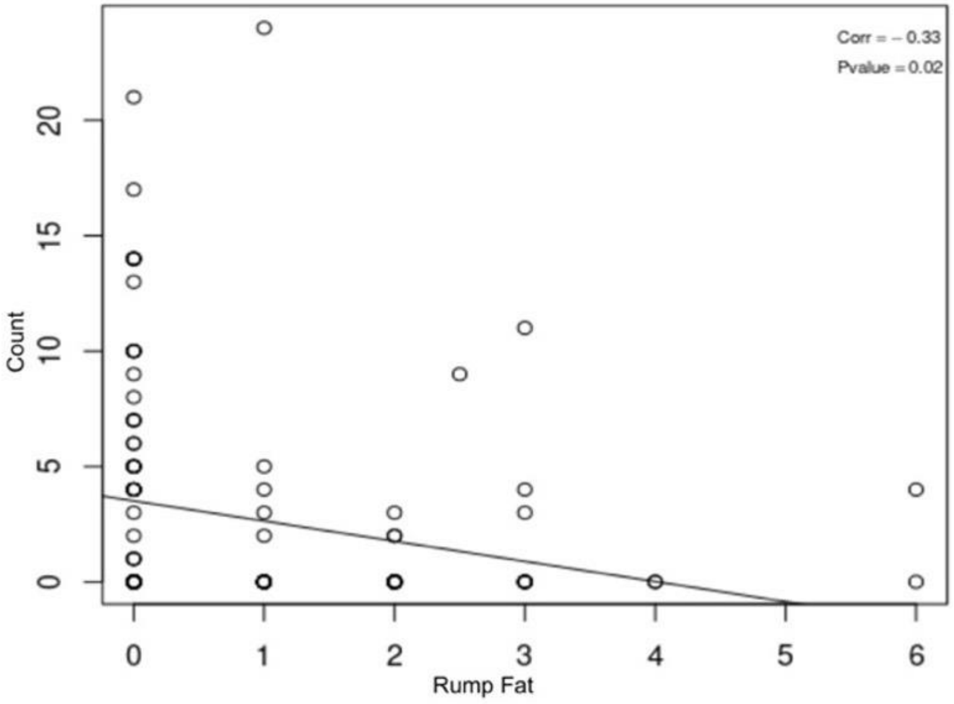

Corr = − 0.33
Pvalue = 0.02
Count
0
5
10
15
20
0
1
2
3
4
5
6
Rump Fat

Figure 6. Correlation plots showing the relationship between ASVs assigned to the family Ruminococcaceae and a) Loin Thickness (ASV ID e89b812979716c96d01b6162a152c846) and b) Rump Fat (ASV ID fd66cf9df106c8a96ce8689645536d56).

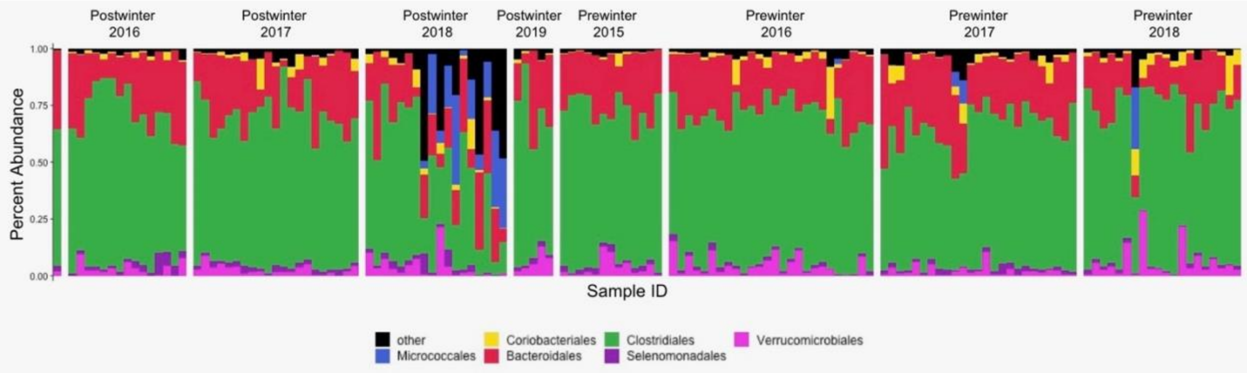


Figure 7. The relative abundance of common bacterial orders in deer with repeated measurements. Each colored column represents an individual deer sample. Sample data is grouped by geography.

TABLES

Table 1. Weighted Unifrac PERMANOVA of adult deer. Sample data evaluated for the effects of season, winter, and geography. (degrees of freedom (DF), p-value (P))

Variable	**DF**	**Sum of Sqs**	**Mean Sqs**	**F Model**	**R2**	**P**
Season	1	0.295	0.295	20.191	0.017	0.001
Overwinter	4	0.506	0.126	8.653	0.029	0.001
Geography	141	4.802	0.034	2.331	0.278	0.001
Season:Overwinter	3	0.295	0.098	6.721	0.017	0.001
Season:Geography	60	1.768	0.029	2.017	0.102	0.001
Overwinter:Geography	142	3.375	0.024	1.627	0.195	0.001
Season:Overwinter:Geography	13	0.389	0.03	2.049	0.023	0.001
Residuals	**400**	**5.844**	**0.015**	**NA**	**0.338**	**NA**
Total	**764**	**17.275**	**NA**	**NA**	**1**	**NA**

Table 2. Counts of deer by age group. Deer are recorded as six months old at the first capture after their birth. Their age is noted at each subsequent capture. Deer are grouped by lifestyle into age groups.

Age Group	**Age Range**	**Sample Count**
Newborn	0 - 0.5 years	156
Yearling	0.5 - 2.5 years	68
Adult	2.5 - 12.5 years	765

Table 3. Weighted Unifrac distance PERMANOVA analysis of a) newborn and b) yearling deer. (degrees of freedom (DF), p-value (P))

A

Variable	**DF**	**Sum of Sqs**	**Mean Sqs**	**F Model**	**R2**	**P**
Overwinter	3	0.226	0.075	4.203	0.065	0.001
Geography	73	1.722	0.024	1.318	0.498	0.006
Overwinter:Geography	17	0.402	0.024	1.323	0.116	0.057
Residuals	**62**	**1.109**	**0.018**	**NA**	**0.321**	**NA**
Total	**155**	**3.459**	**NA**	**NA**	**1**	**NA**

B

Variable	**DF**	**Sum of Sqs**	**Mean Sqs**	**F Model**	**R2**	**P**
Season	1	0.057	0.057	4.955	0.048	0.003
Overwinter	3	0.054	0.018	1.577	0.046	0.099
Geography	41	0.792	0.019	1.69	0.671	0.007
Season:Overwinter	2	0.029	0.015	1.29	0.025	0.228
Season:Geography	7	0.1	0.014	1.246	0.084	0.218
Overwinter:Geography	1	0.012	0.012	1.029	0.01	0.348
Residuals	**12**	**0.137**	**0.011**	**NA**	**0.116**	**NA**
Total	**67**	**1.18**	**NA**	**NA**	**1**	**NA**

Table 4. Weighted Unifrac PERMANOVA of deer with repeated measurements. Sample data evaluated for the effects of geography, overwinter, and season. (degrees of freedom (DF), p-value (P))

Variable	**DF**	**Sum of Sqs**	**Mean Sqs**	**F Model**	**R2**	**P**
Season	1	0.063	0.063	3.938	0.019	0.004
Overwinter	4	0.21	0.052	3.295	1.062	0.001
Geography	33	1.164	0.035	2.215	0.346	0.001
Individual Deer	1	0.007	0.007	0.425	0.002	0.899
Season:Overwinter	3	0.154	0.051	3.223	0.046	0.001
Season:Geography	15	0.372	0.025	1.556	0.111	0.014
Overwinter:Geography	40	0.64	0.016	1.004	0.19	0.465
Season:Overwinter:Geography	6	0.116	0.019	1.217	0.035	0.223
Residuals	**40**	**0.637**	**0.016**	**NA**	**0.189**	**NA**
Total	**143**	**3.361**	**NA**	**NA**	**1**	**NA**

Table 5. Longitudinal Mixed Effects Model of deer with repeated measurements by geography. (Coef. (Coefficient), Std. Err. (Standard Error), p-value (P))

Variable	**Coef.**	**Std.Err.**	**z**	**P**
Intercept	0.707	0.076	9.288	0
Geography[T.Monroe]	0.285	0.462	0.616	0.538
Geography[T.Oquirrh-Stansbury]	-0.288	0.235	-1.223	0.221
Geography[T.Pine Valley]	-0.362	0.19	-1.901	0.057
Geography[T.San Juan]	1.64E+15	2.35E+15	0.696	0.486
Geography[T.Wasatch-Manti]	-0.277	0.053	-5.179	0
Date	-0.023	0.005	-4.85	0
Date:Geography[T.Monroe]	-0.061	0.083	-0.732	0.464
Date:Geography[T.Oquirrh-Stansbury]	0.056	0.049	1.147	0.251
Date:Geography[T.Pine Valley]	0.052	0.025	2.106	0.035
Date:Geography[T.San Juan]	-5.47E+14	7.85E+14	-0.696	0.486
Date:Geography[T.Wasatch-Manti]	0.046			
Group Var	0.008			

SUPPLEMENTAL MATERIAL

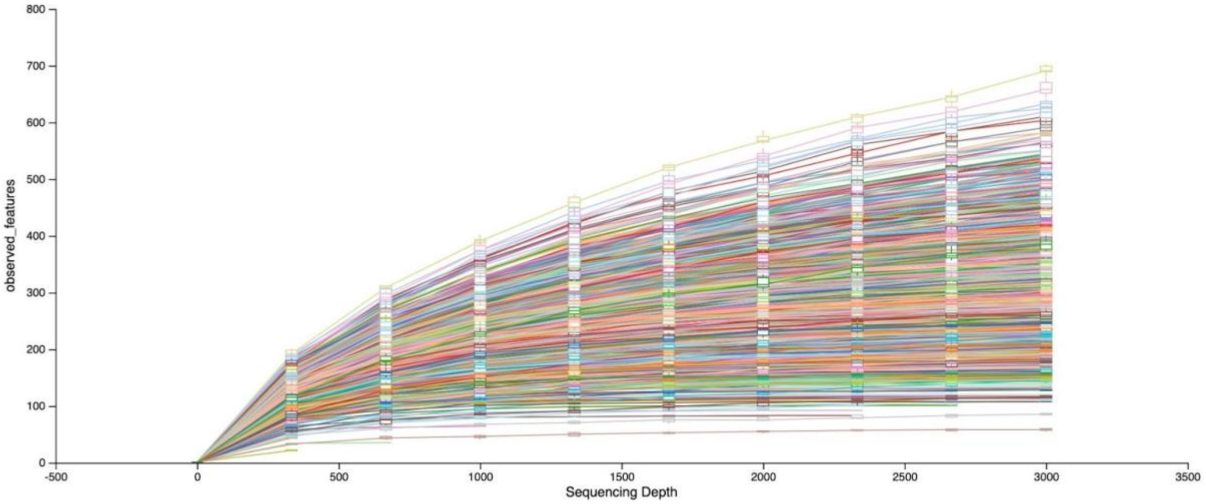


Figure S1: Rarefaction curve using read. Depth of 3000 reads.

Table S1. Bray Curtis, unweighted unifrac, and weighted unifrac distance PERMANOVA analysis of all sampled deer. (degrees of freedom (DF), p-value (P))

a) Bray Curtis

Variable	**DF**	**Sum of Sqs**	**Mean Sqs**	**F Model**	**R2**	**P**
Age	2	1.396	0.698	3.221	0.005	0.001
Season	1	4.422	4.422	20.407	0.017	0.001
Overwinter	4	3.507	0.877	4.046	0.013	0.001
Geography	158	59.458	0.376	1.736	0.224	0.001
Age:Season	1	0.316	0.316	1.457	0.001	0.017
Age:Overwinter	6	1.681	0.28	1.293	0.006	0.002
Season:Overwinter	3	2.129	0.71	3.275	0.008	0.001
Age:Geography	97	24.429	0.252	1.162	0.092	0.001
Season:Geography	62	18.417	0.297	1.371	0.069	0.001
Overwinter:Geography	148	38.764	0.262	1.209	0.146	0.001
Age:Season:Overwinter	2	0.438	0.219	1.01	0.002	0.42
Age:Season:Geography	4	0.859	0.215	0.991	0.003	0.533
Age:Overwinter:Geography	13	3.282	0.252	1.165	0.012	0.004
Season:Overwinter:Geography	13	3.685	0.283	1.308	0.014	0.001
Residuals	**474**	**102.722**	**0.217**	**NA**	**0.387**	**NA**
Total	**988**	**265.507**	**NA**	**NA**	**1**	**NA**

b) Unweighted Unifrac

Variable	**DF**	**Sum of Sqs**	**Mean Sqs**	**F Model**	**R2**	**P**
Age	2	0.671	0.336	2.523	0.004	0.001
Season	1	1.886	1.886	14.174	0.012	0.001
Overwinter	4	2.684	0.671	5.042	0.017	0.001
Geography	158	33.015	0.209	1.57	0.21	0.001
Age:Season	1	0.12	0.12	0.901	0.001	0.706
Age:Overwinter	6	1.079	0.18	1.352	0.007	0.001
Season:Overwinter	3	1.191	0.397	2.983	0.008	0.001
Age:Geography	97	14.396	0.148	1.115	0.092	0.001
Season:Geography	62	10.726	0.173	1.3	0.068	0.001
Overwinter:Geography	148	23.047	0.156	1.17	0.147	0.001
Age:Season:Overwinter	2	0.281	0.141	1.057	0.002	0.305
Age:Season:Geography	4	0.501	0.125	0.941	0.003	0.711
Age:Overwinter:Geography	13	1.98	0.152	1.144	0.013	0.013
Season:Overwinter:Geography	13	2.22	0.171	1.284	0.014	0.001
Residuals	**474**	**63.069**	**0.133**	**NA**	**0.402**	**NA**
Total	**988**	**156.866**	**NA**	**NA**	**1**	**NA**

c) Weighted Unifrac

Variable	**DF**	**Sum of Sqs**	**Mean Sqs**	**F Model**	**R2**	**P**
Age	2	0.132	0.066	4.391	0.006	0.001
Season	1	0.333	0.333	22.177	0.015	0.001
Overwinter	4	0.638	0.16	10.641	0.029	0.001
Geography	158	5.469	0.035	2.308	0.248	0.001
Age:Season	1	0.016	0.016	1.068	0.001	0.336
Age:Overwinter	6	0.121	0.02	1.346	0.005	0.085
Season:Overwinter	3	0.295	0.098	6.559	0.013	0.001
Age:Geography	97	1.871	0.019	1.286	0.085	0.002
Season:Geography	62	1.783	0.029	1.917	0.081	0.001
Overwinter:Geography	148	3.565	0.024	1.606	0.162	0.001
Age:Season:Overwinter	2	0.029	0.014	0.965	0.001	0.438
Age:Season:Geography	4	0.05	0.013	0.841	0.002	0.667
Age:Overwinter:Geography	13	0.245	0.019	1.258	0.011	0.076
Season:Overwinter:Geography	13	0.396	0.03	2.032	0.018	0.001
Residuals	**474**	**7.11**	**0.015**	**NA**	**0.322**	**NA**
Total	**988**	**22.055**	**NA**	**NA**	**1**	**NA**

Table S2. Bray Curtis, unweighted unifrac, and weighted unifrac distance PERMANOVA analysis of deer sample geography subsets. (degrees of freedom (DF), p-value (P))

a) Cache

Bray Curtis

Variable	**DF**	**Sum of Sqs**	**Mean Sqs**	**F Model**	**R2**	**P**
Overwinter	2	1.085	0.542	2.4	0.035	0.001
Season	1	1.073	1.073	4.75	0.035	0.001
Overwinter:Season	2	0.923	0.461	2.042	0.03	0.001
Residuals	122	27.566	0.226	NA	0.899	NA
Total	127	30.647	NA	NA	1	NA

Unweighted Unifrac

Variable	**DF**	**Sum of Sqs**	**Mean Sqs**	**F Model**	**R2**	**P**
Overwinter	2	0.681	0.341	2.356	0.035	0.001
Season	1	0.696	0.696	4.817	0.035	0.001
Overwinter:Season	2	0.6	0.3	2.076	0.031	0.001
Residuals	122	17.639	0.145	NA	0.899	NA
Total	127	19.617	NA	NA	1	NA

Weighted Unifrac

Variable	**DF**	**Sum of Sqs**	**Mean Sqs**	**F Model**	**R2**	**P**
Overwinter	2	0.118	0.059	3.912	0.055	0.001
Season	1	0.112	0.112	7.45	0.052	0.001
Overwinter:Season	2	0.073	0.036	2.415	0.034	0.006
Residuals	122	1.834	0.015	NA	0.859	NA
Total	127	2.136	NA	NA	1	NA

b) Monroe

Bray Curtis

Variable	DF	Sum of Sqs	Mean Sqs	F Model	R2	P
Overwinter	4	1.955	0.489	1.91	0.083	0.001
Season	1	0.503	0.503	1.966	0.021	0.002
Residuals	82	20.98	0.256	NA	0.895	NA
Total	87		NA	NA	1	NA

Unweighted Unifrac

Variable	DF	Sum of Sqs	Mean Sqs	F Model	R2	P
Overwinter	4	1.214	0.304	1.96	0.086	0.001
Season	1	0.248	0.248	1.603	0.018	0.002
Residuals	82	12.699	0.155	NA	0.897	NA
Total	87	14.162	NA	NA	1	NA

Weighted Unifrac

Variable	DF	Sum of Sqs	Mean Sqs	F Model	R2	P
Overwinter	4	0.173	0.043	2.406	0.103	0.001
Season	1	0.028	0.028	1.549	0.017	0.133
Residuals	82	1.475	0.018	NA	0.88	NA
Total	87	1.676	NA	NA	1	NA

c) Oquirrh-Stansbury

Bray Curtis

Variable	DF	Sum of Sqs	Mean Sqs	F Model	R2	P
Overwinter	3	2.047	0.682	2.686	0.094	0.001
Season	1	0.365	0.365	1.435	0.017	0.019
Overwinter:Season	1	0.395	0.395	1.554	0.018	0.012
Residuals	75	19.054	0.254	NA	0.872	NA
Total	80	21.861	NA	NA	1	NA

Unweighted Unifrac

Variable	DF	Sum of Sqs	Mean Sqs	F Model	R2	P
Overwinter	3	1.451	0.484	3.298	0.113	0.001
Season	1	0.226	0.226	1.538	0.018	0.035
Overwinter:Season	1	0.187	0.187	1.275	0.015	0.106
Residuals	75	10.997	0.147	NA	0.855	NA
Total	80	12.86	NA	NA	1	NA

Weighted Unifrac

Variable	DF	Sum of Sqs	Mean Sqs	F Model	R2	P
Overwinter	3	0.305	0.102	4.243	0.141	0.001
Season	1	0.019	0.019	0.784	0.009	0.532
Overwinter:Season	1	0.037	0.037	1.556	0.017	0.16
Residuals	75	1.797	0.024	NA	0.833	NA
Total	80	2.158	NA	NA	1	NA

d) Pine Valley

Bray Curtis

Variable	DF	Sum of Sqs	Mean Sqs	F Model	R2	P
Overwinter	3	1.73	0.577	2.563	0.059	0.001
Season	1	1.15	1.15	5.111	0.039	0.001
Overwinter:Season	2	1.277	0.638	2.837	0.043	0.001
Residuals	112	25.201	0.225	NA	0.858	NA
Total	118	29.358	NA	NA	1	NA

Unweighted Unifrac

Variable	DF	Sum of Sqs	Mean Sqs	F Model	R2	P
Overwinter	3	0.869	0.29	2.109	0.049	0.001
Season	1	0.808	0.808	5.884	0.046	0.001
Overwinter:Season	2	0.626	0.313	2.28	0.035	0.001
Residuals	112	15.384	0.137	NA	0.87	NA
Total	118	17.687	NA	NA	1	NA

Weighted Unifrac

Variable	DF	Sum of Sqs	Mean Sqs	F Model	R2	P
Overwinter	3	0.238	0.079	4.184	0.086	0.001
Season	1	0.218	0.218	11.507	0.079	0.001
Overwinter:Season	2	0.191	0.095	5.019	0.069	0.001
Residuals	112	2.126	0.019	NA	0.767	NA
Total	118	2.774	NA	NA	1	NA

e) San Juan

Bray Curtis

Variable	**DF**	**Sum of Sqs**	**Mean Sqs**	**F Model**	**R2**	**P**
Overwinter	3	2.065	0.688	2.786	0.081	0.001
Season	1	0.409	0.409	1.656	0.016	0.004
Residuals	93	22.974	0.247	NA	0.903	NA
Total	97	25.448	NA	NA	1	NA

Unweighted Unifrac

Variable	**DF**	**Sum of Sqs**	**Mean Sqs**	**F Model**	**R2**	**P**
Overwinter	3	1.62	0.54	4.014	0.113	0.001
Season	1	0.21	0.21	1.559	0.015	0.024
Residuals	93	12.513	0.135	NA	0.872	NA
Total	97	14.343	NA	NA	1	NA

Weighted Unifrac

Variable	**DF**	**Sum of Sqs**	**Mean Sqs**	**F Model**	**R2**	**P**
Overwinter	3	0.506	0.169	9.736	0.236	0.001
Season	1	0.029	0.029	1.666	0.013	0.11
Residuals	93	1.611	0.017	NA	0.751	NA
Total	97	2.146	NA	NA	1	NA

f) South Slope

Bray Curtis

Variable	DF	Sum of Sqs	Mean Sqs	F Model	R2	P
Overwinter	2	1.064	0.532	2.376	0.079	0.001
Season	1	0.59	0.59	2.635	0.044	0.001
Residuals	53	11.863	0.224	NA	0.878	NA
Total	56	13.516	NA	NA	1	NA

Unweighted Unifrac

Variable	DF	Sum of Sqs	Mean Sqs	F Model	R2	P
Overwinter	2	0.569	0.285	2.074	0.07	0.001
Season	1	0.282	0.282	2.054	0.035	0.002
Residuals	53	7.274	0.137	NA	0.895	NA
Total	56	8.125	NA	NA	1	NA

Weighted Unifrac

Variable	DF	Sum of Sqs	Mean Sqs	F Model	R2	P
Overwinter	2	0.114	0.057	3.177	0.103	0.002
Season	1	0.042	0.042	2.363	0.038	0.042
Residuals	53	0.949	0.018	NA	0.859	NA
Total	56	1.105	NA	NA	1	NA

g) Wasatch Manti

Bray Curtis

Variable	DF	Sum of Sqs	Mean Sqs	F Model	R2	P
Overwinter	3	1.95	0.65	2.697	0.038	0.001
Season	1	2.308	2.308	9.578	0.045	0.001
Overwinter:Season	3	2.634	0.878	3.643	0.051	0.001
Residuals	186	44.826	0.241	NA	0.867	NA
Total	193	51.719	NA	NA	1	NA

Unweighted Unifrac

Variable	DF	Sum of Sqs	Mean Sqs	F Model	R2	P
Overwinter	3	1.181	0.394	2.646	0.038	0.001
Season	1	1.013	1.013	6.809	0.033	0.001
Overwinter:Season	3	1.266	0.422	2.838	0.041	0.001
Residuals	186	27.665	0.149	NA	0.889	NA
Total	193	31.125	NA	NA	1	NA

Weighted Unifrac

Variable	DF	Sum of Sqs	Mean Sqs	F Model	R2	P
Overwinter	3	0.301	0.1	5.285	0.067	0.001
Season	1	0.189	0.189	9.94	0.042	0.001
Overwinter:Season	3	0.5	0.167	8.768	0.11	0.001
Residuals	186	3.536	0.019	NA	0.781	NA
Total	193		NA	NA	1	NA

Table S3. Bray Curtis, unweighted unifrac, and weighted unifrac distance PERMANOVA analysis of deer sample overwinter subsets. (degrees of freedom (DF), p-value (P))

a) **Overwinter 2015**

Bray Curtis

Variable	**DF**	**Sum of Sqs**	**Mean Sqs**	**F Model**	**R2**	**P**
Geography	47	14.805	0.315	1.467	0.434	0.001
Residuals	90	19.328	0.215	NA	0.566	NA
Total	137	34.133	NA	NA	1	NA

Unweighted Unifrac

Variable	**DF**	**Sum of Sqs**	**Mean Sqs**	**F Model**	**R2**	**P**
Geography	47	8.395	0.179	1.375	0.418	0.001
Residuals	90	11.695	0.13	NA	0.582	NA
Total	137	20.09	NA	NA	1	NA

Weighted Unifrac

Variable	**DF**	**Sum of Sqs**	**Mean Sqs**	**F Model**	**R2**	**P**
Geography	47	1.108	0.024	1.935	0.503	0.001
Residuals	90	1.097	0.012	NA	0.497	NA
Total	137	2.206	NA	NA	1	NA

b) Overwinter 2016

Bray Curtis

Variable	**DF**	**Sum of Sqs**	**Mean Sqs**	**F Model**	**R2**	**P**
Geography	98	31.428	0.321	1.411	0.437	0.001
Residuals	178	40.466	0.227	NA	0.563	NA
Total	276	71.893	NA	NA	1	NA

Unweighted Unifrac

Variable	**DF**	**Sum of Sqs**	**Mean Sqs**	**F Model**	**R2**	**P**
Geography	98	18.275	0.186	1.338	0.424	0.001
Residuals	178	24.805	0.139	NA	0.576	NA
Total	276	43.08	NA	NA	1	NA

Weighted Unifrac

Variable	**DF**	**Sum of Sqs**	**Mean Sqs**	**F Model**	**R2**	**P**
Geography	98	2.813	0.029	1.859	0.506	0.001
Residuals	178	2.749	0.015	NA	0.494	NA
Total	276	5.562	NA	NA	1	NA

c) Overwinter 2017

Bray Curtis

Variable	**DF**	**Sum of Sqs**	**Mean Sqs**	**F Model**	**R2**	**P**
Geography	72	24.494	0.34	1.385	0.492	0.001
Residuals	103	25.303	0.246	NA	0.508	NA
Total	175	49.797	NA	NA	1	NA

Unweighted Unifrac

Variable	**DF**	**Sum of Sqs**	**Mean Sqs**	**F Model**	**R2**	**P**
Geography	72	14.461	0.201	1.327	0.481	0.001
Residuals	103	15.586	0.151	NA	0.519	NA
Total	175	30.047	NA	NA	1	NA

Weighted Unifrac

Variable	**DF**	**Sum of Sqs**	**Mean Sqs**	**F Model**	**R2**	**P**
Geography	72	2.697	0.037	1.587	0.526	0.001
Residuals	103	2.43	0.024	NA	0.474	NA
Total	175	5.126	NA	NA	1	NA

d) Overwinter 2018

Bray Curtis

Variable	**DF**	**Sum of Sqs**	**Mean Sqs**	**F Model**	**R2**	**P**
Geography	69	21.682	0.314	1.43	0.54	0.001
Residuals	84	18.455	0.22	NA	0.46	NA
Total	153	40.137	NA	NA	1	NA

Unweighted Unifrac

Variable	**DF**	**Sum of Sqs**	**Mean Sqs**	**F Model**	**R2**	**P**
Geography	69	12.16	0.176	1.296	0.516	0.001
Residuals	84	11.424	0.136	NA	0.484	NA
Total	153	23.584	NA	NA	1	NA

Weighted Unifrac

Variable	**DF**	**Sum of Sqs**	**Mean Sqs**	**F Model**	**R2**	**P**
Geography	69	2.247	0.033	2.101	0.633	0.001
Residuals	84	1.302	0.015	NA	0.367	NA
Total	153	3.549	NA	NA	1	NA

Table S4. Bray Curtis, unweighted unifrac, and weighted unifrac distance PERMANOVA analysis of deer sample season subsets. (degrees of freedom (DF), p-value (P))

a) Prewinter

Bray Curtis

Variable	DF	Sum of Sqs	Mean Sqs	F Model	R2	P
Overwinter	3	1.978	0.659	3.137	0.015	0.001
Geography	121	39.779	0.329	1.564	0.308	0.001
Overwinter:Geography	119	30.5	0.256	1.219	0.236	0.001
Residuals	270	56.754	0.21	NA	0.44	NA
Total	513	129.011	NA	NA	1	NA

Unweighted Unifrac

Variable	DF	Sum of Sqs	Mean Sqs	F Model	R2	P
Overwinter	3	1.569	0.523	4.041	0.02	0.001
Geography	121	23.733	0.196	1.515	0.302	0.001
Overwinter:Geography	119	18.311	0.154	1.189	0.233	0.001
Residuals	270	34.952	0.129	NA	0.445	NA
Total	513	78.565	NA	NA	1	NA

Weighted Unifrac

Variable	DF	Sum of Sqs	Mean Sqs	F Model	R2	P
Overwinter	3	0.313	0.104	7.611	0.03	0.001
Geography	121	3.696	0.031	2.231	0.351	0.001
Overwinter:Geography	119	2.81	0.024	1.725	0.267	0.001
Residuals	270	3.697	0.014	NA	0.352	NA
Total	513	10.515	NA	NA	1	NA

b) Post winter

Bray Curtis

Variable	**DF**	**Sum of Sqs**	**Mean Sqs**	**F Model**	**R2**	**P**
Overwinter	4	3.49	0.872	4	0.049	0.001
Geography	80	29.108	0.364	1.668	0.41	0.001
Overwinter:Geography	36	10.067	0.28	1.282	0.142	0.001
Residuals	130	28.354	0.218	NA	0.399	NA
Total	250	71.019	NA	NA	1	NA

Unweighted Unifrac

Variable	**DF**	**Sum of Sqs**	**Mean Sqs**	**F Model**	**R2**	**P**
Overwinter	4	1.822	0.456	3.307	0.044	0.001
Geography	80	16.004	0.2	1.452	0.384	0.001
Overwinter:Geography	36	5.957	0.165	1.201	0.143	0.001
Residuals	130	17.906	0.138	NA	0.43	NA
Total	250	41.689	NA	NA	1	NA

Weighted Unifrac

Variable	**DF**	**Sum of Sqs**	**Mean Sqs**	**F Model**	**R2**	**P**
Overwinter	4	0.496	0.124	7.549	0.076	0.001
Geography	80	2.906	0.036	2.209	0.447	0.001
Overwinter:Geography	36	0.962	0.027	1.625	0.148	0.001
Residuals	130	2.138	0.016	NA	0.329	NA
Total	250	6.501	NA	NA	1	NA

Table S5. Full ANCOM of adult deer samples by geography at all taxonomic levels.

Phylum

	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Cache	Monroe	Oquirrh-Stansbury	Pine Valley	San Juan	South Slope	Wasatch-Manti	Cache_sem	Monroe_sem	Oquirrh-Stansbury_sem	Pine Valley_sem	San Juan_sem	South Slope_sem	Wasatch-Manti_sem
1	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Betaproteobacteriales	f__Burkholderiaceae	g__Parasutterella	s__uncultured Burkholderiales bacterium	abffa3394d919c0bd8224959cb45798d	p__Proteobacteria	0.0245	0.0220	0.0474	0.0461	0.0344	0.0605	0.0405	0.0034	0.0035	0.0093	0.0094	0.0052	0.0088	0.0060
2	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Eggerthellaceae			5652786c2ac5a26c44dcc5df9d02a26a	p__Actinobacteria	0.0098	0.0054	0.0083	0.0065	0.0059	0.0052	0.0065	0.0011	0.0009	0.0011	0.0006	0.0007	0.0011	0.0007
3	k__Bacteria	p__Spirochaetes	c__Spirochaetia	o__Spirochaetales	f__Spirochaetaceae	g__Treponema 2	s__gut metagenome	0b852cc0e76d9d69725def313aff40a4	p__Spirochaetes	0.0053	0.0054	0.0144	0.0104	0.0045	0.0050	0.0097	0.0012	0.0016	0.0051	0.0025	0.0004	0.0015	0.0020
4	k__Bacteria	p__Planctomycetes	c__Planctomycetacia	o__Pirellulales	f__Pirellulaceae	g__p-1088-a5 gut group	s__uncultured bacterium	53ab9d2256ec104ad802edd822fa6eea	p__Planctomycetes	0.0019	0.0019	0.0021	0.0009	0.0010	0.0007	0.0008	0.0003	0.0005	0.0004	0.0003	0.0004	0.0001	0.0002

Class

	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Cache	Monroe	Oquirrh-Stansbury	Pine Valley	San Juan	South Slope	Wasatch-Manti	Cache_sem	Monroe_sem	Oquirrh-Stansbury_sem	Pine Valley_sem	San Juan_sem	South Slope_sem	Wasatch-Manti_sem
1	k__Bacteria	p__Tenericutes	c__Mollicutes	o__Mollicutes RF39				591b47df2174d8219d296319bce9ec06	c__Mollicutes	0.0232	0.0209	0.0316	0.0245	0.0334	0.0601	0.0257	0.0033	0.0035	0.0052	0.0036	0.0052	0.0088	0.0033
2	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Eggerthellaceae			5652786c2ac5a26c44dcc5df9d02a26a	c__Coriobacteriia	0.2366	0.2539	0.2663	0.1894	0.2542	0.2086	0.2251	0.0088	0.0115	0.0128	0.0084	0.0109	0.0121	0.0072
3	k__Bacteria	p__Bacteroidetes	c__Bacteroidia	o__Bacteroidales	f__Bacteroidales RF16 group	g__uncultured bacterium	s__uncultured bacterium	2f490dcda9ddc6af0b6df7f129c3a1a2	c__Bacteroidia	0.0098	0.0054	0.0083	0.0065	0.0059	0.0052	0.0065	0.0011	0.0009	0.0011	0.0006	0.0007	0.0011	0.0007
4	k__Bacteria	p__Proteobacteria	c__Deltaproteobacteria	o__Desulfovibrionales	f__Desulfovibrionaceae	g__Mailhella	s__uncultured bacterium	1336a28dddc8a3b68c94c900deac13cc	c__Deltaproteobacteria	0.0014	0.0019	0.0026	0.0029	0.0028	0.0015	0.0023	0.0001	0.0002	0.0004	0.0004	0.0003	0.0003	0.0003
5	k__Bacteria	p__Spirochaetes	c__Spirochaetia	o__Spirochaetales	f__Spirochaetaceae	g__Treponema 2	s__gut metagenome	0b852cc0e76d9d69725def313aff40a4	c__Spirochaetia	0.0019	0.0019	0.0021	0.0009	0.0010	0.0007	0.0008	0.0003	0.0005	0.0004	0.0003	0.0004	0.0001	0.0002
6	k__Bacteria	p__Planctomycetes	c__Planctomycetacia	o__Pirellulales	f__Pirellulaceae	g__p-1088-a5 gut group	s__uncultured bacterium	53ab9d2256ec104ad802edd822fa6eea	c__Planctomycetacia	0.0019	0.0016	0.0043	0.0033	0.0018	0.0022	0.0017	0.0002	0.0002	0.0004	0.0004	0.0003	0.0006	0.0002

Order

	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Cache	Monroe	Oquirrh-Stansbury	Pine Valley	San Juan	South Slope	Wasatch-Manti	Cache_sem	Monroe_sem	Oquirrh-Stansbury_sem	Pine Valley_sem	San Juan_sem	South Slope_sem	Wasatch-Manti_sem
1	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Eggerthellaceae			5652786c2ac5a26c44dcc5df9d02a26a	o__Coriobacteriales	0.0232	0.0209	0.0316	0.0245	0.0334	0.0601	0.0257	0.0033	0.0035	0.0052	0.0036	0.0052	0.0088	0.0033
2	k__Bacteria	p__Bacteroidetes	c__Bacteroidia	o__Bacteroidales	f__Bacteroidales RF16 group	g__uncultured bacterium	s__uncultured bacterium	2f490dcda9ddc6af0b6df7f129c3a1a2	o__Bacteroidales	0.2366	0.2538	0.2663	0.1894	0.2542	0.2086	0.2241	0.0088	0.0115	0.0128	0.0084	0.0109	0.0121	0.0072
3	k__Bacteria	p__Proteobacteria	c__Deltaproteobacteria	o__Desulfovibrionales	f__Desulfovibrionaceae	g__Mailhella	s__uncultured bacterium	1336a28dddc8a3b68c94c900deac13cc	o__Desulfovibrionales	0.0098	0.0054	0.0083	0.0065	0.0059	0.0052	0.0064	0.0011	0.0009	0.0011	0.0006	0.0007	0.0011	0.0007
4	k__Bacteria	p__Spirochaetes	c__Spirochaetia	o__Spirochaetales	f__Spirochaetaceae	g__Treponema 2	s__gut metagenome	0b852cc0e76d9d69725def313aff40a4	o__Spirochaetales	0.0014	0.0018	0.0026	0.0029	0.0028	0.0015	0.0023	0.0001	0.0002	0.0004	0.0004	0.0003	0.0003	0.0003
5	k__Bacteria	p__Planctomycetes	c__Planctomycetacia	o__Pirellulales	f__Pirellulaceae	g__p-1088-a5 gut group	s__uncultured bacterium	53ab9d2256ec104ad802edd822fa6eea	o__Pirellulales	0.0019	0.0019	0.0021	0.0009	0.0010	0.0007	0.0008	0.0003	0.0005	0.0004	0.0003	0.0004	0.0001	0.0002

Family

	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Cache	Monroe	Oquirrh-Stansbury	Pine Valley	San Juan	South Slope	Wasatch-Manti	Cache_sem	Monroe_sem	Oquirrh-Stansbury_sem	Pine Valley_sem	San Juan_sem	South Slope_sem	Wasatch-Manti_sem
1	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae	g__Lachnospiraceae AC2044 group	s__uncultured bacterium	2736805946a93ec36ef2e53dd9e0d444	f__Lachnospiraceae	0.0025	0.0047	0.0041	0.0051	0.0073	0.0096	0.0037	0.0005	0.0010	0.0009	0.0012	0.0013	0.0023	0.0008
2	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Eggerthellaceae			5652786c2ac5a26c44dcc5df9d02a26a	f__Eggerthellaceae	0.0006	0.0006	0.0019	0.0007	0.0011	0.0016	0.0007	0.0001	0.0002	0.0005	0.0001	0.0003	0.0003	0.0001
3	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Christensenellaceae	g__Christensenellaceae R-7 group		f45ad971967c4657765552d7032edff2	f__Christensenellaceae	0.0192	0.0148	0.0243	0.0178	0.0240	0.0463	0.0201	0.0028	0.0024	0.0040	0.0025	0.0038	0.0068	0.0027
4	k__Bacteria	p__Cyanobacteria	c__Melainabacteria	o__Gastranaerophilales	f__unculturedbacterium	g__uncultured bacterium	s__uncultured bacterium	760c0439f3671cf207b20d7df453530a	f__unculturedbacterium	0.0007	0.0005	0.0008	0.0005	0.0007	0.0017	0.0009	0.0001	0.0001	0.0002	0.0001	0.0001	0.0003	0.0001

5	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Atopobiaceae	g__uncultured	s__uncultured bacterium	d975df96de3ddc81f9fb10f7da2451ba	f__Atopobiaceae	0.0710	0.0905	0.0647	0.0650	0.0814	0.0713	0.0742	0.0024	0.0047	0.0034	0.0033	0.0045	0.0049	0.0024
6	k__Bacteria	p__Bacteroidetes	c__Bacteroidia	o__Bacteroidales	f__Bacteroidaceae	g__Bacteroides	s__uncultured Bacteroides sp.	2ffc6290b27a96b4b16e9f14288cb398	f__Bacteroidaceae	0.0022	0.0023	0.0043	0.0029	0.0019	0.0018	0.0030	0.0002	0.0004	0.0006	0.0004	0.0003	0.0003	0.0007
7	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__FamilyXIII	g__[Eubacterium] nodatum group	s__uncultured rumen bacterium	0e6cdcf43fc9937e0f12e5823f869f1d	f__FamilyXIII	0.0849	0.0853	0.0830	0.0819	0.0993	0.1294	0.0788	0.0036	0.0053	0.0053	0.0052	0.0065	0.0094	0.0033
8	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__uncultured			342e4aeb0756f87d88fb79c015823f0b	f__uncultured	0.0036	0.0029	0.0060	0.0050	0.0060	0.0049	0.0036	0.0003	0.0003	0.0009	0.0006	0.0009	0.0005	0.0005
9	k__Bacteria	p__Spirochaetes	c__Spirochaetia	o__Spirochaetales	f__Spirochaetaceae	g__Treponema 2	s__gut metagenome	0b852cc0e76d9d69725def313aff40a4	f__Spirochaetaceae	0.1346	0.1277	0.1079	0.1281	0.1416	0.1439	0.1570	0.0057	0.0047	0.0040	0.0054	0.0056	0.0094	0.0060
10	k__Bacteria	p__Planctomycetes	c__Planctomycetacia	o__Pirellulales	f__Pirellulaceae	g__p-1088-a5 gut group	s__uncultured bacterium	53ab9d2256ec104ad802edd822fa6eea	f__Pirellulaceae	0.0098	0.0054	0.0083	0.0065	0.0059	0.0052	0.0064	0.0011	0.0009	0.0011	0.0006	0.0007	0.0011	0.0007
11	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Coriobacteriaceae			23ceb404b178b5fa41a9dcea34ff2590	f__Coriobacteriaceae	0.0019	0.0019	0.0021	0.0009	0.0010	0.0007	0.0008	0.0003	0.0005	0.0004	0.0003	0.0004	0.0001	0.0002

Genus

	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Cache	Monroe	Oquirrh-Stansbury	Pine Valley	San Juan	South Slope	Wasatch-Manti	Cache_sem	Monroe_sem	Oquirrh-Stansbury_sem	Pine Valley_sem	San Juan_sem	South Slope_sem	Wasatch-Manti_sem
1	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae	g__LachnospiraceaeAC2044group	s__uncultured bacterium	2736805946a93ec36ef2e53dd9e0d444	g__LachnospiraceaeAC2044group	0.0017	0.0034	0.0022	0.0039	0.0046	0.0059	0.0024	0.0004	0.0008	0.0005	0.0010	0.0009	0.0020	0.0007
2	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Ruminococcaceae	g__RuminococcaceaeUCG-005		676b9a46a8c27708d446a56e623d5cae	g__RuminococcaceaeUCG-005	0.0097	0.0065	0.0120	0.0072	0.0107	0.0259	0.0093	0.0018	0.0011	0.0023	0.0011	0.0018	0.0042	0.0016
3	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae	g__Marvinbryantia	s__uncultured bacterium	8ccb0b837b1928b352be7ec31b1ebea0	g__Marvinbryantia	0.0050	0.0033	0.0075	0.0043	0.0059	0.0119	0.0048	0.0008	0.0006	0.0014	0.0008	0.0010	0.0021	0.0007
4	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae			b2741f7164c1f459772e44f162f8ed72	0.0023	0.0020	0.0015	0.0034	0.0027	0.0035	0.0022	0.0002	0.0004	0.0002	0.0004	0.0004	0.0004	0.0002	
5	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Ruminococcaceae	g__RuminococcaceaeUCG-014	s__uncultured bacterium	44458b368e56225bf308c22a45364f6a	g__RuminococcaceaeUCG-014	0.0007	0.0007	0.0006	0.0006	0.0006	0.0013	0.0008	0.0001	0.0001	0.0001	0.0001	0.0001	0.0002	0.0001
6	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Ruminococcaceae	g__uncultured	s__uncultured bacterium	c5779af7d5c74086a7b2dc363e14e43b	g__uncultured	0.0007	0.0005	0.0008	0.0005	0.0007	0.0017	0.0008	0.0001	0.0001	0.0002	0.0001	0.0001	0.0003	0.0001
7	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Christensenellaceae	g__ChristensenellaceaeR-7group		f45ad971967c4657765552d7032edff2	g__ChristensenellaceaeR-7group	0.0710	0.0905	0.0647	0.0650	0.0814	0.0713	0.0742	0.0024	0.0047	0.0034	0.0033	0.0045	0.0049	0.0024
8	k__Bacteria	p__Cyanobacteria	c__Melainabacteria	o__Gastranaerophilales	f__uncultured bacterium	g__uncultured bacterium	s__uncultured bacterium	760c0439f3671cf207b20d7df453530a	g__unculturedbacterium	0.0194	0.0169	0.0324	0.0208	0.0273	0.0194	0.0184	0.0015	0.0022	0.0034	0.0036	0.0037	0.0027	0.0012
9	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae	g__Lachnoclostridium	s__[Clostridium] fimetarium	a106476d2ca8b9838c81834e0df24e07	g__Lachnoclostridium	0.0073	0.0084	0.0109	0.0064	0.0091	0.0044	0.0059	0.0006	0.0008	0.0010	0.0006	0.0009	0.0006	0.0005
10	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae	g__LachnospiraceaeNK3A20group		42ef77fda0b4d9a6d38bdc2f268244cd	g__LachnospiraceaeNK3A20group	0.0050	0.0028	0.0073	0.0048	0.0048	0.0036	0.0042	0.0004	0.0003	0.0007	0.0004	0.0009	0.0004	0.0003
11	k__Bacteria	p__Bacteroidetes	c__Bacteroidia	o__Bacteroidales	f__Bacteroidaceae	g__Bacteroides	s__uncultured Bacteroides sp.	2ffc6290b27a96b4b16e9f14288cb398	g__Bacteroides	0.0029	0.0028	0.0033	0.0007	0.0025	0.0016	0.0017	0.0003	0.0004	0.0005	0.0001	0.0003	0.0003	0.0002
12	k__Bacteria	p__Bacteroidetes	c__Bacteroidia	o__Bacteroidales	f__Rikenellaceae	g__Alistipes	s__uncultured bacterium	0ac2f3b44d082014fe520489e91f696a	g__Alistipes	0.0022	0.0023	0.0043	0.0029	0.0019	0.0018	0.0030	0.0002	0.0004	0.0006	0.0004	0.0003	0.0003	0.0007
13	k__Bacteria	p__Spirochaetes	c__Spirochaetia	o__Spirochaetales	f__Spirochaetaceae	g__Treponema2	s__gut metagenome	0b852cc0e76d9d69725def313aff40a4	g__Treponema2	0.0846	0.0851	0.0827	0.0816	0.0990	0.1291	0.0785	0.0036	0.0053	0.0053	0.0052	0.0065	0.0094	0.0033
14	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Ruminococcaceae	g__RuminococcaceaeNK4A214group		f3399186bc359971449154a9ed6c993d	g__RuminococcaceaeNK4A214group	0.0006	0.0007	0.0012	0.0009	0.0022	0.0017	0.0010	0.0001	0.0001	0.0003	0.0002	0.0006	0.0003	0.0002
15	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae	g__LachnospiraceaeUCG-008	s__uncultured rumen bacterium	3b77d6685b131c1aaf551a640bf92cb7	g__LachnospiraceaeUCG-008	0.0769	0.0680	0.0538	0.0693	0.0676	0.0761	0.0863	0.0047	0.0031	0.0025	0.0039	0.0029	0.0070	0.0040
16	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Ruminococcaceae	g__Ruminococcus1	s__uncultured rumen bacterium	1eef6b4fa9e05345145297832dcb294d	g__Ruminococcus1	0.0011	0.0008	0.0012	0.0008	0.0018	0.0020	0.0013	0.0001	0.0001	0.0002	0.0002	0.0003	0.0002	0.0002
17	k__Bacteria	p__Planctomycetes	c__Planctomycetacia	o__Pirellulales	f__Pirellulaceae	g__p-1088-a5gutgroup	s__uncultured bacterium	53ab9d2256ec104ad802edd822fa6eea	g__p-1088-a5gutgroup	0.0008	0.0006	0.0017	0.0005	0.0004	0.0003	0.0006	0.0001	0.0001	0.0003	0.0001	0.0001	0.0001	0.0001
18	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae	g__Roseburia	s__uncultured bacterium	a52870de46564c8c421f002ad6f14eb2	g__Roseburia	0.0026	0.0022	0.0017	0.0035	0.0022	0.0039	0.0037	0.0002	0.0002	0.0002	0.0003	0.0002	0.0005	0.0004
19	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Eggerthellaceae	g__Enterorhabdus	s__uncultured rumen bacterium	970384d9bdf4671ac2282157a5b2bed6	g__Enterorhabdus	0.0024	0.0029	0.0030	0.0033	0.0043	0.0043	0.0035	0.0002	0.0003	0.0002	0.0002	0.0003	0.0003	0.0002
20	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Ruminococcaceae	g__Intestinimonas		af7b05d178aafc277d6d2cec7acf4b0e	g__Intestinimonas	0.0016	0.0018	0.0015	0.0024	0.0022	0.0025	0.0035	0.0002	0.0003	0.0002	0.0002	0.0003	0.0004	0.0006
21	k__Bacteria	p__Bacteroidetes	c__Bacteroidia	o__Bacteroidales	f__Rikenellaceae	g__dgA-11gutgroup	s__uncultured bacterium	f4b353a7d70b3834124d5fe462a6abf9	g__dgA-11gutgroup	0.0031	0.0033	0.0054	0.0019	0.0022	0.0024	0.0018	0.0004	0.0005	0.0006	0.0002	0.0004	0.0004	0.0002

