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Role of modified diets in modulating gut integrity and microbiome –immune axis in mice .

A Thesis

Submitted to the Council of the College of Veterinary Medicine/University of Al-Qadisiyah in Partial Fulfillment of the Requirements for the Degree of Doctorate of Philosophy in Microbiology and Parasitology

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بسم الله الرحمن الرحيم

(فَتَعَالَى اللَّهُ الْمَلِكُ الْحَقُّ وَلَا تَعْجَلْ بِالْقُرْآنِ مِن قَبْلِ أَن يُقْضَىٰ إِلَيْكَ وَحْيُهُ وَقُل رَّبِّ زِدْنِي عِلْمًا)

صدق الله العلي العظيم

(طه الآية :**114**)

Dedication

To the one sent by God as a guide, a messenger of glad tidings, and a warner to all the worlds:

Prophet Muhammad (Peace and blessings be upon him and his progeny)

To the one who offered his life and his two sons in sacrifice for the religion of God:

Muhammad Muhammad Sadiq al-Sadr (May his soul be sanctified)

To the one who has filled my life with grace, peace, and stability:

My Dear Wife

To those who are the light of my eyes and my greatest joy:

My Children (Ali, Abbas, and the Fawatim)

Hussein… 2026

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Hussein Imran Kareem 2026

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Abstract

Diets greatly affect a host's gut microbiome and immune responses. Lipid-rich foods, such as those including egg yolks, contain phospholipids, cholesterol, fat-soluble vitamins, and essential fatty acids, all of which impact microbiome activity, the physiology of the gut, and immune functions. The differences in the impact of goose eggs versus chicken eggs on the microbiome-immune axis, however, are understudied. For this reason, the study at hand aimed to examine the impact goose versus chicken egg yolk supplementation had on gut microbiome, cytokine responses, and histomorphological analysis of the gut.

Under the same environmental and experimental control conditions, thirty laboratory mice divided into one of three groups, one of which served as a control and the others supplemented either with chicken or goose egg yolk. After varying two-week and one-month intervals, the gut microbiome was assessed using 16S rRNA amplicon sequencing. The blood was assessed for immune responses by measuring two cytokines, IL-6 and IL-10, and gut microbiome disorders were assessed via morphometry histological images. The data was assessed using a one-way ANOVA, and a p value of < 0.05 was set as the threshold for statistical significance.

In this study, a large proportion of resource allocation was shown to be used for gut microbiome.Microbial community assessments revealed a significant boost in beneficial taxa among yolk supplemented groups as compared to the control groups through the relative abundance analysis. Prominent examples of this effect include the taxa within the genera Ligilactobacillus, Limosilactobacillus, and Bacteroides ($P < 0.05$), with respect to significant enrichment. In the chicken yolk group, Ligilactobacillus apodemi revealed a significant transient increase at day 14. Bacteroides, as a relative abundance, reached 53–55%, and exhibited a decline, lead to day 30 at a relative abundance of 3% and exemplifying of

rapid Early successional and community restructuring. The goose yolk group, in contrast, showed a greater degree of sustained microbial stabilization and characterized with sustainable enrichment of beneficial taxa and the less temporal variability of the predominant microbes. As evidenced by the Chao1 and Bray Curtis indices, subsequent analysis of α and β diversity showed significant reorganization of the microbial communities in relation to the control groups, and through the yolk supplementation. Within both yolk treatment groups, microbial community improvement and restructuring was observed, including an increase in microbial richness during the early feeding period ($P < 0.05$), along with an increase in Shannon's diversity, Simpson's index, and Phylogenetic diversity.

Dietary changes strongly affected the concentration of the cytokines in the blood. The concentration of IL-6 within the blood in the goose yolk group was at (310 ± 95 pg/mL) at day 14, in comparison to the control group at (85 ± 62 pg/mL) ($P < 0.05$).

On the other hand, the chicken egg yolk group demonstrated the most IL-6 at day 30 (410 ± 210 pg/mL), which was significant compared to the control and goose yolk groups ($P < 0.05$), exhibiting a delayed pattern of inflammatory response. There was also significant difference among treatments of the signal of Anti-inflammation. Even though the IL-10 level in serum increased in all groups over time, the chicken yolk group presented the highest level of IL-10 at day 30 (460 ± 150 pg/mL), which was significant compared to the control group ($P < 0.05$) thereby confirming the activation of the compensatory Anti-inflammation regulatory pathways that were caused by the diet-induced microbial and metabolic adaptation.

Histomorphometric assessment from the intestinal tissues showed significant structural improvement upon supplementation of egg yolk. In

the duodenum, the chicken egg yolk group demonstrated a significant increase of mean villus length measured to be 0.4536 mm compared to 0.4088 mm in the control group and 0.5183 mm in the goose yolk group ($P < 0.05$). A similar trend was demonstrated in the jejunum, with control measuring 0.3156 mm, chicken yolk measuring 0.3451 mm, and goose yolk measuring 0.3866 mm ($P < 0.05$). In the control group of the ileum, villus length measured 0.2365 mm, the chicken yolk group measured 0.2841 mm, and the goose yolk group measured 0.3082 mm ($P < 0.05$). The yolk groups showed a significant increase in villus width, villus area, and crypt depth compared to the control group in all sections of the intestine ($P < 0.05$) which was a reflection of the improved epithelial renewal, Absorptive Surface Expansion and functional capacity of the mucosa.

Under the experimental conditions of this study, all the parameters described showed that supplementation of both egg yolk types altered the gut microbiota, immune response, and gut tissue structure. However, the supplementation of goose egg yolk showed more pronounced beneficial gut microbiota, more balanced immune response, and more profound intestinal (gut) tissue structure compared to supplementation of chicken egg yolk, in this study.

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List of Abbreviations

Abbrev-	Terms
DNA	Deoxyribonucleic Acid
EDTA	Ethylenediaminetetraacetic Acid
FODMAP	Fermentable Oligosaccharides Disaccharides Monosaccharides And Polyols
GABA	Gamma-aminobytric acid
GALT	Gut-associated lymphoid tissue
PCR	Polymerase Chain Reaction
PH	Potential of Hydrogen
SCFA	Short Chain Fatty Acid
TMAO	Trimethylamine N-oxide
AhR	Aryl hydrocarbon receptor
SPF	specific pathogen-free conditions.
16SrRNA	16S ribosomal Ribonucleic Acid
NGS	Next generation sequencing
OTU	Operation taxonomic units
ASV	Amplicon sequence variants
ELISA	Enzyme linked immune sorbent assay
IL-6	Interleukin-6
IL-10	Interleukin-10

HRP	Horseradish Peroxidase.
H&E	Heamatoxlyin and Eosin stain
DPX	**D**istrene **P**lasticizer **X**ylene
SEM	Standard Error of the Mean
ANOVA	Analysis of Variance
DASH	Dietary Approaches to Stop Hypertension

Chapter one

Introduction

1.1. Introduction

The gastrointestinal tract comprises a dynamic ecosystem of microorganisms that include bacteria, archaea, fungi, viruses, and also noncellular microorganisms known as the gut microbiome. This microbial assemblage digests food, metabolizes nutrients, formulates various bioactive substances, preserves the integrity of the epithelial barrier, and modulates the immune homeostasis of the host. The gut microbiome also performs other important roles in host health regulation and communication with intestinal immune tissues. This interaction is what de Vos *et al.* (2022) and Bermúdez-Humarán . (2022) refer to as the microbiome–immune axis. The functioning of this microbiome–immune axis is vital for healthy gut balance, and the immune system ultimately helps the host to protect microbial pathogens. However, a disruption of the microbial ecosystem or dysbiosis is related to many health disorders, and they include chronic systemic inflammation, metabolic alteration, immune dysregulation, and damage to neurophysiological signaling that regulate the quality of health (Mayer *et al*., 2024).

Of all the environmental factors that affect the gut microbiome, research suggests that diet is the most powerful, rapid, and consistent environmental factor that can alter the gut microbiome. The substrates in the diet and the metabolites that are derived from the gut microbiome can change the microflora dynamics, the competition for resources, and the metabolism of the gut microflora. The dynamics of the microbiome, their competition for resources, and their metabolism can then change the structure and functioning of the gut microbiome. The fermentation of food substrates by the gut microbes and the metabolites derived from the gut microbes can produce other multimodal gut metabolites which provide immunological activity by signaling to both local and distant immune systems

(Rowland *et al*., 2018; Patloka *et al*., 2024). There exists a considerable amount of experimental and translational findings that show that gut microbiome diversity and gut microbiome dominant flora can be altered by a change in diet. In addition, the gut microbiome can alter the dominant flora, and the gut microbiome can change the diet. The gut microbiome can change the dominant flora, and the gut microbiome can change the diet. The findings show that the structure of the gut microbiome and the immune system are dependent on the diet. The composition of the gut microbiome is altered by the diet. The gut microbiome is dependent on the diet. The gut microbiome is a dependent organic component of the structure and the host immune response.

Potentially modifiable pathways of lipid absorption, bile acid metabolism, 'food' sources of microbes, and inflammatory signaling pathways are some of the microbiome-regulating effects of dietary lipids. Microbial composition can drastically rearrange due to lipid-rich diets, resulting in varying effects on the gut lining, metabolic equilibrium, and the release of signaling molecules. As for diets high in fermentable carbohydrates and fibers, these tend to enrich microbial communities, increase beneficial microbiota, and increase the production of protective metabolites, such as increases in butyrate that reinforce the gut lining and reduce inflammation (Louis and Flint ., 2017; Makki *et al*., 2018; Deehan *et al*., 2020; Zheng et al., 2024) Conversely, the consequences are more harmful for the gut biome and for the host, with an association of high dietary fats with low substrate fermentability, that include low microbial diversity, coupled with decreased protective metabolites, impaired gut associated lymphoid tissue (GALT) immunity, and an increased risk of metabolic disorders (Scott *et al*. 2013; Gomes *et al*. 2022). The quality of the lipids that are ingested by the host plays a greater role in the

composition of microbial communities and in regulating the host–microbiome partnerships than the quantity of the lipids.

There have been an increasing number of studies focusing on naturally occurring food-derived bioactive compounds that positively adjust the gut microbiome and the immune system. Egg yolk contains many bioactive compounds, such as phospholipids, cholesterol, fat-soluble vitamins, essential fatty acids, and many choline and other nutrient compounds, that may influence the gut microbiome and the physiology of the gut. The differences in the composition of the egg yolk of different avian species may result in different biological impacts on the patterns of gut microbiome colonization, gut shapes and immune system responses. The differences in the lipid and fatty acid composition of goose egg yolk and chicken egg yolk, as well as the differences in cholesterol and phospholipid levels and the number of the vitamins, indicate that the impact of goose egg yolk and chicken egg yolk on the gut microbiome may be different. Although the different lipid compounds in eggs are of great scientific nutritional value, there is a clear lack of studies done in a comparative manner to evaluate the differences in the egg-derived lipids and their impact on the gut microbiome, the immune system gut signaling and the structural changes of the gut.

Mouse models constitute a well-structured test system for the study of diet–microbiome–immune interactions due to expert control of the components of diet, environment, exposure, sampling time, and assessment of the biological event of interest in a context of laboratory standardization. Controlled murine dietary models have been instrumental in the study of the effects of nutritional interventions on microbial range, succession, immune mediator expression, and intestinal histological changes. Furthermore, the gut-brain axis suggests that certain probiotic and

psychobiotic genera, along with other beneficial microbes, may utilize microbial signaling and immune system influencing activities to modulate intestinal inflammation and the intestinal permeability barrier as well as other host systems. However, knowledge on the long-term effects of certain dietary lipids, derived from natural animal sources, on the microbiome–immune axis remain largely unexplored.

1.2 Aim of the Study

This study aimed to examine the impact of dietary supplementation with goose and chicken egg yolk on the gut microbiome–immune axis of mice using a controlled laboratory setting. More specifically, this research sought to understand gut microbiome composition and diversity, global immune system responses, and the histomorphological changes to the gut associated with various lengths of dietary supplementation. In addition, this research aimed to understand the effects of the two yolk types in the context of host–microbiome interactions by virtue of their impact on gut health, thus, offering a model to understand the species-specific dietary lipids, microbial ecology, and the associated immune regulatory activity.

1.3 Objectives of the Study

- Assess the impact of goose egg yolk and chicken egg yolk supplementation on the gut microbiome of mice through the use of 16S rRNA sequencing.
- Evaluate the impact of dietary egg yolk supplementation on microbial diversity, as measured by key metrics of alpha diversity (i.e., Chao1 richness, Shannon and Simpson diversity, Faith's phylogenetic diversity) and beta diversity.

- Evaluate the impact of dietary supplementation on the gut microbiome in terms of the key species and genera most affected, with an emphasis on gut health and microbial stability.
- Evaluate the shifts in the immune system, brought on by dietary supplementation, by quantifying the serum concentration of the key inflammatory (i.e., interleukin-6) and anti-inflammatory (i.e., interleukin-10) cytokines.
- Examine the impact of dietary yolk supplementation on histomorphological changes to the intestine by assessing the histological changes to the villi and crypts of the duodenum, jejunum, and ileum.
- This study plan aims to examine the effects of goose vs chicken yolk on the microbial restructuring process as well as other biological responses such as gut cell development and immunological response.
- This study aims to understand the effect of diet on controlled microbial changes, immune responses, as well as structural changes in the gut, using the variability of dietary lipids as the variable to examine the microbiome-immune response relationship.

Chapter two

Literatures Review

2. Literature Review

2.1.1 Overview of the gut microbiome

The gut microbiome is a collection of microorganisms including bacteria, viruses, archaea, fungi, and protozoa (Mukherjee *et al*., 2020; Matijašić *et al*.,2020). In mice, it begins developing at the time of birth. Age, diet, and environment contribute to alterations in composition and function of the gastrointestinal microbiome (Zmora *et al.*,2019; Pilla & Suchodolski, 2020). The microbiome aids in digestion, nutrient absorption, and host pathogen defense (Valles-Colomer *et al*., 2023). Individual diet and nutrient composition influences the microbiome composition (Song *et al*., 2020; Wan *et al*., 2021). High-fat and low-fiber diets result in low microbial diversity, whereas high-fiber diets promote the growth of beneficial microbes (Ceballos *et al*., 2021; Galica *et al*., 2022; Rinninella et al., 2023; Baars *et al*., 2024).

2.1.2 The immune system and its interaction with the microbiota

Gut-associated lymphoid tissue (GALT) is the largest immune system organ. It contains immune cells that communicate with gut microbes and their products (Martyniak *et al*., 2021; Bemark *et al*., 2024). Such interactions aid in immune system fir equilibrium. They are thwart low-grade inflammation, and immune defense (Lin *et al* ., 2023). GALT teaches the body to distinguish between harmful and beneficial microbes. This mechanism is known as immune tolerance. It enables beneficial microbes to inhabit the gut without immune response, and simultaneously subdues pathogenic microbes. This state of equilibrium is critical for gut and overall health.

