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Aquacultured Rainbow Trout (*Oncorhynchus mykiss*) Possess a Large Core Intestinal Microbiota That Is Resistant to Variation in Diet and Rearing Density

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As global aquaculture fish production continues to expand, an improved understanding of how environmental factors interact in fish health and production is needed. Significant advances have been made toward economical alternatives to costly fishmeal-based diets, such as grain-based formulations, and toward defining the effect of rearing density on fish health and production. Little research, however, has examined the effects of fishmeal- and grain-based diets in combination with alterations in rearing density. Moreover, it is unknown whether interactions between rearing density and diet impact the composition of the fish intestinal microbiota, which might in turn impact fish health and production. We fed aquacultured adult rainbow trout (*Oncorhynchus mykiss*) fishmeal- or grain-based diets, reared them under high- or low-density conditions for 10 months in a single aquaculture facility, and evaluated individual fish growth, production, fin indices, and intestinal microbiota composition using 16S rRNA gene sequencing. We found that the intestinal microbiotas were dominated by a shared core microbiota consisting of 52 bacterial lineages observed across all individuals, diets, and rearing densities. Variations in diet and rearing density resulted in only minor changes in intestinal microbiota composition despite significant effects of these variables on fish growth, performance, fillet quality, and welfare. Significant interactions between diet and rearing density were observed only in evaluations of fin indices and the relative abundance of the bacterial genus *Staphylococcus*. These results demonstrate that aquacultured rainbow trout can achieve remarkable consistency in intestinal microbiota composition and suggest the possibility of developing novel aquaculture strategies without overtly altering intestinal microbiota composition.

As aquaculture's contribution to global food fish consumption continues to increase (1), alternatives to fishmeal as the traditional protein source in aquaculture feeds need to be researched, refined, and adopted for sustainable industry growth (2, 3). Much research has focused on all-plant-protein diets and their impact on fish performance (4), palatability (5), and digestibility (6); water quality (7); intestinal inflammation (8); and the community of microorganisms residing in the intestine (microbiota) (9). Overall, significant advances have been made in alternative protein diet formulations in recent years, so that the growth performance of fish fed grain-based diets has been reported to be comparable to that of fish fed traditional fishmeal-based diets (7, 10). Limited research, however, has examined the effects of grain-based feeds in combination with alterations in fish-rearing density. Provided that a given aquaculture system's carrying capacity can support increases in fish biomass, larger harvests can, in theory, be attained by increasing the rearing density as fish are raised to market size. Inappropriately high rearing densities, however, can have negative effects on fish production and are commonly associated with decreased growth, decreased feed intake, reduced feed efficiency, and greater fin erosion (11). Whether these density-associated changes in performance and welfare are consistent when fish are fed either fishmeal- or grain-based diets remains unclear. Moreover, it remains unknown whether interactions between fish-rearing density and diet composition impact the composition of the intestinal microbiota. This gap in our knowledge is significant,

because processes such as intestinal inflammation, dietary energy harvest, and behavior in other vertebrate species are due in part to alterations in intestinal microbiota composition (12–19).

A fundamental challenge in host-associated microbial ecology is determining the extent to which microbial lineages in a given host are shared among other hosts. Previous studies have shown that a subset of microbial lineages harbored by an individual host might also be found in many or all other individual hosts, a concept often referred to as a “core microbiota.” This term can be variably defined based on the taxonomic level or the degree of ubiquity and abundance among individual hosts under a given experimental condition, in a given environment, or in a given host species (20, 21). Although detection of a core microbiota is strongly affected by sample number, sampling depth, and many

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genetic and environmental factors, these factors can be addressed through careful experimental design. The relatively consistent environmental, dietary, and husbandry parameters inherent in aquaculture facilities provide attractive opportunities to explore the potential for a core microbiota in animal hosts. As new strategies for aquaculture enhancements are developed, it will be important to determine whether core microbiotas occur in aquaculture settings and whether such cores are affected by husbandry variation.

Our current information on the gut microbiota of rainbow trout (*Oncorhynchus mykiss*) is derived from analysis of culturable microorganisms (22–24) and culture-independent studies using fingerprinting and sequencing of 16S rRNA and other microbial genes (9, 23, 25–27). These studies have revealed that the rainbow trout gut microbiota is dominated by the bacterial phyla *Proteobacteria* and *Firmicutes*, the same phyla that dominate the intestines of many other fishes (16, 28, 29). In contrast to these methodologies, high-throughput pyrosequencing of 16S rRNA genes permits unbiased identification of rare, as well as abundant, bacterial members of the gut microbiota at low cost per sequence. The gut microbiota of aquacultured trout has previously been analyzed by pyrosequencing of the *cpn60* gene (9, 30), but not the more commonly studied 16S rRNA gene. In this study, we tested whether long-term differences in rearing density and diet, alone and in combination, lead to alterations in animal performance, welfare, fillet quality, or gut microbiota using 16S rRNA gene pyrosequencing.

MATERIALS AND METHODS

Experimental treatments, fish performance data collection, and processing attributes. All experiments involving rainbow trout were conducted in compliance with the requirements of the Animal Welfare Act (9CFR) and were approved by the Freshwater Institute's Institutional Animal Care and Use Committee.

A flowthrough fish culture system consisting of 12 circular 500-liter tanks was employed in this study, using water from a spring source with approximately constant 12.5°C temperature. Eyed rainbow trout eggs were procured from Troutlodge, Inc. (Sumner, WA); hatched alevins were then transferred to two of the 12 flowthrough tanks for introduction to feed. Fishmeal-based starter feed was used for all fish during this acclimation period. When the fish reached approximately 10 g, they were recombined in one tank and then randomly distributed in equal numbers to all 12 flowthrough tanks. The fish were subsequently fed either the experimental fishmeal- or grain-based feed (Table 1) for the remainder of the study and were reared in one of two density ranges: either 20 to 40 kg/m³ (low density) or 40 to 80 kg/m³ (high density). As the tanks approached the maximum density (40 or 80 kg/m³) for their specific treatment, fish were culled to reduce densities to low-end levels (20 or 40 kg/m³). The diet and density treatments were randomly allocated within the 12-tank system, so that each of the four diet/density treatment groups was replicated in three study tanks. Monthly length and weight assessments were made for each tank over the 10-month study to update their biomass increase and to guide density adjustments. All sampled fish were first anesthetized (75 mg/liter tricaine methanesulfonate [MS-222; Tricaine-S; Western Chemical Inc., Ferndale, WA]) prior to collection of performance data. Dead animals were removed and recorded daily to assess cumulative survival. Feed was administered by an in-house-designed computer-operated program to identical feeders for all 12 experimental tanks, with feeding events approximately once per hour. Daily feed levels were determined using standardized feed charts for rainbow trout; however, minor adjustments to daily feeding amounts were occasionally made based on visual observations of increased appetite or satiation. Overall thermal growth coefficients (TGC) and feed conversion ratios (FCR) were

TABLE 1 Nutritional compositions of the fishmeal- and grain-based experimental diets utilized

Ingredient	Amt (g/kg)	
	Fishmeal diet	Grain-based diet
Fish meal ^a	312.7	
Blood meal ^b	74.7	
Soy protein concentrate ^c		289.1
Corn gluten meal ^d		251.7
Soybean meal ^e	192.4	
Wheat gluten meal ^e		46.5
Wheat flour ^f	284.0	
Menhaden oil ^g	112.0	167.4
Vitamin premix ^h	7.5	7.5
Lysine		11.1
Methionine		2.8
Taurine		5.0
Dicalcium phosphate		36.5
Trace mineral premix ⁱ	1.0	1.0
Choline CL	2.0	2.0
Ascorbic acid ^j	2.0	2.0
Astaxanthin ^k		0.2
Total protein (%)	41.0	47.5
Total fat (%)	15.1	18.0

^a Omega Proteins; Menhaden Special Select; 628 g/kg protein.

^b IDF Inc.; 832 g/kg protein.

^c Solae; Pro-Fine VF; 693 g/kg crude protein.

^d Cargill; 602.0 g/kg protein.

^e ADM Inc.; 480 g/kg protein.

^f Manildra Milling; 120 g/kg protein.

^g Omega Proteins Inc.

^h United States Fish and Wildlife Service (USFWS) no. 30. Amounts contributed per kilogram of diet were as follows: vitamin A (as retinol palmitate), 10,000 IU; vitamin D₃, 720 IU; vitamin E (as DL- α -tocopherol acetate), 530 IU; niacin, 330 mg; calcium pantothenate, 160 mg; riboflavin, 80 mg; thiamine mononitrate, 50 mg; pyridoxine hydrochloride, 45 mg; menadione sodium bisulfate, 25 mg; folic acid, 13 mg; biotin, 1 mg; vitamin B₁₂, 30 μ g.

ⁱ USFWS no. 3. Amounts contributed (mg/kg of diet) were as follows: zinc, 37; manganese, 10; iodine, 5; copper, 1.

^j Rovimix Stay-C; 35%; DSM Nutritional Products.

^k Carophyl Pink; DSM Nutritional Products.

calculated for each tank at the end of the study period, based on the final performance data, and compared between treatments as follows: $TGC = [(\text{final mean weight}^{1/3} - \text{initial mean weight}^{1/3}) / (\text{days during interval} \times \text{mean temperature})] \times 1,000$ and $FCR = \text{feed}_{\text{cumulative}} / \text{biomass gain}$, where weight is in grams, length is in millimeters, and temperature is in °C. At study's end (312 days posthatch), 5 randomly selected fish were removed from each tank, euthanized with an overdose (200 mg/liter) of MS-222, eviscerated, and processed to yield butterfly fillets. The butterfly fillet is produce when the head, viscera, and vertebral column and ribs have been removed. The dress yield (percent) (i.e., the head-on gutted yield) was calculated as follows: $\text{eviscerated weight} / \text{whole weight} \times 100$. The pectoral girdle, belly flaps (approximately 1-cm strips along the ventral midline), and skin were removed from the butterfly fillets. The fillets were weighed, and the fillet yield (percent) was calculated as follows: $\text{fillet weight} / \text{whole weight} \times 100$.

16S rRNA gene sequencing and analyses. At 312 days posthatch (after 214 days under study treatment protocols), 3 fish/tank (2 or 3 tanks/treatment combination; 33 fish total) were randomly selected and euthanized with 200 mg/liter MS-222 (Western Chemical Inc., Ferndale, WA), and uniform 5-cm midintestine segments were carefully resected, flash frozen in liquid nitrogen, and stored at -80°C . Intestinal samples were shipped overnight on dry ice to the Core for Applied Genomics and Ecology, University of Nebraska (Lincoln, NE). Total genomic DNA was extracted from intestinal samples using Qiagen (Valencia, CA) Stool Kits.

From the resulting DNA, the V₁-V₃ region of bacterial 16S rRNA genes was amplified using F8 and R518 primers tagged with the A and B Roche 454 Titanium sequencing adapters. The F8 primers were modified to contain an 8-base barcode unique to each sample (see Table S1 in the supplemental material). Pyrosequencing was performed by pooling all samples in a single region of a 2-region Titanium PicoTitre plate. Sequence data were filtered and analyzed with QIIME (31) using default parameters with the following exceptions: we removed sequences with ≥ 50 consecutive bases possessing an average quality score of < 25 or with lengths of < 150 or $> 1,000$ bases. Sequences were then grouped by trout sample based on their barcodes; we used the QIIME denoiser algorithm (32) to denoise the sequences. The denoised sequences were binned by the UCLUST method into operational taxonomic units (OTUs) using a threshold of 97% or higher sequence identity. Representative sequences from each OTU were then aligned to the Greengenes core set (version gg_otus_4feb2011/taxonomies/greengenes_tax_rdp_train.txt) using PyNast (33). The representative sequences from each OTU were also taxonomically classified using the RDP Classifier program (34). Consensus lineages were assigned at each taxonomic level if $\geq 90\%$ of the sequences in the OTU agreed with the classification. We also used the QIIME ChimeraSlayer algorithm to identify and exclude from subsequent analysis any OTUs with chimeric representative sequences. Additionally, OTUs assigned to the phylum *Cyanobacteria* were considered potential plant chloroplast contaminants and removed from the analysis. After the above filtering steps, a total of 185,216 high-quality bacterial 16S rRNA gene sequences remained for analysis. OTUs and their consensus lineages are tabulated in Table S4 in the supplemental material. To determine the relative abundance of each bacterial taxon, OTUs were binned according to their consensus lineages (see Table S3 in the supplemental material). To assess the degree of dissimilarity between the gut microbiotas of different samples, we conducted weighted and unweighted UniFrac analyses using 1,345 sequences from each sample. UniFrac distance matrices were graphically represented using principal-coordinates analysis (PCoA). Additionally, we calculated nonphylogenetic distances between samples by performing binary Jaccard analyses. To determine the bacterial diversity within individuals, we calculated Chao1, Shannon diversity index, and phylogenetic-distance values for each sample (see Table S2 in the supplemental material). LEfSe software (35) was used to identify discriminatory bacterial groups between conditions using sequences that had been taxonomically classified with RDP Classifier in QIIME. Taxa identified as discriminatory between two conditions were further subjected to two-way analysis of variance (ANOVA), followed by Bonferroni posttest using GraphPad Prism software. All analyses were performed using default parameters.

Fin quality assessments. During the final sampling event, 25 fish from each tank were anesthetized and measured for fork length. Then, using digital microcalipers, the maximum length (i.e., the longest ray) of the following fins was measured to the nearest 0.1 mm: left and right pectoral, left and right pelvic, dorsal, ventral, and the top and bottom poles of the caudal fin. Fin indices (36) for all eight measured fins or fin components were then calculated by dividing their individual lengths by the fork length.

Fillet quality and contaminant analyses. Fillet samples collected for processing attribute evaluation were sent to West Virginia University (Morgantown, WV) for the following assessments: cook yield, instrumental texture, proximate composition, and fatty acid profiles. Standard laboratory methods were used to determine the fillet cook yield and texture (37). Analyses of fillet moisture, fat, protein, and ash were performed according to AOAC-approved methods (38). Total lipids were extracted from muscle according to the method of Bligh and Dyer (39). Fatty acid analysis was performed on powdered muscle and minced visceral adipose tissue. Fatty acids were methylated using the method described by Fritsche and Johnston (40). Nonadecanoic acid (19:0) was used as an internal standard. Fatty acid methyl esters (FAMES) were quantified using a Varian CP-3800 Gas Chromatograph (Varian Analytical Instruments, Walnut Creek, CA, USA) equipped with a flame ionization detector. FAMES were

identified based on comparison to retention times of standard FAMES (Supelco quantitative standard FAME 37; Sigma-Aldrich, St. Louis, MO, USA). Peak area counts were computed by an integrator using the Star GC workstation version 6 software (Varian Inc.) and reported as percent fatty acid.

To determine pesticide and polychlorinated biphenyl (PCB) levels, at study's end, 3 fish were randomly selected from each of the 6 high-density tanks, euthanized with MS-222, and filleted. These 18 fillet samples were sent fresh on ice to Northeast Analytical Inc. (Schenectady, NY), where they were processed, homogenized, and analyzed. The Soxhlet extraction method (EPA Method 3540C) was employed for all fillet samples; analysis for organochlorine pesticides was performed by EPA Method 8081. Analysis for PCB congeners was performed by Comprehensive Quantitative Congener Specific PCB Method (Northeast Analytical Inc. Standard Operating Procedure NE133_02); a total of 209 PCB congeners were quantified. The pesticides quantified included aldrin, alpha-chlordane, alpha-benzene hexachloride (BHC), beta-BHC, chlordane, delta-BHC, dieldrin, endosulfan I, endosulfan II, endosulfan sulfate, endrin, endrin aldehyde, endrin ketone, gammachlordane, gamma-BHC, heptachlor, heptachlor epoxide, hexachlorobenzene, methoxychlor, p,p'-DDD (dichlorodiphenyldichloroethane), p,p'-DDE (dichlorodiphenyldichloroethylene), p,p'-DDT (dichlorodiphenyltrichloroethane), and toxaphene.

Histopathology evaluations. At study's end, the 5 fish per tank randomly selected for processing attribute assessment also had standardized 3-cm sections of the posterior intestine removed and fixed in 10% neutral buffered formalin (3.7% formaldehyde). The fixed samples were sent to the Washington Animal Disease Diagnostic Laboratory (Pullman, WA) for histopathology evaluation. A 0- to 5-point grading scale was developed to quantify the extent and severity of intestinal inflammation, with 0 representing normal healthy tissue and 5 denoting severe inflammation with loss of mucosal integrity across most or all of the tissue evaluated. All animals displayed at least minimal inflammation, and severe inflammation (i.e., a score of 4) was observed in only one fish from the low-density, fishmeal diet group.

Statistical analysis. Measurements of final fish performance, health, and yield were assessed for treatment effects using multivariable ANOVA, with diet, density, and diet-density interaction as independent variables. Contaminant data were analyzed with ANOVA for diet effects only. An alpha level of 0.05 was used to determine statistical significance. Relative abundances of bacterial taxa were considered significant by LEfSe (35) analysis if the Kruskal-Wallis test yielded an alpha value of < 0.05 , the pairwise Wilcoxon test yielded an alpha value of < 0.05 , and the logarithmic LDA effect score reached 2.0. LEfSe results were confirmed if two-way ANOVA yielded a *P* value of < 0.05 . Relative abundances of core OTUs were normalized by log₁₀ transformation (41) prior to determining statistical significance using pairwise Student's *t* tests and a 5% false-discovery rate.

Nucleotide sequence accession number. The 16S rRNA gene sequence data have been submitted to MG-RAST under accession number 4509015.3 (<http://metagenomics.anl.gov/linkin.cgi?metagenome=4509015.3>).

RESULTS

Rainbow trout intestines possess a large core microbiota that persists following long-term alteration in rearing density and diet. We sought to define the effects of diet composition and rearing density on the rainbow trout intestinal microbiota through 16S rRNA gene sequencing. Fish were raised together under identical conditions and fed a fishmeal-based diet until they averaged approximately 10 g, and then they were randomly distributed to flowthrough tanks and reared at high or low density and fed either fishmeal- or grain-based diets for 214 days. Genomic DNA was extracted from the midintestines of these animals, and their respective bacterial communities were evaluated using 454 pyrosequencing.

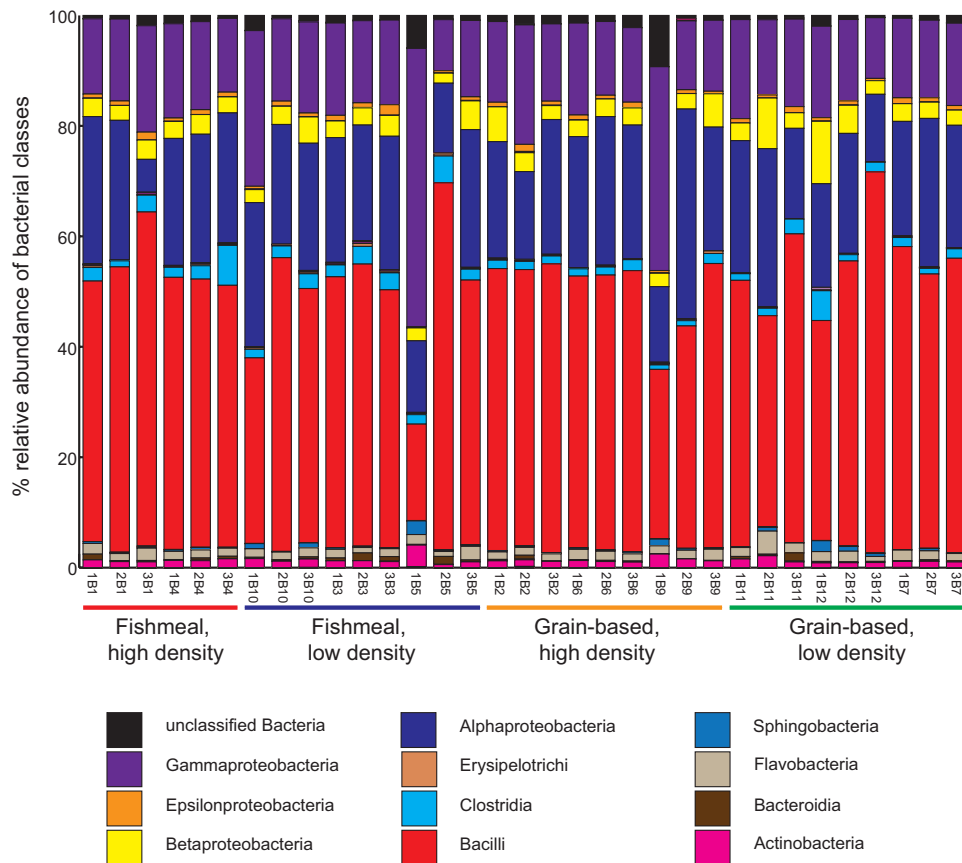


FIG 1 16S rRNA gene sequences reveal similarities between intestinal microbiotas of rainbow trout raised under different diet and density conditions. Shown are relative abundances of bacterial classes in each sample. The labels under each column are sample names corresponding to individual fish. Numerical suffixes indicate the tank number, numerical prefixes identify biological replicates drawn from a given tank, and the letter B acts as a delimiter to separate the tank number from the fish number. The legend includes only taxa constituting 0.005% or more of at least one sample. For each treatment condition, samples were taken from 2 or 3 different tanks, and 3 biological samples were analyzed per tank.

quencing of the V_1 - V_3 region of 16S rRNA genes (3 fish/tank; 2 or 3 tanks/condition; $5,612 \pm 2,671$ sequences/fish). We binned the resulting 185,216 16S rRNA gene sequences into 3,376 OTUs defined by 97% pairwise sequence identity and then classified the taxonomy of each OTU. We found that the relative diversities (see Table S2 in the supplemental material) and abundances of bacterial classes (Fig. 1) in the intestine were strikingly similar in most individuals across different diet and rearing density conditions. All bacterial communities were dominated by the classes *Bacilli* ($48.6\% \pm 9.3\%$ of sequences per sample), *Alphaproteobacteria* ($21.8\% \pm 5.8\%$), *Gammaproteobacteria* ($17.1\% \pm 7.6\%$), *Betaproteobacteria* ($3.8\% \pm 2.0\%$), and *Clostridia* ($2.2\% \pm 1.3\%$). This strong similarity among all samples at the class level raised the possibility that the rainbow trout intestines harbored a shared set of OTUs or a core gut microbiota.

To determine the extent to which OTUs were shared across individuals and treatment groups, we first identified the OTUs present in every individual within a given treatment group (operationally defined here as a “treatment core”) and then evaluated the overlap between different treatment cores to identify those OTUs shared among all sequenced individuals (operationally defined here as the “shared core”) (Fig. 2A). Surprisingly, we found that the majority of OTUs within each treatment core was shared among all four conditions, yielding a shared core of 52 OTUs. This

large shared core contained greater than half of the OTUs that appear in each treatment core (Fig. 2A) and constituted 81.6% of all sequences in this study (Fig. 2B). In agreement with the overall abundances of bacterial taxa (Fig. 1), we found that the shared core is composed primarily of the bacterial classes *Bacilli*, *Alphaproteobacteria*, and *Gammaproteobacteria* (Fig. 2B). As expected from the similarity in overall bacterial composition between samples (Fig. 1), treatment cores were not markedly different from each other or from the shared core (Fig. 2C to F; see Fig. S1 in the supplemental material). Additionally, sequences in OTUs within the shared core constituted 81.8% to 89.8% of all sequences in each treatment group (Fig. 2C to F). These results indicate that the tested variations in diet and rearing density did not exert large, long-term alterations on the gut microbiota of rainbow trout.

Variations in diet and rearing density cause minor changes to the rainbow trout gut bacterial community. We next sought to determine whether variations in diet and rearing density evoked any consistent alterations in gut bacterial community composition. Although treatment cores were highly similar to each other and to the shared core (Fig. 2B to F), we did identify OTUs within each treatment core that were not observed in the shared core (operationally defined here as the “treatment accessory cores”) (Fig. 2G to J). OTUs within each treatment accessory core constituted a small fraction of the sequences within their respective

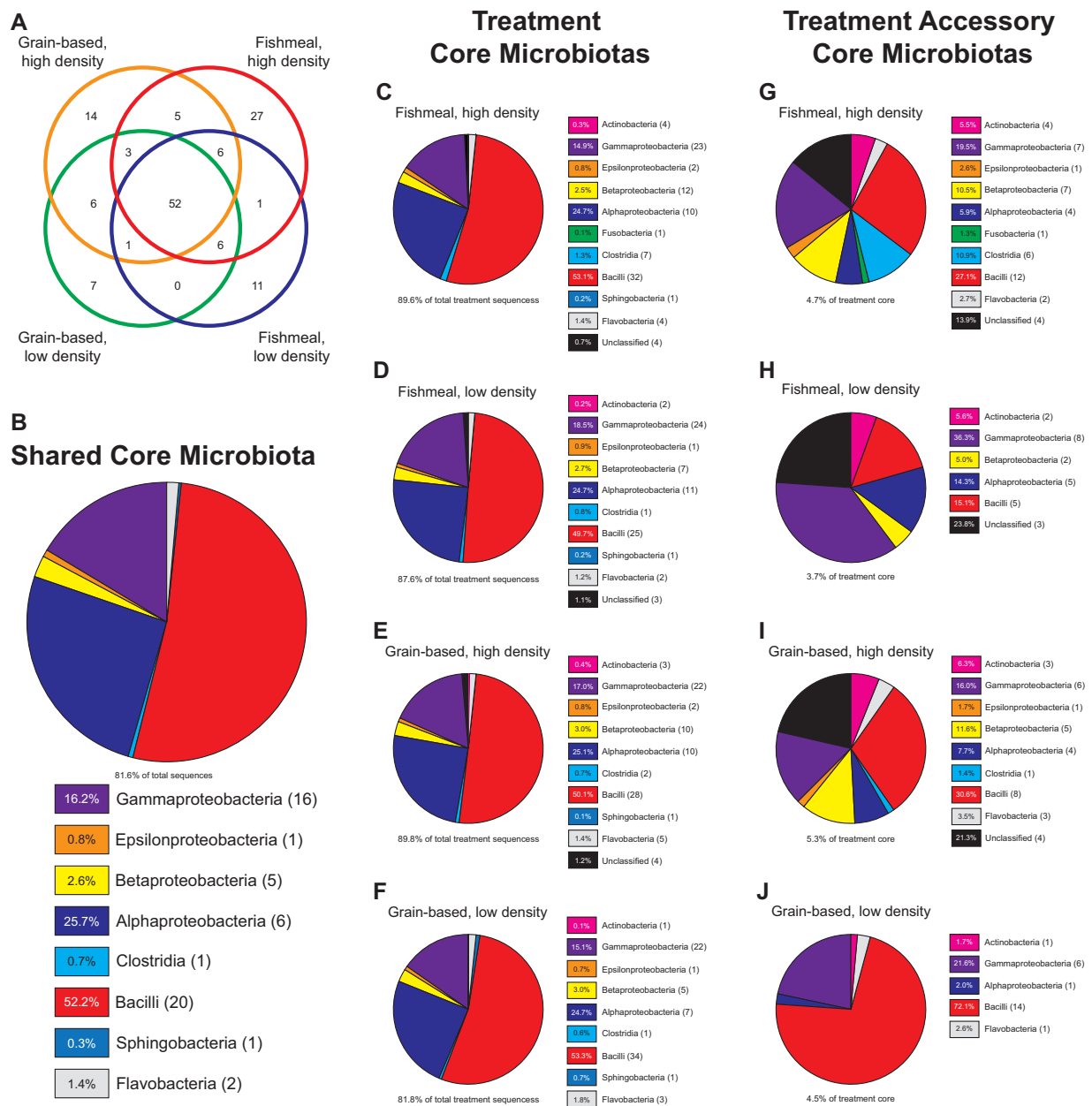


FIG 2 Core microbiotas shared between rainbow trout raised under different diet and density conditions. (A) Numbers of OTUs (97% sequence identity) shared by all individuals within each specific treatment condition (treatment cores) and within all treatment conditions (shared core). The numbers indicate the OTUs shared by overlapping circles. Of the 3,376 OTUs identified in this study, 52 comprised the shared core, and an additional 87 OTUs were included in one or more treatment cores. (B) Composition of the shared core microbiota (the 52 OTUs present in all individuals) for all treatment conditions. The relative abundances of the bacterial classes present are shown in the chart legend; the numbers in parentheses following the legend labels denote the number of OTUs in the core microbiota belonging to the corresponding bacterial class. (C to F) Compositions of the treatment core microbiotas for each of the four treatment groups. The relative abundances of the bacterial classes present are shown in the chart legend; the numbers in parentheses following the legend labels denote the number of OTUs in the core microbiota belonging to the corresponding bacterial class. The text below the pie charts shows the contribution of the core microbiota to the entire microbiota of trout under each treatment condition. (G to J) Compositions of the accessory core microbiotas for each treatment condition (i.e., OTUs present in each individual under a given treatment condition but not in each individual under all treatment conditions). The relative abundances of the bacterial classes present are shown in the chart legend; the numbers in parentheses following the legend labels denote the number of OTUs in the core microbiota belonging to the corresponding bacterial class. The text below the pie charts shows the contribution of the accessory core microbiota to the treatment core microbiota of trout under each treatment condition. (See Tables S5 to S13 in the supplemental material.)

treatment cores (3.7% to 5.3%), but comparison of treatment accessory cores revealed distinct differences between diet and rearing density treatments. Although the relative abundances of bacterial classes were similar in both high-density accessory cores,

we observed a relative increase in *Clostridia* abundance and diversity in the accessory core of the fishmeal high-density treatment (Fig. 2G and I; see Fig. S1 in the supplemental material). In contrast, we observed pronounced differences between the two low-

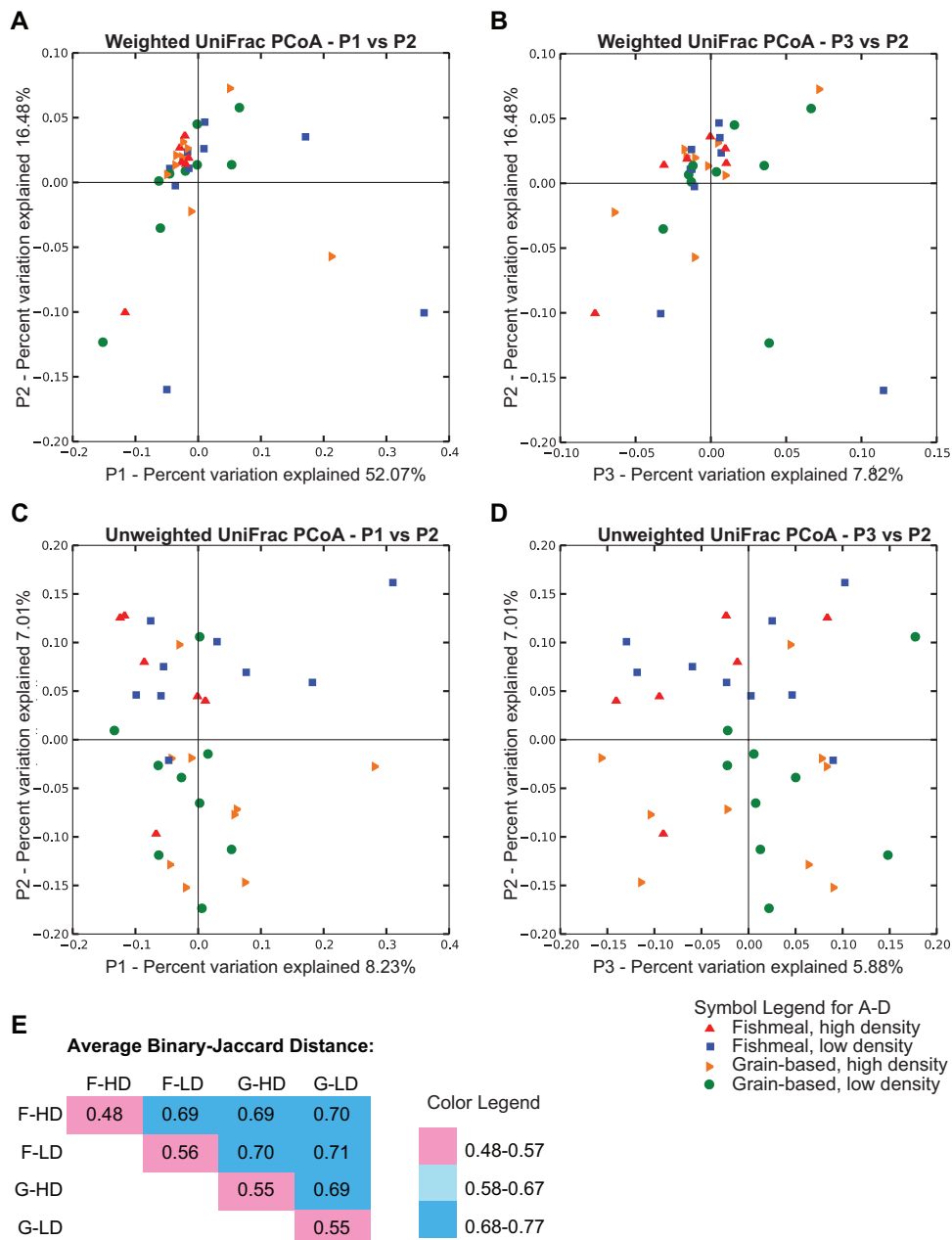


FIG 3 Beta diversity estimates of the rainbow trout intestinal microbiota. (A to D) Use of UniFrac to measure phylogenetic distances between the gut microbiotas of individual trout from all treatment groups. (A and B) Weighted UniFrac PCoA plotted against the PC1 versus PC2 axes (A) and the PC2 versus PC3 axes (B). (C and D) Unweighted UniFrac PCoA plotted against the PC1 versus PC2 axes (C) and the PC2 versus PC3 axes (D). (E) Average binary Jaccard (nonphylogenetic) distances between the gut microbiotas of individuals in the same treatment group and between individuals from different treatment groups. F-HD, fishmeal, high density; F-LD, fishmeal, low density; G-HD, grain based, high density; G-LD, grain based, low density.

density accessory cores compared to each other and to the high-density accessory cores. For example, the grain-based low-density accessory core displayed marked increases in the abundance and diversity of the class *Bacilli* compared to other accessory cores (Fig. 2J; see Fig. S1 in the supplemental material). These results suggest that the tested variations in diet and rearing density are sufficient to induce specific alterations in the diversity and proportional abundance of relatively rare members of the gut microbiota.