22	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Eggerthellaceae	g__DNF00809	s__uncultured bacterium	66811a8459bf3ea91bfadd93b9e89b30	g__DNF00809	0.0017	0.0024	0.0006	0.0018	0.0062	0.0021	0.0036	0.0002	0.0003	0.0002	0.0006	0.0010	0.0004	0.0005
23	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae	g__Dorea	s__uncultured Lachnospiraceae bacterium	8b7da9c1ada1542d528e901e2ae188a2	g__Dorea	0.0020	0.0013	0.0019	0.0014	0.0022	0.0020	0.0021	0.0003	0.0002	0.0006	0.0002	0.0004	0.0004	0.0003
24	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae	g__LachnospiraceaeUCG-002		fed72a43184176a8bd5a22d1085810bb	g__LachnospiraceaeUCG-002	0.0010	0.0012	0.0006	0.0005	0.0021	0.0039	0.0015	0.0001	0.0002	0.0001	0.0001	0.0003	0.0005	0.0002
25	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae	g__[Eubacterium]ruminantiumgroup	s__uncultured bacterium	87d3f2609b7a539a4dd3a1f0dbf55be5	g__[Eubacterium]ruminantiumgroup	0.0014	0.0010	0.0012	0.0007	0.0013	0.0018	0.0015	0.0001	0.0001	0.0002	0.0001	0.0002	0.0002	0.0001
26	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Family XIII	g__Mogibacterium		c6fca45c10aa1cc65be59dd3747b944c	g__Mogibacterium	0.0027	0.0043	0.0027	0.0036	0.0056	0.0061	0.0042	0.0002	0.0004	0.0003	0.0004	0.0006	0.0005	0.0003
27	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Ruminococcaceae	g__RuminococcaceaeUCG-004	s__uncultured rumen bacterium	b3670e366d8f5cdca0dcaca3446afeea	g__RuminococcaceaeUCG-004	0.0105	0.0084	0.0043	0.0090	0.0100	0.0071	0.0154	0.0016	0.0014	0.0006	0.0011	0.0022	0.0020	0.0023
28	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Atopobiaceae	g__Olsenella	s__uncultured rumen bacterium	00e738570656a285b72e284041c25d73	g__Olsenella	0.0052	0.0023	0.0029	0.0041	0.0017	0.0028	0.0029	0.0006	0.0002	0.0003	0.0004	0.0002	0.0003	0.0002
29	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Eggerthellaceae	g__Slackia	s__Slackia heliotrinireducens DSM 20476	9565c2e5069204f315bd9a8c442fe42e	g__Slackia	0.0134	0.0111	0.0111	0.0178	0.0109	0.0123	0.0111	0.0006	0.0008	0.0007	0.0010	0.0006	0.0009	0.0005
30	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae	g__Coprococcus3		621f8a9a7ea593faabaf13e589f13c5c	g__Coprococcus3	0.0014	0.0014	0.0011	0.0011	0.0018	0.0018	0.0013	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001
31	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae	g__LachnospiraceaeFE2018group	s__bacterium FE2018	c16f401190744becd626d95f171908e0	g__LachnospiraceaeFE2018group	0.2538	0.2518	0.1918	0.2612	0.2088	0.2145	0.2433	0.0069	0.0091	0.0098	0.0091	0.0067	0.0100	0.0065
32	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Eggerthellaceae	g__Parvibacter	s__uncultured bacterium	7f3e8fd83d05d1aa89b8d12764c800a7	g__Parvibacter	0.0093	0.0068	0.0183	0.0104	0.0082	0.0103	0.0088	0.0008	0.0009	0.0016	0.0010	0.0009	0.0013	0.0008
33	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae	g__[Eubacterium]halliigroup	s__uncultured rumen bacterium	52399935d8572a471a3ef33ae2e9e358	g__[Eubacterium]halliigroup	0.0147	0.0082	0.0154	0.0074	0.0068	0.0118	0.0071	0.0013	0.0010	0.0014	0.0007	0.0008	0.0016	0.0006
34	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.0098	0.0073	0.0093	0.0095	0.0083	0.0091	0.0077	0.0005	0.0005	0.0005	0.0004	0.0004	0.0005	0.0004
35	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.0079	0.0047	0.0058	0.0061	0.0058	0.0050	0.0061	0.0009	0.0009	0.0006	0.0005	0.0007	0.0011	0.0007
36	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.0019	0.0019	0.0021	0.0009	0.0010	0.0007	0.0008	0.0003	0.0005	0.0004	0.0003	0.0004	0.0001	0.0002

Species

	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Cache	Monroe	Oquirrh-Stansbury	Pine Valley	San Juan	South Slope	Wasatch-Manti	Cache_sem	Monroe_sem	Oquirrh-Stansbury_sem	Pine Valley_sem	San Juan_sem	South Slope_sem	Wasatch-Manti_sem
1	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae	g__Lachnospiraceae AC2044 group	s__unculturedbacterium	2736805946a93ec36ef2e53dd9e0d444	s__unculturedbacterium	0.0010	0.0022	0.0013	0.0023	0.0030	0.0045	0.0014	0.0002	0.0005	0.0003	0.0008	0.0005	0.0019	0.0003
2	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Ruminococcaceae	g__Ruminococcaceae UCG-005		676b9a46a8c27708d446a56e623d5cae	0.0090	0.0061	0.0114	0.0069	0.0102	0.0239	0.0088	0.0017	0.0011	0.0021	0.0010	0.0017	0.0040	0.0015	
3	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Ruminococcaceae	g__[Eubacterium] coprostanoligenes group	s__unculturedrumenbacterium	0c0a33b98b4deeb2e02dd9047bae5e75	s__unculturedrumenbacterium	0.0013	0.0009	0.0020	0.0014	0.0013	0.0028	0.0015	0.0003	0.0002	0.0004	0.0004	0.0003	0.0005	0.0002
4	k__Bacteria	p__Bacteroidetes	c__Bacteroidia	o__Bacteroidales	f__Prevotellaceae	g__Prevotellaceae UCG-004	s__unculturedBacteroidalesbacterium	3f5f06413aff8c8df6793dbd7840c8e6	s__unculturedBacteroidalesbacterium	0.0035	0.0024	0.0054	0.0027	0.0044	0.0088	0.0032	0.0005	0.0005	0.0012	0.0005	0.0007	0.0017	0.0006
5	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae	g__Dorea	s__unculturedLachnospiraceaebacterium	8b7da9c1ada1542d528e901e2ae188a2	s__unculturedLachnospiraceaebacterium	0.0023	0.0020	0.0015	0.0034	0.0027	0.0035	0.0022	0.0002	0.0004	0.0002	0.0004	0.0004	0.0004	0.0002
6	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Christensenellaceae	g__Christensenellaceae R-7 group	s__unculturedprokaryote	8f6419d99de5edba82778c3ddd5ad01d	s__unculturedprokaryote	0.0006	0.0006	0.0005	0.0005	0.0005	0.0009	0.0006	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001
7	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae	g__Lachnospiraceae FE2018 group	s__bacteriumFE2018	c16f401190744becd626d95f171908e0	s__bacteriumFE2018	0.0007	0.0005	0.0008	0.0005	0.0007	0.0017	0.0008	0.0001	0.0001	0.0002	0.0001	0.0001	0.0003	0.0001
8	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Ruminococcaceae	g__Ruminococcaceae UCG-005	s__metagenome	d2f3a0cc7f229ff0461ba3d0c7765bb9	s__metagenome	0.0176	0.0239	0.0198	0.0126	0.0208	0.0179	0.0179	0.0011	0.0030	0.0021	0.0014	0.0022	0.0030	0.0011
9	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.0195	0.0206	0.0160	0.0136	0.0206	0.0173	0.0199	0.0011	0.0014	0.0013	0.0011	0.0017	0.0016	0.0009
10	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.0194	0.0169	0.0324	0.0208	0.0273	0.0194	0.0184	0.0015	0.0022	0.0034	0.0036	0.0037	0.0027	0.0012
11	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.0179	0.0174	0.0216	0.0085	0.0213	0.0153	0.0194	0.0015	0.0019	0.0027	0.0008	0.0023	0.0025	0.0019
12	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.0070	0.0081	0.0106	0.0063	0.0089	0.0043	0.0057	0.0005	0.0008	0.0011	0.0006	0.0009	0.0006	0.0004
13	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.0050	0.0028	0.0073	0.0048	0.0048	0.0036	0.0042	0.0004	0.0003	0.0007	0.0004	0.0009	0.0004	0.0003

14	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.0054	0.0046	0.0071	0.0022	0.0059	0.0071	0.0041	0.0012	0.0008	0.0015	0.0003	0.0016	0.0014	0.0007
15	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.0258	0.0346	0.0411	0.0200	0.0389	0.0222	0.0305	0.0028	0.0043	0.0052	0.0022	0.0039	0.0030	0.0026
16	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.0029	0.0028	0.0033	0.0007	0.0025	0.0016	0.0017	0.0003	0.0004	0.0005	0.0001	0.0003	0.0003	0.0002
17	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.0022	0.0023	0.0043	0.0029	0.0019	0.0018	0.0030	0.0002	0.0004	0.0006	0.0004	0.0003	0.0003	0.0007
18	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.0515	0.0531	0.0539	0.0517	0.0626	0.0809	0.0479	0.0025	0.0036	0.0033	0.0036	0.0041	0.0061	0.0021
19	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.0138	0.0144	0.0105	0.0123	0.0128	0.0210	0.0134	0.0008	0.0012	0.0012	0.0009	0.0010	0.0017	0.0006
20	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.0093	0.0068	0.0075	0.0073	0.0101	0.0123	0.0071	0.0007	0.0010	0.0007	0.0007	0.0012	0.0015	0.0006
21	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.0005	0.0004	0.0008	0.0005	0.0009	0.0005	0.0005	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0000
22	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.0769	0.0680	0.0538	0.0693	0.0676	0.0761	0.0863	0.0047	0.0031	0.0025	0.0039	0.0029	0.0070	0.0040
23	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.0011	0.0008	0.0012	0.0008	0.0018	0.0020	0.0013	0.0001	0.0001	0.0002	0.0002	0.0003	0.0002	0.0002
24	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.0017	0.0010	0.0011	0.0022	0.0014	0.0023	0.0021	0.0002	0.0001	0.0002	0.0002	0.0002	0.0003	0.0004
25	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.0008	0.0012	0.0007	0.0012	0.0009	0.0016	0.0016	0.0001	0.0002	0.0001	0.0001	0.0001	0.0003	0.0002
26	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.0012	0.0011	0.0008	0.0016	0.0017	0.0023	0.0016	0.0001	0.0001	0.0001	0.0001	0.0002	0.0002	0.0001
27	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.0002	0.0011	0.0007	0.0005	0.0017	0.0011	0.0008	0.0001	0.0001	0.0001	0.0001	0.0001	0.0002	0.0001
28	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.0013	0.0014	0.0010	0.0020	0.0018	0.0023	0.0032	0.0002	0.0002	0.0001	0.0002	0.0002	0.0004	0.0006
29	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.0022	0.0028	0.0041	0.0012	0.0012	0.0015	0.0012	0.0003	0.0005	0.0005	0.0002	0.0002	0.0003	0.0001
30	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.0017	0.0024	0.0006	0.0018	0.0060	0.0021	0.0036	0.0002	0.0003	0.0002	0.0006	0.0009	0.0004	0.0005
31	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.0012	0.0007	0.0008	0.0009	0.0014	0.0011	0.0009	0.0002	0.0001	0.0003	0.0002	0.0003	0.0002	0.0001
32	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.0003	0.0007	0.0003	0.0003	0.0012	0.0013	0.0007	0.0001	0.0001	0.0001	0.0001	0.0002	0.0002	0.0001
33	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.0009	0.0007	0.0007	0.0003	0.0010	0.0014	0.0010	0.0001	0.0001	0.0002	0.0001	0.0002	0.0002	0.0001
34	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.0004	0.0005	0.0005	0.0006	0.0010	0.0008	0.0010	0.0001	0.0001	0.0001	0.0001	0.0001	0.0002	0.0001
35	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.0011	0.0018	0.0011	0.0012	0.0018	0.0024	0.0016	0.0001	0.0002	0.0002	0.0001	0.0002	0.0003	0.0001
36	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.0104	0.0083	0.0040	0.0088	0.0097	0.0068	0.0152	0.0016	0.0014	0.0006	0.0011	0.0022	0.0020	0.0023
37	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.0020	0.0031	0.0035	0.0021	0.0029	0.0029	0.0030	0.0002	0.0004	0.0008	0.0002	0.0005	0.0004	0.0003
38	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.0051	0.0023	0.0029	0.0040	0.0017	0.0028	0.0029	0.0006	0.0002	0.0003	0.0004	0.0002	0.0003	0.0002
39	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.0106	0.0084	0.0085	0.0149	0.0087	0.0096	0.0090	0.0005	0.0007	0.0007	0.0009	0.0006	0.0008	0.0004
40	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.0974	0.1079	0.0693	0.1086	0.0801	0.0687	0.0972	0.0051	0.0071	0.0043	0.0060	0.0040	0.0054	0.0044
41	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.0019	0.0009	0.0013	0.0019	0.0007	0.0017	0.0013	0.0002	0.0002	0.0002	0.0002	0.0001	0.0003	0.0001
42	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.0069	0.0054	0.0128	0.0075	0.0056	0.0076	0.0065	0.0006	0.0008	0.0012	0.0006	0.0006	0.0010	0.0005
43	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.0007	0.0004	0.0019	0.0011	0.0007	0.0008	0.0006	0.0001	0.0001	0.0003	0.0002	0.0001	0.0003	0.0001

44	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.0047	0.0028	0.0064	0.0021	0.0024	0.0046	0.0026	0.0007	0.0006	0.0009	0.0003	0.0006	0.0011	0.0004
45	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.0087	0.0050	0.0078	0.0050	0.0039	0.0062	0.0039	0.0011	0.0007	0.0010	0.0006	0.0004	0.0009	0.0003
46	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.0160	0.0113	0.0151	0.0157	0.0129	0.0137	0.0161	0.0008	0.0010	0.0011	0.0012	0.0011	0.0012	0.0008

ASV

	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Cache	Monroe	Oquirrh-Stansbury	Pine Valley	San Juan	South Slope	Wasatch-Manti	Cache_sem	Monroe_sem	Oquirrh-Stansbury_sem	Pine Valley_sem	San Juan_sem	South Slope_sem	Wasatch-Manti_sem
1	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae			bad7e742798b5fcc520ff82e75b256a9	bad7e742798b5fcc520ff82e75b256a9	0.0028	0.0013	0.0034	0.0014	0.0022	0.0038	0.0016	0.0004	0.0003	0.0011	0.0003	0.0004	0.0008	0.0003
2	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae			3d27de5d0b52f339f4eaa9c50384334c	3d27de5d0b52f339f4eaa9c50384334c	0.0023	0.0019	0.0015	0.0034	0.0026	0.0034	0.0022	0.0002	0.0004	0.0002	0.0004	0.0004	0.0004	0.0002
3	k__Bacteria	p__Bacteroidetes	c__Bacteroidia	o__Bacteroidales	f__Bacteroidaceae	g__Bacteroides	s__uncultured Bacteroides sp.	c3e04d8dabd507349ece6501d0db1dc2	c3e04d8dabd507349ece6501d0db1dc2	0.0027	0.0032	0.0040	0.0025	0.0020	0.0011	0.0016	0.0005	0.0005	0.0007	0.0004	0.0004	0.0004	0.0002
4	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Ruminococcaceae	g__Ruminococcaceae UCG-014		6931816a41d435d1dbf37323c5911a26	6931816a41d435d1dbf37323c5911a26	0.0004	0.0005	0.0007	0.0004	0.0008	0.0003	0.0008	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001
5	k__Bacteria	p__Bacteroidetes	c__Bacteroidia	o__Bacteroidales	f__Bacteroidaceae	g__Bacteroides	s__uncultured bacterium	58d83b18f6ccfd7b78fb791f2ddd234a	58d83b18f6ccfd7b78fb791f2ddd234a	0.0037	0.0032	0.0030	0.0027	0.0056	0.0013	0.0034	0.0005	0.0007	0.0007	0.0006	0.0008	0.0005	0.0004
6	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae	g__Lachnospiraceae UCG-008	s__uncultured rumen bacterium	c36b3131d775a0370dc732268cda661f	c36b3131d775a0370dc732268cda661f	0.0033	0.0012	0.0022	0.0017	0.0011	0.0022	0.0025	0.0003	0.0003	0.0004	0.0004	0.0002	0.0005	0.0003
7	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae			6e8b661a46e042ac72dcfdc7b2bf1640	6e8b661a46e042ac72dcfdc7b2bf1640	0.0047	0.0056	0.0029	0.0037	0.0030	0.0058	0.0040	0.0005	0.0007	0.0004	0.0004	0.0004	0.0009	0.0004
8	k__Bacteria	p__Bacteroidetes	c__Bacteroidia	o__Bacteroidales	f__Bacteroidaceae	g__Bacteroides	s__uncultured Bacteroides sp.	f4c5cdfccf496b6bebd5f08d5cf59647	f4c5cdfccf496b6bebd5f08d5cf59647	0.0023	0.0053	0.0016	0.0022	0.0024	0.0035	0.0026	0.0003	0.0008	0.0004	0.0003	0.0004	0.0006	0.0003
9	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Eubacteriaceae	g__Anaerofustis	s__uncultured bacterium	5ef44f4083c411fdac4e4e6f247d9fa3	5ef44f4083c411fdac4e4e6f247d9fa3	0.0030	0.0012	0.0030	0.0018	0.0052	0.0032	0.0045	0.0003	0.0003	0.0005	0.0003	0.0005	0.0007	0.0005
10	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae			490ce719e8f2c7d5179f9fd7241b6845	490ce719e8f2c7d5179f9fd7241b6845	0.0070	0.0126	0.0071	0.0087	0.0104	0.0077	0.0060	0.0007	0.0015	0.0007	0.0008	0.0008	0.0009	0.0004
11	k__Bacteria	p__Bacteroidetes	c__Bacteroidia	o__Bacteroidales	f__Prevotellaceae	g__Prevotellaceae UCG-004	s__uncultured Bacteroidales bacterium	7fb294b2a8be9fa72f541d0cfd534e20	7fb294b2a8be9fa72f541d0cfd534e20	0.0031	0.0068	0.0050	0.0017	0.0049	0.0055	0.0058	0.0006	0.0011	0.0008	0.0004	0.0011	0.0023	0.0009
12	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae	g__Coprococcus 3		780ec7a8c3d95c29e344b5a319a26c6d	780ec7a8c3d95c29e344b5a319a26c6d	0.0019	0.0008	0.0047	0.0029	0.0034	0.0015	0.0021	0.0003	0.0002	0.0005	0.0003	0.0009	0.0003	0.0002
13	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Christensenellaceae	g__Christensenellaceae R-7 group		c988bff728b0b7d1de08acc70ca0c8b5	c988bff728b0b7d1de08acc70ca0c8b5	0.0027	0.0007	0.0020	0.0016	0.0008	0.0015	0.0016	0.0003	0.0002	0.0004	0.0002	0.0002	0.0004	0.0002
14	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Ruminococcaceae	g__Ruminococcus 2		5c80af11236e9dbe24572626ca860d27	5c80af11236e9dbe24572626ca860d27	0.0009	0.0009	0.0015	0.0017	0.0006	0.0007	0.0012	0.0001	0.0002	0.0002	0.0003	0.0001	0.0002	0.0001
15	k__Bacteria	p__Bacteroidetes	c__Bacteroidia	o__Bacteroidales	f__Bacteroidaceae	g__Bacteroides	s__uncultured Bacteroides sp.	5d815d63e66ea05ff63fdb7d373ab89d	5d815d63e66ea05ff63fdb7d373ab89d	0.0009	0.0011	0.0006	0.0008	0.0017	0.0022	0.0012	0.0001	0.0003	0.0001	0.0001	0.0003	0.0003	0.0002
16	k__Bacteria	p__Bacteroidetes	c__Bacteroidia	o__Bacteroidales	f__Rikenellaceae	g__dgA-11 gut group	s__uncultured bacterium	151676c9cd991889ffb561d84b8eec23	151676c9cd991889ffb561d84b8eec23	0.0016	0.0024	0.0024	0.0020	0.0025	0.0039	0.0027	0.0002	0.0005	0.0004	0.0003	0.0005	0.0007	0.0005
17	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Christensenellaceae	g__Christensenellaceae R-7 group		840b390a4d20ebb188390ad930002206	840b390a4d20ebb188390ad930002206	0.0024	0.0014	0.0011	0.0029	0.0013	0.0024	0.0012	0.0003	0.0003	0.0002	0.0004	0.0003	0.0007	0.0002
18	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae			dc9ebfb37254a4862c1890b26c9ceea0	dc9ebfb37254a4862c1890b26c9ceea0	0.0012	0.0015	0.0011	0.0011	0.0020	0.0034	0.0011	0.0002	0.0003	0.0002	0.0002	0.0003	0.0004	0.0001
19	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae	g__[Eubacterium] hallii group	s__uncultured rumen bacterium	52399935d8572a471a3ef33ae2e9e358	52399935d8572a471a3ef33ae2e9e358	0.0033	0.0030	0.0037	0.0031	0.0041	0.0051	0.0027	0.0003	0.0004	0.0004	0.0003	0.0005	0.0006	0.0002
20	k__Bacteria	p__Bacteroidetes	c__Bacteroidia	o__Bacteroidales	f__Bacteroidaceae	g__Bacteroides	s__uncultured bacterium	3af3139cb781bd2d501a5aff0710cfd1	3af3139cb781bd2d501a5aff0710cfd1	0.0029	0.0022	0.0014	0.0023	0.0032	0.0043	0.0021	0.0004	0.0003	0.0003	0.0003	0.0004	0.0005	0.0002
21	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Ruminococcaceae	g__Ruminococcaceae UCG-005		a0be1789266a10cd916a271f506775e5	a0be1789266a10cd916a271f506775e5	0.0058	0.0033	0.0037	0.0032	0.0043	0.0049	0.0026	0.0006	0.0007	0.0004	0.0004	0.0006	0.0008	0.0003
22	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Eggerthellaceae	g__Parvibacter	s__uncultured bacterium	767689e92a255c33e33efcd490ffd1e8	767689e92a255c33e33efcd490ffd1e8	0.0004	0.0003	0.0008	0.0004	0.0009	0.0004	0.0005	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0000
23	k__Bacteria	p__Bacteroidetes	c__Bacteroidia	o__Bacteroidales	f__Bacteroidaceae	g__Bacteroides		0f21aefe093632f22b0b00956bb847c9	0f21aefe093632f22b0b00956bb847c9	0.0124	0.0081	0.0061	0.0118	0.0097	0.0070	0.0093	0.0010	0.0008	0.0007	0.0011	0.0010	0.0010	0.0007
24	k__Bacteria	p__Bacteroidetes	c__Bacteroidia	o__Bacteroidales	f__Bacteroidaceae	g__Bacteroides	s__uncultured Bacteroides sp.	47c4c556d8f1e7301a07421179a41c8a	47c4c556d8f1e7301a07421179a41c8a	0.0006	0.0005	0.0002	0.0007	0.0007	0.0007	0.0007	0.0001	0.0001	0.0000	0.0001	0.0001	0.0001	0.0001
25	k__Bacteria	p__Bacteroidetes	c__Bacteroidia	o__Bacteroidales	f__Rikenellaceae	g__dgA-11 gut group	s__uncultured bacterium	694d5bdadd0faf99d3ffb831e6b192a9	694d5bdadd0faf99d3ffb831e6b192a9	0.0007	0.0006	0.0021	0.0012	0.0018	0.0023	0.0015	0.0001	0.0001	0.0004	0.0001	0.0002	0.0003	0.0001

26	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Christensenellaceae	g__Christensenellaceae R-7 group		47b65bf0d498241aebde58bda676787d	47b65bf0d498241aebde58bda676787d	0.0015	0.0013	0.0013	0.0023	0.0033	0.0036	0.0024	0.0001	0.0002	0.0003	0.0003	0.0003	0.0005	0.0002
27	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae			76314928d015d16b68bb07ed7c1e21b7	76314928d015d16b68bb07ed7c1e21b7	0.0018	0.0008	0.0037	0.0004	0.0008	0.0013	0.0019	0.0003	0.0002	0.0006	0.0001	0.0002	0.0003	0.0004
28	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Christensenellaceae	g__Christensenellaceae R-7 group	s__uncultured rumen bacterium	d4357e3deea47933b40f8f2dcb91a5a1	d4357e3deea47933b40f8f2dcb91a5a1	0.0013	0.0011	0.0003	0.0005	0.0015	0.0015	0.0020	0.0002	0.0002	0.0001	0.0001	0.0002	0.0003	0.0002
29	k__Bacteria	p__Firmicutes	c__Negativicutes	o__Selenomonadales	f__Acidaminococcaceae	g__Phascolarctobacterium	s__uncultured bacterium	9dda34760f2d13aeb961a9e6c6484c34	9dda34760f2d13aeb961a9e6c6484c34	0.0006	0.0003	0.0004	0.0004	0.0011	0.0013	0.0007	0.0001	0.0001	0.0001	0.0001	0.0002	0.0002	0.0001
30	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Christensenellaceae	g__Christensenellaceae R-7 group	s__uncultured prokaryote	54cfc62f863781268abd160036377e8f	54cfc62f863781268abd160036377e8f	0.0211	0.0140	0.0016	0.0143	0.0129	0.0211	0.0275	0.0040	0.0025	0.0004	0.0032	0.0022	0.0061	0.0037
31	k__Bacteria	p__Bacteroidetes	c__Bacteroidia	o__Bacteroidales	f__Bacteroidaceae	g__Bacteroides	s__uncultured Bacteroides sp.	e32225b81aa716a1a2f65737ea633bdb	e32225b81aa716a1a2f65737ea633bdb	0.0004	0.0002	0.0013	0.0014	0.0004	0.0006	0.0007	0.0001	0.0001	0.0002	0.0001	0.0001	0.0001	0.0001
32	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Ruminococcaceae	g__Intestinimonas		d2e6ace039779edef77e2b82a7a2d28b	d2e6ace039779edef77e2b82a7a2d28b	0.0015	0.0012	0.0015	0.0005	0.0007	0.0013	0.0007	0.0002	0.0003	0.0002	0.0001	0.0002	0.0003	0.0001
33	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Ruminococcaceae	g__Negativibacillus	s__uncultured bacterium	2c263f2dff6c02138180d8d1c5d57cb5	2c263f2dff6c02138180d8d1c5d57cb5	0.0010	0.0007	0.0009	0.0006	0.0016	0.0018	0.0012	0.0001	0.0001	0.0002	0.0001	0.0003	0.0002	0.0002
34	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Ruminococcaceae	g__Ruminococcaceae UCG-005		3a1a2997703e40d77585a449a6e78134	3a1a2997703e40d77585a449a6e78134	0.0017	0.0009	0.0010	0.0021	0.0013	0.0021	0.0017	0.0002	0.0001	0.0002	0.0002	0.0002	0.0003	0.0001
35	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Ruminococcaceae	g__Ruminococcaceae NK4A214 group	s__uncultured bacterium	0d781bcdb73083f3c69d7646ef50d11c	0d781bcdb73083f3c69d7646ef50d11c	0.0010	0.0007	0.0005	0.0016	0.0011	0.0011	0.0024	0.0002	0.0002	0.0001	0.0002	0.0002	0.0002	0.0006
36	k__Bacteria	p__Bacteroidetes	c__Bacteroidia	o__Bacteroidales	f__Rikenellaceae	g__Rikenellaceae RC9 gut group	s__uncultured bacterium	c0e1394d06f4bf76cb4459f821ff2ad9	c0e1394d06f4bf76cb4459f821ff2ad9	0.0015	0.0021	0.0005	0.0011	0.0049	0.0017	0.0034	0.0002	0.0003	0.0002	0.0004	0.0007	0.0003	0.0005
37	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae			e91a3ef0bbc2bb4b725c061319f6c1e9	e91a3ef0bbc2bb4b725c061319f6c1e9	0.0008	0.0005	0.0005	0.0002	0.0007	0.0007	0.0007	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001
38	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae	g__Lachnospiraceae FE2018 group	s__bacterium FE2018	0fa4bc34e153544af446f3e2a931b8af	0fa4bc34e153544af446f3e2a931b8af	0.0033	0.0021	0.0014	0.0052	0.0014	0.0017	0.0022	0.0005	0.0004	0.0003	0.0009	0.0004	0.0004	0.0002
39	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Ruminococcaceae	g__Oscillibacter	s__uncultured bacterium	9d4c289bdb1187800d8d26b2e79c3141	9d4c289bdb1187800d8d26b2e79c3141	0.0042	0.0017	0.0024	0.0032	0.0009	0.0021	0.0017	0.0006	0.0002	0.0003	0.0003	0.0001	0.0002	0.0002
40	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae	g__Roseburia		1acf72a9cdf729c1fee61a42c4ed24fa	1acf72a9cdf729c1fee61a42c4ed24fa	0.0006	0.0012	0.0007	0.0004	0.0015	0.0010	0.0009	0.0001	0.0002	0.0001	0.0001	0.0002	0.0002	0.0001
41	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Ruminococcaceae	g__Ruminococcaceae UCG-005	s__uncultured Ruminococcaceae bacterium	279feba3a62fac576c217f743f7a0677	279feba3a62fac576c217f743f7a0677	0.0003	0.0005	0.0004	0.0004	0.0004	0.0004	0.0003	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0000
42	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Eggerthellaceae	g__Enterorhabdus	s__uncultured rumen bacterium	d1c7f61ce9e794e8ee7eb5679ac56349	d1c7f61ce9e794e8ee7eb5679ac56349	0.0042	0.0029	0.0029	0.0077	0.0026	0.0035	0.0027	0.0004	0.0005	0.0005	0.0009	0.0004	0.0006	0.0003
43	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae			867a9dbf65311fbccb6cc0e204049ed7	867a9dbf65311fbccb6cc0e204049ed7	0.0174	0.0218	0.0055	0.0211	0.0144	0.0106	0.0223	0.0024	0.0038	0.0007	0.0041	0.0024	0.0018	0.0029
44	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Ruminococcaceae	g__Ruminococcaceae UCG-005	s__uncultured Ruminococcaceae bacterium	88b31220e635f55ad8ef94508e0c9e01	88b31220e635f55ad8ef94508e0c9e01	0.0569	0.0594	0.0416	0.0612	0.0449	0.0434	0.0505	0.0031	0.0044	0.0025	0.0036	0.0024	0.0040	0.0027
45	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Ruminococcaceae	g__Ruminococcaceae UCG-010	s__uncultured bacterium	b607e4b559041f98b124228e93a22163	b607e4b559041f98b124228e93a22163	0.0012	0.0015	0.0004	0.0011	0.0017	0.0008	0.0010	0.0002	0.0003	0.0001	0.0001	0.0003	0.0002	0.0001
46	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Christensenellaceae	g__Christensenellaceae R-7 group	s__uncultured bacterium	a29473531a9411e9238cdfa4259724ed	a29473531a9411e9238cdfa4259724ed	0.0023	0.0020	0.0018	0.0017	0.0022	0.0015	0.0017	0.0002	0.0002	0.0002	0.0001	0.0002	0.0002	0.0001
47	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Ruminococcaceae	g__Ruminococcaceae UCG-005	s__uncultured bacterium	65a5b2887325cbbef45e7f92c4925206	65a5b2887325cbbef45e7f92c4925206	0.0551	0.0444	0.0417	0.0519	0.0524	0.0673	0.0496	0.0024	0.0024	0.0029	0.0022	0.0026	0.0043	0.0023
48	k__Bacteria	p__Verrucomicrobia	c__Verrucomicrobiae	o__Verrucomicrobiales	f__Akkermansiaceae	g__Akkermansia	s__uncultured bacterium	3d06bc82c1661272ff4d2ad1b9754738	3d06bc82c1661272ff4d2ad1b9754738	0.0423	0.0530	0.0371	0.0410	0.0317	0.0319	0.0371	0.0023	0.0042	0.0027	0.0039	0.0025	0.0022	0.0021
49	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae			ad51fa1938c84e3672b65687af154993	ad51fa1938c84e3672b65687af154993	0.0005	0.0002	0.0002	0.0007	0.0002	0.0001	0.0003	0.0001	0.0000	0.0000	0.0001	0.0000	0.0000	0.0000
50	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae	g__Lachnoclostridium		6189358135d90bdbd014afc6e090b7a7	6189358135d90bdbd014afc6e090b7a7	0.0014	0.0011	0.0026	0.0017	0.0012	0.0015	0.0015	0.0002	0.0001	0.0002	0.0002	0.0002	0.0003	0.0001
51	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Christensenellaceae	g__Christensenellaceae R-7 group		c00d3c1d31f08674abc358a60e684a22	c00d3c1d31f08674abc358a60e684a22	0.0012	0.0009	0.0013	0.0019	0.0016	0.0012	0.0008	0.0002	0.0002	0.0002	0.0003	0.0002	0.0004	0.0001
52	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Ruminococcaceae	g__Ruminococcaceae UCG-005		f461f9e9039751fbea88ced0da0b7387	f461f9e9039751fbea88ced0da0b7387	0.0157	0.0086	0.0145	0.0153	0.0043	0.0081	0.0147	0.0008	0.0010	0.0011	0.0012	0.0007	0.0010	0.0008
53	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae			0dce6b552fbebc89009bf164db8c13e6	0dce6b552fbebc89009bf164db8c13e6	0.0036	0.0074	0.0044	0.0055	0.0065	0.0075	0.0106	0.0006	0.0016	0.0013	0.0013	0.0017	0.0017	0.0014

Table S6. Full ANCOM of adult deer samples by overwinter at all taxonomic levels.

Phylum

	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Winter 2015	Winter 2016	Winter 2017	Winter 2018	Winter 2015_sem	Winter 2016_sem	Winter 2017_sem	Winter 2018_sem
1	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Eggerthellaceae			5652786c2ac5a26c44dcc5df9d02a26a	p__Actinobacteria	0.01240821	0.03446014	0.06882576	0.03379654	0.0025458	0.0030444	0.00890756	0.00443353

Class

	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Winter 2015	Winter 2016	Winter 2017	Winter 2018	Winter 2015_sem	Winter 2016_sem	Winter 2017_sem	Winter 2018_sem
1	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Eggerthellaceae			5652786c2ac5a26c44dcc5df9d02a26a	c__Coriobacteriia	0.01213527	0.03342874	0.03511932	0.02831818	0.00253664	0.00303173	0.00395333	0.00323789
2	k__Bacteria	p__Firmicutes	c__Negativicutes	o__Selenomonadales	f__Acidaminococcaceae	g__Phascolarctobacterium	s__uncultured bacterium	9ee4dcc5306dddb3a4a93ad2cdea09ba	c__Negativicutes	0.02195652	0.01580314	0.01727083	0.01474026	0.00105223	0.00046878	0.00095127	0.00070073

Order

	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Winter 2015	Winter 2016	Winter 2017	Winter 2018	Winter 2015_sem	Winter 2016_sem	Winter 2017_sem	Winter 2018_sem
1	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Eggerthellaceae			5652786c2ac5a26c44dcc5df9d02a26a	o__Coriobacteriales	0.01213527	0.03342874	0.03511932	0.02831818	0.00253664	0.00303173	0.00395333	0.00323789
2	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Enterobacteriales	f__Enterobacteriaceae	g__Serratia		ccb0a94bf7770cd9c03f3988a15074a1	o__Enterobacteriales	0.00101449	0.00373913	0.00264394	0.00448701	0.00044437	0.00083407	0.00150343	0.00130307

Family

	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Winter 2015	Winter 2016	Winter 2017	Winter 2018	Winter 2015_sem	Winter 2016_sem	Winter 2017_sem	Winter 2018_sem
1	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Eggerthellaceae			5652786c2ac5a26c44dcc5df9d02a26a	f__Eggerthellaceae	0.00182126	0.00514614	0.00536932	0.0060368	0.00035705	0.00055983	0.00084333	0.00132744
2	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Christensenellaceae	g__Christensenellaceae R-7 group		f45ad971967c4657765552d7032edff2	f__Christensenellaceae	0.0095314	0.02589372	0.0269375	0.0204632	0.00207153	0.00241811	0.00300734	0.00220308
3	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Atopobiaceae	g__uncultured	s__uncultured bacterium	d975df96de3ddc81f9fb10f7da2451ba	f__Atopobiaceae	0.00035266	0.00090942	0.00093561	0.00074026	9.47E-05	9.88E-05	0.00013767	0.00010794
4	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__FamilyXIII	g__[Eubacterium] nodatum group	s__uncultured rumen bacterium	0e6cdcf43fc9937e0f12e5823f869f1d	f__FamilyXIII	0.0693913	0.09711353	0.0853875	0.09153463	0.00292275	0.00335738	0.00445626	0.00443467
5	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__uncultured			342e4aeb0756f87d88fb79c015823f0b	f__uncultured	0.0021087	0.00456401	0.00662311	0.00397835	0.00014078	0.00043086	0.00064182	0.0003082
6	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Enterobacteriales	f__Enterobacteriaceae	g__Serratia		ccb0a94bf7770cd9c03f3988a15074a1	f__Enterobacteriaceae	0.00101449	0.00373913	0.00264394	0.00448701	0.00044437	0.00083407	0.00150343	0.00130307

Genus

	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Winter 2015	Winter 2016	Winter 2017	Winter 2018	Winter 2015_sem	Winter 2016_sem	Winter 2017_sem	Winter 2018_sem
1	k__Bacteria	p__Tenericutes	c__Mollicutes	o__Mollicutes RF39				591b47df2174d8219d296319bce9ec06	0.00107729	0.00323551	0.00337879	0.0046039	0.0002116	0.00040795	0.00055158	0.00124813	
2	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae	g__Marvinbryantia	s__uncultured bacterium	8ccb0b837b1928b352be7ec31b1ebea0	g__Marvinbryantia	0.00440821	0.0127814	0.01308144	0.00901732	0.00126281	0.00140797	0.00168429	0.00113454
3	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae	g__LachnospiraceaeNK3A20group		42ef77fda0b4d9a6d38bdc2f268244cd	g__LachnospiraceaeNK3A20group	0.00188647	0.00616546	0.00737879	0.00579654	0.00039429	0.00067581	0.00093474	0.00075858
4	k__Bacteria	p__Bacteroidetes	c__Bacteroidia	o__Bacteroidales	f__Prevotellaceae	g__PrevotellaceaeUCG-004	s__uncultured bacterium	c9953823fc07cf9230750e75b981e213	g__PrevotellaceaeUCG-004	0.04544203	0.03592874	0.05504167	0.03920563	0.00359876	0.00203244	0.00327827	0.00304359
5	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Family XIII	g__[Eubacterium] brachygroup	s__uncultured rumen bacterium	bc4c99f91ece907f596287fa6c8b8849	g__[Eubacterium]brachygroup	0.00941787	0.00645894	0.00894508	0.00522078	0.00076371	0.00042419	0.00053751	0.00042848
6	k__Bacteria	p__Bacteroidetes	c__Bacteroidia	o__Bacteroidales	f__Rikenellaceae	g__Alistipes	s__uncultured bacterium	0ac2f3b44d082014fe520489e91f696a	g__Alistipes	0.00486715	0.0041715	0.00582955	0.00429654	0.00064631	0.00022573	0.00038168	0.00033668
7	k__Bacteria	p__Spirochaetes	c__Spirochaetia	o__Spirochaetales	f__Spirochaetaceae	g__Treponema2	s__gut metagenome	0b852cc0e76d9d69725def313aff40a4	g__Treponema2	0.00035507	0.00088043	0.00133523	0.0006645	4.38E-05	0.00010679	0.00014356	7.81E-05
8	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Eggerthellaceae	g__Enterorhabdus	s__uncultured rumen bacterium	970384d9bdf4671ac2282157a5b2bed6	g__Enterorhabdus	0.00065217	0.00112077	0.00194129	0.00144805	5.73E-05	0.0001099	0.0001857	0.00015421
9	k__Bacteria	p__Bacteroidetes	c__Bacteroidia	o__Bacteroidales	f__Rikenellaceae	g__dgA-11gutgroup	s__uncultured bacterium	f4b353a7d70b3834124d5fe462a6abf9	g__dgA-11gutgroup	0.00157246	0.00320531	0.00237121	0.00342424	0.00019976	0.0004164	0.00043728	0.00052554

10	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Eggerthellaceae	g__DNF00809	s__uncultured bacterium	66811a8459bf3ea91bfadd93b9e89b30	g__DNF00809	0.00062802	0.0018128	0.00226326	0.00264935	9.03E-05	0.00022102	0.0003626	0.00036828
11	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae	g__LachnospiraceaeUCG-002		fed72a43184176a8bd5a22d1085810bb	g__LachnospiraceaeUCG-002	0.00068841	0.00155435	0.00126515	0.00184416	0.00011382	0.00013254	0.00018319	0.00020558
12	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Ruminococcaceae	g__RuminococcaceaeUCG-004	s__uncultured rumen bacterium	b3670e366d8f5cdca0dcaca3446afeea	g__RuminococcaceaeUCG-004	0.00264493	0.0047343	0.00367424	0.00440476	0.00020829	0.00027338	0.00032713	0.00031186
13	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__FamilyXIII	g__FamilyXIIIAD3011group	s__uncultured rumen bacterium	3563aa94eecf3b94a010c0d7589c9060	g__FamilyXIIIAD3011group	0.00112319	0.0014529	0.00120833	0.0017013	8.54E-05	6.78E-05	8.74E-05	9.78E-05
14	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Atopobiaceae	g__Olsenella	s__uncultured rumen bacterium	00e738570656a285b72e284041c25d73	g__Olsenella	0.0011256	0.00114855	0.00172348	0.00134632	0.00034387	0.00017964	0.0002111	0.00028623
15	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae	g__LachnospiraceaeFE2018group	s__bacterium FE2018	c16f401190744becd626d95f171908e0	g__LachnospiraceaeFE2018group	0.00041787	0.00073309	0.00125947	0.00047835	8.07E-05	9.82E-05	0.00015898	6.45E-05

Species

	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Winter 2015	Winter 2016	Winter 2017	Winter 2018	Winter 2015_sem	Winter 2016_sem	Winter 2017_sem	Winter 2018_sem
1	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Ruminococcaceae	g__Ruminococcaceae UCG-014	s__unculturedbacterium	44458b368e56225bf308c22a45364f6a	s__unculturedbacterium	0.0006715	0.00213647	0.00212121	0.00267749	0.00013989	0.00028618	0.00031317	0.00093169
2	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Ruminococcaceae	g__[Eubacterium] coprostanoligenes group	s__unculturedrumenbacterium	0c0a33b98b4deeb2e02dd9047bae5e75	s__unculturedrumenbacterium	0.00421256	0.01195894	0.01243371	0.00835714	0.00118875	0.00130636	0.00162234	0.00104898
3	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae	g__Lachnospiraceae FE2018 group	s__bacteriumFE2018	c16f401190744becd626d95f171908e0	s__bacteriumFE2018	0.00061594	0.00183816	0.0020928	0.00108874	0.00012996	0.00023697	0.00030601	0.00014047
4	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Atopobiaceae	g__Olsenella		90699a2dcfc417e5236afcf489f4e1bc	0.00124396	0.00422101	0.00499811	0.00452165	0.00028422	0.000501	0.00069752	0.0006557	
5	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.02355314	0.02100362	0.03420455	0.02428788	0.00268951	0.00151744	0.00243417	0.00240941
6	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.0092343	0.00627295	0.00863258	0.00500649	0.00075782	0.00041312	0.00052537	0.00041838
7	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.000157	0.00062923	0.00121591	0.00088745	2.87E-05	9.74E-05	0.00016228	0.00013814
8	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.00154589	0.0031244	0.00229924	0.00334632	0.00019533	0.00040928	0.00042839	0.00051882
9	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.00027053	0.000843	0.00123864	0.00163636	4.64E-05	8.85E-05	0.00019421	0.00023994
10	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.00192029	0.00299275	0.00218561	0.00333983	0.00031979	0.00027428	0.00024147	0.00030593
11	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.00425121	0.00343357	0.00392045	0.00353896	0.000336	0.00022043	0.00046762	0.0003235
12	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.00057971	0.000843	0.00132197	0.00061472	8.72E-05	9.16E-05	0.00015317	0.00012774

ASV

	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Winter 2015	Winter 2016	Winter 2017	Winter 2018	Winter 2015_sem	Winter 2016_sem	Winter 2017_sem	Winter 2018_sem
1	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae			bad7e742798b5fcc520ff82e75b256a9	bad7e742798b5fcc520ff82e75b256a9	0.00058696	0.00175242	0.00183523	0.00186147	0.00013391	0.00025174	0.00025842	0.00064417
2	k__Bacteria	p__Bacteroidetes	c__Bacteroidia	o__Bacteroidales	f__Prevotellaceae	g__Prevotellaceae UCG-004	s__uncultured bacterium	800cbb4cdf5b762aa3747cd38db617ff	800cbb4cdf5b762aa3747cd38db617ff	0.00061111	0.00212681	0.00303598	0.00270563	0.00012637	0.00027343	0.00045204	0.00054926
3	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Ruminococcaceae	g__[Eubacterium] coprostanoligenes group	s__uncultured rumen bacterium	8527656cc703fff58f61c315702383b8	8527656cc703fff58f61c315702383b8	0.00911353	0.00921498	0.01578598	0.01145887	0.00163616	0.00091495	0.00177352	0.00192777
4	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Atopobiaceae	g__Olsenella		3c98804657c3a3bba509f24ddf64cf18	3c98804657c3a3bba509f24ddf64cf18	0.00143237	0.00134783	0.00065152	0.00148052	0.00016511	0.00015856	0.00011982	0.00019125
5	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Ruminococcaceae	g__Ruminococcaceae UCG-005		3a1a2997703e40d77585a449a6e78134	3a1a2997703e40d77585a449a6e78134	0.01751932	0.02313043	0.00842045	0.01656061	0.00255416	0.00311399	0.00136315	0.00302455
6	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae	g__Lachnospiraceae FE2018 group	s__bacterium FE2018	0fa4bc34e153544af446f3e2a931b8af	0fa4bc34e153544af446f3e2a931b8af	0.0014372	0.00261111	0.00187311	0.0030303	0.00018212	0.0003055	0.00034419	0.00050382
7	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Eggerthellaceae	g__Enterorhabdus	s__uncultured rumen bacterium	d1c7f61ce9e794e8ee7eb5679ac56349	d1c7f61ce9e794e8ee7eb5679ac56349	0.00160628	0.00277174	0.00195076	0.00306277	0.00031614	0.00027089	0.00024018	0.00030258
8	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae			867a9dbf65311fbccb6cc0e204049ed7	867a9dbf65311fbccb6cc0e204049ed7	0.02389614	0.01779831	0.00835606	0.01672078	0.00449784	0.00173047	0.00067424	0.00213233

Table S7. Full ANCOM of adult deer samples by season at all taxonomic levels.