Dietary fiber fermentation produces Short Chain Fatty Acids (SCFA) that impact the emergence of regulatory T cells (Brown *et al* .,2022; Elbrashy *et*

al .,2024; Skawratananond *et al* .,2025). Some microbial by-products influence the production of cytokines and modulate the immune response, both at the level of the innate and adaptive immunity (Kumar *et al* ., 2023). The immune system alters the composition of the microbial population by the release of antimicrobial peptides and immunoglobulin A (IgA) (Liu *et al*.,2023). Such bidirectional communication is fundamental for defense and homeostasis of the host (Cani,2018;Codazzi *et al*.,2024). Changes in such communication can result in dysfunction of the barrier, systemic inflammation, and immunological diseases (Ullah *et al* .,2023; Chandra *et al* ., 2023).

2.1.3 The gut–immune–metabolic interface

The microbiome–immune system axis also affects metabolism. Certain microbial by-products, like SCFAs, bile acids, and derivatives of tryptophan, affect the metabolism of energy, glucose, and lipids (Franzago *et al* ., 2023; Sedlak *et al* ., 2023). These metabolites function as chemical messengers between gut microbes and the other tissues of the body (Juul *et al* ., 2021). Changes in diet can alter the gut microbiome. This may raise the risk of type 2 diabetes, obesity, and heart disease (Beulens *et al* ., 2022). This can lead to insulin resistance and changes in fat metabolism (Beulens *et al* ., 2022;Salzberg .,2022).

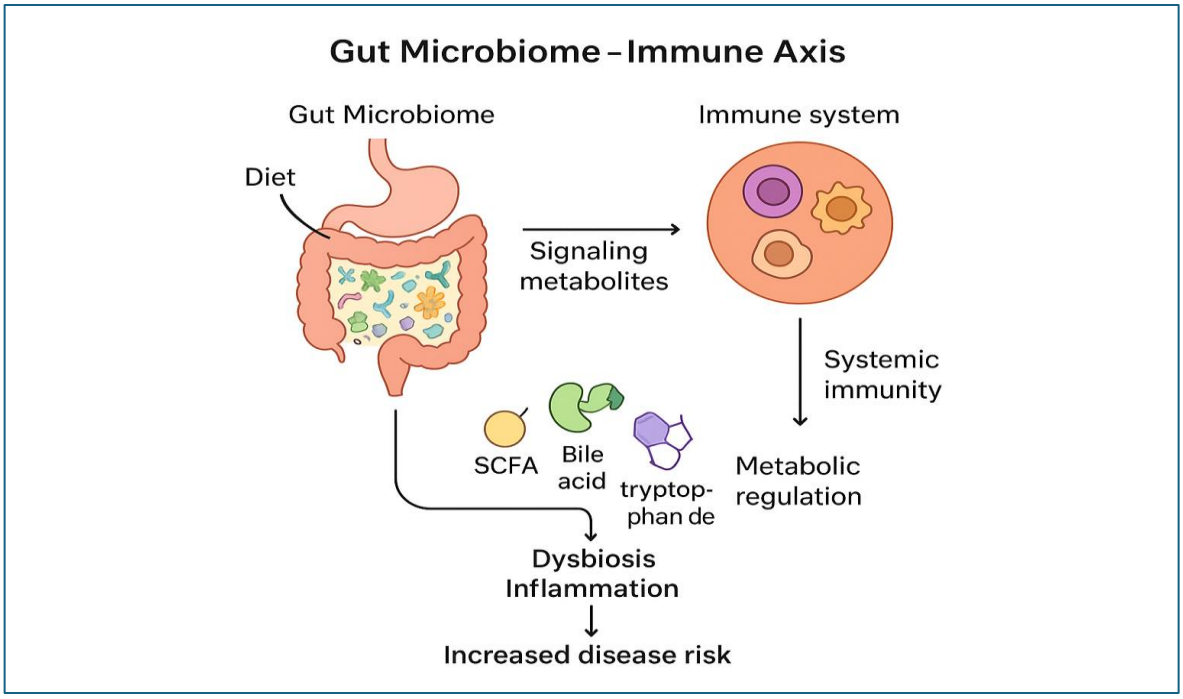


Figure 2-1: Overview of the Gut Microbiome–Immune Axis. "Source: Prepared by the researcher using AI-assisted scientific illustration based on published literature, ChatGPT."

2.2. Dietary Modulation of the Gut Microbiome in Mice

2.2.1. Macronutrient composition and microbiome shifts

The amount and type of protein, fat, and carbohydrates affect gut microbes. A high-fat diet can raise the Firmicutes/Bacteroidetes ratio. It can also lower the variety of microbes (Pandey *et al* .,2024;2023; Mayer et al .,2022). This is linked to more inflammation and problems with metabolism. Diets high in protein can increase bacteria that make harmful substances such as ammonia and hydrogen sulfide (Huaiquipán *et al* .,2023). Fiber-rich foods help good bacteria grow. They also produce short-chain fatty acids that keep the gut healthy (Holscher, H. D., 2017; Galica *et al* ., 2022). A balanced diet helps keep the microbiome stable (Wan *et al* ., 2021; Lee, D. B. , 2025). In

mice, changing macronutrient levels in their food can quickly alter the bacteria present (Cullen *et al*.,2020; Sasson *et al* ., 2021).

2.2.2. Micronutrients and phytochemicals

Vitamins and minerals also shape gut microbes in mice. A lack of vitamin D can change microbial balance and weaken the gut barrier (Martyniak *et al* ., 2021). Plant polyphenols act like prebiotics. They help good bacteria grow and stop harmful microbes (Wan *et al* ., 2021). Selenium and zinc can improve immunity and change microbial diversity (Szczuko *et al* ., 2021). Too little or too much of certain nutrients can harm the microbiome's stability (Gantenbein & Kanaka-Gantenbein, 2021). Diets rich in flavonoids can raise levels of Lactobacillus and Bifidobacterium in mice (Franzago *et al* ., 2023). Both macro- and micronutrients should be considered when studying how diet changes the gut microbiome.

2.2.3. Specialized or modified diets

Some diets change gut microbes in strong ways. Ketogenic diets increase bacteria that grow well in low-carb settings (Arifuzzaman *et al* .,2024; Kumar .,2024). Eating less or fasting for periods can increase microbial diversity. It can also promote bacteria linked to longer life and better metabolism (Franzago *et al* ., 2023; Schoonakker *et al* .,2024). Gluten-free and low-FODMAP diets may help reduce inflammation in sensitive animals. But they may also lower good bacteria if fiber intake is too low (Reddel *et al*., 2019; Gill *et al* .,2022). Elemental diets have pre-digested nutrients. They can lower the number of gut microbes and change immune responses (Zhang *et al* ., 2022). Such diets are useful for research on how food changes the microbiome and immunity.

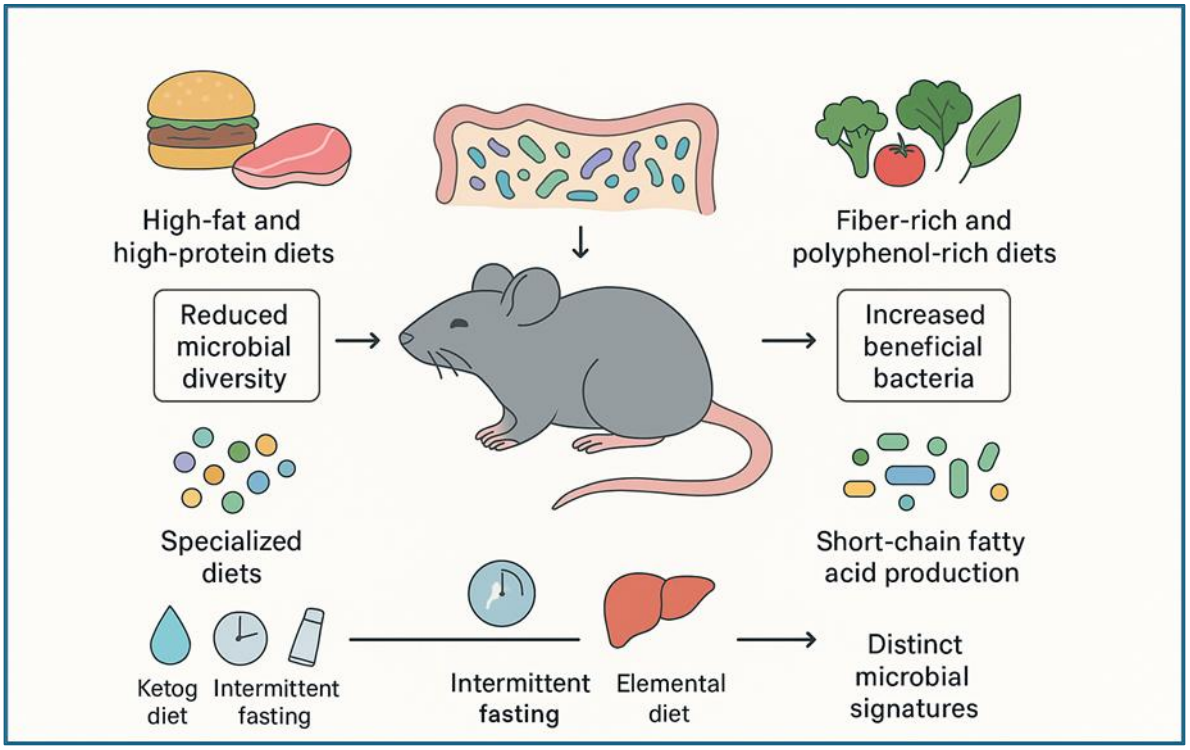


Figure 2-2: Dietary Modulation of the Gut Microbiome in Mice. "Source: Prepared by the researcher using AI-assisted scientific illustration based on published literature, ChatGPT."

This image shows how diet affects gut microbes in mice. High-fat and high-protein diets can cause imbalance. Fiber and polyphenols help good bacteria grow and make short-chain fatty acids. Special diets like ketogenic, fasting, and elemental diets lead to unique microbial patterns. These changes can affect both immunity and metabolism.

2.3. Mechanisms Linking Diet to Immune Modulation via the Microbiome

2.3.1. Barrier function and gut permeability

The gut barrier is where microbes and the immune system meet. It is made of cells, mucus, and tight junctions (Dmytriv *et al* .,2024). Diet changes can

weaken this barrier by altering microbes and their products (Kumar *et al* ., 2025; Shiratori *et al* .,2024). Low-fiber or high-fat diets may lower good bacteria and make the gut “leaky” (Chae *et al* .,2024). Short-chain fatty acids from fiber help repair the lining and keep junctions tight, Dietary patterns particularly those rich in fiber promote the growth of bacteria that produce short-chain fatty acids (SCFAs), notably butyrate. Butyrate serves as the primary energy source for colonocytes and directly strengthens barrier integrity by up regulating tight junction protein expression and stimulating mucin production (Kumar *et al* ., 2025; Shiratori *et al* ., 2024). Polyphenols can protect the barrier by reducing stress and inflammation (Han *et al* ., 2025; Li *et al* .,2025). When the barrier is weak, microbial parts can enter the blood. This can trigger the immune system and cause inflammation (Chae *et al* ., 2024; Shiratori *et al* ., 2024).

2.3.2. Microbial metabolites and immune signaling

Diet changes can alter which metabolites microbes make. These include SCFAs, bile acids, and tryptophan products (Franzago *et al* ., 2023). SCFAs help create regulatory T cells. They also block pathways that cause inflammation (Naomi *et al* ., 2019). Certain bile acids regulate macrophage and dendritic cell function, shaping immune tolerance () Simultaneously, microbial transformation of bile acids and tryptophan regulates the activity of macrophages and dendritic cells, ensuring the body maintains immune tolerance rather than overreacting to stimuli (Franzago *et al* ., 2023). The combination of these pathways shows the importance of a diet-modulated microbiome in systemic inflammation. Aryl hydrocarbon receptor (AhR) modulators and tryptophan metabolites activate mucosal immunity and epithelial defense (Seo & Kown, 2023; Huang, 2024). Metabolic endotoxemia

and chronic inflammation result from high-fat diets due to increased levels of lipopolysaccharides (Loh *et al* ., 2024; Jawamis *et al* ., 2025). In mice, the alteration of a metabolite profile, due to changes in diet composition, impacts cytokine production and the homeostasis of the immune system (Huaiquipán *et al* ., 2023).

2.3.3. Cytokine Profile as a Marker of Diet-Induced Immune Modification:

Cytokines are soluble immune mediators and show the host's inflammatory and regulatory immune responses. Cytokine profiling is of significance in diet–microbiome studies since microbial metabolites and components of bacterial structure can affect the activation of immune cells and the secretion of pro-inflammatory cytokines. Interleukin-6 (IL-6), considered a pro-inflammatory cytokine, is released during immune activation, barrier perturbation, and metabolic stress. On the other hand, interleukin-10 (IL-10) is an anti-inflammatory cytokine and is released during immune control to help limit inflammation and supports immune tolerance. Changes in diet can lead to indirect alterations of cytokine balance due to changes in the microbiome and/or the inhibition of some components that alter gut permeability and/or the interaction of underlying gut-associated lymphoid tissue, to list a few. Hence, the balance of IL-6 and IL-10 can show changes, in terms of the immune response, in the tissue as an effect of dietary changes and changes in the gut microbiome (Martyniak *et al*., 2021; Bermúdez-Humarán *et al* . 2022; Kumar *et al* . 2023; Marginean *et al*., 2023).

3.3 Shaping of systemic immunity by microbiota

The gut microbiome influences systemic immune responses beyond the local level. The gut, via gut-brain and gut-lung axes, can communicate with the lungs and the brain (Loh *et al* ., 2024). High-fiber diets helped in preparing the systemic immune defense by increasing the expression of anti-inflammatory cytokines and enhancing the activity of macrophages (Yusuf *et al* ., 2022). The systemic immunity of the body can be improved by fermented foods and probiotics through the modulation of the gut microbiota by increasing the number of beneficial bacteria and decreasing the levels of inflammatory cytokines (Stiemsma *et al* ., 2020). Systemic immune regulation can be adversely affected by diet-induced dysbiosis, increasing the likelihood of autoimmune or neurodegenerative disorders (Kujawa *et al* ., 2023; Chandra *et al* ., 2023). The Diversity of the gut microbiota can be positively affected by a healthy diet and can improve both the innate and adaptive immunity, thus, decreasing the incidence of diseases (Halper-Stromberg & Dalal, 2023).