We next sought to determine whether the different diet-by-

rearing-density treatments were sufficient to evoke alterations in the overall composition of gut bacterial communities. To do so, we compared diversities between samples from different treatment groups (i.e., beta diversity). PCoA of weighted UniFrac distances (an evaluation of community structure) showed that samples clustered together, regardless of diet or rearing density (Fig. 3A and B) and consistent with our observation of a large shared core microbiota. In contrast, PCoA of unweighted UniFrac distances (an evaluation of community membership that does not consider abundances) showed slight clustering of samples from

the same treatment group (Fig. 3C and D). In accord with this, binary Jaccard analysis (a nonphylogenetic measure of community similarity) revealed that microbial communities from individual samples within the same treatment group were more similar to each other than to those from other treatment groups (Fig. 3E).

We next determined whether the similarity of gut bacterial communities within each treatment group is associated with differential abundances of specific bacterial taxa using LEfSe software (35), followed by 2-way ANOVA. This analysis identified several taxa within the phylum *Firmicutes* that were significantly discriminatory for diet type. The relative abundance of the family *Lactobacillaceae* and its included genus *Lactobacillus* were significantly enriched in fish fed a grain-based diet under both density conditions (Fig. 4A and B). Although there was no significant effect of diet on the relative abundance of the family *Streptococcaceae*, the included genus *Streptococcus* was enriched in fish fed a grain-based diet and was the only taxon to display a significant interaction between diet and density conditions (Fig. 4C and D). The relative abundances of the family *Staphylococcaceae* and its included genus *Staphylococcus* were significantly enriched in fish fed a grain-based diet, with the major effect being observed under low-density conditions (Fig. 4E and F). In contrast, the relative abundances of the family *Clostridiales* and its included genus *Clostridia* were significantly affected by diet, with a trend toward increased relative abundance in fishmeal-fed animals (Fig. 4G and H). Together, these results indicate that the tested diet and rearing-density combinations caused consistent alterations in a limited number of bacterial community members and that differences between treatments were sufficient to create treatment-specific bacterial community profiles in these animals.

Long-term alteration in diet and rearing density do not impact intestinal histopathology. Because grain-based diets have previously been associated with intestinal inflammation in fish (42, 43), we next sought to determine if alterations in diet and rearing density were sufficient to alter intestinal histopathology. All animals displayed at least a minimal level of intestinal inflammation, but intestinal inflammation was not affected by treatment ($P > 0.05$) (see Table S20 in the supplemental material). These data suggest that the tested diets and rearing densities were not sufficient to significantly alter the severity of intestinal inflammation.

Rainbow trout performance, survival, and fin condition are significantly affected by diet and rearing density. Additionally, we determined if variations in diet and rearing conditions impacted fish performance and health. By study's end, statistically significant differences in fish weights were detected, with higher weights being observed in fishmeal diet groups relative to grain-based-diet groups. Rearing density, however, did not significantly affect the final fish weight (Table 2 and Fig. 5). Despite lower final weights, however, fish fed grain-based diets were better able to utilize dietary energy for growth, as indicated by the significantly greater feed efficiency (i.e., lower feed conversion rates) in these groups (Table 2). Again, no significant association between density and feed conversion was determined. Survival was generally high (>96%) among all treatment groups; however, significantly higher survival was observed in grain-based-diet treatment groups (Table 2).

Because fin erosion is an established indicator of fish welfare under culture conditions (44, 45), we measured fin indices (i.e.,

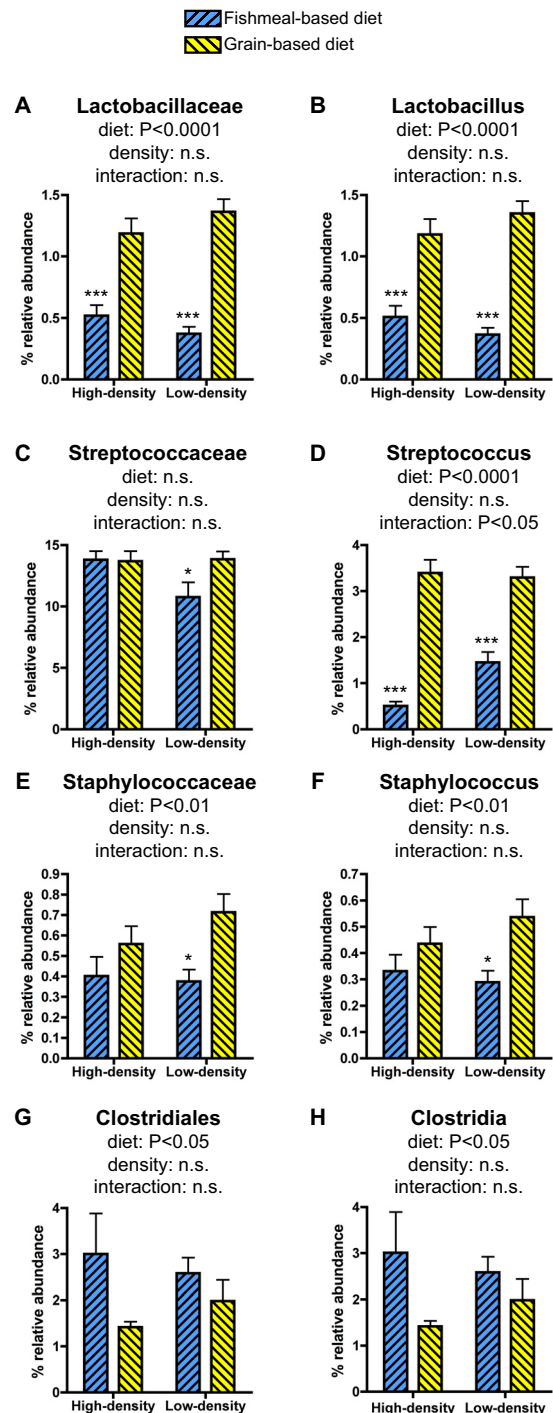


FIG 4 Bacterial taxa identified as discriminatory between experimental conditions. Bacterial taxa identified by LEfSe as discriminatory between experimental conditions were subjected to 2-way ANOVA and Bonferroni posttests. The taxa that were confirmed as significant by 2-way ANOVA are shown (with the exception of panel C). The data are plotted as mean percent relative abundance \pm standard error of the mean (SEM), with the ANOVA P value summary for diet, density, and interaction between diet and density shown above each graph. The asterisks indicate significant differences between low-density and high-density samples under the same diet conditions identified by Bonferroni posttest (*, $P < 0.05$; ***, $P > 0.001$). (See Tables S14 to S19 in the supplemental material.)

TABLE 2 Fish performance and processing and fillet quality attributes for each diet/density treatment group at study's end

Parameter	Value (mean ± standard error)			
	Fishmeal diet		Grain-based diet	
	High density	Low density	High density	Low density
Fish performance				
Final wt (g) ^a	925 ± 12	807 ± 26	663 ± 40	691 ± 46
Survival (%) ^a	96.4 ± 0.5	97.1 ± 0.7	97.9 ± 0.2	97.6 ± 0.5
FCR (overall) ^a	1.18 ± 0.02	1.15 ± 0.03	1.02 ± 0.06	1.10 ± 0.01
TGC (overall)	2.46 ± 0.04	2.45 ± 0.04	2.42 ± 0.07	2.33 ± 0.08
Processing attributes				
Dress yield (%) ^a	86.1 ± 0.4	85.4 ± 0.5	87.7 ± 0.4	88.9 ± 0.4
Fillet index (%)	49.8 ± 0.5	49.7 ± 0.6	50.3 ± 0.3	50.8 ± 0.5
Fillet attributes				
Cook yield (%)	84.3 ± 0.6	84.8 ± 0.5	85.0 ± 0.4	84.4 ± 0.5
Texture (Kramer g/g wt) ^b	340 ± 20	334 ± 18	316 ± 11	344 ± 11
Proximate analysis				
Moisture (%)	70.6 ± 0.3	70.4 ± 0.2	70.4 ± 0.2	70.8 ± 0.3
Fat (%)	8.8 ± 0.4	8.7 ± 0.3	9.10 ± 0.3	8.8 ± 0.4
Protein (%) ^a	20.2 ± 0.2	20.4 ± 0.1	20.6 ± 0.1	20.7 ± 0.1
Ash (%)	1.2 ± 0.0	1.3 ± 0.0	1.3 ± 0.0	1.3 ± 0.0
Fatty acids (mg/g tissue)				
Omega-3				
ALA (C _{18:3n3})	0.75 ± 0.23	0.84 ± 0.19	0.86 ± 0.27	1.18 ± 0.04
EPA (C _{20:5n3}) ^a	3.41 ± 0.13	3.05 ± 0.17	2.10 ± 0.09	2.19 ± 0.07
DHA (C _{22:6n3}) ^a	11.3 ± 0.65	10.3 ± 0.44	8.92 ± 0.23	10.0 ± 0.77
Total omega-3 ^a	15.5 ± 0.68	14.1 ± 0.34	11.9 ± 0.31	13.8 ± 0.57
Omega-6				
DGLA (C _{20:3n6})	1.13 ± 0.17	1.01 ± 0.26	1.00 ± 0.24	1.13 ± 0.16
Eicosadienoic acid (C _{20:2n6}) ^a	9.65 ± 0.24	9.55 ± 0.20	13.2 ± 0.24	13.7 ± 0.14
Total omega-6 ^a	10.8 ± 0.13	10.6 ± 0.25	14.2 ± 0.16	14.8 ± 0.23

^a Parameter showed a statistically significant difference between diet treatment groups using ANOVA ($P < 0.05$); no statistical differences were determined between density treatment groups, and no statistical interactions between treatments were detected.

^b Kramer shear force is a measure of sample firmness. Samples are sheared by blades and force-deformation curves, from which the Kramer values are derived, are obtained.

the length of the longest ray of each rayed fin relative to the fork length) as a means of evaluating fish welfare. Although no major fin erosion was noted qualitatively on any of the sampled fish, fin indices were significantly higher in grain-based-diet treatment groups for all measured fins (Table 3), indicating healthier fins overall in these groups. Statistical interaction between diet and density was observed when modeling these main effects and their associations with indices for the pectoral (left and right), dorsal, and pelvic (left and right) fins. In these cases, the overall trend was an increase in the fin index when fish were fed grain-based diets but a decrease in the fin index associated with the increased-density treatment. Together, these data show that the tested alterations in diet and rearing density were sufficient to independently and interactively modify rainbow trout health and performance.

Rainbow trout diet and rearing density alter processing attributes and product quality. Fish from the grain-based-diet treatment groups had significantly greater dress yield than fish from the fishmeal diet groups (Table 2). There was a small but statistically significantly higher percentage of protein in fillets from fish fed a grain-based diet, and these fish also contained significantly higher fillet levels of eicosadienoic acid and total omega-6 fatty acids. However, fish fed fishmeal-based feed had fillets with significantly higher levels of EPA, DHA, and total omega-3 fatty acids. No statistical differences were noted between treatment groups for fillet contaminants (see Table S21 in the

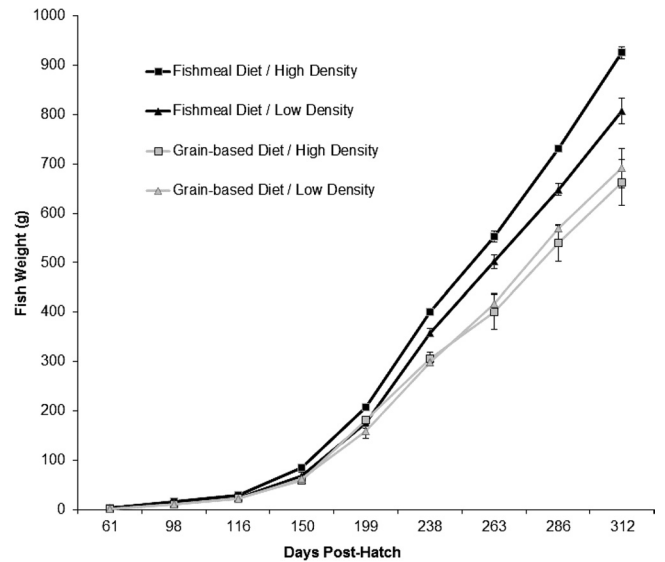


FIG 5 Average rainbow trout weights for the duration of the experiment. The data points represent means of 20 to 60 trout sampled at each monthly growth performance assessment up to 312 days posthatch. The error bars represent standard errors.

supplemental material). Among all pesticides examined, only DDE and PCBs were detected. Levels of DDE and total PCBs in both treatment groups were very low, and as measured, would be of little or no concern to human health (the maximum DDE levels detected were >750 times lower than FDA limits [5 ppm] for the edible portions of fish; PCB levels were >250 times lower than FDA limits [2 ppm] for food fish). No density effects ($P < 0.05$) were noted for any of the processing and product quality parameters investigated (Table 2). These results indicate that the tested variations in diet, not rearing density, had a marked impact on yield and nutrient content.

DISCUSSION

Diet composition and rearing density have been identified as environmental factors that can impact the health and physiology of rainbow trout. Furthermore, the diet type is known to impact the composition of the intestinal microbiota in a variety of animal species. The study reported here is the first to test whether diet and rearing density interact in rainbow trout to impact the gut micro-

TABLE 3 Indices of rainbow trout fins in each treatment group

Fin	Index (mean ± standard error)			
	Fishmeal diet		Grain-based diet	
	High density	Low density	High density	Low density
Pectoral (left) ^{a,b}	0.104 ± 0.002	0.108 ± 0.001	0.114 ± 0.001	0.117 ± 0.002
Pectoral (right) ^{a,b}	0.106 ± 0.001	0.107 ± 0.001	0.115 ± 0.001	0.118 ± 0.002
Dorsal ^{a,b}	0.088 ± 0.003	0.088 ± 0.005	0.091 ± 0.003	0.095 ± 0.004
Pelvic (left) ^{a,b}	0.088 ± 0.001	0.088 ± 0.001	0.090 ± 0.003	0.096 ± 0.003
Pelvic (right) ^{a,b}	0.097 ± 0.001	0.097 ± 0.001	0.102 ± 0.001	0.104 ± 0.001
Ventral ^a	0.097 ± 0.001	0.099 ± 0.002	0.102 ± 0.001	0.104 ± 0.002
Caudal (upper) ^a	0.105 ± 0.001	0.109 ± 0.002	0.109 ± 0.001	0.113 ± 0.001
Caudal (lower) ^a	0.103 ± 0.002	0.105 ± 0.001	0.109 ± 0.001	0.112 ± 0.002

^a Fin showed statistically significant differences between diet treatment groups ($P < 0.05$); no statistical differences were determined between the density treatment groups.

^b Fin showed statistically significant interaction ($P < 0.05$) between diet and density treatments.

biota composition, health, and fish performance metrics. Our results reveal consistent effects of diet composition on fish growth and product quality and novel interactions between diet and rearing density on fish welfare. Despite these marked changes in fish health and yield, the tested alterations in diet and rearing density were not sufficient to significantly alter an unexpectedly large core microbiota in the intestines of aquacultured rainbow trout. As discussed below, these results have important implications for aquaculture of rainbow trout and other finfish, as well as for our understanding of vertebrate gut microbial ecology.

Characterization of the microbial lineages ubiquitous in any habitat is an important step toward understanding the determinants of microbiota membership and the respective roles of its members and for developing effective approaches for managing and manipulating that microbial ecosystem. Deep sequencing of 16S rRNA genes from the intestines of humans, mice, and zebrafish sampled from different populations and geographic locations have suggested that very few bacterial OTUs are common among all individuals from a given host species and that they represent a minor portion of the overall community membership (20, 28, 46). In contrast, we found that all of the individual aquacultured rainbow trout analyzed in this study possessed very similar intestinal bacterial communities dominated by a large shared core microbiota comprised of 52 OTUs. Moreover, the relative abundances of most of these shared OTUs were largely unaffected by tested alterations in diet or rearing density. Since the sequencing depth of this study was not sufficient to saturate diversity in any sample (see Fig. S2 in the supplemental material), the size of this shared core microbiota may be even larger than our data indicate.

The factors underlying the large size of this shared core gut microbiota remain unknown and represent an important subject for future research. The aquacultured trout studied here were raised under identical husbandry conditions prior to the start of the experimental manipulations, and it is possible that early colonization events are strong determinants of bacterial community composition, greatly dampening the impact of the experimental manipulations. It is also possible that the large core microbiota might be due to rearing these animals in flowthrough tanks without water recirculation, likely limiting environmental variation among tanks and individuals during the experimental manipulations. Importantly, the aquacultured trout analyzed here were obtained from a single commercial supplier and raised in a single aquaculture facility, thereby limiting the environmental and host genetic variation and increasing the likelihood of similar microbiota membership. Previous studies have suggested that gut microbiota compositions can vary markedly among domesticated zebrafish and mice from different vivarium facilities (28, 47–49). We therefore expect that comparisons of gut microbiota from rainbow trout obtained from different aquaculture facilities or caught in the wild would reveal a smaller shared core microbiota than that reported here. Previous evaluations of gut microbiota composition in wild rainbow trout identified many of the bacterial genera that we observed in the shared core in this study (e.g., *Aeromonas*, *Acinetobacter*, *Escherichia*, *Pseudomonas*, *Streptococcus*, and *Enterococcus*) (50). These and many other genera observed within the shared core reported here have also been identified in culture-independent and culture-based evaluations of gut microbiota composition in aquacultured trout and other salmonids (9, 22, 30, 52–57). However, these previous reports did not identify these genera in all animals within the respective studies. This could be due at least in part to the limited sampling depths and the inherent

limitations of the respective culture-based and culture-independent methods utilized in these studies.

To provide a more robust frame of reference for interpreting our observations, we compared our results with the only other published study that used deep sequencing to evaluate gut microbiota composition in aquacultured rainbow trout (30). This previous study by Desai and colleagues differed from ours in several ways, including the specific intestinal region analyzed (luminal contents of the distal intestine versus the whole midintestine in our study), the bacterial gene targeted for deep sequencing (*cpn60* versus 16S rRNA gene in our study), the source of tank water (recirculating versus flowthrough in our study), and other aspects of animal husbandry. We detected no bacterial species or genera that were present in all animals across both studies; however, many of the genera within the shared core that we report here were frequently detected in the animals analyzed by Desai and colleagues. Of the 52 OTUs that comprise the shared core in our study, 44 were confidently assigned to one of 26 genera by RDP Classifier. Of those 26 genera, 8 (*Weissella*, *Acidovorax*, *Citrobacter*, *Aeromonas*, *Enterococcus*, *Lactococcus*, *Pseudomonas*, and *Klebsiella*) were observed by Desai and colleagues in at least half of the trout sampled in their study, and they observed an additional 10 genera (*Erwinia*, *Leuconostoc*, *Escherichia/Shigella*, *Streptococcus*, *Veillonella*, *Acinetobacter*, *Bacillus*, *Sphingomonas*, *Chryseobacterium*, and *Pantoea*) in at least one animal (30). This suggests that the shared core microbiota observed in our study is not a “true” core microbiota possessed by all rainbow trout. Although we have operationally defined the core microbiota as those OTUs possessed by 100% of the samples in a group, others have suggested that the criteria for core microbiota can be relaxed to include OTUs present in less than 100% of samples or deeper taxonomic levels (21, 58). Using this relaxed definition, the frequent detection of several bacterial genera in rainbow trout from diverse populations and locations suggests that these genera may be members of a true core microbiota shared by many or all aquacultured rainbow trout. Additional studies are needed to directly compare individual animals from different aquaculture facilities and wild fish to determine whether a true core microbiota exists in rainbow trout and to determine how variations in husbandry techniques and animal provenance impact the composition of the gut microbiota in rainbow trout.

Despite the dominance of the shared core we observed, analysis of the accessory core microbiotas—the set of OTUs present in all individuals in at least one experimental group but not in the shared core—revealed several significant differences between experimental conditions. For example, fish fed a grain-based diet were enriched for the genera *Lactobacillus* and *Streptococcus* compared to those fed a fishmeal-based diet. The relative abundance of the genus *Streptococcus* was the only one in the study to display a significant statistical interaction between diet and density, where the effect of diet was greater in fish raised at high density. Moreover, the relative abundance of one *Streptococcus* OTU—the only OTU in the shared core microbiota with a statistically significant variation among treatment groups—was increased in both groups fed the grain-based diet (see Fig. S3 in the supplemental material). The genera *Lactobacillus* and *Streptococcus* contain species that are used as probiotics in mammals and fish (58, 59). These diet-dependent differences in the gut microbial community structure raise the possibility that minority members may contribute to the physio-

logical differences, such as growth rate, that we observed between fish raised on the fishmeal-based versus the grain-based diet.

Early studies report an association between alternative protein diets and decreased fish growth (60–62), likely in response to intestinal inflammation brought about by dietary antinutritional factors (38, 60). Subsequent research has demonstrated improved performance with newer plant-based diet formulations (7, 10, 63) with reduced antinutritional factors (64). We did not detect differences in intestinal inflammation between treatment groups, and furthermore, the grain-based-feed treatment groups, despite slower growth, had better feed conversion than groups fed a fishmeal-based diet. Fin condition is an indicator of fish welfare (65), but its etiology is a complex, multifactorial process (66). We found that fin indices were significantly better in the grain-based-diet treatment groups. Barrows and Lellis (67) suggest an association between fin health and elements within the protein and/or mineral fraction(s) of diets; however, in our study, it is difficult to identify specific dietary components' impacts on fin condition. Lower fin indices were found in the high-density treatment groups, as has been previously noted by others (41, 68–70), underscoring the importance of maintaining an appropriate density range.

In summary, we find that variations in rearing density and diet composition within the context of a single aquaculture facility are sufficient to interactively alter rainbow trout growth, performance, fillet quality, and welfare. However, these tested variations in rainbow trout husbandry had only minor effects on the gut microbiota composition and did not markedly alter a surprisingly large core microbiota shared among all animals in the study. Although the shared core microbiota we observed in this cohort of aquacultured rainbow trout may not be a “true” core microbiota shared among all aquacultured or wild rainbow trout, our results do reveal that rainbow trout gut microbiota composition can achieve remarkable consistency within the context of a single aquaculture facility. This should encourage additional research and implementation of alternative diets and husbandry practices for trout production by reducing concerns over the potential impact on the structure and function of the gut microbiota.

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The use of trade names does not imply endorsement by the U.S. government.

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Aquacultured rainbow trout (*Oncorhynchus mykiss*) possess a large core intestinal microbiota that is resistant to variation in diet and rearing density

Running title: Core microbiota in the rainbow trout intestine

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CONTENTS SUMMARY:

A summary of the samples used for pyrosequencing (Table S1); a summary of the alpha diversity of the samples (Table S2); a list of the bacterial genera observed in each rainbow trout intestine (Table S3); a list of OTUs observed in each rainbow trout intestine (Table S4); a list of OTUs in the shared core microbiota from each rainbow trout intestine (Table S5); lists of OTUs in each treatment core microbiota from each rainbow trout intestine (Tables S6-S9); lists of OTUs in treatment accessory cores from each rainbow trout intestine (Tables S10-13); LEfSe results for each pair-wise comparison performed (Tables S14-S19); average intestinal inflammation scores in each treatment group (Table S20); end-of-study results for measured fish fillet contaminant concentrations in each diet treatment group (Table S21); proportion of treatment core OTUs each bacterial class contributes (Figure S1); alpha rarefaction for each sample (Figure S2); average relative abundances of each shared core OTUs in each treatment (Figure S3).

Table S1. Description of 16S rRNA gene pyrosequencing datasets generated in this study

Sample Name	Diet	Density	Tank #	Pyrosequencing Barcode	# Sequences ¹
1B1	fishmeal-based	high	1	AACGATCC	8 650
2B1	fishmeal-based	high	1	ATGCGGTT	7 983
3B1	fishmeal-based	high	1	CTCACTGT	3 224
1B4	fishmeal-based	high	4	ACAGACTC	3 190
2B4	fishmeal-based	high	4	CAGTAGTC	3 307
3B4	fishmeal-based	high	4	GACAACTC	10 362
1B3	fishmeal-based	low	3	AAGGCCTT	2 561
2B3	fishmeal-based	low	3	CACACAGT	5 920
3B3	fishmeal-based	low	3	GAAGTGG	8 889
1B5	fishmeal-based	low	5	ACCTACCT	2 917
2B5	fishmeal-based	low	5	CCAATTCC	5 902
3B5	fishmeal-based	low	5	GAGAGACT	9 386
1B10	fishmeal-based	low	10	AGGAACCA	3 827
2B10	fishmeal-based	low	10	CGCCAATA	9 515
3B10	fishmeal-based	low	10	GGAATTGG	2 813
1B2	grain-based	high	2	AATCCGG	4 351
2B2	grain-based	high	2	CAACTGCA	3 515
3B2	grain-based	high	2	CTGTGACA	9 047
1B6	grain-based	high	6	ACGAAGCA	4 854
2B6	grain-based	high	6	CCGGAATT	5 652
3B6	grain-based	high	6	GCAATACC	8 532
1B9	grain-based	high	9	AGCTGATC	6 179
2B9	grain-based	high	9	CGATAAGG	3 779
3B9	grain-based	high	9	GCTAGGAA	6 658
1B7	grain-based	low	7	AGACCTGT	3 112
2B7	grain-based	low	7	CCTTCAA	4 626
3B7	grain-based	low	7	GCGCAATT	5 421
1B11	grain-based	low	11	ATATCCGG	2 661
2B11	grain-based	low	11	CGTAGGTT	7 214
3B11	grain-based	low	11	GGCGAATA	1 345
1B12	grain-based	low	12	ATCCGCAA	6 563
2B12	grain-based	low	12	CTACCTTG	10 797
3B12	grain-based	low	12	GGTACGAA	2 464

Footnotes:

1. Number of sequences remaining for analysis after filtering for low-quality sequence reads, denoising of sequences, chimera slaying, and removal of Cyanobacteria sequences

Table S2. Alpha diversity estimates of 16S rRNA gene sequence datasets

Experimental Group	Sample Name	Observed Species ¹		Chao1 ¹		Shannon Index ¹		Phylogenetic Distance ¹	
		Individual	Average ²	Individual	Average ²	Individual	Average ²	Individual	Average ²
Fishmeal-based, high density	1B1	158.10	158.97+/-14.77	315.22	334.65+/-37.68	4.79	4.86+/-0.22	17.57	17.95+/-1.41
	2B1	129.00		285.65		4.43		15.16	
	3B1	177.00		404.31		5.15		19.52	
	1B4	166.80		356.70		4.91		19.02	
	2B4	159.10		314.94		4.87		18.56	
	3B4	163.80		331.10		5.01		17.85	
Fishmeal-based, low density	1B3	177.90	167.19+/-16.85	376.17	353.17+/-50.70	5.12	4.98+/-0.33	20.39	19.00+/-1.16
	2B3	170.90		381.38		4.92		19.07	
	3B3	176.00		385.07		5.06		19.53	
	1B5	195.50		458.41		5.57		20.33	
	2B5	136.20		307.45		4.32		17.37	
	3B5	159.60		310.25		4.93		18.62	
	1B10	176.50		353.23		5.24		19.75	
	2B10	146.20		283.24		4.68		16.81	
3B10	165.90	323.33	5.02	19.11					
Grain-based, high density	1B2	161.60	160.72+/-18.56	343.45	339.33+/-63.74	5.07	4.97+/-0.29	18.19	18.32+/-1.63
	2B2	162.70		360.35		5.03		19.63	
	3B2	138.50		256.86		4.72		16.33	
	1B6	144.50		288.79		4.83		16.85	
	2B6	153.50		315.41		4.84		17.87	
	3B6	152.00		304.24		4.87		16.95	
	1B9	205.40		496.90		5.68		21.94	
	2B9	154.40		338.06		4.61		17.92	
	3B9	173.90		349.90		5.11		19.15	
Grain-based, low density	1B7	153.60	165.56+/-13.89	305.52	335.38+/-49.61	4.85	5.04+/-0.24	17.01	17.89+/-1.38
	2B7	173.40		341.83		5.06		18.60	
	3B7	166.20		351.57		4.95		18.47	
	1B11	159.10		299.93		5.03		16.46	
	2B11	182.60		377.23		5.32		19.30	
	3B11	163.00		321.19		5.05		17.11	
	1B12	187.00		439.20		5.49		20.25	
	2B12	166.60		329.85		5.04		18.21	
3B12	138.50	252.08	4.58	15.64					

Footnotes:

1. All alpha diversity values were calculated using 1 092 randomly sampled sequences from each sample. Values for each sample were iteratively generated ten times and averaged.
2. Averages +/- standard deviation for each experimental group.