Phylum

	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Post-Winter	Pre-Winter	Post-Winter_sem	Pre-Winter_sem
1	k__Bacteria	p__Planctomycetes	c__Planctomycetacia	o__Pirellulales	f__Pirellulaceae	g__p-1088-a5 gut group	s__uncultured bacterium	53ab9d2256ec104ad802edd822fa6eea	p__Planctomycetes	0.0100239	0.00544444	0.00078977	0.00030627

Class

	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Post-Winter	Pre-Winter	Post-Winter_sem	Pre-Winter_sem
1	k__Bacteria	p__Spirochaetes	c__Spirochaetia	o__Spirochaetales	f__Spirochaetaceae	g__Treponema 2	s__gut metagenome	0b852cc0e76d9d69725def313aff40a4	c__Spirochaetia	0.0100239	0.00544444	0.00078977	0.00030627
2	k__Bacteria	p__Planctomycetes	c__Planctomycetacia	o__Pirellulales	f__Pirellulaceae	g__p-1088-a5 gut group	s__uncultured bacterium	53ab9d2256ec104ad802edd822fa6eea	c__Planctomycetacia	0.00062151	0.00161404	0.0001521	0.00015664

Order

	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Post-Winter	Pre-Winter	Post-Winter_sem	Pre-Winter_sem
1	k__Bacteria	p__Spirochaetes	c__Spirochaetia	o__Spirochaetales	f__Spirochaetaceae	g__Treponema 2	s__gut metagenome	0b852cc0e76d9d69725def313aff40a4	o__Spirochaetales	0.01	0.00544379	0.00079062	0.00030626
2	k__Bacteria	p__Planctomycetes	c__Planctomycetacia	o__Pirellulales	f__Pirellulaceae	g__p-1088-a5 gut group	s__uncultured bacterium	53ab9d2256ec104ad802edd822fa6eea	o__Pirellulales	0.00062151	0.00161404	0.0001521	0.00015664

Family

	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Post-Winter	Pre-Winter	Post-Winter_sem	Pre-Winter_sem
1	k__Bacteria	p__Bacteroidetes	c__Bacteroidia	o__Bacteroidales	f__Rikenellaceae	g__Rikenellaceae RC9 gut group	s__uncultured bacterium	5f666e483f64c68dfae78fd13975ab7c	f__Rikenellaceae	0.03954714	0.05624301	0.00289077	0.00184413
2	k__Bacteria	p__Bacteroidetes	c__Bacteroidia	o__Bacteroidales	f__Prevotellaceae	g__Prevotellaceae UCG-004	s__uncultured bacterium	c9953823fc07cf9230750e75b981e213	f__Prevotellaceae	0.05712616	0.07073229	0.00354631	0.00204545
3	k__Bacteria	p__Planctomycetes	c__Planctomycetacia	o__Pirellulales	f__Pirellulaceae	g__p-1088-a5 gut group	s__uncultured bacterium	53ab9d2256ec104ad802edd822fa6eea	f__Pirellulaceae	0.01	0.00544379	0.00079062	0.00030626

Genus

	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Post-Winter	Pre-Winter	Post-Winter_sem	Pre-Winter_sem
1	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae			b2741f7164c1f459772e44f162f8ed72	0.03099203	0.04777908	0.00244153	0.00169168	
2	k__Bacteria	p__Bacteroidetes	c__Bacteroidia	o__Bacteroidales	f__Rikenellaceae	g__RikenellaceaeRC9gutgroup	s__uncultured bacterium	5f666e483f64c68dfae78fd13975ab7c	g__RikenellaceaeRC9gutgroup	0.04579814	0.05837882	0.00325824	0.00184901
3	k__Bacteria	p__Bacteroidetes	c__Bacteroidia	o__Bacteroidales	f__Prevotellaceae	g__PrevotellaceaeUCG-004	s__uncultured bacterium	c9953823fc07cf9230750e75b981e213	g__PrevotellaceaeUCG-004	0.09239841	0.06409227	0.00411932	0.00124584
4	k__Bacteria	p__Planctomycetes	c__Planctomycetacia	o__Pirellulales	f__Pirellulaceae	g__p-1088-a5gutgroup	s__uncultured bacterium	53ab9d2256ec104ad802edd822fa6eea	g__p-1088-a5gutgroup	0.0010425	0.00047758	8.66E-05	4.63E-05
5	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae	g__[Eubacterium]ventriosumgroup		ec549257240a32514c730a66973e267a	g__[Eubacterium]ventriosumgroup	0.00887517	0.00471605	0.00073546	0.00024982

Species

	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Post-Winter	Pre-Winter	Post-Winter_sem	Pre-Winter_sem
1	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae			b2741f7164c1f459772e44f162f8ed72	0.01504515	0.02958869	0.00170541	0.00129943	
2	k__Bacteria	p__Bacteroidetes	c__Bacteroidia	o__Bacteroidales	f__Prevotellaceae	g__Prevotellaceae UCG-004	s__unculturedbacterium	c9953823fc07cf9230750e75b981e213	s__unculturedbacterium	0.0167251	0.02034698	0.00164457	0.00100275
3	k__Bacteria	p__Bacteroidetes	c__Bacteroidia	o__Bacteroidales	f__Rikenellaceae	g__Rikenellaceae RC9 gut group	s__unculturedBacteroidalesbacterium	a6a4a6e6aedaf32a82d240d64ee8209a	s__unculturedBacteroidalesbacterium	0.02486853	0.03267706	0.00249401	0.00146187
4	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae	g__[Eubacterium] ventriosum group	s__unculturedrumenbacterium	4a52579a9155d0aa02872eada55a6414	s__unculturedrumenbacterium	0.09239841	0.06409227	0.00411932	0.00124584
5	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.00102523	0.00047109	8.58E-05	4.61E-05
6	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.00102789	0.00211761	9.99E-05	0.0001695
7	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.00494024	0.00301819	0.00031756	0.00015311
8	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.0180332	0.01321702	0.00087511	0.00039092
9	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.00887251	0.00471605	0.00073529	0.00024982

ASV

	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Post-Winter	Pre-Winter	Post-Winter_sem	Pre-Winter_sem
1	k__Bacteria	p__Bacteroidetes	c__Bacteroidia	o__Bacteroidales	f__Bacteroidaceae	g__Bacteroides		cf987feccd74b47f83a9e8dffb23c0c3	cf987feccd74b47f83a9e8dffb23c0c3	0.00738247	0.00334893	0.00094139	0.00034312
2	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae			bad7e742798b5fcc520ff82e75b256a9	bad7e742798b5fcc520ff82e75b256a9	0.00293891	0.004718	0.00030911	0.00023171
3	k__Bacteria	p__Planctomycetes	c__Planctomycetacia	o__Pirellulales	f__Pirellulaceae	g__p-1088-a5 gut group	s__uncultured bacterium	53ab9d2256ec104ad802edd822fa6eea	53ab9d2256ec104ad802edd822fa6eea	0.00808499	0.01244509	0.00127793	0.00087394
4	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Christensenellaceae	g__Christensenellaceae R-7 group		f8a30689dee232805c05ee738a3b47bf	f8a30689dee232805c05ee738a3b47bf	0.00115007	0.00298571	0.00015288	0.00024272

5	k__Bacteria	p__Bacteroidetes	c__Bacteroidia	o__Bacteroidales	f__Prevotellaceae	g__Prevotellaceae UCG-004	s__uncultured bacterium	800cbb4cdf5b762aa3747cd38db617ff	800cbb4cdf5b762aa3747cd38db617ff	0.00464807	0.00774984	0.00054854	0.00037082
6	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae			6e8b661a46e042ac72dcfdc7b2bf1640	6e8b661a46e042ac72dcfdc7b2bf1640	0.00133997	0.00265107	0.00012293	0.00012837
7	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Ruminococcaceae	g__Ruminococcaceae UCG-005		4b09f1ee861ce88c31d75ea75d8afcda	4b09f1ee861ce88c31d75ea75d8afcda	0.0020571	0.00086615	0.00020283	6.52E-05
8	k__Bacteria	p__Bacteroidetes	c__Bacteroidia	o__Bacteroidales	f__Bacteroidaceae	g__Bacteroides	s__uncultured Bacteroides sp.	5d815d63e66ea05ff63fdb7d373ab89d	5d815d63e66ea05ff63fdb7d373ab89d	0.03777689	0.00792853	0.00363998	0.00087162
9	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Christensenellaceae	g__Christensenellaceae R-7 group		840b390a4d20ebb188390ad930002206	840b390a4d20ebb188390ad930002206	0.00242231	0.00084276	0.00045979	6.75E-05
10	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Ruminococcaceae	g__Ruminococcaceae NK4A214 group	s__uncultured bacterium	24adfd04805b5bf0804d7c6843c49524	24adfd04805b5bf0804d7c6843c49524	0.00096813	0.00364003	0.00016343	0.00032432
11	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Ruminococcaceae	g__[Eubacterium] coprostanoligenes group	s__uncultured bacterium	78dedcf7eb47d7b606eb31cc7d287299	78dedcf7eb47d7b606eb31cc7d287299	0.00565206	0.00321832	0.00052864	0.00024761
12	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Ruminococcaceae	g__Ruminococcaceae UCG-005		14f43ef69a9c221129271f49a6bbf29d	14f43ef69a9c221129271f49a6bbf29d	0.00196282	0.00359649	0.0001462	0.00012328
13	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Ruminococcaceae	g__Ruminococcaceae UCG-005		3a1a2997703e40d77585a449a6e78134	3a1a2997703e40d77585a449a6e78134	0.0028579	0.00487459	0.00021744	0.00018377
14	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae			867a9dbf65311fbccb6cc0e204049ed7	867a9dbf65311fbccb6cc0e204049ed7	0.03069323	0.01113255	0.0031693	0.00077218
15	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Ruminococcaceae	g__[Eubacterium] coprostanoligenes group		35252cd698224c71c910904c42d3f017	35252cd698224c71c910904c42d3f017	0.00351129	0.00468356	0.00039838	0.00021461
16	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae	g__Lachnoclostridium		6189358135d90bdbd014afc6e090b7a7	6189358135d90bdbd014afc6e090b7a7	0.00856175	0.00425796	0.00073369	0.00024282

Table S8. Full ANCOM of newborn deer samples by geography and overwinter at all taxonomic levels.

a) Geography

Phylum

	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Cache	Monroe	Oquirrh-Stansbury	Pine Valley	San Juan	South Slope	Wasatch-Manti	Cache_sem	Monroe_sem	Oquirrh-Stansbury_sem	Pine Valley_sem	San Juan_sem	South Slope_sem	Wasatch-Manti_sem

Class

	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Cache	Monroe	Oquirrh-Stansbury	Pine Valley	San Juan	South Slope	Wasatch-Manti	Cache_sem	Monroe_sem	Oquirrh-Stansbury_sem	Pine Valley_sem	San Juan_sem	South Slope_sem	Wasatch-Manti_sem
1	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Eggerthellaceae			5652786c2ac5a26c44dcc5df9d02a26a	c__Coriobacteriia	0.04286364	0.0522	0.02479487	0.00448333	0.01246667	0.0752037	0.03519608	0.01230639	0.0265069 4	0.00955309	0.0010135	0.0029746	0.020039	0.01271119

Order

	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Cache	Monroe	Oquirrh-Stansbury	Pine Valley	San Juan	South Slope	Wasatch-Manti	Cache_sem	Monroe_sem	Oquirrh-Stansbury_sem	Pine Valley_sem	San Juan_sem	South Slope_sem	Wasatch-Manti_sem
1	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Eggerthellaceae			5652786c2ac5a26c44dcc5df9d02a26a	o__Coriobacteriales	0.04286364	0.0522	0.02479487	0.00448333	0.01246667	0.0752037	0.03519608	0.01230639	0.0265069 4	0.00955309	0.0010135	0.0029746	0.020039	0.01271119

Family

	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Cache	Monroe	Oquirrh-Stansbury	Pine Valley	San Juan	South Slope	Wasatch-Manti	Cache_sem	Monroe_sem	Oquirrh-Stansbury_sem	Pine Valley_sem	San Juan_sem	South Slope_sem	Wasatch-Manti_sem
1	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Eggerthellaceae			5652786c2ac5a26c44dcc5df9d02a26a	f__Eggerthellaceae	0.03230303	0.03783333	0.02005128	0.00305	0.00921905	0.05831481	0.02594118	0.00941341	0.0178034 7	0.00812157	0.00056209	0.0023	0.016935	0.00951466

Genus

	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Cache	Monroe	Oquirrh-Stansbury	Pine Valley	San Juan	South Slope	Wasatch-Manti	Cache_sem	Monroe_sem	Oquirrh-Stansbury_sem	Pine Valley_sem	San Juan_sem	South Slope_sem	Wasatch-Manti_sem
1	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Eggerthellaceae	g__Enterorhabdus	s__uncultured rumen bacterium	970384d9bdf4671ac2282157a5b2bed6	g__Enterorhabdus	0.01465152	0.019	0.01153846	0.00096667	0.0045619	0.03157407	0.01376471	0.00392464	0.0089649 5	0.00547469	0.0003306	0.00135699	0.0096297	0.00525772
2	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Eggerthellaceae	g__DNF00809	s__uncultured bacterium	66811a8459bf3ea91bfadd93b9e89b30	g__DNF00809	0.01048485	0.0098	0.00538462	0.00065	0.00234286	0.01355556	0.00615686	0.0041794	0.0051714 3	0.0020823	0.00025418	0.00054447	0.00427207	0.00272382
3	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Eggerthellaceae	g__Parvibacter	s__uncultured bacterium	7f3e8fd83d05d1aa89b8d12764c800a7	g__Parvibacter	0.00307576	0.00236667	0.00112821	0.00073333	0.00060952	0.0042963	0.00129412	0.00059375	0.0009931 2	0.00029123	0.00019285	0.00013142	0.00113244	0.00033319

Species

	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Cache	Monroe	Oquirrh-Stansbury	Pine Valley	San Juan	South Slope	Wasatch-Manti	Cache_sem	Monroe_sem	Oquirrh-Stansbury_sem	Pine Valley_sem	San Juan_sem	South Slope_sem	Wasatch-Manti_sem
1	k__Bacteria	p__Firmicutes	c__Negativicutes	o__Selenomonadales	f__Acidaminococcaceae	g__Phascolarctobacterium	s__unculturedbacterium	9ee4dcc5306dddb3a4a93ad2cdea09ba	s__unculturedbacterium	0.01371212	0.01776667	0.01064103	0.00093333	0.00432381	0.0295	0.01290196	0.00362081	0.0083228 2	0.00491443	0.00033386	0.00124883	0.00878837	0.00481519
2	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Eggerthellaceae	g__Enterorhabdus	s__unculturedrumenbacterium	970384d9bdf4671ac2282157a5b2bed6	s__unculturedrumenbacterium	0.00733333	0.0076	0.00441026	0.00023333	0.00188571	0.00987037	0.00398039	0.00331096	0.0043653 5	0.00186898	0.00016772	0.00050339	0.00378595	0.00170051
3	k__Bacteria	p__Firmicutes	c__Negativicutes	o__Selenomonadales	f__Acidaminococcaceae	g__Phascolarctobacterium	s__unculturedVeillonellaceaebacterium	45c3713fc12801a8730faba2e3dfc57b	s__unculturedVeillonellaceaebacterium	0.00357576	0.00086667	0.00125641	9.00E-04	0.00050476	0.00194444	0.00111765	0.00044688	0.000445	0.00062834	0.00035384	0.00018805	0.00044055	0.00047567
4	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Ruminococcaceae	g__Ruminococcaceae UCG-005	s__metagenome	d2f3a0cc7f229ff0461ba3d0c7765bb9	s__metagenome	0.01486364	0.00273333	0.01346154	0.01521667	0.00742857	0.0042037	0.01037255	0.00213186	0.0010986	0.00221737	0.00163501	0.00172354	0.00094209	0.00181021
5	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.00168182	0.00803333	0.00207692	0.00103333	0.00558095	0.00259259	0.00258824	0.0007361	0.0025148 7	0.0011267	0.00068778	0.00102957	0.00121464	0.00192942

ASV

	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Cache	Monroe	Oquirrh-Stansbury	Pine Valley	San Juan	South Slope	Wasatch-Manti	Cache_sem	Monroe_sem	Oquirrh-Stansbury_sem	Pine Valley_sem	San Juan_sem	South Slope_sem	Wasatch-Manti_sem
1	k__Bacteria	p__Bacteroidetes	c__Bacteroidia	o__Bacteroidales	f__Bacteroidaceae	g__Bacteroides	s__uncultured bacterium	58d83b18f6ccfd7b78fb791f2ddd234a	58d83b18f6ccfd7b78fb791f2ddd234a	0.00304545	0.0045	0.002	0.00683333	0.00605714	0.00166667	0.00468627	0.00132706	0.0012365 3	0.00113102	0.00145246	0.0011201	0.00101549	0.00384604
2	k__Bacteria	p__Bacteroidetes	c__Bacteroidia	o__Bacteroidales	f__Bacteroidaceae	g__Bacteroides		0f21aefe093632f22b0b00956bb847c9	0f21aefe093632f22b0b00956bb847c9	0.0009697	0.001	0.00407692	0.00125	0.00867619	0.00027778	0.00098039	0.00048045	0.0004527	0.00284579	0.00032881	0.00170327	0.00011824	0.0005243
3	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Ruminococcaceae	g__Ruminococcaceae UCG-005	s__uncultured Ruminococcaceae bacterium	d2bb065e12a3db145a18dff35dd42493	d2bb065e12a3db145a18dff35dd42493	0.02057576	0.01006667	0.00597436	0.0222	0.01373333	0.0067963	0.00872549	0.00391874	0.0030424	0.0019606	0.00536102	0.00270159	0.00362655	0.00240646

4	k__Bacteria	p__Firmicutes	c__Negativicutes	o__Selenomonadales	f__Acidaminococcaceae	g__Phascolarctobacterium	s__uncultured bacterium	9dda34760f2d13aeb961a9e6c6484c34	9dda34760f2d13aeb961a9e6c6484c34	0.01413636	0.00193333	0.01323077	0.01485	0.00411429	0.00212963	0.00933333	0.00211623	0.00095426	0.00231783	0.00156916	0.00125877	0.00064112	0.00165165

b) Overwinter

Phylum

	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Winter 2015	Winter 2016	Winter 2017	Winter 2018	Winter 2015_sem	Winter 2016_sem	Winter 2017_sem	Winter 2018_sem

Class

	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Winter 2015	Winter 2016	Winter 2017	Winter 2018	Winter 2015_sem	Winter 2016_sem	Winter 2017_sem	Winter 2018_sem
1	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Eggerthellaceae			5652786c2ac5a26c44dcc5df9d02a26a	c__Coriobacteriia	0.00576984	0.04684959	0.01240741	0.03483333	0.0009816	0.0071455	0.00509562	0.02916667

Order

	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Winter 2015	Winter 2016	Winter 2017	Winter 2018	Winter 2015_sem	Winter 2016_sem	Winter 2017_sem	Winter 2018_sem
1	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Eggerthellaceae			5652786c2ac5a26c44dcc5df9d02a26a	o__Coriobacteriales	0.00576984	0.04684959	0.01240741	0.03483333	0.0009816	0.0071455	0.00509562	0.02916667

Family

	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Winter 2015	Winter 2016	Winter 2017	Winter 2018	Winter 2015_sem	Winter 2016_sem	Winter 2017_sem	Winter 2018_sem
1	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Eggerthellaceae			5652786c2ac5a26c44dcc5df9d02a26a	f__Eggerthellaceae	0.00379365	0.03557724	0.01007407	0.02833333	0.00063828	0.00557977	0.00420272	0.02433333

Genus

	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Winter 2015	Winter 2016	Winter 2017	Winter 2018	Winter 2015_sem	Winter 2016_sem	Winter 2017_sem	Winter 2018_sem
1	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Eggerthellaceae			5652786c2ac5a26c44dcc5df9d02a26a	0.00019048	0.00269106	0.00025926	0.003	0.00011537	0.00051316	0.00014463	0.00233333	
2	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Eggerthellaceae	g__Enterorhabdus	s__uncultured rumen bacterium	970384d9bdf4671ac2282157a5b2bed6	g__Enterorhabdus	0.00157143	0.01853659	0.00392593	0.01116667	0.00043692	0.00299882	0.00164502	0.01016667
3	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Eggerthellaceae	g__DNF00809	s__uncultured bacterium	66811a8459bf3ea91bfadd93b9e89b30	g__DNF00809	0.00075397	0.00931707	0.00366667	0.00683333	0.00018599	0.00170637	0.00167314	0.0065

Species

	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Winter 2015	Winter 2016	Winter 2017	Winter 2018	Winter 2015_sem	Winter 2016_sem	Winter 2017_sem	Winter 2018_sem
1	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Eggerthellaceae			5652786c2ac5a26c44dcc5df9d02a26a	0.00019048	0.00269106	0.00025926	0.003	0.00011537	0.00051316	0.00014463	0.00233333	
2	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Eggerthellaceae	g__Enterorhabdus	s__unculturedrumenbacterium	970384d9bdf4671ac2282157a5b2bed6	s__unculturedrumenbacterium	0.00155556	0.01727236	0.00377778	0.01116667	0.00043801	0.00274866	0.00152651	0.01016667
3	k__Bacteria	p__Actinobacteria	c__Coriobacteriia	o__Coriobacteriales	f__Eggerthellaceae	g__DNF00809	s__unculturedbacterium	66811a8459bf3ea91bfadd93b9e89b30	s__unculturedbacterium	0.00039683	0.0069065	0.0022963	0.0035	0.00016155	0.00139054	0.00101142	0.00316667

ASV

	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Winter 2015	Winter 2016	Winter 2017	Winter 2018	Winter 2015_sem	Winter 2016_sem	Winter 2017_sem	Winter 2018_sem

Table S9. Full ANCOM of yearling deer samples by geography, overwinter, and season at all taxonomic levels.

a) Geography

Phylum

	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Cache	Monroe	Oquirrh-Stansbury	Pine Valley	San Juan	South Slope	Wasatch-Manti	Cache_sem	Monroe_sem	Oquirrh-Stansbury_sem	Pine Valley_sem	San Juan_sem	South Slope_sem	Wasatch-Manti_sem

Class

	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Cache	Monroe	Oquirrh-Stansbury	Pine Valley	San Juan	South Slope	Wasatch-Manti	Cache_sem	Monroe_sem	Oquirrh-Stansbury_sem	Pine Valley_sem	San Juan_sem	South Slope_sem	Wasatch-Manti_sem

Order

	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Cache	Monroe	Oquirrh-Stansbury	Pine Valley	San Juan	South Slope	Wasatch-Manti	Cache_sem	Monroe_sem	Oquirrh-Stansbury_sem	Pine Valley_sem	San Juan_sem	South Slope_sem	Wasatch-Manti_sem

Family

	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Cache	Monroe	Oquirrh-Stansbury	Pine Valley	San Juan	South Slope	Wasatch-Manti	Cache_sem	Monroe_sem	Oquirrh-Stansbury_sem	Pine Valley_sem	San Juan_sem	South Slope_sem	Wasatch-Manti_sem

Genus

	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Cache	Monroe	Oquirrh-	Pine Valley	San Juan	South	Wasatch-	Cache_sem	Monroe_sem	Oquirrh-Stansb	Pine Valle	San Juan_sem	South Slop	Wasatch-Mant

												Stansbury			Slope	Manti			ury_sem	y_sem		e_sem	i_sem
Species																							
	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Cache	Monroe	Oquirrh-Stansbury	Pine Valley	San Juan	South Slope	Wasatch-Manti	Cache_sem	Monroe_sem	Oquirrh-Stansbury_sem	Pine Valley_sem	San Juan_sem	South Slope_sem	Wasatch-Manti_sem
ASV																							
	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Cache	Monroe	Oquirrh-Stansbury	Pine Valley	San Juan	South Slope	Wasatch-Manti	Cache_sem	Monroe_sem	Oquirrh-Stansbury_sem	Pine Valley_sem	San Juan_sem	South Slope_sem	Wasatch-Manti_sem
1	k__Bacteria	p__Firmicutes	c__Negativicutes	o__Selenomonadales	f__Acidaminococcaceae	g__Phascolarctobacterium	s__uncultured bacterium	9dda34760f2d13aeb961a9e6c6484c34	9dda34760f2d13aeb961a9e6c6484c34	0.01280952	0.00381818	0.02326667	0.01038889	0.00305556	0.00383333	0.01433333	0.00192842	0.0021184	0.00865987	0.00296325	0.00135378	0.0030608	0.00138811

b) Overwinter																
Phylum																
	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Winter 2015	Winter 2016	Winter 2017	Winter 2018	Winter 2015_sem	Winter 2016_sem	Winter 2017_sem	Winter 2018_sem
Class																
	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Winter 2015	Winter 2016	Winter 2017	Winter 2018	Winter 2015_sem	Winter 2016_sem	Winter 2017_sem	Winter 2018_sem
Order																
	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Winter 2015	Winter 2016	Winter 2017	Winter 2018	Winter 2015_sem	Winter 2016_sem	Winter 2017_sem	Winter 2018_sem
Family																
	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Winter 2015	Winter 2016	Winter 2017	Winter 2018	Winter 2015_sem	Winter 2016_sem	Winter 2017_sem	Winter 2018_sem
Genus																
	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Winter 2015	Winter 2016	Winter 2017	Winter 2018	Winter 2015_sem	Winter 2016_sem	Winter 2017_sem	Winter 2018_sem
Species																
	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Winter 2015	Winter 2016	Winter 2017	Winter 2018	Winter 2015_sem	Winter 2016_sem	Winter 2017_sem	Winter 2018_sem
ASV																
	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Winter 2015	Winter 2016	Winter 2017	Winter 2018	Winter 2015_sem	Winter 2016_sem	Winter 2017_sem	Winter 2018_sem

c) Season													
Phylum													
	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Post-Winter	Pre-Winter	Post-Winter_sem	Pre-Winter_sem
Class													
	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Post-Winter	Pre-Winter	Post-Winter_sem	Pre-Winter_sem
Order													
	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Post-Winter	Pre-Winter	Post-Winter_sem	Pre-Winter_sem
Family													
	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Post-Winter	Pre-Winter	Post-Winter_sem	Pre-Winter_sem
1	k__Bacteria	p__Bacteroidetes	c__Bacteroidia	o__Bacteroidales	f__Prevotellaceae	g__Prevotellaceae UCG-004	s__uncultured bacterium	c9953823fc07cf9230750e75b981e213	f__Prevotellaceae	0.0285873	0.05854348	0.00881392	0.00523787
2	k__Bacteria	p__Planctomycetes	c__Planctomycetacia	o__Pirellulales	f__Pirellulaceae	g__p-1088-a5 gut group	s__uncultured bacterium	53ab9d2256ec104ad802edd822fa6eea	f__Pirellulaceae	0.01446032	0.00376087	0.00333702	0.00058093
Genus													
	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Post-Winter	Pre-Winter	Post-Winter_sem	Pre-Winter_sem
1	k__Bacteria	p__Bacteroidetes	c__Bacteroidia	o__Bacteroidales	f__Prevotellaceae	g__Prevotellaceae UCG-004	s__uncultured bacterium	c9953823fc07cf9230750e75b981e213	g__PrevotellaceaeUCG-004	0.0258254	0.05337681	0.00864477	0.00509366
2	k__Bacteria	p__Planctomycetes	c__Planctomycetacia	o__Pirellulales	f__Pirellulaceae	g__p-1088-a5gutgroup	s__uncultured bacterium	53ab9d2256ec104ad802edd822fa6eea	g__p-1088-a5gutgroup	0.01328571	0.0036087	0.00328201	0.00055992
Species													
	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Post-Winter	Pre-Winter	Post-Winter_sem	Pre-Winter_sem
1	k__Bacteria	p__Bacteroidetes	c__Bacteroidia	o__Bacteroidales	f__Prevotellaceae	g__Prevotellaceae UCG-004	s__unculturedbacterium	c9953823fc07cf9230750e75b981e213	s__unculturedbacterium	0.00968254	0.03231884	0.00399361	0.00410333
2	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.01328571	0.0036087	0.00328201	0.00055992
ASV													

	kingdom	phylum	class	order	family	genus	species	ASV	get(taxonomic_level)	Post-Winter	Pre-Winter	Post-Winter_sem	Pre-Winter_sem
1	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae			bad7e742798b5fcc520ff82e75b256a9	bad7e742798b5fcc520ff82e75b256a9	0.00439683	0.01218841	0.00345574	0.00275558
2	k__Bacteria	p__Planctomycetes	c__Planctomycetacia	o__Pirellulales	f__Pirellulaceae	g__p-1088-a5 gut group	s__uncultured bacterium	53ab9d2256ec104ad802edd822fa6eea	53ab9d2256ec104ad802edd822fa6eea	0.00311111	0.00831159	0.00113023	0.00131486
3	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Christensenellaceae	g__Christensenellaceae R-7 group		f8a30689dee232805c05ee738a3b47bf	f8a30689dee232805c05ee738a3b47bf	0.04149206	0.00510145	0.0106767	0.00212732
4	k__Bacteria	p__Bacteroidetes	c__Bacteroidia	o__Bacteroidales	f__Prevotellaceae	g__Prevotellaceae UCG-004	s__uncultured bacterium	800cbb4cdf5b762aa3747cd38db617ff	800cbb4cdf5b762aa3747cd38db617ff	0.01328571	0.00335507	0.00328201	0.00052978

Table S10. Full proximate analysis. Includes statistically significant correlations for each deer sample subset (each geography, overwinter year, season) at each taxonomic level.

Phylum													
Sample Subset	Taxonomic Level	LFR2	BCSR2	RFR2	LF_Coeff	BCS_Coeff	RF_Coeff	LF_Adj._Pval	BCS_Adj._Pval	RF_Adj._Pval	LF_N	BCS_N	RF_N
2015	Level , p__Firmicutes	0.045464	0.195573	0.179447	-0.17991	-0.40674	-0.35092	1	0.002916	0.036538	99	99	99
2017	Level , p__Bacteroidetes	0.017933	0.031528	0.049888	0.149412	0.183118	0.278215	1	1	0.005168	226	225	225
2017	Level , p__Firmicutes	0.014521	0.041956	0.058416	-0.11386	-0.20305	-0.28538	1	0.496858	0.003097	226	225	225
2017	Level , p__Spirochaetes	0.015865	0.045724	0.067186	0.133258	0.277544	0.352937	1	0.005418	1.19E-05	226	225	225
2017	Level , p__Tenericutes	0.016205	0.021123	0.026455	0.161983	0.164103	0.283165	1	1	0.003633	226	225	225
2015_PreWinter	Level , p__Firmicutes	0.036974	0.194299	0.187479	-0.16521	-0.41639	-0.38076	1	0.010679	0.042409	79	79	79
Adult	Level , p__Bacteroidetes	0.007056	0.009929	0.015744	0.088382	0.118858	0.152206	1	0.765993	0.019093	761	763	760
Adult	Level , p__Spirochaetes	0.006281	0.015556	0.018225	0.123345	0.219218	0.221502	0.494256	7.14E-07	5.09E-07	761	763	760
All	Level , p__Bacteroidetes	0.006586	0.011876	0.015737	0.0823	0.130013	0.150697	1	0.143337	0.011156	828	830	827
All	Level , p__Spirochaetes	0.006408	0.013231	0.016722	0.121434	0.201551	0.207734	0.382438	3.89E-06	1.35E-06	828	830	827
Cache	Level , p__Elusimicrobia	0.070532	0.105353	0.102716	0.204415	0.285762	0.309016	1	0.137773	0.049481	128	128	128
Cache	Level , p__Spirochaetes	0.115919	0.108152	0.088514	0.300256	0.371886	0.339608	0.073503	0.001977	0.011252	128	128	128
PostWinter	Level , p__Kiritimatiellaeota	0.009915	0.02877	0.020568	-0.17672	-0.23404	-0.25102	1	0.045928	0.014507	251	251	251
Wasatch-Manti	Level , p__Planctomycetes	0.052887	0.00826	0.011487	-0.27976	-0.03751	-0.10437	0.015128	1	1	194	194	194
Winter18-19	Level , p__Spirochaetes	0.000984	0.034001	0.031647	0.041766	0.285548	0.313252	1	0.050978	0.011752	154	154	154
Yearling	Level , p__Planctomycetes	0.115623	0.173283	0.090132	-0.32487	-0.41329	-0.37174	0.489914	0.034098	0.130832	67	67	67
Class													
Sample Subset	Taxonomic Level	LFR2	BCSR2	RFR2	LF_Coeff	BCS_Coeff	RF_Coeff	LF_Adj._Pval	BCS_Adj._Pval	RF_Adj._Pval	LF_N	BCS_N	RF_N
2015	Level , p__Firmicutes , c__Clostridia	0.046202	0.195543	0.181112	-0.18502	-0.41109	-0.35977	1	0.002346	0.025215	99	99	99
2017	Level , p__Bacteroidetes , c__Bacteroidia	0.017933	0.031528	0.049888	0.149412	0.183118	0.278215	1	1	0.005168	226	225	225
2017	Level , p__Firmicutes , c__Clostridia	0.016086	0.043362	0.059021	-0.11792	-0.20091	-0.27615	1	0.554192	0.005974	226	225	225
2017	Level , p__Spirochaetes , c__Spirochaetia	0.015865	0.045724	0.067186	0.133258	0.277544	0.352937	1	0.005418	1.19E-05	226	225	225
2017	Level , p__Tenericutes , c__Mollicutes	0.016205	0.021123	0.026455	0.161983	0.164103	0.283165	1	1	0.003633	226	225	225
2015_PreWinter	Level , p__Firmicutes , c__Clostridia	0.033158	0.183594	0.179891	-0.15925	-0.39761	-0.36332	1	0.022522	0.078848	79	79	79
Adult	Level , p__Bacteroidetes , c__Bacteroidia	0.007056	0.009929	0.015744	0.088382	0.118858	0.152206	1	0.765993	0.019093	761	763	760
Adult	Level , p__Spirochaetes , c__Spirochaetia	0.006281	0.015556	0.018225	0.123345	0.219218	0.221502	0.494256	7.14E-07	5.09E-07	761	763	760
All	Level , p__Bacteroidetes , c__Bacteroidia	0.006586	0.011876	0.015737	0.0823	0.130013	0.150697	1	0.143337	0.011156	828	830	827
All	Level , p__Spirochaetes , c__Spirochaetia	0.006408	0.013231	0.016722	0.121434	0.201551	0.207734	0.382438	3.89E-06	1.35E-06	828	830	827
Cache	Level , p__Elusimicrobia , c__Elusimicrobia	0.070532	0.105353	0.102716	0.204415	0.285762	0.309016	1	0.137773	0.049481	128	128	128
Cache	Level , p__Spirochaetes , c__Spirochaetia	0.115919	0.108152	0.088514	0.300256	0.371886	0.339608	0.073503	0.001977	0.011252	128	128	128
Monroe	Level , p__Proteobacteria , c__Alphaproteobacteria	0.048775	0.097025	0.108875	0.322953	0.338373	0.467067	0.198476	0.12381	0.000499	87	86	86
PostWinter	Level , p__Kiritimatiellaeota , c__Kiritimatiellae	0.009915	0.02877	0.020568	-0.17672	-0.23404	-0.25102	1	0.045928	0.014507	251	251	251
Wasatch-Manti	Level , p__Planctomycetes , c__Planctomycetacia	0.052887	0.00826	0.011487	-0.27976	-0.03751	-0.10437	0.015128	1	1	194	194	194
Winter18-19	Level , p__Spirochaetes , c__Spirochaetia	0.000984	0.034001	0.031647	0.041766	0.285548	0.313252	1	0.050978	0.011752	154	154	154
Yearling	Level , p__Planctomycetes , c__Planctomycetacia	0.115623	0.173283	0.090132	-0.32487	-0.41329	-0.37174	0.489914	0.034098	0.130832	67	67	67
Yearling	Level , p__Proteobacteria , c__Gammaproteobacteria	0.027841	0.056258	0.031317	-0.40861	-0.24431	-0.24817	0.040018	1	1	67	67	67
Order													
Sample Subset	Taxonomic Level	LFR2	BCSR2	RFR2	LF_Coeff	BCS_Coeff	RF_Coeff	LF_Adj._Pval	BCS_Adj._Pval	RF_Adj._Pval	LF_N	BCS_N	RF_N
2015	Level , p__Firmicutes , c__Clostridia , o__Clostridiales	0.046202	0.195543	0.181112	-0.18502	-0.41109	-0.35977	1	0.002346	0.025215	99	99	99
2017	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales	0.017971	0.031427	0.049722	0.149135	0.182768	0.277831	1	1	0.00531	226	225	225
2017	Level , p__Firmicutes , c__Clostridia , o__Clostridiales	0.016079	0.04336	0.059019	-0.11792	-0.20091	-0.27615	1	0.554192	0.005974	226	225	225
2017	Level , p__Spirochaetes , c__Spirochaetia , o__Spirochaetales	0.015865	0.045724	0.067186	0.133258	0.277544	0.352937	1	0.005418	1.19E-05	226	225	225
2017	Level , p__Tenericutes , c__Mollicutes , o__Izimaplasmatales	0.005766	0.013243	0.022618	0.098353	0.198921	0.266983	1	0.613054	0.011217	226	225	225
2018	Level , p__Actinobacteria , c__Actinobacteria , o__Micrococcales	0.031917	0.040397	0.035878	-0.08932	-0.23656	-0.2853	1	0.348158	0.031075	167	167	167
2018	Level , p__Proteobacteria , c__Alphaproteobacteria , o__Rhizobiales	0.002819	0.006544	0.008822	-0.11801	-0.22009	-0.28331	1	0.712106	0.034622	167	167	167
2015_PreWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales	0.033158	0.183594	0.179891	-0.15925	-0.39761	-0.36332	1	0.022522	0.078848	79	79	79
Adult	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales	0.00718	0.0102	0.016155	0.089708	0.120414	0.155295	1	0.656012	0.012966	761	763	760

Adult	Level , p__Proteobacteria , c__Alphaproteobacteria , o__Rhizobiales	0.000999	0.00232	0.002367	-0.11513	-0.17232	-0.18095	1	0.001285	0.000389	761	763	760
Adult	Level , p__Proteobacteria , c__Alphaproteobacteria , o__Rhodospirillales	0.001723	0.019405	0.015538	0.072392	0.173054	0.182455	1	0.001159	0.000312	761	763	760
Adult	Level , p__Spirochaetes , c__Spirochaetia , o__Spirochaetales	0.006281	0.015556	0.018225	0.123345	0.219218	0.221502	0.494256	7.14E-07	5.09E-07	761	763	760
All	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales	0.006685	0.012153	0.01612	0.083481	0.131555	0.153609	1	0.119675	0.00754	828	830	827
All	Level , p__Proteobacteria , c__Alphaproteobacteria , o__Rhodospirillales	0.000636	0.012051	0.009821	0.08279	0.159067	0.168282	1	0.003422	0.000938	828	830	827
All	Level , p__Spirochaetes , c__Spirochaetia , o__Spirochaetales	0.006408	0.013231	0.016722	0.121434	0.201551	0.207734	0.382438	3.89E-06	1.35E-06	828	830	827
All	Level , p__Tenericutes , c__Mollicutes , o__Izimaplasmatales	0.00489	0.00425	0.004373	0.098088	0.133134	0.149445	1	0.099282	0.013173	828	830	827
Cache	Level , p__Elusimicrobia , c__Elusimicrobia , o__Elusimicrobiales	0.070532	0.105353	0.102716	0.204415	0.285762	0.309016	1	0.137773	0.049481	128	128	128
Cache	Level , p__Spirochaetes , c__Spirochaetia , o__Spirochaetales	0.115919	0.108152	0.088514	0.300256	0.371886	0.339608	0.073503	0.001977	0.011252	128	128	128
Cache	Level , p__Verrucomicrobia , c__Verrucomicrobiae , o__Opitutales	0.024262	0.024844	0.022844	0.287389	0.315883	0.283168	0.128598	0.035968	0.15364	128	128	128
Monroe	Level , p__Proteobacteria , c__Alphaproteobacteria , o__Rhodospirillales	0.039089	0.091077	0.108989	0.270772	0.32471	0.415438	0.97373	0.196622	0.005987	87	86	86
Monroe	Level , p__Tenericutes , c__Mollicutes , o__Izimaplasmatales	0.000219	0.102982	0.058874	0.089619	0.417328	0.442579	1	0.005505	0.001705	87	86	86
PineValley	Level , p__Actinobacteria , c__Actinobacteria , o__Micrococcales	0.040859	0.045632	0.028904	-0.26233	-0.33999	-0.24394	0.515463	0.018435	0.965071	116	119	116
PostWinter	Level , p__Kiritimatiellaeota , c__Kiritimatiellae , o__WCHB1-41	0.009915	0.02877	0.020568	-0.17672	-0.23404	-0.25102	1	0.045928	0.014507	251	251	251
Wasatch-Manti	Level , p__Planctomycetes , c__Planctomycetacia , o__Pirellulales	0.053407	0.00802	0.011069	-0.28503	-0.03405	-0.09243	0.010899	1	1	194	194	194
Wasatch-Manti	Level , p__Proteobacteria , c__Alphaproteobacteria , o__Rhizobiales	0.007615	0.009178	0.012083	-0.0988	-0.18602	-0.26518	1	1	0.036159	194	194	194
Winter17-18	Level , p__Actinobacteria , c__Actinobacteria , o__Corynebacteriales	0.00435	0.026316	0.021898	-0.04719	-0.29471	-0.31827	1	0.013174	0.003095	176	175	175
Winter17-18	Level , p__Actinobacteria , c__Actinobacteria , o__Propionibacteriales	0.004338	0.016888	0.014998	-0.08237	-0.29317	-0.32796	1	0.014417	0.001645	176	175	175
Winter17-18	Level , p__Proteobacteria , c__Alphaproteobacteria , o__Rhizobiales	0.004792	0.017588	0.015537	-0.18394	-0.32923	-0.33348	1	0.001512	0.001136	176	175	175
Winter18-19	Level , p__Spirochaetes , c__Spirochaetia , o__Spirochaetales	0.000984	0.034001	0.031647	0.041766	0.285548	0.313252	1	0.050978	0.011752	154	154	154
Yearling	Level , p__Planctomycetes , c__Planctomycetacia , o__Pirellulales	0.115623	0.173283	0.090132	-0.32487	-0.41329	-0.37174	0.489914	0.034098	0.130832	67	67	67
Family													
Sample Subset	Taxonomic Level	LFR2	BCSR2	RFR2	LF_Coeff	BCS_Coeff	RF_Coeff	LF_Adj._Pval	BCS_Adj._Pval	RF_Adj._Pval	LF_N	BCS_N	RF_N
2015	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae	0.122668	0.07679	0.074327	0.383024	0.309112	0.257636	0.009026	0.18323	0.993797	99	99	99
2016	Level , p__Tenericutes , c__Mollicutes , o__Mollicutes RF39 ,	0.008519	0.028848	0.026238	0.164828	0.251986	0.240416	1	0.018973	0.044216	237	240	237
2017	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Prevotellaceae	0.038284	0.058076	0.088164	0.214443	0.255572	0.37906	0.26663	0.023814	9.52E-07	226	225	225
2017	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae	0.015936	0.018296	0.034164	0.181644	0.194774	0.285862	1	0.75415	0.00299	226	225	225
2017	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae	0.035942	0.067104	0.090176	-0.25546	-0.26641	-0.35506	0.023242	0.011658	9.80E-06	226	225	225
2017	Level , p__Spirochaetes , c__Spirochaetia , o__Spirochaetales , f__Spirochaetaceae	0.015865	0.045724	0.067186	0.133258	0.277544	0.352937	1	0.005418	1.19E-05	226	225	225
2017	Level , p__Tenericutes , c__Mollicutes , o__Izimaplasmatales , f__gut metagenome	0.013427	0.007699	0.011608	0.154784	0.231915	0.282444	1	0.101856	0.003826	226	225	225
2017	Level , p__Tenericutes , c__Mollicutes , o__Mollicutes RF39 ,	0.022564	0.013826	0.017099	0.156918	0.139573	0.251663	1	1	0.030578	226	225	225
2018	Level , p__Actinobacteria , c__Actinobacteria , o__Micrococcales , f__Microbacteriaceae	0.000541	0.007447	0.008543	-0.12254	-0.22994	-0.28922	1	0.466838	0.025077	167	167	167
2019	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales ,	0.144683	0.371855	0.214261	0.537248	0.282624	0.371106	0.04867	1	1	32	32	32
2019	Level , p__Proteobacteria , c__Gammaproteobacteria , o__Betaproteobacteriales , f__Burkholderiaceae	0.147968	0.018822	0.014112	-0.54031	-0.07165	-0.03205	0.04518	1	1	32	32	32
2017_PostWinter	Level , p__Firmicutes , c__Negativicutes , o__Selenomonadales , f__Veillonellaceae	0.008427	0.005921	0.02118	-0.08078	-0.21954	-0.35931	1	1	0.033147	95	95	95
2017_PostWinter	Level , p__Tenericutes , c__Mollicutes , o__Izimaplasmatales , f__gut metagenome	0.004014	0.071171	0.111856	0.139564	0.303071	0.36403	1	0.269034	0.027301	95	95	95
2019_PostWinter	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales ,	0.144298	0.383139	0.272944	0.592479	0.307207	0.339892	0.011304	1	1	32	32	32
Adult	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales ,	0.001678	0.001223	0.001755	0.095262	0.15533	0.159556	1	0.012471	0.007509	761	763	760
Adult	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Muribaculaceae	0.005841	0.01124	0.006696	0.098931	0.166948	0.176337	1	0.002703	0.00076	761	763	760
Adult	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Prevotellaceae	0.010868	0.017162	0.024295	0.137116	0.170119	0.201204	0.112702	0.001748	1.68E-05	761	763	760
Adult	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae	0.007063	0.004958	0.010202	0.140592	0.114983	0.144735	0.075858	1	0.04721	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae	0.020585	0.022942	0.028633	-0.14033	-0.14031	-0.1711	0.078137	0.076967	0.001592	761	763	760
Adult	Level , p__Proteobacteria , c__Alphaproteobacteria , o__Rhodospirillales , f__uncultured	0.001723	0.019405	0.015538	0.072392	0.173054	0.182455	1	0.001159	0.000312	761	763	760