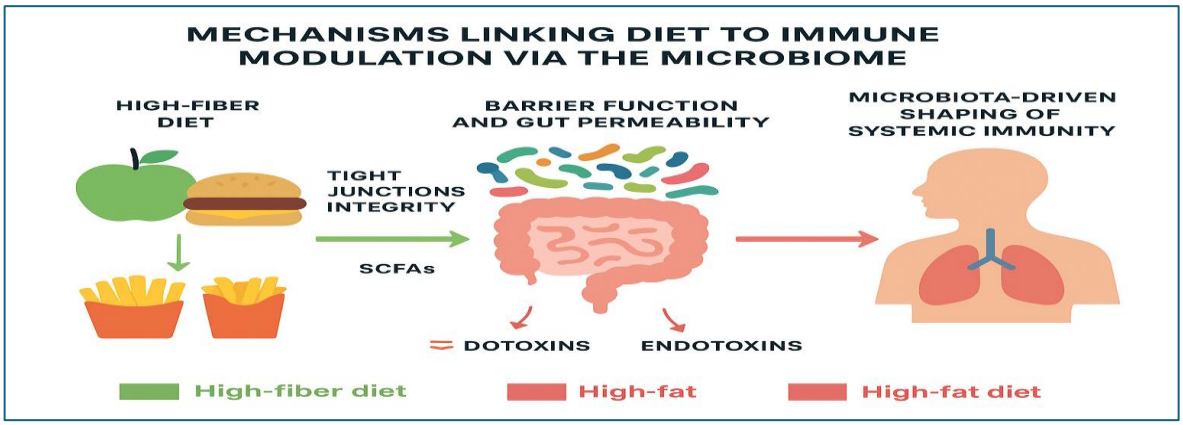


Figure 2-3: Ways Diet Impacts Microbiome and Immune Function. "Source: Prepared by the researcher using AI-assisted scientific illustration based on published literature, ChatGPT."

These mechanisms explain how different diets impact the gut microbiome and in turn affect barrier mechanisms and the production of metabolites. A diet rich in fiber enhances the integrity of tight junctions, increases SCFA production, and strengthens immune tolerance. In contrast, a diet high in fats, increases the permeability of the gut, the load of endotoxins, and inflammation. The impact of the microbiome is not only local and reaches distant organs through the gut-brain and gut-lung axes.

2.4. Experimental Models to Investigate Interactions Among Diet, Microbiome, and the Immune System

2.4.1. Mouse Strains and Genetic Backgrounds

Varied immune responses and microbiome compositions across different strains of mice. For example, the more common strains, C57BL/6 and BALB/c, have different degrees of susceptibility to diet-driven changes in microbiota (Huaiquipán *et al* ., 2023; Simoes *et al* ., 2025). The genetic backgrounds of mice have been shown to correlate with host microbial diversity, immune cell profiles, and the host's metabolic syndrome (Lin *et al* ., 2023; Cahana and Fuad, 2020). Germ-free mice are raised in a sterile environment and are ideal for testing the effects of microbiota, as they can be supplemented with specific bacterial populations (Mukherjee *et al* ., 2020; Bose *et al* ., 2024). Gnotobiotic mice have specific microorganisms and are especially useful for targeted diet and microbiome studies (Pilla & Suchodolski, 2020). Humanized mice, which are colonized with human gut microbiota, can be used to study the effects of various diets more closely to human physiology (Halper-Stromberg & Dalal, 2023). The choice

of strain and the source of microbiota are both critical for reproducibility and interpretation of diet and immune studies.

2.4.2 Protocols for diet intervention

To avoid confounding results, experimental diets for mice need to be uniform. Purified ingredient diets are utilized by researchers to control the composition of the diets in terms of macro and micronutrients (Loh et al ., 2024). Standard chow is commonly used as a reference for the assessment of microbes and immune response in high-fat, high-protein, and high-fiber diets (Galica *et al* ., 2022; Meyer *et al* .,2024). Specialized regimens like ketogenic diets or intermittent fasting are applied to study the metabolic and inflammatory impact (Kamel *et al* ., 2024). To avoid or minimize microbial load prior to the application of controlled microbiota, elemental diets (i.e., pre-digested) are used (Sasson *et al* ., 2021). The duration of feeding is considered because there are changes in the microbiome that occur in a few days and in the immune system, changes may occur in weeks (Ceballos *et al* ., 2021).

2.4.3 Analytical Approaches

The analysis of both the microbiome and immune system has seen great advancements with modern techniques. For instance, 16S rRNA gene sequencing has the potential to show the bacterial diversity present, as well as the relative abundances of different species (Wan *et al* ., 2021). As for shotgun metagenomics, it can be used to show the functional genes which have been modified by diet (Valles-Colomer *et al* ., 2023). As for the analysis of metabolites, it can be used to show the metabolites produced by the microbes in response to diet, such as short-chain fatty acids (SCFAs), bile

acids, and derivatives of tryptophan (Franzago *et al* ., 2023). Flow cytometry is an immune analysis technique that can profile subpopulations of immune cells, while cytokine assays are inflammatory mediator cytokine (Martyniak *et al* ., 2021). On the other hand, histology is a technique used to study the structure of gut tissues and can be used to visualize the damage to the gut barrier or the presence of immune cells in a tissue (Dunleavy *et al* ., 2023). A comprehensive understanding of the effects of diet on an experimental model can be obtained by integrating the microbiome, metabolome and immune datasets (Umu *et al* ., 2024).

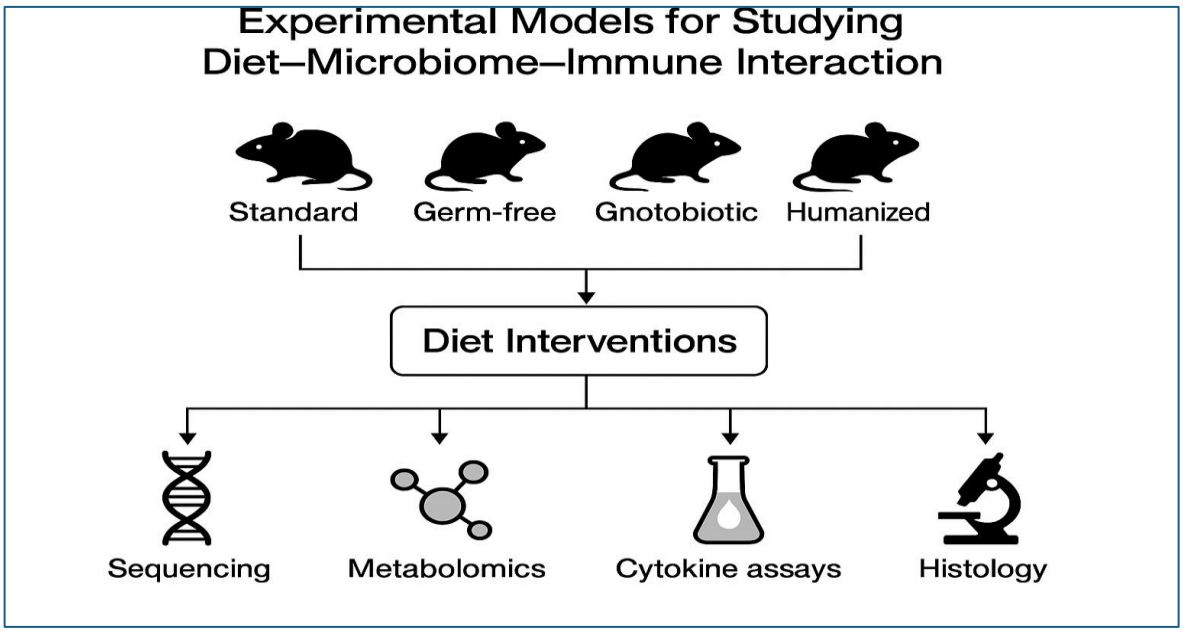


Figure 2-4: Models for Examining Interactions of Diet, Microbiome, and Immunity. "Source: Prepared by the researcher using AI-assisted scientific illustration based on published literature, ChatGPT."

This figure captures the central experimental techniques and different types of mouse models (including standard, germ-free, gnotobiotic, and humanized) combined with controlled dietary interventions to assess alterations in the microbiome and immune system. Sequencing,

metabolomics, cytokine assays, and histology are applied to examine the effects of diets on the structure of microbial communities and the immune system.

2.5 Effects of Diet on the Microbiome and the Immune System

2.5.1 Dietary Fat and Inflammation

High amounts of dietary fat contribute to the gut microbiome becoming increasingly inflammatory. In mouse studies, reduction in microbial diversity and increase in the relative abundance of pro-inflammatory microorganisms have been observed (Juul *et al* ., 2021). Dietary fat increases the abundance of lipopolysaccharide, leading to metabolic endotoxemia and inflammation throughout the body (Baars *et al* ., 2024). Dietary fat reduces the strength of the intestinal barrier, which allows the passage of bacterial antigens into the blood. Cytokines such as TNF-α and IL-6 become elevated after long-term exposure to high-fat diets (Ceballos *et al* ., 2021). The inflammation caused by such diets may lead to insulin resistance, immune dysfunction associated with obesity, and increased risk of pathogen infection (Beulens *et al* ., 2022;Selman et al.,2025).

2.5.2 Dietary Fiber and Prebiotic Intake

Dietary fibers are useful in the growth of beneficial intestinal bacteria such as Bifidobacterium and Lactobacillus (Galica *et al* ., 2022). The breakdown of fiber in the intestines produces short-chain fatty acids, including acetate, propionate, and butyrate.

The immune system is aided by these acids remaining calm and balanced (Naomi *et al* ., 2021). Prebiotic fibers such as inulin and fructo-

oligosaccharides reinforce the body's protective barriers of the gut while also decreasing certain inflammatory signals (Martyniak *et al* ., 2021). In experimental mice, additional fiber in the diet, as opposed to in a high-fat (harmful) diet, was able to improve a more beneficial condition of the gut microbiome (Franzago *et al* ., 2023). Prebiotic consumption is also believed to assist the immune system in warding off infections and in reducing the odds of developing autoimmune disorders (Kujawa *et al* ., 2023). Raised Protein Consumption and Dysbiosis An excess of the consumption of protein alters bacterial activity and functions within the gut. Specifically, it is suggested a larger proportion of bacterial activity may revolve around the degradation of proteins as opposed to carbohydrates which is accompanied by the production of by-products, such as ammonia and phenols, which are responsible for the degeneration of the gut lining (Loh *et al* ., 2024). In addition, high levels of protein that is of animal origin may also lead to the proliferation of pathogenic gut bacteria and the reduction of beneficial gut microbes (Huaiquipán *et al* ., 2023). Dysbiosis is a condition of gut microbial imbalance which is known to lower immune health as well as increase the incidence of inflammatory conditions of the gut (Halper-Stromberg & Dalal, 2023). Some researchers propose that the consumption of proteins originating from plants is not as likely to correlate with these negative outcomes. This is possibly due to the presence of dietary fibers and the coincident consumption of protective phytochemicals (polyphenols) that are typical in vegetables (Wan *et al* ., 2021;Van Buiten *et al*.,2024).

2.5.3 High-Protein Diets and Gut Imbalance

Eating too much protein changes how gut bacteria work. It can make them break down more proteins instead of carbs. This process creates by-products

like ammonia and phenols that can hurt the gut lining (Vernia *et al* ., 2021). High amounts of animal protein may increase harmful bacteria and reduce the good ones (Huaiquipán *et al* ., 2023). This imbalance, called dysbiosis, can weaken the immune system and raise the risk of gut inflammation (Halper-Stromberg & Dalal, 2023). Some studies suggest plant-based proteins are less likely to cause these problems. This may be because they also have fiber and healthy plant chemicals like polyphenols (Wan *et al* ., 2021).

2.5.4 Micronutrient-modified diets

Specific micronutrients, such as vitamins A and D, as well as the mineral zinc, impact microbiome–immune interactions. Vitamins, such as vitamin D, are modulating factors in the production of antimicrobial peptides and the differentiation of various immune cells (Akimbekov *et al* ., 2020; Martyniak *et al* ., 2021). Zinc defciency may lead to the breakdown of barrier integrity and the development of microbial shifts that are pro-inflammatory (Szczuko *et al* ., 2021). Diets that are rich in polyphenols and other antioxidants may inhibit the growth of detrimental bacterial populations, while promoting the growth of beneficial microbiota (Wan *et al* ., 2021; Wang *et al* ., 2023; Bhatnagar *et al* ., 2024). In experiments with mice Selenium supplementation improved immune response and count to pathogens (Pilla & Suchodolski, 2020; Doaei *et al* ., 2023). Trusting the balance of micronutrients is essential to sustaining a healthy gut–immune axis.

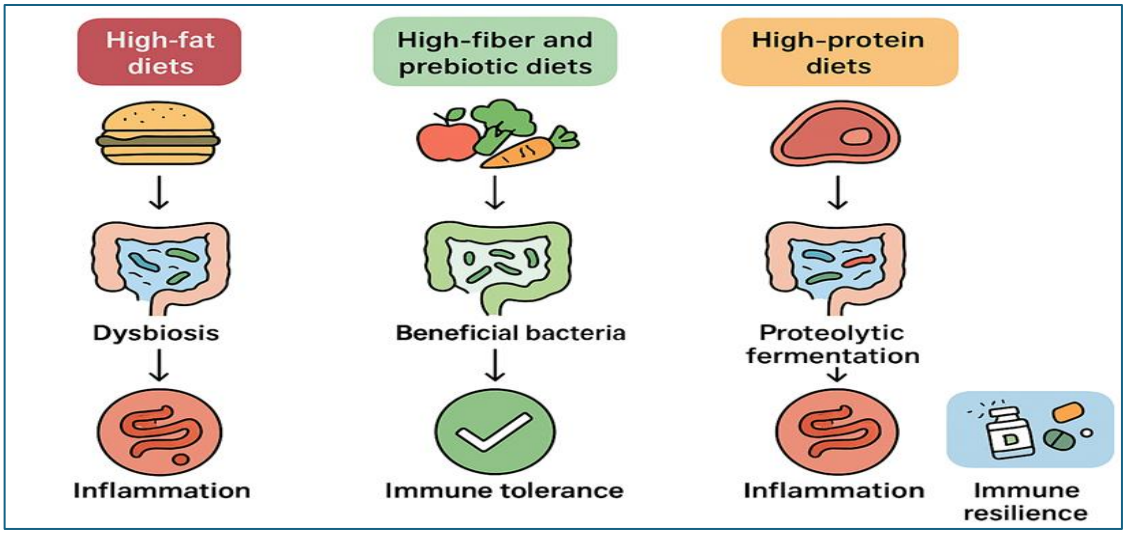


Figure 2-5: Changes in Microbiome-Immune Interactions From Select Dietary Changes. "Source: Prepared by the researcher using AI-assisted scientific illustration based on published literature, ChatGPT."

Dietary impacts on the gut microbiome and immune system modulation are compared. A high-fat diet causes dysbiosis and inflammation and disrupts gut barriers. In contrast, high-fiber and prebiotic diets increase beneficial bacteria and short-chain fatty acids (SCFAs), and help immune systems 'calm' (tolerance). High-protein diets, particularly from animals, can cause inflammation and 'bad' bacteria' (proteolytic) fermentation. A diet with adequate micronutrients improves gut barrier function and immune system resilience (reduces oxidative stress). The distilled knowledge from mouse models informs the diet-microbiome-immune system interactions and the roles in human disease. Changes in the microbiome have been associated with the development of type 2 diabetes, inflammatory bowel disease, and neurodegenerative diseases (Singh *et al*.,2017; Dawson *et al* ., 2025; Baars *et al* ., 2024; Kujawa *et al* ., 2023). Increased consumption of fiber and plant-based foods is associated with improved diversity of the microbiome and

reduced inflammation (Gantenbein & Kanaka-Gantenbein, 2021; Galica *et al* ., 2022). Dietary changes are often implemented in clinical practice, alongside medication, to rebalance the microbiome and improve immune response (Martyniak *et al* ., 2021; Du *et al* ., 2024). For instance, prebiotics and probiotics have been explored to enhance gut barrier and decrease inflammation in patients with IBD (Halper-Stromberg & Dalal, 2023). However, there are important considerations to address in the translation of findings from mice to humans due to the differences in the composition and function of the microbiota (Mukherjee *et al* ., 2020; Montenegro *et al* ., 2023).