Firmicutes: Bacilli: Bacillales: Paenibacillaceae: Paenibacillus	0.01%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.02%	0.00%	0.07%	0.00%	0.01%	0.03%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.05%	0.03%	0.00%	0.03%	0.02%	0.04%	0.00%	0.03%	0.00%	0.03%	0.01%	0.00%
Firmicutes: Bacilli: Bacillales: Paenibacillaceae: Saccharibacillus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.08%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.08%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Firmicutes: Bacilli: Bacillales: Paenibacillaceae: unclassified genus	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.10%	0.00%	0.00%	0.05%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.06%	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	0.01%	0.00%	
Firmicutes: Bacilli: Bacillales: Planococcaceae: Bhangavaea	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.04%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Firmicutes: Bacilli: Bacillales: Planococcaceae: Kurthia	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Firmicutes: Bacilli: Bacillales: Planococcaceae: Planococcus	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.03%	0.00%	0.00%	0.03%	0.01%	0.04%	0.00%	0.00%	0.02%	0.00%	0.02%	0.00%	0.01%	0.02%	0.00%	0.00%	0.00%	0.02%	0.03%	0.07%	0.00%	0.00%	
Firmicutes: Bacilli: Bacillales: Planococcaceae: Planimicrobium	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.02%	0.00%	0.02%	0.00%	0.02%	0.00%	0.00%	0.00%	0.04%	0.00%	0.01%	0.00%	0.01%	
Firmicutes: Bacilli: Bacillales: Planococcaceae: Sprossarcina	0.00%	0.01%	0.06%	0.00%	0.00%	0.10%	0.00%	0.00%	0.03%	0.00%	0.01%	0.03%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	
Firmicutes: Bacilli: Bacillales: Planococcaceae: unclassified genus	0.01%	0.04%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.03%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	
Firmicutes: Bacilli: Bacillales: Staphylococcaceae: Gemella	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.04%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.01%	0.00%	0.03%	0.00%	0.02%	0.02%	0.04%	0.00%	0.00%	0.01%	
Firmicutes: Bacilli: Bacillales: Staphylococcaceae: Jeikeibacillus	0.02%	0.00%	0.00%	0.03%	0.00%	0.03%	0.08%	0.03%	0.01%	0.03%	0.00%	0.01%	0.03%	0.04%	0.04%	0.11%	0.06%	0.15%	0.00%	0.12%	0.06%	0.02%	0.03%	0.00%	0.03%	0.04%	0.09%	0.30%	0.11%	0.04%	
Firmicutes: Bacilli: Bacillales: Staphylococcaceae: Macrocococcus	0.05%	0.00%	0.00%	0.09%	0.00%	0.18%	0.00%	0.02%	0.08%	0.00%	0.04%	0.05%	0.07%	0.07%	0.22%	0.00%	0.02%	0.00%	0.00%	0.05%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Firmicutes: Bacilli: Bacillales: Staphylococcaceae: Mesocomicoccus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Firmicutes: Bacilli: Bacillales: Staphylococcaceae: Salinicoccus	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.02%	0.00%	0.02%	0.04%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Firmicutes: Bacilli: Bacillales: Staphylococcaceae: Staphylococcus	0.25%	0.30%	0.12%	0.56%	0.30%	0.44%	0.47%	0.22%	0.37%	0.07%	0.22%	0.22%	0.21%	0.46%	0.36%	0.83%	0.28%	0.45%	0.23%	0.48%	0.40%	0.23%	0.42%	0.60%	0.29%	0.78%	0.59%	0.34%	0.71%	0.67%	
Firmicutes: Bacilli: Bacillales: Thermocycloninotocaceae: Thermocycloninotus	0.00%	0.00%	0.03%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Firmicutes: Bacilli: Bacillales: Thermocycloninotocaceae: unclassified genus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Firmicutes: Bacilli: Bacillales: unclassified family: unclassified genus	0.02%	0.00%	0.03%	0.03%	0.09%	0.11%	0.12%	0.00%	0.06%	0.21%	0.02%	0.02%	0.10%	0.09%	0.07%	0.05%	0.03%	0.02%	0.00%	0.02%	0.05%	0.13%	0.00%	0.02%	0.00%	0.04%	0.15%	0.04%	0.01%	0.00%	
Firmicutes: Bacilli: Lactobacillales: Aerococcaceae: Abrotropia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Firmicutes: Bacilli: Lactobacillales: Aerococcaceae: Aerococcus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Firmicutes: Bacilli: Lactobacillales: Aerococcaceae: Eremococcus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Firmicutes: Bacilli: Lactobacillales: Aerococcaceae: Globicatella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Firmicutes: Bacilli: Lactobacillales: Carnobacteriaceae: Atopostipes	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Firmicutes: Bacilli: Lactobacillales: Carnobacteriaceae: Carnobacterium	0.01%	0.00%	0.03%	0.06%	0.03%	0.02%	0.12%	0.02%	0.03%	2.54%	36.53%	0.4%	0.05%	0.05%	0.00%	0.02%	0.03%	0.02%	0.02%	0.58%	0.02%	0.08%	0.03%	0.02%	0.00%	0.09%	0.00%	0.08%	0.00%	0.05%	
Firmicutes: Bacilli: Lactobacillales: Carnobacteriaceae: Deserzina	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.04%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Firmicutes: Bacilli: Lactobacillales: Carnobacteriaceae: Granulicatella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	
Firmicutes: Bacilli: Lactobacillales: Carnobacteriaceae: Manniicatibacillus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Firmicutes: Bacilli: Lactobacillales: Carnobacteriaceae: Trichococcus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Firmicutes: Bacilli: Lactobacillales: Carnobacteriaceae: unclassified genus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Firmicutes: Bacilli: Lactobacillales: Enterococcaceae: Enterococcus	0.92%	1.23%	1.09%	1.22%	0.94%	0.99%	1.17%	0.98%	0.85%	0.31%	0.47%	0.93%	0.65%	0.91%	1.03%	0.76%	1.37%	1.16%	1.30%	1.10%	0.89%	0.52%	0.74%	0.86%	0.77%	1.02%	0.87%	0.83%	0.64%	0.89%	
Firmicutes: Bacilli: Lactobacillales: Enterococcaceae: unclassified genus	0.00%	0.01%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Firmicutes: Bacilli: Lactobacillales: Enterococcaceae: Vogococcus	0.00%	0.01%	0.06%	0.03%	0.03%	0.11%	0.04%	0.05%	0.03%	0.00%	0.03%	0.00%	0.07%	0.04%	0.07%	0.06%	0.01%	0.06%	0.04%	0.00%	0.00%	0.03%	0.06%	0.03%	0.02%	0.04%	0.08%	0.00%	0.05%	0.00%	
Firmicutes: Bacilli: Lactobacillales: Lactobacillaceae: Lactobacillus	0.55%	0.36%	0.71%	0.82%	0.24%	0.37%	0.35%	0.59%	0.60%	0.07%	0.27%	0.3%	0.34%	0.45%	0.25%	1.52%	0.97%	1.19%	1.03%	1.10%	1.11%	0.83%	0.85%	2.03%	1.77%	1.19%	1.49%	1.47%	1.58%	1.64%	
Firmicutes: Bacilli: Lactobacillales: Lactobacillaceae: Pedococcus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Firmicutes: Bacilli: Lactobacillales: Lactobacillaceae: unclassified genus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Firmicutes: Bacilli: Lactobacillales: Leuconostocaceae: Leuconostoc	9.11%	10.69%	10.73%	9.25%	8.92%	8.48%	9.37%	10.54%	7.50%	1.85%	5.57%	8.40%	6.01%	9.63%	9.17%	8.96%	8.31%	11.45%	8.53%	8.49%	9.53%	4.61%	6.72%	8.14%	9.81%	9.22%	7.89%	6.00%	10.26%	6.70%	
Firmicutes: Bacilli: Lactobacillales: Leuconostocaceae: unclassified genus	0.31%	0.34%	0.62%	0.50%	0.42%	0.40%	0.55%	0.17%	0.22%	0.63%	0.32%	0.19%	0.30%	0.19%	0.28%	0.19%	0.34%	0.39%	0.25%	0.33%	0.18%	0.19%	0.35%	0.16%	0.48%	0.44%	0.34%	0.25%	0.45%	0.20%	
Firmicutes: Bacilli: Lactobacillales: Leuconostocaceae: Weissella	21.64%	25.30%	27.76%	22.73%	23.47%	21.81%	22.22%	24.34%	22.77%	4.25%	14.33%	23.20%	15.91%	28.44%	22.57%	21.39%	21.99%	22.33%	22.05%	22.09%	12.45%	18.18%	22.60%	27.38%	20.19%	22.39%	21.46%	16.58%	23.57%	18.25%	
Firmicutes: Bacilli: Lactobacillales: Streptococcaceae: Lactococcus	10.92%	11.51%	14.52%	10.78%	11.70%	10.12%	10.27%	11.06%	10.12%	2.88%	0.29%	10.64%	10.00%	12.88%	9.88%	10.22%	11.64%	11.04%	11.37%	10.16%	10.57%	5.02%	8.52%	9.61%	10.12%	10.87%	10.46%	11.09%	6.98%	13.09%	
Firmicutes: Bacilli: Lactobacillales: Streptococcaceae: Streptococcus	1.91%	0.93%	2.30%	1.97%	1.39%	2.12%	1.85%	1.77%	2.33%	0.27%	1.32%	2.26%	0.76%	1.19%	1.24%	3.49%	4.32%	3.09%	2.76%	3.63%	3.91%	1.85%	2.83%	4.75%	3.76%	4.05%	4.59%	2.93%	2.83%	2.91%	
Firmicutes: Bacilli: Lactobacillales: Streptococcaceae: unclassified genus	0.53%	0.49%	0.43%	0.28%	0.39%	0.31%	0.31%	0.39%	0.39%	0.21%	0.35%	0.16																			

Proteobacteria:Gammaproteobacteria:Pseudomonadales:Moraxellaceae:Enhydrobacter	0.91%	0.56%	0.53%	0.88%	0.51%	0.75%	0.62%	0.49%	0.57%	0.17%	0.39%	0.81%	0.52%	0.61%	0.75%	0.64%	0.63%	0.65%	0.58%	0.30%	0.68%	0.34%	0.48%	0.62%	0.67%	0.69%	0.89%	0.90%	0.53%	0.67%	0.50%	0.68%	0.37%
Proteobacteria:Gammaproteobacteria:Pseudomonadales:Moraxellaceae:Moraxella	0.00%	0.01%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria:Gammaproteobacteria:Pseudomonadales:Moraxellaceae:Peñicillibac	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria:Gammaproteobacteria:Pseudomonadales:Moraxellaceae:Psychrobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.08%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria:Gammaproteobacteria:Pseudomonadales:Moraxellaceae:unclassified genus	0.29%	0.51%	0.99%	1.00%	0.67%	0.40%	0.55%	0.84%	0.71%	0.27%	0.44%	0.77%	0.73%	0.61%	0.28%	0.62%	0.80%	0.43%	0.74%	0.51%	0.53%	0.44%	0.58%	0.75%	0.90%	0.76%	0.52%	0.56%	0.50%	0.37%	0.49%	0.57%	0.41%
Proteobacteria:Gammaproteobacteria:Pseudomonadales:Pseudomonadaceae:Azorhizophilus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria:Gammaproteobacteria:Pseudomonadales:Pseudomonadaceae:Cellvibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria:Gammaproteobacteria:Pseudomonadales:Pseudomonadaceae:Pseudomonas	0.43%	0.70%	0.37%	0.38%	0.82%	0.34%	0.74%	0.52%	0.49%	19.95%	0.24%	0.35%	8.57%	0.55%	1.28%	0.51%	0.17%	0.18%	0.45%	0.62%	0.29%	13.85%	0.77%	0.42%	0.13%	0.45%	0.65%	1.09%	1.73%	0.22%	1.01%	0.61%	0.32%
Proteobacteria:Gammaproteobacteria:Pseudomonadales:Pseudomonadaceae:unclassified genus	0.05%	0.01%	0.03%	0.00%	0.03%	0.04%	0.04%	0.03%	0.07%	1.92%	0.08%	0.01%	0.84%	0.04%	0.04%	0.07%	0.14%	0.02%	0.06%	0.04%	0.02%	1.18%	0.08%	0.06%	0.00%	0.00%	0.07%	0.08%	0.17%	0.00%	0.17%	0.07%	0.04%
Proteobacteria:Gammaproteobacteria:Pseudomonadales:unclassified family:unclassified genus	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria:Gammaproteobacteria:Salinisphaerales:Salinisphaeraeae:Salinisphaera	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria:Gammaproteobacteria:unclassified order:unclassified family:unclassified genus	0.00%	0.00%	0.03%	0.03%	0.09%	0.04%	0.08%	0.07%	0.02%	0.34%	0.05%	0.06%	0.10%	0.04%	0.04%	0.00%	0.03%	0.07%	0.00%	0.04%	0.05%	0.16%	0.05%	0.05%	0.05%	0.04%	0.02%	0.04%	0.04%	0.07%	0.11%	0.06%	0.00%
Proteobacteria:Gammaproteobacteria:Vibrionales:Vibrionaceae:Photobacterium	0.01%	0.00%	0.00%	0.00%	0.06%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria:Gammaproteobacteria:Vibrionales:Vibrionaceae:unclassified genus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria:Gammaproteobacteria:Vibrionales:Vibrionaceae:Vibrio	0.00%	0.00%	0.00%	0.03%	0.00%	0.03%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.03%	0.03%	0.04%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria:Gammaproteobacteria:Xanthomonadales:Sinobacteraceae:Siroidobacter	0.00%	0.00%	0.00%	0.09%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria:Gammaproteobacteria:Xanthomonadales:Xanthomonadaceae:Lycobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria:Gammaproteobacteria:Xanthomonadales:Xanthomonadaceae:Pseudoxanthomonas	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria:Gammaproteobacteria:Xanthomonadales:Xanthomonadaceae:Stenotrophomonas	0.06%	0.11%	0.03%	0.03%	0.06%	0.15%	0.08%	0.02%	0.03%	0.51%	0.05%	0.00%	0.21%	0.02%	0.00%	0.06%	0.06%	0.02%	0.06%	0.11%	0.01%	0.24%	0.03%	0.06%	0.00%	0.04%	0.02%	0.04%	0.17%	0.00%	0.20%	0.07%	0.00%
Proteobacteria:Gammaproteobacteria:Xanthomonadales:Xanthomonadaceae:unclassified genus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria:Gammaproteobacteria:Xanthomonadales:Xanthomonadaceae:Wohlfahrtimonas	0.00%	0.00%	0.00%	0.03%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria:Gammaproteobacteria:Xanthomonadales:Xanthomonadaceae:Xanthomonas	0.02%	0.04%	0.06%	0.00%	0.03%	0.02%	0.00%	0.00%	0.03%	0.00%	0.00%	0.01%	0.00%	0.06%	0.00%	0.00%	0.03%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria:unclassified class:unclassified order:unclassified family:unclassified genus	0.02%	0.05%	0.03%	0.09%	0.15%	0.00%	0.16%	0.05%	0.04%	0.10%	0.00%	0.04%	0.10%	0.00%	0.07%	0.00%	0.03%	0.02%	0.02%	0.05%	0.02%	0.15%	0.13%	0.00%	0.00%	0.06%	0.00%	0.11%	0.15%	0.00%	0.49%	0.13%	0.04%
Spirochaetes:Spirochaetales:Spirochaetaeae:Treponema	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
SR1:SR1_genera_incertae_sedis:unclassified order:unclassified family:unclassified genus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Synergistetes:Synergistia:Synergistales:Synergistaceae:unclassified genus	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Tenericutes:Mollicutes:Anaeroplasmatales:Anaeroplasmataceae:Anaeroplasma	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Tenericutes:Mollicutes:Mycoplasmatales:Mycoplasmataceae:Mycoplasma	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
TM7:TM7_genera_incertae_sedis:unclassified order:unclassified family:unclassified genus	0.02%	0.00%	0.06%	0.09%	0.09%	0.04%	0.08%	0.07%	0.03%	0.03%	0.10%	0.04%	0.03%	0.02%	0.21%	0.02%	0.14%	0.04%	0.02%	0.12%	0.00%	0.03%	0.37%	0.05%	0.03%	0.02%	0.09%	0.04%	0.03%	0.22%	0.08%	0.07%	0.04%
Verrucomicrobia:Opitutae:Opitutales:Opitutaceae:Opitulus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Verrucomicrobia:Spartobacteria:Spartobacteria_genera_incertae_sedis:unclassified family:unclassified genus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Verrucomicrobia:unclassified class:unclassified order:unclassified family:unclassified genus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Verrucomicrobia:Verrucomicrobiae:Verrucomicrobiales:Verrucomicrobiaceae:Akkermansia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
unclassified phylum:unclassified class:unclassified order:unclassified family:unclassified genus	0.57%	0.65%	1.80%	1.41%	1.03%	0.49%	1.25%	0.88%	0.79%	5.90%	0.66%	0.86%	2.72%	0.56%	0.92%	1.08%	1.54%	1.47%	1.36%	0.92%	2.20%	9.24%	0.61%	0.83%	0.48%	0.80%	1.31%	0.71%	0.72%	0.45%	1.87%	0.66%	0.32%

Footnotes:

1. Values represent the relative abundance, by percent, of each listed genus observed within each sample.
2. Taxonomic assignment determined using RDP classifier to compare a representative sequence from each OTU to reference sequences in the greengenes database.

2361	Proteobacteria:Betaproteobacteria:Hydrogenophiales:Hydrogenophilaceae:Hydrogenophilus	4	0	0	0	0	1	0	6	0	2	1	4	0	0	0	0	0	0	1	1	0	2	1	0	0	0	2	0	1	5	0	0	2	1	
4529	Proteobacteria:Betaproteobacteria:Hydrogenophiales:Hydrogenophilaceae:Hydrogenophilus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0		
1589	Proteobacteria:Betaproteobacteria:Hydrogenophiales:Hydrogenophilaceae:Petrobacter	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
135	Proteobacteria:Betaproteobacteria:Methylophilales:Methylophilaceae	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
1305	Proteobacteria:Betaproteobacteria:Methylophilales:Methylophilaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1		
1685	Proteobacteria:Betaproteobacteria:Methylophilales:Methylophilaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0		
4563	Proteobacteria:Betaproteobacteria:Methylophilales:Methylophilaceae:Methylobacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		
3046	Proteobacteria:Betaproteobacteria:Methylophilales:Methylophilaceae:Methylophilus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
90	Proteobacteria:Betaproteobacteria:Neisseriales:Neisseriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
530	Proteobacteria:Betaproteobacteria:Neisseriales:Neisseriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
1137	Proteobacteria:Betaproteobacteria:Neisseriales:Neisseriaceae	0	2	0	0	0	0	1	0	0	0	2	0	0	0	0	2	4	4	0	3	4	0	0	0	0	0	0	0	0	0	0	0	2	0	
1170	Proteobacteria:Betaproteobacteria:Neisseriales:Neisseriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
1264	Proteobacteria:Betaproteobacteria:Neisseriales:Neisseriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
1286	Proteobacteria:Betaproteobacteria:Neisseriales:Neisseriaceae	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
2136	Proteobacteria:Betaproteobacteria:Neisseriales:Neisseriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	
2226	Proteobacteria:Betaproteobacteria:Neisseriales:Neisseriaceae	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2838	Proteobacteria:Betaproteobacteria:Neisseriales:Neisseriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2889	Proteobacteria:Betaproteobacteria:Neisseriales:Neisseriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3007	Proteobacteria:Betaproteobacteria:Neisseriales:Neisseriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3753	Proteobacteria:Betaproteobacteria:Neisseriales:Neisseriaceae	1	5	0	1	0	3	0	5	1	0	1	2	0	1	1	1	1	0	1	1	4	1	0	1	2	0	1	0	2	0	0	0	0		
4459	Proteobacteria:Betaproteobacteria:Neisseriales:Neisseriaceae	1	2	0	2	1	2	0	1	0	0	1	2	0	0	1	1	0	0	0	1	6	0	0	0	0	2	0	3	4	1	0	0	0	0	
4764	Proteobacteria:Betaproteobacteria:Neisseriales:Neisseriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
412	Proteobacteria:Betaproteobacteria:Neisseriales:Neisseriaceae:Aquifales	3	2	0	1	1	1	0	0	0	1	3	0	0	0	0	0	0	0	0	1	4	0	0	0	0	0	0	0	0	0	0	0	0	0	
3730	Proteobacteria:Betaproteobacteria:Neisseriales:Neisseriaceae:Kingella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
662	Proteobacteria:Betaproteobacteria:Neisseriales:Neisseriaceae:Microvirgula	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
792	Proteobacteria:Betaproteobacteria:Neisseriales:Neisseriaceae:Microvirgula	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2509	Proteobacteria:Betaproteobacteria:Neisseriales:Neisseriaceae:Microvirgula	43	25	25	24	10	45	8	32	10	8	29	98	6	23	27	17	39	40	19	24	40	16	17	21	16	22	7	26	50	3	11	17	13		
1226	Proteobacteria:Betaproteobacteria:Neisseriales:Neisseriaceae:Neisseria	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4002	Proteobacteria:Betaproteobacteria:Neisseriales:Neisseriaceae:Neisseria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
352	Proteobacteria:Betaproteobacteria:Neisseriales:Neisseriaceae:Urburueella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3798	Proteobacteria:Betaproteobacteria:Neisseriales:Neisseriaceae:Urburueella	2	2	0	0	1	0	0	2	0	0	2	0	0	1	2	0	2	1	1	1	2	1	0	2	2	0	0	1	1	0	0	0	0	0	
730	Proteobacteria:Betaproteobacteria:Neisseriales:Neisseriaceae:Vitrosocilla	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3212	Proteobacteria:Betaproteobacteria:Neisseriales:Neisseriaceae:Vitrosocilla	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4246	Proteobacteria:Betaproteobacteria:Neisseriales:Neisseriaceae:Vitrosocilla	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
5201	Proteobacteria:Betaproteobacteria:Neisseriales:Neisseriaceae:Vitrosocilla	2	11	9	4	1	11	1	20	1	8	9	6	0	3	9	2	2	6	5	5	7	4	0	4	5	4	1	7	3	0	3	4	4		
5340	Proteobacteria:Betaproteobacteria:Neisseriales:Neisseriaceae:Vitrosocilla	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5357	Proteobacteria:Betaproteobacteria:Neisseriales:Neisseriaceae:Vitrosocilla	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
727	Proteobacteria:Betaproteobacteria:Neisseriales:Neisseriaceae:Vogesella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1934	Proteobacteria:Betaproteobacteria:Neisseriales:Neisseriaceae:Vogesella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2532	Proteobacteria:Betaproteobacteria:Neisseriales:Neisseriaceae:Vogesella	3	1	1	0	1	1	0	0	5	1	1	1	1	0	0	0	1	2	0	0	2	4	0	1	0	1	108	41	0	0	0	0	0	0	
3896	Proteobacteria:Betaproteobacteria:Neisseriales:Neisseriaceae:Vogesella	1	6	3	2	4	7	1	15	4	1	3	19	0	5	14	3	2	4	6	6	9	4	2	1	1	1	2	3	6	0	6	10	5		
4684	Proteobacteria:Betaproteobacteria:Neisseriales:Neisseriaceae:Vogesella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4747	Proteobacteria:Betaproteobacteria:Neisseriales:Neisseriaceae:Vogesella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4888	Proteobacteria:Betaproteobacteria:Neisseriales:Neisseriaceae:Vogesella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4967	Proteobacteria:Betaproteobacteria:Neisseriales:Neisseriaceae:Vogesella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5018	Proteobacteria:Betaproteobacteria:Neisseriales:Neisseriaceae:Vogesella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5266	Proteobacteria:Betaproteobacteria:Neisseriales:Neisseriaceae:Vogesella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5274	Proteobacteria:Betaproteobacteria:Neisseriales:Neisseriaceae:Vogesella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2201	Proteobacteria:Betaproteobacteria:Nitrosomonadales:Nitrosomonadaceae	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2929	Proteobacteria:Betaproteobacteria:Nitrosomonadales:Nitrosomonadaceae:Nitrospirilla	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1791	Proteobacteria:Betaproteobacteria:Rhodocyclales:Rhodocyclaceae	0	0																																	