Adult	Level , p__Spirochaetes , c__Spirochaetia , o__Spirochaetales , f__Spirochaetaceae	0.006281	0.015556	0.018225	0.123345	0.219218	0.221502	0.494256	7.14E-07	5.09E-07	761	763	760
Adult	Level , p__Tenericutes , c__Mollicutes , o__Mollicutes RF39 ,	0.004623	0.008068	0.008423	0.088804	0.119158	0.153825	1	0.743512	0.015602	761	763	760
All	Level , p__Actinobacteria , c__Actinobacteria , o__Frankiales , f__Geodermatophilaceae	0.005121	0.00538	0.003461	-0.07252	-0.1623	-0.14854	1	0.002161	0.014849	828	830	827
All	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Muribaculaceae	0.005013	0.010519	0.005121	0.088024	0.162869	0.161016	1	0.00199	0.002695	828	830	827
All	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Prevotellaceae	0.013666	0.021689	0.02836	0.1532	0.192278	0.221311	0.007882	1.96E-05	1.02E-07	828	830	827
All	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae	0.007605	0.005947	0.010565	0.143197	0.125729	0.149572	0.029314	0.234184	0.012955	828	830	827
All	Level , p__Firmicutes , c__Bacilli , o__Bacillales , f__Staphylococcaceae	0.004198	0.000745	0.001973	-0.14438	-0.05289	-0.07966	0.025221	1	1	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales ,	0.005287	0.02393	0.025683	0.17814	0.144996	0.163772	0.000205	0.022832	0.001815	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae	0.026015	0.026933	0.030769	-0.14918	-0.15654	-0.18238	0.013497	0.004871	0.000106	828	830	827
All	Level , p__Kiritimatiellaeota , c__Kiritimatiellae , o__WCHB1-41 , f__uncultured rumen bacterium	0.014486	0.00331	0.00101	-0.14067	-0.09219	-0.08775	0.040328	1	1	828	830	827
All	Level , p__Proteobacteria , c__Alphaproteobacteria , o__Rhodospirillales , f__uncultured	0.000636	0.012051	0.009821	0.08279	0.159067	0.168282	1	0.003422	0.000938	828	830	827
All	Level , p__Spirochaetes , c__Spirochaetia , o__Spirochaetales , f__Spirochaetaceae	0.006408	0.013231	0.016722	0.121434	0.201551	0.207734	0.382438	3.89E-06	1.35E-06	828	830	827
All	Level , p__Tenericutes , c__Mollicutes , o__Mollicutes RF39 ,	0.004133	0.012061	0.011282	0.126005	0.142271	0.163713	0.230346	0.032338	0.001831	828	830	827
Cache	Level , p__Actinobacteria , c__Coriobacteriia , o__Coriobacteriales , f__uncultured	0.038907	0.116505	0.116591	0.166906	0.337792	0.360515	1	0.012341	0.003728	128	128	128
Cache	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Barnesiellaceae	0.029748	0.002898	0.000576	0.343101	0.337627	0.309378	0.009406	0.012445	0.048664	128	128	128
Cache	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae	0.106999	0.06586	0.053709	0.356955	0.375523	0.362206	0.004524	0.001606	0.003398	128	128	128
Cache	Level , p__Elusimicrobia , c__Elusimicrobia , o__Elusimicrobiales , f__Elusimicrobiaceae	0.070532	0.105353	0.102716	0.204415	0.285762	0.309016	1	0.137773	0.049481	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales ,	0.076838	0.092668	0.089466	0.315883	0.321595	0.335476	0.035969	0.027427	0.013872	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae	0.075782	0.119424	0.07697	-0.29257	-0.33861	-0.30836	0.102996	0.011837	0.05099	128	128	128
Cache	Level , p__Spirochaetes , c__Spirochaetia , o__Spirochaetales , f__Spirochaetaceae	0.115919	0.108152	0.088514	0.300256	0.371886	0.339608	0.073503	0.001977	0.011252	128	128	128
Cache	Level , p__Verrucomicrobia , c__Verrucomicrobiae , o__Opitutales , f__Puniceicoccaceae	0.024262	0.024844	0.022844	0.287389	0.315883	0.283168	0.128598	0.035968	0.15364	128	128	128
Monroe	Level , p__Proteobacteria , c__Alphaproteobacteria , o__Rhodospirillales , f__uncultured	0.039089	0.091077	0.108989	0.270772	0.32471	0.415438	0.97373	0.196622	0.005987	87	86	86
Monroe	Level , p__Tenericutes , c__Mollicutes , o__Izimaplasmatales , f__uncultured bacterium	0.002741	0.108599	0.064397	0.135235	0.403009	0.395744	1	0.010277	0.013957	87	86	86
OquirrhStansbury	Level , p__Cyanobacteria , c__Melainabacteria , o__Gastranaerophilales , f__uncultured rumen bacterium	0.020542	0.102195	0.083887	0.126387	0.473068	0.445912	1	0.000664	0.002446	81	81	81
PineValley	Level , p__Actinobacteria , c__Actinobacteria , o__Micrococcales , f__Micrococcaceae	0.045874	0.045372	0.026948	-0.29317	-0.3571	-0.25432	0.162865	0.007973	0.681145	116	119	116
PineValley	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Muribaculaceae	0.02147	0.075595	0.085642	0.183509	0.325528	0.275327	1	0.036085	0.322249	116	119	116
PineValley	Level , p__Firmicutes , c__Bacilli , o__Lactobacillales , f__Enterococcaceae	0.000284	0.001598	0.00834	-0.21698	-0.33407	-0.31329	1	0.024369	0.071498	116	119	116
PostWinter	Level , p__Kiritimatiellaeota , c__Kiritimatiellae , o__WCHB1-41 , f__uncultured rumen bacterium	0.043611	0.062215	0.048273	-0.20575	-0.29158	-0.2961	0.261882	0.000656	0.00045	251	251	251
Wasatch-Manti	Level , p__Actinobacteria , c__Actinobacteria , o__Micrococcales , f__Microbacteriaceae	0.003741	0.014958	0.019199	-0.20958	-0.21195	-0.29141	0.651405	0.583677	0.007273	194	194	194
Wasatch-Manti	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Prevotellaceae	0.084265	0.027862	0.0448	0.319296	0.196441	0.258093	0.001102	1	0.054278	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales ,	0.034233	0.039668	0.057078	0.219599	0.214234	0.286084	0.40628	0.524518	0.010204	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Eubacteriaceae	0.023345	0.051781	0.068309	0.204141	0.231747	0.316138	0.834632	0.222797	0.001378	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae	0.078579	0.036352	0.056334	-0.2571	-0.16356	-0.26224	0.057418	1	0.042863	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae	0.047503	0.106135	0.080268	0.231737	0.342049	0.357889	0.222909	0.000204	5.82E-05	194	194	194
Wasatch-Manti	Level , p__Planctomycetes , c__Planctomycetacia , o__Pirellulales , f__Pirellulaceae	0.053407	0.00802	0.011069	-0.28503	-0.03405	-0.09243	0.010899	1	1	194	194	194
Winter16-17	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Prevotellaceae	0.004335	0.006383	0.012746	0.103367	0.160441	0.239436	1	1	0.017568	273	276	273
Winter16-17	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae	0.012673	0.010501	0.023857	0.164824	0.143253	0.246984	1	1	0.010068	273	276	273
Winter16-17	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae	0.055969	0.058466	0.082106	-0.24269	-0.28293	-0.36388	0.013848	0.000491	1.56E-07	273	276	273
Winter17-18	Level , p__Actinobacteria , c__Actinobacteria , o__Corynebacteriales , f__Nocardiaceae	0.004434	0.025556	0.021256	-0.06734	-0.27805	-0.30055	1	0.034101	0.009303	176	175	175
Winter17-18	Level , p__Actinobacteria , c__Actinobacteria , o__Propionibacteriales , f__Nocardioidaceae	0.004338	0.016888	0.014998	-0.08237	-0.29317	-0.32796	1	0.014417	0.001645	176	175	175
Winter17-18	Level , p__Proteobacteria , c__Alphaproteobacteria , o__Rhizobiales , f__Devosiaceae	0.002901	0.013353	0.011224	-0.07945	-0.24926	-0.27132	1	0.153952	0.049235	176	175	175
Winter18-19	Level , p__Kiritimatiellaeota , c__Kiritimatiellae , o__WCHB1-41 , f__uncultured rumen bacterium	0.041786	0.034209	0.033467	-0.14812	-0.21252	-0.28877	1	1	0.043305	154	154	154
Winter18-19	Level , p__Spirochaetes , c__Spirochaetia , o__Spirochaetales , f__Spirochaetaceae	0.000984	0.034001	0.031647	0.041766	0.285548	0.313252	1	0.050978	0.011752	154	154	154
Yearling	Level , p__Planctomycetes , c__Planctomycetacia , o__Pirellulales , f__Pirellulaceae	0.115623	0.173283	0.090132	-0.32487	-0.41329	-0.37174	0.489914	0.034098	0.130832	67	67	67

Genus													
Sample Subset	Taxonomic Level	LFR2	BCSR2	RFR2	LF_Coeff	BCS_Coeff	RF_Coeff	LF_Adj._Pval	BCS_Adj._Pval	RF_Adj._Pval	LF_N	BCS_N	RF_N
2015	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Prevotellaceae , g__Prevotellaceae UCG-004	0.038306	0.085096	0.064809	0.272824	0.344447	0.305814	0.622985	0.047614	0.206124	99	99	99
2015	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group	0.113748	0.066896	0.062758	0.367381	0.300793	0.249879	0.01817	0.245962	1	99	99	99
2015	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae FE2018 group	0.133611	0.035402	0.013655	-0.39154	-0.23179	-0.16199	0.006074	1	1	99	99	99
2016	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Coprococcus 3	0.011356	0.036977	0.044325	0.243184	0.193499	0.24691	0.037035	0.625897	0.029079	237	240	237
2016	Level , p__Tenericutes , c__Mollicutes , o__Mollicutes RF39 , ,	0.008519	0.028848	0.026238	0.164828	0.251986	0.240416	1	0.018973	0.044216	237	240	237
2017	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Prevotellaceae , g__Prevotellaceae UCG-004	0.044756	0.062944	0.092869	0.203524	0.269828	0.382295	0.475868	0.009248	6.85E-07	226	225	225
2017	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__dgA-11 gut group	0.040935	0.045955	0.063746	0.213699	0.190579	0.297116	0.277623	0.926187	0.001298	226	225	225
2017	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group	0.017672	0.016584	0.030297	0.199412	0.202494	0.28669	0.587516	0.511191	0.002816	226	225	225
2017	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__uncultured , g__uncultured bacterium	5.50E-06	0.002696	0.012407	0.132316	0.171348	0.284748	1	1	0.003242	226	225	225
2017	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae ,	0.042581	0.070027	0.081351	-0.2461	-0.28366	-0.34991	0.042118	0.003507	1.58E-05	226	225	225
2017	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Tyzzerella 3	4.30E-06	0.008258	0.007531	-0.12878	-0.16242	-0.25549	1	1	0.023943	226	225	225
2017	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminiclostridium 6	0.009237	0.021465	0.036172	0.203403	0.189439	0.260155	0.478859	0.978669	0.017673	226	225	225
2017	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcus 1	0.00515	0.028664	0.043822	0.132569	0.169097	0.269929	1	1	0.009184	226	225	225
2017	Level , p__Spirochaetes , c__Spirochaetia , o__Spirochaetales , f__Spirochaetaceae , g__Treponema 2	0.015935	0.045549	0.066973	0.133352	0.277469	0.352879	1	0.005447	1.20E-05	226	225	225
2017	Level , p__Tenericutes , c__Mollicutes , o__Izimaplasmatales , f__gut metagenome , g__gut metagenome	0.013427	0.007699	0.011608	0.154784	0.231915	0.282444	1	0.101856	0.003826	226	225	225
2017	Level , p__Tenericutes , c__Mollicutes , o__Mollicutes RF39 , ,	0.022564	0.013826	0.017099	0.156918	0.139573	0.251663	1	1	0.030578	226	225	225
2018	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Dorea , s__uncultured bacterium	0.064397	0.095806	0.115657	0.196136	0.249183	0.276432	1	0.194528	0.049929	167	167	167
2018	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae UCG-001	0.018548	0.033742	0.046892	0.157537	0.219617	0.285182	1	0.726303	0.031279	167	167	167
2018	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Negativibacillus	0.054858	0.048694	0.064284	0.324855	0.224114	0.309087	0.003076	0.600579	0.008047	167	167	167
2018	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminiclostridium 9	0.085089	0.13023	0.130802	0.290051	0.396956	0.394445	0.023951	1.82E-05	2.22E-05	167	167	167
2018	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-013	0.020041	0.056332	0.074211	0.130833	0.208076	0.288826	1	1	0.025626	167	167	167
2018	Level , p__Proteobacteria , c__Gammaproteobacteria , o__Betaproteobacteriales , f__Burkholderiaceae , g__Delftia	0.081963	0.04781	0.025252	-0.25455	-0.30075	-0.28343	0.150478	0.013097	0.034383	167	167	167
2019	Level , p__Actinobacteria , c__Coriobacteriia , o__Coriobacteriales , f__Atopobiaceae , g__uncultured	0.02726	0.181473	0.293598	0.212358	0.408536	0.536249	1	0.648462	0.04986	32	32	32
2019	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , ,	0.144683	0.371855	0.214261	0.537248	0.282624	0.371106	0.04867	1	1	32	32	32
2019	Level , p__Proteobacteria , c__Deltaproteobacteria , o__Desulfovibrionales , f__Desulfovibrionaceae , g__Bilophila	0.035205	5.26E-05	0.225734	0.097708	0.105621	0.542387	1	1	0.042932	32	32	32
2015_PostWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Papillibacter	0.408497	0.039717	0.006916	0.712995	-0.01062	0.171495	0.008355	1	1	20	20	20
2015_PreWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae UCG-001	0.126597	0.18311	0.152962	-0.33418	-0.39948	-0.37744	0.206416	0.020947	0.047852	79	79	79
2016_PostWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Faecalibacterium	0.000583	0.240382	0.101411	0.002786	0.439342	0.225037	1	0.029443	1	59	59	59
2016_PostWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Flavonifractor	0.01071	0.021614	0.091721	0.23079	0.312609	0.441132	1	0.939726	0.02775	59	59	59
2017_PostWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Peptostreptococcaceae , g__Romboutsia	0.13078	0.088677	0.019267	-0.39817	-0.22912	-0.1592	0.006119	1	1	95	95	95
2017_PostWinter	Level , p__Tenericutes , c__Mollicutes , o__Izimaplasmatales , f__gut metagenome , g__gut metagenome	0.004014	0.071171	0.111856	0.139564	0.303071	0.36403	1	0.269034	0.027301	95	95	95
2019_PostWinter	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , ,	0.144298	0.383139	0.272944	0.592479	0.307207	0.339892	0.011304	1	1	32	32	32
2019_PostWinter	Level , p__Proteobacteria , c__Gammaproteobacteria , o__Betaproteobacteriales , f__Burkholderiaceae	0.123188	0.02541	0.017236	-0.53724	-0.1449	-0.08773	0.048684	1	1	32	32	32
Adult	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , ,	0.001678	0.001223	0.001755	0.095262	0.15533	0.159556	1	0.012471	0.007509	761	763	760
Adult	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Muribaculaceae , g__uncultured bacterium	0.006196	0.010858	0.006294	0.104403	0.164671	0.173866	1	0.003679	0.00108	761	763	760
Adult	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Prevotellaceae , g__Prevotellaceae UCG-004	0.015912	0.021289	0.026332	0.151706	0.19647	0.231391	0.020092	3.40E-05	8.15E-08	761	763	760

Adult	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__dgA-11 gut group	0.024507	0.011867	0.016432	0.196067	0.149043	0.177187	3.77E-05	0.027287	0.000673	761	763	760
Adult	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group	0.006711	0.004227	0.008923	0.145761	0.122059	0.152613	0.041385	0.555735	0.018152	761	763	760
Adult	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__uncultured , g__uncultured bacterium	0.001072	0.009142	0.016328	0.100469	0.160482	0.187375	1	0.006415	0.000149	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae ,	0.024712	0.027651	0.030799	-0.15549	-0.15283	-0.17955	0.012509	0.017096	0.000478	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminiclostridium 6	0.009139	0.003564	0.0035	0.150122	0.097029	0.121808	0.024425	1	0.581688	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminiclostridium 9	0.023879	0.015573	0.012649	0.204715	0.167528	0.162375	9.20E-06	0.002498	0.005191	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-009	0.023627	0.027138	0.015436	0.163488	0.187975	0.192689	0.004423	0.000129	6.55E-05	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010	0.017677	0.019276	0.015329	0.179377	0.197427	0.198823	0.000482	2.92E-05	2.47E-05	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-013	0.020645	0.033658	0.02736	0.146497	0.175487	0.186499	0.037899	0.000821	0.00017	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcus 1	0.000329	0.003497	0.004376	0.081313	0.122764	0.149637	1	0.517279	0.026193	761	763	760
Adult	Level , p__Proteobacteria , c__Alphaproteobacteria , o__Rhodospirillales , f__uncultured , g__gut metagenome	0.0024	0.017693	0.017942	0.090166	0.1617	0.16954	1	0.005465	0.001975	761	763	760
Adult	Level , p__Spirochaetes , c__Spirochaetia , o__Spirochaetales , f__Spirochaetaceae , g__Treponema 2	0.006281	0.015556	0.018225	0.123345	0.219218	0.221502	0.494256	7.14E-07	5.09E-07	761	763	760
Adult	Level , p__Tenericutes , c__Mollicutes , o__Mollicutes RF39 , ,	0.004623	0.008068	0.008423	0.088804	0.119158	0.153825	1	0.743512	0.015602	761	763	760
All	Level , p__Actinobacteria , c__Actinobacteria , o__Micrococcales , f__Microbacteriaceae ,	0.004999	0.005139	0.004849	-0.14063	-0.14487	-0.16364	0.040484	0.023209	0.001851	828	830	827
All	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Muribaculaceae , g__uncultured bacterium	0.005379	0.010283	0.004915	0.095779	0.16176	0.16148	1	0.002334	0.002522	828	830	827
All	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Prevotellaceae , g__Prevotellaceae UCG-004	0.016849	0.025416	0.030077	0.161975	0.214451	0.247506	0.002321	3.59E-07	4.31E-10	828	830	827
All	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__dgA-11 gut group	0.023255	0.009117	0.015419	0.181159	0.122993	0.155049	0.000127	0.317856	0.006196	828	830	827
All	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group	0.006997	0.004985	0.009027	0.150684	0.133363	0.156185	0.011055	0.096614	0.0053	828	830	827
All	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__uncultured , g__uncultured bacterium	7.49E-05	0.006081	0.011654	0.080927	0.155927	0.183168	1	0.005304	9.35E-05	828	830	827
All	Level , p__Firmicutes , c__Bacilli , o__Bacillales , f__Staphylococcaceae , g__Staphylococcus	0.004198	0.000745	0.001973	-0.14438	-0.05289	-0.07966	0.025221	1	1	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , ,	0.005287	0.02393	0.025683	0.17814	0.144996	0.163772	0.000205	0.022832	0.001815	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae ,	0.028406	0.028816	0.030592	-0.16413	-0.16167	-0.18852	0.001702	0.002365	3.89E-05	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__[Eubacterium] ventriosum group	0.022522	0.011091	0.011512	-0.14052	-0.12421	-0.13711	0.041058	0.277709	0.063126	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae FCS020 group	0.013196	0.000252	0.000137	0.14938	0.055216	0.041296	0.013146	1	1	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Tyzzerella 3	0.005512	0.010436	0.007329	-0.10783	-0.12401	-0.14918	1	0.283815	0.01364	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminiclostridium 6	0.00733	0.003063	0.003765	0.151203	0.10412	0.138606	0.010314	1	0.052545	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminiclostridium 9	0.026924	0.024373	0.017559	0.170305	0.18972	0.181559	0.000684	3.02E-05	0.000121	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-009	0.021201	0.023365	0.014051	0.160999	0.164364	0.178392	0.002668	0.001602	0.0002	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010	0.017967	0.017316	0.014108	0.180343	0.189616	0.193033	0.000145	3.07E-05	1.82E-05	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-013	0.019094	0.027706	0.022953	0.140442	0.165479	0.180884	0.041469	0.001362	0.000135	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcus 1	3.80E-06	0.003172	0.004351	0.109129	0.132647	0.154028	1	0.105188	0.007122	828	830	827
All	Level , p__Kiritimatiellaeota , c__Kiritimatiellae , o__WCHB1-41 , f__uncultured rumen bacterium , g__uncultured rumen bacterium	0.014486	0.00331	0.00101	-0.14067	-0.09219	-0.08775	0.040328	1	1	828	830	827
All	Level , p__Planctomycetes , c__Planctomycetacia , o__Pirellulales , f__Pirellulaceae , g__p-1088-a5 gut group	0.018366	0.015236	0.012368	-0.11956	-0.11448	-0.14598	0.468525	0.791073	0.020725	828	830	827
All	Level , p__Proteobacteria , c__Alphaproteobacteria , o__Rhodospirillales , f__uncultured ,	0.003592	0.009011	0.006715	0.103548	0.144703	0.152326	1	0.023709	0.008969	828	830	827
All	Level , p__Spirochaetes , c__Spirochaetia , o__Spirochaetales , f__Spirochaetaceae , g__Treponema 2	0.006408	0.013231	0.016722	0.121434	0.201551	0.207734	0.382438	3.89E-06	1.35E-06	828	830	827
All	Level , p__Tenericutes , c__Mollicutes , o__Mollicutes RF39 , ,	0.004133	0.012061	0.011282	0.126005	0.142271	0.163713	0.230346	0.032338	0.001831	828	830	827
Cache	Level , p__Actinobacteria , c__Coriobacteriia , o__Coriobacteriales , f__Eggerthellaceae ,	0.032503	0.046294	0.044179	0.218197	0.29043	0.314089	1	0.112938	0.039122	128	128	128
Cache	Level , p__Actinobacteria , c__Coriobacteriia , o__Coriobacteriales , f__uncultured , g__uncultured bacterium	0.038907	0.116505	0.116591	0.166906	0.337792	0.360515	1	0.012341	0.003728	128	128	128
Cache	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Barnesiellaceae , g__uncultured	0.029875	0.002882	0.000564	0.345886	0.339338	0.310233	0.008141	0.011408	0.046786	128	128	128

Cache	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Prevotellaceae , g__Prevotellaceae UCG-004	0.061393	0.04214	0.031527	0.3025	0.355871	0.342698	0.066494	0.004797	0.009604	128	128	128
Cache	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__dgA-11 gut group	0.081494	0.137197	0.108349	0.255625	0.356095	0.32586	0.459321	0.004739	0.02232	128	128	128
Cache	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group	0.108318	0.060362	0.051022	0.370449	0.389159	0.379221	0.002145	0.00072	0.001297	128	128	128
Cache	Level , p__Elusimicrobia , c__Elusimicrobia , o__Elusimicrobiales , f__Elusimicrobiaceae , g__Elusimicrobium	0.070532	0.105353	0.102716	0.204415	0.285762	0.309016	1	0.137773	0.049481	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , ,	0.076838	0.092668	0.089466	0.315883	0.321595	0.335476	0.035969	0.027427	0.013872	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae ,	0.064876	0.110706	0.070469	-0.25276	-0.32714	-0.31082	0.511473	0.020968	0.045532	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__[Eubacterium] ventriosum group	0.03353	0.055038	0.050154	-0.20323	-0.32672	-0.33297	1	0.021409	0.015724	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae ,	0.110588	0.110802	0.084775	0.36173	0.339964	0.31645	0.003488	0.01105	0.035022	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminiclostridium	0.047915	0.117362	0.112861	0.2368	0.311592	0.316443	0.911332	0.04394	0.035035	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminiclostridium 6	0.108897	0.110385	0.084857	0.325921	0.313477	0.278865	0.022255	0.040256	0.183675	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminiclostridium 9	0.123813	0.11252	0.082626	0.371773	0.372825	0.345914	0.00199	0.001875	0.00813	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010	0.118892	0.120694	0.095176	0.403551	0.454119	0.424544	0.000297	9.33E-06	7.56E-05	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-013	0.055822	0.110601	0.106734	0.326073	0.406428	0.394595	0.022091	0.000248	0.000518	128	128	128
Cache	Level , p__Spirochaetes , c__Spirochaetia , o__Spirochaetales , f__Spirochaetaceae , g__Treponema 2	0.115919	0.108152	0.088514	0.300256	0.371886	0.339608	0.073503	0.001977	0.011252	128	128	128
Cache	Level , p__Verrucomicrobia , c__Verrucomicrobiae , o__Opitutales , f__Puniceicoccaceae , g__Cerasicoccus	0.023244	0.024231	0.022552	0.256988	0.317529	0.281666	0.436235	0.033284	0.163571	128	128	128
Monroe	Level , p__Tenericutes , c__Mollicutes , o__Izimaplasmatales , f__uncultured bacterium , g__uncultured bacterium	0.002741	0.108599	0.064397	0.135235	0.403009	0.395744	1	0.010277	0.013957	87	86	86
OquirrhStansbury	Level , p__Cyanobacteria , c__Melainabacteria , o__Gastranaerophilales , f__uncultured rumen bacterium , g__uncultured rumen bacterium	0.020542	0.102195	0.083887	0.126387	0.473068	0.445912	1	0.000664	0.002446	81	81	81
PineValley	Level , p__Actinobacteria , c__Actinobacteria , o__Micrococcales , f__Micrococcaceae , g__Arthrobacter	0.045874	0.045372	0.026948	-0.29317	-0.3571	-0.25432	0.162865	0.007973	0.681145	116	119	116
PineValley	Level , p__Firmicutes , c__Bacilli , o__Lactobacillales , f__Enterococcaceae , g__Enterococcus	0.000284	0.001598	0.00834	-0.21698	-0.33407	-0.31329	1	0.024369	0.071498	116	119	116
PostWinter	Level , p__Kiritimatiellaeota , c__Kiritimatiellae , o__WCHB1-41 , f__uncultured rumen bacterium , g__uncultured rumen bacterium	0.043611	0.062215	0.048273	-0.20575	-0.29158	-0.2961	0.261882	0.000656	0.00045	251	251	251
SanJuan	Level , p__Actinobacteria , c__Coriobacteriia , o__Coriobacteriales , f__Atopobiaceae ,	0.053956	1.63E-05	0.001944	-0.35349	-0.17571	-0.17737	0.034926	1	1	98	98	98
Wasatch-Manti	Level , p__Actinobacteria , c__Actinobacteria , o__Micrococcales , f__Microbacteriaceae ,	0.017189	0.011704	0.013827	-0.19487	-0.18092	-0.26256	1	1	0.042062	194	194	194
Wasatch-Manti	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Prevotellaceae , g__Prevotellaceae UCG-004	0.064271	0.007979	0.018078	0.278555	0.140571	0.215002	0.016283	1	0.505872	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , ,	0.034233	0.039668	0.057078	0.219599	0.214234	0.286084	0.40628	0.524518	0.010204	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Eubacteriaceae , g__Anaerofustis	0.023345	0.051781	0.068309	0.204141	0.231747	0.316138	0.834632	0.222797	0.001378	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae ,	0.083788	0.042266	0.06373	-0.27507	-0.1962	-0.28035	0.020128	1	0.014581	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Tyzzerella 3	0.039561	0.03304	0.035999	-0.22699	-0.18025	-0.29187	0.282967	1	0.00706	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Tyzzerella 4	0.035503	0.05374	0.049825	0.268392	0.290924	0.295403	0.029967	0.007502	0.005615	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae ,	0.027941	0.08508	0.068169	0.21595	0.312668	0.319864	0.483687	0.001757	0.001059	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group	0.05823	0.069227	0.060972	0.234746	0.324622	0.346763	0.191164	0.000752	0.000142	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Negativibacillus	0.057939	0.088665	0.081934	0.284007	0.259735	0.32301	0.011624	0.049452	0.000845	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminiclostridium 6	0.008891	0.001554	0.001076	0.298642	0.197476	0.278399	0.004541	1	0.016439	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminiclostridium 9	0.061469	0.063483	0.047933	0.263444	0.308709	0.341361	0.039985	0.002308	0.000215	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae NK4A214 group	0.048763	0.089518	0.115491	0.232288	0.283754	0.375207	0.216757	0.011808	1.36E-05	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-002	0.013525	0.000848	0.001478	0.068702	0.177881	0.267248	1	1	0.032049	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-009	0.07747	0.095117	0.078973	0.259618	0.32421	0.389808	0.049783	0.000775	3.74E-06	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010	0.069897	0.104936	0.086866	0.277301	0.333243	0.398965	0.017579	0.000399	1.61E-06	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-013	0.090959	0.067565	0.061326	0.316094	0.247562	0.294528	0.001382	0.097205	0.005945	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__uncultured	0.064839	0.102896	0.107226	0.292119	0.298227	0.367472	0.006947	0.004667	2.64E-05	194	194	194

Winter16-17	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Prevotellaceae , g__Prevotellaceae UCG-004	0.012587	0.015448	0.02238	0.123777	0.179545	0.268185	1	0.760819	0.001914	273	276	273
Winter16-17	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group	0.016093	0.013585	0.025505	0.191491	0.16784	0.267694	0.403584	1	0.001992	273	276	273
Winter16-17	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae ,	0.057464	0.059302	0.079512	-0.23739	-0.30128	-0.37644	0.020371	9.30E-05	3.50E-08	273	276	273
Winter16-17	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Tyzzerella 3	0.001616	0.03237	0.038435	-0.07202	-0.19624	-0.27574	1	0.289299	0.001022	273	276	273
Winter16-17	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae NK4A214 group	0.047784	0.018602	0.021954	0.235484	0.193257	0.207647	0.023348	0.345837	0.151424	273	276	273
Winter16-17	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010	0.012282	0.015498	0.006157	0.228745	0.210937	0.223612	0.037508	0.115467	0.05332	273	276	273
Winter16-17	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__uncultured	0.022333	0.051541	0.049042	0.152795	0.198433	0.235178	1	0.25323	0.023864	273	276	273
Winter17-18	Level , p__Actinobacteria , c__Actinobacteria , o__Corynebacteriales , f__Nocardiaceae , g__Williamsia	0.005669	0.019703	0.017046	-0.06486	-0.27681	-0.30005	1	0.036514	0.009588	176	175	175
Winter17-18	Level , p__Actinobacteria , c__Actinobacteria , o__Micrococcales , f__Microbacteriaceae ,	0.012378	0.016486	0.014696	-0.22404	-0.2804	-0.31782	0.492325	0.029915	0.003185	176	175	175
Winter17-18	Level , p__Actinobacteria , c__Actinobacteria , o__Propionibacteriales , f__Nocardioidaceae , g__Aeromicrobium	0.001157	0.014447	0.013465	-0.05223	-0.26632	-0.29106	1	0.064327	0.016308	176	175	175
Winter17-18	Level , p__Actinobacteria , c__Actinobacteria , o__Propionibacteriales , f__Nocardioidaceae , g__Nocardioides	0.016257	0.026672	0.019208	-0.10688	-0.23626	-0.27889	1	0.287999	0.032541	176	175	175
Winter17-18	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Blautia	0.011294	0.064557	0.036508	0.141011	0.345444	0.325909	1	0.000497	0.001884	176	175	175
Winter17-18	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Dorea	0.013894	0.044695	0.011328	0.122505	0.298679	0.27273	1	0.010409	0.045627	176	175	175
Winter17-18	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae AC2044 group	0.011823	0.043759	0.032778	0.121872	0.280706	0.303435	1	0.029414	0.007815	176	175	175
Winter17-18	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-013	0.025031	0.11852	0.109626	0.188041	0.352055	0.382333	1	0.00031	3.11E-05	176	175	175
Winter17-18	Level , p__Proteobacteria , c__Alphaproteobacteria , o__Rhizobiales , f__Devosiaceae , g__Devosia	0.002901	0.013353	0.011224	-0.07945	-0.24926	-0.27132	1	0.153952	0.049235	176	175	175
Winter17-18	Level , p__Proteobacteria , c__Gammaproteobacteria , o__Betaproteobacteriales , f__Burkholderiaceae , g__Delftia	0.056837	0.039794	0.017954	-0.26866	-0.31719	-0.29907	0.054876	0.003317	0.010169	176	175	175
Winter18-19	Level , p__Kiritimatiellaeota , c__Kiritimatiellae , o__WCHB1-41 , f__uncultured rumen bacterium , g__uncultured rumen bacterium	0.041786	0.034209	0.033467	-0.14812	-0.21252	-0.28877	1	1	0.043305	154	154	154
Winter18-19	Level , p__Spirochaetes , c__Spirochaetia , o__Spirochaetales , f__Spirochaetaceae , g__Treponema 2	0.000981	0.034218	0.031773	0.041802	0.28574	0.313364	1	0.050488	0.011678	154	154	154
Yearling	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__uncultured ,	0.003491	0.163535	0.116734	0.078882	0.423772	0.314757	1	0.023608	0.63521	67	67	67
Yearling	Level , p__Planctomycetes , c__Planctomycetacia , o__Pirellulales , f__Pirellulaceae , g__p-1088-a5 gut group	0.119601	0.172765	0.084939	-0.32217	-0.42777	-0.37929	0.525505	0.020457	0.103778	67	67	67
Species													
Sample Subset	Taxonomic Level	LFR2	BCSR2	RFR2	LF_Coeff	BCS_Coeff	RF_Coeff	LF_Adj._Pval	BCS_Adj._Pval	RF_Adj._Pval	LF_N	BCS_N	RF_N
2015	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Prevotellaceae , g__Prevotellaceae UCG-004 , s__uncultured bacterium	0.026904	0.092183	0.076276	0.264978	0.36679	0.337125	0.795536	0.018644	0.063794	99	99	99
2015	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae FE2018 group , s__bacterium FE2018	0.130751	0.035167	0.01336	-0.39131	-0.23422	-0.1639	0.00614	1	1	99	99	99
2015	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Oscillibacter ,	0.007436	0.047282	0.033286	-0.15416	-0.35074	-0.32067	1	0.036812	0.12	99	99	99
2016	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Coprococcus 3 ,	0.03478	0.052945	0.054062	0.302133	0.238375	0.289893	0.000512	0.046417	0.001352	237	240	237
2016	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Marvinbryantia , s__uncultured bacterium	0.031422	0.032451	0.033257	0.213581	0.261928	0.287245	0.221965	0.009556	0.001658	237	240	237
2016	Level , p__Tenericutes , c__Mollicutes , o__Mollicutes RF39 , , ,	0.008519	0.028848	0.026238	0.164828	0.251986	0.240416	1	0.018973	0.044216	237	240	237
2017	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Prevotellaceae , g__Prevotellaceae UCG-004 , s__uncultured bacterium	0.033137	0.062428	0.080899	0.225111	0.313503	0.397383	0.147213	0.000361	1.41E-07	226	225	225
2017	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Prevotellaceae , g__Prevotellaceae UCG-004 , s__uncultured Bacteroidales bacterium	0.019928	0.014541	0.029602	0.139688	0.174244	0.307239	1	1	0.000594	226	225	225
2017	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__dgA-11 gut group , s__uncultured bacterium	0.040935	0.045955	0.063746	0.213699	0.190579	0.297116	0.277623	0.926187	0.001298	226	225	225
2017	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group ,	0.046291	0.03664	0.055736	0.249968	0.193112	0.288214	0.033037	0.818503	0.002519	226	225	225
2017	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , s__uncultured Bacteroidales bacterium	0.004204	0.002824	0.00609	0.163826	0.202562	0.271232	1	0.5094	0.0084	226	225	225
2017	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__uncultured , g__uncultured bacterium , s__uncultured bacterium	5.50E-06	0.002696	0.012407	0.132316	0.171348	0.284748	1	1	0.003242	226	225	225
2017	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , ,	0.042581	0.070027	0.081351	-0.2461	-0.28366	-0.34991	0.042118	0.003507	1.58E-05	226	225	225
2017	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Coprococcus 3 , s__uncultured bacterium	0.027031	0.04681	0.060152	-0.16345	-0.23327	-0.30636	1	0.094086	0.000636	226	225	225

2017	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Tyzzerella 3 , s__uncultured rumen bacterium	0.000625	0.0163	0.018193	-0.11238	-0.18745	-0.27197	1	1	0.007985	226	225	225
2017	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminiclostridium 9 ,	0.016267	0.072681	0.064512	0.183382	0.230636	0.270959	1	0.109737	0.008559	226	225	225
2017	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 ,	0.016593	0.036716	0.043029	0.156674	0.202763	0.248992	1	0.504176	0.036192	226	225	225
2017	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcus 1 ,	0.005201	0.01726	0.023319	0.21333	0.171874	0.286276	0.283213	1	0.002902	226	225	225
2017	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcus 1 , s__uncultured bacterium	0.003719	0.018798	0.029571	0.128732	0.17443	0.24584	1	1	0.044054	226	225	225
2017	Level , p__Firmicutes , c__Negativicutes , o__Selenomonadales , f__Acidaminococcaceae , g__Phascolarctobacterium , s__uncultured Veillonellaceae bacterium	0.016345	0.008928	0.006661	0.172119	0.220995	0.24478	1	0.189978	0.047038	226	225	225
2017	Level , p__Spirochaetes , c__Spirochaetia , o__Spirochaetales , f__Spirochaetaceae , g__Treponema 2 ,	0.000805	0.025134	0.024929	0.073924	0.219494	0.251851	1	0.206501	0.030216	226	225	225
2017	Level , p__Spirochaetes , c__Spirochaetia , o__Spirochaetales , f__Spirochaetaceae , g__Treponema 2 , s__uncultured bacterium	0.017996	0.02575	0.046312	0.146931	0.22516	0.296211	1	0.150303	0.00139	226	225	225
2017	Level , p__Tenericutes , c__Mollicutes , o__Izimaplasmatales , f__gut metagenome , g__gut metagenome , s__gut metagenome	0.013427	0.007699	0.011608	0.154784	0.231915	0.282444	1	0.101856	0.003826	226	225	225
2017	Level , p__Tenericutes , c__Mollicutes , o__Mollicutes RF39 , , ,	0.022564	0.013826	0.017099	0.156918	0.139573	0.251663	1	1	0.030578	226	225	225
2018	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Roseburia ,	3.35E-05	0.032023	0.03151	0.035031	0.270332	0.280673	1	0.068555	0.039879	167	167	167
2018	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Negativibacillus , s__uncultured bacterium	0.054858	0.048694	0.064284	0.324855	0.224114	0.309087	0.003076	0.600579	0.008047	167	167	167
2018	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminiclostridium 9 ,	0.047742	0.125623	0.124553	0.21676	0.353477	0.329841	0.818015	0.000466	0.002243	167	167	167
2018	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , s__uncultured bacterium	0.007669	0.06495	0.040745	0.119091	0.298744	0.295116	1	0.014692	0.01805	167	167	167
2018	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-013 , s__uncultured bacterium	0.022558	0.061	0.069537	0.143364	0.238877	0.313952	1	0.313576	0.006015	167	167	167
2018	Level , p__Proteobacteria , c__Gammaproteobacteria , o__Betaproteobacteriales , f__Burkholderiaceae , g__Delftia ,	0.081963	0.04781	0.025252	-0.25455	-0.30075	-0.28343	0.150478	0.013097	0.034383	167	167	167
2019	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , , ,	0.144683	0.371855	0.214261	0.537248	0.282624	0.371106	0.04867	1	1	32	32	32
2019	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__metagenome	0.006355	0.023972	0.38604	0.028168	0.274642	0.595975	1	1	0.010214	32	32	32
2015_PostWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Papillibacter , s__uncultured bacterium	0.277491	0.082121	0.002599	0.697445	-0.0338	0.148102	0.012604	1	1	20	20	20
2016_PostWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Faecalibacterium ,	0.000583	0.240382	0.101411	0.002786	0.439342	0.225037	1	0.029443	1	59	59	59
2017_PostWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Peptostreptococcaceae , g__Romboutsia , s__uncultured bacterium	0.134309	0.077756	0.016616	-0.40923	-0.25024	-0.16503	0.003636	1	1	95	95	95
2017_PostWinter	Level , p__Tenericutes , c__Mollicutes , o__Izimaplasmatales , f__gut metagenome , g__gut metagenome , s__gut metagenome	0.004014	0.071171	0.111856	0.139564	0.303071	0.36403	1	0.269034	0.027301	95	95	95
2017_PreWinter	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides ,	0.002064	0.072471	0.065012	0.106559	0.302086	0.348277	1	0.062088	0.006366	131	130	130
2018_PostWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae NK3A20 group ,	0.025432	0.020967	0.002234	-0.5157	-0.28166	-0.1482	0.012974	1	1	45	45	45
2018_PostWinter	Level , p__Proteobacteria , c__Alphaproteobacteria , o__Acetobacterales , f__Acetobacteraceae , g__Roseomonas , s__Roseomonas ludipueritiae	0.226968	0.017928	0.001685	0.513926	0.256145	0.243053	0.013728	1	1	45	45	45
2019_PostWinter	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , , ,	0.144298	0.383139	0.272944	0.592479	0.307207	0.339892	0.011304	1	1	32	32	32
2019_PostWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__metagenome	0.00798	0.046049	0.484748	0.028168	0.274642	0.595975	1	1	0.010214	32	32	32
Adult	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , , ,	0.001678	0.001223	0.001755	0.095262	0.15533	0.159556	1	0.012471	0.007509	761	763	760
Adult	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Muribaculaceae , g__uncultured bacterium , s__uncultured bacterium	0.006196	0.010858	0.006294	0.104403	0.164671	0.173866	1	0.003679	0.00108	761	763	760
Adult	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Prevotellaceae , g__Prevotellaceae UCG-004 , s__uncultured bacterium	0.013775	0.018551	0.020307	0.178425	0.205478	0.236274	0.000554	7.77E-06	3.20E-08	761	763	760
Adult	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Prevotellaceae , g__Prevotellaceae UCG-004 , s__uncultured Bacteroidales bacterium	0.005292	0.00661	0.010717	0.088849	0.122846	0.169729	1	0.512944	0.001924	761	763	760
Adult	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__dgA-11 gut group , s__uncultured bacterium	0.024507	0.011867	0.016432	0.196067	0.149043	0.177187	3.77E-05	0.027287	0.000673	761	763	760
Adult	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group ,	0.017856	0.007363	0.009616	0.19737	0.133863	0.162901	3.06E-05	0.159236	0.004843	761	763	760
Adult	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , s__uncultured Bacteroidales bacterium	0.000397	0.000548	0.002571	0.120389	0.120838	0.150472	0.666321	0.62863	0.023649	761	763	760

Adult	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__uncultured , g__uncultured bacterium , s__uncultured bacterium	0.001072	0.009142	0.016328	0.100469	0.160482	0.187375	1	0.006415	0.000149	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , ,	0.024712	0.027651	0.030799	-0.15549	-0.15283	-0.17955	0.012509	0.017096	0.000478	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Coprococcus 3 ,	0.011591	0.008273	0.005176	0.163289	0.114609	0.135534	0.004541	1	0.135709	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Dorea , s__uncultured bacterium	0.007555	0.011999	0.013388	0.102778	0.154791	0.156639	1	0.013353	0.010931	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Tyzzerella 3 , s__uncultured rumen bacterium	0.00361	0.009322	0.009837	-0.09429	-0.1298	-0.16788	1	0.247664	0.002478	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group ,	0.004125	0.002853	0.004198	0.111206	0.10439	0.144429	1	1	0.048948	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminiclostridium 6 , s__uncultured bacterium	0.009378	0.003175	0.002878	0.152348	0.096971	0.122621	0.018554	1	0.535741	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminiclostridium 9 ,	0.018	0.023602	0.01989	0.171269	0.193656	0.184383	0.001532	5.33E-05	0.000234	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-009 , s__uncultured bacterium	0.024047	0.027446	0.01551	0.165069	0.189918	0.193723	0.003579	9.56E-05	5.57E-05	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 ,	0.023223	0.02037	0.018873	0.157694	0.176378	0.173009	0.009438	0.000722	0.001218	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium	0.008039	0.013294	0.008638	0.181291	0.202669	0.205502	0.000364	1.24E-05	8.24E-06	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured Ruminococcaceae bacterium	0.012786	0.006394	0.00706	0.169974	0.159567	0.155319	0.001834	0.00723	0.012927	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-013 , s__uncultured bacterium	0.017633	0.029599	0.021906	0.138891	0.175162	0.178913	0.092181	0.000859	0.000524	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-014 , s__unidentified	0.007753	0.012192	0.009799	0.117094	0.162086	0.152551	0.922459	0.005193	0.018291	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcus 1 ,	0.000503	0.000823	0.000618	0.114742	0.12172	0.162974	1	0.575163	0.004796	761	763	760
Adult	Level , p__Firmicutes , c__Negativicutes , o__Selenomonadales , f__Acidaminococcaceae , g__Phascolarctobacterium , s__uncultured Veillonellaceae bacterium	0.004592	0.001049	0.001239	0.11591	0.124706	0.154881	1	0.42373	0.013662	761	763	760
Adult	Level , p__Proteobacteria , c__Alphaproteobacteria , o__Rhodospirillales , f__uncultured , g__gut metagenome , s__gut metagenome	0.0024	0.017693	0.017942	0.090166	0.1617	0.16954	1	0.005465	0.001975	761	763	760
Adult	Level , p__Proteobacteria , c__Deltaproteobacteria , o__Desulfovibrionales , f__Desulfovibrionaceae , g__uncultured ,	0.007027	0.0033	0.003656	-0.14559	-0.09748	-0.09914	0.04223	1	1	761	763	760
Adult	Level , p__Spirochaetes , c__Spirochaetia , o__Spirochaetales , f__Spirochaetaceae , g__Treponema 2 ,	0.000941	0.010595	0.008218	0.080358	0.16512	0.157965	1	0.003463	0.009223	761	763	760
Adult	Level , p__Spirochaetes , c__Spirochaetia , o__Spirochaetales , f__Spirochaetaceae , g__Treponema 2 , s__uncultured bacterium	0.007679	0.008488	0.013928	0.091235	0.148052	0.160616	1	0.030783	0.006541	761	763	760
Adult	Level , p__Tenericutes , c__Mollicutes , o__Mollicutes RF39 , , ,	0.004623	0.008068	0.008423	0.088804	0.119158	0.153825	1	0.743512	0.015602	761	763	760
All	Level , p__Actinobacteria , c__Actinobacteria , o__Micrococcales , f__Microbacteriaceae , ,	0.004999	0.005139	0.004849	-0.14063	-0.14487	-0.16364	0.040484	0.023209	0.001851	828	830	827
All	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Muribaculaceae , g__uncultured bacterium , s__uncultured bacterium	0.005379	0.010283	0.004915	0.095779	0.16176	0.16148	1	0.002334	0.002522	828	830	827
All	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Prevotellaceae , g__Prevotellaceae UCG-004 , s__uncultured bacterium	0.017697	0.023801	0.026065	0.202865	0.222949	0.257124	3.20E-06	6.88E-08	4.90E-11	828	830	827
All	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Prevotellaceae , g__Prevotellaceae UCG-004 , s__uncultured Bacteroidales bacterium	0.003225	0.006519	0.009494	0.089045	0.132677	0.171556	1	0.104825	0.000574	828	830	827
All	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__dgA-11 gut group , s__uncultured bacterium	0.023255	0.009117	0.015419	0.181159	0.122993	0.155049	0.000127	0.317856	0.006196	828	830	827
All	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group ,	0.017877	0.007277	0.008994	0.204062	0.140628	0.154446	2.58E-06	0.03977	0.006729	828	830	827
All	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , s__uncultured Bacteroidales bacterium	0.000454	0.000794	0.002624	0.12805	0.132741	0.160228	0.182567	0.104026	0.003013	828	830	827
All	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__uncultured , g__uncultured bacterium , s__uncultured bacterium	7.49E-05	0.006081	0.011654	0.080927	0.155927	0.183168	1	0.005304	9.35E-05	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , , ,	0.005287	0.02393	0.025683	0.17814	0.144996	0.163772	0.000205	0.022832	0.001815	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , ,	0.028406	0.028816	0.030592	-0.16413	-0.16167	-0.18852	0.001702	0.002365	3.89E-05	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__[Eubacterium] ventriosum group , s__uncultured rumen bacterium	0.022426	0.011041	0.011327	-0.14001	-0.12507	-0.13567	0.043747	0.252155	0.075194	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Coprococcus 3 ,	0.00972	0.011924	0.008415	0.176541	0.142719	0.171718	0.000263	0.030553	0.00056	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Dorea , s__uncultured bacterium	0.006499	0.011275	0.012302	0.092039	0.149547	0.148247	1	0.012588	0.015425	828	830	827

All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae FCS020 group , s__uncultured bacterium	0.012919	0.000256	0.000151	0.145737	0.053628	0.040359	0.021169	1	1	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Tyzzerella 3 , s__uncultured rumen bacterium	0.008723	0.018933	0.017112	-0.12086	-0.17257	-0.2046	0.406869	0.000471	2.39E-06	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group ,	0.004242	0.003331	0.004484	0.109385	0.111356	0.146585	1	1	0.019161	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Candidatus Soleaferrea , s__uncultured Ruminococcaceae bacterium	0.006119	0.017175	0.009854	-0.05467	-0.15377	-0.14497	1	0.007133	0.023616	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminiclostridium 6 , s__uncultured bacterium	0.007463	0.002896	0.003248	0.15025	0.104865	0.139559	0.011713	1	0.046711	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminiclostridium 9 ,	0.021283	0.029302	0.024521	0.159616	0.19643	0.187419	0.003245	9.59E-06	4.67E-05	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-009 , s__uncultured bacterium	0.021717	0.023188	0.013891	0.162365	0.165182	0.179028	0.002195	0.001422	0.000181	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 ,	0.021418	0.018466	0.01869	0.153606	0.168445	0.175376	0.007459	0.000878	0.00032	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium	0.008418	0.011998	0.007601	0.183427	0.194533	0.194119	8.82E-05	1.33E-05	1.51E-05	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured Ruminococcaceae bacterium	0.015655	0.006332	0.007167	0.197654	0.168633	0.167159	8.05E-06	0.000854	0.001107	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-013 , s__uncultured bacterium	0.018987	0.027093	0.020592	0.145414	0.173653	0.183386	0.02207	0.000399	9.02E-05	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-014 , s__unidentified	0.011082	0.015713	0.011969	0.099141	0.144702	0.143264	1	0.023713	0.029348	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcus 1 ,	8.18E-05	0.000681	0.000777	0.149967	0.119111	0.159709	0.012163	0.485268	0.003242	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__uncultured ,	0.011293	0.010737	0.007894	0.128949	0.136586	0.140059	0.164672	0.065524	0.0439	828	830	827
All	Level , p__Firmicutes , c__Negativicutes , o__Selenomonadales , f__Acidaminococcaceae , g__Phascolarctobacterium , s__uncultured Veillonellaceae bacterium	0.00515	0.00231	0.002376	0.11887	0.133504	0.158538	0.504446	0.095006	0.003822	828	830	827
All	Level , p__Kiritimatiellaeota , c__Kiritimatiellae , o__WCHB1-41 , f__uncultured rumen bacterium , g__uncultured rumen bacterium , s__uncultured rumen bacterium	0.014486	0.00331	0.00101	-0.14067	-0.09219	-0.08775	0.040328	1	1	828	830	827
All	Level , p__Planctomycetes , c__Planctomycetacia , o__Pirellulales , f__Pirellulaceae , g__p-1088-a5 gut group , s__uncultured bacterium	0.018392	0.015224	0.012363	-0.11959	-0.11453	-0.14603	0.466757	0.787112	0.020576	828	830	827
All	Level , p__Proteobacteria , c__Alphaproteobacteria , o__Rhodospirillales , f__uncultured , ,	0.003592	0.009011	0.006715	0.103548	0.144703	0.152326	1	0.023709	0.008969	828	830	827
All	Level , p__Spirochaetes , c__Spirochaetia , o__Spirochaetales , f__Spirochaetaceae , g__Treponema 2 ,	0.001866	0.010639	0.008856	0.101042	0.163876	0.155424	1	0.00172	0.005885	828	830	827
All	Level , p__Spirochaetes , c__Spirochaetia , o__Spirochaetales , f__Spirochaetaceae , g__Treponema 2 , s__uncultured bacterium	0.006164	0.006046	0.01131	0.085251	0.142489	0.157152	1	0.031459	0.004636	828	830	827
All	Level , p__Tenericutes , c__Mollicutes , o__Mollicutes RF39 , , ,	0.004133	0.012061	0.011282	0.126005	0.142271	0.163713	0.230346	0.032338	0.001831	828	830	827
Cache	Level , p__Actinobacteria , c__Coriobacteriia , o__Coriobacteriales , f__Eggerthellaceae , ,	0.032503	0.046294	0.044179	0.218197	0.29043	0.314089	1	0.112938	0.039122	128	128	128
Cache	Level , p__Actinobacteria , c__Coriobacteriia , o__Coriobacteriales , f__uncultured , g__uncultured bacterium , s__uncultured bacterium	0.038907	0.116505	0.116591	0.166906	0.337792	0.360515	1	0.012341	0.003728	128	128	128
Cache	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Barnesiellaceae , g__uncultured ,	0.034734	0.01048	0.003474	0.363283	0.347085	0.320017	0.003202	0.007647	0.029575	128	128	128
Cache	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Prevotellaceae , g__Prevotellaceae UCG-004 , s__uncultured bacterium	0.050899	0.033559	0.021917	0.30357	0.376868	0.347017	0.063373	0.001486	0.007675	128	128	128
Cache	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__dgA-11 gut group , s__uncultured bacterium	0.081494	0.137197	0.108349	0.255625	0.356095	0.32586	0.459321	0.004739	0.02232	128	128	128
Cache	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group ,	0.076008	0.067381	0.057234	0.366894	0.442696	0.438207	0.00262	2.14E-05	2.95E-05	128	128	128
Cache	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , s__uncultured Bacteroidales bacterium	0.050609	0.022017	0.016622	0.319311	0.348153	0.319241	0.030587	0.007231	0.03069	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , , ,	0.076838	0.092668	0.089466	0.315883	0.321595	0.335476	0.035969	0.027427	0.013872	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , ,	0.064876	0.110706	0.070469	-0.25276	-0.32714	-0.31082	0.511473	0.020968	0.045532	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__[Eubacterium] ventriosum group , s__uncultured rumen bacterium	0.035091	0.059354	0.055964	-0.21081	-0.33623	-0.34233	1	0.013356	0.00979	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae UCG-010 ,	0.05561	0.071499	0.068404	0.239453	0.324999	0.319757	0.829941	0.023274	0.029945	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , ,	0.110588	0.110802	0.084775	0.36173	0.339964	0.31645	0.003488	0.01105	0.035022	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminiclostridium 9 ,	0.068885	0.10529	0.090423	0.280225	0.329883	0.290502	0.173645	0.018327	0.112586	128	128	128

Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminiclostridium 9 , s__Colidextribacter massiliensis	0.079229	0.028257	0.013374	0.363526	0.287179	0.275021	0.003159	0.129751	0.214926	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , s__metagenome	0.128488	0.088844	0.078048	0.377626	0.326537	0.322225	0.001423	0.021596	0.02661	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 ,	0.099547	0.132757	0.120266	0.334978	0.407252	0.384545	0.014223	0.000235	0.000949	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium	0.082578	0.084454	0.060861	0.418607	0.465002	0.439647	0.000112	4.10E-06	2.66E-05	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured Ruminococcaceae bacterium	0.076241	0.037054	0.028793	0.34857	0.331851	0.289152	0.007075	0.016626	0.119294	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-013 , s__uncultured bacterium	0.059669	0.129941	0.124266	0.320448	0.396854	0.391281	0.028973	0.000451	0.000634	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-014 , s__unidentified	0.045267	0.129373	0.111885	0.257287	0.309218	0.281099	0.431311	0.049024	0.167473	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__uncultured ,	0.042638	0.045768	0.028875	0.266783	0.344538	0.330757	0.298754	0.008732	0.017553	128	128	128
Cache	Level , p__Verrucomicrobia , c__Verrucomicrobiae , o__Opitutales , f__Puniceicoccaceae , g__Cerasicoccus , s__uncultured bacterium	0.023244	0.024231	0.022552	0.256988	0.317529	0.281666	0.436235	0.033284	0.163571	128	128	128
Monroe	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__uncultured , s__uncultured rumen bacterium	0.011137	0.005639	0.007833	0.363225	0.171118	0.281507	0.047376	1	0.74361	87	86	86
Monroe	Level , p__Tenericutes , c__Mollicutes , o__Izimaplasmatales , f__uncultured bacterium , g__uncultured bacterium , s__uncultured bacterium	0.002741	0.108599	0.064397	0.135235	0.403009	0.395744	1	0.010277	0.013957	87	86	86
OquirrhStansbury	Level , p__Cyanobacteria , c__Melainabacteria , o__Gastranaerophilales , f__uncultured rumen bacterium , g__uncultured rumen bacterium , s__uncultured rumen bacterium	0.020542	0.102195	0.083887	0.126387	0.473068	0.445912	1	0.000664	0.002446	81	81	81
OquirrhStansbury	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Family XIII , g__Family XIII AD3011 group , s__uncultured bacterium	0.056965	0.04196	0.043755	0.284533	0.408306	0.374152	0.813245	0.012503	0.046961	81	81	81
OquirrhStansbury	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Oscillibacter ,	0.077487	0.128001	0.101482	-0.27152	-0.40669	-0.41312	1	0.013354	0.010253	81	81	81
PineValley	Level , p__Actinobacteria , c__Actinobacteria , o__Micrococcales , f__Micrococcaceae , g__Arthrobacter ,	0.045874	0.045372	0.026948	-0.29317	-0.3571	-0.25432	0.162865	0.007973	0.681145	116	119	116
PineValley	Level , p__Firmicutes , c__Bacilli , o__Lactobacillales , f__Enterococcaceae , g__Enterococcus ,	0.000284	0.001598	0.00834	-0.21698	-0.33407	-0.31329	1	0.024369	0.071498	116	119	116
PostWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Family XIII , g__Family XIII AD3011 group , s__uncultured bacterium	1.01E-05	0.020329	0.023867	-0.04936	-0.29383	-0.28572	1	0.000545	0.001059	251	251	251
PostWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 ,	0.013323	0.045035	0.049906	0.101926	0.208973	0.234497	1	0.217134	0.044564	251	251	251
PostWinter	Level , p__Kiritimatiellaeota , c__Kiritimatiellae , o__WCHB1-41 , f__uncultured rumen bacterium , g__uncultured rumen bacterium , s__uncultured rumen bacterium	0.043611	0.062215	0.048273	-0.20575	-0.29158	-0.2961	0.261882	0.000656	0.00045	251	251	251
PreWinter	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides ,	0.007763	0.020218	0.022329	0.097672	0.176277	0.211954	1	0.031038	0.000712	510	512	509
SanJuan	Level , p__Actinobacteria , c__Coriobacteriia , o__Coriobacteriales , f__Atopobiaceae , ,	0.053956	1.63E-05	0.001944	-0.35349	-0.17571	-0.17737	0.034926	1	1	98	98	98
SanJuan	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__uncultured , s__uncultured bacterium	0.108585	0.006746	0.008793	-0.35286	-0.08396	-0.11571	0.035847	1	1	98	98	98
Wasatch-Manti	Level , p__Actinobacteria , c__Actinobacteria , o__Micrococcales , f__Microbacteriaceae , ,	0.017189	0.011704	0.013827	-0.19487	-0.18092	-0.26256	1	1	0.042062	194	194	194
Wasatch-Manti	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Prevotellaceae , g__Prevotellaceae UCG-004 , s__uncultured bacterium	0.071971	0.032986	0.049608	0.340965	0.194968	0.284857	0.000222	1	0.011022	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , , ,	0.034233	0.039668	0.057078	0.219599	0.214234	0.286084	0.40628	0.524518	0.010204	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Eubacteriaceae , g__Anaerofustis , s__uncultured bacterium	0.021703	0.057067	0.080993	0.194482	0.243705	0.327332	1	0.119598	0.000617	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , ,	0.083788	0.042266	0.06373	-0.27507	-0.1962	-0.28035	0.020128	1	0.014581	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Coprococcus 3 ,	0.025882	0.03243	0.026002	0.332692	0.253974	0.314295	0.000415	0.068373	0.001568	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Tyzzerella 3 , s__uncultured rumen bacterium	0.038525	0.035537	0.049155	-0.24228	-0.24279	-0.36445	0.128991	0.125573	3.39E-05	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Tyzzerella 4 , s__uncultured bacterium	0.035352	0.053835	0.049617	0.267022	0.29148	0.294848	0.032476	0.007239	0.005822	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , ,	0.027941	0.08508	0.068169	0.21595	0.312668	0.319864	0.483687	0.001757	0.001059	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group ,	0.052586	0.038006	0.043644	0.253448	0.272549	0.34221	0.070398	0.023419	0.000202	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group , s__uncultured bacterium	0.030444	0.041529	0.027455	0.142453	0.271396	0.256615	1	0.025086	0.058989	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Negativibacillus , s__uncultured bacterium	0.057939	0.088665	0.081934	0.284007	0.259735	0.32301	0.011624	0.049452	0.000845	194	194	194

Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminiclostridium 6 , s__uncultured bacterium	0.00837	0.001251	0.000925	0.297469	0.196039	0.276662	0.004905	1	0.018276	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminiclostridium 9 , s__Colidextribacter massiliensis	0.049133	0.035095	0.042968	0.266663	0.197291	0.243903	0.033166	1	0.118344	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae NK4A214 group , s__uncultured bacterium	0.046498	0.096842	0.11565	0.234076	0.308215	0.393025	0.197858	0.002387	2.79E-06	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , s__uncultured Ruminococcaceae bacterium	0.05123	0.059266	0.050332	0.205786	0.24182	0.285117	0.774863	0.132195	0.010843	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-009 , s__uncultured bacterium	0.07747	0.095117	0.078973	0.259618	0.32421	0.389808	0.049783	0.000775	3.74E-06	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 ,	0.05642	0.06339	0.050245	0.236574	0.299084	0.348224	0.173966	0.00441	0.000126	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium	0.05841	0.123891	0.103348	0.26891	0.348106	0.421106	0.029067	0.000127	1.88E-07	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-013 , s__uncultured bacterium	0.075882	0.052613	0.043206	0.292174	0.231919	0.264778	0.006923	0.22086	0.037013	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-014 , s__unidentified	0.044019	0.027737	0.029702	0.267391	0.239227	0.246009	0.031781	0.151521	0.105709	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcus 1 ,	0.002805	0.001172	0.000115	0.276757	0.108961	0.156582	0.018171	1	1	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcus 1 , s__uncultured bacterium	0.01204	0.000976	0.003994	0.261177	0.151641	0.26073	0.045548	1	0.046725	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__uncultured , s__uncultured bacterium	0.024547	0.080757	0.089277	0.199038	0.228375	0.282989	1	0.264061	0.012385	194	194	194
Winter15-16	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcus 2 ,	0.006117	0.046881	0.019176	-0.17792	-0.30452	-0.19234	1	0.038897	1	138	138	138
Winter16-17	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Prevotellaceae , g__Prevotellaceae UCG-004 , s __uncultured bacterium	0.035004	0.013838	0.016016	0.23018	0.220039	0.292181	0.033947	0.063315	0.000245	273	276	273
Winter16-17	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group ,	0.022519	0.026328	0.027749	0.200865	0.167768	0.252932	0.230627	1	0.006411	273	276	273
Winter16-17	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , s__uncultured Bacteroidales bacterium	0.00231	0.000822	0.006362	0.184418	0.149898	0.240452	0.605487	1	0.016316	273	276	273
Winter16-17	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , ,	0.057464	0.059302	0.079512	-0.23739	-0.30128	-0.37644	0.020371	9.30E-05	3.50E-08	273	276	273
Winter16-17	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Coprococcus 3 , s__uncultured bacterium	0.018494	0.028232	0.029662	-0.11767	-0.20795	-0.23709	1	0.139858	0.020813	273	276	273
Winter16-17	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Tyzzerella 3 , s__uncultured rumen bacterium	0.005094	0.026381	0.030148	-0.09609	-0.22412	-0.27481	1	0.047971	0.001106	273	276	273
Winter16-17	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group ,	0.005674	0.027557	0.032484	0.120767	0.198872	0.258586	1	0.246534	0.004131	273	276	273
Winter16-17	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae NK4A214 group , s__uncultured bacterium	0.046174	0.014977	0.016471	0.228076	0.174219	0.187818	0.039284	1	0.499092	273	276	273
Winter16-17	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured Ruminococcaceae bacterium	0.002276	0.000514	4.00E-07	0.235007	0.133886	0.162633	0.024156	1	1	273	276	273
Winter16-17	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__uncultured ,	0.038976	0.01721	0.009679	0.22623	0.162558	0.194246	0.044607	1	0.343275	273	276	273
Winter17-18	Level , p__Actinobacteria , c__Actinobacteria , o__Corynebacteriales , f__Nocardiaceae , g__Williamsia ,	0.005669	0.019703	0.017046	-0.06486	-0.27681	-0.30005	1	0.036514	0.009588	176	175	175
Winter17-18	Level , p__Actinobacteria , c__Actinobacteria , o__Micrococcales , f__Microbacteriaceae , ,	0.012378	0.016486	0.014696	-0.22404	-0.2804	-0.31782	0.492325	0.029915	0.003185	176	175	175
Winter17-18	Level , p__Actinobacteria , c__Actinobacteria , o__Propionibacteriales , f__Nocardioidaceae , g__Aeromicrobium ,	0.001157	0.014447	0.013465	-0.05223	-0.26632	-0.29106	1	0.064327	0.016308	176	175	175
Winter17-18	Level , p__Actinobacteria , c__Actinobacteria , o__Propionibacteriales , f__Nocardioidaceae , g__Nocardioides ,	0.016257	0.026672	0.019208	-0.10688	-0.23626	-0.27889	1	0.287999	0.032541	176	175	175
Winter17-18	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides ,	0.000707	0.043998	0.038866	0.100104	0.280013	0.318423	1	0.030574	0.003064	176	175	175
Winter17-18	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Blautia ,	0.011744	0.0626	0.033965	0.139498	0.323763	0.299656	1	0.002168	0.009817	176	175	175
Winter17-18	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-013 , s__uncultured bacterium	0.025266	0.13453	0.116423	0.208976	0.380925	0.398988	0.946696	3.48E-05	7.91E-06	176	175	175
Winter17-18	Level , p__Proteobacteria , c__Alphaproteobacteria , o__Rhizobiales , f__Devosiaceae , g__Devosia ,	0.002901	0.013353	0.011224	-0.07945	-0.24926	-0.27132	1	0.153952	0.049235	176	175	175
Winter17-18	Level , p__Proteobacteria , c__Gammaproteobacteria , o__Betaproteobacteriales , f__Burkholderiaceae , g__Delftia ,	0.056837	0.039794	0.017954	-0.26866	-0.31719	-0.29907	0.054876	0.003317	0.010169	176	175	175
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Tyzzerella 3 , s__uncultured rumen bacterium	0.023773	0.033351	0.031863	-0.1418	-0.26624	-0.28863	1	0.130189	0.043612	154	154	154

Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured Ruminococcaceae bacterium	0.018849	0.070365	0.102743	0.116676	0.314539	0.325718	1	0.010937	0.005782	154	154	154
Winter18-19	Level , p__Kiritimatiellaeota , c__Kiritimatiellae , o__WCHB1-41 , f__uncultured rumen bacterium , g__uncultured rumen bacterium , s__uncultured rumen bacterium	0.041786	0.034209	0.033467	-0.14812	-0.21252	-0.28877	1	1	0.043305	154	154	154
Yearling	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Prevotellaceae , g__Prevotellaceae UCG-004 , s__uncultured bacterium	0.131271	0.086749	0.103344	0.43173	0.352796	0.365278	0.017717	0.228423	0.158805	67	67	67
Yearling	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__uncultured , ,	0.003491	0.163535	0.116734	0.078882	0.423772	0.314757	1	0.023608	0.63521	67	67	67
Yearling	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , s__metagenome	0.164986	0.173899	0.208763	0.386476	0.283252	0.410219	0.082817	1	0.037884	67	67	67
Yearling	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-014 , s__unidentified	0.04506	0.123567	0.077318	0.268126	0.439983	0.42174	1	0.013056	0.025375	67	67	67
Yearling	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcus 1 ,	0.054352	0.000128	5.05E-05	0.431674	0.34082	0.358442	0.017753	0.319497	0.19413	67	67	67
Yearling	Level , p__Planctomycetes , c__Planctomycetacia , o__Pirellulales , f__Pirellulaceae , g__p-1088-a5 gut group , s__uncultured bacterium	0.119601	0.172765	0.084939	-0.32217	-0.42777	-0.37929	0.525505	0.020457	0.103778	67	67	67
ASV													
Sample Subset	Taxonomic Level	LFR2	BCSR2	RFR2	LF_Coeff	BCS_Coeff	RF_Coeff	LF_Adj._Pval	BCS_Adj._Pval	RF_Adj._Pval	LF_N	BCS_N	RF_N
2015	Level , p__Actinobacteria , c__Coriobacteriia , o__Coriobacteriales , f__Eggerthellaceae , g__DNF00809 , s__uncultured bacterium , 535cfd6b9eaf931b8a0a152015fc7603	0.024404	0.038194	0.048681	-0.37001	-0.14945	-0.08291	0.016191	1	1	99	99	99
2015	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 5a93cb46df25c6a6e053456b94264970	0.111318	0.080403	0.095659	0.355577	0.130377	0.20318	0.030104	1	1	99	99	99
2015	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 657b53eec5cc03a34d4d673a58c65689	0.102025	0.02151	0.014273	0.357068	0.26368	0.268217	0.028274	0.8278	0.71976	99	99	99
2015	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae FE2018 group , s__bacterium FE2018 , 0fa4bc34e153544af446f3e2a931b8af	0.138756	0.031775	0.010395	-0.40398	-0.23634	-0.16897	0.00334	1	1	99	99	99
2015	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , , , 6fb8eb193f5d0673db6bd7c380ad98c6	0.090434	0.094752	0.099783	0.355453	0.331754	0.299457	0.030261	0.078708	0.257671	99	99	99
2015	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Oscillibacter , , ef44e026034244f99ad961589cded471	0.069401	0.117107	0.084002	-0.25861	-0.39521	-0.31932	0.96516	0.005104	0.126183	99	99	99
2015	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , s__uncultured bacterium , 7adcbba7d451427c8e384471fb4d9b80	0.096778	0.006339	0.008604	-0.34778	-0.27661	-0.28981	0.04158	0.55221	0.358154	99	99	99
2016	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Muribaculaceae , g__uncultured bacterium , s__uncultured bacterium , 612b1eac3e95c5ad3f38048179efa072	0.005287	0.014571	0.013533	0.04994	0.240274	0.221335	1	0.041093	0.141967	237	240	237
2016	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , , , , a29894c639f10bfa998c059f74ec48d7	0.004215	0.019499	0.019598	0.099581	0.244106	0.252223	1	0.032044	0.020465	237	240	237
2016	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 7cc01e38f36bb6f650c12bd229839582	8.61E-05	0.024396	0.012849	0.083408	0.249421	0.244212	1	0.022545	0.034659	237	240	237
2016	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 8df8651bddbd747ee536d321428120f9	0.034362	0.018306	0.018794	-0.25985	-0.17569	-0.23854	0.01219	1	0.049797	237	240	237
2016	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Coprococcus 3 , , 780ec7a8c3d95c29e344b5a319a26c6d	0.030639	0.037502	0.037058	0.286399	0.224209	0.270171	0.00177	0.111677	0.005896	237	240	237
2016	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Marvinbryantia , s__uncultured bacterium , 39a0eba5cec3d61b5a72f86754ca1e2a	0.031448	0.013036	0.012743	0.188044	0.208013	0.246925	0.868851	0.285636	0.029051	237	240	237
2016	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , s__uncultured Ruminococcaceae bacterium , 0a7e34e68bffaec4e495b31786b31c0d	0.051785	0.000167	0.00047	0.296864	0.121147	0.134511	0.000782	1	1	237	240	237
2016	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , 94f75b32f2b0377dd60ceb9b2eb26973	0.031586	0.049953	0.049698	0.210423	0.231619	0.240446	0.26511	0.071025	0.044134	237	240	237
2017	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides , s__uncultured bacterium , 4f79c257c93f08d09a79987b27a3dfe9	0.008779	0.046927	0.023657	0.142188	0.240647	0.266059	1	0.060564	0.011937	226	225	225
2017	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides , s__uncultured Bacteroides sp. , 5e34611a72e7b6239039b8c404dd5595	0.004084	0.022157	0.028786	-0.05634	-0.21814	-0.26705	1	0.222518	0.011163	226	225	225
2017	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Muribaculaceae , g__uncultured bacterium , s__uncultured bacterium , 788a07d650668a784b6c713618e6f59d	0.009946	0.017905	0.016242	0.102781	0.231434	0.277176	1	0.104755	0.00556	226	225	225
2017	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Prevotellaceae , g__Prevotellaceae UCG-004 , s__uncultured bacterium , 19d31b001318d82f6e59d1a478ef8a80	0.00988	0.01323	0.019257	0.183231	0.206706	0.249414	1	0.411011	0.035247	226	225	225
2017	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Prevotellaceae , g__Prevotellaceae	0.027219	0.032487	0.043683	0.182439	0.287199	0.346387	1	0.002713	2.18E-05	226	225	225

	UCG-004 , s__uncultured bacterium , 415406680b4f6ebe91936977ea5f1e48												
2017	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , s__uncultured Bacteroidales bacterium , 0aab184e2191664a04c41d10d101d70c	0.011621	0.047811	0.068724	0.171728	0.238342	0.24747	1	0.069605	0.039809	226	225	225
2017	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , s__uncultured Bacteroidales bacterium , 4f916b9e6d00b0b7dfbc82f1768beb72	0.011748	0.014601	0.021694	0.184879	0.252173	0.289467	1	0.029603	0.002298	226	225	225
2017	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Christensenellaceae , g__Christensenellaceae R-7 group , , 3e638e44c1ef67bf6503944b4e8aea2c	0.013735	0.042633	0.034621	-0.1527	-0.25101	-0.21013	1	0.03188	0.343172	226	225	225
2017	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Christensenellaceae , g__Christensenellaceae R-7 group , , 53cda7b5f8fff34af36319ce1763ce00	0.000447	0.023541	0.023888	-0.11806	-0.22451	-0.2504	1	0.155947	0.033129	226	225	225
2017	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Christensenellaceae , g__Christensenellaceae R-7 group , , a4431161388367c379b9a879542994b3	0.006475	0.055591	0.039567	-0.14755	-0.26919	-0.27656	1	0.009657	0.005808	226	225	225
2017	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Christensenellaceae , g__Christensenellaceae R-7 group , , f8a30689dee232805c05ee738a3b47bf	0.021748	0.009126	0.003329	0.194617	0.209047	0.263033	0.747393	0.363416	0.014613	226	225	225
2017	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 17d6cc9d7f73afa3bdccea307b776b95	0.001059	0.000862	0.001832	0.082576	0.21716	0.254029	1	0.234843	0.026295	226	225	225
2017	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 3d27de5d0b52f339f4eaa9c50384334c	0.021327	0.063578	0.072169	-0.22867	-0.29847	-0.33052	0.11998	0.001171	8.79E-05	226	225	225
2017	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 76314928d015d16b68bb07ed7c1e21b7	0.005732	0.015193	0.016872	0.199783	0.239564	0.31344	0.576535	0.064668	0.000363	226	225	225
2017	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 867a9dbf65311fbccb6cc0e204049ed7	0.032819	0.051963	0.069085	-0.26237	-0.28557	-0.36773	0.014771	0.003055	2.93E-06	226	225	225
2017	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 8df8651bddbd747ee536d321428120f9	0.028172	0.05399	0.054061	-0.18911	-0.29428	-0.2903	0.979056	0.001607	0.00216	226	225	225
2017	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , bad7e742798b5fcc520ff82e75b256a9	0.037655	0.056671	0.066898	-0.29531	-0.33517	-0.39246	0.001424	5.88E-05	2.38E-07	226	225	225
2017	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__[Eubacterium] ruminantium group , s__uncultured bacterium , d0e2a33156b62e774f7ffcdb9e512e01	0.012616	0.011615	0.011086	0.149423	0.17937	0.253806	1	1	0.026675	226	225	225
2017	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Blautia , , a36a43c162afd14d5434eacc5546af32	0.001757	0.041005	0.023658	-0.08002	-0.25956	-0.23066	1	0.018377	0.109569	226	225	225
2017	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Coprococcus 3 , s__uncultured bacterium , efc5b27119b872096124c1f77e3837db	0.018688	0.077212	0.081601	-0.13043	-0.33395	-0.3854	1	6.54E-05	4.98E-07	226	225	225
2017	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnoclostridium 10 , s__uncultured bacterium , b64826495fc83c6140b1c86abd222201	0.002108	0.005604	0.006901	0.151616	0.202635	0.277838	1	0.507503	0.005307	226	225	225
2017	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Tyzzerella 3 , s__uncultured rumen bacterium , ebdd9551834b21f202410ad555805be5	0.004005	0.034067	0.041295	-0.1439	-0.2333	-0.32614	1	0.09393	0.000127	226	225	225
2017	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group , , 35252cd698224c71c910904c42d3f017	0.006952	0.019244	0.016638	0.167225	0.223197	0.256829	1	0.167939	0.021955	226	225	225
2017	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group , s__uncultured bacterium , d76904084359ae3ec664c1f460423bc4	0.050988	0.048401	0.02988	-0.23884	-0.27748	-0.24718	0.065773	0.005443	0.040534	226	225	225
2017	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group , s__uncultured bacterium , e78fae7e795a110a3d0552f48c6f3778	0.008167	0.065164	0.07384	0.125568	0.244469	0.273377	1	0.047948	0.007246	226	225	225
2017	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae NK4A214 group , s__uncultured bacterium , 24adfd04805b5bf0804d7c6843c49524	0.03713	0.024098	0.044086	0.195504	0.154915	0.262456	0.715145	1	0.015183	226	225	225
2017	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae NK4A214 group , s__uncultured bacterium , eef237868deb059c696bdc15f925e43b	0.014376	0.022064	0.032955	-0.1522	-0.16138	-0.29023	1	1	0.002171	226	225	225
2017	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , , 14f43ef69a9c221129271f49a6bbf29d	0.016328	0.040132	0.050284	0.153845	0.199638	0.258554	1	0.591243	0.019626	226	225	225
2017	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , , 3a1a2997703e40d77585a449a6e78134	0.012493	0.027932	0.044181	-0.09495	-0.18928	-0.29837	1	0.986036	0.00118	226	225	225
2017	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , s__uncultured rumen bacterium , 48f1e8cf3e520701d22faf7ce9a53c4e	0.025334	0.073835	0.110643	0.168724	0.220293	0.249907	1	0.197553	0.034169	226	225	225
2017	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , s__uncultured Ruminococcaceae bacterium , 0a7e34e68bffaec4e495b31786b31c0d	0.020005	0.021634	0.01316	0.278548	0.275669	0.292594	0.00486	0.006179	0.001823	226	225	225
2017	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , s__uncultured Ruminococcaceae bacterium , b867ec33eb48cd092e2e6dcc4d00d9c3	0.03612	0.03682	0.040106	0.21382	0.213252	0.253491	0.275801	0.290381	0.027218	226	225	225

2017	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , 17c9e8abd586ece0513aced0ea7ed577	0.011499	0.03627	0.051727	0.162283	0.240069	0.255211	1	0.062721	0.024374	226	225	225
2017	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , 3cf6f7fd518dbd251dba5e6a7126d3bb	0.007353	0.0186	0.02542	0.153119	0.191368	0.249905	1	0.891343	0.034174	226	225	225
2017	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , fe27bc4f741e069fc11654baa029f59f	0.014642	0.043452	0.048912	0.150876	0.197339	0.252131	1	0.663779	0.029682	226	225	225
2017	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcus 1 , s__uncultured bacterium , 0eedd0f89cc92e032578905bde583193	0.028066	0.091734	0.180519	0.209651	0.239298	0.257273	0.345027	0.065713	0.021331	226	225	225
2017	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcus 2 , , 5c80af11236e9dbe24572626ca860d27	0.044959	0.043087	0.036755	-0.22644	-0.24795	-0.25359	0.136437	0.038626	0.027039	226	225	225
2017	Level , p__Firmicutes , c__Negativicutes , o__Selenomonadales , f__Acidaminococcaceae , g__Phascolarctobacterium , s__uncultured Veillonellaceae bacterium , 43c44256ecd605ae8c670ac3dead8fea	0.020375	0.007797	0.007122	0.184501	0.218872	0.244237	1	0.213724	0.048639	226	225	225
2017	Level , p__Planctomycetes , c__Planctomycetacia , o__Pirellulales , f__Pirellulaceae , g__p-1088-a5 gut group , s__uncultured bacterium , 53ab9d2256ec104ad802edd822fa6eea	0.004264	0.016575	0.017218	-0.13012	-0.21985	-0.27779	1	0.202454	0.005325	226	225	225
2017	Level , p__Planctomycetes , c__Planctomycetacia , o__Pirellulales , f__Pirellulaceae , g__p-1088-a5 gut group , s__uncultured bacterium , c320f7e5d90b6cec1456bbd956ab8a8c	0.005939	0.018514	0.035945	0.085436	0.201453	0.251995	1	0.539149	0.029939	226	225	225
2017	Level , p__Spirochaetes , c__Spirochaetia , o__Spirochaetales , f__Spirochaetaceae , g__Treponema 2 , s__uncultured bacterium , 06fb1a72c5c93904cdf18e71b84e5fba	0.006212	0.038908	0.067446	0.068452	0.230345	0.262925	1	0.111609	0.014719	226	225	225
2017	Level , p__Spirochaetes , c__Spirochaetia , o__Spirochaetales , f__Spirochaetaceae , g__Treponema 2 , s__uncultured bacterium , 6619eb4628f7f376558c6a9427bd24cc	0.007883	0.041217	0.04682	0.068264	0.227667	0.259702	1	0.130268	0.018205	226	225	225
2017	Level , p__Tenericutes , c__Mollicutes , o__Izimaplasmatales , f__gut metagenome , g__gut metagenome , s__gut metagenome , 846fddf565d24f0c9e77b3bd92f7cad0	0.004445	0.011896	0.022237	0.155056	0.248867	0.290758	1	0.036478	0.002089	226	225	225
2017	Level , p__Tenericutes , c__Mollicutes , o__Mollicutes RF39 , , , , 02f112286be3e1d1c3ad712de887546b	0.034388	0.038975	0.034914	0.233045	0.238015	0.274059	0.092938	0.070984	0.006912	226	225	225
2018	Level , p__Actinobacteria , c__Actinobacteria , o__Micrococcales , f__Micrococcaceae , g__Arthrobacter , , 0c3cfeb668abf80ab2fa7db967ad446d	0.031236	0.025919	0.019378	-0.11909	-0.26223	-0.29611	1	0.103294	0.017068	167	167	167
2018	Level , p__Actinobacteria , c__Actinobacteria , o__Micrococcales , f__Micrococcaceae , g__Arthrobacter , , 78fe427154e97652282bb3816b0cb548	0.043012	0.039857	0.034424	-0.09303	-0.23375	-0.27752	1	0.394826	0.047158	167	167	167
2018	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 9def80b81f4d74edcf03f40e25596f96	0.038956	0.100902	0.098482	0.173693	0.282333	0.318178	1	0.036485	0.004652	167	167	167
2018	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , s__uncultured bacterium , 5d1315329b7e125ce9f78391c0411525	0.016657	0.095791	0.04855	0.177625	0.285494	0.260757	1	0.030753	0.111105	167	167	167
2018	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , s__uncultured bacterium , cb0be1adbef8a093692b519ff7612dfb	0.027094	0.054784	0.043354	0.193421	0.279794	0.247623	1	0.041793	0.209384	167	167	167
2018	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-013 , s__uncultured bacterium , f9108f7b1a28bd62f9fd39ecbde49f1b	0.016328	0.018149	0.016353	0.16233	0.233605	0.278081	1	0.397303	0.045771	167	167	167
2018	Level , p__Proteobacteria , c__Gammaproteobacteria , o__Betaproteobacteriales , f__Burkholderiaceae , g__Delftia , , 3259e7445475eebc79d267126760b2d6	0.081963	0.04781	0.025252	-0.25455	-0.30075	-0.28343	0.150478	0.013097	0.034383	167	167	167
2019	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 2cb542b093102fdc46852ed96813952d	0.006206	0.02254	0.376971	0.028168	0.274642	0.595975	1	1	0.010214	32	32	32
2019	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , e07d8b8733c1dea20b81cdf974f1b834	0.008321	0.059494	0.50543	0.028182	0.277986	0.596285	1	1	0.010122	32	32	32
2019	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Marvinbryantia , , 5d5f16dbc10db37b21b3a3e19d150788	0.008321	0.059494	0.50543	0.028182	0.277986	0.596285	1	1	0.010122	32	32	32
2019	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae NK4A214 group , , a0b0bbc9821580e52c0133ba4732bb42	0.015563	0.218578	0.195808	0.114681	0.494321	0.54268	1	0.128993	0.042624	32	32	32
2019	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae NK4A214 group , s__uncultured bacterium , 7f6f95fb40c69b9e48f5c2ffad4d97f2	0.042454	0.231175	0.268732	0.212358	0.408536	0.536249	1	0.648462	0.04986	32	32	32
2019	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , 34ff4b3ade536446df58d456746bc360	0.002419	0.073203	0.285149	-0.05369	0.28104	0.536249	1	1	0.04986	32	32	32
2019	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-013 , s__uncultured bacterium , c890805c56cd7f4b33d20fa098b57cb8	0.213958	0.015415	0.011935	0.59904	0.127528	-0.05591	0.009336	1	1	32	32	32
2015_PostWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Christensenellaceae , g__Christensenellaceae R-7 group , s__uncultured prokaryote , 6b5007ffeea03955e21a333ffbeca617	0.151227	0.012985	0.015803	0.709645	-0.07816	0.060903	0.009149	1	1	20	20	20

2015_PostWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 8df8651bddbd747ee536d321428120f9	0.143516	0.08906	0.473127	0.292341	0.280682	0.655289	1	1	0.034229	20	20	20
2015_PostWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , c39dcf11813994c2c56444ab03bb9854	0.215175	0.124299	0.50685	0.36271	0.351546	0.715571	1	1	0.007785	20	20	20
2015_PostWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Papillibacter , s__uncultured bacterium , 0e6952efdc3fb4e094174d0d0799b775	0.277491	0.082121	0.002599	0.697445	-0.0338	0.148102	0.012604	1	1	20	20	20
2015_PostWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , fe27bc4f741e069fc11654baa029f59f	0.245577	0.060941	0.015682	0.726075	0.047325	0.16138	0.005791	1	1	20	20	20
2015_PostWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-013 , s__uncultured bacterium , 5429fc62e8cd8ac4a8dd5392f36eb82d	0.031277	0.111976	0.343099	0.186985	0.387612	0.668202	1	1	0.025621	20	20	20
2015_PreWinter	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__uncultured , g__uncultured bacterium , s__uncultured bacterium , f806136c6bb583e214457f2649a40861	4.20E-06	0.053489	0.066025	0.110498	0.316787	0.391633	1	0.351476	0.028296	79	79	79
2015_PreWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Intestinimonas , , 91223ec5064454a1134c9d67dffa8f34	0.097362	0.00633	9.03E-05	-0.42357	-0.14546	-0.07977	0.007936	1	1	79	79	79
2015_PreWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-014 , s__unidentified rumen bacterium JW32	1.80E-06	0.006976	0.015741	0.135137	0.318339	0.400626	1	0.33558	0.020035	79	79	79
2016_PostWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Faecalibacterium , , 38d04a8c957eaede278db809b89d2e77	0.002774	0.123567	0.046167	-0.04519	0.453108	0.254691	1	0.018512	1	59	59	59
2016_PostWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , , 5eef6e3161171e33f388ab3880aea291	0.002128	0.111146	0.191774	0.055132	0.26716	0.423921	1	1	0.048404	59	59	59
2016_PreWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 76314928d015d16b68bb07ed7c1e21b7	0.000711	0.008677	0.009136	0.162905	0.26295	0.277956	1	0.063087	0.030662	178	181	178
2016_PreWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__uncultured , s__uncultured rumen bacterium 4C0d-17 , 4f9d66c2156036c80c8a5482cca688e7	0.021772	0.005116	0.027849	0.197266	0.198081	0.272597	1	1	0.041315	178	181	178
2017_PostWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Peptostreptococcaceae , g__Romboutsia , s__uncultured bacterium , 3670d267896c76b16273a832e54a2b7c	0.134309	0.077756	0.016616	-0.40923	-0.25024	-0.16503	0.003636	1	1	95	95	95
2017_PostWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Oscillibacter , s__uncultured bacterium , 9d4c289bdb1187800d8d26b2e79c3141	0.031735	0.070701	0.158428	0.186631	0.280168	0.351142	1	0.566345	0.04606	95	95	95
2017_PostWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae NK4A214 group , , a0b0bbc9821580e52c0133ba4732bb42	0.008166	0.023073	0.041512	0.179653	0.282981	0.392831	1	0.518508	0.007816	95	95	95
2017_PreWinter	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides , s__uncultured Bacteroides sp. , 5e34611a72e7b6239039b8c404dd5595	0	0.074065	0.0643	-0.07507	-0.3089	-0.31955	1	0.045389	0.02739	131	130	130
2017_PreWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Intestinimonas , s__uncultured bacterium , 4b450c09e18572f11046ee84ae7db8aa	0.000873	0.037655	0.028618	-0.07755	-0.31446	-0.30505	1	0.034941	0.054225	131	130	130
2017_PreWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminiclostridium 9 , s__Colidextribacter massiliensis , 7ea417aef7384868d35d18f4b6ca04e9	1.70E-06	0.033057	0.033803	-0.06326	-0.29253	-0.33911	1	0.095167	0.010299	131	130	130
2017_PreWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae NK4A214 group , s__uncultured rumen bacterium , ae8855dfdf478e5b3a59664ed9c30743	0.004231	0.092941	0.077837	-0.09037	-0.37482	-0.38421	1	0.00145	0.000832	131	130	130
2017_PreWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-002 , s__uncultured bacterium , 1023461f5893d13cfdabbd37580aef33	0.023964	0.063019	0.077077	-0.26063	-0.27652	-0.33254	0.346082	0.188363	0.014412	131	130	130
2017_PreWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , s__uncultured Ruminococcaceae bacterium , 0a7e34e68bffaec4e495b31786b31c0d	0.016901	0.005143	0.001307	0.342622	0.186888	0.186074	0.008095	1	1	131	130	130
2018_PostWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , bdfd51e4ee9933559261ff98abfcb5e1	0.007587	0.210028	0.380854	0.304206	0.45145	0.502833	1	0.083411	0.019401	45	45	45
2018_PostWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Shuttleworthia , s__uncultured bacterium , a806f6a5d38a9a21dce89cb969852214	0.100651	0.227798	0.050229	-0.36863	-0.5021	-0.31992	0.572121	0.01984	1	45	45	45
2018_PostWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminiclostridium 1 , s__uncultured bacterium , fca3a27e0fe28ae34652d1b9f7c59a5f	0.258227	0.209689	0.220004	0.520881	0.492587	0.531006	0.010984	0.026431	0.00787	45	45	45
2018_PostWinter	Level , p__Proteobacteria , c__Alphaproteobacteria , o__Acetobacterales , f__Acetobacteraceae , g__Roseomonas , s__Roseomonas ludipueritiae , d65ac55e38188ad863c0586dd00d524a	0.226968	0.017928	0.001685	0.513926	0.256145	0.243053	0.013728	1	1	45	45	45
2018_PreWinter	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Prevotellaceae , g__Prevotellaceae UCG-004 , s__uncultured bacterium , 415406680b4f6ebe91936977ea5f1e48	0.01858	0.096852	0.112838	0.076012	0.311075	0.329544	1	0.05948	0.025632	122	122	122
2018_PreWinter	Level , p__Spirochaetes , c__Spirochaetia , o__Spirochaetales , f__Spirochaetaceae , g__Treponema 2 , s__uncultured bacterium , 6619eb4628f7f376558c6a9427bd24cc	0.006822	0.091045	0.113135	-0.02944	0.318524	0.353617	1	0.042631	0.007876	122	122	122

2019_PostWinter	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides , , fe2e425ff10e99c7bd12697e09e4ce67	0.014809	0.155326	0.155871	0.157402	0.457152	0.540861	1	0.272864	0.044571	32	32	32
2019_PostWinter	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Barnesiellaceae , g__uncultured , s__uncultured Porphyromonadaceae bacterium , acf4482133d9a6ac65607f0b7916f896	0.053856	0.207774	0.516112	0.192027	0.257352	0.59769	1	1	0.009714	32	32	32
2019_PostWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 2cb542b093102fdc46852ed96813952d	0.005288	0.014876	0.321188	0.028168	0.274642	0.595975	1	1	0.010214	32	32	32
2019_PostWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , , , a664b1d386d2a0a0f825514940f8b38f	0.012664	0.120999	0.293598	0.103208	0.380204	0.536249	1	1	0.04986	32	32	32
2019_PostWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae NK4A214 group , , a0b0bbc9821580e52c0133ba4732bb42	0.08407	0.263306	0.156405	0.2258	0.512807	0.541607	1	0.08609	0.043764	32	32	32
2019_PostWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae NK4A214 group , s__uncultured bacterium , 7f6f95fb40c69b9e48f5c2ffad4d97f2	0.035097	0.209221	0.285375	0.212358	0.408536	0.536249	1	0.648462	0.04986	32	32	32
2019_PostWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-009 , s__uncultured bacterium , 6b30d20342ff8ed12379a07e1d01f587	0.007439	0.036694	0.451875	0.028168	0.274642	0.595975	1	1	0.010214	32	32	32
2019_PostWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , , 8bc67c5c6e762b15ca6a281e8d82fa35	0.000576	0.013798	0.285375	-0.05369	0.175479	0.536249	1	1	0.04986	32	32	32
2019_PostWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , 8ad28808b394163393ca95ed22f8a4b1	0.018666	0.190993	0.399024	0.108049	0.3112	0.595975	1	1	0.010214	32	32	32
2019_PostWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , a0f88f9875f2d2c51997b4c0877e7de6	0.005388	0.015631	0.327305	0.028168	0.274642	0.595975	1	1	0.010214	32	32	32
2019_PostWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-013 , s__uncultured bacterium , 6bdece54ce89a8f63e1a1dbafac3e1ff	0.001134	0.07274	0.293598	-0.05369	0.28104	0.536249	1	1	0.04986	32	32	32
2019_PostWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-013 , s__uncultured bacterium , cdda125799871dc50c40d6f871e825d4	0.006569	0.073875	0.399024	0.028168	0.28104	0.595975	1	1	0.010214	32	32	32
2019_PostWinter	Level , p__Verrucomicrobia , c__Verrucomicrobiae , o__Verrucomicrobiales , f__Akkermansiaceae , g__Akkermansia , s__uncultured bacterium , fc39e03f567b300f5ba14e43a58ef063	0.214636	0.046135	0.025677	-0.55064	-0.29164	-0.22798	0.034953	1	1	32	32	32
Adult	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides , s__uncultured Bacteroides sp. , 5d815d63e66ea05ff63fdb7d373ab89d	0.000338	0.010329	0.008588	0.04703	0.150276	0.15686	1	0.023459	0.010627	761	763	760
Adult	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Muribaculaceae , g__uncultured bacterium , s__uncultured bacterium , 20e4028000d0bdf4ddb8b4d6d7236258	0.002783	0.010941	0.010656	0.081779	0.16238	0.153201	1	0.004995	0.016868	761	763	760
Adult	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Muribaculaceae , g__uncultured bacterium , s__uncultured bacterium , 612b1eac3e95c5ad3f38048179efa072	5.01E-05	0.015087	0.01732	0.02352	0.173985	0.168455	1	0.001016	0.002292	761	763	760
Adult	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Muribaculaceae , g__uncultured bacterium , s__uncultured bacterium , e70e6f1be806650d3cbe3bb7b588dd6e	0.005861	0.007242	0.005755	0.094077	0.194664	0.169728	1	4.54E-05	0.001924	761	763	760
Adult	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Prevotellaceae , g__Prevotellaceae UCG-004 , s__uncultured bacterium , 19d31b001318d82f6e59d1a478ef8a80	0.009855	0.012942	0.011458	0.162825	0.154398	0.150683	0.00483	0.014033	0.023044	761	763	760
Adult	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Prevotellaceae , g__Prevotellaceae UCG-004 , s__uncultured bacterium , 415406680b4f6ebe91936977ea5f1e48	0.025312	0.027371	0.027248	0.185621	0.241322	0.244411	0.000191	1.09E-08	6.42E-09	761	763	760
Adult	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__dgA-11 gut group , s__uncultured bacterium , 151676c9cd991889ffb561d84b8eec23	0.01734	0.001287	0.001709	0.151834	0.074363	0.086345	0.019776	1	1	761	763	760
Adult	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , s__uncultured Bacteroidales bacterium , 2cdeaee65031b825a1165c1e7ac2fc2d	0.009146	0.010572	0.014163	0.126535	0.141073	0.146257	0.355438	0.070429	0.039399	761	763	760
Adult	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , s__uncultured Bacteroidales bacterium , 4d2656901ad4babf34990d43497a2bca	0.010122	0.007409	0.005496	0.106151	0.148097	0.140878	1	0.030614	0.07408	761	763	760
Adult	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , s__uncultured Bacteroidales bacterium , 4f916b9e6d00b0b7dfbc82f1768beb72	0.007228	0.006231	0.005835	0.119149	0.167009	0.17204	0.753807	0.002681	0.001396	761	763	760
Adult	Level , p__Cyanobacteria , c__Melainabacteria , o__Gastranaerophilales , , , , 10304c2abda761627220b6f202cf0f40	0.000601	0.019435	0.017873	0.026314	0.142088	0.146366	1	0.062588	0.038889	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Christensenellaceae , g__Christensenellaceae R-7 group , , f8a30689dee232805c05ee738a3b47bf	0.022968	0.011504	0.009548	0.194052	0.186654	0.227105	5.19E-05	0.000158	1.82E-07	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 467b4334451ebbd88fec172eac048e0e	0.014558	0.00262	0.001144	0.161567	0.140614	0.143889	0.005703	0.074279	0.052168	761	763	760

Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 523c9229e6cdf0b04cb2551794041d34	0.006767	0.023148	0.010258	0.088626	0.172155	0.144538	1	0.001316	0.048323	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 5489c2eaf6c505895fcb2870091af37f	0.002907	0.002241	0.003914	0.097823	0.1182	0.151591	1	0.817438	0.020604	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 5b5ece78a87c22d7da8a3377a00cd2f8	0.008648	0.022713	0.016057	0.113015	0.15291	0.157158	1	0.01692	0.010229	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 657b53eec5cc03a34d4d673a58c65689	0.011778	0.009442	0.008764	0.121463	0.147954	0.163483	0.598234	0.031152	0.004483	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 76314928d015d16b68bb07ed7c1e21b7	0.000443	0.00893	0.010087	0.112585	0.21321	0.227519	1	2.07E-06	1.69E-07	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 867a9dbf65311fbccb6cc0e204049ed7	0.027193	0.026545	0.028357	-0.14407	-0.14836	-0.15206	0.050589	0.029667	0.019448	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 8df8651bddbd747ee536d321428120f9	0.011943	0.016293	0.014859	-0.16192	-0.16191	-0.17181	0.005443	0.005318	0.001441	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , bad7e742798b5fcc520ff82e75b256a9	0.034679	0.038901	0.040259	-0.23449	-0.2433	-0.27228	4.39E-08	7.34E-09	1.67E-11	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , bdfd51e4ee9933559261ff98abfcb5e1	0.002966	0.019881	0.020604	0.160384	0.20272	0.20724	0.00666	1.23E-05	6.15E-06	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , bf49a90284d596106b657efe32d36dd9	0.00348	0.002558	0.002144	0.106844	0.150797	0.164981	1	0.022	0.00367	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , cad5af3533fcd506a12e6794a4722d04	0.008051	0.004345	0.006583	-0.14508	-0.08982	-0.12437	0.044891	1	0.448079	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae XPB1014 group , , d3d62061e77c8e7e87fca28a6d89ac53	0.002299	0.008905	0.009712	0.072033	0.156991	0.170981	1	0.010088	0.001618	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Syntrophococcus , s__uncultured rumen bacterium , b3335be5b925014b97454ca38c3bf5ef	0.017552	0.010377	0.010426	-0.15075	-0.13476	-0.14004	0.022604	0.144152	0.081588	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Tyzzerella 3 , s__uncultured rumen bacterium , ebdd9551834b21f202410ad555805be5	0.005334	0.013719	0.016567	-0.12783	-0.17052	-0.2191	0.310402	0.001653	7.84E-07	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , , , 5dad1dc79c35f84ce8cae394d8a91b73	0.011905	0.018839	0.013452	0.153612	0.203885	0.196581	0.015845	1.01E-05	3.54E-05	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , , , 6fb8eb193f5d0673db6bd7c380ad98c6	0.022596	0.013933	0.024335	0.155733	0.130578	0.150513	0.012125	0.227884	0.023529	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , , , 935c2b2e0d3a4b87b5a140288ebe95e3	0.011462	0.016479	0.016617	0.148674	0.112167	0.123192	0.029145	1	0.505502	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , , , fffd39a0a31309c0234a9e0da2ec9449	0.020088	0.016686	0.014636	0.148511	0.103346	0.108899	0.029729	1	1	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group , , 0ad791d40c0601fdfb6947d17c4c4372	0.000695	0.000541	0.000347	0.124996	0.16344	0.155469	0.417122	0.004338	0.012683	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group , , 35252cd698224c71c910904c42d3f017	0.008718	0.00486	0.003421	0.189989	0.192661	0.198874	9.80E-05	6.23E-05	2.45E-05	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group , , 67c46fdb2e3ec08a9ffb3a207124ff72	0.00255	0.009293	0.008466	0.080058	0.145885	0.154476	1	0.039964	0.014377	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group , , d0f21207086935b1aaa9a1c905af19f1	0.003031	0.00117	0.002633	0.120514	0.118122	0.150441	0.658066	0.823728	0.023738	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group , s__uncultured bacterium , 9e7318bcf7eeb3491ad16ecc05bd6b58	0.006124	0.013328	0.012793	0.086702	0.14818	0.146758	1	0.03031	0.037107	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group , s__uncultured bacterium , e89b812979716c96d01b6162a152c846	0.008592	0.028172	0.02469	0.096124	0.178239	0.171573	1	0.000552	0.00149	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__GCA-900066225 , , 3174faaa3f054fd27f6c7bd82356f33a	0.01684	0.005766	0.006071	-0.16873	-0.13627	-0.14655	0.002176	0.12177	0.03805	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Intestinimonas , , 91223ec5064454a1134c9d67dffa8f34	0.013144	0.020777	0.017852	0.135379	0.176588	0.166498	0.13689	0.000701	0.002992	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Negativibacillus , s__uncultured bacterium , 2c263f2dff6c02138180d8d1c5d57cb5	0.003825	0.005471	0.007504	0.092496	0.153452	0.166825	1	0.015807	0.002862	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Oscillibacter , s__uncultured bacterium , 8c037ab6aac2ee433ec5bcf766480efe	0.01333	0.011373	0.00964	-0.12698	-0.14338	-0.1601	0.339275	0.053777	0.006993	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminiclostridium 9 , , d136306da31f27b197b563aa866114e2	0.012317	0.016442	0.015965	0.144262	0.170103	0.173329	0.049441	0.001752	0.001165	761	763	760

Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae NK4A214 group , s__uncultured bacterium , 24adfd04805b5bf0804d7c6843c49524	0.012034	0.014054	0.020497	0.124159	0.157426	0.192094	0.454699	0.009539	7.19E-05	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae NK4A214 group , s__uncultured bacterium , eef237868deb059c696bdc15f925e43b	0.02084	0.015017	0.014816	-0.16072	-0.15118	-0.19943	0.00637	0.020979	2.24E-05	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , , 14f43ef69a9c221129271f49a6bbf29d	0.03531	0.020301	0.025706	0.197673	0.16913	0.196679	2.92E-05	0.002004	3.49E-05	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , , 3a1a2997703e40d77585a449a6e78134	0.021372	0.021531	0.019649	-0.11128	-0.15334	-0.17426	1	0.016038	0.001022	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , , 643af4b801bb60813fd7dcfaf7e209ff	0.015707	0.013758	0.010791	0.161554	0.194661	0.190579	0.005712	4.54E-05	9.10E-05	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , , b0d148c179e7590ffeb4f5701ab388ac	0.003616	2.75E-05	8.31E-05	0.156137	0.083529	0.102772	0.011517	1	1	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , s__uncultured bacterium , 5d1315329b7e125ce9f78391c0411525	0.011879	0.033659	0.030183	0.108394	0.166926	0.152181	1	0.002712	0.019153	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , s__uncultured bacterium , 7adcbba7d451427c8e384471fb4d9b80	0.003207	0.000744	0.001622	-0.11622	-0.11813	-0.14465	1	0.82319	0.04771	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , s__uncultured bacterium , cb0be1adbef8a093692b519ff7612dfb	0.021561	0.009319	0.008548	0.163066	0.116632	0.135353	0.004678	0.953143	0.138455	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , s__uncultured Ruminococcaceae bacterium , 0a7e34e68bffaec4e495b31786b31c0d	0.012532	0.012402	0.007475	0.218402	0.193774	0.203296	8.67E-07	5.23E-05	1.19E-05	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , s__uncultured Ruminococcaceae bacterium , b867ec33eb48cd092e2e6dcc4d00d9c3	0.01199	0.01188	0.009481	0.134139	0.149142	0.165953	0.157051	0.026956	0.00322	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , , 6f6af6e1fa18c9ff48f621aa88547fe3	0.012286	0.011471	0.007762	0.098874	0.161865	0.133895	1	0.005347	0.162674	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , 06fba16f3d8a8d7248e32043d246d7db	0.010671	0.015187	0.005825	0.113044	0.146849	0.122331	1	0.035598	0.551707	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , 3cf6f7fd518dbd251dba5e6a7126d3bb	0.027278	0.014718	0.009087	0.219005	0.194776	0.20513	7.78E-07	4.46E-05	8.76E-06	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , fe27bc4f741e069fc11654baa029f59f	0.010563	0.02446	0.019947	0.130897	0.185232	0.186071	0.22367	0.000196	0.000181	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , ffb81be0f493cef5f436913cf7f89fac	0.013331	0.010306	0.007651	0.156196	0.15197	0.141817	0.011431	0.019024	0.066457	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured Ruminococcaceae bacterium , 4527170be8e5e15c661c7b4e1b96fbb2	0.018425	0.017384	0.020218	0.133165	0.168926	0.169875	0.174804	0.002062	0.001886	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-013 , s__uncultured bacterium , 04a0ffb69d9670c5cf62a2f436d27b98	0.023202	0.015429	0.009931	-0.18587	-0.18459	-0.19472	0.000184	0.000216	4.76E-05	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-013 , s__uncultured bacterium , 919c896da2430a031fd8cddd44df39be	0.016	0.018076	0.019318	0.123771	0.141724	0.160062	0.4732	0.065305	0.007031	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-013 , s__uncultured bacterium , ee2e47eef6b792e2754bdd4970452a07	0.000584	0.009403	0.003679	0.03932	0.145275	0.133516	1	0.042983	0.169595	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-014 , , 47b9b0ed577f9a81a42fb4a44242c98b	0.000249	0.014312	0.015342	-0.03527	-0.14369	-0.1538	1	0.051842	0.015652	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-014 , , 5216b09776e2e3e8d020f51e9eda13a8	0.008069	0.011823	0.009011	0.125078	0.16062	0.169939	0.413619	0.0063	0.001869	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-014 , , 8bf3dd6e298b7ca2ccba11e1fa45191c	0.005662	0.01503	0.00969	-0.08988	-0.16246	-0.15697	1	0.004939	0.010485	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-014 , s__uncultured rumen bacterium , f0bdde976b450093645a7190731566a9	0.000981	0.003985	0.003544	0.105932	0.187144	0.192076	1	0.000146	7.21E-05	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-014 , s__unidentified , 8c007ef3ada9cee8a897aa0393e77d24	0.009237	0.026359	0.02747	0.102765	0.147437	0.157302	1	0.033161	0.010043	761	763	760
Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcus 1 , , c196274bb1694853b1e3defc904b97b4	0.004967	0.010897	0.018744	0.095829	0.132225	0.152966	1	0.190592	0.017371	761	763	760

Adult	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcus 2 , s__uncultured rumen bacterium , 9c05fa86e3062f1150c232747186350d	0.006982	0.014581	0.010635	0.140879	0.186222	0.177366	0.073385	0.000169	0.000656	761	763	760
Adult	Level , p__Firmicutes , c__Negativicutes , o__Selenomonadales , f__Acidaminococcaceae , g__Phascolarctobacterium , s__uncultured Veillonellaceae bacterium , 43c44256ecd605ae8c670ac3dead8fea	0.005049	0.000928	0.00134	0.116583	0.124191	0.152814	0.969477	0.446896	0.017703	761	763	760
Adult	Level , p__Planctomycetes , c__Planctomycetacia , o__Pirellulales , f__Pirellulaceae , g__p-1088-a5 gut group , s__uncultured bacterium , 53ab9d2256ec104ad802edd822fa6eea	0.014911	0.01173	0.011055	-0.10056	-0.11997	-0.1531	1	0.685882	0.017083	761	763	760
Adult	Level , p__Spirochaetes , c__Spirochaetia , o__Spirochaetales , f__Spirochaetaceae , g__Treponema 2 , s__uncultured bacterium , 6619eb4628f7f376558c6a9427bd24cc	0.008724	0.018925	0.020954	0.047356	0.172333	0.17502	1	0.001283	0.000917	761	763	760
Adult	Level , p__Tenericutes , c__Mollicutes , o__Mollicutes RF39 , f__uncultured bacterium , g__uncultured bacterium , s__uncultured bacterium , cf172bbb51cb13d1532d9ed534c108d2	0.01247	0.015092	0.009352	-0.146	-0.18795	-0.19678	0.040211	0.000129	3.43E-05	761	763	760
All	Level , p__Actinobacteria , c__Actinobacteria , o__Bifidobacteriales , f__Bifidobacteriaceae , g__Aeriscardovia , s__uncultured bacterium , dccfc97f0380b1552ca04c9123f05c6c	0.004259	0.016448	0.009488	0.0876	0.140113	0.118996	1	0.042413	0.500886	828	830	827
All	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Muribaculaceae , g__uncultured bacterium , s__uncultured bacterium , 20e4028000d0bdf4ddb8b4d6d7236258	0.005098	0.007604	0.006719	0.092825	0.15337	0.146655	1	0.007531	0.018988	828	830	827
All	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Muribaculaceae , g__uncultured bacterium , s__uncultured bacterium , 612b1eac3e95c5ad3f38048179efa072	0.000426	0.012867	0.01618	0.035861	0.181413	0.172678	1	0.000118	0.000484	828	830	827
All	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Muribaculaceae , g__uncultured bacterium , s__uncultured bacterium , e70e6f1be806650d3cbe3bb7b588dd6e	0.004489	0.005643	0.003936	0.092679	0.183059	0.154591	1	9.06E-05	0.006596	828	830	827
All	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Prevotellaceae , g__Prevotellaceae UCG-004 , s__uncultured bacterium , 19d31b001318d82f6e59d1a478ef8a80	0.012515	0.009369	0.009408	0.178206	0.162781	0.169678	0.000203	0.002015	0.000762	828	830	827
All	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Prevotellaceae , g__Prevotellaceae UCG-004 , s__uncultured bacterium , 415406680b4f6ebe91936977ea5f1e48	0.024516	0.02874	0.029383	0.190094	0.241144	0.251055	2.94E-05	1.58E-09	1.95E-10	828	830	827
All	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Prevotellaceae , g__Prevotellaceae UCG-004 , s__uncultured bacterium , 800cbb4cdf5b762aa3747cd38db617ff	0.001505	0.002396	0.004263	0.113543	0.131432	0.158497	0.881542	0.121411	0.003844	828	830	827
All	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Prevotellaceae , g__Prevotellaceae UCG-004 , s__uncultured bacterium , c9953823fc07cf9230750e75b981e213	0.003529	0.006259	0.007985	0.075313	0.11201	0.139385	1	1	0.04773	828	830	827
All	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__dgA-11 gut group , s__uncultured bacterium , 151676c9cd991889ffb561d84b8eec23	0.01627	0.00122	0.002254	0.150077	0.053777	0.067832	0.011986	1	1	828	830	827
All	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , s__uncultured Bacteroidales bacterium , 4d2656901ad4babf34990d43497a2bca	0.009774	0.00807	0.005324	0.097647	0.155418	0.148119	1	0.005689	0.015685	828	830	827
All	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , s__uncultured Bacteroidales bacterium , 4f916b9e6d00b0b7dfbc82f1768beb72	0.006365	0.008493	0.008995	0.117562	0.170733	0.178031	0.579796	0.000623	0.000212	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , , , , 603b2984c0554068f813d2c08844f3e8	0.013413	0.008866	0.006386	0.141112	0.115002	0.12812	0.038136	0.749275	0.1825	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Christensenellaceae , g__Christensenellaceae R-7 group , , b0ee948362f852234206b43d4424c840	4.46E-05	0.001677	0.001818	0.074337	0.131321	0.146656	1	0.123004	0.018984	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Christensenellaceae , g__Christensenellaceae R-7 group , , f8a30689dee232805c05ee738a3b47bf	0.023005	0.011561	0.009513	0.197204	0.192951	0.227896	8.70E-06	1.75E-05	2.75E-08	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 467b4334451ebbd88fec172eac048e0e	0.01701	0.005032	0.003879	0.157919	0.146758	0.147234	0.004118	0.018169	0.01761	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 5489c2eaf6c505895fcb2870091af37f	0.004248	0.001947	0.002757	0.103658	0.117995	0.14161	1	0.546767	0.036167	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 657b53eec5cc03a34d4d673a58c65689	0.015547	0.019728	0.016675	0.112312	0.145495	0.157143	0.999633	0.021408	0.004642	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 6e8b661a46e042ac72dcfdc7b2bf1640	0.011832	0.010429	0.004857	0.130011	0.152554	0.149493	0.145633	0.008411	0.013089	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 76314928d015d16b68bb07ed7c1e21b7	0.000134	0.007316	0.007311	0.099424	0.198837	0.207125	1	6.29E-06	1.51E-06	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 867a9dbf65311fbccb6cc0e204049ed7	0.021397	0.022484	0.023402	-0.13133	-0.15156	-0.15424	0.124817	0.009615	0.00692	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 8df8651bddbd747ee536d321428120f9	0.013607	0.019332	0.018217	-0.16911	-0.15819	-0.17875	0.000818	0.003872	0.000189	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , bad7e742798b5fcc520ff82e75b256a9	0.038439	0.040904	0.040983	-0.24878	-0.25956	-0.29028	3.15E-10	2.51E-11	1.33E-14	828	830	827

All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , bdfd51e4ee9933559261ff98abfcb5e1	0.004074	0.019984	0.02121	0.157018	0.200593	0.204062	0.004668	4.61E-06	2.63E-06	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , bf49a90284d596106b657efe32d36dd9	0.00405	0.002745	0.002401	0.113141	0.141513	0.157568	0.9186	0.035587	0.004376	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Coprococcus 3 , , 780ec7a8c3d95c29e344b5a319a26c6d	0.009627	0.008347	0.007453	0.158404	0.11883	0.150778	0.003847	0.500122	0.011037	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Coprococcus 3 , s__uncultured bacterium , efc5b27119b872096124c1f77e3837db	0.002191	0.008415	0.011967	-0.03055	-0.10282	-0.14516	1	1	0.023022	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae XPB1014 group , , d3d62061e77c8e7e87fca28a6d89ac53	0.003879	0.009287	0.010796	0.073752	0.147661	0.158521	1	0.016146	0.003831	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Tyzzerella 3 , s__uncultured rumen bacterium , ebdd9551834b21f202410ad555805be5	0.011124	0.023378	0.022066	-0.15234	-0.19807	-0.23713	0.008848	7.20E-06	4.07E-09	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Tyzzerella 4 , s__uncultured bacterium , 61ae7b6ab2e57a91c9bcb98ae9bde8d8	0.004314	0.013292	0.011003	0.099161	0.130644	0.162086	1	0.133169	0.002313	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , , , 5dad1dc79c35f84ce8cae394d8a91b73	0.016041	0.020241	0.010238	0.136953	0.180887	0.161316	0.063766	0.000128	0.002582	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , , , 5e6f162e2e88970cf3c01694a92e0692	0.021204	0.001872	0.002876	0.153212	0.076246	0.08413	0.007869	1	1	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , , , 6fb8eb193f5d0673db6bd7c380ad98c6	0.025654	0.013415	0.022058	0.15242	0.145161	0.163452	0.008758	0.02235	0.001901	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , , , 935c2b2e0d3a4b87b5a140288ebe95e3	0.011281	0.026025	0.024209	0.166028	0.150727	0.167326	0.00129	0.010756	0.00108	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , , , fffd39a0a31309c0234a9e0da2ec9449	0.019187	0.017595	0.015423	0.175921	0.125591	0.136226	0.00029	0.237837	0.070264	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group , , 35252cd698224c71c910904c42d3f017	0.00987	0.00509	0.00395	0.193386	0.189715	0.18887	1.68E-05	3.02E-05	3.67E-05	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group , , d0f21207086935b1aaa9a1c905af19f1	0.004036	0.001306	0.002304	0.122316	0.117063	0.145292	0.347246	0.603618	0.022646	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group , s__uncultured bacterium , 0241c9abc5c494a335538186f7f6d8bd	0.000666	1.02E-05	0.000193	-0.14241	-0.04441	-0.05552	0.03237	1	1	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group , s__uncultured bacterium , e89b812979716c96d01b6162a152c846	0.007897	0.024978	0.019922	0.101712	0.176383	0.166097	1	0.000262	0.001294	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Candidatus Soleaferrea , s__uncultured Ruminococcaceae bacterium , 37b27c5991bb542fcaf77e178d5559dc	0.006119	0.017175	0.009854	-0.05467	-0.15377	-0.14497	1	0.007133	0.023616	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__GCA-900066225 , , 3174faaa3f054fd27f6c7bd82356f33a	0.009472	0.004444	0.004967	-0.15245	-0.12856	-0.13972	0.008722	0.16967	0.045772	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Intestinimonas , , 91223ec5064454a1134c9d67dffa8f34	0.011038	0.009978	0.008179	0.110352	0.152617	0.133683	1	0.008341	0.095359	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Negativibacillus , s__uncultured bacterium , 2c263f2dff6c02138180d8d1c5d57cb5	0.0024	0.00832	0.009894	0.079941	0.138806	0.154275	1	0.049896	0.006887	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Oscillibacter , , ef44e026034244f99ad961589cded471	0.010302	0.016926	0.015909	-0.09701	-0.13839	-0.15263	1	0.052519	0.00861	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Oscillibacter , s__uncultured bacterium , 5dd4e467291bcdfb96ebe5c3739a3b19	0.00922	0.009915	0.010377	-0.09169	-0.10031	-0.13971	1	1	0.04587	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Oscillibacter , s__uncultured bacterium , 5e8888de220cdef4f3d7fd7bb8765649	0.000468	0.009559	0.010103	0.084082	0.130004	0.144956	1	0.143489	0.023647	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Oscillibacter , s__uncultured bacterium , 8c037ab6aac2ee433ec5bcf766480efe	0.012587	0.012161	0.009758	-0.13472	-0.1517	-0.15777	0.083523	0.009437	0.004252	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminiclostridium 1 , s__uncultured bacterium , a0c0cc1fbcb3d1a239d38ea783e427b2	0.014026	0.005442	0.005527	-0.14724	-0.09441	-0.10998	0.017411	1	1	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminiclostridium 9 , , d136306da31f27b197b563aa866114e2	0.015901	0.021832	0.02314	0.130596	0.150784	0.161365	0.136053	0.010674	0.002564	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae NK4A214 group , s__uncultured bacterium , 24adfd04805b5bf0804d7c6843c49524	0.011152	0.022457	0.024241	0.116177	0.178356	0.193147	0.670846	0.000192	1.78E-05	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae NK4A214 group , s__uncultured bacterium , eef237868deb059c696bdc15f925e43b	0.024421	0.018672	0.016353	-0.17367	-0.16718	-0.20456	0.00041	0.001061	2.40E-06	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-002 ,	0.011592	0.00103	0.002702	0.15034	0.07095	0.116994	0.011573	1	0.619452	828	830	827

	s__uncultured bacterium , 3a22296adc9621145bbea6b9a982b33b												
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , , 14f43ef69a9c221129271f49a6bbf29d	0.039472	0.018288	0.022833	0.211147	0.179143	0.202053	7.01E-07	0.00017	3.77E-06	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , , 3a1a2997703e40d77585a449a6e78134	0.0229	0.02334	0.019963	-0.10514	-0.14239	-0.15942	1	0.031871	0.003379	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , , 4b09f1ee861ce88c31d75ea75d8afcda	0.008009	0.002399	0.003393	0.150444	0.137889	0.15349	0.011414	0.055867	0.007663	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , , 643af4b801bb60813fd7dcfaf7e209ff	0.013063	0.015727	0.011196	0.181701	0.216404	0.217923	0.000116	2.47E-07	1.98E-07	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , , b0d148c179e7590ffeb4f5701ab388ac	0.004701	6.18E-05	5.30E-06	0.178085	0.090606	0.117779	0.000207	1	0.570177	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , s__uncultured bacterium , 7adcbba7d451427c8e384471fb4d9b80	0.004391	0.001714	0.002638	-0.11421	-0.11356	-0.1428	0.82346	0.870267	0.031116	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , s__uncultured bacterium , c6871ddd810bed33ca43a7fcc8ef97ef	0.00714	0.002872	0.003974	0.126656	0.112649	0.141682	0.213995	0.95505	0.035842	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , s__uncultured Ruminococcaceae bacterium , 0a7e34e68bffaec4e495b31786b31c0d	0.009354	0.009596	0.005397	0.226823	0.19586	0.210229	3.33E-08	1.06E-05	8.51E-07	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , s__uncultured Ruminococcaceae bacterium , b867ec33eb48cd092e2e6dcc4d00d9c3	0.005895	0.008481	0.007203	0.139523	0.157776	0.177783	0.046492	0.004102	0.00022	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , , 6f6af6e1fa18c9ff48f621aa88547fe3	0.013133	0.018438	0.017498	0.088652	0.154567	0.141974	1	0.006395	0.034551	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , , cb63664dbe1e8b80ae021f688dbcac7c	0.009766	0.009225	0.00673	0.144769	0.11855	0.124982	0.023979	0.51535	0.26026	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , 06fba16f3d8a8d7248e32043d246d7db	0.020027	0.011551	0.004846	0.126026	0.142749	0.132382	0.229793	0.030435	0.111248	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , 3cf6f7fd518dbd251dba5e6a7126d3bb	0.02035	0.01398	0.011174	0.193487	0.191316	0.197961	1.65E-05	2.31E-05	7.77E-06	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , 58b05226e0db81427785eabe4dd537a3	0.006789	0.009044	0.010777	0.127527	0.138273	0.151297	0.193827	0.053283	0.010297	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , 9cd0c5f0e97b7b772b17a04db71a35be	0.010749	0.00601	0.005096	0.155425	0.084451	0.081906	0.005817	1	1	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , f271890d9555d0632d4e84e236514c32	0.006153	0.015394	0.008308	0.092936	0.156809	0.155035	1	0.004693	0.006208	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , fe27bc4f741e069fc11654baa029f59f	0.019126	0.034807	0.031458	0.158735	0.171784	0.175492	0.003673	0.000531	0.000315	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , ffb81be0f493cef5f436913cf7f89fac	0.006747	0.004927	0.003361	0.146351	0.124755	0.118749	0.019552	0.261266	0.514299	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured Ruminococcaceae bacterium , 4527170be8e5e15c661c7b4e1b96fbb2	0.019735	0.018061	0.021371	0.147928	0.174272	0.178386	0.015916	0.000363	0.0002	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured Ruminococcaceae bacterium , 59d7c945f9a0c393b02ed42268b2ecc9	0.003604	0.000165	0.000206	0.156943	0.075683	0.068894	0.004716	1	1	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-013 , s__uncultured bacterium , 04a0ffb69d9670c5cf62a2f436d27b98	0.022706	0.0165	0.011322	-0.18063	-0.19143	-0.18571	0.000138	2.26E-05	6.18E-05	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-014 , , 47b9b0ed577f9a81a42fb4a44242c98b	0.000785	0.013806	0.014918	-0.01347	-0.13313	-0.14591	1	0.099284	0.020909	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-014 , , 5216b09776e2e3e8d020f51e9eda13a8	0.014091	0.024034	0.018225	0.120076	0.142948	0.157196	0.443134	0.029677	0.004608	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-014 , , 8bf3dd6e298b7ca2ccba11e1fa45191c	0.008106	0.016546	0.011841	-0.1196	-0.17264	-0.16937	0.466539	0.000467	0.000797	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-014 , s__uncultured rumen bacterium , f0bdde976b450093645a7190731566a9	0.003801	0.006286	0.005079	0.106028	0.167625	0.176369	1	0.000992	0.000275	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-014 , s__unidentified , 8c007ef3ada9cee8a897aa0393e77d24	0.006059	0.018504	0.018167	0.083871	0.142718	0.144207	1	0.030558	0.026027	828	830	827

All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcus 1 , s__uncultured bacterium , 0eedd0f89cc92e032578905bde583193	0.009053	0.021064	0.037954	0.141487	0.116156	0.134868	0.036385	0.664145	0.082762	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcus 2 , s__uncultured rumen bacterium , 9c05fa86e3062f1150c232747186350d	0.007908	0.019523	0.013351	0.144166	0.187456	0.174648	0.025908	4.40E-05	0.000358	828	830	827
All	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__uncultured , s__uncultured bacterium , 5afe6c5ef01bcf7642c0834291348e74	0.013459	0.011716	0.008272	0.15006	0.114839	0.112286	0.012013	0.762094	1	828	830	827
All	Level , p__Firmicutes , c__Negativicutes , o__Selenomonadales , f__Acidaminococcaceae , g__Phascolarctobacterium , s__uncultured Veillonellaceae bacterium , 43c44256ecd605ae8c670ac3dead8fea	0.005451	0.002162	0.0024	0.120968	0.129279	0.153471	0.402312	0.156071	0.007683	828	830	827
All	Level , p__Planctomycetes , c__Planctomycetacia , o__Pirellulales , f__Pirellulaceae , g__p-1088-a5 gut group , s__uncultured bacterium , 53ab9d2256ec104ad802edd822fa6eea	0.01948	0.01843	0.016005	-0.12036	-0.13369	-0.17357	0.429952	0.092907	0.000423	828	830	827
All	Level , p__Spirochaetes , c__Spirochaetia , o__Spirochaetales , f__Spirochaetaceae , g__Treponema 2 , s__uncultured bacterium , 6619eb4628f7f376558c6a9427bd24cc	0.004017	0.010395	0.012668	0.042582	0.161253	0.162427	1	0.002509	0.002203	828	830	827
All	Level , p__Tenericutes , c__Mollicutes , o__Mollicutes RF39 , f__uncultured bacterium , g__uncultured bacterium , s__uncultured bacterium , cf172bbb51cb13d1532d9ed534c108d2	0.015354	0.018071	0.012599	-0.16734	-0.18474	-0.2086	0.001064	6.89E-05	1.15E-06	828	830	827
Cache	Level , p__Actinobacteria , c__Coriobacteriia , o__Coriobacteriales , f__Eggerthellaceae , , , 9eae5276dc67ae7da7f903cb61281ba7	0.046616	0.099462	0.082024	0.271942	0.366855	0.366545	0.243374	0.002626	0.002671	128	128	128
Cache	Level , p__Actinobacteria , c__Coriobacteriia , o__Coriobacteriales , f__uncultured , g__uncultured bacterium , s__uncultured bacterium , 3ef24da812dc1308e7638ca3e3d58447	0.035002	0.091089	0.104582	0.186717	0.321203	0.346613	1	0.027947	0.007839	128	128	128
Cache	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides , s__uncultured Bacteroides sp. , 5d815d63e66ea05ff63fdb7d373ab89d	0.00383	0.038041	0.026622	0.059865	0.312846	0.341051	1	0.041457	0.010452	128	128	128
Cache	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , , 178417778aaabd0e4afe7335a4753d70	0.063729	0.162815	0.162459	0.253517	0.309625	0.330357	0.497184	0.048116	0.017904	128	128	128
Cache	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , , b4a54ca39ab88e6a1a2d965e087bbaea	0.010267	0.010871	0.009372	0.173607	0.295001	0.32468	1	0.092657	0.023637	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Christensenellaceae , g__Christensenellaceae R-7 group , , eafd9f6c12dc2afceee988cfc4fbeb6c	0.064174	0.110412	0.103787	0.280799	0.325912	0.329959	0.169567	0.022264	0.018259	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , bad7e742798b5fcc520ff82e75b256a9	0.079293	0.137989	0.093259	-0.42175	-0.51932	-0.51499	9.11E-05	4.31E-08	6.39E-08	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae XPB1014 group , , d3d62061e77c8e7e87fca28a6d89ac53	0.021647	0.1206	0.095701	0.292077	0.356535	0.346727	0.105202	0.004628	0.007792	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , , , 5dad1dc79c35f84ce8cae394d8a91b73	0.075485	0.063459	0.047882	0.297715	0.315733	0.304883	0.082257	0.036223	0.05973	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , , , 5e6f162e2e88970cf3c01694a92e0692	0.163537	0.22523	0.208182	0.420815	0.481658	0.46083	9.70E-05	1.10E-06	5.64E-06	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , , , 935c2b2e0d3a4b87b5a140288ebe95e3	0.100366	0.123928	0.117528	0.299453	0.285367	0.312594	0.076174	0.140086	0.041946	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , , , a47e513280aa60fee2fb695f49b019b3	0.040287	0.078265	0.056601	0.233367	0.317694	0.309153	1	0.033025	0.049171	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group , , 0ad791d40c0601fdfb6947d17c4c4372	3.28E-05	0.017058	0.015605	0.210576	0.351131	0.356776	1	0.00618	0.004568	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group , , 35252cd698224c71c910904c42d3f017	0.069852	0.07386	0.062138	0.334309	0.345469	0.273652	0.014708	0.00832	0.22718	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group , s__uncultured bacterium , c65b0bd6c7f2549ba5c15aeddb753368	0.08534	0.026069	0.007846	0.322414	0.228406	0.195216	0.026369	1	1	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group , s__uncultured bacterium , e78fae7e795a110a3d0552f48c6f3778	0.071077	0.172132	0.183303	0.280599	0.322449	0.343242	0.170979	0.026325	0.009338	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Intestinimonas , , 91223ec5064454a1134c9d67dffa8f34	0.014427	0.036273	0.027131	0.199943	0.325556	0.305838	1	0.022653	0.057201	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Intestinimonas , , b0112ca7dd6152bd4943b69af95d5548	0.048152	0.015605	0.008637	0.334918	0.272782	0.230136	0.014266	0.235286	1	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Oscillibacter , s__uncultured bacterium , 613399746627c5f4075cc499502a8521	0.058119	0.124701	0.103043	0.234941	0.369826	0.335635	0.9725	0.002222	0.013761	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Oscillibacter , s__uncultured bacterium , 8c037ab6aac2ee433ec5bcf766480efe	0.047727	0.057627	0.039695	-0.23263	-0.32401	-0.29181	1	0.024417	0.106436	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae NK4A214 group , s__uncultured bacterium , 24adfd04805b5bf0804d7c6843c49524	0.048421	0.068991	0.05361	0.196823	0.336852	0.315865	1	0.012942	0.035999	128	128	128

Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae NK4A214 group , s__uncultured bacterium , 6dfb4291462e75654b7cffb4bffd9cca	0.037489	0.035087	0.009814	0.246551	0.319288	0.260624	0.643084	0.030621	0.379668	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae NK4A214 group , s__uncultured bacterium , eef237868deb059c696bdc15f925e43b	0.063482	0.05304	0.029089	-0.21913	-0.31686	-0.29688	1	0.03435	0.08532	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , , 14f43ef69a9c221129271f49a6bbf29d	0.048897	0.077697	0.061818	0.229913	0.328489	0.318719	1	0.019629	0.031459	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , , 4b09f1ee861ce88c31d75ea75d8afcda	0.085228	0.047777	0.027178	0.342467	0.369833	0.321769	0.009719	0.002221	0.027199	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , , 643af4b801bb60813fd7dcfaf7e209ff	0.033747	0.011112	0.009475	0.352836	0.304213	0.304393	0.005644	0.061565	0.061066	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , s__uncultured bacterium , 81f138623974b6263ca765135ea7eecc	0.011849	0.020039	0.009119	0.23045	0.330088	0.285808	1	0.018143	0.137505	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , s__uncultured Ruminococcaceae bacterium , 0a7e34e68bffaec4e495b31786b31c0d	0.051923	0.03931	0.019942	0.338889	0.407497	0.373193	0.011672	0.000231	0.001836	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , , 6f6af6e1fa18c9ff48f621aa88547fe3	0.014494	0.051488	0.02386	0.19318	0.320001	0.296657	1	0.029599	0.086178	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , , 8dec791b026a7eee38b463da9ea888b5	0.053987	0.040376	0.023616	0.256343	0.311795	0.313309	0.447019	0.043529	0.040572	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , , cb63664dbe1e8b80ae021f688dbcac7c	0.087215	0.054472	0.041604	0.371469	0.276261	0.266758	0.002025	0.204355	0.299047	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , , dd67c7ed8f9591a64cebfd20c4e995d8	0.043268	0.08911	0.081516	0.2688	0.346777	0.34422	0.275871	0.007772	0.008877	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , 25b49730f8da4b6647b8e526a78c2601	0.048979	0.114947	0.10587	0.218958	0.31301	0.316058	1	0.041141	0.035675	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , 3cf6f7fd518dbd251dba5e6a7126d3bb	0.109906	0.134273	0.098019	0.380174	0.398748	0.37891	0.001227	0.000401	0.001321	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , 6d8df274f92be96c184e009ae57de8dd	0.026134	0.054578	0.071891	0.194052	0.293283	0.320822	1	0.099851	0.02846	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , f271890d9555d0632d4e84e236514c32	0.074707	0.077065	0.05974	0.256057	0.346209	0.317389	0.451887	0.008006	0.033506	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-013 , s__uncultured bacterium , 04a0ffb69d9670c5cf62a2f436d27b98	0.068734	0.058165	0.034498	-0.34732	-0.37554	-0.37307	0.007554	0.001605	0.001848	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-014 , , 8bf3dd6e298b7ca2ccba11e1fa45191c	0.023708	0.057236	0.036173	-0.22616	-0.37482	-0.3697	1	0.001673	0.002238	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcus 1 , s__uncultured bacterium , 0eedd0f89cc92e032578905bde583193	0.079003	0.125776	0.194535	0.255369	0.305015	0.332888	0.463781	0.059374	0.01579	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcus 1 , s__uncultured bacterium , 6b3b389f19a8a7d2f7a9cab742c68abd	0.020238	0.034765	0.036407	0.245099	0.323521	0.329791	0.67793	0.025	0.018411	128	128	128
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcus 2 , , 5c80af11236e9dbe24572626ca860d27	0.0699	0.090979	0.061119	-0.28222	-0.3328	-0.31062	0.159823	0.01586	0.045962	128	128	128
Cache	Level , p__Spirochaetes , c__Spirochaetia , o__Spirochaetales , f__Spirochaetaceae , g__Treponema 2 , s__uncultured bacterium , 6619eb4628f7f376558c6a9427bd24cc	0.098737	0.077146	0.063671	0.255728	0.34488	0.313738	0.457547	0.008579	0.039769	128	128	128
Cache	Level , p__Tenericutes , c__Mollicutes , o__Mollicutes RF39 , f__uncultured bacterium , g__uncultured bacterium , s__uncultured bacterium , cf172bbb51cb13d1532d9ed534c108d2	0.033747	0.053937	0.03731	-0.27233	-0.38612	-0.36619	0.239562	0.000864	0.002725	128	128	128
Cache	Level , p__Verrucomicrobia , c__Verrucomicrobiae , o__Verrucomicrobiales , f__Akkermansiaceae , g__Akkermansia , s__uncultured bacterium , 3d06bc82c1661272ff4d2ad1b9754738	0.053725	0.04134	0.048892	0.248084	0.283932	0.310882	0.608032	0.148802	0.045407	128	128	128
Monroe	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Prevotellaceae , g__Prevotellaceae UCG-004 , s__uncultured bacterium , 3326971d1942c5f2708bf4f307283d46	0.016028	0.032253	0.031906	0.315323	0.315122	0.385213	0.254993	0.268679	0.021484	87	86	86
Monroe	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , c8e2464aa1450360474c3536172e389b	0.020334	0.004527	0.004004	0.285264	0.303007	0.365009	0.644026	0.393065	0.047245	87	86	86
Monroe	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group , , 35252cd698224c71c910904c42d3f017	0.004816	0.128155	0.082579	0.087944	0.399798	0.288855	1	0.011776	0.601206	87	86	86
Monroe	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group , s__uncultured bacterium , 78dedcf7eb47d7b606eb31cc7d287299	0.000569	0.083313	0.06059	-0.13553	-0.40627	-0.4197	1	0.008936	0.00495	87	86	86

Monroe	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , , 56003b2bba761cce087c719091198479	0.038489	0.117395	0.066415	0.200974	0.364797	0.297161	1	0.047625	0.469668	87	86	86
Monroe	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcus 1 , s__uncultured bacterium , 6b3b389f19a8a7d2f7a9cab742c68abd	0.000528	0.158959	0.14499	0.113966	0.367089	0.378783	1	0.043666	0.027761	87	86	86
Monroe	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__uncultured , s__uncultured rumen bacterium , 14816748d4b4023e3f40abf6478596e4	0.043018	0.000529	0.001681	0.41203	0.129782	0.219338	0.006379	1	1	87	86	86
OquirrhStansbury	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Family XIII , g__Family XIII AD3011 group , s__uncultured bacterium , 2708e0c821aa20a79a8a0bd5f8112231	0.047775	0.029762	0.032938	0.251698	0.3907	0.326244	1	0.025178	0.239387	81	81	81
OquirrhStansbury	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae NK4A136 group , , cd40cd1e6fea89a0185e95224cd334b8	0.078509	0.139683	0.074089	-0.33339	-0.3881	-0.263	0.190751	0.027829	1	81	81	81
OquirrhStansbury	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__uncultured , s__uncultured bacterium , ac4fa418085ad29d9846952e3946e0dc	0.131239	0.07561	0.049898	-0.4235	-0.33469	-0.28509	0.006617	0.18292	0.801001	81	81	81
OquirrhStansbury	Level , p__Spirochaetes , c__Spirochaetia , o__Spirochaetales , f__Spirochaetaceae , g__Treponema 2 , , 84ce9017161bb7a9f82c825cfd3d24b6	0.000805	0.076219	0.083239	0.140567	0.372935	0.368067	1	0.049101	0.05858	81	81	81
PineValley	Level , p__Actinobacteria , c__Actinobacteria , o__Micrococcales , f__Micrococcaceae , g__Arthrobacter , , 78fe427154e97652282bb3816b0cb548	0.050567	0.055596	0.031976	-0.26353	-0.39277	-0.31108	0.494051	0.001184	0.078491	116	119	116
PineValley	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Muribaculaceae , g__uncultured bacterium , s__uncultured bacterium , 2ebbbc265b3fcdcae540f6610ff25d97	0.024325	0.07034	0.089757	0.285595	0.370272	0.336433	0.21877	0.004046	0.02576	116	119	116
PineValley	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Alistipes , s__uncultured bacterium , d3f77865b15d42354bced1c1dd4a8b9b	0.027318	0.139602	0.153192	0.189987	0.342375	0.359737	1	0.01645	0.008473	116	119	116
PineValley	Level , p__Firmicutes , c__Bacilli , o__Lactobacillales , f__Enterococcaceae , g__Enterococcus , , 5a1f1721139ae50f3f16b30e699e5e77	0.043511	0.045015	0.014518	-0.23765	-0.3221	-0.28981	1	0.042113	0.185789	116	119	116
PineValley	Level , p__Firmicutes , c__Bacilli , o__Lactobacillales , f__Streptococcaceae , g__Streptococcus , , 11435364553451d8ad9a00283ee743d3	0.053262	0.028349	0.006514	-0.34307	-0.21219	-0.12687	0.018934	1	1	116	119	116
PineValley	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Family XIII , g__Family XIII UCG-001 , s__uncultured rumen bacterium , 3a3366cddbd8dcc7e93e6a307b9c6d09	0.056847	0.049753	0.016527	-0.15892	-0.32148	-0.24733	1	0.043302	0.862429	116	119	116
PineValley	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , c39dcf11813994c2c56444ab03bb9854	0.064696	0.058171	0.059251	0.259107	0.311097	0.348606	0.577234	0.06828	0.014568	116	119	116
PineValley	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Shuttleworthia , s__uncultured bacterium , a806f6a5d38a9a21dce89cb969852214	0.076312	0.02365	0.002388	-0.33438	-0.23496	-0.14409	0.028288	1	1	116	119	116
PineValley	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , , , 57defc0463af1e2cb133bae952cb3c6d	0.071845	0.08224	0.039402	-0.20705	-0.33022	-0.3191	1	0.029121	0.055747	116	119	116
PineValley	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , s__uncultured Ruminococcaceae bacterium , 88b31220e635f55ad8ef94508e0c9e01	0.057597	0.068936	0.059885	0.296491	0.336415	0.262621	0.142739	0.021832	0.510261	116	119	116
PineValley	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-009 , s__uncultured bacterium , 6b30d20342ff8ed12379a07e1d01f587	0.04638	0.074944	0.055935	0.155659	0.32091	0.31629	1	0.044408	0.062919	116	119	116
PineValley	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcus 1 , , 0bd75b752c551cc50cacc8ccae702f6d	0.000144	0.03672	0.088557	0.167375	0.239651	0.346143	1	1	0.016379	116	119	116
PostWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Family XIII , g__Family XIII AD3011 group , s__uncultured bacterium , 2708e0c821aa20a79a8a0bd5f8112231	7.37E-05	0.019759	0.023977	-0.04101	-0.25239	-0.26027	1	0.01317	0.007477	251	251	251
PostWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , e914a5b86e224f2d703988f7a78e6dd5	0.017719	0.022777	0.026346	0.147941	0.23402	0.188058	1	0.04598	0.697352	251	251	251
PostWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Intestinimonas , s__uncultured bacterium , 4b450c09e18572f11046ee84ae7db8aa	0.030328	2.03E-05	9.00E-07	0.23771	0.029769	0.067453	0.036045	1	1	251	251	251
PostWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Oscillibacter , s__uncultured bacterium , 9d4c289bdb1187800d8d26b2e79c3141	0.012617	0.06307	0.114208	0.129884	0.21304	0.296172	1	0.170733	0.000448	251	251	251
PostWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , , 3837bf36b72bf5389451996608c2b573	0.007271	0.013062	0.019118	0.090433	0.18693	0.263701	1	0.740241	0.005811	251	251	251
PreWinter	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Muribaculaceae , g__uncultured bacterium , s__uncultured bacterium , 612b1eac3e95c5ad3f38048179efa072	0.003114	0.012302	0.015585	0.026889	0.176769	0.196542	1	0.029575	0.004039	510	512	509
PreWinter	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Muribaculaceae , g__uncultured bacterium , s__uncultured bacterium , e70e6f1be806650d3cbe3bb7b588dd6e	0.007128	0.008238	0.00628	0.082474	0.186561	0.16466	1	0.011022	0.096978	510	512	509
PreWinter	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Prevotellaceae , g__Prevotellaceae UCG-004 , s__uncultured bacterium , 415406680b4f6ebe91936977ea5f1e48	0.011598	0.012614	0.014076	0.097721	0.179776	0.186342	1	0.021962	0.011851	510	512	509
PreWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 76314928d015d16b68bb07ed7c1e21b7	0.01131	0.027944	0.02864	0.120747	0.201037	0.220912	1	0.002327	0.000244	510	512	509

PreWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , bdfd51e4ee9933559261ff98abfcb5e1	0.001053	0.0184	0.018825	0.123633	0.177754	0.166865	1	0.026842	0.079205	510	512	509
PreWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae NK3A20 group , s__uncultured rumen bacterium , b335b50e0d595d60d82ea63bc1dec6e6	0.00101	0.014474	0.016144	-0.0378	-0.16606	-0.19738	1	0.082038	0.003687	510	512	509
PreWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group , s__uncultured bacterium , e89b812979716c96d01b6162a152c846	0.01314	0.042559	0.034869	0.098369	0.194915	0.170677	1	0.004557	0.055488	510	512	509
PreWinter	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__uncultured , s__uncultured rumen bacterium 4C0d-17 , 4f9d66c2156036c80c8a5482cca688e7	0.001699	0.011483	0.01078	0.116772	0.171794	0.158921	1	0.047877	0.162282	510	512	509
SanJuan	Level , p__Actinobacteria , c__Coriobacteriia , o__Coriobacteriales , f__Atopobiaceae , , , b966a7f68f0ced6e8ed2232d57492639	0.059684	0.000876	0.003184	-0.35196	-0.17322	-0.1814	0.037192	1	1	98	98	98
SanJuan	Level , p__Actinobacteria , c__Coriobacteriia , o__Coriobacteriales , f__Coriobacteriaceae , g__Enorma , , 6a8fbbcc585203e85ca9d61d28ac5ef6	0.055804	0.001043	0.000126	-0.35072	-0.05295	-0.03434	0.039132	1	1	98	98	98
SanJuan	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Prevotellaceae , g__Prevotellaceae UCG-004 , s__uncultured bacterium , c9953823fc07cf9230750e75b981e213	0.045403	0.057837	0.077504	0.246037	0.314431	0.357998	1	0.15829	0.028954	98	98	98
SanJuan	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Alistipes , s__uncultured bacterium , dac0ec947a6f2f0f3b4c30bfe1c8dcaf	0.023655	0.074684	0.107529	0.170875	0.353521	0.331091	1	0.034876	0.085101	98	98	98
SanJuan	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae FE2018 group , s__bacterium FE2018 , 0fa4bc34e153544af446f3e2a931b8af	0.072395	0.023872	0.018994	-0.36357	-0.21459	-0.20017	0.022881	1	1	98	98	98
SanJuan	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Marvinbryantia , s__uncultured bacterium , 67dbf7327629420d5c6de90d3d3b3387	0.085996	0.023568	0.01614	-0.3808	-0.17242	-0.14579	0.010746	1	1	98	98	98
SanJuan	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__uncultured , s__uncultured bacterium , 08f0198179a1816c2558db142abd4475	0.111844	0.006632	0.007602	-0.35832	-0.11461	-0.15526	0.028563	1	1	98	98	98
SanJuan	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , , , 6fb8eb193f5d0673db6bd7c380ad98c6	0.109876	0.044679	0.083514	0.367422	0.365289	0.365423	0.019395	0.021259	0.021137	98	98	98
SanJuan	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , s__uncultured bacterium , cb0be1adbef8a093692b519ff7612dfb	0.090076	0.02689	0.050979	0.318641	0.29624	0.367508	0.135758	0.299742	0.019322	98	98	98
SouthSlope	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Christensenellaceae , g__Christensenellaceae R-7 group , s__uncultured bacterium , 7d7161e8f91e49e15abffcb3a00c1c29	0.026928	0.06142	0.065161	-0.3226	-0.4301	-0.36373	0.820123	0.047887	0.308672	57	57	57
SouthSlope	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae UCG-010 , s__uncultured bacterium , fa1cc733db7bd6ca322c4e6b120fd1ff	0.119539	0.073799	0.080773	-0.46056	-0.30323	-0.32828	0.017792	1	0.721837	57	57	57
SouthSlope	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Tyzzerella 4 , s__uncultured bacterium	0.084256	0.198625	0.186378	-0.30005	-0.44564	-0.43259	1	0.029234	0.044325	57	57	57
SouthSlope	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , , , 1a872ea9afe2569307b95f2209c11ff6	0.209297	0.032481	0.078527	-0.44997	-0.21132	-0.26871	0.025374	1	1	57	57	57
Wasatch-Manti	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides , , 6e1aad1b91d2817d2c517ecabbe9d947	0.047338	0.026715	0.026997	0.264428	0.224603	0.269337	0.037772	0.318418	0.028344	194	194	194
Wasatch-Manti	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides , s__uncultured Bacteroides sp. , 7ec9b84d721b02d9682830a09cb19b67	0.064716	0.016123	0.009827	-0.26049	-0.15154	-0.12208	0.047364	1	1	194	194	194
Wasatch-Manti	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Prevotellaceae , g__Prevotellaceae UCG-004 , s__uncultured bacterium , 19d31b001318d82f6e59d1a478ef8a80	0.088369	0.035262	0.047494	0.366674	0.205421	0.226831	2.82E-05	0.787799	0.285194	194	194	194
Wasatch-Manti	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Prevotellaceae , g__Prevotellaceae UCG-004 , s__uncultured bacterium , 415406680b4f6ebe91936977ea5f1e48	0.081917	0.062474	0.068803	0.357249	0.329793	0.370615	6.14E-05	0.000515	2.02E-05	194	194	194
Wasatch-Manti	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , , b4a54ca39ab88e6a1a2d965e087bbaea	0.032746	0.005108	0.003606	0.271831	0.184236	0.203475	0.024444	1	0.859997	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , , , , 603b2984c0554068f813d2c08844f3e8	0.04519	0.0435	0.045353	0.220514	0.228886	0.29597	0.388731	0.257391	0.005412	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Christensenellaceae , g__Christensenellaceae R-7 group , , f8a30689dee232805c05ee738a3b47bf	0.084211	0.059297	0.084472	0.337021	0.332237	0.445036	0.0003	0.00043	1.54E-08	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Christensenellaceae , g__Christensenellaceae R-7 group , s__uncultured rumen bacterium , d4357e3deea47933b40f8f2dcb91a5a1	0.023368	0.011709	0.022646	0.219098	0.215164	0.31053	0.416195	0.502029	0.002037	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Christensenellaceae , g__uncultured , s__uncultured bacterium , 2514ab64f1103278920ee2937e90b3f8	0.025809	0.082101	0.068597	0.166401	0.251084	0.274736	1	0.080213	0.020536	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Clostridiales vadinBB60 group , g__uncultured bacterium , s__uncultured bacterium , c3c517702356fe333d5d917ba981c486	0.033084	0.053114	0.047686	0.15182	0.271773	0.266599	1	0.024529	0.033289	194	194	194

Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Eubacteriaceae , g__Anaerofustis , s__uncultured bacterium , 5ef44f4083c411fdac4e4e6f247d9fa3	0.020688	0.052799	0.075402	0.190503	0.239349	0.32291	1	0.150557	0.000851	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 362e07bafe709327c30bf460413f41d1	0.025921	0.065397	0.06996	0.199185	0.25068	0.29307	1	0.08201	0.006534	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 5032c3118fa9237afa024f02fc89c393	0.021905	0.015231	0.031091	-0.21313	-0.19115	-0.31334	0.552485	1	0.001676	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 5b5ece78a87c22d7da8a3377a00cd2f8	0.048045	0.097521	0.089843	0.274434	0.227896	0.302996	0.020912	0.270457	0.003399	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 76314928d015d16b68bb07ed7c1e21b7	4.80E-06	5.00E-06	0.000457	0.231177	0.218918	0.277834	0.229334	0.419816	0.017017	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 867a9dbf65311fbccb6cc0e204049ed7	0.066433	0.028998	0.050118	-0.26644	-0.17001	-0.23111	0.033596	1	0.230117	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , bad7e742798b5fcc520ff82e75b256a9	0.110708	0.058081	0.078574	-0.40471	-0.26249	-0.34767	9.38E-07	0.042253	0.000132	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , c39dcf11813994c2c56444ab03bb9854	0.046334	0.058089	0.05748	0.230776	0.22768	0.264996	0.234033	0.273383	0.036548	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , c742bf9d46d840950f47989590e21f9d	0.007868	0.035117	0.032963	-0.1129	-0.2658	-0.29375	1	0.034879	0.006255	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Coprococcus 3 , , 780ec7a8c3d95c29e344b5a319a26c6d	0.097036	0.062827	0.069093	0.335916	0.236231	0.299847	0.000326	0.177079	0.004193	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Tyzzerella 3 , s__uncultured rumen bacterium , ebdd9551834b21f202410ad555805be5	0.038936	0.031313	0.045033	-0.25034	-0.22224	-0.3597	0.083572	0.357468	5.02E-05	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Tyzzerella 4 , s__uncultured bacterium , 2937b97c81d9b0bbf872e2e9ccad7c12	0.061075	0.050895	0.062912	0.264127	0.24655	0.293345	0.038436	0.102672	0.006419	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Tyzzerella 4 , s__uncultured bacterium , 90daac5db92425b36e2cb42c69ac8394	0.003466	0.031414	0.034981	0.121658	0.245629	0.288236	1	0.107891	0.008906	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , , , 5e6f162e2e88970cf3c01694a92e0692	0.064143	0.022969	0.023655	0.282152	0.15387	0.149698	0.013047	1	1	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , , , 935c2b2e0d3a4b87b5a140288ebe95e3	0.012676	0.054638	0.056285	0.225946	0.238977	0.30201	0.297981	0.153518	0.003631	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group , , 35252cd698224c71c910904c42d3f017	0.039545	0.043009	0.038649	0.329787	0.249899	0.311299	0.000515	0.085594	0.001931	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group , s__uncultured bacterium , 9e7318bcf7eeb3491ad16ecc05bd6b58	0.032594	0.02956	0.033683	0.308656	0.232403	0.249472	0.002316	0.215502	0.087615	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group , s__uncultured bacterium , e89b812979716c96d01b6162a152c846	0.037038	0.087919	0.067066	0.257411	0.349264	0.332833	0.056407	0.000116	0.000411	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Negativibacillus , s__uncultured bacterium , 2c263f2dff6c02138180d8d1c5d57cb5	0.069904	0.04543	0.046664	0.281786	0.257189	0.325952	0.013346	0.057115	0.000683	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae NK4A214 group , s__uncultured bacterium , 24adfd04805b5bf0804d7c6843c49524	0.048767	0.062034	0.077041	0.230892	0.239081	0.302748	0.232661	0.152683	0.003456	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae NK4A214 group , s__uncultured bacterium , eef237868deb059c696bdc15f925e43b	0.039167	0.018167	0.026097	-0.23108	-0.17663	-0.296	0.230517	1	0.005402	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-002 , s__uncultured bacterium , 3a22296adc9621145bbea6b9a982b33b	0.044466	0.035059	0.049558	0.21348	0.225113	0.26354	0.543441	0.310507	0.039763	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , , 14f43ef69a9c221129271f49a6bbf29d	0.097644	0.058134	0.062053	0.371292	0.234557	0.315154	1.91E-05	0.193028	0.001477	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , , 4b09f1ee861ce88c31d75ea75d8afcda	0.060103	0.033678	0.030888	0.298295	0.282784	0.355693	0.004646	0.012544	6.96E-05	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , , 643af4b801bb60813fd7dcfaf7e209ff	0.029882	0.030019	0.029208	0.326043	0.294186	0.32807	0.000678	0.006078	0.000585	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , , b0d148c179e7590ffeb4f5701ab388ac	0.010649	0.004172	0.001255	0.303248	0.234629	0.277775	0.003342	0.192317	0.017078	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , , f0448d5c6f327fa5617910b0eaca9315	0.034094	0.013556	0.027421	-0.23527	-0.16759	-0.29562	0.186071	1	0.005537	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , s__uncultured bacterium , 1bc1e2315852d26ed11f14c956f78556	0.038681	0.008798	0.004876	-0.26657	-0.08143	-0.00967	0.033349	1	1	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 ,	0.033093	0.079297	0.078088	0.216508	0.238055	0.299108	0.471048	0.16109	0.004403	194	194	194

	s__uncultured bacterium , 3f3a58f9b4be11437feb676680c41867												
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , s__uncultured bacterium , cb0be1adbef8a093692b519ff7612dfb	0.045742	0.004281	0.005201	0.262844	0.134568	0.17409	0.041391	1	1	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , s__uncultured Ruminococcaceae bacterium , 0a7e34e68bffaec4e495b31786b31c0d	0.074258	0.014345	0.020025	0.355754	0.202116	0.300271	6.93E-05	0.91388	0.004077	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , s__uncultured Ruminococcaceae bacterium , 279feba3a62fac576c217f743f7a0677	0.028723	0.040495	0.056273	0.187753	0.192411	0.298477	1	1	0.00459	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , s__uncultured Ruminococcaceae bacterium , b867ec33eb48cd092e2e6dcc4d00d9c3	0.02772	0.036162	0.028423	0.217039	0.259415	0.306048	0.459299	0.050359	0.002767	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , s__uncultured Ruminococcaceae bacterium , d2bb065e12a3db145a18dff35dd42493	0.01556	0.012576	0.011707	0.190578	0.235447	0.31871	1	0.18439	0.001149	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-009 , s__uncultured bacterium , a759076415a35f844098586e3fe503a0	0.025027	0.021527	0.017743	0.180765	0.207994	0.271544	1	0.700731	0.024865	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-009 , s__uncultured bacterium , da82330b4c04cc56a3bda8335ab5ae46	0.028645	0.068605	0.065726	0.129886	0.251539	0.306734	1	0.07823	0.002641	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , , 3837bf36b72bf5389451996608c2b573	0.034758	0.050668	0.028483	0.207572	0.269095	0.23066	0.7144	0.028752	0.235402	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , 3cf6f7fd518dbd251dba5e6a7126d3bb	0.061477	0.090318	0.073215	0.29716	0.316757	0.377495	0.005006	0.001319	1.12E-05	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , b607e4b559041f98b124228e93a22163	0.009723	0.040551	0.028213	0.112866	0.233336	0.259775	1	0.205487	0.049338	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , f1128d1d6b92bfd1b74354361a830f18	0.015738	0.046125	0.035435	0.150841	0.235113	0.291572	1	0.187596	0.007196	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , fe27bc4f741e069fc11654baa029f59f	0.040479	0.105458	0.132095	0.238318	0.319453	0.387056	0.158893	0.00109	4.80E-06	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , ffb81be0f493cef5f436913cf7f89fac	0.044707	0.028115	0.020787	0.268618	0.1319	0.155578	0.029572	1	1	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured Ruminococcaceae bacterium , 59d7c945f9a0c393b02ed42268b2ecc9	0.049823	0.008435	0.003459	0.305445	0.159322	0.175136	0.002882	1	1	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-013 , s__uncultured bacterium , ee2e47eef6b792e2754bdd4970452a07	0.002254	0.061331	0.062777	0.070549	0.229548	0.262572	1	0.248972	0.042045	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-014 , , 6931816a41d435d1dbf37323c5911a26	0.054708	0.0091	0.008068	0.275282	0.078068	0.123004	0.01987	1	1	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcus 2 , s__uncultured rumen bacterium , 9c05fa86e3062f1150c232747186350d	0.025542	0.043681	0.037597	0.177383	0.292139	0.321099	1	0.006939	0.000969	194	194	194
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcus 2 , s__uncultured rumen bacterium , c0658f58e8a1e751fd0663f830b2ec77	0.081856	0.043346	0.024151	-0.25011	-0.27691	-0.2706	0.08462	0.018002	0.026295	194	194	194
Wasatch-Manti	Level , p__Verrucomicrobia , c__Verrucomicrobiae , o__Verrucomicrobiales , f__Akkermansiaceae , g__Akkermansia , s__uncultured bacterium , fc39e03f567b300f5ba14e43a58ef063	0.000223	0.042727	0.03723	0.109871	0.282213	0.269163	1	0.012997	0.028636	194	194	194
Winter15-16	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides , , e1c61a1046f394f90672780aa61452eb	0.091097	0.024421	0.0234	-0.34694	-0.1706	-0.22535	0.004226	1	1	138	138	138
Winter15-16	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Marinifilaceae , g__Odoribacter , s__uncultured Bacteroidales bacterium , 7443089b1bdc7d7f18152e4843339ddb	0.046118	0.131829	0.13794	0.233415	0.333769	0.336619	0.809375	0.00872	0.007475	138	138	138
Winter16-17	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Muribaculaceae , g__uncultured bacterium , s__uncultured bacterium , 612b1eac3e95c5ad3f38048179efa072	0.002014	0.009035	0.015555	0.038164	0.221706	0.238284	1	0.056562	0.019096	273	276	273
Winter16-17	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Prevotellaceae , g__Prevotellaceae UCG-004 , s__uncultured bacterium , 415406680b4f6ebe91936977ea5f1e48	0.041106	0.020787	0.01985	0.225553	0.284826	0.314404	0.046722	0.000416	3.06E-05	273	276	273
Winter16-17	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Prevotellaceae , g__Prevotellaceae UCG-004 , s__uncultured bacterium , 800cbb4cdf5b762aa3747cd38db617ff	0.014507	0.009308	0.013321	0.190567	0.18213	0.227432	0.425905	0.658426	0.041071	273	276	273
Winter16-17	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Christensenellaceae , g__Christensenellaceae R-7 group , , f8a30689dee232805c05ee738a3b47bf	0.027715	0.024066	0.01962	0.206201	0.263021	0.322635	0.165823	0.002625	1.35E-05	273	276	273

Winter16-17	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Christensenellaceae , g__Christensenellaceae R-7 group , s__uncultured prokaryote , 907c20d0298042d65b40e73cd413f191	0.023726	0.045658	0.041758	0.172006	0.204333	0.22788	1	0.175826	0.039821	273	276	273
Winter16-17	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 76314928d015d16b68bb07ed7c1e21b7	0.00023	0.004086	0.00414	0.150685	0.305007	0.351301	1	6.54E-05	6.51E-07	273	276	273
Winter16-17	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 8df8651bddbd747ee536d321428120f9	0.031951	0.028963	0.02775	-0.18424	-0.24328	-0.25212	0.611419	0.012169	0.006825	273	276	273
Winter16-17	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , bad7e742798b5fcc520ff82e75b256a9	0.043852	0.052317	0.06505	-0.2241	-0.29881	-0.36229	0.051592	0.000117	1.87E-07	273	276	273
Winter16-17	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , bf49a90284d596106b657efe32d36dd9	0.008823	0.000374	0.001358	0.176098	0.186304	0.231461	0.958341	0.519296	0.031036	273	276	273
Winter16-17	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Roseburia , , db57d0dcb87bff6649a748ed003444a9	0.017758	0.018434	0.033239	-0.12902	-0.13459	-0.24145	1	1	0.015172	273	276	273
Winter16-17	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Tyzzerella 3 , s__uncultured rumen bacterium , ebdd9551834b21f202410ad555805be5	0.005953	0.030585	0.037179	-0.11019	-0.24093	-0.30457	1	0.014495	7.84E-05	273	276	273
Winter16-17	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , , , 0b265531d775f26000397e0eb8488666	0.005445	0.025768	0.028851	0.134515	0.238865	0.273125	1	0.016866	0.001273	273	276	273
Winter16-17	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , , , 6fb8eb193f5d0673db6bd7c380ad98c6	0.024878	0.027392	0.044692	0.207027	0.218755	0.243953	0.157456	0.069018	0.012616	273	276	273
Winter16-17	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group , , 35252cd698224c71c910904c42d3f017	0.010272	0.021103	0.010973	0.201212	0.292619	0.305525	0.225791	0.000207	7.17E-05	273	276	273
Winter16-17	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group , s__uncultured bacterium , 04d3a3e424fd1df07d5947eaf3356350	0.018957	0.01293	0.008441	0.115496	0.202941	0.245159	1	0.191806	0.011537	273	276	273
Winter16-17	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group , s__uncultured bacterium , e89b812979716c96d01b6162a152c846	0.008699	0.050482	0.041912	0.0896	0.239888	0.246515	1	0.015647	0.010427	273	276	273
Winter16-17	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Intestinimonas , , 91223ec5064454a1134c9d67dffa8f34	0.065947	0.03179	0.023041	0.257616	0.247454	0.228752	0.004458	0.008892	0.03749	273	276	273
Winter16-17	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae NK4A214 group , s__uncultured bacterium , 24adfd04805b5bf0804d7c6843c49524	0.019656	0.030791	0.048449	0.164187	0.184836	0.245113	1	0.564846	0.011577	273	276	273
Winter16-17	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae NK4A214 group , s__uncultured bacterium , eef237868deb059c696bdc15f925e43b	0.018201	0.021503	0.035591	-0.16128	-0.1655	-0.27758	1	1	0.000875	273	276	273
Winter16-17	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , , 14f43ef69a9c221129271f49a6bbf29d	0.09208	0.030303	0.04996	0.280013	0.222718	0.26993	0.000711	0.0528	0.001658	273	276	273
Winter16-17	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , , 4b09f1ee861ce88c31d75ea75d8afcda	0.009162	0.009709	0.015284	0.15872	0.214443	0.254335	1	0.091877	0.005754	273	276	273
Winter16-17	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , s__uncultured Ruminococcaceae bacterium , 0a7e34e68bffaec4e495b31786b31c0d	0.033262	0.002364	0.004043	0.236283	0.163964	0.188166	0.022052	1	0.489241	273	276	273
Winter16-17	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , s__uncultured Ruminococcaceae bacterium , b867ec33eb48cd092e2e6dcc4d00d9c3	0.025459	0.018708	0.018002	0.16988	0.19853	0.232094	1	0.25173	0.029687	273	276	273
Winter16-17	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , 3cf6f7fd518dbd251dba5e6a7126d3bb	0.034655	0.01118	0.006891	0.282671	0.228782	0.273506	0.000566	0.03472	0.001233	273	276	273
Winter16-17	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , 445bce2f402a960305c18a62ad519346	0.011034	0.018275	0.021286	0.14804	0.211211	0.22497	1	0.113438	0.048619	273	276	273
Winter16-17	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , fe27bc4f741e069fc11654baa029f59f	0.023458	0.06272	0.05779	0.2091	0.266881	0.270959	0.138136	0.001916	0.001524	273	276	273
Winter17-18	Level , p__Actinobacteria , c__Actinobacteria , o__Corynebacteriales , f__Nocardiaceae , g__Williamsia , , 9fa38da5c450085b30000c85dc27fa94	0.005475	0.021669	0.018653	-0.06486	-0.27681	-0.30005	1	0.036514	0.009588	176	175	175
Winter17-18	Level , p__Actinobacteria , c__Actinobacteria , o__Micrococcales , f__Microbacteriaceae , , , c8c2a3359cf6cd5820689d3dace7afc4	0.013403	0.018668	0.015714	-0.18537	-0.26844	-0.27851	1	0.057464	0.033242	176	175	175
Winter17-18	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides , s__uncultured bacterium , 58d83b18f6ccfd7b78fb791f2ddd234a	0.003902	0.03503	0.025352	-0.14964	-0.27837	-0.26643	1	0.0335	0.063942	176	175	175
Winter17-18	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Muribaculaceae , g__uncultured bacterium , s__uncultured bacterium , 75e91c227f9685c1f605d737ff6881b8	0.068854	0.032951	0.031401	0.332635	0.234433	0.249219	0.001138	0.313632	0.154255	176	175	175
Winter17-18	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group , s__uncultured bacterium , e89b812979716c96d01b6162a152c846	0.033069	0.090933	0.105726	0.196	0.299712	0.31426	1	0.009785	0.003995	176	175	175

Winter17-18	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Oscillibacter , , 1568eda601bd7389122116059b025faf	0.020638	0.022028	0.005958	-0.11845	-0.30108	-0.31042	1	0.00901	0.005085	176	175	175
Winter17-18	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Oscillibacter , s__uncultured bacterium , 5dd4e467291bcdfb96ebe5c3739a3b19	0.04144	0.048519	0.032435	-0.18734	-0.27203	-0.26703	1	0.047388	0.061953	176	175	175
Winter17-18	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae NK4A214 group , s__uncultured bacterium , 24adfd04805b5bf0804d7c6843c49524	0.021935	0.043303	0.062345	0.166349	0.27654	0.31387	1	0.037057	0.004094	176	175	175
Winter17-18	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , s__uncultured Ruminococcaceae bacterium , 0a7e34e68bffaec4e495b31786b31c0d	0.018605	0.005494	0.000932	0.279496	0.198517	0.195876	0.030307	1	1	176	175	175
Winter17-18	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , fb7c6fc8ca9c22e7d46bd8afe9174369	0.081201	0.028665	0.025669	0.274264	0.180859	0.173123	0.040493	1	1	176	175	175
Winter17-18	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , fe27bc4f741e069fc11654baa029f59f	0.015718	0.035705	0.024894	0.151467	0.251057	0.276426	1	0.140806	0.037289	176	175	175
Winter17-18	Level , p__Proteobacteria , c__Gammaproteobacteria , o__Betaproteobacteriales , f__Burkholderiaceae , g__Delftia , , 3259e7445475eebc79d267126760b2d6	0.056837	0.039794	0.017954	-0.26866	-0.31719	-0.29907	0.054876	0.003317	0.010169	176	175	175
Winter18-19	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Prevotellaceae , g__Prevotellaceae UCG-004 , s__uncultured bacterium , 415406680b4f6ebe91936977ea5f1e48	0.028285	0.119873	0.138296	0.125485	0.303748	0.318839	1	0.019768	0.008584	154	154	154
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , bad7e742798b5fcc520ff82e75b256a9	0.038114	0.046399	0.040205	-0.21486	-0.29643	-0.31706	1	0.029148	0.009496	154	154	154
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae XPB1014 group , , 2dc6173bbe6466f22d87d430ced59323	0.019223	0.037409	0.030022	-0.13541	-0.29385	-0.31082	1	0.033345	0.013449	154	154	154
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Syntrophococcus , s__uncultured rumen bacterium , b3335be5b925014b97454ca38c3bf5ef	0.028792	0.028016	0.033002	-0.20122	-0.22275	-0.29254	1	0.845625	0.035683	154	154	154
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Oscillibacter , , ef44e026034244f99ad961589cded471	0.059147	0.072755	0.055549	-0.15513	-0.28007	-0.29803	1	0.066975	0.026806	154	154	154
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , s__uncultured bacterium , 2727ad9acd3f4e925c3a88edfc793c09	0.024773	0.096692	0.106174	0.095961	0.282528	0.325851	1	0.059298	0.005737	154	154	154
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , s__uncultured bacterium , 550985f124fbf352dc630914fcdf2557	0.024832	0.105854	0.085569	0.150568	0.291713	0.270639	1	0.037246	0.105784	154	154	154
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , s__uncultured Ruminococcaceae bacterium , 0a7e34e68bffaec4e495b31786b31c0d	0.006057	0.05572	0.037445	0.200895	0.298382	0.300957	1	0.026309	0.022953	154	154	154
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured Ruminococcaceae bacterium , 4527170be8e5e15c661c7b4e1b96fbb2	0.007278	0.065566	0.089505	0.088064	0.276899	0.295126	1	0.078246	0.031208	154	154	154
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-013 , s__uncultured bacterium , ee2e47eef6b792e2754bdd4970452a07	0.039429	0.026152	0.033966	0.238683	0.267753	0.287509	0.442377	0.121268	0.04617	154	154	154
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-014 , , 8bf3dd6e298b7ca2ccba11e1fa45191c	0.023676	0.028491	0.023396	-0.16384	-0.28597	-0.3174	1	0.049916	0.009312	154	154	154
Winter18-19	Level , p__Spirochaetes , c__Spirochaetia , o__Spirochaetales , f__Spirochaetaceae , g__Treponema 2 , s__uncultured bacterium , 6619eb4628f7f376558c6a9427bd24cc	0.015774	0.112412	0.132844	0.0475	0.320975	0.36272	1	0.0076	0.000583	154	154	154
Winter18-19	Level , p__Tenericutes , c__Mollicutes , o__Mollicutes RF39 , f__uncultured bacterium , g__uncultured bacterium , s__uncultured bacterium , cf172bbb51cb13d1532d9ed534c108d2	0.018128	0.022223	0.016805	-0.27344	-0.3096	-0.30676	0.092518	0.014382	0.016799	154	154	154
Yearling	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Prevotellaceae , g__Prevotellaceae UCG-004 , s__uncultured bacterium , 800cbb4cdf5b762aa3747cd38db617ff	0.076224	0.075154	0.129148	0.49132	0.441185	0.485206	0.001624	0.01248	0.002119	67	67	67
Yearling	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , c39dcf11813994c2c56444ab03bb9854	0.165756	0.086118	0.054642	0.46546	0.302029	0.301168	0.004837	0.870436	0.888764	67	67	67
Yearling	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , , , a664b1d386d2a0a0f825514940f8b38f	0.055277	0.087617	0.159996	0.225973	0.321936	0.44031	1	0.528698	0.012897	67	67	67
Yearling	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Negativibacillus , s__uncultured bacterium , 7fea681644517d3e38e3abf2fdcfc425	0.178913	0.00884	0.011592	0.434732	0.182117	0.176845	0.015869	1	1	67	67	67
Yearling	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , , 643af4b801bb60813fd7dcfaf7e209ff	0.008283	0.021189	0.013407	0.431174	0.388871	0.412777	0.01808	0.076733	0.034702	67	67	67
Yearling	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , , b0d148c179e7590ffeb4f5701ab388ac	0.162321	0.030936	0.053432	0.465986	0.187765	0.292984	0.004735	1	1	67	67	67
Yearling	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , s__metagenome , fd66cf9df106c8a96ce8689645536d56	0.134442	0.026313	0.03957	0.414937	0.117049	0.243763	0.032205	1	1	67	67	67

Yearling	Level , p__Planctomycetes , c__Planctomycetacia , o__Pirellulales , f__Pirellulaceae , g__p-1088-a5 gut group , s__uncultured bacterium , 53ab9d2256ec104ad802edd822fa6eea	0.123024	0.176562	0.087747	-0.33269	-0.46664	-0.407	0.398366	0.00461	0.042263	67	67	67

Table S11. Full future/predictive analysis. Includes statistically significant correlations for each deer sample subset (each geography, overwinter year, season) at each taxonomic level.

Phylum													
Sample Subset	Taxonomic Level	LFR2	BCSR2	RFR2	LF_Coeff	BCS_Coeff	RF_Coeff	LF_Adj._Pval	BCS_Adj._Pval	RF_Adj._Pval	LF_N	BCS_N	RF_N
Winter15-16	Level , p__Verrucomicrobia	0.069403	0.146441	0.128483	-0.25918	-0.3654	-0.56878	1	1	0.044437	28	28	28
Wasatch-Manti	Level , p__Verrucomicrobia	0.257272	0.169604	0.083936	-0.53758	-0.39331	-0.3072	0.005376	0.315047	1	46	46	46
Class													
Sample Subset	Taxonomic Level	LFR2	BCSR2	RFR2	LF_Coeff	BCS_Coeff	RF_Coeff	LF_Adj._Pval	BCS_Adj._Pval	RF_Adj._Pval	LF_N	BCS_N	RF_N
Winter15-16	Level , p__Verrucomicrobia , c__Verrucomicrobiae	0.069403	0.146441	0.128483	-0.25918	-0.3654	-0.56878	1	1	0.044437	28	28	28
Wasatch-Manti	Level , p__Verrucomicrobia , c__Verrucomicrobiae	0.257272	0.169604	0.083936	-0.53758	-0.39331	-0.3072	0.005376	0.315047	1	46	46	46
Order													
Sample Subset	Taxonomic Level	LFR2	BCSR2	RFR2	LF_Coeff	BCS_Coeff	RF_Coeff	LF_Adj._Pval	BCS_Adj._Pval	RF_Adj._Pval	LF_N	BCS_N	RF_N
Winter18-19	Level , p__Verrucomicrobia , c__Verrucomicrobiae , o__Opitutales	0.023644	0.708247	0.146976	-0.16244	0.911374	0.359185	1	0.005626	1	9	9	9
Wasatch-Manti	Level , p__Verrucomicrobia , c__Verrucomicrobiae , o__Verrucomicrobiales	0.247623	0.18567	0.092181	-0.50234	-0.38367	-0.29935	0.01723	0.390328	1	46	46	46
Family													
Sample Subset	Taxonomic Level	LFR2	BCSR2	RFR2	LF_Coeff	BCS_Coeff	RF_Coeff	LF_Adj._Pval	BCS_Adj._Pval	RF_Adj._Pval	LF_N	BCS_N	RF_N
OquirrhStansbury	Level , p__Tenericutes , c__Mollicutes , o__Mollicutes RF39 , f__uncultured rumen bacterium	0.671905	0.05787	0.024327	-0.8956	-0.43319	-0.13182	0.009825	1	1	9	9	9
Winter18-19	Level , p__Verrucomicrobia , c__Verrucomicrobiae , o__Opitutales , f__Puniceicoccaceae	0.023644	0.708247	0.146976	-0.16244	0.911374	0.359185	1	0.005626	1	9	9	9
Wasatch-Manti	Level , p__Verrucomicrobia , c__Verrucomicrobiae , o__Verrucomicrobiales , f__Akkermansiaceae	0.247623	0.18567	0.092181	-0.50234	-0.38367	-0.29935	0.01723	0.390328	1	46	46	46
Genus													
Sample Subset	Taxonomic Level	LFR2	BCSR2	RFR2	LF_Coeff	BCS_Coeff	RF_Coeff	LF_Adj._Pval	BCS_Adj._Pval	RF_Adj._Pval	LF_N	BCS_N	RF_N
SanJuan	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae UCG-008	0.723389	0.244755	0.028877	-0.86071	0.371849	0.094132	0.048563	1	1	8	8	8
SanJuan	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-013	0.683175	0.087445	0.027232	-0.87427	0.304901	-0.11115	0.036099	1	1	8	8	8
OquirrhStansbury	Level , p__Tenericutes , c__Mollicutes , o__Mollicutes RF39 , f__uncultured rumen bacterium , g__uncultured rumen bacterium	0.671905	0.05787	0.024327	-0.8956	-0.43319	-0.13182	0.009825	1	1	9	9	9
Monroe	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Pygmaiobacter	0.418439	0.068808	0.03034	0.839839	0.146427	0.414578	0.041504	1	1	9	9	9
Winter15-16	Level , p__Proteobacteria , c__Deltaproteobacteria , o__Desulfovibrionales , f__Desulfovibrionaceae , g__Desulfovibrio	0.062332	0.221183	0.293674	-0.13631	0.439305	0.585519	1	0.541483	0.029761	28	28	28
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Defluviitaleaceae ,	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Butyrivibrio	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospira	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__uncultured	0.018496	0.577284	0.086604	0.170437	-0.88396	-0.35755	1	0.014056	1	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Caproiciproducens	0.006918	0.674128	0.127551	0.066778	-0.85309	-0.36423	1	0.031099	1	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Oscillibacter	0.010612	0.908836	0.195652	-0.05485	0.943308	0.483302	1	0.001216	1	9	9	9
Winter18-19	Level , p__Planctomycetes , c__Planctomycetacia , o__Pirellulales , f__Pirellulaceae , g__CPla-4 termite group	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Proteobacteria , c__Deltaproteobacteria , o__Desulfovibrionales , f__Desulfovibrionaceae , g__uncultured	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Verrucomicrobia , c__Verrucomicrobiae , o__Opitutales , f__Puniceicoccaceae , g__Cerasicoccus	0.029665	0.690684	0.144227	-0.14859	0.907222	0.429058	1	0.006577	1	9	9	9
Yearling	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Dorea	0.110013	0.005094	0.638617	0.082659	0.009213	0.831984	1	1	0.04868	9	9	9
Yearling	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminiclostridium 1	0.077494	0.012648	0.156311	-0.83893	0	-0.3365	0.042293	1	1	9	9	9
Wasatch-Manti	Level , p__Verrucomicrobia , c__Verrucomicrobiae , o__Verrucomicrobiales , f__Akkermansiaceae , g__Akkermansia	0.247623	0.18567	0.092181	-0.50234	-0.38367	-0.29935	0.01723	0.390328	1	46	46	46
Monroe	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Family XIII , g__Anaerovorax	0.21123	0.127229	0.976351	0.626722	0.315668	1	0.638009	1	0	9	9	9
Monroe	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Hydrogenoanaerobacterium	0.21123	0.127229	0.976351	0.626722	0.315668	1	0.638009	1	0	9	9	9
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group	0.191091	0.093962	0.022387	0.498951	0.299248	0.138975	0.019149	1	1	46	46	46

SanJuan	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcus 1	0.159417	0.423244	0.888693	0.323359	0.756154	0.938558	1	0.239539	0.004428	8	8	8
PineValley	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminiclostridium 9	0.150517	0.000133	8.97E-05	-0.61361	-0.19921	-0.17138	0.042455	1	1	23	23	23
SanJuan	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-009	0.080438	0.604999	0.523824	-0.01198	0.987878	0.876811	1	3.53E-05	0.03402	8	8	8
Monroe	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae ,	0.032981	0.492999	0.032607	-0.35598	0.860059	-0.06847	1	0.026422	1	9	9	9
Species													
Sample Subset	Taxonomic Level	LFR2	BCSR2	RFR2	LF_Coeff	BCS_Coeff	RF_Coeff	LF_Adj._Pval	BCS_Adj._Pval	RF_Adj._Pval	LF_N	BCS_N	RF_N
SanJuan	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides , s__uncultured Bacteroides sp.	0.747797	0.168294	0.004368	-0.88095	0.109109	-0.20869	0.030803	1	1	8	8	8
SanJuan	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-013 , s__uncultured bacterium	0.690218	0.017612	0.097555	-0.88095	0.169725	-0.24551	0.030803	1	1	8	8	8
OquirrhStansbury	Level , p__Tenericutes , c__Mollicutes , o__Mollicutes RF39 , f__uncultured rumen bacterium , g__uncultured rumen bacterium , s__uncultured rumen bacterium	0.671905	0.05787	0.024327	-0.8956	-0.43319	-0.13182	0.009825	1	1	9	9	9
OquirrhStansbury	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-014 , s__unidentified	0.574556	0.002618	0.160019	-0.85253	-0.27136	0.094916	0.031498	1	1	9	9	9
Monroe	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Pygmaiobacter , s__uncultured bacterium	0.418439	0.068808	0.03034	0.839839	0.146427	0.414578	0.041504	1	1	9	9	9
PineValley	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-002 ,	0.294414	0.185274	0.06043	-0.66225	-0.31336	-0.29491	0.013253	1	1	23	23	23
Monroe	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Family XIII , g__Family XIII AD3011 group , s__uncultured Clostridiales Family XIII bacterium	0.279125	0.088109	0.875	0.631676	0.275334	0.992157	0.612243	1	1.26E-06	9	9	9
Wasatch-Manti	Level , p__Verrucomicrobia , c__Verrucomicrobiae , o__Verrucomicrobiales , f__Akkermansiaceae , g__Akkermansia , s__uncultured bacterium	0.247623	0.18567	0.092181	-0.50234	-0.38367	-0.29935	0.01723	0.390328	1	46	46	46
Monroe	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Family XIII , g__Anaerovorax , s__uncultured bacterium	0.21123	0.127229	0.976351	0.626722	0.315668	1	0.638009	1	0	9	9	9
SanJuan	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-009 , s__uncultured bacterium	0.080438	0.604999	0.523824	-0.01198	0.987878	0.876811	1	3.53E-05	0.03402	8	8	8
OquirrhStansbury	Level , p__Spirochaetes , c__Spirochaetia , o__Spirochaetales , f__Spirochaetaceae , g__Treponema 2 , s__uncultured bacterium	0.078714	0.485745	0.228553	-0.37774	-0.84848	-0.49605	1	0.034483	1	9	9	9
Wasatch-Manti	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae NK3A20 group ,	0.072456	0.026296	0.041021	-0.47789	-0.2525	-0.18957	0.036009	1	1	46	46	46
Monroe	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , ,	0.032981	0.492999	0.032607	-0.35598	0.860059	-0.06847	1	0.026422	1	9	9	9
Winter15-16	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , s__uncultured bacterium	0.016447	0.136618	0.241779	-0.10127	-0.27914	-0.57248	1	1	0.040746	28	28	28
Winter15-16	Level , p__Proteobacteria , c__Deltaproteobacteria , o__Desulfovibrionales , f__Desulfovibrionaceae , g__Desulfovibrio ,	0.062332	0.221183	0.293674	-0.13631	0.439305	0.585519	1	0.541483	0.029761	28	28	28
Winter17-18	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Flavonifractor , s__uncultured bacterium	0.279212	0.371664	0.055688	-0.55071	-0.62795	-0.26634	0.092355	0.015434	1	26	26	26
Winter18-19	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Alistipes ,	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Defluviitaleaceae , ,	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Defluviitaleaceae , g__Defluviitaleaceae UCG-011 , s__uncultured rumen bacterium	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Family XIII , g__Anaerovorax ,	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Butyrivibrio , s__uncultured bacterium	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Coprococcus 2 , s__uncultured rumen bacterium	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospira , s__uncultured bacterium	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Peptococcaceae , g__uncultured , s__uncultured rumen bacterium	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Caproiciproducens , s__uncultured bacterium	0.006918	0.674128	0.127551	0.066778	-0.85309	-0.36423	1	0.031099	1	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Oscillibacter , s__uncultured bacterium	0.012064	0.757175	0.090074	0.14532	0.900931	0.419627	1	0.008222	1	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminiclostridium 1 ,	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae NK4A214 group , s__uncultured Ruminococcaceae bacterium	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-014 , s__gut metagenome	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9

Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-014 , s__uncultured Clostridiales bacterium	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcus 1 , s__uncultured bacterium	0.249346	0.636647	0	-0.16807	0.939336	0.137505	1	0.001535	1	9	9	9
Winter18-19	Level , p__Planctomycetes , c__Planctomycetacia , o__Pirellulales , f__Pirellulaceae , g__CPla-4 termite group , s__uncultured bacterium	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Proteobacteria , c__Deltaproteobacteria , o__Desulfovibrionales , f__Desulfovibrionaceae , g__uncultured ,	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Verrucomicrobia , c__Verrucomicrobiae , o__Opitutales , f__Puniceicoccaceae , g__Cerasicoccus , s__uncultured bacterium	0.029665	0.690684	0.144227	-0.14859	0.907222	0.429058	1	0.006577	1	9	9	9
Yearling	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Christensenellaceae , g__Christensenellaceae R-7 group , s__uncultured prokaryote	0.148713	0.103611	0.557622	-0.07831	-0.36853	-0.83198	1	1	0.04868	9	9	9
ASV													
Sample Subset	Taxonomic Level	LFR2	BCSR2	RFR2	LF_Coeff	BCS_Coeff	RF_Coeff	LF_Adj._Pval	BCS_Adj._Pval	RF_Adj._Pval	LF_N	BCS_N	RF_N
Winter18-19	Level , p__Actinobacteria , c__Coriobacteriia , o__Coriobacteriales , f__Eggerthellaceae , g__DNF00809 , s__uncultured bacterium , cc550942f1e8bafe26a02eb5e1270d4a	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Actinobacteria , c__Coriobacteriia , o__Coriobacteriales , f__Eggerthellaceae , g__Enterorhabdus , s__uncultured rumen bacterium , f104af55eb9783d10ba2949a6010cb03	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides , , 0ad91f8efd56830986e079b0a5beff69	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides , s__uncultured bacterium , 37fbb20546ec612c6d4155759ae0c6de	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides , s__uncultured bacterium , 4f79c257c93f08d09a79987b27a3dfe9	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides , s__uncultured bacterium , 58c28ae87ca7406a25dc96d8c28c5f8e	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides , s__uncultured Bacteroides sp. , cc4491591a55666ca43817d2342c6de3	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides , s__uncultured Bacteroides sp. , e65158f90463e81877fe57c6e03d852a	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidales RF16 group , g__uncultured bacterium , s__uncultured bacterium , 64df65c0834a61aef79c50d7788b820f	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidales RF16 group , g__uncultured bacterium , s__uncultured bacterium , c9d684bba3da3b10e6765ba5ba4e0540	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Marinifilaceae , g__Odoribacter , s__uncultured Bacteroidales bacterium , 7443089b1bdc7d7f18152e4843339ddb	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Alistipes , , fda58443b32dc58e21aa15bd5233c2ef	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__dgA-11 gut group , s__uncultured bacterium , d7ab40e7cb86b70178fae67aa58bf79a	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , , 311ebf66738c3863ce8a87878b802716	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , , 5f049987abc5381047973e67c7cf5c57	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , , 63d4f6266bdaa68f8afe42cebdabdce7	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , , d55ce07ae6c95b2c0abff009ff5a2ef5	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , , d73e89aef2e5b5afcf4850b94e5bedee	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , , e23d452b4fd2f7dc644c1b1078dcbfc0	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , , e26b001846ff06fbf964a08ad851d010	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , , fcd8f9ed05d02dcb55f575a3d056f78a	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9

Winter18-19	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , s__uncultured bacterium , 15d52082785b94061a4d24c022dfe58a	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , s__uncultured bacterium , 1947abf485e33587f8ece476a5d6e90a	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , s__uncultured bacterium , 42d926de1f8a0e756fd65238d0aca0ab	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , s__uncultured Bacteroidales bacterium , 0c6bd93dda347c21944955c466cc069b	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , s__uncultured Bacteroidales bacterium , 445cc84e1a0745e5a9a080bff3357ba5	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , s__uncultured Bacteroidales bacterium , ea84033bd4296d79a2bed718320aa15f	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__uncultured , , , 362c0aca15c808ff6833b4d1002d6927	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__uncultured , , , 99e6f0160ee687cfcc0e3c9c3d0bc020	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__uncultured , g__uncultured bacterium , s__uncultured bacterium , 3a09837ec2c2f446e46dc14ea56cc1f2	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Cyanobacteria , c__Melainabacteria , o__Gastranaerophilales , f__uncultured bacterium , g__uncultured bacterium , s__uncultured bacterium , 6e9716c7aecae8d9cc9de5d7e2313728	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Cyanobacteria , c__Melainabacteria , o__Gastranaerophilales , f__uncultured bacterium , g__uncultured bacterium , s__uncultured bacterium , 7592acd5b1da7b2887350006572869c4	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Cyanobacteria , c__Melainabacteria , o__Gastranaerophilales , f__uncultured rumen bacterium , g__uncultured rumen bacterium , s__uncultured rumen bacterium , 08b63c64da753172d54839aad8012500	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Cyanobacteria , c__Melainabacteria , o__Gastranaerophilales , f__uncultured rumen bacterium , g__uncultured rumen bacterium , s__uncultured rumen bacterium , 8543a4b127b368f9350aca469202ef2e	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , , , , 82b389bc494bbf9e093737f064ab1f1b	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , , , , 902a56ab3632418756f17771e7e49d03	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , , , , f0e910faeb7250bcefb43953a1d41b0f	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Christensenellaceae , g__Christensenellaceae R-7 group , , 172ea4b46c095fd206e12c6ee11726ed	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Christensenellaceae , g__Christensenellaceae R-7 group , , 4ec90b581f56a738a2bff213c8217419	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Christensenellaceae , g__Christensenellaceae R-7 group , , 9a5ee9df292b4c446baad6bdd61a1e39	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Christensenellaceae , g__Christensenellaceae R-7 group , s__uncultured prokaryote , 2370ac99ccee38df44578cf545660686	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Clostridiales vadinBB60 group , g__uncultured bacterium , s__uncultured bacterium , d64df63b40615528f057f17cc7dbc1be	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Clostridiales vadinBB60 group , g__uncultured bacterium , s__uncultured bacterium , e87e05d4925069f6c221bfeed90e6873	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Defluviitaleaceae , , , 0c8b515e2935abe30d029214b41e0114	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Defluviitaleaceae , g__Defluviitaleaceae UCG-011 , s__uncultured rumen bacterium , ba0b56b5bba4452da2a4755c1dfb0da3	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Family XIII , g__[Eubacterium] brachy group , s__uncultured bacterium , 711b5d8095c2c106d9fa1e41d78638ba	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Family XIII , g__Anaerovorax , , e15d1438d077f3695d2ff766797d7538	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 165dd2ea271b298f1e35387db1323d01	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9

Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 2c14fb46c1500059c2e0952a2c221e2b	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 365efb653bc1440f429c22aced646cab	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 4bd1d7cb3efd8441f50525c1f7989a8c	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 587ea6ee208cf9bc0413c22e403bb3db	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 66375b6d6f0da60a8328e98e087be4f3	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 852a7c19f2de2456a06fd8f16859cc9f	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , b5bdf3563a2f8064b354904cf1e4d417	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , ba025de4afb8bfa15e4d265bc6ac61cb	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , c0024d3ee6f299d3d726575f2e3850d1	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , c87dd3bf5533fa30c83c19435da28ea9	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , fe9d941d307005f1c6624cf67983439d	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Butyrivibrio , s__uncultured bacterium , 7cb2ed6d82ced11912cffa367efae5d4	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Coprococcus 2 , s__uncultured rumen bacterium , d08c75b2300fcd140f5bfa3b3c31ba68	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Eisenbergiella , s__uncultured bacterium , a6c49275f8c7c9dc9414429df7b2ddf9	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospira , s__uncultured bacterium , f5c04813aebcc1fbb3400c329b36b97d	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae AC2044 group , , db2849fa8551b6da02aa16a7fe89ead0	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae AC2044 group , s__uncultured bacterium , af9a0a7d7266d7a7fe66250d169563d8	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae NK4A136 group , , 3d0f03d59874d61e5313abdd457204a1	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae NK4A136 group , , cb04070d129098e773809b675383224f	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae UCG-002 , , fed72a43184176a8bd5a22d1085810bb	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae UCG-008 , s__uncultured rumen bacterium , 995e549859964b02c8a1e2c7df990c9c	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Tyzzerella 4 , s__uncultured bacterium , 5329f48b92f736ce783eae7141df61fd	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Peptococcaceae , g__uncultured , s__uncultured organism , 699937f910096d3fffd9e4ac2bcefabf	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Peptococcaceae , g__uncultured , s__uncultured rumen bacterium , 75b8dd8daf5b46aacb71fd6064053246	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , , , 6ef99eee3d838bc845b5cbdb91b40728	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , , , a28eb16d1939c8e8d0e3aae3fb7e6f68	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , , , e30583def59fe47d3db7ad7bf6386c1f	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , , , ecc216f584a67d08df55bcd4085126fc	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group , , 5bfcd4e866c9d2fe68bf5943a88f9ec9	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group , , 6b93494279e6534d3bc450dd0fac2f31	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9

Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group , , 7a23ce1affd0853366b1d6aca092bd50	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group , s__uncultured bacterium , 0ef9bd8f4d197642c35edb7dae77f4bf	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group , s__uncultured bacterium , 47395a65217aabd8e6bc32535c1d3935	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group , s__uncultured bacterium , c3cfa0a15eb14e6273591d3340f7dbd1	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group , s__uncultured rumen bacterium , 01c8e74d731a5e8adaaa48c6ecf5c60d	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminiclostridium 1 , , 071bdc3d8a0758d84f6aad3f2eae23d0	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminiclostridium 1 , s__uncultured bacterium , b3d5c571585fb646d6f799cdd93e527d	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminiclostridium 5 , s__uncultured bacterium , 49c12d4a1f7d0b947b5c946e8b1d6efe	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae NK4A214 group , , 32a514ebdc214d1392d92339c730bf21	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae NK4A214 group , s__uncultured bacterium , 1ae2cc80aa7b7d69580eddcf8fee7667	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae NK4A214 group , s__uncultured Ruminococcaceae bacterium , 8f89754b4ad9752c2f049a2718286415	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , , c83378510cd33f6b3a257e2157ebbda4	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , , e71614c67455bc104e33a90695963c6d	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , s__uncultured bacterium , 1feee2eabc771b19261e7d43ecba55b4	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , s__uncultured bacterium , 2912df83c711fa71a055930da24bb68d	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , s__uncultured bacterium , ceb559749d5959661af052b35aa994ca	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , , 162381b67421379ed4974ccc32e9365b	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , , 478309ae9044726666097ffbaa212d88	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , , 5eef6e3161171e33f388ab3880aea291	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , , caca8d3f8217572e0f344473c9c4400a	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , 75fbb5ab93622f97cae5c3ea7575f376	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , 934333f2d17fc923b8d8158c74520f27	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , 94f75b32f2b0377dd60ceb9b2eb26973	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , dcbe7b08e26e87b570224fd8563dfb9c	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , e25714a0d31e957ef4074308b63f62dd	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , e31b99e67ce39c53ba174320a77fee27	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9

Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , e49ad4019da9ed9e1e649f86842797a7	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , e8b3c9826eb91e9cb1d134e6813d7c50	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , f3105871c4275f0f32c38dad8e92009f	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured Ruminococcaceae bacterium , 04ad0900f6ca40a4cfdd5aa5fe573031	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-013 , , 13f2aa7eee082413fe8ef99ea0f3588d	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-013 , , 59ca783b6bb69ac6bc4afc54ff188b38	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-013 , , 6715a46bfbf50463108c811598ad6fa3	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-013 , , 956ce06a0b7cf5b9656f71cfed63c943	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-013 , , e0cad1b2d41686cabc7acc9de6349001	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-013 , s__uncultured bacterium , 0f5441096fd3635602702bfab9b971f7	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-014 , , def163b9aa63ea47f493808878b43b8b	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-014 , s__gut metagenome , b9dd197c0eb8d3fa81037e099d48ac3c	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-014 , s__uncultured Clostridiales bacterium , d7fa3f5574ce9bacf68641b06073115b	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcus 1 , s__uncultured bacterium , a06c4ec058b3a1eac806b45e8dd0c14e	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcus 1 , s__uncultured bacterium , e37caaac0fdaf6b21036bb953f999dec	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__uncultured , s__uncultured bacterium , 9f483400ad9333110a3839d71bb0533d	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__uncultured , s__uncultured rumen bacterium , 4c5750493c6b27b454ba4a62332e0be2	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Planctomycetes , c__Planctomycetacia , o__Pirellulales , f__Pirellulaceae , g__CPla-4 termite group , s__uncultured bacterium , 82301d5a4e033e8f76025d58b6661749	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Proteobacteria , c__Deltaproteobacteria , o__Desulfovibrionales , f__Desulfovibrionaceae , g__uncultured , , fdf3ddf6fccab762e73f544dcb9935b6	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Tenericutes , c__Mollicutes , o__Izimaplasmatales , f__gut metagenome , g__gut metagenome , s__gut metagenome , 19130642aef003861546251fe5ac1980	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Tenericutes , c__Mollicutes , o__Mollicutes RF39 , , , , 80643135b723018b2c06f31b41fcf111	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Tenericutes , c__Mollicutes , o__Mollicutes RF39 , f__uncultured bacterium , g__uncultured bacterium , s__uncultured bacterium , 11efd508b9c8e7e11baec33d6264f041	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Winter18-19	Level , p__Verrucomicrobia , c__Verrucomicrobiae , o__Opitutales , f__Puniceicoccaceae , g__uncultured , s__metagenome , fa00e291ccbf836d84198b3d81548fa2	0.025636	0.129032	1	0.206257	0.365963	1	1	1	0	9	9	9
Monroe	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides , s__uncultured Bacteroides sp. , cc4491591a55666ca43817d2342c6de3	0.23452	0.123832	0.997514	0.626722	0.315668	1	0.638009	1	0	9	9	9
Monroe	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , , b9a3b8fa5bfc2cdee48fe4d1222f848d	0.256304	0.116642	0.994913	0.626722	0.315668	1	0.638009	1	0	9	9	9
Monroe	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Family XIII , g__Anaerovorax , s__uncultured bacterium , 63d3c7980625915ad6aa2319045a2c43	0.21123	0.127229	0.976351	0.626722	0.315668	1	0.638009	1	0	9	9	9
Monroe	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , e91a3ef0bbc2bb4b725c061319f6c1e9	0.190808	0.127971	0.945313	0.626722	0.315668	1	0.638009	1	0	9	9	9
Monroe	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , , , ec92ce8c965c1b6806146c78187e1e26	0.190808	0.127971	0.945313	0.626722	0.315668	1	0.638009	1	0	9	9	9

Monroe	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , s__uncultured Bacteroidales bacterium , 4e886de8a62d80d5afc301f1520e221e	0.185807	0.127898	0.936293	0.626722	0.315668	1	0.638009	1	0	9	9	9
Monroe	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , , 6cbfb98e95fb5dd3473def3120a87a5b	0.212449	0.147352	0.920863	0.392759	0.521486	0.867722	1	1	0.021866	9	9	9
Monroe	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Peptococcaceae , g__uncultured , , 94e013bebc4a60786b4c437da1d08fe4	0.171242	0.127182	0.907209	0.626722	0.315668	1	0.638009	1	0	9	9	9
Monroe	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Christensenellaceae , g__Christensenellaceae R-7 group , , 47b65bf0d498241aebde58bda676787d	0.161979	0.126358	0.886658	0.626722	0.315668	1	0.638009	1	0	9	9	9
Monroe	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Family XIII , g__Family XIII AD3011 group , s__uncultured Clostridiales Family XIII bacterium , a3d5e6336565023ba25de0cc482b3453	0.279125	0.088109	0.875	0.631676	0.275334	0.992157	0.612243	1	1.26E-06	9	9	9
Monroe	Level , p__Tenericutes , c__Mollicutes , o__Mollicutes RF39 , f__uncultured bacterium , g__uncultured bacterium , s__uncultured bacterium , ec91d6e7ee1d1976bba7405d55191b93	0.279125	0.088109	0.875	0.631676	0.275334	0.992157	0.612243	1	1.26E-06	9	9	9
Monroe	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group , s__uncultured bacterium , 31e3e7b39a611d8f5cf4aae2b4e42cde	0.153125	0.125317	0.865596	0.626722	0.315668	1	0.638009	1	0	9	9	9
Monroe	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides , s__uncultured Bacteroides sp. , 1d27345c3ca213f566b298db05466f81	0.137548	0.122899	0.825273	0.626722	0.315668	1	0.638009	1	0	9	9	9
Monroe	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminiclostridium 9 , , 4689da95a6dd6e65a83d91ef7414fa6e	0.265472	0.060183	0.695652	0.626722	0.23068	0.96875	0.638009	1	0.000155	9	9	9
SanJuan	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , d0a83c56ecb5c212c13c5a560676842a	0.117661	0.326687	0.54863	0.450564	0.662757	0.877584	1	0.586174	0.033404	8	8	8
Monroe	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides , s__uncultured Bacteroides sp. , 5a8d1319bd03e8dd95264884d3d6c1f7	0.075936	0.061537	0.546488	0.322264	0.189631	0.840606	1	1	0.040845	9	9	9
OquirrhStansbury	Level , p__Cyanobacteria , c__Melainabacteria , o__Gastranaerophilales , f__uncultured bacterium , g__uncultured bacterium , s__uncultured bacterium , d2c6f923beaca7d179f9ff79dd3e0b94	0.012029	0.000275	0.376812	-0.10685	-0.35142	-0.85737	1	1	0.028164	9	9	9
SanJuan	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides , , b5f53a1242a34fa06a0813c4052e9efd	0.11074	0.762602	0.370951	-0.46371	0.875	0.590671	1	0.035492	0.98504	8	8	8
OquirrhStansbury	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__F082 , g__uncultured bacterium , s__uncultured bacterium , 48cdfdd31abcab60abb822d8edf0724c	0.00938	0.002359	0.36235	-0.17897	-0.49055	-0.8339	1	1	0.046857	9	9	9
Winter18-19	Level , p__Verrucomicrobia , c__Verrucomicrobiae , o__Opitutales , f__Puniceicoccaceae , g__Cerasicoccus , s__uncultured bacterium , de00d94f498382837fe5aa1916328d48	0.026994	0.76981	0.343019	-0.0874	0.907222	0.572078	1	0.006577	0.967448	9	9	9
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , , , edddb10de1c1d1e1d6d4d41b249a4890	0.137855	0.184981	0.299785	0.452849	0.444657	0.656283	0.524528	0.593996	0.007068	26	26	26
Cache	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , , 2a0836f5337b66512ae45f0c0aa40d18	0.127925	0.300771	0.291703	0.512484	0.551659	0.657567	0.193237	0.090579	0.006809	26	26	26
Monroe	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Prevotellaceae , g__Prevotellaceae UCG-004 , s__uncultured bacterium , 3326971d1942c5f2708bf4f307283d46	0.149438	0.013903	0.272464	0.322264	0.189631	0.840606	1	1	0.040845	9	9	9
OquirrhStansbury	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminiclostridium 5 , s__uncultured bacterium , c071ae7d96e9d60afba4bc07616c1aae	0.036899	0.710304	0.271376	-0.23505	-0.90468	-0.50745	1	0.00721	1	9	9	9
Monroe	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group , , 5bfcd4e866c9d2fe68bf5943a88f9ec9	0.15302	0.001275	0.267658	0.463254	-0.06848	0.840606	1	1	0.040845	9	9	9
PineValley	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , , , 23b64b0d53b14a08f23ee0e0a806baf1	0.394918	0.399823	0.232643	-0.63814	-0.75948	-0.54648	0.024185	0.000606	0.160414	23	23	23
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , , 4f772fd0da3342d44a7b7bf3461a2c38	0.363183	0.168759	0.219957	0.536074	0.475428	0.630678	0.123763	0.366645	0.014362	26	26	26
Winter16-17	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , 2b1c6c0ba15f446196e1dfaf6088f4be	0.00994	0.047225	0.196911	0.107379	0.334073	0.504548	1	0.493653	0.001796	62	62	62
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , s__uncultured Ruminococcaceae bacterium , b867ec33eb48cd092e2e6dcc4d00d9c3	0.140488	0.274201	0.185371	0.340624	0.581383	0.379711	1	0.047832	1	26	26	26
Yearling	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides , , 6d3ed464e5af8d7ac4221254e8db59b2	0.301724	0.093137	0.601557	-0.47458	-0.28141	-0.87831	1	1	0.016506	9	9	9
Yearling	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides , s__uncultured Bacteroides sp. , 5a8d1319bd03e8dd95264884d3d6c1f7	0.093102	0.656701	0.63792	0.316745	0.699534	0.837436	1	0.323515	0.043617	9	9	9
Yearling	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 ,	0.03965	0.478733	0.607211	0.066918	0.479651	0.857395	1	1	0.028148	9	9	9

	s__uncultured bacterium , 7d12937301a5867893a812824e4c7409												
Yearling	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-014 , , 6931816a41d435d1dbf37323c5911a26	0.405152	0.372741	0.005304	0.8864	0.293609	-0.01869	0.013081	1	1	9	9	9
SanJuan	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group , s__uncultured bacterium , 78dedcf7eb47d7b606eb31cc7d287299	0.797401	0.021904	0.181992	-0.9084	0.018752	-0.32278	0.014333	1	1	8	8	8
Cache	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Alistipes , s__uncultured bacterium , 49ee58b13c10af6b5c97d9da479e4abb	0.058671	0.144889	0.176883	0.440529	0.574136	0.64696	0.631733	0.056199	0.009218	26	26	26
Winter16-17	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , , , 5dad1dc79c35f84ce8cae394d8a91b73	0.035523	0.03671	0.169006	0.172206	0.340655	0.530964	1	0.418056	0.000559	62	62	62
PineValley	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Christensenellaceae , g__Christensenellaceae R-7 group , s__uncultured prokaryote , f7bbc9acddff1fc57f714041837540c1	0.050177	0.291066	0.164936	-0.30665	-0.65999	-0.45737	1	0.01405	0.648902	23	23	23
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Caproiciproducens , s__uncultured bacterium , eb85206d10b8dc3e9b6aa22813a79542	0.006918	0.674128	0.127551	0.066778	-0.85309	-0.36423	1	0.031099	1	9	9	9
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae UCG-008 , s__uncultured rumen bacterium , c36b3131d775a0370dc732268cda661f	0.020396	0.658602	0.104167	0.034045	-0.8608	-0.41781	1	0.025958	1	9	9	9
Winter17-18	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , , 37942b8745b7e8727f0b9994c6a419ad	0.317894	0.351351	0.094943	-0.57257	-0.64834	-0.40414	0.058161	0.008867	1	26	26	26
Winter17-18	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae UCG-010 , , 5e3bb8f786fdf77707037446396e20a1	0.178161	0.416509	0.094353	-0.40361	-0.68188	-0.3511	1	0.003249	1	26	26	26
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 3d27de5d0b52f339f4eaa9c50384334c	0.004985	0.797438	0.091912	-0.0693	-0.85759	-0.28347	1	0.02802	1	9	9	9
PineValley	Level , p__Firmicutes , c__Bacilli , o__Lactobacillales , f__Streptococcaceae , g__Streptococcus , , 11435364553451d8ad9a00283ee743d3	0.343942	0.174264	0.088288	-0.61386	-0.53286	-0.35445	0.04222	0.203468	1	23	23	23
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Christensenellaceae , g__Christensenellaceae R-7 group , , 48bf2db09ac2eabd51feeb5e73d0645f	0.269477	0.17873	0.083449	-0.50218	-0.5935	-0.36264	0.232509	0.036225	1	26	26	26
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 262bd4b729869bc9ce1764ff73530444	0.029586	0.087672	0.082531	0.445562	0.498337	0.582074	0.585973	0.248787	0.047093	26	26	26
Winter17-18	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group , s__uncultured bacterium , e89b812979716c96d01b6162a152c846	0.110574	0.232813	0.081188	0.392275	0.606885	0.413497	1	0.026304	0.929515	26	26	26
Monroe	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , , , 935c2b2e0d3a4b87b5a140288ebe95e3	0.429399	0.066506	0.077005	0.874467	0.149445	0.606128	0.018332	1	0.752316	9	9	9
Winter17-18	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Christensenellaceae , g__Christensenellaceae R-7 group , , 53cda7b5f8fff34af36319ce1763ce00	0.144121	0.117548	0.073453	-0.50098	-0.61858	-0.46199	0.237517	0.019655	0.454995	26	26	26
SanJuan	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 867a9dbf65311fbccb6cc0e204049ed7	0.79657	0.005733	0.072748	-0.89392	0.201571	-0.05267	0.022017	1	1	8	8	8
PineValley	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , a17518c2a816f7d83cd9e71e0251ea78	0.354948	0.184356	0.072318	-0.61655	-0.40463	-0.29582	0.039779	1	1	23	23	23
Winter17-18	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , , , f81bff87ac9e92a3e3226e83a194bdb1	0.066084	0.242595	0.067903	-0.4326	-0.65223	-0.39141	0.7097	0.007941	1	26	26	26
Winter17-18	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 21effaa101d2ca4835fee11f54743a31	0.027942	0.014255	0.06281	-0.27418	-0.35322	-0.59784	1	1	0.032703	26	26	26
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , 7ba75135650451ac9f9bbbafae8b7174	0.001937	0.720046	0.055804	-0.14003	-0.86248	-0.2455	1	0.024916	1	9	9	9
Cache	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , , 50bdeea35a8d2507925cac78cae74a6c	0.383241	0.095175	0.054096	-0.59383	-0.36417	-0.27715	0.035941	1	1	26	26	26
Wasatch-Manti	Level , p__Actinobacteria , c__Coriobacteriia , o__Coriobacteriales , f__Eggerthellaceae , g__Enterorhabdus , s__uncultured rumen bacterium , eb570318b4cc9b0883ffc4f35d06a6b5	0.07646	0.040907	0.04186	-0.4679	-0.33277	-0.33887	0.047926	1	0.977098	46	46	46
Winter18-19	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae UCG-002 , s__uncultured rumen bacterium , 7e5b20120976d898eafbc8d5a137f0b1	0.138508	0.514868	0.039902	-0.2784	-0.85739	-0.24405	1	0.028148	1	9	9	9
PineValley	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Tyzzerella 4 , s__uncultured bacterium , 2937b97c81d9b0bbf872e2e9ccad7c12	0.295361	0.071222	0.025335	-0.72518	-0.42016	-0.30179	0.00208	1	1	23	23	23
Winter15-16	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 467b4334451ebbd88fec172eac048e0e	0.228021	0.001017	0.010656	0.571165	-0.12087	0.234725	0.042026	1	1	28	28	28
Winter15-16	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Tyzzerella 4 , s__uncultured bacterium , 530f97bbdff6b7a4f1d9512d1a43b43f	0.193688	0.010434	0.007181	0.59862	0.178683	-0.03001	0.021414	1	1	28	28	28

SanJuan	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , , 232c6391a23e610926b271734b7730c0	0.695136	0.090738	0.00056	-0.88786	0.32291	0.013079	0.025888	1	1	8	8	8
Winter15-16	Level , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__uncultured , g__uncultured bacterium , s__uncultured bacterium , f806136c6bb583e214457f2649a40861	0.052212	0.098853	0.000174	-0.1736	0.584311	0.102309	1	0.030656	1	28	28	28
SanJuan	Level , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , f1128d1d6b92bfd1b74354361a830f18	0.842496	0.1469	3.03E-05	-0.93223	0.214575	-0.11851	0.005914	1	1	8	8	8

Table S12. Full latitude analysis. Includes statistically significant correlations for adult deer samples at each taxonomic level.

Phylum					
Sample Subset	Taxonomic Level	Latitude_R2	Latitude_Coeff	Latitude_Adj._Pval	Latitude_N
Adult	Level , k__Bacteria , p__Kiritimatiellaeota	0.019198	0.180814	0.000373	764
Adult	Level , k__Bacteria , p__Spirochaetes	0.007508	0.179268	0.000468	764
Class					
Sample Subset	Taxonomic Level	Latitude_R2	Latitude_Coeff	Latitude_Adj._Pval	Latitude_N
Adult	Level , k__Bacteria , p__Kiritimatiellaeota , c__Kiritimatiellae	0.019198	0.180814	0.000373	764
Adult	Level , k__Bacteria , p__Proteobacteria , c__Deltaproteobacteria	0.017447	-0.15977	0.006957	764
Adult	Level , k__Bacteria , p__Spirochaetes , c__Spirochaetia	0.007508	0.179268	0.000468	764
Order					
Sample Subset	Taxonomic Level	Latitude_R2	Latitude_Coeff	Latitude_Adj._Pval	Latitude_N
Adult	Level , k__Bacteria , p__Kiritimatiellaeota , c__Kiritimatiellae , o__WCHB1-41	0.019198	0.180814	0.000373	764
Adult	Level , k__Bacteria , p__Proteobacteria , c__Deltaproteobacteria , o__Desulfovibrionales	0.017495	-0.15977	0.006958	764
Adult	Level , k__Bacteria , p__Spirochaetes , c__Spirochaetia , o__Spirochaetales	0.007508	0.179268	0.000468	764
Family					
Sample Subset	Taxonomic Level	Latitude_R2	Latitude_Coeff	Latitude_Adj._Pval	Latitude_N
Adult	Level , k__Bacteria , p__Actinobacteria , c__Coriobacteriia , o__Coriobacteriales , f__uncultured	0.009429	0.146847	0.035249	764
Adult	Level , k__Bacteria , p__Proteobacteria , c__Deltaproteobacteria , o__Desulfovibrionales , f__Desulfovibrionaceae	0.017495	-0.15977	0.006958	764
Adult	Level , k__Bacteria , p__Spirochaetes , c__Spirochaetia , o__Spirochaetales , f__Spirochaetaceae	0.007508	0.179268	0.000468	764
Genus					
Sample Subset	Taxonomic Level	Latitude_R2	Latitude_Coeff	Latitude_Adj._Pval	Latitude_N
Adult	Level , k__Bacteria , p__Actinobacteria , c__Coriobacteriia , o__Coriobacteriales , f__Eggerthellaceae , g__Enterorhabdus	0.007407	0.15937	0.007328	764
Adult	Level , k__Bacteria , p__Actinobacteria , c__Coriobacteriia , o__Coriobacteriales , f__uncultured , g__uncultured bacterium	0.00981	0.148135	0.03016	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Muribaculaceae ,	0.012677	0.183811	0.000238	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Prevotellaceae , g__Prevotellaceae UCG-004	0.026709	0.154728	0.013307	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__hoa5-07d05 gut group	0.020158	0.152744	0.017084	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__uncultured , g__uncultured bacterium	0.019288	0.193181	5.64E-05	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Dorea	0.017726	-0.15528	0.012404	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae AC2044 group	0.014275	0.150052	0.023859	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae UCG-001	0.032801	-0.18133	0.000345	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae UCG-008	0.016167	0.1982	2.53E-05	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Flavonifractor	0.010509	-0.15663	0.010441	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Negativibacillus	0.0318	-0.14878	0.027879	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminiclostridium 5	0.007217	-0.18307	0.000267	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcus 1	0.066589	0.241824	9.57E-09	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcus 2	0.027504	-0.1687	0.002097	764
Adult	Level , k__Bacteria , p__Planctomycetes , c__Planctomycetacia , o__Pirellulales , f__Pirellulaceae , g__CPla-4 termite group	0.021243	0.177216	0.00063	764
Adult	Level , k__Bacteria , p__Spirochaetes , c__Spirochaetia , o__Spirochaetales , f__Spirochaetaceae , g__Treponema 2	0.007508	0.179268	0.000468	764
Species					
Sample Subset	Taxonomic Level	Latitude_R2	Latitude_Coeff	Latitude_Adj._Pval	Latitude_N
Adult	Level , k__Bacteria , p__Actinobacteria , c__Coriobacteriia , o__Coriobacteriales , f__uncultured , g__uncultured bacterium , s__uncultured bacterium	0.00981	0.148135	0.03016	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides , s__uncultured Bacteroides sp.	0.023977	-0.15027	0.023217	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Muribaculaceae , ,	0.012677	0.183811	0.000238	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Prevotellaceae , g__Prevotellaceae UCG-004 , s__uncultured Bacteroidales bacterium	0.012033	0.144948	0.044251	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__hoa5-07d05 gut group , s__uncultured Bacteroidales bacterium	0.020158	0.152744	0.017084	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , s__uncultured bacterium	0.004838	0.14722	0.033696	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__uncultured , g__uncultured bacterium , s__uncultured bacterium	0.019288	0.193181	5.64E-05	764

Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Dorea , s__uncultured Lachnospiraceae bacterium	0.035733	-0.24684	3.48E-09	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae AC2044 group , s__uncultured bacterium	0.013413	0.153142	0.016253	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae UCG-001 , s__uncultured Lachnospiraceae bacterium	0.026568	-0.1623	0.004984	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae UCG-008 , s__uncultured rumen bacterium	0.012166	0.220242	5.80E-07	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Peptococcaceae , g__uncultured , s__uncultured organism	0.029736	-0.18426	0.000223	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__GCA-900066225 , s__uncultured bacterium	0.013374	-0.15751	0.009322	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Negativibacillus , s__uncultured bacterium	0.0318	-0.14878	0.027879	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminiclostridium 5 , s__uncultured bacterium	0.007721	-0.18749	0.000137	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcus 1 ,	0.031992	0.231722	6.88E-08	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcus 1 , s__Ruminococcus flavefaciens	0.021176	0.169778	0.001807	764
Adult	Level , k__Bacteria , p__Planctomycetes , c__Planctomycetacia , o__Pirellulales , f__Pirellulaceae , g__CPla-4 termite group , s__uncultured bacterium	0.021243	0.177216	0.00063	764
Adult	Level , k__Bacteria , p__Spirochaetes , c__Spirochaetia , o__Spirochaetales , f__Spirochaetaceae , g__Treponema 2 , s__uncultured bacterium	0.009154	0.205621	7.43E-06	764
ASV					
Sample Subset	Taxonomic Level	Latitude_R2	Latitude_Coeff	Latitude_Adj._Pval	Latitude_N
Adult	Level , k__Bacteria , p__Actinobacteria , c__Actinobacteria , o__Bifidobacteriales , f__Bifidobacteriaceae , , , 126aad2abec832f510f3c7cd31e6bc51	0.049618	-0.27899	3.05E-12	764
Adult	Level , k__Bacteria , p__Actinobacteria , c__Actinobacteria , o__Bifidobacteriales , f__Bifidobacteriaceae , , , 4a2331b8afa1fed7cb7ec37e8e96c398	0.022461	0.155048	0.012778	764
Adult	Level , k__Bacteria , p__Actinobacteria , c__Coriobacteriia , o__Coriobacteriales , f__Eggerthellaceae , g__DNF00809 , s__uncultured bacterium , 0f34383489f2b1b49ab017e0a59b3a10	0.009559	0.146586	0.036372	764
Adult	Level , k__Bacteria , p__Actinobacteria , c__Coriobacteriia , o__Coriobacteriales , f__Eggerthellaceae , g__DNF00809 , s__uncultured bacterium , 2011717e31d71111649c03cf31ae51a5	0.035622	0.227509	1.52E-07	764
Adult	Level , k__Bacteria , p__Actinobacteria , c__Coriobacteriia , o__Coriobacteriales , f__Eggerthellaceae , g__DNF00809 , s__uncultured bacterium , e26e258eaa272633fa02627125500be5	0.025142	0.24966	1.95E-09	764
Adult	Level , k__Bacteria , p__Actinobacteria , c__Coriobacteriia , o__Coriobacteriales , f__Eggerthellaceae , g__Enterorhabdus , s__uncultured bacterium , 08e47e2fe6593384c4d66397f2b24d33	0.021582	0.180097	0.000414	764
Adult	Level , k__Bacteria , p__Actinobacteria , c__Coriobacteriia , o__Coriobacteriales , f__Eggerthellaceae , g__Enterorhabdus , s__uncultured bacterium , 1c23fa2c54bf0c32d54a94562cad54b3	0.01229	0.155063	0.012753	764
Adult	Level , k__Bacteria , p__Actinobacteria , c__Coriobacteriia , o__Coriobacteriales , f__Eggerthellaceae , g__Enterorhabdus , s__uncultured rumen bacterium , d1c7f61ce9e794e8ee7eb5679ac56349	0.013104	0.167979	0.002316	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides , , 6e1aad1b91d2817d2c517ecabbe9d947	0.017667	0.215746	1.29E-06	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides , , b51d420b1793b22542b31899dac0e901	0.006431	0.149053	0.026966	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides , , e1c61a1046f394f90672780aa61452eb	0.025776	0.183856	0.000237	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides , , ec1f3306e8cb1e9b22014c4faa507994	0.009307	0.202541	1.24E-05	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides , , fe2e425ff10e99c7bd12697e09e4ce67	0.027832	0.280044	2.38E-12	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides , s__uncultured bacterium , 613db2b57b24d50434aa76fcd7de3e72	0.030985	0.236929	2.52E-08	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides , s__uncultured bacterium , d806520feb876b8bebb412b2780c8126	0.016726	0.149688	0.02495	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides , s__uncultured Bacteroides sp. , 47c4c556d8f1e7301a07421179a41c8a	0.022798	0.216177	1.20E-06	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides , s__uncultured Bacteroides sp. , 509ee24fc5fc0f658f5798c90c0a7793	0.016079	-0.14469	0.045607	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides , s__uncultured Bacteroides sp. , 5a8d1319bd03e8dd95264884d3d6c1f7	0.075626	-0.30425	6.06E-15	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides , s__uncultured Bacteroides sp. , 6b55f9b3ed37c51826a0054d98f0f6a5	0.022592	0.16234	0.004958	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides , s__uncultured Bacteroides sp. , a9fcfc8a4c9e91c6452f10664cfa94f9	0.015763	0.153448	0.015641	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides , s__uncultured Bacteroides sp. , b26a09ee06ac491ae808a870a7d99328	0.030646	-0.2487	2.37E-09	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides , s__uncultured Bacteroides sp. , cafd0eeb509485881fa1d7ef8e8a2018	0.022271	-0.17082	0.001564	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides , s__uncultured Bacteroides sp. , ceee10093571b81388d86b71ee3ea8e8	0.031121	-0.21228	2.38E-06	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Barnesiellaceae , g__uncultured , , bce3174b3dc6bc7efe54c5434245e5a1	0.006809	-0.18054	0.000388	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__F082 , g__uncultured bacterium , s__uncultured bacterium , dfb829edabc20b913bb87b943f1982b5	0.013132	0.188454	0.000118	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Marinifilaceae , g__Sanguibacteroides , s__Gabonibacter massiliensis , 85e1fa16a155933723022abb6adf8c47	0.017162	-0.15623	0.010994	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Muribaculaceae , , , 77f6bd8148f14e0531997c6bd854a173	0.007789	0.174268	0.000962	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Muribaculaceae , g__uncultured bacterium , s__uncultured bacterium , 08bbfbcff6792a84c9123e823bfc021f	0.014515	-0.14676	0.035611	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Muribaculaceae , g__uncultured bacterium , s__uncultured bacterium , 5f1d5f3323c6d03ab3f3323b2c4e5457	0.011174	0.199464	2.06E-05	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Muribaculaceae , g__uncultured bacterium , s__uncultured bacterium , 612b1eac3e95c5ad3f38048179efa072	0.004304	0.181398	0.000342	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Muribaculaceae , g__uncultured bacterium , s__uncultured bacterium , 75e91c227f9685c1f605d737ff6881b8	0.004116	0.274249	9.14E-12	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Prevotellaceae , g__Prevotellaceae UCG-004 , s__uncultured bacterium , 19d31b001318d82f6e59d1a478ef8a80	0.008702	0.176654	0.000684	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Prevotellaceae , g__Prevotellaceae UCG-004 , s__uncultured bacterium , 415406680b4f6ebe91936977ea5f1e48	0.014726	0.213422	1.95E-06	764

Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Prevotellaceae , g__Prevotellaceae UCG-004 , s__uncultured Bacteroidales bacterium , 202d553345f839ac47f58ffb7e7e8489	0.013929	0.143962	0.049741	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Alistipes , s__uncultured bacterium , dac0ec947a6f2f0f3b4c30bfe1c8dcaf	0.004939	-0.15257	0.017454	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Alistipes , s__uncultured bacterium , f71b78a43df7a5b5393736615f76d31f	0.020207	0.186255	0.000165	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__dgA-11 gut group , s__uncultured bacterium , 694d5bdadd0faf99d3ffb831e6b192a9	0.032511	0.166732	0.002747	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , , 26a68677933f681ed791f9302dc3ab56	0.000136	-0.15266	0.017258	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , , 5530b7c9f10c5b683ed5f32a73b7e3c9	0.013416	0.144598	0.046129	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , , 68055e2bb9273d9ce9feed6130a8c3b0	0.016526	-0.16081	0.00607	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , , b4120f2c61083cd674d2ab176c0d61fd	0.015107	0.165558	0.003221	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , s__uncultured bacterium , 43b764831af49aa1cb6c5d4062a55aff	0.029553	0.262256	1.34E-10	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , s__uncultured bacterium , c911c19e16d95159d4c611c8e8cc1b62	0.023532	0.146374	0.037312	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , s__uncultured bacterium , e0073a7e55271bc1c1730c2bc18bb76b	0.013423	0.145317	0.042344	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , s__uncultured Bacteroidales bacterium , 0c6bd93dda347c21944955c466cc069b	0.003783	-0.14694	0.034857	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , s__uncultured Bacteroidales bacterium , 4a65aa8a64b8e292b509686fc8b4253b	0.015154	-0.16555	0.003224	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , s__uncultured Bacteroidales bacterium , 4e886de8a62d80d5afc301f1520e221e	0.013429	0.230176	9.22E-08	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , s__uncultured Bacteroidales bacterium , 850188d4c809d1d7d9310ce542a67b67	0.005956	-0.1645	0.003714	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__uncultured , , , 583e66c4e3dd97194fc16ca29f34690a	0.01953	0.149637	0.025105	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__uncultured , g__uncultured bacterium , s__uncultured bacterium , 0b304999a8c36243a16cff856ab6450e	0.022888	0.17972	0.000438	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__uncultured , g__uncultured bacterium , s__uncultured bacterium , 3a09837ec2c2f446e46dc14ea56cc1f2	0.004114	0.144854	0.04475	764
Adult	Level , k__Bacteria , p__Cyanobacteria , c__Melainabacteria , o__Gastranaerophilales , , , , 10304c2abda761627220b6f202cf0f40	0.027039	0.180045	0.000417	764
Adult	Level , k__Bacteria , p__Cyanobacteria , c__Melainabacteria , o__Gastranaerophilales , f__uncultured bacterium , g__uncultured bacterium , s__uncultured bacterium , 97bd437a522627fd056a3447ac301b15	0.012248	-0.16214	0.005092	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Christensenellaceae , g__Christensenellaceae R-7 group , , 8579eaf08132041b20e3ec72f4690aa5	0.018999	-0.15232	0.018015	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Christensenellaceae , g__Christensenellaceae R-7 group , , 8f21db493e23f4b6bcad5fd904b2859f	0.010122	0.205458	7.63E-06	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Christensenellaceae , g__Christensenellaceae R-7 group , s__uncultured rumen bacterium , d4357e3deea47933b40f8f2dcb91a5a1	0.011181	0.14957	0.025313	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 244e776175bd9f10fd5eb8a20125aeaf	0.020047	-0.17324	0.001113	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 3d27de5d0b52f339f4eaa9c50384334c	0.004374	-0.1468	0.035433	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 76314928d015d16b68bb07ed7c1e21b7	0.026528	0.256194	4.95E-10	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , bdfd51e4ee9933559261ff98abfcb5e1	0.00662	0.1536	0.015343	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , bf49a90284d596106b657efe32d36dd9	0.016733	0.275812	6.38E-12	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , e697603d42fd7e764a0577666029b917	0.022645	-0.16187	0.005279	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , e91a3ef0bbc2bb4b725c061319f6c1e9	0.023998	0.17676	0.000673	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , ebce6bd04f41abc6281f7288838e5a10	0.027077	-0.20166	1.44E-05	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Dorea , s__uncultured Lachnospiraceae bacterium , 7722095207dc88f7b6509a7fd0316c32	0.040613	-0.25148	1.33E-09	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae AC2044 group , s__uncultured bacterium , 22b6fe0f1fdc573f9c7e86f6118b0b46	0.015647	0.158715	0.007979	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae NK3A20 group , s__uncultured rumen bacterium , 6461aa292e74eb0808f60b07dbc183eb	0.015869	0.183563	0.000248	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae NK3A20 group , s__uncultured rumen bacterium , b335b50e0d595d60d82ea63bc1dec6e6	0.01755	-0.20335	1.09E-05	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae UCG-001 , s__uncultured Lachnospiraceae bacterium , 44f73400ac069f18fee7d1f5031dc5f3	0.04506	-0.25075	1.55E-09	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae UCG-002 , , 31da3c46e046fd766c2101acd0d03126	0.010217	0.147966	0.030784	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae UCG-002 , s__uncultured rumen bacterium , 771cfecf5b7d352227b38c3aff188c5a	0.015785	-0.1592	0.007493	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae UCG-008 , s__uncultured rumen bacterium , c36b3131d775a0370dc732268cda661f	0.016894	0.261207	1.68E-10	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae XPB1014 group , , d3d62061e77c8e7e87fca28a6d89ac53	0.008187	0.166448	0.002855	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Marvinbryantia , s__uncultured rumen bacterium , fb9112e06c4132bc4c4ed09e60c83f9f	0.017407	-0.14737	0.033108	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Shuttleworthia , s__uncultured bacterium , 83ba8fdfd37671b116879799d59281a2	0.021625	-0.19009	9.15E-05	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Shuttleworthia , s__uncultured bacterium , a806f6a5d38a9a21dce89cb969852214	0.023629	-0.2032	1.11E-05	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Peptococcaceae , g__uncultured , s__uncultured organism , 699937f910096d3fffd9e4ac2bcefabf	0.018079	-0.1461	0.038568	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group , , 3b2ee55450ad72152fad229e135d236a	0.021278	0.174904	0.000879	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group , , 6cb638b6da370a7178baf6c42f01d0d1	0.019901	0.162702	0.004725	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group , , 9ea2af650fdaa7d59cdceef2ae3dd3c8	0.011747	-0.18925	0.000104	764

Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Flavonifractor , , e7f1a685324388d65300722f5ad81849	0.023499	-0.1478	0.031398	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__GCA-900066225 , , 3174faaa3f054fd27f6c7bd82356f33a	0.012882	0.149854	0.024446	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__GCA-900066225 , s__uncultured bacterium , 76a03b63f89b05912ddbc95c4d87b8f0	0.026581	-0.15883	0.007859	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Negativibacillus , s__uncultured bacterium , 61b8a1a526bf34889651da32c5e38455	0.021378	-0.17769	0.000589	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminiclostridium 1 , s__uncultured bacterium , a0c0cc1fbcb3d1a239d38ea783e427b2	0.016389	0.1462	0.038101	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminiclostridium 5 , s__uncultured bacterium , 11c70bd377cae9ede1dfe90276c7cca3	0.02155	-0.14771	0.031753	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminiclostridium 5 , s__uncultured bacterium , d605376d01e3bec87cca2756e1c351fa	0.018501	-0.15933	0.007364	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae NK4A214 group , s__uncultured bacterium , 697c15ce3ca09600b446dbc4a563fd98	0.015292	-0.14914	0.026672	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae NK4A214 group , s__uncultured bacterium , 6dfb4291462e75654b7cffb4bffd9cca	0.022627	-0.14445	0.046944	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae NK4A214 group , s__uncultured rumen bacterium , ae8855dfdf478e5b3a59664ed9c30743	0.025737	-0.16339	0.004313	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-005 , s__uncultured rumen bacterium , 48f1e8cf3e520701d22faf7ce9a53c4e	0.026605	0.215841	1.27E-06	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , , 03d67bf322771ff8ee3fab2a830959cc	0.031347	-0.18264	0.000284	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , , 2071bd5239b0f81ae816ec40d2283451	0.004435	-0.14854	0.028716	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , 7619cfddadf5f2452a1f595a63d9a9e6	0.027551	-0.19123	7.66E-05	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , 7b3af146bebf7184c0353671fcd1d611	0.016873	-0.1887	0.000113	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-013 , s__uncultured bacterium , 04a0ffb69d9670c5cf62a2f436d27b98	0.025001	0.192484	6.29E-05	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-014 , , 3838c7991557e5b2d199885188f5b661	0.009915	0.164007	0.00397	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-014 , s__uncultured rumen bacterium , f0bdde976b450093645a7190731566a9	0.012273	0.161622	0.005453	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcus 1 , , 03662dcd104aec9fb8fb45a72761a1ec	0.011417	0.154256	0.014126	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcus 1 , , 7602ae516855b78ea4ee0a4801e5ee33	0.016275	0.200555	1.72E-05	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcus 1 , , c196274bb1694853b1e3defc904b97b4	0.034388	0.22776	1.45E-07	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcus 1 , s__uncultured bacterium , 6b3b389f19a8a7d2f7a9cab742c68abd	0.019847	0.148842	0.02767	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcus 1 , s__uncultured bacterium , a9f84b44a6b243a1d0224b71a651983c	0.019924	0.199439	2.07E-05	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcus 1 , s__uncultured bacterium , d98f8d98687a48f0ba8442c0cbc5e1c0	0.011085	0.184581	0.000212	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Negativicutes , o__Selenomonadales , f__Acidaminococcaceae , g__Phascolarctobacterium , s__uncultured bacterium , 92c85de832fc150cce384bd21d83f5ca	0.035074	-0.18105	0.00036	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Negativicutes , o__Selenomonadales , f__Acidaminococcaceae , g__Phascolarctobacterium , s__uncultured bacterium , 9dda34760f2d13aeb961a9e6c6484c34	0.023111	0.179468	0.000454	764
Adult	Level , k__Bacteria , p__Planctomycetes , c__Planctomycetacia , o__Pirellulales , f__Pirellulaceae , g__CPla-4 termite group , s__uncultured bacterium , 82301d5a4e033e8f76025d58b6661749	0.017211	0.169485	0.001882	764
Adult	Level , k__Bacteria , p__Proteobacteria , c__Deltaproteobacteria , o__Desulfovibrionales , f__Desulfovibrionaceae , g__Mailhella , s__uncultured bacterium , 2febaa04d25bfef12a4b879d634d70dc	0.02289	-0.17861	0.000515	764
Adult	Level , k__Bacteria , p__Spirochaetes , c__Spirochaetia , o__Spirochaetales , f__Spirochaetaceae , g__Treponema 2 , s__uncultured bacterium , 6619eb4628f7f376558c6a9427bd24cc	0.030629	0.175407	0.000818	764
Adult	Level , k__Bacteria , p__Verrucomicrobia , c__Verrucomicrobiae , o__Verrucomicrobiales , f__Akkermansiaceae , g__Akkermansia , s__uncultured bacterium , 1b77636b96aa24bda840b90a0a76e4bc	0.016621	0.1448	0.045033	764
Adult	Level , k__Bacteria , p__Verrucomicrobia , c__Verrucomicrobiae , o__Verrucomicrobiales , f__Akkermansiaceae , g__Akkermansia , s__uncultured bacterium , 5102ddb2fcb7ac7ebd0d28c9474847ba	0.013092	-0.17665	0.000684	764

Table S13. Full elevation analysis. Includes statistically significant correlations for adult deer samples at each taxonomic level.

Phylum					
Sample Subset	Taxonomic Level	Elevation_R2	Elevation_Coeff	Elevation_Adj.Pval	Elevation_N
Class					
Sample Subset	Taxonomic Level	Elevation_R2	Elevation_Coeff	Elevation_Adj.Pval	Elevation_N
Order					
Sample Subset	Taxonomic Level	Elevation_R2	Elevation_Coeff	Elevation_Adj.Pval	Elevation_N
Family					
Sample Subset	Taxonomic Level	Elevation_R2	Elevation_Coeff	Elevation_Adj.Pval	Elevation_N
Adult	Level , k__Bacteria , p__Actinobacteria , c__Coriobacteriia , o__Coriobacteriales ,	0.012054	0.162158	0.005079	764

Genus					
Sample Subset	Taxonomic Level	Elevation_R2	Elevation_Coeff	Elevation_Adj.Pval	Elevation_N
Adult	Level , k__Bacteria , p__Actinobacteria , c__Coriobacteriia , o__Coriobacteriales , ,	0.012054	0.162158	0.005079	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Family XIII , g__Family XIII AD3011 group	0.017994	-0.17206	0.001314	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae FE2018 group	0.014893	0.187648	0.000133	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae NK4B4 group	0.015802	-0.17786	0.000574	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Caproiciproducens	0.036221	-0.14855	0.028669	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminiclostridium 5	0.016818	-0.15908	0.007606	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-002	0.017047	-0.14474	0.045343	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-014	0.004916	-0.15488	0.01305	764
Species					
Sample Subset	Taxonomic Level	Elevation_R2	Elevation_Coeff	Elevation_Adj.Pval	Elevation_N
Adult	Level , k__Bacteria , p__Actinobacteria , c__Coriobacteriia , o__Coriobacteriales , , ,	0.012054	0.162158	0.005079	764
Adult	Level , k__Bacteria , p__Actinobacteria , c__Coriobacteriia , o__Coriobacteriales , f__Eggerthellaceae , g__DNF00809 ,	0.00934	0.14843	0.029098	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae FE2018 group , s__bacterium FE2018	0.014532	0.188658	0.000114	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae NK4B4 group , s__uncultured bacterium	0.016356	-0.18631	0.000163	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminiclostridium 5 , s__uncultured bacterium	0.015823	-0.15348	0.015579	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae NK4A214 group , s__uncultured rumen bacterium	0.049212	-0.20887	4.28E-06	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-002 , s__uncultured bacterium	0.018547	-0.16107	0.005864	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-014 ,	0.00447	-0.16279	0.004668	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-014 , s__uncultured bacterium	0.016117	-0.17974	0.000437	764
ASV					
Sample Subset	Taxonomic Level	Elevation_R2	Elevation_Coeff	Elevation_Adj.Pval	Elevation_N
Adult	Level , k__Bacteria , p__Actinobacteria , c__Actinobacteria , o__Bifidobacteriales , f__Bifidobacteriaceae , , , 126aad2abec832f510f3c7cd31e6bc51	0.01039	-0.16531	0.003332	764
Adult	Level , k__Bacteria , p__Actinobacteria , c__Coriobacteriia , o__Coriobacteriales , f__Eggerthellaceae , g__DNF00809 , s__uncultured bacterium , babbd17ea6acd534511cbdd8089b5592	0.008981	0.150868	0.021574	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides , , 6e1aad1b91d2817d2c517ecabbe9d947	0.029682	0.183381	0.000254	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides , , cf95ac1e123ec4a3b6354ef1e6488777	0.017996	0.148225	0.02983	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides , s__uncultured bacterium , 178542b2981e5592d0b652e266d829d5	0.014923	0.158086	0.008657	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides , s__uncultured Bacteroides sp. , 2ffc6290b27a96b4b16e9f14288cb398	0.020185	0.163961	0.003995	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides , s__uncultured Bacteroides sp. , 47c4c556d8f1e7301a07421179a41c8a	0.013142	0.182928	0.000272	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides , s__uncultured Bacteroides sp. , 5a8d1319bd03e8dd95264884d3d6c1f7	0.039603	-0.18259	0.000286	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides , s__uncultured Bacteroides sp. , a31e7ca794e6663ff211ef3d61773b9c	0.021196	-0.16507	0.003441	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Bacteroidaceae , g__Bacteroides , s__uncultured Bacteroides sp. , f4c5cdfccf496b6bebd5f08d5cf59647	0.020714	-0.15999	0.006756	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Alistipes , s__uncultured bacterium , 49ee58b13c10af6b5c97d9da479e4abb	0.015246	-0.17356	0.001064	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , , 26a68677933f681ed791f9302dc3ab56	0.004071	-0.14528	0.042548	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , s__uncultured Bacteroidales bacterium , 0c6bd93dda347c21944955c466cc069b	0.017001	-0.18357	0.000247	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , s__uncultured Bacteroidales bacterium , 3fc97fb46eade0a81422d3fb740e3dba	0.005179	0.147229	0.033657	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , s__uncultured Bacteroidales bacterium , 5dec64bfb7ed2f7fa18d2280c98d4491	0.012893	-0.21427	1.68E-06	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__Rikenellaceae , g__Rikenellaceae RC9 gut group , s__uncultured Bacteroidales bacterium , 8d8aad38a560be76cfe9350fb6f9020c	0.0056	-0.19171	7.11E-05	764
Adult	Level , k__Bacteria , p__Bacteroidetes , c__Bacteroidia , o__Bacteroidales , f__uncultured , , , 02c150baa32454e2fee2e1b84407c9a2	0.023964	-0.20734	5.56E-06	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Christensenellaceae , g__Christensenellaceae R-7 group , , 3e638e44c1ef67bf6503944b4e8aea2c	0.020521	-0.17373	0.001038	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Christensenellaceae , g__Christensenellaceae R-7 group , , 69aef149c527db753db41797d9fd9742	0.016705	-0.15495	0.012943	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Christensenellaceae , g__Christensenellaceae R-7 group , , 7e5e2897270e1e9c359e1511bd725c68	0.020739	-0.17199	0.001328	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Christensenellaceae , g__Christensenellaceae R-7 group , , f45ad971967c4657765552d7032edff2	0.015036	0.150155	0.023558	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Christensenellaceae , g__Christensenellaceae R-7 group , s__uncultured prokaryote , 053434fe25c31935f8edc6557b7cebd8	0.030475	0.184503	0.000215	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 244e776175bd9f10fd5eb8a20125aeaf	0.030647	-0.14598	0.039118	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 867a9dbf65311fbccb6cc0e204049ed7	0.009632	0.174336	0.000953	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , 9d1801f353bd327f4c87a3acca800256	0.007455	-0.15171	0.019429	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , dc9ebfb37254a4862c1890b26c9ceea0	0.046121	-0.18418	0.000226	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , , , ebce6bd04f41abc6281f7288838e5a10	0.048266	-0.20196	1.37E-05	764

Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Lachnospiraceae FE2018 group , s__bacterium FE2018 , 0fa4bc34e153544af446f3e2a931b8af	0.017286	0.224379	2.72E-07	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Lachnospiraceae , g__Marvinbryantia , s__uncultured bacterium , 39a0eba5cec3d61b5a72f86754ca1e2a	0.012904	0.146408	0.037159	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , , , 5e6f162e2e88970cf3c01694a92e0692	0.044649	-0.14804	0.030523	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__[Eubacterium] coprostanoligenes group , , 6b93494279e6534d3bc450dd0fac2f31	0.027808	-0.14769	0.031832	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Intestinimonas , , 91223ec5064454a1134c9d67dffa8f34	0.016934	0.167161	0.002591	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Negativibacillus , s__uncultured bacterium , 61b8a1a526bf34889651da32c5e38455	0.050485	-0.18743	0.000138	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Oscillibacter , s__uncultured bacterium , 6abee690210d97b024c227c0a9c3882f	0.025566	0.182219	0.000303	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae NK4A214 group , s__uncultured rumen bacterium , ae8855dfdf478e5b3a59664ed9c30743	0.057829	-0.19122	7.68E-05	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-002 , s__uncultured bacterium , 3a22296adc9621145bbea6b9a982b33b	0.020722	-0.15737	0.009493	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-010 , s__uncultured bacterium , 72d5d6ca0cb143a33a518c330ce5aa64	0.024018	-0.14783	0.031296	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__Ruminococcaceae UCG-014 , s__uncultured bacterium , 24c1566a353ec4b38bf34b9ef043db95	0.010425	-0.1551	0.01269	764
Adult	Level , k__Bacteria , p__Firmicutes , c__Clostridia , o__Clostridiales , f__Ruminococcaceae , g__uncultured , , cff37584a712ea6db7767c8b449d718c	0.000963	-0.16242	0.004906	764
Adult	Level , k__Bacteria , p__Proteobacteria , c__Deltaproteobacteria , o__Desulfovibrionales , f__Desulfovibrionaceae , g__Mailhella , s__uncultured bacterium , 758204d53a5a2bdb308cc43775c74310	0.019258	0.144195	0.048387	764