Table 2-1 : Composition of goose egg yolk, chicken egg yolk, and the standard diet (Karsten *et al*., 2010; Abeyrathne *et al*., 2022; Kucharska-Gaca *et al*., 2023; U.S. Department of Agriculture, Agricultural Research Service, 2026)

Component	Goose egg yolk: pasture-raised	Chicken egg yolk: caged egg	Standard laboratory diet / AIN-93M control
Moisture	45–49%	52–56%	≤7–10%
Dry matter	51–55%	44–48%	90–93%
Crude protein	16–18%	14.8–15.9%	12.6–14.0%
Total lipid / crude fat	31–35%	24.9–26.5%	4.0–4.1%
Carbohydrate / nitrogen-free extract	0.5–2.0%	3.0–3.6%	67.5–69.4%
Ash / minerals	1.5–2.2%	1.5–2.0%	2.2–3.9%

Component	Goose egg yolk: pasture-raised	Chicken egg yolk: caged egg	Standard laboratory diet / AIN-93M control
Crude fiber	0%	0%	4.8–5.0%
Cholesterol	1.0–1.4%	1.0–1.1%	Not applicable / trace
Phospholipids	~30–33% of yolk lipid	~30–33% of yolk lipid	Not applicable
Triacylglycerols	~62–65% of yolk lipid	~62–65% of yolk lipid	Not applicable
Cholesterol fraction of yolk lipid	~4–5% of yolk lipid	~4–5% of yolk lipid	Not applicable
Saturated fatty acids	High; commonly 30–36% of total fatty acids	Commonly 30–35% of total fatty acids	Low; depends on soybean oil
Monounsaturated fatty acids	Relatively high; may exceed chicken yolk	Moderate to high	Low to moderate
Polyunsaturated fatty acids	Present; pasture feeding may increase omega-3 fraction	Present; usually more dependent on commercial feed	Mainly from soybean oil
Omega-3 fatty acids	Expected to be relatively higher due to pasture exposure	Usually lower in caged eggs unless feed is enriched	Low to moderate
Omega-6:omega-3 ratio	Expected to be lower than caged eggs	Usually higher than pasture-derived eggs	Depends on oil source
Vitamin A	Present; may be higher with pasture access	Present	Added in vitamin mix

Component	Goose egg yolk: pasture-raised	Chicken egg yolk: caged egg	Standard laboratory diet / AIN-93M control
Vitamin E	Present; may be higher with pasture access	Present	Added in vitamin mix
Choline	High	High	Added as choline bitartrate
Calcium	Present	Present	~0.5%
Phosphorus	Present	Present	~0.23% or higher depending on formula

2.6: Translational and Clinical Relevance

2.6.1 Implications for human health

Findings from mouse models help explain how diet–microbiome–immune interactions influence disease in humans. Evidence links microbiome changes to conditions such as type 2 diabetes, inflammatory bowel disease, and neurodegenerative disorders (Dawson *et al* .,2025; Baars *et al* ., 2024; Kujawa *et al* ., 2023). Diets high in fiber and plant-based foods are associated with better microbial diversity and lower inflammation (Gantenbein & Kanaka-Gantenbein, 2021; Galica *et al* ., 2022). In clinical settings, dietary interventions are used to complement medical treatments, aiming to restore microbial balance and enhance immune function (Martyniak *et al* ., 2021; Du *et al* .,2024). For example, prebiotics and probiotics have been tested to improve gut barrier integrity and reduce inflammatory symptoms in IBD

patients (Halper-Stromberg & Dalal, 2023). However, translation from mice to humans requires caution because of differences in microbiota composition and metabolism (Mukherjee *et al* ., 2020; Montenegro *et al* .,2023).

2.6.2 Potential therapeutic applications

Changing the diet can be a useful way to improve the gut microbiome and create personalized nutrition plans. Specific eating patterns mayhelp lower the risk of disease, boost how well treatments work, and support a healthy immune system (Franzago *et al* ., 2023; Gates *et al* ., 2022). For people with metabolic problems, adjusting the balance of proteins, fats, and carbohydrates can make the body respond better to insulin. It can also help reduce ongoing inflammation (Juul *et al* ., 2021). In conditions like Alzheimer's disease, using probiotics and foods high in polyphenols may lower inflammation and support brain function (Naomi *et al* ., 2021;Van Buiten *et al*.,2024; Espirito Santo *et al*.,2021). For heart health, diets such as the Mediterranean diet and the DASH diet can improve how blood vessels work. These benefits may be partly due to positive changes in the gut microbiome (Gantenbein & Kanaka-Gantenbein, 2021). Future treatments might mix dietary changes with drugs that target the microbiome or with fecal microbiota transplants. More large studies are needed to find the best diet plans for different groups of patients (Beulens *et al* ., 2022).

2.6.3 Possible clinical uses

Diet change can potentially improve gut microbiome as well as establish personalized nutrition strategies. Certain dietary patterns can reduce disease risk, enhance treatment efficacy, and promote healthy immune function (Franzago *et al* ., 2023). For individuals with metabolic disorders,

optimizing the ratio of protein, fat, and carbohydrate can enhance insulin sensitivity. In the study conducted by Loh *et al* . (2024), ongoing inflammation is said to be diminished by the use of certain probiotics and foods high in polyphenols, in addition to the aforementioned benefits linked to Alzheimer's disease. Inflammation and brain function can be supported by the combination of the two (Graf *et al*., 2015;Naomi *et al* , 2021; Espirito Santo *et al*.,2021;Van Buiten *et al*.,2024). In regards to brain function and inflammation, the Mediterranean and DASH diets are said to improve how the blood vessels function (Gantenbein & Kanaka-Gantenbein, 2021). Such benefits could be a result of positive alterations within the gut microbiome. Potential combination treatments are aimed at dietary changes in conjunction with microbiome-targeting drugs and/or fecal microbiota transplantation. In regard to the best dietary plan for a target group of patients, further studies are warranted (Beulens *et al* , 2022).

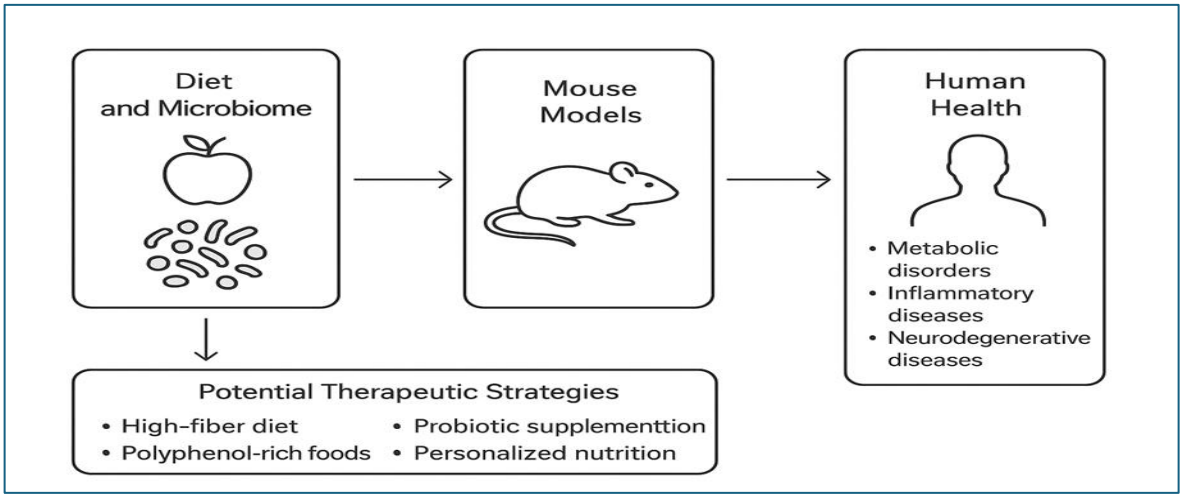


Figure 2-6: The Translational and Clinical Relevance of the Diet-Microbiome-Immune System Axis. "Source: Prepared by the researcher using AI-assisted scientific illustration based on published literature, ChatGPT."

Application of findings in mouse research to humans. Pathways are shown from the dietary modulation of the microbiome to the clinic of metabolic, inflammatory, and neurodegenerative disorders. Examples of such potentially therapeutic strategies are high-fiber diets, probiotics, polyphenol-rich foods, and individualized dietary plans. The figure also depicts the gap between preclinical and clinical research.

2. 7: Knowledge Gaps and Future Research Directions.

2.7.1 Current mouse models limitations.

Mouse models are vital in studying the interactions between diets, the microbiome, and the immune system, although they do have limitations. Mouse gut microbiota differ from those of humans (Mukherjee *et al* ., 2020; Arnesen *et al* .,2025). The dietary responses to interventions may diverge from those in humans (Pilla & Suchodolski, 2020; Bertorello *et al* .,2024). Environmental factors (such as housing, temperature and exposure to pathogens or stress) can alter a microbiome and immune system response (Theophilus *et al* .,2023). Laboratory diets lack the variability of human diets and can result in a loss of translational value (Huaiquipán *et al* ., 2023). Furthermore, the use of young, healthy male mice in most experiments limits the understanding of these factors (Ceballos *et al* ., 2021). Optimizing these parameters may enhance the utility of preclinical models.

2.7.2 Merging multi-omics methodologies

The multiple layers involved in the diet-microbiome-immune axis integration include genomics, metabolomics, proteomics, and transcriptomics (Valles-Colomer *et al* ., 2023; Chen *et al* ., 2024), yet most analyses focus on one layer, leading to the loss of important interactions across microbial, metabolite, and immune systems (Franzago *et al* ., 2023). The integration of these layers allows the diet, microbial, and immune networks (Naomi *et al* ., 2021) to be fully realized. The advanced models and machine learning aimed at immune outcomes via microbes may allow us to identify specific dietary (Du *et al* ., 2024) components. Progress can be made in the effort of standardization of the analytical processes and in the sharing of data.

2.7.3 Long-term impacts and intergenerational effects

However, the long-term effects are less understood (Sasson *et al* ., 2021; Magalhães *et al* .,2024). Even after returning to a normalized diet, the changes in the diet-induced microbiome may continue to persist for months to years (Halper-Stromberg & Dalal, 2023; Huang *et al* .,2025). Additionally, the maternal diet in pregnancy can also alter the microbiome and immune system of the offspring, which can have long-term effects on health (Beulens *et al* ., 2022). These effects, possibly through epigenetic changes, are hypothesized to span multiple generations, as suggested by some animal studies (Franzago *et al* ., 2023; Ren *et al* .,2024). The effect of various diets on immune function and microbiome composition throughout the life span, and over multiple generations, is an area that deserves further attention for research.

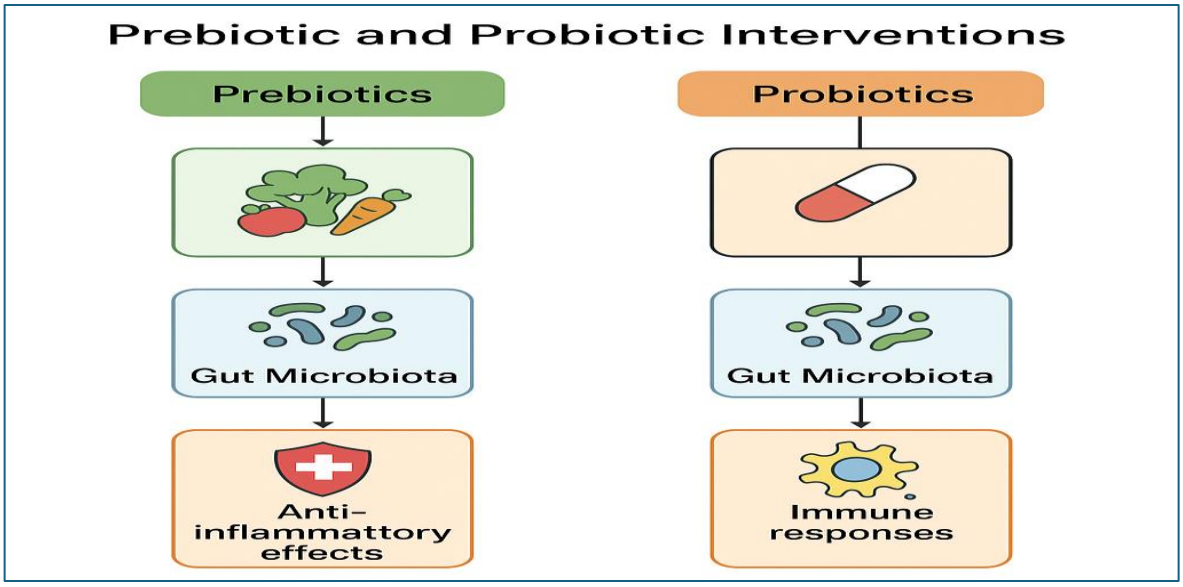


Figure 2-7: The Prebiotic and Probiotic Intervention . "Source: Prepared by the researcher using AI-assisted scientific illustration based on published literature, ChatGPT."

2.8. Metagenomics in Diet–Microbiome–Immune Research

2.8.1 Principles of metagenomics

Metagenomics involves analyzing genetic material from surroundings, such as from microbial life forms from bacteria to fungi in a mouse's gut (Valles-Colomer *et al* ., 2023;Du *et al* .,2024). This approach identifies both culturable and non-culturable microbes (Huaiquipán *et al* ., 2023). Mukherjee *et al* ., (2020) describe how this approach helps scientists study the effect of different diets on microbial populations. Extensive gene sequencing (high throughput sequencing) is used by researchers to describe the potential functions of the microbes in given sample (Wan *et al* . 2021). This is important in clarifying how diet-dependent alterations of gut microbiome modulate immunity and metabolism (Balakrishnan *et al* ., 2024). Subsequently, computerized algorithms are employed to associate microbial

genes with products such as short-chain fatty acids and bile acids, which can modulate immunity (Naomi *et al* ., 2021; Melo *et al* .,2023).

2.8.2 The role of diet in microbiome research

Mouse studies have corroborated the effect of diet on the functioning of gut microbes. For instance, a high fiber diet has been shown to increase the presence of microbial genes involved in the degradation of complex polysaccharides and the production of short-chain fatty acids (Galica *et al* ., 2022).

On the other hand, a high fat diet can increase the number of genes related to the alteration of bile acids and the production of biliary toxins (Loh *et al* ., 2024). Such alterations can cause an imbalance in the immune system, affect the integrity of the gut barrier, and trigger inflammation (Martyniak *et al* ., 2021). In models of inflammatory bowel disease, metagenomics has revealed a decrease in beneficial microbial genes during inflammatory flare ups. These functions may return following prebiotic consumption (Halper-Stromberg & Dalal, 2023). In addition, the latest clinical studies highlight that compliance with a Mediterranean-style diet boosts the anti-inflammatory and butyrate-producing, gut lining protective, microbial profile (Ghosh *et al* ., 2024). Shotgun sequencing also captures small but notable changes in rare microbes (Pilla & Suchodolski, 2020). This links microbial gene clusters to immune system and disease risk.