Table S5. Shared core microbiota of the rainbow trout Intestine¹

#OTU ID ²	Consensus Lineage ³	Fishmeal-based, high density						Fishmeal-based, low density						Grain-based, high density						Grain-based, low density														
		B1	B1	B1	B4	B4	B4	B10	B210	B10	B3	B3	B3	B5	B5	B5	B2	B2	B2	B6	B6	B6	B9	B9	B9	B11	B11	B11	B12	B12	B12	B17	B17	B17
3213	Bacteroidetes:Flavobacteria:Flavobacteriales:Flavobacteriaceae:Chryseobacterium	61	60	37	29	18	64	19	48	13	17	24	70	5	23	75	25	25	54	51	44	43	23	26	35	15	35	10	34	60	14	18	31	21
4854	Bacteroidetes:Flavobacteria:Flavobacteriales:Flavobacteriaceae:Cloacibacterium	61	15	11	2	18	48	22	28	19	11	11	25	2	16	96	15	9	33	21	27	32	15	16	77	16	230	4	117	56	3	26	16	23
681	Bacteroidetes:Sphingobacteria:Sphingobacteriales:Cytosphaerae:Flectobacillus	19	9	6	1	10	9	4	3	19	5	7	3	9	4	13	3	3	8	8	7	16	7	8	9	2	32	1	117	65	8	3	12	5
4912	Firmicutes: Bacilli: Bacillales: Bacillaceae: Bacillus	25	3	21	5	4	64	2	31	4	17	9	36	2	15	44	21	8	20	8	10	37	8	5	20	4	13	2	7	21	5	1	43	18
1568	Firmicutes: Bacilli: Bacillales: Staphylococaceae: Staphylococcus	16	24	1	13	8	23	3	25	6	8	9	15	2	11	13	20	4	17	7	17	21	8	14	21	5	26	1	10	29	5	2	21	19
1199	Firmicutes: Bacilli: Lactobacillales: Enterococcaceae: Enterococcus	19	26	11	12	5	27	8	16	8	9	12	22	4	6	18	11	10	20	23	15	20	7	9	7	4	15	4	11	29	6	6	6	12
2572	Firmicutes: Bacilli: Lactobacillales: Enterococcaceae: Enterococcus	42	52	21	23	19	52	11	56	13	13	35	34	5	14	48	21	23	53	28	29	34	16	15	32	11	20	7	15	45	4	9	27	22
3978	Firmicutes: Bacilli: Lactobacillales: Leuconostocaceae	27	27	20	16	14	41	7	29	5	13	10	18	1	18	28	9	6	29	19	14	28	11	7	23	9	17	6	13	43	7	5	21	24
1328	Firmicutes: Bacilli: Lactobacillales: Leuconostocaceae: Leuconostoc	781	836	329	286	289	863	223	907	255	233	606	657	52	318	764	382	285	770	398	473	786	275	248	532	202	413	136	424	939	145	279	353	494
977	Firmicutes: Bacilli: Lactobacillales: Leuconostocaceae: Weissella	7	13	7	4	5	10	4	12	6	5	9	12	1	4	12	12	3	14	2	13	11	7	4	7	6	3	4	8	4	2	5	7	
1372	Firmicutes: Bacilli: Lactobacillales: Leuconostocaceae: Weissella	131	136	81	68	49	174	60	160	35	46	117	142	17	67	188	58	71	163	88	95	145	71	51	107	41	95	28	114	212	29	64	73	82
4905	Firmicutes: Bacilli: Lactobacillales: Leuconostocaceae: Weissella	1700	1827	769	632	700	2013	528	2204	584	507	1284	1820	102	749	1935	886	652	1774	961	1115	1685	658	614	1333	512	1065	281	1043	2257	358	754	828	1086
5017	Firmicutes: Bacilli: Lactobacillales: Leuconostocaceae: Weissella	14	15	17	4	8	18	3	15	3	2	7	23	1	6	20	9	10	13	7	10	13	8	4	18	3	8	1	7	21	9	12	5	9
384	Firmicutes: Bacilli: Lactobacillales: Streptococcaceae	37	39	11	9	13	29	3	27	10	7	20	25	6	14	28	13	19	25	17	15	14	9	15	17	9	14	7	13	32	5	5	6	14
277	Firmicutes: Bacilli: Lactobacillales: Streptococcaceae: Lactococcus	16	23	10	6	7	10	1	18	4	1	9	19	1	3	22	12	5	13	5	7	21	4	2	11	2	11	3	2	17	3	5	6	1
894	Firmicutes: Bacilli: Lactobacillales: Streptococcaceae: Lactococcus	421	421	198	174	171	525	114	576	128	137	311	360	38	180	495	200	205	459	260	286	437	179	140	291	125	211	64	227	534	86	137	203	264
1265	Firmicutes: Bacilli: Lactobacillales: Streptococcaceae: Lactococcus	42	29	19	19	18	55	15	65	15	12	21	46	2	11	33	23	7	38	12	21	49	9	12	29	6	16	8	31	46	10	15	25	33
1434	Firmicutes: Bacilli: Lactobacillales: Streptococcaceae: Lactococcus	199	188	108	46	74	178	57	245	44	41	141	190	22	72	175	82	89	211	107	90	178	75	69	125	58	90	46	111	237	71	74	130	122
2767	Firmicutes: Bacilli: Lactobacillales: Streptococcaceae: Lactococcus	17	31	16	6	7	22	4	18	4	7	9	28	2	10	23	16	5	17	16	19	9	6	21	3	6	6	12	20	9	5	10	13	
2942	Firmicutes: Bacilli: Lactobacillales: Streptococcaceae: Lactococcus	238	228	82	67	100	233	63	287	75	56	137	219	18	75	207	86	76	236	134	127	175	73	76	144	62	133	47	107	253	94	66	99	120
708	Firmicutes: Bacilli: Lactobacillales: Streptococcaceae: Streptococcus	20	15	1	2	2	86	2	9	7	3	7	9	2	5	21	3	2	14	2	1	8	3	3	8	4	1	3	7	9	2	3	11	3
997	Firmicutes: Bacilli: Lactobacillales: Streptococcaceae: Streptococcus	56	13	19	27	21	44	6	42	11	18	22	83	1	26	62	20	3	21	15	25	45	9	13	66	10	29	7	15	27	7	20	22	33
5231	Firmicutes: Bacilli: Lactobacillales: Streptococcaceae: Streptococcus	32	29	43	14	10	51	9	24	7	17	38	70	3	24	84	105	137	213	105	155	230	94	81	186	51	163	18	150	221	42	76	138	183
2533	Firmicutes: Clostridia: Clostridiales: Veillonellaceae: Veillonella	70	48	31	20	27	62	15	88	30	17	40	62	5	37	51	29	28	50	33	37	63	14	9	34	21	29	16	17	62	11	18	11	34
0	Proteobacteria: Alphaproteobacteria: Rhizobiales: Bradyrhizobiacae	44	40	4	15	16	74	7	54	12	19	31	56	7	12	60	35	16	50	31	49	50	18	44	30	14	26	3	30	52	6	12	25	34
3190	Proteobacteria: Alphaproteobacteria: Rhizobiales: Bradyrhizobiacae	56	47	7	17	20	85	43	43	26	8	42	68	26	19	102	22	30	59	39	46	64	72	50	51	36	78	6	77	84	9	19	39	23
2938	Proteobacteria: Alphaproteobacteria: Sphingomonadales: Sphingomonadaceae	156	124	17	54	53	164	113	142	49	41	70	170	66	77	178	75	32	132	93	119	140	86	118	129	58	222	17	104	177	27	57	100	62
1945	Proteobacteria: Alphaproteobacteria: Sphingomonadales: Sphingomonadaceae: Sphingomonas	1882	1650	131	582	610	1876	705	1651	485	429	968	1612	189	552	1727	683	418	1777	882	1141	1593	523	1104	1113	469	1489	166	864	1755	214	484	931	940
3461	Proteobacteria: Alphaproteobacteria: Sphingomonadales: Sphingomonadaceae: Sphingomonas	49	48	1	19	14	72	32	51	16	16	20	62	11	12	59	25	11	50	30	37	47	13	38	43	13	43	7	24	55	8	18	35	43
4139	Proteobacteria: Alphaproteobacteria: Sphingomonadales: Sphingomonadaceae: Sphingomonas	26	34	4	5	7	34	22	25	18	13	27	41	6	9	23	14	5	21	17	40	35	16	18	22	9	44	5	12	33	12	13	19	23
2263	Proteobacteria: Betaproteobacteria: Burkholderiales: Burkholderiales: Incertae sedis: Aquabacterium	15	8	9	5	8	12	6	18	7	2	13	12	2	3	40	5	3	16	4	11	10	7	7	49	8	98	1	9	30	2	4	7	7
1855	Proteobacteria: Betaproteobacteria: Burkholderiales: Comamonadaceae: Acidovorax	37	26	10	2	10	25	8	35	11	8	17	56	3	10	68	19	15	26	19	11	14	9	5	39	8	63	8	13	41	7	14	11	24
2759	Proteobacteria: Betaproteobacteria: Burkholderiales: Comamonadaceae: Acidovorax	64	42	18	10	27	56	18	54	17	14	32	40	3	16	107	64	9	42	24	30	44	15	20	112	16	187	4	21	48	15	20	22	31
3468	Proteobacteria: Betaproteobacteria: Burkholderiales: Comamonadaceae: Diaphorobacter	35	18	5	13	12	25	11	37	11	5	15	15	2	14	105	26	12	32	15	22	26	12	10	81	6	119	2	12	49	5	16	9	8
2509	Proteobacteria: Betaproteobacteria: Neisseriales: Neisseriaceae: Microvirgula	43	25	25	24	10	45	8	32	10	8	29	98	6	23	27	17	39	40	19	24	40	16	17	21	16	22	7	26	50	3	11	17	13
2794	Proteobacteria: Epsilonproteobacteria: Campylobacteriales: Campylobacteriaceae: Arcobacter	58	53	38	14	21	67	16	73	15	22	41	148	4	23	42	34	42	52	37	32	72	21	24	25	21	21	38	60	6	25	33	32	
446	Proteobacteria: Gammaproteobacteria: Aeromonadales: Aeromonadaceae: Aeromonas	15	23	6	6	6	18	6	20	6	2	13	23	1	5	6	12	8	27	10	13	20	12	5	15	6	11	1	21	22	2	4	9	8
4341	Proteobacteria: Gammaproteobacteria: Enterobacteriales: Enterobacteriaceae	22	14	14	4	5	22	1	21	6	5	15	21	1	1	5	10	8	14	30	14	11	9	12	12	6	11	3	5	29	4	6	6	17
3841	Proteobacteria: Gammaproteobacteria: Enterobacteriales: Enterobacteriaceae: Citrobacter	372	336	185	149	137	345	108	408	107	113	255	426	62	156	342	159	219																

Table S6. Fishmeal-based, high density treatment core microbiota¹

#OTU ID ²	Consensus Lineage ³	1B1	2B1	3B1	1B4	2B4	3B4
4842	Actinobacteria;Actinobacteria;Actinomycetales;Actinomycetaceae;Actinomyces	5	2	2	2	1	3
2074	Actinobacteria;Actinobacteria;Actinomycetales;Corynebacteriaceae;Corynebacterium	2	2	3	3	1	4
2949	Actinobacteria;Actinobacteria;Actinomycetales;Corynebacteriaceae;Corynebacterium	16	5	1	2	1	8
3338	Actinobacteria;Actinobacteria;Actinomycetales;Corynebacteriaceae;Corynebacterium	6	2	2	4	4	5
4906	Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae	7	3	2	1	1	1
3213	Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Chryseobacterium	61	60	37	29	18	64
80	Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Chryseobacterium	6	2	7	3	3	6
4854	Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Cloacibacterium	61	15	11	2	18	48
681	Bacteroidetes;Sphingobacteria;Sphingobacteriales;Cytophagaceae;Flectobacillus	19	9	6	1	10	9
111	Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus	8	1	2	2	2	28
4912	Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus	25	3	21	5	4	64
1568	Firmicutes;Bacilli;Bacillales;Staphylococcaceae;Staphylococcus	16	24	1	13	8	23
1199	Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;Enterococcus	19	26	11	12	5	27
2572	Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;Enterococcus	42	52	21	23	19	52
5230	Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;Enterococcus	4	13	3	3	5	11
4699	Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;Vagococcus	1	5	2	1	1	10
1802	Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus	6	6	8	5	4	10
1815	Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus	28	12	11	11	1	13
3978	Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae	27	27	20	16	14	41
1328	Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Leuconostoc	781	836	329	286	289	863
1052	Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Leuconostoc	1	4	10	3	1	6
1417	Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Leuconostoc	3	3	2	3	1	6
977	Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Weissella	7	13	7	4	5	10
1372	Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Weissella	131	136	81	68	49	174
4905	Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Weissella	1700	1827	769	632	700	2013
5017	Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Weissella	14	15	17	4	8	18
1138	Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Weissella	5	5	3	4	5	13
1588	Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Weissella	1	2	3	2	2	3
384	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae	37	39	11	9	13	29
277	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactococcus	16	23	10	6	7	10
894	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactococcus	421	421	198	174	171	525
1265	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactococcus	42	29	19	19	18	55
1404	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactococcus	199	188	108	46	74	178
2767	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactococcus	17	31	16	6	7	22
2942	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactococcus	238	228	82	67	100	233
4516	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactococcus	4	3	3	6	3	5
95	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Streptococcus	2	3	2	1	1	4
1323	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Streptococcus	24	7	3	8	7	31
708	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Streptococcus	20	15	1	2	2	66
997	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Streptococcus	56	13	19	27	21	44
5231	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Streptococcus	32	29	43	14	10	51
2897	Firmicutes;Clostridia;Clostridiales	4	1	1	2	1	3
5459	Firmicutes;Clostridia;Clostridiales;Clostridiaceae;Clostridium	1	2	4	2	2	11
1673	Firmicutes;Clostridia;Clostridiales;Incertae Sedis XI	16	1	7	3	5	13
781	Firmicutes;Clostridia;Clostridiales;Peptococcaceae;Peptococcus	4	1	1	3	2	2
4580	Firmicutes;Clostridia;Clostridiales;Peptostreptococcaceae	9	8	7	3	3	33
2533	Firmicutes;Clostridia;Clostridiales;Veillonellaceae;Veillonella	70	48	31	20	27	62
3480	Firmicutes;Clostridia;Clostridiales;Veillonellaceae;Veillonella	4	1	3	2	2	3
2022	Fusobacteria;Fusobacteria;Fusobacteriales;Fusobacteriaceae	2	1	6	1	4	7
1410	Proteobacteria;Alphaproteobacteria;Alphaproteobacteria_incertae_sedis;Novispirillum	2	2	3	3	8	4
1864	Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;Asticcacaulis	9	1	1	1	1	1
2338	Proteobacteria;Alphaproteobacteria;Rhizobiales	15	7	2	2	3	8
0	Proteobacteria;Alphaproteobacteria;Rhizobiales;Bradyrhizobiaceae	44	40	4	15	16	74
3190	Proteobacteria;Alphaproteobacteria;Rhizobiales;Bradyrhizobiaceae	56	47	7	17	20	85
1316	Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae	5	5	1	3	3	3
2938	Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae	156	124	17	54	53	164
1945	Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas	1882	1650	131	582	610	1876
3461	Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas	49	48	1	19	14	72
4139	Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas	26	34	4	5	7	34

1816	Proteobacteria;Betaproteobacteria;Burkholderiales	5	6	1	1	4	4
5544	Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae	3	2	1	2	2	3
2263	Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiales_incertae_sedis;Aquabacterium	15	8	9	5	8	12
2016	Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Acidovorax	6	4	4	6	1	4
1855	Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Acidovorax	37	26	10	2	10	25
2759	Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Acidovorax	64	42	18	10	27	56
3903	Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Comamonas	5	1	3	2	3	13
3468	Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Diaphorobacter	35	18	5	13	12	25
2509	Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae;Microvirgula	43	25	25	24	10	45
5201	Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae;Vitreoscilla	2	11	9	4	1	11
3896	Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae;Vogesella	1	6	3	2	4	7
5399	Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Azonexus	5	1	4	1	3	4
2794	Proteobacteria;Epsilonproteobacteria;Campylobacteriales;Campylobacteraceae;Arcobacter	58	53	38	14	21	67
85	Proteobacteria;Epsilonproteobacteria;Campylobacteriales;Campylobacteraceae;Sulfurospirillum	7	9	6	2	8	8
446	Proteobacteria;Gammaproteobacteria;Aeromonadales;Aeromonadaceae;Aeromonas	15	23	6	6	6	18
3236	Proteobacteria;Gammaproteobacteria;Aeromonadales;Aeromonadaceae;Aeromonas	3	6	4	2	1	1
4341	Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae	22	14	14	4	5	22
4497	Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae	22	26	12	10	11	16
3841	Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Citrobacter	372	336	185	149	137	345
460	Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Erwinia	21	11	5	6	10	20
3492	Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Escherichia/Shigella	20	29	10	10	31	16
1488	Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Klebsiella	25	45	26	15	14	66
3907	Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Pantoea	17	23	6	2	12	28
3848	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae	5	7	12	8	4	5
5154	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae	20	29	19	23	15	35
197	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Acinetobacter	10	13	3	3	3	10
563	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Acinetobacter	7	6	6	4	2	9
526	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Acinetobacter	97	83	36	54	37	123
893	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Acinetobacter	53	62	32	31	31	51
1370	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Acinetobacter	61	74	30	32	32	63
2675	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Acinetobacter	189	220	133	108	90	243
1192	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Enhydrobacter	11	10	6	6	2	13
2828	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Enhydrobacter	52	23	8	15	11	48
3197	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Enhydrobacter	16	12	2	7	4	17
2252	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae;Pseudomonas	4	9	1	4	5	18
5089	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae;Pseudomonas	15	1	2	1	4	4
684	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae;Pseudomonas	9	34	9	7	12	9
922	unclassified Bacteria	3	2	2	1	1	5
1386	unclassified Bacteria	5	8	3	9	6	4
3794	unclassified Bacteria	23	23	21	14	14	16
4670	unclassified Bacteria	14	11	3	1	8	21

Footnotes:

1. OTUs appearing in every fish reared at high density on a fishmeal diet. Table values constitute the number of times a give OTU is observed in each sample.
2. Sequences were grouped in an OTU if they share 97% or more identity to a representative sequence
3. Taxonomy assigned if at least 90% of sequences in the OTU are in agreement for the classification

Table S7. Fishmeal-based, low density treatment core microbiota¹

#OTU ID ²	Consensus Lineage ³	1B10	2B10	3B10	1B3	2B3	3B3	1B5	2B5	3B5
2949	Actinobacteria;Actinobacteria;Actinomycetales;Corynebacteriaceae;Corynebacterium	4	5	3	3	11	14	2	1	20
4311	Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;Leifsonia	5	11	1	1	4	7	1	5	9
3213	Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Chryseobacterium	19	48	13	17	24	70	5	23	75
4854	Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Cloacibacterium	22	28	19	11	11	25	2	16	96
681	Bacteroidetes;Sphingobacteria;Sphingobacteriales;Cytophagaceae;Flectobacillus	4	3	19	5	7	3	9	4	13
4912	Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus	2	31	4	17	9	36	2	15	44
111	Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus	8	14	6	5	4	9	13	3	6
1568	Firmicutes;Bacilli;Bacillales;Staphylococcaceae;Staphylococcus	3	25	6	8	9	15	2	11	13
1199	Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;Enterococcus	8	16	8	9	12	22	4	6	18
2572	Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;Enterococcus	11	56	13	13	35	34	5	14	48
3526	Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus	5	10	1	1	5	7	1	3	8
3978	Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae	7	29	5	13	10	18	1	18	28
1328	Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Leuconostoc	223	907	255	233	606	657	52	318	764
1052	Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Leuconostoc	4	3	1	6	11	4	1	6	11
977	Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Weissella	4	12	6	5	9	12	1	4	12
1372	Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Weissella	60	160	35	46	117	142	17	67	168
4905	Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Weissella	528	2204	584	507	1284	1820	102	749	1935
5017	Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Weissella	3	15	3	2	7	23	1	6	20
1138	Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Weissella	4	11	2	1	4	4	1	5	10
384	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae	3	27	10	7	20	25	6	14	28
277	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactococcus	1	18	4	1	9	19	1	3	22
894	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactococcus	114	576	128	137	311	360	38	180	495
1265	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactococcus	15	65	15	12	21	46	2	11	33
1404	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactococcus	57	245	44	41	141	190	22	72	175
2767	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactococcus	4	18	4	7	9	29	2	10	23
2942	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactococcus	63	287	75	56	137	219	18	75	207
708	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Streptococcus	2	9	7	3	7	9	2	5	21
997	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Streptococcus	6	42	11	18	22	83	1	26	62
5231	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Streptococcus	9	24	7	17	38	70	3	24	84
1323	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Streptococcus	2	7	6	6	14	18	1	7	30
2533	Firmicutes;Clostridia;Clostridiales;Veillonellaceae;Veillonella	15	88	30	17	40	62	5	37	51
649	Proteobacteria;Alphaproteobacteria;Rhizobiales	3	16	1	1	6	9	7	4	8
2338	Proteobacteria;Alphaproteobacteria;Rhizobiales	3	4	5	2	5	8	8	4	11
0	Proteobacteria;Alphaproteobacteria;Rhizobiales;Bradyrhizobiaceae	7	54	12	19	31	56	7	12	60
3190	Proteobacteria;Alphaproteobacteria;Rhizobiales;Bradyrhizobiaceae	43	43	26	8	42	68	26	19	102
5588	Proteobacteria;Alphaproteobacteria;Sphingomonadales	9	9	7	6	3	23	3	7	10
2938	Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae	113	142	49	41	70	170	66	77	178
2751	Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae	4	1	1	3	4	4	2	3	6
3451	Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Novosphingobium	10	8	1	4	3	14	7	4	12
1945	Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas	705	1651	485	429	968	1612	189	552	1727
3461	Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas	32	51	16	16	20	62	11	12	59
4139	Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas	22	25	18	13	27	41	6	9	23
3105	Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Burkholderia	1	16	2	3	5	6	1	8	12
2263	Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiales_incertae_sedis;Aquabacterium	6	18	7	2	13	12	2	3	40
1855	Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Acidovorax	8	35	11	8	17	56	3	10	68
2759	Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Acidovorax	18	54	17	14	32	40	3	16	107
2016	Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Acidovorax	3	3	10	4	4	6	3	3	5
3468	Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Diaphorobacter	11	37	11	5	15	15	2	14	105
2509	Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae;Microvirgula	8	32	10	8	29	98	6	23	27
2794	Proteobacteria;Epsilonproteobacteria;Campylobacteriales;Campylobacteriaceae;Arcobacter	16	73	15	22	41	148	4	23	42
446	Proteobacteria;Gammaproteobacteria;Aeromonadales;Aeromonadaceae;Aeromonas	6	20	6	2	13	23	1	5	6
4341	Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae	1	21	6	5	15	21	1	1	5
1814	Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Cedecea	1	4	1	5	1	2	4	1	6
3841	Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Citrobacter	108	408	107	113	255	426	62	156	342
460	Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Erwinia	166	14	12	11	7	15	246	5	10
3492	Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Escherichia/Shigella	9	20	34	15	23	24	13	15	15
1488	Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Klebsiella	12	46	15	15	39	53	6	25	43
4017	Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Morganella	1	5	5	3	2	6	2	2	7
3907	Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Pantoea	193	16	12	6	11	4	325	1	21

5558	Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Serratia	5	26	26	11	3	20	25	1	35
3848	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae	11	10	3	3	12	17	2	11	14
5154	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae	12	47	5	11	36	45	4	12	55
526	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Acinetobacter	17	123	30	32	71	110	10	37	112
893	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Acinetobacter	11	59	20	19	37	67	9	26	50
1370	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Acinetobacter	16	102	21	20	55	64	2	34	99
2675	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Acinetobacter	37	257	66	57	142	196	22	121	185
563	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Acinetobacter	6	3	1	5	3	7	2	5	10
2828	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Enhydrobacter	10	25	14	11	17	26	1	12	37
3197	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Enhydrobacter	6	26	1	2	7	16	1	4	24
1192	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Enhydrobacter	4	7	6	3	4	8	3	7	13
2006	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae	30	4	1	1	1	4	52	4	1
1438	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae;Pseudomonas	45	9	3	3	7	3	95	2	1
684	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae;Pseudomonas	225	28	19	8	13	17	402	6	14
2252	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae;Pseudomonas	29	7	10	7	5	3	50	4	5
1386	unclassified Bacteria	70	4	2	4	6	5	146	5	4
3794	unclassified Bacteria	9	16	2	9	26	21	4	16	35
4670	unclassified Bacteria	7	12	4	2	6	21	2	3	13

Footnotes:

1. OTUs appearing in every fish reared at low density on a fishmeal diet. Table values constitute the number of times a give OTU is observed in each sample.
2. Sequences were grouped in an OTU if they share 97% or more identity to a representative sequence
3. Taxonomy assigned if at least 90% of sequences in the OTU are in agreement for the classification

Table S8. Grain-based, high density treatment core microbiota¹

#OTU ID ²	Consensus Lineage ³	1B2	2B2	3B2	1B6	2B6	3B6	1B9	2B9	3B9
2949	Actinobacteria;Actinobacteria;Actinomycetales;Corynebacteriaceae;Corynebacterium	2	1	14	6	5	12	2	3	5
4311	Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;Leifsonia	12	1	15	7	4	11	3	6	1
4183	Actinobacteria;Actinobacteria;Actinomycetales;Propionibacteriaceae;Propionibacterium	3	8	10	3	5	12	3	4	7
4906	Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae	2	3	7	3	4	8	4	1	1
3213	Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Chryseobacterium	25	25	54	51	44	43	23	26	35
80	Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Chryseobacterium	4	1	10	7	6	2	1	1	1
1695	Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Chryseobacterium	1	4	2	1	4	7	2	1	2
4854	Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Cloacibacterium	15	9	33	21	27	32	15	16	77
681	Bacteroidetes;Sphingobacteria;Sphingobacteriales;Cytophagaceae;Flectobacillus	3	3	8	8	7	16	7	8	9
763	Firmicutes;Bacilli;Bacillales;Bacillaceae	18	4	11	6	10	14	3	7	11
4912	Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus	21	8	20	8	10	37	8	5	20
1568	Firmicutes;Bacilli;Bacillales;Staphylococcaceae;Staphylococcus	20	4	17	7	17	21	8	14	21
2642	Firmicutes;Bacilli;Bacillales;Staphylococcaceae;Staphylococcus	15	6	19	4	10	9	5	2	17
1199	Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;Enterococcus	11	10	20	23	15	20	7	9	7
2572	Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;Enterococcus	21	23	53	28	29	34	16	15	32
3870	Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;Enterococcus	1	1	6	5	1	3	2	1	2
1802	Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus	43	22	63	27	35	66	28	24	98
1815	Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus	8	6	22	8	7	11	5	5	10
361	Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus	5	3	11	4	6	3	7	2	13
3526	Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus	3	2	4	2	3	12	1	1	2
3978	Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae	9	6	29	19	14	28	11	7	23
1328	Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Leuconostoc	382	285	770	398	473	786	275	248	532
977	Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Weissella	12	3	14	2	13	11	7	4	7
1372	Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Weissella	58	71	163	88	95	145	71	51	107
4905	Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Weissella	886	652	1774	961	1115	1685	658	614	1333
5017	Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Weissella	9	10	13	7	10	13	8	4	18
384	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae	13	19	25	17	15	14	9	15	17
277	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactococcus	12	5	13	5	7	21	4	2	11
894	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactococcus	200	205	459	260	286	437	179	140	291
1265	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactococcus	23	7	38	12	21	49	9	12	29
1404	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactococcus	82	89	211	107	90	178	75	69	125
2767	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactococcus	16	5	17	17	16	19	9	6	21
2942	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactococcus	86	76	236	134	127	175	73	76	144
3017	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactococcus	1	2	6	5	5	2	4	2	3
708	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Streptococcus	3	2	14	2	1	8	3	3	8
997	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Streptococcus	20	3	21	15	25	45	9	13	66
5231	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Streptococcus	105	137	213	105	155	230	94	81	186
2667	Firmicutes;Clostridia;Clostridiales;Lachnospiraceae	3	1	2	3	5	7	2	2	11
2533	Firmicutes;Clostridia;Clostridiales;Veillonellaceae;Veillonella	29	28	50	33	37	63	14	9	34
3629	Proteobacteria;Alphaproteobacteria;Caulobacteriales;Caulobacteraceae	3	3	11	2	2	14	1	3	1
649	Proteobacteria;Alphaproteobacteria;Rhizobiales	7	3	5	4	9	9	2	1	7
0	Proteobacteria;Alphaproteobacteria;Rhizobiales;Bradyrhizobiaceae	35	16	50	31	49	50	18	44	30
3190	Proteobacteria;Alphaproteobacteria;Rhizobiales;Bradyrhizobiaceae	22	30	59	39	46	64	72	50	51
5588	Proteobacteria;Alphaproteobacteria;Sphingomonadales	11	2	12	2	9	5	4	6	8
2938	Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae	75	32	132	93	119	140	86	118	129
3451	Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Novosphingobium	3	4	6	4	2	10	6	4	15
1945	Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas	683	418	1777	882	1141	1593	523	1104	1113
3461	Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas	25	11	50	30	37	47	13	38	43
4139	Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas	14	5	21	17	40	35	16	18	22
3105	Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Burkholderia	80	4	17	11	8	39	3	6	11
2263	Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiales_incertae_sedis;Aquabacterium	5	3	16	4	11	10	7	7	49
1855	Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Acidovorax	19	15	26	19	11	14	9	5	39
2759	Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Acidovorax	64	9	42	24	30	44	15	20	112
2016	Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Acidovorax	1	5	4	2	2	7	5	4	7
4227	Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Acidovorax	2	1	8	4	4	4	3	3	4
5543	Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Comamonas	3	1	1	1	1	4	1	2	3
3468	Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Diaphorobacter	26	12	32	15	22	26	12	10	81
2509	Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae;Microvirgula	17	39	40	19	24	40	16	17	21
3896	Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae;Vogesella	3	2	4	6	6	9	4	2	1

2794	Proteobacteria;Epsilonproteobacteria;Campylobacterales;Campylobacteraceae;Arcobacter	34	42	52	37	32	72	21	24	25
85	Proteobacteria;Epsilonproteobacteria;Campylobacterales;Campylobacteraceae;Sulfurospirillum	2	1	12	6	3	12	4	1	3
446	Proteobacteria;Gammaproteobacteria;Aeromonadales;Aeromonadaceae;Aeromonas	12	8	27	10	13	20	12	5	15
5100	Proteobacteria;Gammaproteobacteria;Aeromonadales;Aeromonadaceae;Aeromonas	2	2	4	3	2	6	3	3	4
4341	Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae	10	8	14	30	14	11	9	12	12
4497	Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae	9	7	21	8	14	25	4	10	8
3841	Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Citrobacter	159	219	354	276	198	381	162	166	244
460	Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Erwinia	17	5	10	12	8	13	314	4	11
3492	Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Escherichia/Shigella	14	8	27	15	14	16	28	13	14
1488	Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Klebsiella	16	20	41	31	30	43	19	14	27
3907	Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Pantoea	9	3	15	12	16	14	402	1	5
5558	Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Serratia	39	2	1	4	3	17	34	6	21
3848	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae	6	10	12	6	4	13	13	6	14
5154	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae	19	13	25	27	22	25	11	16	30
526	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Acinetobacter	69	45	97	56	57	94	29	41	64
893	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Acinetobacter	34	30	64	31	52	50	14	12	31
1370	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Acinetobacter	19	24	63	46	37	67	28	22	47
2675	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Acinetobacter	87	257	289	112	144	176	61	62	130
2828	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Enhydrobacter	14	10	33	17	12	33	12	7	17
3197	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Enhydrobacter	8	7	17	7	3	18	6	6	13
1192	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Enhydrobacter	6	5	8	3	2	5	3	5	8
2006	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae	3	3	2	2	2	2	63	1	4
684	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae;Pseudomonas	8	1	13	10	24	18	623	16	10
1614	Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Stenotrophomonas	3	2	2	3	4	1	9	1	2
922	unclassified Bacteria	4	15	20	5	8	9	12	5	6
1386	unclassified Bacteria	1	4	1	5	7	6	179	1	7
3794	unclassified Bacteria	14	19	85	9	18	43	8	2	15
4670	unclassified Bacteria	5	2	7	5	8	4	5	4	5

Footnotes:

1. OTUs appearing in every fish reared at high density on a soy diet. Table values constitute the number of times a give OTU is observed in each sample.
2. Sequences were grouped in an OTU if they share 97% or more identity to a representative sequence
3. Taxonomy assigned if at least 90% of sequences in the OTU are in agreement for the classification

Table S9. Grain-based, low density treatment core microbiota¹

#OTU ID ²	Consensus Lineage ³	1B11	2B11	3B11	1B12	2B12	3B12	1B7	2B7	3B7
2454	Actinobacteria;Actinobacteria;Actinomycetales;Nocardiaaceae;Gordonia	2	9	1	2	3	2	1	4	4
3213	Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Chryseobacterium	15	35	10	34	60	14	18	31	21
1695	Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Chryseobacterium	2	4	5	3	15	1	4	4	5
4854	Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Cloacibacterium	16	230	4	17	56	3	26	16	23
681	Bacteroidetes;Sphingobacteria;Sphingobacteriales;Cytophagaceae;Flectobacillus	2	32	1	117	65	8	3	12	5
763	Firmicutes;Bacilli;Bacillales;Bacillaceae	6	14	3	12	26	6	3	7	23
4912	Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus	4	13	2	7	21	5	1	43	18
111	Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus	3	15	2	11	29	1	5	3	12
3974	Firmicutes;Bacilli;Bacillales;Bacillaceae;Virgibacillus	8	7	3	12	18	5	4	11	16
740	Firmicutes;Bacilli;Bacillales;Staphylococcaceae;Jeotgalicoccus	5	1	4	7	4	4	1	11	5
1568	Firmicutes;Bacilli;Bacillales;Staphylococcaceae;Staphylococcus	5	26	1	10	29	5	2	21	19
2642	Firmicutes;Bacilli;Bacillales;Staphylococcaceae;Staphylococcus	4	20	5	5	20	5	6	10	10
1199	Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;Enterococcus	4	15	4	11	29	6	6	6	12
2572	Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;Enterococcus	11	20	7	15	45	4	9	27	22
1802	Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus	20	87	15	42	63	15	38	43	54
1815	Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus	6	5	3	9	16	2	6	7	13
361	Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus	1	13	1	10	9	3	4	3	8
3978	Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae	9	17	6	13	43	7	5	21	24
1328	Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Leuconostoc	202	413	136	424	939	145	279	353	494
1052	Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Leuconostoc	6	15	1	10	22	56	6	10	3
977	Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Weissella	6	6	3	4	8	4	2	5	7
1372	Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Weissella	41	95	28	114	212	29	64	73	82
4905	Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Weissella	512	1065	281	1043	2257	358	754	828	1086
5017	Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Weissella	3	8	1	7	21	9	12	5	9
1588	Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Weissella	1	1	1	5	2	2	1	3	2
1138	Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Weissella	1	8	1	7	13	1	5	3	5
384	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae	9	14	7	13	32	5	5	6	14
5461	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae	1	9	1	4	5	4	1	4	3
277	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactococcus	2	11	3	2	17	3	5	6	1
894	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactococcus	125	211	64	227	534	86	137	203	264
1265	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactococcus	6	16	8	31	46	10	15	25	33
1404	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactococcus	58	90	46	111	237	71	74	130	122
2767	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactococcus	3	6	6	12	20	9	5	10	13
2942	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactococcus	62	133	47	107	253	94	66	99	120
3017	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactococcus	2	5	1	5	5	2	3	5	4
708	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Streptococcus	4	1	3	7	9	2	3	11	3
997	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Streptococcus	10	29	7	15	27	7	20	22	33
5231	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Streptococcus	51	163	18	150	221	42	76	138	183
1323	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Streptococcus	7	15	5	5	18	2	2	8	9
2533	Firmicutes;Clostridia;Clostridiales;Veillonellaceae;Veillonella	21	29	16	17	62	11	18	11	34
2338	Proteobacteria;Alphaproteobacteria;Rhizobiales	2	2	1	6	9	3	3	5	3
0	Proteobacteria;Alphaproteobacteria;Rhizobiales;Bradyrhizobiaceae	14	26	3	30	52	6	12	25	34
3190	Proteobacteria;Alphaproteobacteria;Rhizobiales;Bradyrhizobiaceae	36	78	6	77	84	9	19	39	23
2938	Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae	58	222	17	104	177	27	57	100	62
1945	Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas	469	1489	166	864	1755	214	484	931	940
3461	Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas	13	43	7	24	55	8	18	35	43
4139	Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas	9	44	5	12	33	12	13	19	23
2263	Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiales_incertae_sedis;Aquabacterium	8	98	1	9	30	2	4	7	7
1855	Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Acidovorax	8	63	8	13	41	7	14	11	24
2759	Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Acidovorax	16	187	4	21	48	15	20	22	31
3468	Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Diaphorobacter	6	119	2	12	49	5	16	9	8
2509	Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae;Microvirgula	16	22	7	26	50	3	11	17	13
2794	Proteobacteria;Epsilonproteobacteria;Campylobacteriales;Campylobacteriaceae;Arcobacter	21	30	11	38	60	6	25	33	32
446	Proteobacteria;Gammaproteobacteria;Aeromonadales;Aeromonadaceae;Aeromonas	6	11	1	21	22	2	4	9	8
5100	Proteobacteria;Gammaproteobacteria;Aeromonadales;Aeromonadaceae;Aeromonas	2	2	2	7	7	1	2	3	3
4341	Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae	6	11	3	5	29	4	6	6	17
4497	Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae	3	12	5	7	25	4	6	13	11
4121	Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae	5	2	3	2	12	2	4	9	3
3841	Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Citrobacter	135	189	59	195	345	77	104	156	245
460	Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Erwinia	11	42	1	10	24	6	13	7	7
3492	Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Escherichia/Shigella	5	69	3	284	165	12	5	9	9
1488	Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Klebsiella	17	24	7	18	80	13	15	23	22
3907	Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Pantoea	18	60	2	15	27	15	8	10	15
5558	Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Serratia	6	19	4	7	39	8	13	29	12
3848	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae	4	11	2	11	18	4	5	12	8

5154	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae	11	23	3	21	41	6	21	21	20
526	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Acinetobacter	25	58	23	49	132	21	32	69	57
893	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Acinetobacter	5	19	15	40	52	5	20	29	42
1370	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Acinetobacter	24	37	6	29	69	20	19	29	42
2675	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Acinetobacter	63	117	48	84	210	39	98	90	138
197	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Acinetobacter	5	5	2	4	8	1	2	5	3
563	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Acinetobacter	2	4	2	8	10	1	4	2	2
2828	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Enhydrobacter	15	28	7	14	32	6	13	22	25
3197	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Enhydrobacter	6	5	2	8	26	1	2	7	13
684	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae;Pseudomonas	12	59	1	34	29	4	2	6	19

Footnotes:

1. OTUs appearing in every fish reared at low density on a soy diet. Table values constitute the number of times a give OTU is observed in each sample.
2. Sequences were grouped in an OTU if they share 97% or more identity to a representative sequence
3. Taxonomy assigned if at least 90% of sequences in the OTU are in agreement for the classification

Table S10. Fishmeal-based, high density accessory core¹

#OTU ID ²	Consensus Lineage ³	1B1	2B1	3B1	1B4	2B4	3B4
4842	Actinobacteria;Actinobacteria;Actinomycetales;Actinomycetaceae;Actinomyces	5	2	2	2	1	3
2949	Actinobacteria;Actinobacteria;Actinomycetales;Corynebacteriaceae;Corynebacterium	16	5	1	2	1	8
2074	Actinobacteria;Actinobacteria;Actinomycetales;Corynebacteriaceae;Corynebacterium	2	2	3	3	1	4
3338	Actinobacteria;Actinobacteria;Actinomycetales;Corynebacteriaceae;Corynebacterium	6	2	2	4	4	5
4906	Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae	7	3	2	1	1	1
80	Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Chryseobacterium	6	2	7	3	3	6
111	Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus	8	1	2	2	2	28
5230	Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;Enterococcus	4	13	3	3	5	11
4699	Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;Vagococcus	1	5	2	1	1	10
1802	Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus	6	6	8	5	4	10
1815	Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus	28	12	11	11	1	13
1052	Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Leuconostoc	1	4	10	3	1	6
1417	Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Leuconostoc	3	3	2	3	1	6
1588	Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Weissella	1	2	3	2	2	3
1138	Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Weissella	5	5	3	4	5	13
4516	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactococcus	4	3	3	6	3	5
1323	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Streptococcus	24	7	3	8	7	31
95	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Streptococcus	2	3	2	1	1	4
2897	Firmicutes;Clostridia;Clostridiales	4	1	1	2	1	3
5459	Firmicutes;Clostridia;Clostridiales;Clostridiaceae;Clostridium	1	2	4	2	2	11
1673	Firmicutes;Clostridia;Clostridiales;Incertae Sedis XI	16	1	7	3	5	13
781	Firmicutes;Clostridia;Clostridiales;Peptococcaceae;Peptococcus	4	1	1	3	2	2
4580	Firmicutes;Clostridia;Clostridiales;Peptostreptococcaceae	9	8	7	3	3	33
3480	Firmicutes;Clostridia;Clostridiales;Veillonellaceae;Veillonella	4	1	3	2	2	3
2022	Fusobacteria;Fusobacteria;Fusobacteriales;Fusobacteriaceae	2	1	6	1	4	7
1410	Proteobacteria;Alphaproteobacteria;Alphaproteobacteria_incertae_sedis;Novispirillum	2	2	3	3	8	4
1864	Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;Asticcacaulis	9	1	1	1	1	1
2338	Proteobacteria;Alphaproteobacteria;Rhizobiales	15	7	2	2	3	8
1316	Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae	5	5	1	3	3	3
1816	Proteobacteria;Betaproteobacteria;Burkholderiales	5	6	1	1	4	4
5544	Proteobacteria;Betaproteobacteria;Burkholderiales;Alcaligenaceae	3	2	1	2	2	3
2016	Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Acidovorax	6	4	4	6	1	4
3903	Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Comamonas	5	1	3	2	3	13
5201	Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae;Vitreoscilla	2	11	9	4	1	11
3896	Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae;Vogesella	1	6	3	2	4	7
5399	Proteobacteria;Betaproteobacteria;Rhodocyclales;Rhodocyclaceae;Azonexus	5	1	4	1	3	4
85	Proteobacteria;Epsilonproteobacteria;Campylobacteriales;Campylobacteraceae;Sulfurospirillum	7	9	6	2	8	8
3236	Proteobacteria;Gammaproteobacteria;Aeromonadales;Aeromonadaceae;Aeromonas	3	6	4	2	1	1
4497	Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae	22	26	12	10	11	16
197	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Acinetobacter	10	13	3	3	3	10
563	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Acinetobacter	7	6	6	4	2	9
1192	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Enhydrobacter	11	10	6	6	2	13
2252	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae;Pseudomonas	4	9	1	4	5	18
5089	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae;Pseudomonas	15	1	2	1	4	4
922	unclassified Bacteria	3	2	2	1	1	5
1386	unclassified Bacteria	5	8	3	9	6	4
3794	unclassified Bacteria	23	23	21	14	14	16
4670	unclassified Bacteria	14	11	3	1	8	21

Footnotes:

1. OTUs that are observed in every fish reared at high density on a fishmeal diet but not necessarily in fish raised under different diet and/or density conditions. Table values constitute the number of times a give OTU is observed in each sample.
2. Sequences were grouped in an OTU if they share 97% or more identity to a representative sequence.
3. Taxonomy assigned if at least 90% of sequences in the OTU are in agreement for the classification.

Table S11. Fishmeal-based, low density accessory core¹

#OTU ID ²	Consensus Lineage ³	1B10	2B10	3B10	1B3	2B3	3B3	1B5	2B5	3B5
2949	Actinobacteria;Actinobacteria;Actinomycetales;Corynebacteriaceae;Corynebacterium	4	5	3	3	11	14	2	1	20
4311	Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;Leifsonia	5	11	1	1	4	7	1	5	9
111	Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus	8	14	6	5	4	9	13	3	6
3526	Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus	5	10	1	1	5	7	1	3	8
1052	Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Leuconostoc	4	3	1	6	11	4	1	6	11
1138	Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Weissella	4	11	2	1	4	4	1	5	10
1323	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Streptococcus	2	7	6	6	14	18	1	7	30
649	Proteobacteria;Alphaproteobacteria;Rhizobiales	3	16	1	1	6	9	7	4	8
2338	Proteobacteria;Alphaproteobacteria;Rhizobiales	3	4	5	2	5	8	8	4	11
5588	Proteobacteria;Alphaproteobacteria;Sphingomonadales	9	9	7	6	3	23	3	7	10
2751	Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae	4	1	1	3	4	4	2	3	6
3451	Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Novosphingobium	10	8	1	4	3	14	7	4	12
3105	Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Burkholderia	1	16	2	3	5	6	1	8	12
2016	Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Acidovorax	3	3	10	4	4	6	3	3	5
1814	Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Cedecea	1	4	1	5	1	2	4	1	6
4017	Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Morganella	1	5	5	3	2	6	2	2	7
5558	Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Serratia	5	26	26	11	3	20	25	1	35
563	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Acinetobacter	6	3	1	5	3	7	2	5	10
1192	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Enhydrobacter	4	7	6	3	4	8	3	7	13
2006	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae	30	4	1	1	1	4	52	4	1
1438	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae;Pseudomonas	45	9	3	3	7	3	95	2	1
2252	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae;Pseudomonas	29	7	10	7	5	3	50	4	5
1386	unclassified Bacteria	70	4	2	4	6	5	146	5	4
3794	unclassified Bacteria	9	16	2	9	26	21	4	16	35
4670	unclassified Bacteria	7	12	4	2	6	21	2	3	13

Footnotes:

1. OTUs that are observed in every fish reared at low density on a fishmeal diet but not necessarily in fish raised under different diet and/or density conditions. Table values constitute the number of times a give OTU is observed in each sample.
2. Sequences were grouped in an OTU if they share 97% or more identity to a representative sequence
3. Taxonomy assigned if at least 90% of sequences in the OTU are in agreement for the classification

Table S12. Grain-based, high density accessory core¹

#OTU ID ²	Consensus Lineage ³	1B2	2B2	3B2	1B6	2B6	3B6	1B9	2B9	3B9
2949	Actinobacteria;Actinobacteria;Actinomycetales;Corynebacteriaceae;Corynebacterium	2	1	14	6	5	12	2	3	5
4311	Actinobacteria;Actinobacteria;Actinomycetales;Microbacteriaceae;Leifsonia	12	1	15	7	4	11	3	6	1
4183	Actinobacteria;Actinobacteria;Actinomycetales;Propionibacteriaceae;Propionibacterium	3	8	10	3	5	12	3	4	7
4906	Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae	2	3	7	3	4	8	4	1	1
1695	Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Chryseobacterium	1	4	2	1	4	7	2	1	2
80	Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Chryseobacterium	4	1	10	7	6	2	1	1	1
763	Firmicutes;Bacilli;Bacillales;Bacillaceae	18	4	11	6	10	14	3	7	11
2642	Firmicutes;Bacilli;Bacillales;Staphylococcaceae;Staphylococcus	15	6	19	4	10	9	5	2	17
3870	Firmicutes;Bacilli;Lactobacillales;Enterococcaceae;Enterococcus	1	1	6	5	1	3	2	1	2
361	Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus	5	3	11	4	6	3	7	2	13
3526	Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus	3	2	4	2	3	12	1	1	2
1802	Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus	43	22	63	27	35	66	28	24	98
1815	Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus	8	6	22	8	7	11	5	5	10
3017	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactococcus	1	2	6	5	5	2	4	2	3
2667	Firmicutes;Clostridia;Clostridiales;Lachnospiraceae	3	1	2	3	5	7	2	2	11
3629	Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae	3	3	11	2	2	14	1	3	1
649	Proteobacteria;Alphaproteobacteria;Rhizobiales	7	3	5	4	9	9	2	1	7
5588	Proteobacteria;Alphaproteobacteria;Sphingomonadales	11	2	12	2	9	5	4	6	8
3451	Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Novosphingobium	3	4	6	4	2	10	6	4	15
3105	Proteobacteria;Betaproteobacteria;Burkholderiales;Burkholderiaceae;Burkholderia	80	4	17	11	8	39	3	6	11
4227	Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Acidovorax	2	1	8	4	4	4	3	3	4
2016	Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Acidovorax	1	5	4	2	2	7	5	4	7
5543	Proteobacteria;Betaproteobacteria;Burkholderiales;Comamonadaceae;Comamonas	3	1	1	1	1	4	1	2	3
3896	Proteobacteria;Betaproteobacteria;Neisseriales;Neisseriaceae;Vogesella	3	2	4	6	6	9	4	2	1
85	Proteobacteria;Epsilonproteobacteria;Campylobacteriales;Campylobacteraceae;Sulfurospirillum	2	1	12	6	3	12	4	1	3
5100	Proteobacteria;Gammaproteobacteria;Aeromonadales;Aeromonadaceae;Aeromonas	2	2	4	3	2	6	3	3	4
4497	Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae	9	7	21	8	14	25	4	10	8
5558	Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Serratia	39	2	1	4	3	17	34	6	21
1192	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Enhydrobacter	6	5	8	3	2	5	3	5	8
2006	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae	3	3	2	2	2	2	63	1	4
1614	Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Stenotrophomonas	3	2	2	3	4	1	9	1	2
922	unclassified Bacteria	4	15	20	5	8	9	12	5	6
1386	unclassified Bacteria	1	4	1	5	7	6	179	1	7
3794	unclassified Bacteria	14	19	85	9	18	43	8	2	15
4670	unclassified Bacteria	5	2	7	5	8	4	5	4	5

Footnotes:

1. OTUs that are observed in every fish reared at high density on a soy diet but not necessarily in fish raised under different diet and/or density conditions. Table values constitute the number of times a give OTU is observed in each sample.
2. Sequences were grouped in an OTU if they share 97% or more identity to a representative sequence
3. Taxonomy assigned if at least 90% of sequences in the OTU are in agreement for the classification

Table S13. Grain-based, low density accessory core¹

#OTU ID ²	Consensus Lineage ³	1B11	2B11	3B11	1B12	2B12	3B12	1B7	2B7	3B7
2454	Actinobacteria;Actinobacteria;Actinomycetales;Nocardiaceae;Gordonia	2	9	1	2	3	2	1	4	4
1695	Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Chryseobacterium	2	4	5	3	15	1	4	4	5
763	Firmicutes;Bacilli;Bacillales;Bacillaceae	6	14	3	12	26	6	3	7	23
111	Firmicutes;Bacilli;Bacillales;Bacillaceae;Bacillus	3	15	2	11	29	1	5	3	12
3974	Firmicutes;Bacilli;Bacillales;Bacillaceae;Virgibacillus	8	7	3	12	18	5	4	11	16
740	Firmicutes;Bacilli;Bacillales;Staphylococcaceae;Jeotgalicoccus	5	1	4	7	4	4	1	11	5
2642	Firmicutes;Bacilli;Bacillales;Staphylococcaceae;Staphylococcus	4	20	5	5	20	5	6	10	10
361	Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus	1	13	1	10	9	3	4	3	8
1802	Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus	20	87	15	42	63	15	38	43	54
1815	Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus	6	5	3	9	16	2	6	7	13
1052	Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Leuconostoc	6	15	1	10	22	56	6	10	3
1588	Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Weissella	1	1	1	5	2	2	1	3	2
1138	Firmicutes;Bacilli;Lactobacillales;Leuconostocaceae;Weissella	1	8	1	7	13	1	5	3	5
5461	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae	1	9	1	4	5	4	1	4	3
3017	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactococcus	2	5	1	5	5	2	3	5	4
1323	Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Streptococcus	7	15	5	5	18	2	2	8	9
2338	Proteobacteria;Alphaproteobacteria;Rhizobiales	2	2	1	6	9	3	3	5	3
5100	Proteobacteria;Gammaproteobacteria;Aeromonadales;Aeromonadaceae;Aeromonas	2	2	2	7	7	1	2	3	3
4121	Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae	5	2	3	2	12	2	4	9	3
4497	Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae	3	12	5	7	25	4	6	13	11
5558	Proteobacteria;Gammaproteobacteria;Enterobacteriales;Enterobacteriaceae;Serratia	6	19	4	7	39	8	13	29	12
197	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Acinetobacter	5	5	2	4	8	1	2	5	3
563	Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Acinetobacter	2	4	2	8	10	1	4	2	2

Footnotes:

1. OTUs that are observed in every fish reared at low density on a soy diet but not necessarily in fish raised under different diet and/or density conditions. Table values constitute the number of times a given OTU is observed in each sample.
2. Sequences were grouped in an OTU if they share 97% or more identity to a representative sequence
3. Taxonomy assigned if at least 90% of sequences in the OTU are in agreement for the classification

Table S14. LEfSe comparison of all fishmeal-based groups against all grain-based groups

Taxon ¹	Log10 [(mean relative abundance) x (10 ⁶)] from group with higher relative abundance of taxon	Group with significantly higher logarithmic LDA score	Logarithmic LDA score of higher-scoring group
Bacteria	6		
Bacteria.Acidobacteria	0		
Bacteria.Acidobacteria.Acidobacteria	0		
Bacteria.Acidobacteria.Acidobacteria Gp1	0		
Bacteria.Acidobacteria.Acidobacteria Gp1.Gp1	0		
Bacteria.Acidobacteria.Acidobacteria Gp1.Gp1.unclassified family	0		
Bacteria.Acidobacteria.Acidobacteria Gp1.Gp1.unclassified family.unclassified genus	0		
Bacteria.Acidobacteria.Acidobacteria Gp16	0		
Bacteria.Acidobacteria.Acidobacteria Gp16.Gp16	0		
Bacteria.Acidobacteria.Acidobacteria Gp16.Gp16.unclassified family	0		
Bacteria.Acidobacteria.Acidobacteria Gp16.Gp16.unclassified family.unclassified genus	0		
Bacteria.Acidobacteria.Acidobacteria Gp2	0		
Bacteria.Acidobacteria.Acidobacteria Gp2.Gp2	0		
Bacteria.Acidobacteria.Acidobacteria Gp2.Gp2.unclassified family	0		
Bacteria.Acidobacteria.Acidobacteria Gp2.Gp2.unclassified family.unclassified genus	0		
Bacteria.Acidobacteria.Acidobacteria Gp3	0		
Bacteria.Acidobacteria.Acidobacteria Gp3.Gp3	0		
Bacteria.Acidobacteria.Acidobacteria Gp3.Gp3.unclassified family	0		
Bacteria.Acidobacteria.Acidobacteria Gp3.Gp3.unclassified family.unclassified genus	0		
Bacteria.Acidobacteria.Acidobacteria Gp4	0		
Bacteria.Acidobacteria.Acidobacteria Gp4.Gp4	0		
Bacteria.Acidobacteria.Acidobacteria Gp4.Gp4.unclassified family	0		
Bacteria.Acidobacteria.Acidobacteria Gp4.Gp4.unclassified family.unclassified genus	0		
Bacteria.Acidobacteria.Acidobacteria Gp5	0		
Bacteria.Acidobacteria.Acidobacteria Gp5.Gp5	0		
Bacteria.Acidobacteria.Acidobacteria Gp5.Gp5.unclassified family	0		
Bacteria.Acidobacteria.Acidobacteria Gp5.Gp5.unclassified family.unclassified genus	0		
Bacteria.Acidobacteria.Acidobacteria Gp6	0		
Bacteria.Acidobacteria.Acidobacteria Gp6.Gp6	0		
Bacteria.Acidobacteria.Acidobacteria Gp6.Gp6.unclassified family	0		
Bacteria.Acidobacteria.Acidobacteria Gp6.Gp6.unclassified family.unclassified genus	0		
Bacteria.Acidobacteria.Acidobacteria Gp7	0		
Bacteria.Acidobacteria.Acidobacteria Gp7.Gp7	0		
Bacteria.Acidobacteria.Acidobacteria Gp7.Gp7.unclassified family	0		
Bacteria.Acidobacteria.Acidobacteria Gp7.Gp7.unclassified family.unclassified genus	0		
Bacteria.Actinobacteria	3.165897344		
Bacteria.Actinobacteria.Actinobacteria	3.165897344		
Bacteria.Actinobacteria.Actinobacteria.Acidimicrobiales	0		
Bacteria.Actinobacteria.Actinobacteria.Acidimicrobiales.Acidimicrobiaceae	0		
Bacteria.Actinobacteria.Actinobacteria.Acidimicrobiales.Acidimicrobiaceae.unclassified genus	0		
Bacteria.Actinobacteria.Actinobacteria.Acidimicrobiales.lamiaceae	0		
Bacteria.Actinobacteria.Actinobacteria.Acidimicrobiales.lamiaceae.lamia	0		
Bacteria.Actinobacteria.Actinobacteria.Acidimicrobiidae incertae sedis	0		
Bacteria.Actinobacteria.Actinobacteria.Acidimicrobiidae incertae sedis.Iumatobacter	0		
Bacteria.Actinobacteria.Actinobacteria.Acidimicrobiidae incertae sedis.Iumatobacter.unclassified genus	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales	3.165897344		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Actinomycetaceae	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Actinomycetaceae.Actinomycetes	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Actinomycetaceae.Arcanobacterium	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Actinomycetaceae.unclassified genus	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Beutenbergiaceae	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Beutenbergiaceae.Satana	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Beutenbergiaceae.Seriniabacter	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Bogoriellaceae	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Bogoriellaceae.Georgia	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Bogoriellaceae.unclassified genus	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Brevibacteriaceae	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Brevibacteriaceae.Brevibacterium	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Cellulomonadaceae	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Cellulomonadaceae.Cellulomonas	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Cellulomonadaceae.unclassified genus	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Corynebacteriaceae	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Corynebacteriaceae.Corynebacterium	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Corynebacteriaceae.Turicella	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Corynebacteriaceae.unclassified genus	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Dermabacteraceae	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Dermabacteraceae.Brachybacterium	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Dermacoccaceae	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Dermacoccaceae.Dermacoccus	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Dietziaceae	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Dietziaceae.Dietzia	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Geodermatophilaceae	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Geodermatophilaceae.Blastococcus	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Geodermatophilaceae.unclassified genus	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Intrasporangiaceae	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Intrasporangiaceae.Janibacter	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Intrasporangiaceae.Knoellia	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Intrasporangiaceae.Omithinimicrobium	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Intrasporangiaceae.Tetrasphaera	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Intrasporangiaceae.unclassified genus	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Jonesiaceae	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Jonesiaceae.Jonesia	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Microbacteriaceae	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Microbacteriaceae.Agrococcus	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Microbacteriaceae.Clavibacter	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Microbacteriaceae.Curtobacterium	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Microbacteriaceae.Frigoribacterium	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Microbacteriaceae.Leifsonia	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Microbacteriaceae.Leucobacter	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Microbacteriaceae.Microbacterium	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Microbacteriaceae.Plantibacter	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Microbacteriaceae.Pseudoclavibacter	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Microbacteriaceae.unclassified genus	0		

Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Micrococcaceae	3.165897344		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Micrococcaceae.Arthrobacter	3.165897344		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Micrococcaceae.Kocuria	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Micrococcaceae.Micrococcus	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Micrococcaceae.Nesterenkonia	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Micrococcaceae.Rothia	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Micrococcaceae.unclassified_genus	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Micromonosporaceae	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Micromonosporaceae.Luedemannella	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Micromonosporaceae.Micromonospora	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Mycobacteriaceae	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Mycobacteriaceae.Mycobacterium	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Nocardiaceae	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Nocardiaceae.Gordonia	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Nocardiaceae.Rhodococcus	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Nocardiaceae.unclassified_genus	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Nocardiaceae.Williamsia	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Nocardioidaceae	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Nocardioidaceae.Aeromicrobium	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Nocardioidaceae.Marmoricola	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Nocardioidaceae.Nocardioides	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Nocardioidaceae.Pimelobacter	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Nocardioidaceae.unclassified_genus	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Nocardiopsaceae	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Nocardiopsaceae.Nocardiopsis	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Nocardiopsaceae.unclassified_genus	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Propionibacteriaceae	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Propionibacteriaceae.Friedmanniella	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Propionibacteriaceae.Microlunatus	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Propionibacteriaceae.Propionibacterium	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Propionibacteriaceae.unclassified_genus	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Pseudonocardiaceae	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Pseudonocardiaceae.Pseudonocardiopsis	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Pseudonocardiaceae.Pseudonocardia	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Pseudonocardiaceae.Saccharopolyspora	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Pseudonocardiaceae.unclassified_genus	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Sanguibacteraceae	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Sanguibacteraceae.Sanguibacter	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Streptomycetaceae	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Streptomycetaceae.Streptomyces	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Streptomycetaceae.unclassified_genus	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.unclassified_family	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.unclassified_family.unclassified_genus	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Yaniellaceae	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Yaniellaceae.Yaniella	0		
Bacteria.Actinobacteria.Actinobacteria.Bifidobacteriales	0		
Bacteria.Actinobacteria.Actinobacteria.Bifidobacteriales.Bifidobacteriaceae	0		
Bacteria.Actinobacteria.Actinobacteria.Bifidobacteriales.Bifidobacteriaceae.Aeriscardovia	0		
Bacteria.Actinobacteria.Actinobacteria.Bifidobacteriales.Bifidobacteriaceae.Bifidobacterium	0		
Bacteria.Actinobacteria.Actinobacteria.Bifidobacteriales.Bifidobacteriaceae.unclassified_genus	0		
Bacteria.Actinobacteria.Actinobacteria.Coriobacteriales	0		
Bacteria.Actinobacteria.Actinobacteria.Coriobacteriales.Coriobacteriaceae	0		
Bacteria.Actinobacteria.Actinobacteria.Coriobacteriales.Coriobacteriaceae.Asaccharobacter	0		
Bacteria.Actinobacteria.Actinobacteria.Coriobacteriales.Coriobacteriaceae.Atopobium	0		
Bacteria.Actinobacteria.Actinobacteria.Coriobacteriales.Coriobacteriaceae.Collinsella	0		
Bacteria.Actinobacteria.Actinobacteria.Coriobacteriales.Coriobacteriaceae.Eggerthella	0		
Bacteria.Actinobacteria.Actinobacteria.Coriobacteriales.Coriobacteriaceae.Olsenella	0		
Bacteria.Actinobacteria.Actinobacteria.Coriobacteriales.Coriobacteriaceae.Paraeggerthella	0		
Bacteria.Actinobacteria.Actinobacteria.Coriobacteriales.Coriobacteriaceae.unclassified_genus	0		
Bacteria.Actinobacteria.Actinobacteria.Rubrobacteriales	0		
Bacteria.Actinobacteria.Actinobacteria.Rubrobacteriales.Rubrobacteraceae	0		
Bacteria.Actinobacteria.Actinobacteria.Rubrobacteriales.Rubrobacteraceae.Rubrobacter	0		
Bacteria.Actinobacteria.Actinobacteria.Solirubrobacteriales	0		
Bacteria.Actinobacteria.Actinobacteria.Solirubrobacteriales.Conexibacteraceae	0		
Bacteria.Actinobacteria.Actinobacteria.Solirubrobacteriales.Conexibacteraceae.Conexibacter	0		
Bacteria.Actinobacteria.Actinobacteria.Solirubrobacteriales.Solirubrobacteraceae	0		
Bacteria.Actinobacteria.Actinobacteria.Solirubrobacteriales.Solirubrobacteraceae.Solirubrobacter	0		
Bacteria.Actinobacteria.Actinobacteria.Solirubrobacteriales.unclassified_family	0		
Bacteria.Actinobacteria.Actinobacteria.Solirubrobacteriales.unclassified_family.unclassified_genus	0		
Bacteria.Actinobacteria.Actinobacteria.unclassified_order	0		
Bacteria.Actinobacteria.Actinobacteria.unclassified_order.unclassified_family	0		
Bacteria.Actinobacteria.Actinobacteria.unclassified_order.unclassified_family.unclassified_genus	0		
Bacteria.Aquificae	0		
Bacteria.Aquificae.Aquificae	0		
Bacteria.Aquificae.Aquificae.Aquificales	0		
Bacteria.Aquificae.Aquificae.Aquificales.Hydrogenothermaceae	0		
Bacteria.Aquificae.Aquificae.Aquificales.Hydrogenothermaceae.Sulfurihydrogenibium	0		
Bacteria.Bacteroidetes	4.314707167		
Bacteria.Bacteroidetes.Bacteroidia	3.168303414		
Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales	3.168303414		
Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae	2.780939668		
Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides	2.780939668		
Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Porphyrionadaceae	3.168303414		
Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Porphyrionadaceae.Dysgonomonas	0		
Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Porphyrionadaceae.Porphyrionomonas	0		
Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Porphyrionadaceae.Proteiniphilum	0		
Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Porphyrionadaceae.unclassified_genus	3.168303414		
Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Prevotellaceae	0		
Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Prevotellaceae.Hallella	0		
Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Prevotellaceae.Prevotella	0		
Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Prevotellaceae.unclassified_genus	0		
Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.unclassified_family	0		
Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.unclassified_family.unclassified_genus	0		
Bacteria.Bacteroidetes.Flavobacteria	4.209824075		
Bacteria.Bacteroidetes.Flavobacteria.Flavobacteriales	4.209824075		
Bacteria.Bacteroidetes.Flavobacteria.Flavobacteriales.Cryomorphaceae	0		
Bacteria.Bacteroidetes.Flavobacteria.Flavobacteriales.Cryomorphaceae.Fluvicola	0		
Bacteria.Bacteroidetes.Flavobacteria.Flavobacteriales.Flavobacteriaceae	4.209824075		
Bacteria.Bacteroidetes.Flavobacteria.Flavobacteriales.Flavobacteriaceae.Capnocytophaga	0		
Bacteria.Bacteroidetes.Flavobacteria.Flavobacteriales.Flavobacteriaceae.Chryseobacterium	4.070348208	Fishmeal-based	3.142706388
Bacteria.Bacteroidetes.Flavobacteria.Flavobacteriales.Flavobacteriaceae.Cloacibacterium	3.675880431		
Bacteria.Bacteroidetes.Flavobacteria.Flavobacteriales.Flavobacteriaceae.Flavobacterium	2.864867349		
Bacteria.Bacteroidetes.Flavobacteria.Flavobacteriales.Flavobacteriaceae.Myroides	0		