2.8.3 Challenges and limitations

Metagenomics creates very large datasets. These need strong computer tools and skilled people to study (Valles-Colomer *et al* ., 2023). Current genome databases are still incomplete, so some new microbes and their

functions are hard to identify (Mukherjee *et al* ., 2020). The results can also change depending on sequencing depth, how samples are handled, and how libraries are prepared (Huaiquipán *et al* ., 2023). Metagenomics shows what genes are present, but not whether they are active. To know that researchers need other tools such as meta-transcriptomics (Naomi *et al* ., 2021; Almeida *et al* .,2021). High costs can make it hard to do big diet studies in mice. Shared methods and combining different "omics" approaches can improve results and make them more useful for human health research (Wan *et al* ., 2021).

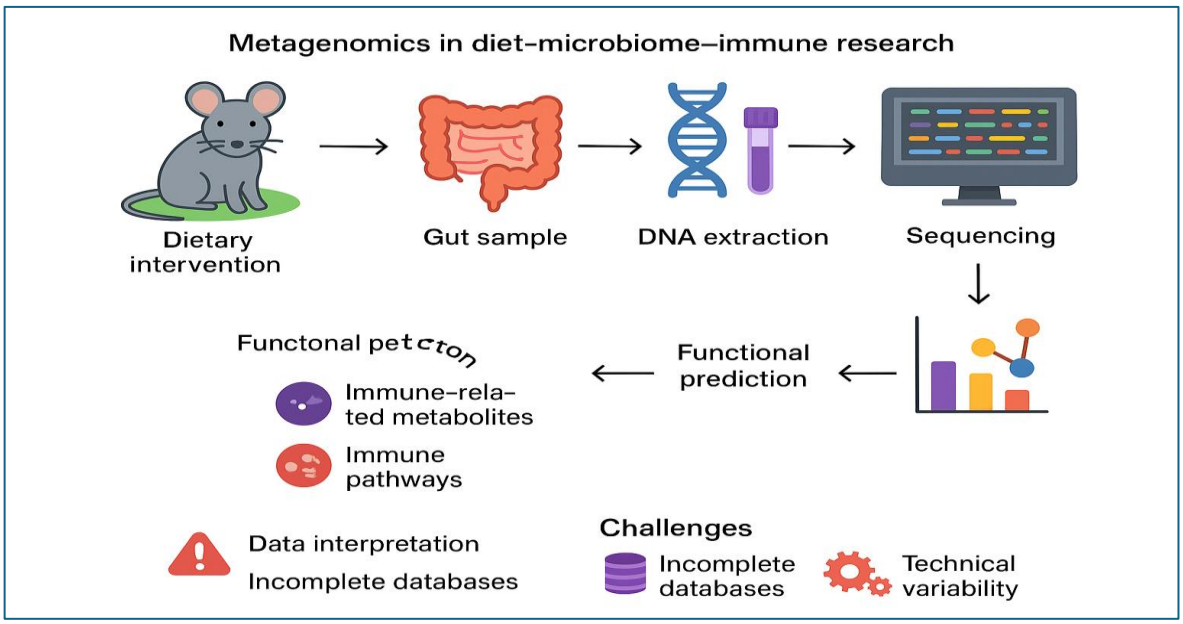


Figure 2-8: **Metagenomics in Diet–Microbiome–Immune Research.** "Source: Prepared by the researcher using AI-assisted scientific illustration based on published literature, ChatGPT."

2.9 Next-Generation Sequencing (NGS) Tools for Microbiome–Immune Analysis

2.9.1 16S rRNA gene sequencing

One of the primary methods utilized for the study of bacterial communities is gene sequencing of the 16S rRNA gene. The methodology focuses on the specific range of target sequences of the gene that confer both the ability to conserve and vary in order to classify the specific organisms in the sample (Wan *et al* ., 2021). The gene in question has a length of approximately 1500 base pairs and is comprised of nine hypervariable regions (V1 to V9). These hypervariable regions are separated by conserved regions and thus allow for the hierarchical classification of the constituent organisms of the gene sample (Bharti & Grimm, 2021). The methodology has been employed in dietary, gut microbiome, and immune response studies, where researchers are interested in the impact of a given dietary alteration on the microbial population (Galica *et al* ., 2022;Salim *et al*.,2023). While the technique is limited in contrast to whole genome sequencing, both in terms of cost and the amount of computing power needed (Pilla & Suchodolski, 2020), it still has a degree of utility even in the case of very closely related bacterial species (Huaiquipán *et al* ., 2023; Yang *et al* ., 2024). Mouse dietary studies where the primary interest is in assessing the more general changes in the microbiome over a specified period, the methodology is still useful (Halper-Stromberg & Dalal, 2023).

2.9.2 Shotgun Metagenomic Sequencing

Shotgun metagenomics reads all the DNA in a sample. This gives a full picture of the microbes and the genes they have (Valles-Colomer *et al* ., 2023). It can reveal how diet changes microbial genes that affect metabolism,

the immune system, and gut health (Franzago *et al* ., 2023). High-fiber diets often raise genes for making short-chain fatty acids. High-fat diets can increase genes linked to toxin production (Loh *et al* ., 2024). Shotgun sequencing is more detailed than 16S sequencing but costs more and needs more data analysis (Mukherjee *et al* ., 2020; Baev,2025;). It is most helpful for finding exact links between changes in the microbiome and certain immune or metabolic pathways (Naomi *et al* ., 2021; Jangi and Hecht, 2024).

2.9.3 Meta-transcriptomics and Immune Gene Expression Profiling

Meta-transcriptomics is a research area that studies the RNA from microbes to determine which genes are active for which genes for each microbe under varying conditions (Naomi *et al* ., 2021). When researchers of diets and the immune system need to analyze the interaction of gut microbiome and host immune system in a more integrative manner, they use a combination of microbial RNA and host RNA-seq data (Baars *et al* ., 2024). This approach is capable of detecting gene expression changes caused by diets in both microbes and immune cells. Working with RNA is a greater challenge because of its rapid degradation relative to DNA and is therefore more difficult to obtain and handle (Huaiquipán *et al* ., 2023).

2.9.4 Future Directions in Sequencing Technologies

The evolving sequencing technologies are also extending the frontiers of microbiome-immune system research. Genome assembly and structural variation detection that short-read methods miss are possible with long-read sequencing techniques like PacBio and Oxford Nanopore (Valles-Colomer *et al* ., 2023). Although capturing contiguous genomes from human gut

metagenomes is achieved by the newly developed Illumina Complete Long Read assay (Maghini *et al* ., 2024), earlier technology (before 2024) lacked this ability and was therefore less effective. Improved strain-level resolution from this technology is crucial for precise attribution of immune modulation to specific bacteria (Pilla & Suchodolski, 2020). The most promising avenue for NGS technology within the diet, microbiome, and immune system research is data-sets that integrate multi-omics (meta-genomics, meta-transcriptomics, meta-metabolomics, and immunomics) (Wernimont *et al* ., 2020; Franzago *et al* ., 2023). Gaining research insights about the immune response induced by diet based on sequencing data will, however, require advances in bioinformatics and machine learning (Bertorello *et al* ., 2024).

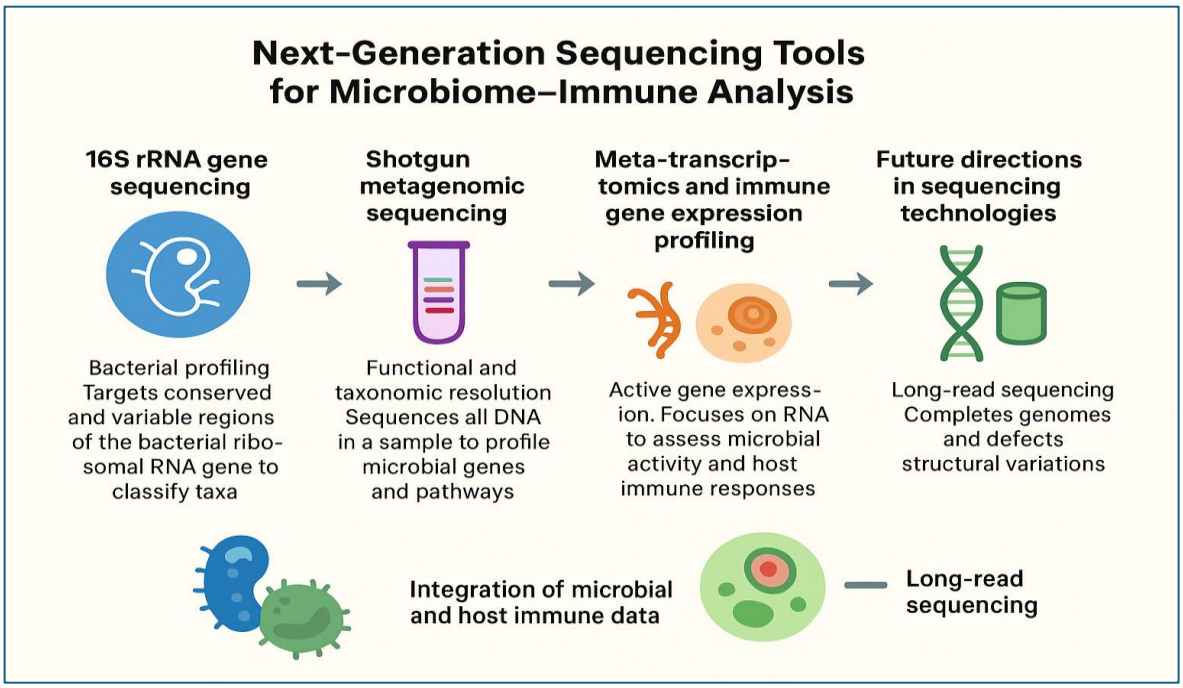


Figure 2-9: Next-Generation Sequencing Tools for Microbiome–Immune Analysis. “Source: Prepared by the researcher using AI-assisted scientific illustration based on published literature, ChatGPT.”

2.9.5. Microbiome Diversity Indices

2.9.5.1.Alpha Diversity

2.9.5.1.1 Chao1 Richness Index

Estimating the number of bacterial taxa within a microbial community can often be achieved by employing the Chao1 richness index. Primarily due to its emphasis on rare taxa, particularly those identified only a few times within sequencing datasets, the index is well suited to observe microbial richness changes resulting from a diet. In diet–microbiome studies, increased Chao1 indexes suggest that the di et al lowed for the development of a more extensive bacterial community, whereas diminished indexes may indicate the contraction of microbial richness or the restriction of particular microbial taxa due to the diet. Considering the rapid shift of gut microbiota associated with diet, the Chao1 index becomes a significant metric for the expansion of gut bacteria and the branched community of gut bacteria in mice as influenced by dietary constituents (David *et al* ., 2014; Wu *et al* ., 2011; Wan *et al* ., 2021).

2.9.5.1.2. Shannon Diversity Index

The Shannon Diversity Index is a popular a-diversity measurement used in gut microbiome analysis. This helps to understand both the different types of species present and their relative abundance. The higher the Shannon value, the marked the abundance and diversity of the microbes in the gut. Conversely, the lower the Shannon value, the less microbial diversity present and instead, was evidence of some microbial dominance, which helps to understand the balance and harmony of the gut. Other than the lower

Shannon value, implications of lower microbial diversity associated with the gut microbiome illuminate gut stability, metabolic, and greater immune activity and regulatory balance. Shannon diversity is impacted by a number of factors in the diet gut, including gut diversity, gut microbial dysbiosis, and gut microbial activity, including gut microbial activity. These factors would likely modulate the microbial growth and substrate that forms in the gut which is governed by gut dysbiosis and fermentation, which results in altered immune signaling (Scott *et al* ., 2013; Gomes *et al* ., 2022; Huaiquipán *et al* ., 2023).

2.9.5.1.3. Simpson Diversity Index

The Simpson Diversity Index evaluates the diversity of microbes by focusing on their dominance in the microbial community. It is the likelihood that, as two organisms are drawn at random from the same sample, that the different taxa they belong to are different from each other. Simpson diversity favors a more even and more diverse microbial community. Simpson diversity works especially well in the realm of nutrition, as certain diets may have the potential to increase the number of certain types of bacteria within the community while decreasing the balance of the community (Scott *et al* ., 2013; Gomes et al ., 2022; Huaiquipán *et al* ., 2023).

2.9.5.1.4.Faith’s Phylogenetic Diversity

Faith’s phylogenetic diversity is measured by analyzing the evolutionary order of diversity between microbiota. Unlike other indices that focus on how many the members are in a community (microbial richness), this particular index is based on how many evolutionary branches the community represents. This allows it to account for whether a diet has the potential to broaden the

evolutionary scope of taxa. Increased diversity in Faith's phylogenetic scores may also signal a wider functional potential in the microbiome, as added metabolic and immunological supports bestowed by phylogenetically different species remain. This is critical in diet-microbiome-immune interrelations, as the microbiota have capacity to sit at the junction of multiple imbalances. The imbalance may aid in the production of different short-chain fatty acids, other bilious acids, and variations in the regulation of the immune factor (Rowland *et al* ., 2018; Franzago *et al* ., 2023; Patloka *et al* ., 2024).

2.9.5.2 Beta Diversity

Whereas alpha diversity is used to measure diversity in a single microbiota sample, beta diversity scores measure comparability between multiple (2 and more) samples. Beta diversity, in particular, is used to signify how different two (or more) microbiota samples are from each other. In gastrointestinal studies, beta diversity will measure whether unique lineages are present in the diet of interest. Beta diversity measures whether a particular diet (in this case, chicken vs goose egg diet vs the control diet) has the potential to alter the overall structure of the microbiota, and is therefore essential for studies involving the goose egg yolk and chicken egg yolk diet (David *et al* ., 2014; Wu *et al* ., 2011; Wan *et al* ., 2021).

2.10. Genus level

2.10.1 Staphylococcus

Staphylococcus is capable of transient expansion through diet-induced intestinal perturbation. Diets rich in lipids alter metabolism of bile-acids, which can lead to anaerobic microbial consumption of oxygen. During this tenuous period, some taxa may increase in abundance, with some of them

being opportunistic. When microbial competition goes back to normal levels and the immune system is working properly, the system tends to be self-correcting. Therefore, the Staphylococcus growth can be seen as the gut system normalizing and regulating the microbial balance, and helps to detect the lipid-induced gut imbalance and the system self-correcting later (Carmody *et al* ., 2024; Du *et al* ., 2025; Di Vincenzo *et al* ., 2024; Wang *et al* ., 2023).

2.10.2 Lactobacillus

Lactobacillus is almost entirely recognized for substantiating gut barrier, and for induction of lactic acid and immune function. It occurs that for the short-term phase of dietary modification, its increase in abundance is possible. Some of the members of this genus can respond quickly and can utilize the sudden change in nutrient availability. However, the lipid-rich bile may be the primary culprit of the negative feedback for the system, as it can increase the bile pressure, which can limit the substrate availability. Thus, the Lactobacillus are showing their protective and adaptable nature in the microbial balance for gut system (Carmody *et al* ., 2024; Du *et al* ., 2025; Howard *et al* ., 2022; Qi & Wang, 2023; Fan *et al* ., 2023).