Bacteria.Bacteroidetes.Flavobacteria.Flavobacteriales.Flavobacteriaceae.Riemerella	0	
Bacteria.Bacteroidetes.Flavobacteria.Flavobacteriales.Flavobacteriaceae.Salinimicrobium	0	
Bacteria.Bacteroidetes.Flavobacteria.Flavobacteriales.Flavobacteriaceae.unclassified_genus	0	
Bacteria.Bacteroidetes.Flavobacteria.Flavobacteriales.Flavobacteriaceae.Wautersiella	0	
Bacteria.Bacteroidetes.Flavobacteria.Flavobacteriales.unclassified_family	0	
Bacteria.Bacteroidetes.Flavobacteria.Flavobacteriales.unclassified_family.unclassified_genus	0	
Bacteria.Bacteroidetes.Sphingobacteria	3,47739161	
Bacteria.Bacteroidetes.Sphingobacteria.Sphingobacteriales	3,47739161	
Bacteria.Bacteroidetes.Sphingobacteria.Sphingobacteriales.Chitinophagaceae	0	
Bacteria.Bacteroidetes.Sphingobacteria.Sphingobacteriales.Chitinophagaceae.Ferruginibacter	0	
Bacteria.Bacteroidetes.Sphingobacteria.Sphingobacteriales.Chitinophagaceae.Filimonas	0	
Bacteria.Bacteroidetes.Sphingobacteria.Sphingobacteriales.Chitinophagaceae.Flavisolibacter	0	
Bacteria.Bacteroidetes.Sphingobacteria.Sphingobacteriales.Chitinophagaceae.unclassified_genus	0	
Bacteria.Bacteroidetes.Sphingobacteria.Sphingobacteriales.Cytophagaceae	3,374850036	
Bacteria.Bacteroidetes.Sphingobacteria.Sphingobacteriales.Cytophagaceae.Adhaeribacter	0	
Bacteria.Bacteroidetes.Sphingobacteria.Sphingobacteriales.Cytophagaceae.Cytophaga	0	
Bacteria.Bacteroidetes.Sphingobacteria.Sphingobacteriales.Cytophagaceae.Dvadobacter	0	
Bacteria.Bacteroidetes.Sphingobacteria.Sphingobacteriales.Cytophagaceae.Ermicicia	0	
Bacteria.Bacteroidetes.Sphingobacteria.Sphingobacteriales.Cytophagaceae.Flectobacillus	3,374850036	
Bacteria.Bacteroidetes.Sphingobacteria.Sphingobacteriales.Cytophagaceae.Hymenobacter	0	
Bacteria.Bacteroidetes.Sphingobacteria.Sphingobacteriales.Cytophagaceae.Pontibacter	0	
Bacteria.Bacteroidetes.Sphingobacteria.Sphingobacteriales.Cytophagaceae.Runella	0	
Bacteria.Bacteroidetes.Sphingobacteria.Sphingobacteriales.Cytophagaceae.Sporocytophaga	0	
Bacteria.Bacteroidetes.Sphingobacteria.Sphingobacteriales.Cytophagaceae.unclassified_genus	0	
Bacteria.Bacteroidetes.Sphingobacteria.Sphingobacteriales.Sphingobacteriaceae	3,34359413	
Bacteria.Bacteroidetes.Sphingobacteria.Sphingobacteriales.Sphingobacteriaceae.Nubsella	0	
Bacteria.Bacteroidetes.Sphingobacteria.Sphingobacteriales.Sphingobacteriaceae.Pedobacter	0	
Bacteria.Bacteroidetes.Sphingobacteria.Sphingobacteriales.Sphingobacteriaceae.Sphingobacterium	3,34359413	
Bacteria.Bacteroidetes.Sphingobacteria.Sphingobacteriales.Sphingobacteriaceae.unclassified_genus	0	
Bacteria.Bacteroidetes.Sphingobacteria.Sphingobacteriales.unclassified_family	0	
Bacteria.Bacteroidetes.Sphingobacteria.Sphingobacteriales.unclassified_family.unclassified_genus	0	
Bacteria.Bacteroidetes.unclassified_class	0	
Bacteria.Bacteroidetes.unclassified_class.unclassified_order	0	
Bacteria.Bacteroidetes.unclassified_class.unclassified_order.unclassified_family	0	
Bacteria.Bacteroidetes.unclassified_class.unclassified_order.unclassified_family.unclassified_genus	0	
Bacteria.Chloroflexi	0	
Bacteria.Chloroflexi.Anaerolineae	0	
Bacteria.Chloroflexi.Anaerolineae.Anaerolineales	0	
Bacteria.Chloroflexi.Anaerolineae.Anaerolineales.Anaerolineaceae	0	
Bacteria.Chloroflexi.Anaerolineae.Anaerolineales.Anaerolineaceae.unclassified_genus	0	
Bacteria.Chloroflexi.Caldilineae	0	
Bacteria.Chloroflexi.Caldilineae.Caldilineales	0	
Bacteria.Chloroflexi.Caldilineae.Caldilineales.Caldilineaceae	0	
Bacteria.Chloroflexi.Caldilineae.Caldilineales.Caldilineaceae.Caldilinea	0	
Bacteria.Chloroflexi.Thermomicrobium	0	
Bacteria.Chloroflexi.Thermomicrobium.Sphaerobacteriales	0	
Bacteria.Chloroflexi.Thermomicrobium.Sphaerobacteriales.Sphaerobacteraceae	0	
Bacteria.Chloroflexi.Thermomicrobium.Sphaerobacteriales.Sphaerobacteraceae.Sphaerobacter	0	
Bacteria.Chloroflexi.Thermomicrobium.unclassified_order	0	
Bacteria.Chloroflexi.Thermomicrobium.unclassified_order.unclassified_family	0	
Bacteria.Chloroflexi.Thermomicrobium.unclassified_order.unclassified_family.unclassified_genus	0	
Bacteria.Chloroflexi.unclassified_class	0	
Bacteria.Chloroflexi.unclassified_class.unclassified_order	0	
Bacteria.Chloroflexi.unclassified_class.unclassified_order.unclassified_family	0	
Bacteria.Chloroflexi.unclassified_class.unclassified_order.unclassified_family.unclassified_genus	0	
Bacteria.Deinococcus_Thermus	0	
Bacteria.Deinococcus_Thermus.Deinococci	0	
Bacteria.Deinococcus_Thermus.Deinococci_Deinococcales	0	
Bacteria.Deinococcus_Thermus.Deinococci_Deinococcales_Deinococcaceae	0	
Bacteria.Deinococcus_Thermus.Deinococci_Deinococcales_Deinococcaceae_Deinococcus	0	
Bacteria.Deinococcus_Thermus.Deinococci_Deinococcales_Trueperaceae	0	
Bacteria.Deinococcus_Thermus.Deinococci_Deinococcales_Trueperaceae_Truepera	0	
Bacteria.Deinococcus_Thermus.Deinococci_Thermales	0	
Bacteria.Deinococcus_Thermus.Deinococci_Thermales_Thermaceae	0	
Bacteria.Deinococcus_Thermus.Deinococci_Thermales_Thermaceae_Meiothermus	0	
Bacteria.Deinococcus_Thermus.Deinococci.unclassified_order	0	
Bacteria.Deinococcus_Thermus.Deinococci.unclassified_order.unclassified_family	0	
Bacteria.Deinococcus_Thermus.Deinococci.unclassified_order.unclassified_family.unclassified_genus	0	
Bacteria.Firmicutes	5,72503841	
Bacteria.Firmicutes.Bacilli	5,716129382	
Bacteria.Firmicutes.Bacilli.Bacillales	4,159959177	
Bacteria.Firmicutes.Bacilli.Bacillales.Alicyclobacillaceae	0	
Bacteria.Firmicutes.Bacilli.Bacillales.Alicyclobacillaceae.Alicyclobacillus	0	
Bacteria.Firmicutes.Bacilli.Bacillales.Bacillaceae	4,011315507	
Bacteria.Firmicutes.Bacilli.Bacillales.Bacillaceae.Anoxybacillus	0	
Bacteria.Firmicutes.Bacilli.Bacillales.Bacillaceae.Bacillus	3,89476401	
Bacteria.Firmicutes.Bacilli.Bacillales.Bacillaceae.Caldalkalibacillus	0	
Bacteria.Firmicutes.Bacilli.Bacillales.Bacillaceae.Cerasibacillus	0	
Bacteria.Firmicutes.Bacilli.Bacillales.Bacillaceae.Exiguobacterium	2,864867349	
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Bacteria.Firmicutes.Bacilli.Bacillales.Bacillaceae.Gracilibacillus	0	
Bacteria.Firmicutes.Bacilli.Bacillales.Bacillaceae.Lentibacillus	0	
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Bacteria.Firmicutes.Bacilli.Bacillales.Bacillaceae.Oceanobacillus	0	
Bacteria.Firmicutes.Bacilli.Bacillales.Bacillaceae.Ornithinibacillus	0	
Bacteria.Firmicutes.Bacilli.Bacillales.Bacillaceae.Tenuibacillus	0	
Bacteria.Firmicutes.Bacilli.Bacillales.Bacillaceae.Terribacillus	0	
Bacteria.Firmicutes.Bacilli.Bacillales.Bacillaceae.Tumebacillus	0	
Bacteria.Firmicutes.Bacilli.Bacillales.Bacillaceae.unclassified_genus	3,383075809	
Bacteria.Firmicutes.Bacilli.Bacillales.Bacillaceae.Ureibacillus	0	
Bacteria.Firmicutes.Bacilli.Bacillales.Bacillaceae.Virgibacillus	0	
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Bacteria.Firmicutes.Bacilli.Bacillales.Bacillales_incertae_sedis.Rummeliibacillus	0	
Bacteria.Firmicutes.Bacilli.Bacillales.Bacillales_incertae_sedis.Solibacillus	0	
Bacteria.Firmicutes.Bacilli.Bacillales.Listeriaceae	0	
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Bacteria.Firmicutes.Bacilli.Bacillales.Listeriaceae.Listeria	0	
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Bacteria.Firmicutes.Bacilli.Bacillales.Paenibacillaceae.Cohnella	0	
Bacteria.Firmicutes.Bacilli.Bacillales.Paenibacillaceae.Oxalophagus	0	

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Bacteria.Firmicutes.Bacilli.Bacillales.Paenibacillaceae.Saccharibacillus	0		
Bacteria.Firmicutes.Bacilli.Bacillales.Paenibacillaceae.unclassified_genus	0		
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Bacteria.Firmicutes.Bacilli.Bacillales.Planococcaceae.Bhargavaea	0		
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Bacteria.Firmicutes.Bacilli.Bacillales.Planococcaceae.Planococcus	0		
Bacteria.Firmicutes.Bacilli.Bacillales.Planococcaceae.Planomicrobium	0		
Bacteria.Firmicutes.Bacilli.Bacillales.Planococcaceae.Sporosarcina	0		
Bacteria.Firmicutes.Bacilli.Bacillales.Planococcaceae.unclassified_genus	0		
Bacteria.Firmicutes.Bacilli.Bacillales.Staphylococcaceae	3.622117197		
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Bacteria.Firmicutes.Bacilli.Bacillales.Staphylococcaceae.Macrocooccus	0		
Bacteria.Firmicutes.Bacilli.Bacillales.Staphylococcaceae.Nosocomiocooccus	0		
Bacteria.Firmicutes.Bacilli.Bacillales.Staphylococcaceae.Saliniococcus	0		
Bacteria.Firmicutes.Bacilli.Bacillales.Staphylococcaceae.Staphylococcus	3.622117197		
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Bacteria.Firmicutes.Bacilli.Lactobacillales.Aerococcaceae.Eremococcus	0		
Bacteria.Firmicutes.Bacilli.Lactobacillales.Aerococcaceae.Globicatella	0		
Bacteria.Firmicutes.Bacilli.Lactobacillales.Carnobacteriaceae	4.47136814		
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Bacteria.Firmicutes.Bacilli.Lactobacillales.Carnobacteriaceae.Granulicatella	0		
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Bacteria.Firmicutes.Bacilli.Lactobacillales.Carnobacteriaceae.Trichococcus	0		
Bacteria.Firmicutes.Bacilli.Lactobacillales.Carnobacteriaceae.unclassified_genus	0		
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Bacteria.Firmicutes.Bacilli.Lactobacillales.Enterococcaceae.Enterococcus	4.034535215		
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Bacteria.Firmicutes.Bacilli.Lactobacillales.Enterococcaceae.Vagococcus	0		
Bacteria.Firmicutes.Bacilli.Lactobacillales.Lactobacillaceae	4.140344892	Grain-based	3.920888601
Bacteria.Firmicutes.Bacilli.Lactobacillales.Lactobacillaceae.Lactobacillus	4.140344892	Grain-based	3.914081554
Bacteria.Firmicutes.Bacilli.Lactobacillales.Lactobacillaceae.Pediococcus	0		
Bacteria.Firmicutes.Bacilli.Lactobacillales.Lactobacillaceae.unclassified_genus	0		
Bacteria.Firmicutes.Bacilli.Lactobacillales.Leuconostocaceae	5.520299293		
Bacteria.Firmicutes.Bacilli.Lactobacillales.Leuconostocaceae.Leuconostoc	5.025245096		
Bacteria.Firmicutes.Bacilli.Lactobacillales.Leuconostocaceae.unclassified_genus	3.340552621		
Bacteria.Firmicutes.Bacilli.Lactobacillales.Leuconostocaceae.Weissella	5.367599599	Fishmeal-based	4.037726214
Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae	5.17349219	Grain-based	3.947605787
Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Lactococcus	5.048149257		
Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus	4.571559816	Grain-based	3.998238502
Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.unclassified_genus	3.383025317		
Bacteria.Firmicutes.Bacilli.Lactobacillales.unclassified_family	2.864867349		
Bacteria.Firmicutes.Bacilli.Lactobacillales.unclassified_family.unclassified_genus	2.864867349		
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Bacteria.Firmicutes.Bacilli.unclassified_order.unclassified_family	0		
Bacteria.Firmicutes.Bacilli.unclassified_order.unclassified_family.unclassified_genus	0		
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Bacteria.Firmicutes.Clostridia.Clostridiales	4.249252681	Fishmeal-based	3.724284724
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Bacteria.Firmicutes.Clostridia.Clostridiales.Clostridiaceae.Clostridium	2.855425792		
Bacteria.Firmicutes.Clostridia.Clostridiales.Clostridiaceae.Thermobrachium	0		
Bacteria.Firmicutes.Clostridia.Clostridiales.Clostridiaceae.unclassified_genus	0		
Bacteria.Firmicutes.Clostridia.Clostridiales.Eubacteriaceae	0		
Bacteria.Firmicutes.Clostridia.Clostridiales.Eubacteriaceae.Eubacterium	0		
Bacteria.Firmicutes.Clostridia.Clostridiales.Eubacteriaceae.unclassified_genus	0		
Bacteria.Firmicutes.Clostridia.Clostridiales.IncertaeSedisXI	2.864867349		
Bacteria.Firmicutes.Clostridia.Clostridiales.IncertaeSedisXI.Anaerococcus	0		
Bacteria.Firmicutes.Clostridia.Clostridiales.IncertaeSedisXI.Anaerosphaera	0		
Bacteria.Firmicutes.Clostridia.Clostridiales.IncertaeSedisXI.Finegoldia	0		
Bacteria.Firmicutes.Clostridia.Clostridiales.IncertaeSedisXI.Gallicola	0		
Bacteria.Firmicutes.Clostridia.Clostridiales.IncertaeSedisXI.Parvimonas	0		
Bacteria.Firmicutes.Clostridia.Clostridiales.IncertaeSedisXI.Peptoniphilus	0		
Bacteria.Firmicutes.Clostridia.Clostridiales.IncertaeSedisXI.Sporanaerobacter	0		
Bacteria.Firmicutes.Clostridia.Clostridiales.IncertaeSedisXI.Tepidimicrobium	0		
Bacteria.Firmicutes.Clostridia.Clostridiales.IncertaeSedisXI.Tissierella	0		
Bacteria.Firmicutes.Clostridia.Clostridiales.IncertaeSedisXI.unclassified_genus	2.864867349		
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Bacteria.Firmicutes.Clostridia.Clostridiales.IncertaeSedisXIII.Anaerovorax	0		
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Bacteria.Firmicutes.Clostridia.Clostridiales.IncertaeSedisXIV	0		
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Bacteria.Firmicutes.Clostridia.Clostridiales.Peptostreptococcaceae.Sporacetigenium	0		
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Bacteria.Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Faecalibacterium	0		
Bacteria.Firmicutes.Clostridia.Clostridiales.Ruminococcaceae.Oscillibacter	0		
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Bacteria.Firmicutes.Clostridia.Clostridiales.Veillonellaceae.Megasphaera	0		
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Bacteria.Firmicutes.Clostridia.Clostridiales.Veillonellaceae.Sporomusa	0		
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Bacteria.Proteobacteria.Alphaproteobacteria.Rhodospirillales.Rhodospirillaceae.unclassified_genus	0	
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Bacteria.Proteobacteria.Alphaproteobacteria.Sphingomonadales.Sphingomonadaceae.Blastomonas	0	
Bacteria.Proteobacteria.Alphaproteobacteria.Sphingomonadales.Sphingomonadaceae.Novosphingobium	0	
Bacteria.Proteobacteria.Alphaproteobacteria.Sphingomonadales.Sphingomonadaceae.Sphingobium	0	
Bacteria.Proteobacteria.Alphaproteobacteria.Sphingomonadales.Sphingomonadaceae.Sphingomonas	5.288179014	
Bacteria.Proteobacteria.Alphaproteobacteria.Sphingomonadales.Sphingomonadaceae.unclassified_genus	4.335299145	
Bacteria.Proteobacteria.Alphaproteobacteria.Sphingomonadales.unclassified_family	0	
Bacteria.Proteobacteria.Alphaproteobacteria.Sphingomonadales.unclassified_family.unclassified_genus	0	
Bacteria.Proteobacteria.Alphaproteobacteria.unclassified_order	0	
Bacteria.Proteobacteria.Alphaproteobacteria.unclassified_order.unclassified_family	0	
Bacteria.Proteobacteria.Alphaproteobacteria.unclassified_order.unclassified_family.unclassified_genus	0	
Bacteria.Proteobacteria.Betaproteobacteria	4.429452046	
Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales	4.378057692	
Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Alcaligenaceae	0	
Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Alcaligenaceae.Achromobacter	0	
Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Alcaligenaceae.Alcaligenes	0	
Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Alcaligenaceae.Sutterella	0	
Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Alcaligenaceae.unclassified_genus	0	
Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Burkholderiaceae	3.072629637	
Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Burkholderiaceae.Burkholderia	3.072629637	
Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Burkholderiaceae.Chilimonas	0	
Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Burkholderiaceae.Cupriavidus	0	
Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Burkholderiaceae.Pandoraea	0	
Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Burkholderiaceae.Polynucleobacter	0	
Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Burkholderiaceae.Ralstonia	0	
Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Burkholderiaceae.unclassified_genus	0	
Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Burkholderiales.incertae_sedis	3.074958299	
Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Burkholderiales.incertae_sedis.Aquabacterium	3.074958299	
Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Burkholderiales.incertae_sedis.Ideonella	0	
Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Burkholderiales.incertae_sedis.Leptothrix	0	
Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Burkholderiales.incertae_sedis.Tepidimonas	0	
Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Burkholderiales.incertae_sedis.unclassified_genus	0	
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Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Comamonadaceae.Acidovorax	4.192250992	
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Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Comamonadaceae.Curvibacter	0	
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Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Comamonadaceae.Diaphorobacter	3.473382719	
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Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Comamonadaceae.Pelomonas	0	
Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Comamonadaceae.Polaromonas	0	
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Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Comamonadaceae.unclassified_genus	0	
Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Comamonadaceae.Variovorax	0	
Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Oxalobacteraceae	2.776244546	
Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Oxalobacteraceae.Duganella	0	
Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Oxalobacteraceae.Herbaspirillum	0	
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Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.unclassified_family	3.374850036	
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Bacteria.Proteobacteria.Betaproteobacteria.Hydrogenophilales.Hydrogenophilaceae	0	
Bacteria.Proteobacteria.Betaproteobacteria.Hydrogenophilales.Hydrogenophilaceae.Hydrogenophilus	0	
Bacteria.Proteobacteria.Betaproteobacteria.Hydrogenophilales.Hydrogenophilaceae.Petrobacter	0	
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Bacteria.Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Kingella	0	
Bacteria.Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Microvirgula	3.561016158	
Bacteria.Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Neisseria	0	
Bacteria.Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.unclassified_genus	0	
Bacteria.Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Uruburuella	0	
Bacteria.Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Vitrosocilla	0	
Bacteria.Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Vogesella	3.077274542	
Bacteria.Proteobacteria.Betaproteobacteria.Nitrosomonadales	0	
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Bacteria.Proteobacteria.Betaproteobacteria.Nitrosomonadales.Nitrosomonadaceae.unclassified_genus	0	
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Bacteria.Proteobacteria.Betaproteobacteria.Rhodocyclales.Rhodocyclaceae	0	
Bacteria.Proteobacteria.Betaproteobacteria.Rhodocyclales.Rhodocyclaceae.Azonexus	0	
Bacteria.Proteobacteria.Betaproteobacteria.Rhodocyclales.Rhodocyclaceae.Azospira	0	
Bacteria.Proteobacteria.Betaproteobacteria.Rhodocyclales.Rhodocyclaceae.Dechloromonas	0	
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Bacteria.Proteobacteria.Betaproteobacteria.Rhodocyclales.Rhodocyclaceae.Propionivibrio	0	
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Bacteria.Proteobacteria.Betaproteobacteria.Rhodocyclales.Rhodocyclaceae.Thaueria	0	

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Bacteria.Proteobacteria.Betaproteobacteria.unclassified_order.unclassified_family	0		
Bacteria.Proteobacteria.Betaproteobacteria.unclassified_order.unclassified_family.unclassified_genus	0		
Bacteria.Proteobacteria.Deltaproteobacteria	0		
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Bacteria.Proteobacteria.Deltaproteobacteria.Bdellovibrionales.Bacteriovoraceae	0		
Bacteria.Proteobacteria.Deltaproteobacteria.Bdellovibrionales.Bacteriovoraceae.Bacteriovorax	0		
Bacteria.Proteobacteria.Deltaproteobacteria.Bdellovibrionales.Bacteriovoraceae.Peredibacter	0		
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Bacteria.Proteobacteria.Deltaproteobacteria.Myxococcales.Polyangiaceae	0		
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Bacteria.Proteobacteria.Deltaproteobacteria.unclassified_order.unclassified_family.unclassified_genus	0		
Bacteria.Proteobacteria.Epsilonproteobacteria	3.945025614		
Bacteria.Proteobacteria.Epsilonproteobacteria.Campylobacteriales	3.945025614		
Bacteria.Proteobacteria.Epsilonproteobacteria.Campylobacteriales.Campylobacteraceae	3.945025614		
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Bacteria.Proteobacteria.Epsilonproteobacteria.Campylobacteriales.Campylobacteraceae.Sulfurospirillum	0		
Bacteria.Proteobacteria.Epsilonproteobacteria.Campylobacteriales.Helicobacteraceae	0		
Bacteria.Proteobacteria.Epsilonproteobacteria.Campylobacteriales.Helicobacteraceae.Helicobacter	0		
Bacteria.Proteobacteria.Epsilonproteobacteria.unclassified_order	0		
Bacteria.Proteobacteria.Epsilonproteobacteria.unclassified_order.unclassified_family	0		
Bacteria.Proteobacteria.Epsilonproteobacteria.unclassified_order.unclassified_family.unclassified_genus	0		
Bacteria.Proteobacteria.Gammaproteobacteria	5.278053005		
Bacteria.Proteobacteria.Gammaproteobacteria.Aeromonadales	2.776244546		
Bacteria.Proteobacteria.Gammaproteobacteria.Aeromonadales.Aeromonadaceae	2.776244546		
Bacteria.Proteobacteria.Gammaproteobacteria.Aeromonadales.Aeromonadaceae.Aeromonas	2.776244546		
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Bacteria.Proteobacteria.Gammaproteobacteria.Alteromonadales.Shewanellaceae	0		
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Bacteria.Proteobacteria.Gammaproteobacteria.Alteromonadales.unclassified_family	0		
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Bacteria.Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Cedecea	0		
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Bacteria.Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Cronobacter	0		
Bacteria.Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Enterobacter	0		
Bacteria.Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Erwinia	3.980292936		
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Bacteria.Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Kluyvera	0		
Bacteria.Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Morganella	0		
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Bacteria.Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Serratia	3.475242752		
Bacteria.Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Trabulsirella	0		
Bacteria.Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.unclassified_genus	4.070047454	Fishmeal-based	3.174289816
Bacteria.Proteobacteria.Gammaproteobacteria.Enterobacteriales.Enterobacteriaceae.Yersinia	0		
Bacteria.Proteobacteria.Gammaproteobacteria.Gammaproteobacteria_incertae_sedis	2.776244546		
Bacteria.Proteobacteria.Gammaproteobacteria.Gammaproteobacteria_incertae_sedis.Solimonas	2.776244546		
Bacteria.Proteobacteria.Gammaproteobacteria.Gammaproteobacteria_incertae_sedis.Solimonas.unclassified_genus	2.776244546		
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Bacteria.Proteobacteria.Gammaproteobacteria.Legionellales.Coxiellaceae	0		
Bacteria.Proteobacteria.Gammaproteobacteria.Legionellales.Coxiellaceae.Aquicella	0		
Bacteria.Proteobacteria.Gammaproteobacteria.Legionellales.Legionellaceae	0		
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Bacteria.Proteobacteria.Gammaproteobacteria.Legionellales.Legionellaceae.unclassified_genus	0		
Bacteria.Proteobacteria.Gammaproteobacteria.Oceanospirillales	0		
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Bacteria.Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae.Aggregatibacter	0		
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Bacteria.Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae.Pasteurella	0		
Bacteria.Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae.unclassified_genus	0		
Bacteria.Proteobacteria.Gammaproteobacteria.Pseudomonadales	5.009299231		
Bacteria.Proteobacteria.Gammaproteobacteria.Pseudomonadales.Moraxellaceae	4.872462513		
Bacteria.Proteobacteria.Gammaproteobacteria.Pseudomonadales.Moraxellaceae.Acinetobacter	4.76593692		
Bacteria.Proteobacteria.Gammaproteobacteria.Pseudomonadales.Moraxellaceae.Alkanindiges	0		
Bacteria.Proteobacteria.Gammaproteobacteria.Pseudomonadales.Moraxellaceae.Enhydrobacter	3.946236603		
Bacteria.Proteobacteria.Gammaproteobacteria.Pseudomonadales.Moraxellaceae.Enhydrobacter	0		
Bacteria.Proteobacteria.Gammaproteobacteria.Pseudomonadales.Moraxellaceae.Perlucciabaca	0		
Bacteria.Proteobacteria.Gammaproteobacteria.Pseudomonadales.Moraxellaceae.Psychrobacter	0		
Bacteria.Proteobacteria.Gammaproteobacteria.Pseudomonadales.Moraxellaceae.unclassified_genus	3.892085122		
Bacteria.Proteobacteria.Gammaproteobacteria.Pseudomonadales.Pseudomonadaceae	4.446207288		

Bacteria.Proteobacteria.Gammaproteobacteria.Pseudomonadales.Pseudomonadaceae.Azorhizophilus	0	
Bacteria.Proteobacteria.Gammaproteobacteria.Pseudomonadales.Pseudomonadaceae.Ceclivibrio	0	
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Bacteria.Proteobacteria.Gammaproteobacteria.Pseudomonadales.Pseudomonadaceae.unclassified_genus	3.34359413	
Bacteria.Proteobacteria.Gammaproteobacteria.Pseudomonadales.unclassified_family	0	
Bacteria.Proteobacteria.Gammaproteobacteria.Pseudomonadales.unclassified_family.unclassified_genus	0	
Bacteria.Proteobacteria.Gammaproteobacteria.Salinisphaerales	0	
Bacteria.Proteobacteria.Gammaproteobacteria.Salinisphaerales.Salinisphaeraceae	0	
Bacteria.Proteobacteria.Gammaproteobacteria.Salinisphaerales.Salinisphaeraceae.Salinisphaera	0	
Bacteria.Proteobacteria.Gammaproteobacteria.unclassified_order	0	
Bacteria.Proteobacteria.Gammaproteobacteria.unclassified_order.unclassified_family	0	
Bacteria.Proteobacteria.Gammaproteobacteria.unclassified_order.unclassified_family.unclassified_genus	0	
Bacteria.Proteobacteria.Gammaproteobacteria.Vibrionales	0	
Bacteria.Proteobacteria.Gammaproteobacteria.Vibrionales.Vibrionaceae	0	
Bacteria.Proteobacteria.Gammaproteobacteria.Vibrionales.Vibrionaceae.Photobacterium	0	
Bacteria.Proteobacteria.Gammaproteobacteria.Vibrionales.Vibrionaceae.unclassified_genus	0	
Bacteria.Proteobacteria.Gammaproteobacteria.Vibrionales.Vibrionaceae.Vibrio	0	
Bacteria.Proteobacteria.Gammaproteobacteria.Xanthomonadales	2.864867349	
Bacteria.Proteobacteria.Gammaproteobacteria.Xanthomonadales.Sinobacteraceae	0	
Bacteria.Proteobacteria.Gammaproteobacteria.Xanthomonadales.Sinobacteraceae.Steroidobacter	0	
Bacteria.Proteobacteria.Gammaproteobacteria.Xanthomonadales.Xanthomonadaceae	2.864867349	
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Bacteria.Proteobacteria.Gammaproteobacteria.Xanthomonadales.Xanthomonadaceae.Pseudoxanthomonas	0	
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Bacteria.Proteobacteria.Gammaproteobacteria.Xanthomonadales.Xanthomonadaceae.unclassified_genus	0	
Bacteria.Proteobacteria.Gammaproteobacteria.Xanthomonadales.Xanthomonadaceae.Wohlfahrtiimonas	0	
Bacteria.Proteobacteria.Gammaproteobacteria.Xanthomonadales.Xanthomonadaceae.Xanthomonas	0	
Bacteria.Proteobacteria.unclassified_class	0	
Bacteria.Proteobacteria.unclassified_class.unclassified_order	0	
Bacteria.Proteobacteria.unclassified_class.unclassified_order.unclassified_family	0	
Bacteria.Proteobacteria.unclassified_class.unclassified_order.unclassified_family.unclassified_genus	0	
Bacteria.Spirochaetes	0	
Bacteria.Spirochaetes.Spirochaetes	0	
Bacteria.Spirochaetes.Spirochaetes.Spirochaetales	0	
Bacteria.Spirochaetes.Spirochaetes.Spirochaetales.Spirochaetaceae	0	
Bacteria.Spirochaetes.Spirochaetes.Spirochaetales.Spirochaetaceae.Treponema	0	
Bacteria.SR1	0	
Bacteria.SR1.SR1_genera_incertae_sedis	0	
Bacteria.SR1.SR1_genera_incertae_sedis.unclassified_order	0	
Bacteria.SR1.SR1_genera_incertae_sedis.unclassified_order.unclassified_family	0	
Bacteria.SR1.SR1_genera_incertae_sedis.unclassified_order.unclassified_family.unclassified_genus	0	
Bacteria.Synergistetes	0	
Bacteria.Synergistetes.Synergistia	0	
Bacteria.Synergistetes.Synergistia.Synergistales	0	
Bacteria.Synergistetes.Synergistia.Synergistales.Synergistaceae	0	
Bacteria.Synergistetes.Synergistia.Synergistales.Synergistaceae.unclassified_genus	0	
Bacteria.Tenericutes	0	
Bacteria.Tenericutes.Mollicutes	0	
Bacteria.Tenericutes.Mollicutes.Anaeroplasmatales	0	
Bacteria.Tenericutes.Mollicutes.Anaeroplasmatales.Anaeroplasmataceae	0	
Bacteria.Tenericutes.Mollicutes.Anaeroplasmatales.Anaeroplasmataceae.Anaeroplasma	0	
Bacteria.Tenericutes.Mollicutes.Mycoplasmatales	0	
Bacteria.Tenericutes.Mollicutes.Mycoplasmatales.Mycoplasmataceae	0	
Bacteria.Tenericutes.Mollicutes.Mycoplasmatales.Mycoplasmataceae.Mycoplasma	0	
Bacteria.TM7	0	
Bacteria.TM7.TM7_genera_incertae_sedis	0	
Bacteria.TM7.TM7_genera_incertae_sedis.unclassified_order	0	
Bacteria.TM7.TM7_genera_incertae_sedis.unclassified_order.unclassified_family	0	
Bacteria.TM7.TM7_genera_incertae_sedis.unclassified_order.unclassified_family.unclassified_genus	0	
Bacteria.unclassified_phylum	4.208046356	
Bacteria.unclassified_phylum.unclassified_class	4.208046356	
Bacteria.unclassified_phylum.unclassified_class.unclassified_order	4.208046356	
Bacteria.unclassified_phylum.unclassified_class.unclassified_order.unclassified_family	4.208046356	
Bacteria.unclassified_phylum.unclassified_class.unclassified_order.unclassified_family.unclassified_genus	4.208046356	
Bacteria.Verrucomicrobia	0	
Bacteria.Verrucomicrobia.Opitutae	0	
Bacteria.Verrucomicrobia.Opitutae.Opitutales	0	
Bacteria.Verrucomicrobia.Opitutae.Opitutales.Opitutaceae	0	
Bacteria.Verrucomicrobia.Opitutae.Opitutales.Opitutaceae.Opitutus	0	
Bacteria.Verrucomicrobia.Spartobacteria	0	
Bacteria.Verrucomicrobia.Spartobacteria.Spartobacteria_genera_incertae_sedis	0	
Bacteria.Verrucomicrobia.Spartobacteria.Spartobacteria_genera_incertae_sedis.unclassified_family	0	
Bacteria.Verrucomicrobia.Spartobacteria.Spartobacteria_genera_incertae_sedis.unclassified_family.unclassified_genus	0	
Bacteria.Verrucomicrobia.unclassified_class	0	
Bacteria.Verrucomicrobia.unclassified_class.unclassified_order	0	
Bacteria.Verrucomicrobia.unclassified_class.unclassified_order.unclassified_family	0	
Bacteria.Verrucomicrobia.unclassified_class.unclassified_order.unclassified_family.unclassified_genus	0	
Bacteria.Verrucomicrobia.Verrucomicrobiae	0	
Bacteria.Verrucomicrobia.Verrucomicrobiae.Verrucomicrobiales	0	
Bacteria.Verrucomicrobia.Verrucomicrobiae.Verrucomicrobiales.Verrucomicrobiaceae	0	
Bacteria.Verrucomicrobia.Verrucomicrobiae.Verrucomicrobiales.Verrucomicrobiaceae.Akkermansia	0	

Footnotes:

1. Taxonomic assignment determined using RDP classifier to compare a representative sequence from each OTU to reference sequences in the greengenes database.

Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Intrasporangiaceae.Knoellia	0	
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Bacteria.Verrucomicrobia.Verrucomicrobiae.Verrucomicrobiales.Verrucomicrobiaceae.Akkermansia	0		

Footnotes:

1. Taxonomic assignment determined using RDP classifier to compare a representative sequence from each OTU to reference sequences in the greengenes database.

Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Micrococcaceae.Arthrobacter	3.101274818		
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Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Micrococcaceae.Rothia	0		
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Bacteria.Bacteroidetes.Flavobacteria	4.216231133		
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Bacteria.Bacteroidetes.Flavobacteria.Flavobacteriales.Flavobacteriaceae.Cloacibacterium	3.568689856		
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Bacteria.Bacteroidetes.Flavobacteria.Flavobacteriales.Flavobacteriaceae.Myroides	0		
Bacteria.Bacteroidetes.Flavobacteria.Flavobacteriales.Flavobacteriaceae.Riemerella	0		

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Bacteria.Bacteroidetes.Flavobacteria.Flavobacteriales.unclassified_family.unclassified_genus	0	
Bacteria.Bacteroidetes.Sphingobacteria	3.101274818	
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Bacteria.Bacteroidetes.Sphingobacteria.Sphingobacteriales.Sphingobacteriaceae.Pedobacter	0	
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Bacteria.Chloroflexi.Anaerolineae	0	
Bacteria.Chloroflexi.Anaerolineae.Anaerolineales	0	
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Bacteria.Deinococcus_Thermus.Deinococci	0	
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Bacteria.Deinococcus_Thermus.Deinococci.Deinococcales.Trueperaceae	0	
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Bacteria.Deinococcus_Thermus.Deinococci.Thermales	0	
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Bacteria.Deinococcus_Thermus.Deinococci.unclassified_order.unclassified_family	0	
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Bacteria.Firmicutes.Bacilli.Bacillales.Bacillaceae.Terribacillus	0	
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Bacteria.Firmicutes.Bacilli.Lactobacillales.Lactobacillaceae.unclassified_genus			
Bacteria.Firmicutes.Bacilli.Lactobacillales.Leuconostocaceae	5.566018816	Fishmeal-based	4.45987679
Bacteria.Firmicutes.Bacilli.Lactobacillales.Leuconostocaceae.Leuconostoc	5.016217517		
Bacteria.Firmicutes.Bacilli.Lactobacillales.Leuconostocaceae.unclassified_genus	3.556749702		
Bacteria.Firmicutes.Bacilli.Lactobacillales.Leuconostocaceae.Weissella	5.416201657	Fishmeal-based	4.340951048
Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae	5.175782145		
Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Lactococcus	5.112000431		
Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus	4.573304732	Grain-based	4.096274975
Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.unclassified_genus	3.559125128		
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Bacteria.Firmicutes.Clostridia.Clostridiales	4.346705098		
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Bacteria.Firmicutes.Clostridia.Clostridiales.IncertaeSedisXI.Parvimonas		0	
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Bacteria.Fusobacteria	0		
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Bacteria.Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae.Pasteurella		0	
Bacteria.Proteobacteria.Gammaproteobacteria.Pasteurellales.Pasteurellaceae.unclassified_genus		0	
Bacteria.Proteobacteria.Gammaproteobacteria.Pseudomonadales		4.994004168	
Bacteria.Proteobacteria.Gammaproteobacteria.Pseudomonadales.Moraxellaceae		4.932445876	
Bacteria.Proteobacteria.Gammaproteobacteria.Pseudomonadales.Moraxellaceae.Acinetobacter		4.828708568	
Bacteria.Proteobacteria.Gammaproteobacteria.Pseudomonadales.Moraxellaceae.Alkanindiges		0	
Bacteria.Proteobacteria.Gammaproteobacteria.Pseudomonadales.Moraxellaceae.Enhydrobacter		4.039659764	
Bacteria.Proteobacteria.Gammaproteobacteria.Pseudomonadales.Moraxellaceae.Moraxella		0	
Bacteria.Proteobacteria.Gammaproteobacteria.Pseudomonadales.Moraxellaceae.Perlicudioba		0	
Bacteria.Proteobacteria.Gammaproteobacteria.Pseudomonadales.Moraxellaceae.Psychrobacter		0	
Bacteria.Proteobacteria.Gammaproteobacteria.Pseudomonadales.Moraxellaceae.unclassified_genus		3.925119696	
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Bacteria.Proteobacteria.Gammaproteobacteria.Pseudomonadales.Pseudomonadaceae.Azorhizophilus		0	

Bacteria.Proteobacteria.Gammaproteobacteria.Pseudomonadales.Pseudomonadaceae.CeIlvibrio	0		
Bacteria.Proteobacteria.Gammaproteobacteria.Pseudomonadales.Pseudomonadaceae.Pseudomonas	4.327329572		
Bacteria.Proteobacteria.Gammaproteobacteria.Pseudomonadales.Pseudomonadaceae.unclassified_genus	3.101274818		
Bacteria.Proteobacteria.Gammaproteobacteria.Pseudomonadales.unclassified_family	0		
Bacteria.Proteobacteria.Gammaproteobacteria.Pseudomonadales.unclassified_family.unclassified_genus	0		
Bacteria.Proteobacteria.Gammaproteobacteria.Salinisphaerales	0		
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Bacteria.Proteobacteria.Gammaproteobacteria.Salinisphaerales.Salinisphaeraeae.Salinisphaera	0		
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Bacteria.Proteobacteria.Gammaproteobacteria.unclassified_order.unclassified_family	0		
Bacteria.Proteobacteria.Gammaproteobacteria.unclassified_order.unclassified_family.unclassified_genus	0		
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Bacteria.Proteobacteria.Gammaproteobacteria.Xanthomonadales.Xanthomonadaceae	0		
Bacteria.Proteobacteria.Gammaproteobacteria.Xanthomonadales.Xanthomonadaceae.Lysobacter	0		
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Bacteria.Proteobacteria.Gammaproteobacteria.Xanthomonadales.Xanthomonadaceae.Xanthomonas	0		
Bacteria.Proteobacteria.unclassified_class	0		
Bacteria.Proteobacteria.unclassified_class.unclassified_order	0		
Bacteria.Proteobacteria.unclassified_class.unclassified_order.unclassified_family	0		
Bacteria.Proteobacteria.unclassified_class.unclassified_order.unclassified_family.unclassified_genus	0		
Bacteria.Spirochaetes	0		
Bacteria.Spirochaetes.Spirochaetes	0		
Bacteria.Spirochaetes.Spirochaetes.Spirochaetales	0		
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Bacteria.Synergistetes	0		
Bacteria.Synergistetes.Synergistia	0		
Bacteria.Synergistetes.Synergistia.Synergistales	0		
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Bacteria.Tenericutes.Mollicutes	0		
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Bacteria.Tenericutes.Mollicutes.Anaeroplasmatales.Anaeroplasmataceae	0		
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Bacteria.Tenericutes.Mollicutes.Mycoplasmatales	0		
Bacteria.Tenericutes.Mollicutes.Mycoplasmatales.Mycoplasmataceae	0		
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Bacteria.TM7	0		
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Bacteria.unclassified_phylum.unclassified_class.unclassified_order.unclassified_family	4.369765597		
Bacteria.unclassified_phylum.unclassified_class.unclassified_order.unclassified_family.unclassified_genus	4.369765597		
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Bacteria.Verrucomicrobia.Opitutae	0		
Bacteria.Verrucomicrobia.Opitutae.Opitutales	0		
Bacteria.Verrucomicrobia.Opitutae.Opitutales.Opitutaceae	0		
Bacteria.Verrucomicrobia.Opitutae.Opitutales.Opitutaceae.Opitutus	0		
Bacteria.Verrucomicrobia.Spartobacteria	0		
Bacteria.Verrucomicrobia.Spartobacteria.Spartobacteria genera incertae sedis	0		
Bacteria.Verrucomicrobia.Spartobacteria.Spartobacteria genera incertae sedis.unclassified_family	0		
Bacteria.Verrucomicrobia.Spartobacteria.Spartobacteria genera incertae sedis.unclassified_family.unclassified_genus	0		
Bacteria.Verrucomicrobia.unclassified_class	0		
Bacteria.Verrucomicrobia.unclassified_class.unclassified_order	0		
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Bacteria.Verrucomicrobia.Verrucomicrobiae	0		
Bacteria.Verrucomicrobia.Verrucomicrobiae.Verrucomicrobiales	0		
Bacteria.Verrucomicrobia.Verrucomicrobiae.Verrucomicrobiales.Verrucomicrobiaceae	0		
Bacteria.Verrucomicrobia.Verrucomicrobiae.Verrucomicrobiales.Verrucomicrobiaceae.Akkermansia	0		

Footnotes:

1. Taxonomic assignment determined using RDP classifier to compare a representative sequence from each OTU to reference sequences in the greengenes database.

Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Micrococcaceae.Arthrobacter	3.387746094		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Micrococcaceae.Kocuria	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Micrococcaceae.Micrococcus	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Micrococcaceae.Nesterenkonia	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Micrococcaceae.Rothia	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Micrococcaceae.unclassified_genus	0		
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Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Nocardiaceae.Rhodococcus	0		
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Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Propionibacteriaceae.Propionibacterium	0		
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Bacteria.Aquificae.Aquificae.Aquificales.Hydrogenothermaceae.Sulfurihydrogenibium	0		
Bacteria.Bacteroidetes	4.39801795		
Bacteria.Bacteroidetes.Bacteroidia	3.390152164		
Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales	3.390152164		
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Bacteria.Bacteroidetes.Flavobacteria.Flavobacteriales.Flavobacteriaceae.Chryseobacterium	4.045262684	Fishmeal-based	3.157342848
Bacteria.Bacteroidetes.Flavobacteria.Flavobacteriales.Flavobacteriaceae.Cloacibacterium	3.851591741		
Bacteria.Bacteroidetes.Flavobacteria.Flavobacteriales.Flavobacteriaceae.Flavobacterium	3.086716098		
Bacteria.Bacteroidetes.Flavobacteria.Flavobacteriales.Flavobacteriaceae.Myroides	0		
Bacteria.Bacteroidetes.Flavobacteria.Flavobacteriales.Flavobacteriaceae.Riemerella	0		

Bacteria.Bacteroidetes.Flavobacteria.Flavobacteriales.Flavobacteriaceae.Salinimicrobium	0	
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Bacteria.Bacteroidetes.Flavobacteria.Flavobacteriales.unclassified_family	0	
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Bacteria.Bacteroidetes.Sphingobacteria	3.692407098	
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Bacteria.Bacteroidetes.Sphingobacteria.Sphingobacteriales.Cytophagaceae.Sporocytophaga	0	
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Bacteria.Bacteroidetes.Sphingobacteria.Sphingobacteriales.Sphingobacteriaceae.Pedobacter	0	
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Bacteria.Chloroflexi.Anaerolineae	0	
Bacteria.Chloroflexi.Anaerolineae.Anaerolineales	0	
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Bacteria.Chloroflexi.Anaerolineae.Anaerolineales.Anaerolineaceae.unclassified_genus	0	
Bacteria.Chloroflexi.Caldilineae	0	
Bacteria.Chloroflexi.Caldilineae.Caldilineales	0	
Bacteria.Chloroflexi.Caldilineae.Caldilineales.Caldilineaceae	0	
Bacteria.Chloroflexi.Caldilineae.Caldilineales.Caldilineaceae.Caldilinea	0	
Bacteria.Chloroflexi.Thermomicrobia	0	
Bacteria.Chloroflexi.Thermomicrobia.Sphaerobacteriales	0	
Bacteria.Chloroflexi.Thermomicrobia.Sphaerobacteriales.Sphaerobacteraceae	0	
Bacteria.Chloroflexi.Thermomicrobia.Sphaerobacteriales.Sphaerobacteraceae.Sphaerobacter	0	
Bacteria.Chloroflexi.Thermomicrobia.unclassified_order	0	
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Bacteria.Deinococcus_Thermus.Deinococci	0	
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Bacteria.Deinococcus_Thermus.Deinococci.Deinococcales.Deinococcaceae	0	
Bacteria.Deinococcus_Thermus.Deinococci.Deinococcales.Deinococcaceae.Deinococcus	0	
Bacteria.Deinococcus_Thermus.Deinococci.Deinococcales.Trueperaceae	0	
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Bacteria.Deinococcus_Thermus.Deinococci.Themales	0	
Bacteria.Deinococcus_Thermus.Deinococci.Themales.Thermaceae	0	
Bacteria.Deinococcus_Thermus.Deinococci.Themales.Thermaceae.Meiothermus	0	
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Bacteria.Deinococcus_Thermus.Deinococci.unclassified_order.unclassified_family.unclassified_genus	0	
Bacteria.Firmicutes	5.741882699	
Bacteria.Firmicutes.Bacilli	5.731425133	
Bacteria.Firmicutes.Bacilli.Bacillales	4.226199611	
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Bacteria.Firmicutes.Bacilli.Bacillales.Bacillaceae.Exiguobacterium	3.086716098	
Bacteria.Firmicutes.Bacilli.Bacillales.Bacillaceae.Geobacillus	0	
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Bacteria.Firmicutes.Bacilli.Bacillales.Bacillaceae.Terribacillus	0	
Bacteria.Firmicutes.Bacilli.Bacillales.Bacillaceae.Tumebacillus	0	
Bacteria.Firmicutes.Bacilli.Bacillales.Bacillaceae.unclassified_genus	3.562260965	
Bacteria.Firmicutes.Bacilli.Bacillales.Bacillaceae.Ureibacillus	0	
Bacteria.Firmicutes.Bacilli.Bacillales.Bacillaceae.Virgibacillus	0	
Bacteria.Firmicutes.Bacilli.Bacillales.Bacillales_incertae_sedis	0	
Bacteria.Firmicutes.Bacilli.Bacillales.Bacillales_incertae_sedis.Rummeliibacillus	0	
Bacteria.Firmicutes.Bacilli.Bacillales.Bacillales_incertae_sedis.Solibacillus	0	
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Bacteria.Firmicutes.Bacilli.Bacillales.Planococcaceae.Sporosarcina	0		
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Bacteria.Firmicutes.Bacilli.Bacillales.Staphylococcaceae.Macrococcus	0		
Bacteria.Firmicutes.Bacilli.Bacillales.Staphylococcaceae.Nosocomiicoccus	0		
Bacteria.Firmicutes.Bacilli.Bacillales.Staphylococcaceae.Saliniicoccus	0		
Bacteria.Firmicutes.Bacilli.Bacillales.Staphylococcaceae.Staphylococcus	3.778249365	Grain-based	3.51558726
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Bacteria.Firmicutes.Bacilli.Lactobacillales.Aerococcaceae.Globicatella	0		
Bacteria.Firmicutes.Bacilli.Lactobacillales.Carnobacteriaceae	4.69321689		
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Bacteria.Firmicutes.Bacilli.Lactobacillales.Enterococcaceae.Vagococcus	0		
Bacteria.Firmicutes.Bacilli.Lactobacillales.Lactobacillaceae	4.156940991	Grain-based	3.748785221
Bacteria.Firmicutes.Bacilli.Lactobacillales.Lactobacillaceae.Lactobacillus	4.156940991	Grain-based	3.749054345
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Bacteria.Firmicutes.Bacilli.Lactobacillales.Leuconostocaceae.unclassified_genus	3.096367484		
Bacteria.Firmicutes.Bacilli.Lactobacillales.Leuconostocaceae.Weissella	5.356507914		
Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae	5.171190096	Grain-based	4.126232247
Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Lactococcus	5.041281712		
Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.Streptococcus	4.56980786	Grain-based	3.992609372
Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae.unclassified_genus	3.081969663		
Bacteria.Firmicutes.Bacilli.Lactobacillales.unclassified_family	3.086716098		
Bacteria.Firmicutes.Bacilli.Lactobacillales.unclassified_family.unclassified_genus	3.086716098		
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Bacteria.Firmicutes.Clostridia.Clostridiales.Eubacteriaceae.Eubacterium	0		
Bacteria.Firmicutes.Clostridia.Clostridiales.Eubacteriaceae.unclassified_genus	0		
Bacteria.Firmicutes.Clostridia.Clostridiales.IncertaeSedisXI	3.086716098		
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Bacteria.Firmicutes.Clostridia.Clostridiales.IncertaeSedisXI.Gallicola	0		
Bacteria.Firmicutes.Clostridia.Clostridiales.IncertaeSedisXI.Parvimonas	0		
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Bacteria.Firmicutes.Clostridia.Clostridiales.IncertaeSedisXI.Tepidimicrobium	0		
Bacteria.Firmicutes.Clostridia.Clostridiales.IncertaeSedisXI.Tissierella	0		
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Bacteria.Proteobacteria.Alphaproteobacteria.Sphingomonadales.Sphingomonadaceae.Sphingomonas	5.262597354		
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Bacteria.Proteobacteria.Alphaproteobacteria.Sphingomonadales.unclassified_family	0		
Bacteria.Proteobacteria.Alphaproteobacteria.Sphingomonadales.unclassified_family.unclassified_genus	0		
Bacteria.Proteobacteria.Alphaproteobacteria.unclassified_order	0		
Bacteria.Proteobacteria.Alphaproteobacteria.unclassified_order.unclassified_family	0		
Bacteria.Proteobacteria.Alphaproteobacteria.unclassified_order.unclassified_family.unclassified_genus	0		
Bacteria.Proteobacteria.Betaproteobacteria	4.522829566		
Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales	4.455610829		
Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Alcaligenaceae	0		
Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Alcaligenaceae.Achromobacter	0		
Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Alcaligenaceae.Alcaligenes	0		
Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Alcaligenaceae.Sutterella	0		
Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Alcaligenaceae.unclassified_genus	0		
Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Burkholderiaceae	0		
Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Burkholderiaceae.Burkholderia	0		
Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Burkholderiaceae.Chilimonas	0		
Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Burkholderiaceae.Cupriavidus	0		
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Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Burkholderiaceae.Polynucleobacter	0		
Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Burkholderiaceae.Ralstonia	0		
Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Burkholderiaceae.unclassified_genus	0		
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Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Burkholderiales_incertae_sedis.Tepidimonas	0		
Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Burkholderiales_incertae_sedis.unclassified_genus	0		
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Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Comamonadaceae.Polaromonas	0		
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Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Oxalobacteraceae.Herbaspirillum	0		
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Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.Oxalobacteraceae.unclassified_genus	3.077274542		
Bacteria.Proteobacteria.Betaproteobacteria.Burkholderiales.unclassified_family	3.675880032		
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Bacteria.Proteobacteria.Betaproteobacteria.Methylophilales	0		
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Bacteria.Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.unclassified_genus	0		
Bacteria.Proteobacteria.Betaproteobacteria.Neisseriales.Neisseriaceae.Urubuella	0		
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Bacteria.Proteobacteria.Epsilonproteobacteria.Campylobacteriales	3.924477168		
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Bacteria.Proteobacteria.Gammaproteobacteria.Aeromonadales	3.077274542		
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Bacteria.Proteobacteria.Gammaproteobacteria.Legionellales.Legionellaceae.unclassified_genus	0		
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Bacteria.Proteobacteria.Gammaproteobacteria.Pseudomonadales	5.044511647		
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Bacteria.Proteobacteria.Gammaproteobacteria.Pseudomonadales.Moraxellaceae.Perlicudiaba	0		
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Bacteria.Proteobacteria.Gammaproteobacteria.unclassified_order.unclassified_family	0		
Bacteria.Proteobacteria.Gammaproteobacteria.unclassified_order.unclassified_family.unclassified_genus	0		
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Bacteria.Proteobacteria.Gammaproteobacteria.Vibrionales.Vibrionaceae	0		
Bacteria.Proteobacteria.Gammaproteobacteria.Vibrionales.Vibrionaceae.Photobacterium	0		
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Bacteria.Proteobacteria.Gammaproteobacteria.Vibrionales.Vibrionaceae.Vibrio	0		
Bacteria.Proteobacteria.Gammaproteobacteria.Xanthomonadales	3.086716098		
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Bacteria.Proteobacteria.Gammaproteobacteria.Xanthomonadales.Sinobacteraceae.Steroidobacter	0		
Bacteria.Proteobacteria.Gammaproteobacteria.Xanthomonadales.Xanthomonadaceae	3.086716098		
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Bacteria.Proteobacteria.unclassified_class.unclassified_order	0		
Bacteria.Proteobacteria.unclassified_class.unclassified_order.unclassified_family	0		
Bacteria.Proteobacteria.unclassified_class.unclassified_order.unclassified_family.unclassified_genus	0		
Bacteria.Spirochaetes	0		
Bacteria.Spirochaetes.Spirochaetes	0		
Bacteria.Spirochaetes.Spirochaetes.Spirochaetales	0		
Bacteria.Spirochaetes.Spirochaetes.Spirochaetales.Spirochaetaceae	0		
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Bacteria.SR1.SR1 genera incertae sedis	0		
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Bacteria.Synergistetes	0		
Bacteria.Synergistetes.Synergistia	0		
Bacteria.Synergistetes.Synergistia.Synergistales	0		
Bacteria.Synergistetes.Synergistia.Synergistales.Synergistaceae	0		
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Bacteria.Tenericutes.Mollicutes.Anaeroplasmatales.Anaeroplasmataceae	0		
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Bacteria.Tenericutes.Mollicutes.Mycoplasmatales.Mycoplasmataceae	0		
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Bacteria.TM7	0		
Bacteria.TM7.TM7 genera incertae sedis	0		
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Bacteria.TM7.TM7 genera incertae sedis.unclassified_order.unclassified_family	0		
Bacteria.TM7.TM7 genera incertae sedis.unclassified_order.unclassified_family.unclassified_genus	0		
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Bacteria.unclassified_phylum.unclassified_class	4.293861782	Fishmeal-based	3.677331359
Bacteria.unclassified_phylum.unclassified_class.unclassified_order	4.293861782	Fishmeal-based	3.677331359
Bacteria.unclassified_phylum.unclassified_class.unclassified_order.unclassified_family	4.293861782	Fishmeal-based	3.677331359
Bacteria.unclassified_phylum.unclassified_class.unclassified_order.unclassified_family.unclassified_genus	4.293861782	Fishmeal-based	3.677331359
Bacteria.Verrucomicrobia	0		
Bacteria.Verrucomicrobia.Opitutae	0		
Bacteria.Verrucomicrobia.Opitutae.Opitutales	0		
Bacteria.Verrucomicrobia.Opitutae.Opitutales.Opitutaceae	0		
Bacteria.Verrucomicrobia.Opitutae.Opitutales.Opitutaceae.Opitutus	0		
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Bacteria.Verrucomicrobia.unclassified_class	0		
Bacteria.Verrucomicrobia.unclassified_class.unclassified_order	0		
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Bacteria.Verrucomicrobia.Verrucomicrobiae.Verrucomicrobiales	0		
Bacteria.Verrucomicrobia.Verrucomicrobiae.Verrucomicrobiales.Verrucomicrobiaceae	0		
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Footnotes:

1. Taxonomic assignment determined using RDP classifier to compare a representative sequence from each OTU to reference sequences in the greengenes database.

Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Micrococcaceae	3.387746094		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Micrococcaceae.Arthrobacter	3.387746094		
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Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Micrococcaceae.Micrococcus	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Micrococcaceae.Nesterenkonia	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Micrococcaceae.Rothia	0		
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Bacteria.Proteobacteria.Gammaproteobacteria.Xanthomonadales.Xanthomonadaceae	3.086716098	
Bacteria.Proteobacteria.Gammaproteobacteria.Xanthomonadales.Xanthomonadaceae.Lysobacter	0	
Bacteria.Proteobacteria.Gammaproteobacteria.Xanthomonadales.Xanthomonadaceae.Pseudoxanthomonas	0	
Bacteria.Proteobacteria.Gammaproteobacteria.Xanthomonadales.Xanthomonadaceae.Stenotrophomonas	3.086716098	
Bacteria.Proteobacteria.Gammaproteobacteria.Xanthomonadales.Xanthomonadaceae.unclassified_genus	0	
Bacteria.Proteobacteria.Gammaproteobacteria.Xanthomonadales.Xanthomonadaceae.Wohlfahrtiimonas	0	
Bacteria.Proteobacteria.Gammaproteobacteria.Xanthomonadales.Xanthomonadaceae.Xanthomonas	0	
Bacteria.Proteobacteria.unclassified_class	0	
Bacteria.Proteobacteria.unclassified_class.unclassified_order	0	
Bacteria.Proteobacteria.unclassified_class.unclassified_order.unclassified_family	0	
Bacteria.Proteobacteria.unclassified_class.unclassified_order.unclassified_family.unclassified_genus	0	
Bacteria.Spirochaetes	0	
Bacteria.Spirochaetes.Spirochaetes	0	
Bacteria.Spirochaetes.Spirochaetes.Spirochaetales	0	
Bacteria.Spirochaetes.Spirochaetes.Spirochaetales.Spirochaetaceae	0	
Bacteria.Spirochaetes.Spirochaetes.Spirochaetales.Spirochaetaceae.Treponema	0	
Bacteria.SR1	0	
Bacteria.SR1.SR1_genera_incertae_sedis	0	
Bacteria.SR1.SR1_genera_incertae_sedis.unclassified_order	0	
Bacteria.SR1.SR1_genera_incertae_sedis.unclassified_order.unclassified_family	0	
Bacteria.SR1.SR1_genera_incertae_sedis.unclassified_order.unclassified_family.unclassified_genus	0	
Bacteria.Synergistetes	0	
Bacteria.Synergistetes.Synergistia	0	
Bacteria.Synergistetes.Synergistia.Synergistales	0	
Bacteria.Synergistetes.Synergistia.Synergistales.Synergistaceae	0	
Bacteria.Synergistetes.Synergistia.Synergistales.Synergistaceae.unclassified_genus	0	
Bacteria.Tenericutes	0	
Bacteria.Tenericutes.Mollicutes	0	
Bacteria.Tenericutes.Mollicutes.Anaeroplasmatales	0	
Bacteria.Tenericutes.Mollicutes.Anaeroplasmatales.Anaeroplasmataceae	0	
Bacteria.Tenericutes.Mollicutes.Anaeroplasmatales.Anaeroplasmataceae.Anaeroplasma	0	
Bacteria.Tenericutes.Mollicutes.Mycoplasmatales	0	
Bacteria.Tenericutes.Mollicutes.Mycoplasmatales.Mycoplasmataceae	0	
Bacteria.Tenericutes.Mollicutes.Mycoplasmatales.Mycoplasmataceae.Mycoplasma	0	
Bacteria.TM7	0	
Bacteria.TM7.TM7_genera_incertae_sedis	0	
Bacteria.TM7.TM7_genera_incertae_sedis.unclassified_order	0	
Bacteria.TM7.TM7_genera_incertae_sedis.unclassified_order.unclassified_family	0	
Bacteria.TM7.TM7_genera_incertae_sedis.unclassified_order.unclassified_family.unclassified_genus	0	
Bacteria.unclassified_phylum	4.293861782	
Bacteria.unclassified_phylum.unclassified_class	4.293861782	
Bacteria.unclassified_phylum.unclassified_class.unclassified_order	4.293861782	
Bacteria.unclassified_phylum.unclassified_class.unclassified_order.unclassified_family	4.293861782	
Bacteria.unclassified_phylum.unclassified_class.unclassified_order.unclassified_family.unclassified_genus	4.293861782	
Bacteria.Verrucomicrobia	0	
Bacteria.Verrucomicrobia.Opitutae	0	
Bacteria.Verrucomicrobia.Opitutae.Opitutales	0	
Bacteria.Verrucomicrobia.Opitutae.Opitutales.Opitutaceae	0	
Bacteria.Verrucomicrobia.Opitutae.Opitutales.Opitutaceae.Opitutus	0	
Bacteria.Verrucomicrobia.Spartobacteria	0	
Bacteria.Verrucomicrobia.Spartobacteria.Spartobacteria_genera_incertae_sedis	0	
Bacteria.Verrucomicrobia.Spartobacteria.Spartobacteria_genera_incertae_sedis.unclassified_family	0	
Bacteria.Verrucomicrobia.Spartobacteria.Spartobacteria_genera_incertae_sedis.unclassified_family.unclassified_genus	0	
Bacteria.Verrucomicrobia.unclassified_class	0	
Bacteria.Verrucomicrobia.unclassified_class.unclassified_order	0	
Bacteria.Verrucomicrobia.unclassified_class.unclassified_order.unclassified_family	0	
Bacteria.Verrucomicrobia.unclassified_class.unclassified_order.unclassified_family.unclassified_genus	0	
Bacteria.Verrucomicrobia.Verrucomicrobiae	0	
Bacteria.Verrucomicrobia.Verrucomicrobiae.Verrucomicrobiales	0	
Bacteria.Verrucomicrobia.Verrucomicrobiae.Verrucomicrobiales.Verrucomicrobiaceae	0	
Bacteria.Verrucomicrobia.Verrucomicrobiae.Verrucomicrobiales.Verrucomicrobiaceae.Akkermansia	0	

Footnotes:

1. Taxonomic assignment determined using RDP classifier to compare a representative sequence from each OTU to reference sequences in the greengenes database.