2.10.3 Ligilactobacillus

Ligilactobacillus is classified among the lactic acid bacteria demonstrating an association with rapid gut microbial adaptation due to dietary changes. An early adaptation to lipid-rich feeding could lead to an increase in the biomass of these bacteria. The production of lactate and cross-feeding interactions are key elements in maintaining equilibrium in the gut epithelium. A later decrease in these populations corresponds to a stable gut community or the

depletion of available fermentable substrates. This behavior is consistent with the initial microbial adjustments of the gut community, which are followed by an ecological equilibrium (Carmody *et al* ., 2024; Du *et al* ., 2025; Santangelo *et al* ., 2023; Pietrzak *et al* ., 2022).

2.10.4 Limosilactobacillus

Limosilactobacillus is a genus of lactic acid bacteria involved in gut homeostasis, production of metabolites, and regulation of the immune response. Some of these bacteria produce lactic acid and other bioactive metabolites that affect the mucosal pH, barrier function, and inflammation. This genus could increase its abundance at the early stages of a lipid-rich diet, but decrease later, due to a competitive or unfavorable gut environment, which may indicate a more advanced metabolic adjustment to yolk lipids (Du *et al* ., 2025; Fan *et al* ., 2023; Bagheri *et al* ., 2022; Barber *et al* ., 2023; Santangelo *et al* ., 2023).

2.10.5 Streptococcus

Streptococcus has species that can strongly adapt to some changes in the mucosa, the availability of carbohydrates, and oxidative changes. Given the lipid composition of the gut, the abundance of some Streptococcus species may decrease when some lipid metabolites from the gut reduce the adhesiveness of some Gram-positive species to the gut mucosa. Egg-yolk lipids, more so the phospholipids, can help to alter the surface mucosa and redirect the colonization of some opportunistic bacteria. Therefore, some variation in the Streptococcus group can be interpreted as some shift in the competition between the mucosal epithelium and the gut microbiota

(Xiao *et al* ., 2024; Carmody *et al* ., 2024; Du *et al* ., 2025; Barber *et al* ., 2023; Bagheri *et al* ., 2022).

2.10.6 Lachnoclostridium

Lachnoclostridium is an anaerobic genus of Clostridia that participate in fermentation and lead to the production of short-chain fatty acids. Clostridia-related metabolism may be supported and even increased by some dietary early exposure. The presence of fermentable substrates and some changes in the luminal environment may lead to some Clostridia-related metabolism. However, some early increases in fermentable substrates and some changes in the luminal environment may be diminished by lipid-rich diets. Regarding microbial competition, some prolonged lipid-rich diets may reduce the abundance of some Clostridia. Due to the contributions of this genus to some butyrylated pathways, the change in the abundance of this genus may be indicative of some moderated shift in the mucosa supply and the subsequent change in the gut (EL-kholy *et al* ., 2025; Xiao *et al* ., 2020; Carmody *et al* ., 2024; Howard *et al* ., 2022; Fan *et al* ., 2023).

2.10.7 Bacteroides

Bacteroides dominates the gastrointestinal microbiota and is recognized for its role in the fermentation of saccharides, bile-acid tolerance, and involvement in lipid metabolism. Due to its bile tolerance and capacity to ferment complex substrates, many species within the genus respondappears to positively respond to fat-rich diets. An increase in the genus may assist in metabolic adaptation during the initial phase, and the genus's decrease at a later point may suggest substrate depletion or a balance in the microbial community. Thus, it is plausible to designate Bacteroides the highlight for

microbial reconstruction of gut metabolism due to diet (Carmody *et al* . 2024; Du *et al* . 2025; Hemmati *et al* . 2023; Gweon ., 2023; Zafar *et al* . 2021).

2.10.8. Phocaeicola

Phocaeicola (Bacteroidota) is another genus of the gut microbiota that includes members that are capable of complex carbohydrate metabolism, including the utilization of mucins. Like Bacteroides, the genus may exhibit a non-linear trip due to its adaptation to bile salt and later resurrect (como(tipo what gives preference to microbial competition post colonization. The flexibility of Phocaeicola renders this genus important in diet-induced gut remodeling. Changes in abundance of the genus Phocaeicola would be indicative of an ecological resilience and revitalization of metabolic equilibrium (Carmody *et al* . 2024; Du *et al* . 2025; Bagheri *et al* . 2022 ; Zafar *et al* . 2021).

2.10.9. Duncaniella

Duncaniella is a genus of anaerobic, carbohydrate fermenting bacteria associated with murine gut microbiomes. Rapid response to diet changes is hypothesized when redox changes in the gut and substrate supply changes. Increased abundance in early phases may indicate active coprophagous fermentation with a subsequent decline indicating resource competition. Therefore, Duncaniella is a good indicator of rare gut microbiota that is dynamic to dietary induced ecological pressures (Carmody *et al* ., 2024; Du *et al* ., 2025; Fan *et al* ., 2023).

2.10.10. Muribaculum

Muribaculum is known to be associated with murine gut carbohydrate fermenters with the capability to produce short chain fatty acids. Various levels of dietary lipids and proteins and changes to yolk-derived nutrients have an effect on the gut. Early abundance changes may allow increased gut metabolite shifting and gut-system communication and may eventually reflect the gut's balance. Therefore, Muribaculum is relevant for interpreting diet-related changes in murine intestinal microbiota (Haneishi *et al* ., 2024; Carmody *et al* ., 2024; Di Vincenzo *et al* ., 2024; Howard *et al* ., 2022; Qi & Wang, 2023).

2.10.11. Paramuribaculum

Paramuribaculum also belongs to murine-associated Bacteroidota and may respond to increased substrate availability and changes in bile-induced pressure. Early abundance changes may indicate primary exposure to dietary lipids; however, later decline may indicate changes in the gut mfocbiota and reduced loss of the gut. Given that gut fermentation is associated to this genus, it may explain the balance of gut microbes and the yolk, dietary-induced changes (Carmody *et al* ., 2024; Di Vincenzo *et al* ., 2024; Barber *et al* ., 2023).

2.10.12. Sangeribacter

Sangeribacter is a gut bacterial genus that may function as an adaptive fermenter with regards to dietary energy availability. Early rise during lipid-augmented feeding may represent temporary access to novel substrates or modified intestinal redox alterations. Later decline may occur as substrate flux normalizes and the balance in the microbial ecosystem is restored. Thus,

this genus may be a short-term responder in the diet-modified gut community (Du et al ., 2025).

2.10.13. Alloprevotella

Alloprevotella is a genus associated with mucin and carbohydrates, and may be strain-sensitive to fermentable substrates. Under lipid and carbohydrate-rich conditions, the community structure may be altered, along with the equilibrium of mucin, fiber, and immune-mediated mucosal alterations. A temporary rise may suggest access to new substrates. Later decline may depict the closing of fermentative support. This genus is therefore useful to assess diet-focused microfaunal shifts in relation to SCFA pathways (Carmody et al ., 2024; Howard *et al* ., 2022; Qi & Wang, 2023; Barber *et al* ., 2023; Bagheri *et al* ., 2022).

2.10.14. Alistipes

Alistipes is an anaerobic genus often linked with protein and amino-acid metabolism, exposure to bile acids, and inflammatory tone. It may elevate during high-fat or lipid dietary patterns because such diets alter bile flow and intestinal oxidative stress. Fewer changes in gut microbes may suggest stabilization of microbiota after high-fat or lipid diets or the balance of fiber-modulated taxa. Thus, Alistipes may be a shortcut of lipid metabolism pathways, tryptophan, and gut immune pathways (Du et al ., 2025; Carmody *et al* ., 2024; Fan *et al* ., 2023; Barber *et al* ., 2023).

2.10.15. Escherichia

Escherichia is a genus (of the family, Enterobacteriaceae) of anaerobes that thrive in the presence of and can survive in the absence of oxygen. This

genus exhibits a surge in intestinal (and) oxidative stress and lining (and) breach of barrier integrity. At later times, the immune system may once again take control and promote (and) restore anaerobic competition. In this regard, the abundance of genus Escherichia is used as an indicator of momentary stress to gut lining (and) the later recovery of the gut lining (Lee, 2024; Di Vincenzo 2024;Du, 2025; Fan, 2023).

2.10.16. Desulfovibrio

Desulfovibrio is a genus of anaerobes that is characterized by its ability to reduce sulfate that is present in the environment. Desulfovibrio have an increase in abundance due to a diet rich in fats and poor in fibers that may affect the flow of dietary fiber in (and) promote stress at the gut lining (and) favor the growth of sulfur-cycling bacteria. Extreme levels of this abundance have been correlated with barrier breach (and) may indicate growth (and) restoration of anaerobic balance at the mucosal lining. Accordingly, Desulfovibrio is very relevant in the assessment of diet-induced stress and recovery (Carmody *et al* ., 2024; Du *et al* ., 2025; Di Vincenzo *et al* ., 2024; Bagheri *et al* ., 2022)

2.10.17. Lawsonia

Lawsonia is a genus of intracellular bacteria that may be affected by renewal at the lining of epithelia, stress at the gastointestinal lining, (and) immune system regulation. A surge in this genus after administering a lipid-rich diet may indicate changes to epithelial dynamics and/or the host-microbiome relationship during intestinal adaptation. A decline occurring later may represent immune system surges, competition, (and) restoration of mucosal homeostasis. At this stage, the Lawsonia genus may be used as a compass to

indicate a diet that alters the epithelia and immune homeostasis (Carmody *et al* ., 2024; Di Vincenzo *et al* ., 2024; Qi & Wang, 2023).

2.11. Species-level

2.11.1. *Adlercreutzia Caecimuris*

is a gut microbe that is responsible for the metabolism of the diet's substances and critical host-microbe relationships. Because dietary substances interact with gut microbes and modify the handicap to the gut substrate, abundance of this species can vary during lipid-dominant feeding due to the availability of intestinal space to substrate.. This species is significant for the study of alterations in metabolism due to the diet in the murine microbiome (Meiners *et al* ., 2025; Patloka *et al* ., 2024; Anto & Blesso, 2022; Islam *et al* ., 2024).

2.11.2.*Staphylococcus aureus*

gut microbe species are typically elevated with increased intestinal permeability, elevated mucus oxidative stress, and greater gut barrier permeability. It is possible for fat/protein-dominant diets to result in an initial mucosal dysbiosis triggered from high *S. aureus*, followed by an interval of dysbiosis and a subsequent decline in S aureus. Anaerobic microbes and anti-inflammatory substances dominate to restore equilibrium thereafter. Staphylococcus aureus may be the predominant and severe response of dysbiosis due to lipid and high protein associated gut dysbiosis (Dang *et al* ., 2023; Abbasi & Khodadadi, 2025; Islam *et al* ., 2024; Hoffman *et al* ., 2023; Gopal *et al* ., 2024; Yadav *et al* ., 2023).

2.11.3.*Staphylococcus capitis*

Staphylococcus capitis is a facultative species that may flourish under nutrient-rich or oxidative intestinal conditions. Its temporary availability during exposure to lipids may correlate with bile-acid, enhancing the secretion of mucosal, and stress of diminished regulation of tight junctions. A subsequent decrease may indicate a restoration of immune control and competitive suppression by anaerobic commensals. Therefore, S. capitis can be described as a short-term opportunistic responder, the early diet-induced inflammation of the gut (Anto & Blesso, 2022; Engin, 2024; Dang *et al* ., 2023; Ciernikova *et al* ., 2023; Patloka *et al* ., 2024; Islam *et al* ., 2024).

2.11.4. *Lactobacillus gallinarum*

Lactobacillus gallinarum is a lactic acid bacterial species that are noted for their probiotic activity and their intestinal homeostasis and regulation metabolism. Their early proliferation under lipid enhanced-diets may be to aid in bile handling, signaling and inhibited inflammation, related to, short-chain fatty acids. This species may, therefore, represent a temporary beneficial responder to yolk-derived dietary substrates (Marchese et al ., 2023; Kaviyarasan *et al* ., 2022; Engin, 2024; Islam *et al* ., 2024; Joyet *et al* ., 2023).

2.11.5. *Lactobacillus gasseri*

Probiotic *Lactobacillus gasseri* forms a connection between metabolic homeostasis, bile-salt hydrolase activity, lipid metabolism, and inflammation in the gut as indicated by research carried out by You, Patloka, Marchese, Hoffman, Abbasi and Khodadadi, and Gopal. Lactobacillus gasseri's mode of subsisting may also signify lipid-rich diet adaptation and gut barrier

functioning. However, chronic lipid pressure will ultimately switch the digestive capability of Lactobacillus gasseri in favor of other anaerobes at the competitive level.

2.11.6.*Ligilactobacillus apodemi*

Ligilactobacillus apodemi 'is level of subsistence may alter in response to nutritional lipids especially in the early phases of nutritional-intervention. In the early phase, a temporary increase in *Ligilactobacillus apodemi* may suggest the supporting role of egg-yolk nurturing to select lactic acid bacteria. Following a temporary increase, a reduction in *Ligilactobacillus apodemi* may be a reflection of a stabilized gut community due to competitive and limited substrates.

2.11.7. *Limosilactobacillus reuteri*

Limosilactobacillus reuteri is a probiotic-associated species whose subsistence may indicate the connectivity of lipids, functional shifts, and the response of gut microbial members to the dietary used. Yang *et al* . (2025) argue that if the dietary exposure of egg-yolk is prolonged, microbial shifts may redistribute gut ecosystems as it ultimately stabilizes. In spite of that, the subsistence of L. reuteri during early dietary exposure supports the notion of specific egg-yolk components providing a habitat for beneficial Lactobacilli.

2.11.8. *Kineothrix alysoides*

Kineothrix alysoides may contribute to the production of short-chain fatty acids through gut fermentation. Depending on gut metabolism and the availability of certain dietary substrates, the incidence of Kineothrix alysoides may change. In the context of dietary egg yolks, fluctuations of this species

may indicate variable fermentation of egg yolk lipids and/or proteins. K. alysoides may provide an insight into the dietary alteration of anaerobic energy metabolism within the gut (Wang *et al* ., 2024).

2.11.9.*Clostridium scindens*

Clostridium scindens has the potential to change bile metabolism and gut–liver signaling, primarily as a buffalo bile metabolism via the alteration of secondary bile acids. Since egg yolk diets are lipid-rich, they may change the pool of bile acids and also influence the population of the species. Changes in *C. scindens* may indicate diet-driven changes in bile metabolism and host metabolic signaling. This species is especially relevant when interpreting the relationship between dietary lipids, microbiota, and gut–liver metabolic systems (Xiao *et al* ., 2025).

2.11.10. *Schaedlerella arabinosiphila*

Schaedlerella arabinosiphila is associated with gut microbiota of the Lachnospiraceae family. This family is known for its ability to promote polysaccharide fermentation and subsequently produce cross-fed nutrients. Changes in diet can also influence this species via changes in the fermentable substrates and modifications in microbial community structures. In egg yolk diets, changes in the availability of lipids and proteins may have a secondary effect of altering carbohydrate fermentation, thus this species provides an indication towards fermentative gut adaptation (Du *et al* ., 2024).

2.11.11. *Bacteroides acidifaciens*

Bacteroides acidifaciens participates in balance of energy assimilation, stability of the gut microbiome, and the digestion of carbohydrates. Typically,

it may vary in proportion, depending on the diet and the availability of the substrate for metabolism. Expected alteration in this group of species may demonstrate change in the metabolism of fermentation and the metabolic interaction of the gut microbes with the host in the alphabets of yolk feeding. Thus, B. acidifaciens is useful for the comprehension of the impact of egg-yolk associated diets on gut functions of the microbes and the involved energy pathways (Jung *et al* ., 2025).

2.11.12. *Phocaeicola vulgatus*

Phocaeicola vulgatus is a species of Bacteroidota and is implicated in the metabolism of lipids, mucin, and complex carbohydrates. It may increase during early exposure to lipid-rich diets as it is able to respond to changes in mucosal substrates of bile and mucin. Later declines may occur as bile-acid signaling, immune pressure, and microbial competition restructure the community. Thus, P. vulgatus may represent an early metabolic response, followed by immune-stabilized microbial adjustment (Islam *et al* ., 2024; Anto & Blesso, 2022; Dang *et al* ., 2023; Abbasi & Khodadadi, 2025; Singar *et al* ., 2024; Meiners *et al* ., 2025).

2.11.13. *Duncaniella muris*

Duncaniella muris is a gut of murine species, associated with fermentation and the metabolism of short chain fecal matter. Its increase may be associated with abrupt dietary changes and high lipid content metabolic substrates. Decrease may subsequently be due to the depletion of these resources and the return of the gut microbial homeostasis to equilibrium. Thus, D. muris serves as a species that shows microbial resilience in high

lipid-related gut adaptation (Ciernikova *et al* ., 2023; Gopal *et al* ., 2024; Engin, 2024; Islam *et al* ., 2024).

Chapter three

Materials and Methods

3. MATERIALS AND METHODS

3.1 Materials

All experiments were done using aseptic laboratory conditions. The reagents used for the nucleic acid analysis were of molecular grade and the reagents used for the histological processing of tissues were of histological grade. All the supplies used were sterile and nuclease-free. All the necessary calibrations and maintenance of the instruments were done before the experiment to ensure any measurements are precise and reproducible.

3.1.1 Equipment

All laboratory instruments used during the experiment were selected based on their accuracy, sensitivity, and compatibility with the molecular microbiology and histopathology workflows.

Table 3.1: Equipment Utilized in the Experimental Procedures

No.	Equipment	Manufacturer	Model	Country
1	Class II Biosafety Cabinet	Thermo Scientific	1300 Series A2	USA
2	Microcentrifuge (refrigerated)	Eppendorf	5424 R	Germany
3	High-speed centrifuge	Thermo Scientific	Sorvall ST16R	USA
4	NanoDrop Spectrophotometer	Thermo Scientific	NanoDrop 2000	USA
5	UV-Vis Spectrophotometer	PerkinElmer	VICTOR Nivo™	USA
6	Bead-Beating Homogenizer	Qiagen	TissueLyser II	Germany

No.	Equipment	Manufacturer	Model	Country
7	Gel Electrophoresis System	Bio-Rad	Mini-Sub Cell GT	USA
8	Electrophoresis Power Supply	Bio-Rad	PowerPac Basic	USA
9	Gel Documentation System	Bio-Rad	GelDoc XR+	USA
10	Thermal Cycler	Bio-Rad	T100	USA
11	Real-Time PCR System	Bio-Rad	CFX96	USA
12	Illumina Sequencing Platform	Illumina	MiSeq i100	USA
13	−80°C Ultra-Low Freezer	Thermo Scientific	TSX Series	USA
14	Automated Microtome	Leica	RM2235	Germany
15	Tissue Processor	Leica	TP1020	Germany
16	Paraffin Embedding Station	Leica	EG1150H	Germany
17	Light Microscope	Olympus	CX43	Japan
18	Water Bath	Memmert	WNB14	Germany
19	Analytical Balance	Sartorius	Entris II	Germany
20	pH Meter	Mettler Toledo	SevenCompact	Switzerland

All instruments were calibrated according to manufacturer recommendations before use. Temperature-sensitive equipment was monitored daily.

3.1.2 Chemicals and Reagents

All reagents were certified molecular biology or histological grade. Storage conditions followed manufacturer instructions.

Table 3.2: Chemicals and Reagents

No.	Reagent	Manufacturer	Catalog No.	Country
1	DNeasy PowerSoil Pro Kit	Qiagen	47014	Germany
2	AMPure XP Beads	Beckman Coulter	A63881	USA
3	Herculase II Fusion DNA Polymerase	Agilent	600675	USA
4	Nextera XT Index Kit	Illumina	FC-131-1096	USA
5	Agarose	Invitrogen	16500500	USA
6	Safe DNA Gel Stain	Thermo Scientific	S33102	USA
7	Tris-Acetate-EDTA Buffer (10X)	Sigma-Aldrich	TAE10X	Germany
8	10% Neutral Buffered Formalin	Merck	1.04003	Germany
9	Hematoxylin	Sigma-Aldrich	H9627	Germany
10	Eosin Y	Sigma-Aldrich	HT110116	Germany
11	Alcian Blue (pH 2.5)	Sigma-Aldrich	A5268	Germany
12	Xylene	Merck	1.08642	Germany
13	Paraffin Wax	Leica	39601095	Germany
14	Ethanol (Absolute & Graded)	Merck	Various	Germany
15	Phosphate Buffered Saline	Gibco	10010023	USA

3.1.3 Experimental Design

A randomized, controlled, dietary intervention model was chosen.

- Animals underwent a 14-day acclimatization period.
- Mice were randomly assigned to one of the three experimental groups (n = 6 per group).
- Dietary supplements were provided for 30 consecutive days
- Two sampling time points for intervention effects were selected (Day 14 and Day 30)
- Longitudinal collection of fecal samples during the intervention period was done
- At Day 30, tissues were collected for analysis

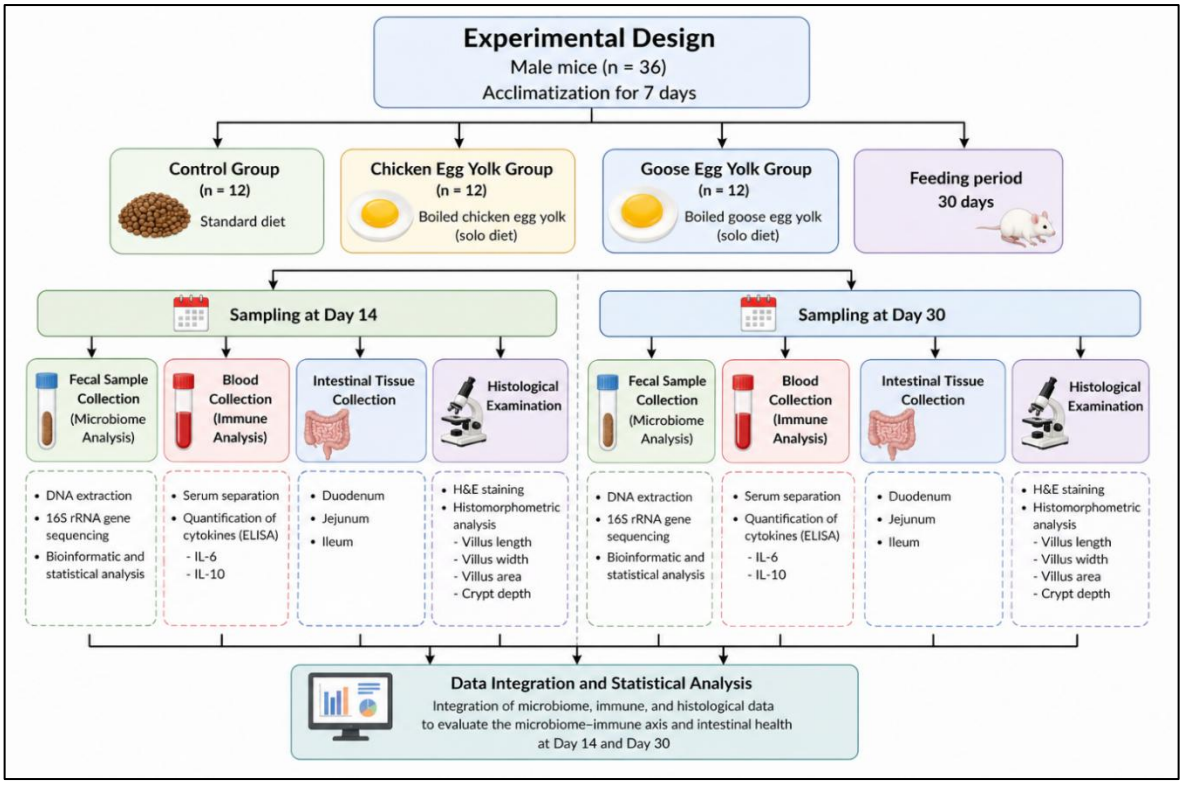


Figure 3-1: Experimental Desigen Source: Prepared by the researcher using AI-assisted scientific illustration based on published literature, ChatGPT."

Experimental Flow Diagram

Acclimatization (14 days)

↓

Random allocation

(Control / Goose Yolk / Chicken Yolk)

↓

Dietary intervention (30 days)

↓

Fecal sampling and serum collection (immune analysis) (Day 14, Day 30)

↓

DNA extraction and quantification

↓

Agarose gel integrity verification

↓

16S rRNA library preparation

↓

Illumina MiSeq sequencing

↓

Bioinformatics processing

↓

Histomorphometric (H&E, Alcian Blue) (at 30 day)

↓

Statistical analysis

3.1.4 Animals

- Male C57BL/6 mice, 8–12 weeks old were obtained from an approved breeding facility for the study.
- At the beginning of the study, their body weights ranged from 20 to 25 g.
- Animals were kept in ventilated cages with specific pathogen-free (SPF) conditions.
- The temperature was kept at 22 ± 2°C.
- Relative humidity was kept at 55 ± 5%.
- A 12-hour light and dark cycle was used.
- Standard chow and water were available ad libitum.
- An ethical approval was granted with approval number 626 (February 5, 2026).

3.2. Method :

3-2-1 Method of Egg Yolk Preparation and Administration

Fresh pasture-raised-goose eggs and cage-chicken eggs were obtained from healthy local flocks under hygienic conditions. The yolks were carefully separated from the egg whites, boiled thoroughly, and then provided individually as the sole dietary component to their respective experimental groups during the feeding period. The control group was maintained on a standard laboratory diet (18–20% crude protein, 4–5% crude fat, 4–6% crude fiber, 5–7% ash, vitamins, minerals, and balanced carbohydrate sources).

3-2-2 Fecal samples collection:

Fecal samples were taken from control group, chicken egg yolk diet group, and goose egg yolk diet group, at two different time points (day 14 and day 30). Aseptically, samples of feces were collected, and swabs were placed in sterile microcentrifuge tubes to avoid contamination, before instantaneous freezing in liquid nitrogen. Samples were kept at -80 degrees until molecular analysis was conducted. This ensured that the microbial DNA collected in the fecal samples, remained intact and was not degraded before the sequencing analysis could be accomplished.

3.2.3 Molecular Analysis

Molecular characterization of gut microbiota was implemented to assess how diet composition (goose egg yolk and chicken egg yolk) affected the gut microbial community structure of the experimental mice. The total genomic DNA obtained from fecal samples, which underwent molecular profiling of bacterial communities, was used for 16S rRNA gene amplicon sequencing. The DNA samples served as templates for the amplification of specific bacterial ribosomal gene segments, which are used for the identification of microbes as they are highly conserved. The next step was to create and analyze sequencing libraries using next-generation sequencing. The sequence data were used in a bioinformatics pipeline and were analyzed for the microbial compositions, their relative abundances, and the diversity indices of the microbes for the different dietary groups and their respective sampling time points.

3.2.3.1 DNA Extraction

DNA samples were isolated from fecal samples using the QIAamp PowerFecal Pro DNA Kit (Cat. No. 51804, Qiagen, Hilden, Germany). 200 mg fecal sample were transferred into the bead-beating tube supplied. Lysis and ceramic beads buffer were added to the tube, and then were subjected to homogenizing using a FastPrep-24™ bead homogenizer from MP Biomedicals located in Santa Ana, CA. After homogenization, a majority of the hard-to-lyse Gram-positive bacteria cells, and the fecal matrix, DNA samples, were lysed.

The QIAamp PowerFecal Pro DNA Kit has a silica spin column system that was used to purify the DNA samples. Subsequently, a number of washing purifications were performed to remove any remaining fecal contaminants, such as proteins, polysaccharides, bile salts, and polymerase chain reaction inhibitors, that could disrupt and hamper DNA from being amplified and provide unrecoverable pieces of evidence for the DNA sample. The purified DNA was then stored in the elution buffer, along with additional protective measures, to further guard the sample. The DNA was stored until further analysis, which was carried out on a 2000 NanoDrop spectrophotometer from the Thermo Fisher Scientific company located in Waltham, MA. The samples were also subjected to 1% agarose gel electrophoresis using ethidium bromide to assess quality and cleanliness of the DNA samples that were extracted.

3-2-3-2 Molecular Target

The target of the first gut microbiome profiling study was the 16S ribosomal RNA gene of bacteria. Microbial sequencing targeting the V3 and V4 variable regions provides good bacterial taxonomic resolution with a high

degree of usefulness in microbiome amplicon sequencing. With respect to the bacterial endogenous control amplification of the 16S ribosomal RNA gene, the forward and reverse primers were Bakt_341F and 805R, respectively, with the former representing a 5' to 3' sequence of CCTACGGGNGGCWGCAG, and the latter of GACTACHVGGGTATCTAATCC.

A total of 25 µL was used to do polymerase chain reactions with the 16S ribosomal RNA gene. Reaction mixtures contained advanced polymerase and the bast, 14 µL of buffer, 4 µL of template, and 1.5 µL each of forward and reverse primers. The reaction mixture was placed in a Veriti™ 96-Well Thermal Cycler (Applied Biosystems, Foster City, CA, USA) to run the polymerase chain reaction. The polymerase chain reaction was evaluated with gel electrophoresis. Gel electrophoresis was used to determine whether the target V3 and V4 regions were successfully amplified. The virome polymerase chain reaction products were placed into the sequencing library.

3.2.3.3 Sequencing and Library Construction

The first sequencing step was to purify with AMPure XPPCR beads (Cat. No. A63881, Beckman Coulter, Brea, CA, USA) to remove sequencing primers and primer addition products. Sequencing cavities are highly affected by the amount of DNA per bead and the presence of primer addition products. To eliminate products, magnetically purifying a bead and culling to the desired amount of amplicon was performed.