Table S19. LEfSe comparison of grain-based, high density against grain-based, low density

Taxon ¹	Log10 [(mean relative abundance) x (10 ⁶)] from group with higher relative abundance of taxon	Group with significantly higher logarithmic LDA score	Logarithmic LDA score of higher-scoring group
Bacteria	6		
Bacteria_Acidobacteria	0		
Bacteria_Acidobacteria_Acidobacteria_Gp1	0		
Bacteria_Acidobacteria_Acidobacteria_Gp1_Gp1	0		
Bacteria_Acidobacteria_Acidobacteria_Gp1_Gp1_unclassified_family	0		
Bacteria_Acidobacteria_Acidobacteria_Gp1_Gp1_unclassified_family_unclassified_genus	0		
Bacteria_Acidobacteria_Acidobacteria_Gp16	0		
Bacteria_Acidobacteria_Acidobacteria_Gp16_Gp16	0		
Bacteria_Acidobacteria_Acidobacteria_Gp16_Gp16_unclassified_family	0		
Bacteria_Acidobacteria_Acidobacteria_Gp16_Gp16_unclassified_family_unclassified_genus	0		
Bacteria_Acidobacteria_Acidobacteria_Gp2	0		
Bacteria_Acidobacteria_Acidobacteria_Gp2_Gp2	0		
Bacteria_Acidobacteria_Acidobacteria_Gp2_Gp2_unclassified_family	0		
Bacteria_Acidobacteria_Acidobacteria_Gp2_Gp2_unclassified_family_unclassified_genus	0		
Bacteria_Acidobacteria_Acidobacteria_Gp3	0		
Bacteria_Acidobacteria_Acidobacteria_Gp3_Gp3	0		
Bacteria_Acidobacteria_Acidobacteria_Gp3_Gp3_unclassified_family	0		
Bacteria_Acidobacteria_Acidobacteria_Gp3_Gp3_unclassified_family_unclassified_genus	0		
Bacteria_Acidobacteria_Acidobacteria_Gp4	0		
Bacteria_Acidobacteria_Acidobacteria_Gp4_Gp4	0		
Bacteria_Acidobacteria_Acidobacteria_Gp4_Gp4_unclassified_family	0		
Bacteria_Acidobacteria_Acidobacteria_Gp4_Gp4_unclassified_family_unclassified_genus	0		
Bacteria_Acidobacteria_Acidobacteria_Gp5	0		
Bacteria_Acidobacteria_Acidobacteria_Gp5_Gp5	0		
Bacteria_Acidobacteria_Acidobacteria_Gp5_Gp5_unclassified_family	0		
Bacteria_Acidobacteria_Acidobacteria_Gp5_Gp5_unclassified_family_unclassified_genus	0		
Bacteria_Acidobacteria_Acidobacteria_Gp6	0		
Bacteria_Acidobacteria_Acidobacteria_Gp6_Gp6	0		
Bacteria_Acidobacteria_Acidobacteria_Gp6_Gp6_unclassified_family	0		
Bacteria_Acidobacteria_Acidobacteria_Gp6_Gp6_unclassified_family_unclassified_genus	0		
Bacteria_Acidobacteria_Acidobacteria_Gp7	0		
Bacteria_Acidobacteria_Acidobacteria_Gp7_Gp7	0		
Bacteria_Acidobacteria_Acidobacteria_Gp7_Gp7_unclassified_family	0		
Bacteria_Acidobacteria_Acidobacteria_Gp7_Gp7_unclassified_family_unclassified_genus	0		
Bacteria_Actinobacteria	3.101274818		
Bacteria_Actinobacteria_Actinobacteria	3.101274818		
Bacteria_Actinobacteria_Actinobacteria_Acidimicrobiales	0		
Bacteria_Actinobacteria_Actinobacteria_Acidimicrobiales_Acidimicrobiaceae	0		
Bacteria_Actinobacteria_Actinobacteria_Acidimicrobiales_Acidimicrobiaceae_unclassified_genus	0		
Bacteria_Actinobacteria_Actinobacteria_Acidimicrobiales_lamiaceae	0		
Bacteria_Actinobacteria_Actinobacteria_Acidimicrobiales_lamiaceae_lamia	0		
Bacteria_Actinobacteria_Actinobacteria_Acidimicrobiales_incertae_sedis	0		
Bacteria_Actinobacteria_Actinobacteria_Acidimicrobiales_incertae_sedis_lumatobacter	0		
Bacteria_Actinobacteria_Actinobacteria_Acidimicrobiales_incertae_sedis_lumatobacter_unclassified_genus	0		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales	3.101274818		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales_Actinomycetaceae	0		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales_Actinomycetaceae_Actinomycetes	0		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales_Actinomycetaceae_Arcanobacterium	0		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales_Actinomycetaceae_unclassified_genus	0		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales_Beutenbergiaceae	0		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales_Beutenbergiaceae_Salana	0		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales_Beutenbergiaceae_Serinebacter	0		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales_Bogoriellaceae	0		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales_Bogoriellaceae_Georgia	0		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales_Bogoriellaceae_unclassified_genus	0		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales_Brevibacteriaceae	0		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales_Brevibacteriaceae_Brevibacterium	0		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales_Cellulomonadaceae	0		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales_Cellulomonadaceae_Cellulomonas	0		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales_Cellulomonadaceae_unclassified_genus	0		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales_Corynebacteriaceae	0		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales_Corynebacteriaceae_Corynebacterium	0		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales_Corynebacteriaceae_Turicella	0		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales_Corynebacteriaceae_unclassified_genus	0		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales_Dermabacteriaceae	0		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales_Dermabacteriaceae_Brachybacterium	0		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales_Dermacoccaceae	0		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales_Dermacoccaceae_Dermacoccus	0		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales_Dietziaceae	0		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales_Dietziaceae_Dietzia	0		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales_Geodermatophilaceae	0		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales_Geodermatophilaceae_Blastococcus	0		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales_Geodermatophilaceae_unclassified_genus	0		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales_Intrasporangiaceae	0		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales_Intrasporangiaceae_Janibacter	0		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales_Intrasporangiaceae_Knoellia	0		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales_Intrasporangiaceae_Omithinimicrobium	0		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales_Intrasporangiaceae_Tetrasphaera	0		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales_Intrasporangiaceae_unclassified_genus	0		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales_Jonesiaceae	0		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales_Jonesiaceae_Jonesia	0		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales_Microbacteriaceae	0		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales_Microbacteriaceae_Agrococcus	0		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales_Microbacteriaceae_Clavibacter	0		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales_Microbacteriaceae_Curtobacterium	0		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales_Microbacteriaceae_Frigoribacterium	0		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales_Microbacteriaceae_Leifsonia	0		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales_Microbacteriaceae_Leucobacter	0		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales_Microbacteriaceae_Microbacterium	0		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales_Microbacteriaceae_Plantibacter	0		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales_Microbacteriaceae_Pseudoclavibacter	0		
Bacteria_Actinobacteria_Actinobacteria_Actinomycetales_Microbacteriaceae_unclassified_genus	0		

Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Micrococcaceae	3.101274818		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Micrococcaceae.Arthrobacter	3.101274818		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Micrococcaceae.Kocuria	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Micrococcaceae.Micrococcus	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Micrococcaceae.Nesterenkonia	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Micrococcaceae.Rothia	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Micrococcaceae.unclassified_genus	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Micromonosporaceae	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Micromonosporaceae.Luedemannella	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Micromonosporaceae.Micromonospora	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Mycobacteriaceae	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Mycobacteriaceae.Mycobacterium	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Nocardiaceae	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Nocardiaceae.Gordonia	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Nocardiaceae.Rhodococcus	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Nocardiaceae.unclassified_genus	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Nocardiaceae.Williamsia	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Nocardioidaceae	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Nocardioidaceae.Aeromicrobium	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Nocardioidaceae.Marmoricola	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Nocardioidaceae.Nocardioides	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Nocardioidaceae.Pimelobacter	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Nocardioidaceae.unclassified_genus	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Nocardiopsaceae	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Nocardiopsaceae.Nocardiopsis	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Nocardiopsaceae.unclassified_genus	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Propionibacteriaceae	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Propionibacteriaceae.Friedmanniella	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Propionibacteriaceae.Microlunatus	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Propionibacteriaceae.Propionibacterium	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Propionibacteriaceae.unclassified_genus	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Pseudonocardiaceae	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Pseudonocardiaceae.Pseudonocardia	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Pseudonocardiaceae.Saccharopolyspora	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Pseudonocardiaceae.unclassified_genus	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Sanguibacteraceae	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Sanguibacteraceae.Sanguibacter	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Streptomycetaceae	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Streptomycetaceae.Streptomyces	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Streptomycetaceae.unclassified_genus	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.unclassified_family	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.unclassified_family.unclassified_genus	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Yaniellaceae	0		
Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Yaniellaceae.Yaniella	0		
Bacteria.Actinobacteria.Actinobacteria.Bifidobacteriales	0		
Bacteria.Actinobacteria.Actinobacteria.Bifidobacteriales.Bifidobacteriaceae	0		
Bacteria.Actinobacteria.Actinobacteria.Bifidobacteriales.Bifidobacteriaceae.Aeriscardovia	0		
Bacteria.Actinobacteria.Actinobacteria.Bifidobacteriales.Bifidobacteriaceae.Bifidobacterium	0		
Bacteria.Actinobacteria.Actinobacteria.Bifidobacteriales.Bifidobacteriaceae.unclassified_genus	0		
Bacteria.Actinobacteria.Actinobacteria.Coriobacteriales	0		
Bacteria.Actinobacteria.Actinobacteria.Coriobacteriales.Coriobacteriaceae	0		
Bacteria.Actinobacteria.Actinobacteria.Coriobacteriales.Coriobacteriaceae.Asaccharobacter	0		
Bacteria.Actinobacteria.Actinobacteria.Coriobacteriales.Coriobacteriaceae.Atopobium	0		
Bacteria.Actinobacteria.Actinobacteria.Coriobacteriales.Coriobacteriaceae.Collinsella	0		
Bacteria.Actinobacteria.Actinobacteria.Coriobacteriales.Coriobacteriaceae.Eggerthella	0		
Bacteria.Actinobacteria.Actinobacteria.Coriobacteriales.Coriobacteriaceae.Olsenella	0		
Bacteria.Actinobacteria.Actinobacteria.Coriobacteriales.Coriobacteriaceae.Paraeggerthella	0		
Bacteria.Actinobacteria.Actinobacteria.Coriobacteriales.Coriobacteriaceae.unclassified_genus	0		
Bacteria.Actinobacteria.Actinobacteria.Rubrobacteriales	0		
Bacteria.Actinobacteria.Actinobacteria.Rubrobacteriales.Rubrobacteraceae	0		
Bacteria.Actinobacteria.Actinobacteria.Rubrobacteriales.Rubrobacteraceae.Rubrobacter	0		
Bacteria.Actinobacteria.Actinobacteria.Solirubrobacteriales	0		
Bacteria.Actinobacteria.Actinobacteria.Solirubrobacteriales.Conexibacteraceae	0		
Bacteria.Actinobacteria.Actinobacteria.Solirubrobacteriales.Conexibacteraceae.Conexibacter	0		
Bacteria.Actinobacteria.Actinobacteria.Solirubrobacteriales.Solirubrobacteraceae	0		
Bacteria.Actinobacteria.Actinobacteria.Solirubrobacteriales.Solirubrobacteraceae.Solirubrobacter	0		
Bacteria.Actinobacteria.Actinobacteria.Solirubrobacteriales.unclassified_family	0		
Bacteria.Actinobacteria.Actinobacteria.Solirubrobacteriales.unclassified_family.unclassified_genus	0		
Bacteria.Actinobacteria.Actinobacteria.unclassified_order	0		
Bacteria.Actinobacteria.Actinobacteria.unclassified_order.unclassified_family	0		
Bacteria.Actinobacteria.Actinobacteria.unclassified_order.unclassified_family.unclassified_genus	0		
Bacteria.Aquificae	0		
Bacteria.Aquificae.Aquificae	0		
Bacteria.Aquificae.Aquificae.Aquificales	0		
Bacteria.Aquificae.Aquificae.Aquificales.Hydrogenothermaceae	0		
Bacteria.Aquificae.Aquificae.Aquificales.Hydrogenothermaceae.Sulfurihydrogenibium	0		
Bacteria.Bacteroidetes	4.39801795		
Bacteria.Bacteroidetes.Bacteroidia	3.081969663		
Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales	3.081969663		
Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae	3.081969663		
Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Bacteroidaceae.Bacteroides	3.081969663		
Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Porphyrionadaceae	0		
Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Porphyrionadaceae.Dysgonomonas	0		
Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Porphyrionadaceae.Porphyrionas	0		
Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Porphyrionadaceae.Proteiniphilum	0		
Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Porphyrionadaceae.unclassified_genus	0		
Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Prevotellaceae	0		
Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Prevotellaceae.Hallella	0		
Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Prevotellaceae.Prevotella	0		
Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Prevotellaceae.unclassified_genus	0		
Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.unclassified_family	0		
Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.unclassified_family.unclassified_genus	0		
Bacteria.Bacteroidetes.Flavobacteria	4.280023713		
Bacteria.Bacteroidetes.Flavobacteria.Flavobacteriales	4.280023713		
Bacteria.Bacteroidetes.Flavobacteria.Flavobacteriales.Cryomorphaceae	0		
Bacteria.Bacteroidetes.Flavobacteria.Flavobacteriales.Cryomorphaceae.Fluvicola	0		
Bacteria.Bacteroidetes.Flavobacteria.Flavobacteriales.Flavobacteriaceae	4.280023713		
Bacteria.Bacteroidetes.Flavobacteria.Flavobacteriales.Flavobacteriaceae.Capnocytophaga	0		
Bacteria.Bacteroidetes.Flavobacteria.Flavobacteriales.Flavobacteriaceae.Chryseobacterium	4.037422441		
Bacteria.Bacteroidetes.Flavobacteria.Flavobacteriales.Flavobacteriaceae.Cloacibacterium	3.851591741		
Bacteria.Bacteroidetes.Flavobacteria.Flavobacteriales.Flavobacteriaceae.Flavobacterium	3.077274542		
Bacteria.Bacteroidetes.Flavobacteria.Flavobacteriales.Flavobacteriaceae.Myroides	0		

Bacteria.Bacteroidetes.Flavobacteria.Flavobacteriales.Flavobacteriaceae.Riemerella	0	
Bacteria.Bacteroidetes.Flavobacteria.Flavobacteriales.Flavobacteriaceae.Salinimicrobium	0	
Bacteria.Bacteroidetes.Flavobacteria.Flavobacteriales.Flavobacteriaceae.unclassified_genus	0	
Bacteria.Bacteroidetes.Flavobacteria.Flavobacteriales.Flavobacteriaceae.Wautersiella	0	
Bacteria.Bacteroidetes.Flavobacteria.Flavobacteriales.unclassified_family	0	
Bacteria.Bacteroidetes.Flavobacteria.Flavobacteriales.unclassified_family.unclassified_genus	0	
Bacteria.Bacteroidetes.Sphingobacteria	3.675880032	
Bacteria.Bacteroidetes.Sphingobacteria.Sphingobacteriales	3.675880032	
Bacteria.Bacteroidetes.Sphingobacteria.Sphingobacteriales.Chitinophagaceae	0	
Bacteria.Bacteroidetes.Sphingobacteria.Sphingobacteriales.Chitinophagaceae.Ferruginibacter	0	
Bacteria.Bacteroidetes.Sphingobacteria.Sphingobacteriales.Chitinophagaceae.Filimonas	0	
Bacteria.Bacteroidetes.Sphingobacteria.Sphingobacteriales.Chitinophagaceae.Flavisolibacter	0	
Bacteria.Bacteroidetes.Sphingobacteria.Sphingobacteriales.Chitinophagaceae.unclassified_genus	0	
Bacteria.Bacteroidetes.Sphingobacteria.Sphingobacteriales.Cytophagaceae	3.675880032	
Bacteria.Bacteroidetes.Sphingobacteria.Sphingobacteriales.Cytophagaceae.Adhaeribacter	0	
Bacteria.Bacteroidetes.Sphingobacteria.Sphingobacteriales.Cytophagaceae.Cytophaga	0	
Bacteria.Bacteroidetes.Sphingobacteria.Sphingobacteriales.Cytophagaceae.Dvadobacter	0	
Bacteria.Bacteroidetes.Sphingobacteria.Sphingobacteriales.Cytophagaceae.Ermicicia	0	
Bacteria.Bacteroidetes.Sphingobacteria.Sphingobacteriales.Cytophagaceae.Flectobacillus	3.675880032	
Bacteria.Bacteroidetes.Sphingobacteria.Sphingobacteriales.Cytophagaceae.Hymenobacter	0	
Bacteria.Bacteroidetes.Sphingobacteria.Sphingobacteriales.Cytophagaceae.Pontibacter	0	
Bacteria.Bacteroidetes.Sphingobacteria.Sphingobacteriales.Cytophagaceae.Runella	0	
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Footnotes:

1. Taxonomic assignment determined using RDP classifier to compare a representative sequence from each OTU to reference sequences in the greengenes database.

Table S20. Average intestinal inflammation scores in each treatment group

Experimental group	Score
Fishmeal-based, high density	1.53 ± 0.17
Fishmeal-based, low density	1.93 ± 0.21
Grain-based, high density	1.73 ± 0.18
Grain-based, low density	1.6 ± 0.19

Table S21. End-of-study results for measured fish fillet contaminant concentrations in each diet treatment group

Contaminant	Fishmeal Diet	Grain-based Diet
DDE ($\mu\text{g/g}$) ¹	0.0059 \pm 0.0006	0.0064 \pm 0.0012
Total PCBs (ppm) ²	0.0069 \pm 0.0009	0.0048 \pm 0.0015

Footnotes:

1. DDE = dichlorodiphenyldichloroethylene

2. PCBs = polychlorinated biphenyls (209 congeners tested).

%OTUs from each class

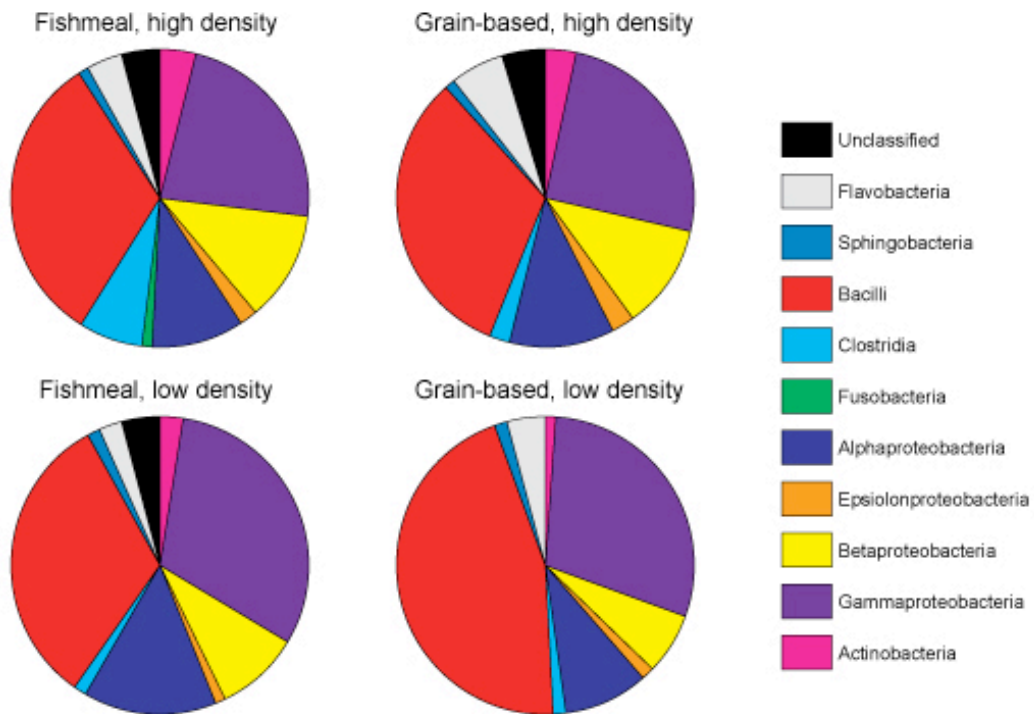


Figure S1. Diversity of rainbow trout treatment core microbiotas. Percentage of the treatment core OTUs from each bacterial class.

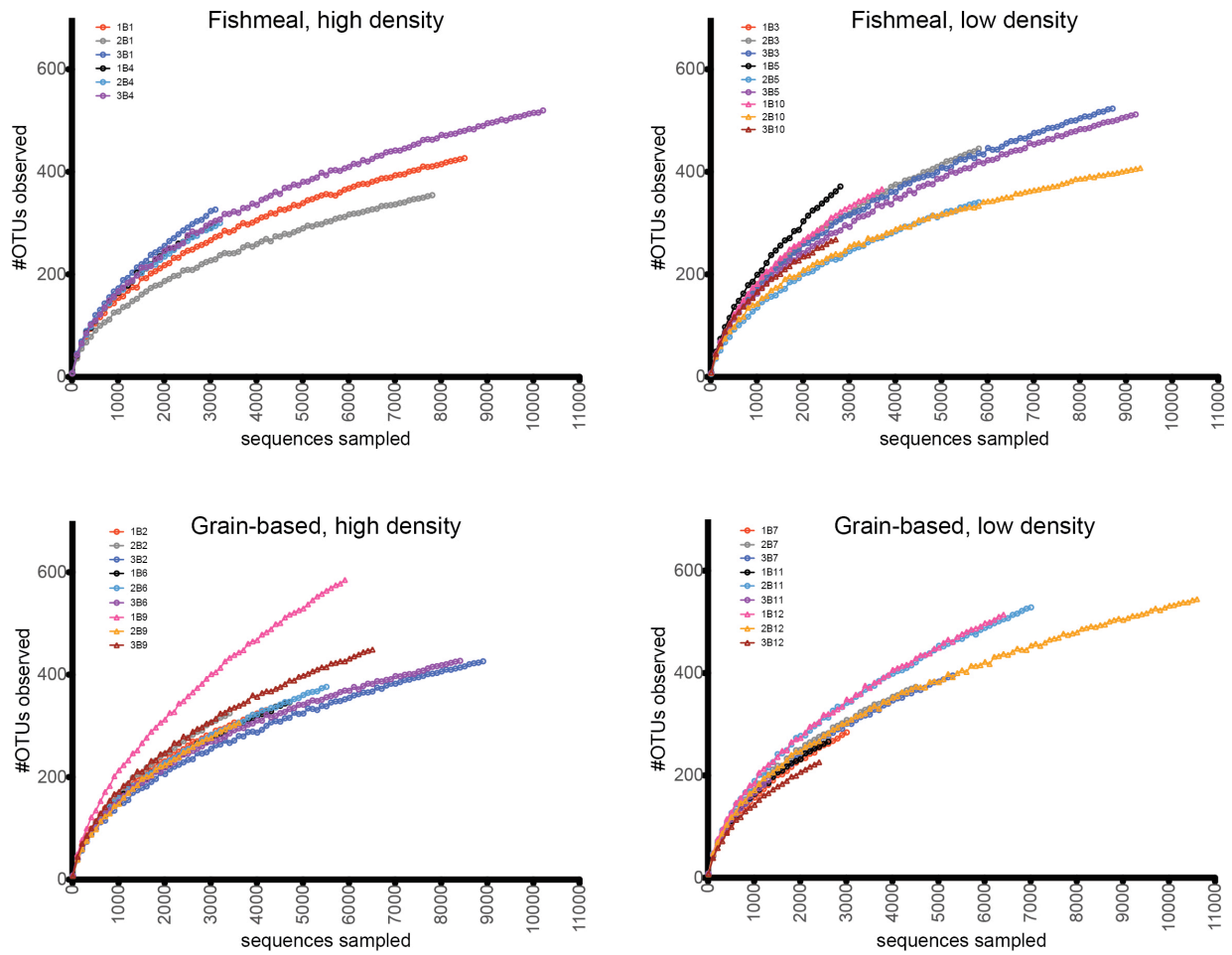


Figure S2. Alpha rarefaction of 16S sequences from rainbow trout intestines. The number of unique observed 16S sequences for each sequenced fish at sampling depths from 10-11000 sequences. Each curve in each panel represents a single animal. Curves are truncated when all sequences in an individual have been sampled.

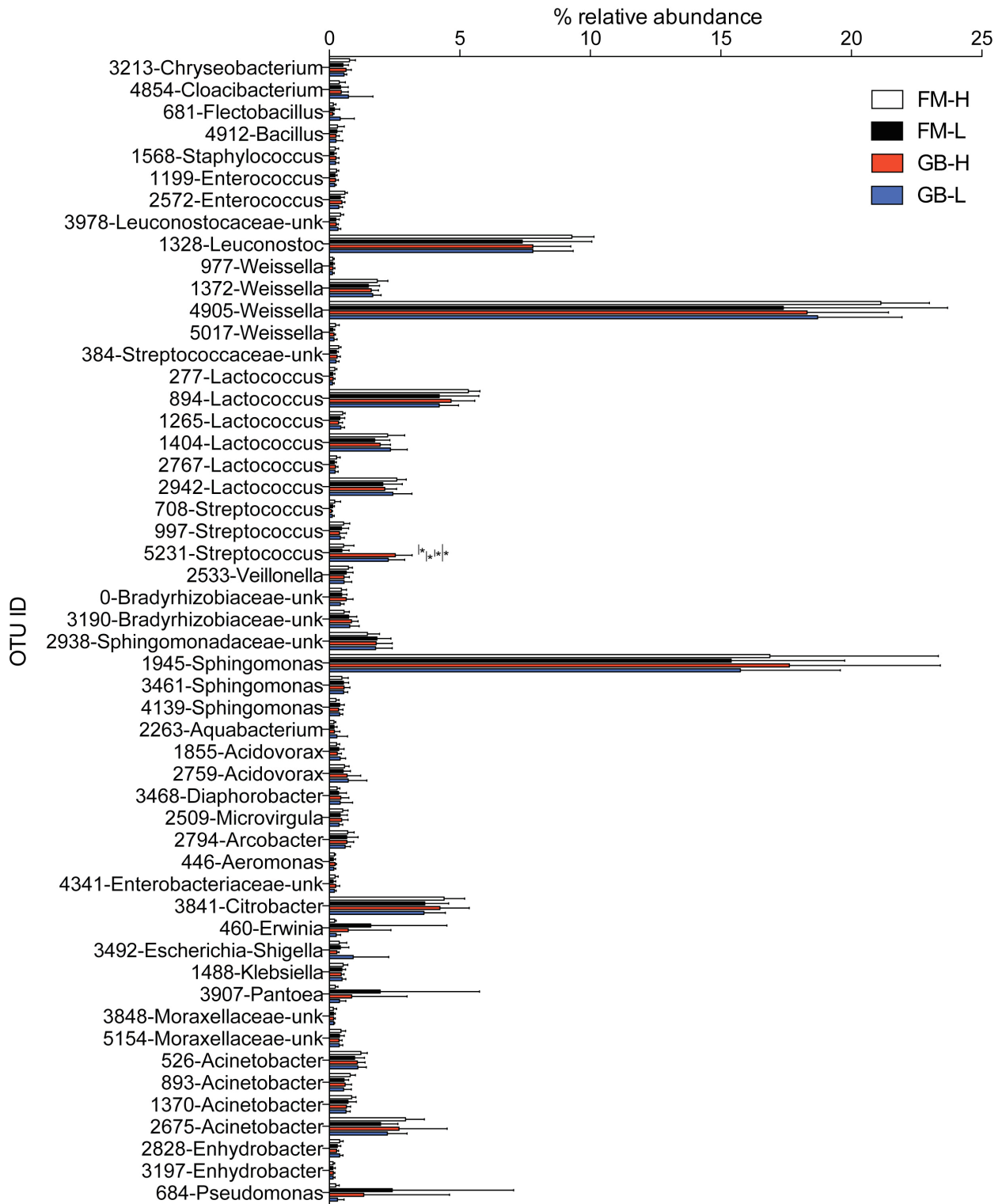


Figure S3. Average relative abundances of 52 shared core OTUs in each treatment. “OTU ID” indicates an arbitrarily assigned OTU number followed by the most detailed taxonomic classification for the OTU. For statistical comparison between treatment groups, OTU counts were standardized by sample and normalized by \log_{10} transformation. Relative abundances between treatment groups were compared by Student’s t-test with a 5% FDR. Asterisks indicate statistically significant differences between treatment groups.