Sequencing libraries were assembled with the Nextera XT DNA Library Preparation Kit (Cat. No. FC-131-1096, Illumina Inc., San Diego, CA, USA). Library concentration was quantified using a Qubit™ 4 Fluorometer and Qubit dsDNA High Sensitivity Assay Kit (Cat. No. Q32851, Thermo Fisher

Scientific, USA). The Illumina MiSeq (Illumina Inc., San Diego, CA, USA) sequenced the libraries and followed by quality checking and adjustment of saturation. Sequencing resulted in paired-end reads that were used to develop the gut microbiome.

3.2.3.4 Bioinformatics Analysis

The bioinformatics processing of the gut microbiome sequencing data from the Illumina MiSeq system was performed and analyzed. The following reads were removed as part of the quality control of the sequencing data: low quality, chimeric, adapter, ambiguous, and short reads. Advanced sequencing data quality control was performed with the DADA2 algorithm, which corrected sequencing errors and generated denoised sequencing data along with high-resolution amplicon sequence variants. Compared to operational taxonomic unit (OTU) clustering, microbial profiling of DADA2 was more precise.

A Bayesian classification method was applied against the NCBI 16S rRNA reference database to classify the generated amplicon sequence variants. For levels of classification where it was achievable, the relative bacterial abundance was assessed at the taxonomic rank of phylum, class, order, family, genus, and species. These results were used to examine the variations of microbial community among groups without treatment, chicken egg yolk, and goose egg yolk across the periods of interest. The generated taxonomic compositions were further employed for subsequent diversity analysis, which includes but is not limited to alpha and beta diversity, and comparisons of group level microbial composition.

3.2.4. Cytokine Targets

We assessed the following cytokines:

- Interleukin-6 (IL-6) – marker of pro-inflammation
- Interleukin-10 (IL-10) – anti-inflammatory cytokine

Mouse-specific ELISA kits were sourced from R&D systems (USA). All reagents were brought to room temperature prior to utilization.

3.2.4.1 Preparation of ELISA Plates

- Used the pre-coated 96-well microplates (capture antibody was immobilized).
- The plates were taken out of the sealed packaging and checked for any defects.
- As per instructions provided, standards were reconstituted with calibrator diluent.
- To establish a standard curve, a series of two-fold dilutions of the standard cytokine were prepared (e.g. from 1000 pg/mL down to 15.6 pg/mL).
- Wells that were meant to be blank and contained only assay buffer were designated as such.

3.2.4.2 Loading the Samples

- Serum samples were thawed on ice and mixed gently by inversion.
- Samples were diluted (1:2 or 1:5) based on expected concentration.

- 100 µL of standards, blanks, and diluted samples were pipetted into their respective wells in doublets.
- The plates were film sealed.
- As per the kit protocol, incubation was carried out for 2 hours at 37°C or for 4°C overnight.

3.2.4.3 Washing Step

- The liquid contents were removed via aspiration in their entirety.
- Wells were washed with 300 µL of wash buffer.
- An automated plate washer was used to repeat this washing five times.
- The plate was tapped against an absorbent to remove any residual buffer.

3.2.4.4 Incubation With Detection Antibodies

- 100 µL of biotinylated detection antibody was placed in each well.
- This was followed by incubation at 37°C for 1 hour.
- As described above, washing was carried out five times.

3.2.4.5 Incubation With Streptavidin-HRP

- 100 µL of streptavidin-HRP solution was introduced into each well.
- This was followed by incubation at 37°C for 30 minutes in the dark.
- Five washes were performed to remove any unbound conjugate.

3.2.4.6 Substrate Development

- 100 µL of TMB substrate solution was introduced.
- The plates were covered and the substrate was incubated (in the absence of light at room temperature) for 10-15 minutes.
- The development of color (indicated by blue color) was assessed by eye.
- 50 µL of stop solution (2N sulfuric acid) was added to each well.
- When reaction stopped, blue color changed to yellow.

3.2.4.7 Measurement of Optical Density

- Absorbance at 450 nm was captured using a microplate reader (PerkinElmer VICTOR Nivo™).
- For background correction, the reference wavelength was set to 570 nm.
- Absorbance values from duplicate wells were averaged.

3.2.4.8 Standard Curve and Concentration Calculating

- Standard curve was plotted using a four-parameter logistic regression model.
- For the standard curve, cytokine concentrations were obtained by interpolation.
- To the final serum concentrations, dilution factors were corrected.
- Results were given in pg/mL.

3.2.4.9 Quality Control

- Duplicate coefficient of variation (CV%) was calculated.
- Repeat measurement was initiated at CV values >10%.
- Standard curve R^2 values were accepted at ≥0.98.
- Control negative wells were verified to have little to no absorbance.

3.2.4.10 Data Interpretation

- Increased inflammation was interpreted from the elevated values of IL-6 .
- Increased anti-inflammatory signaling was interpreted from the elevated values of IL-10.
- To assess the immunological balance, cytokine ratios (IL-10/IL-6) were calculated.

3.3. Histomorphometric

3.3.1. Hematoxylin & Eosin

- Tissues fixed were dehydrated in ascending series of ethanol.
- Clearing was done in xylene.
- Embedding in paraffin was done.
- Sections were cut to 5 m.
- Staining with hematoxylin was done for 5 minutes.
- Staining with eosin was done for 2 minutes.7. Mounting was performed with DPX.

- Measurement of villus height and crypt depth was done.

3.3.2 Alcian Blue

- Deparaffinization was done.
- Sections were stained for 30 minutes with Alcian Blue (pH 2.5).
- Counterstaining was done.
- Evaluation of Goblet cell mucin density was done.

3.4 Statistical Analysis

- Data were expressed as mean ± SEM.
- One-way ANOVA was used.
- Tukey's post-hoc was performed.
- The significance threshold was set at $p < 0.05$.
- Graphs were exported at 600 dpi.

Chapter four

Results

4. Results

4.1. Relative abundance

4.1.1. Genus level

4.1.1.1 Staphylococcus

When mice were put on the modified diet with goose egg yolk, the relative abundance of Staphylococcus genus was present on the 14th day of sample collection with both chicken yolk and control groups. Staphylococcus abundance showed a pronounced early elevation, suggesting possible stimulation of the Staphylococcus genus at an early phase of the dietary adaptative period. However, at the 30th day of collection, the same abundance exhibited a pronounced and significant decline, falling under the values recorded at day 14. The decline suggests that the initial increase was in fact early and that the bacterial population decreased as the study progressed, causing a time-relational disjunction between the initial and later sampling points (Figure 4-1).

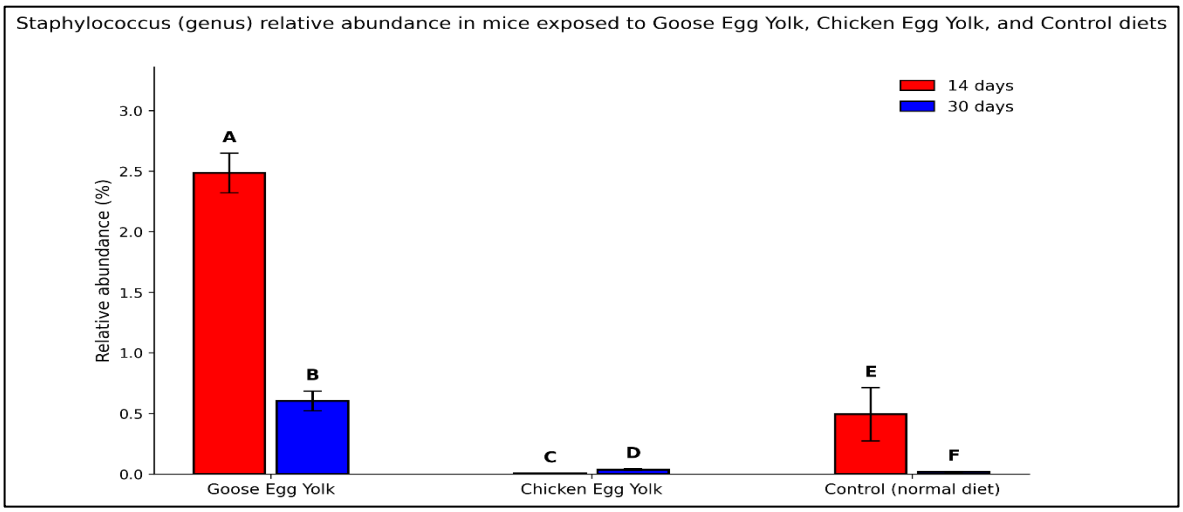


Figure 4-1: Staphylococcus (genus) relative abundance in mice exposed to Goose Egg Yolk, Chicken Egg Yolk, and Control diets.

4.1.1.2 Lactobacillus

Between the various diet groups and time intervals, the abundance of the genus Lactobacillus differed. At 14 days, the control (normal diet) group had the highest abundance (around 35%); the second highest was the goose egg yolk group (around 30%), and the lowest was the chicken egg yolk group (about 5-6%). At 30 days, all groups had a relative abundance which decreased from 14 days. In the control group, this decline was to around 17-18%, and in the goose egg yolk group, this decrease was more substantial, to around 3-4%. The chicken egg yolk group was around 1-2%. This data indicates all treatments had a decrease in the abundance of Lactobacillus between 14 and 30 days, with the most notable decrease seen across the treatments at 14 days (Figure 4-2).

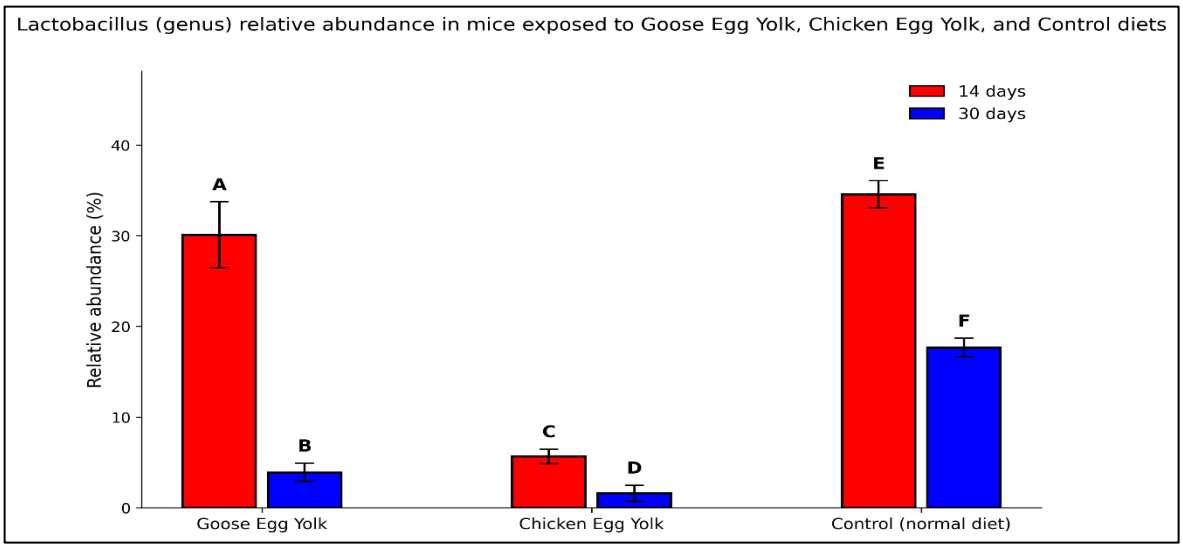


Figure 4-2: Lactobacillus (genus) relative abundance in mice exposed to Goose Egg Yolk, Chicken Egg Yolk, and Control diets.

4.1.1.3 Ligilactobacillus

Our results show that, as of 14 days, the highest relative abundance of the genus Ligilactobacillus was found in the chicken egg yolk group (approx. 53-55%), while the control and goose egg yolk groups were found to have a much lower relative abundance (approx. 5-7%). As of 30 days, the chicken egg yolk group's relative abundance has since markedly decreased to 3-4%. Similarly, the goose egg yolk group showed a decrease to 2-3% from 5-6% at 14 days, while the control group exhibited little to no change from 6-7% at both time stamps. Essentially, the data shows that the chicken egg yolk group experienced a pronounced increase at 14 days, followed by a decrease at 30 days as the other groups experienced little to no change in relative abundance (Figure 4-3).

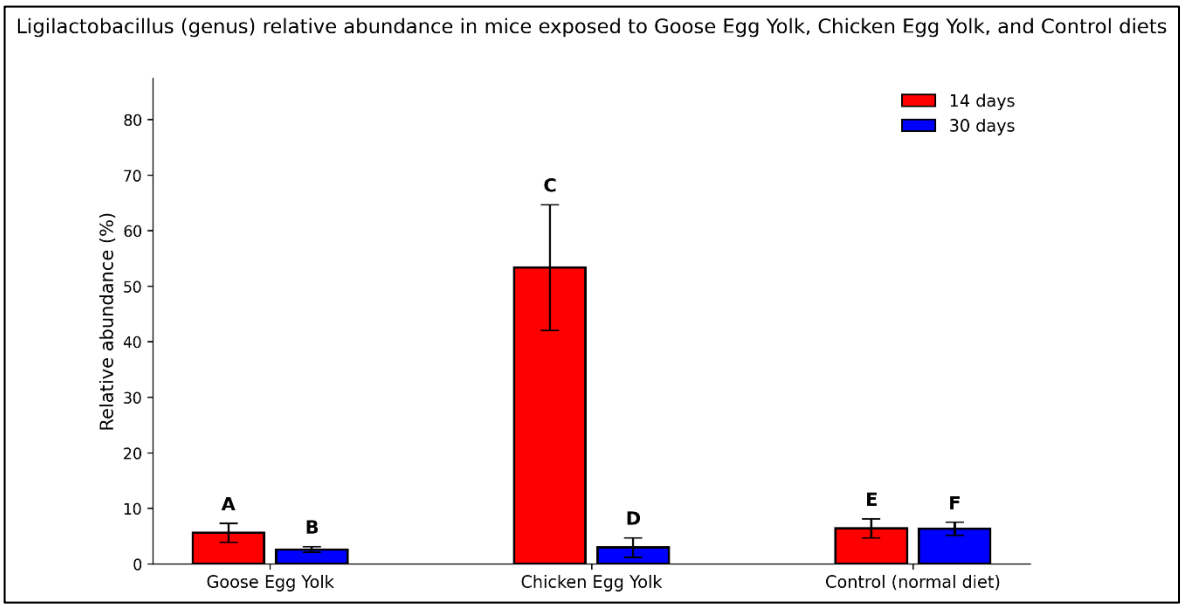


Figure 4-3: Ligilactobacillus (genus) relative abundance in mice exposed to Goose Egg Yolk, Chicken Egg Yolk, and Control diets.

4.1.1.4 Limosilactobacillus

For the first 14 days, the mice who were fed goose egg yolk were way advanced in Limosilactobacillus like in abundance compared to the other diets ($p < 0.05$). This suggested a temporary need for the expansion of the genus under yolk feeding conditions. On the 30th day, this same genus also showed an impressive and significant ($p < 0.05$) decline in comparison to the previously recorded levels. Then, the genus must have experienced a period of time-basal decline growth an augmentation conceptualized during the first two weeks of the experiment (Figure 4-4).

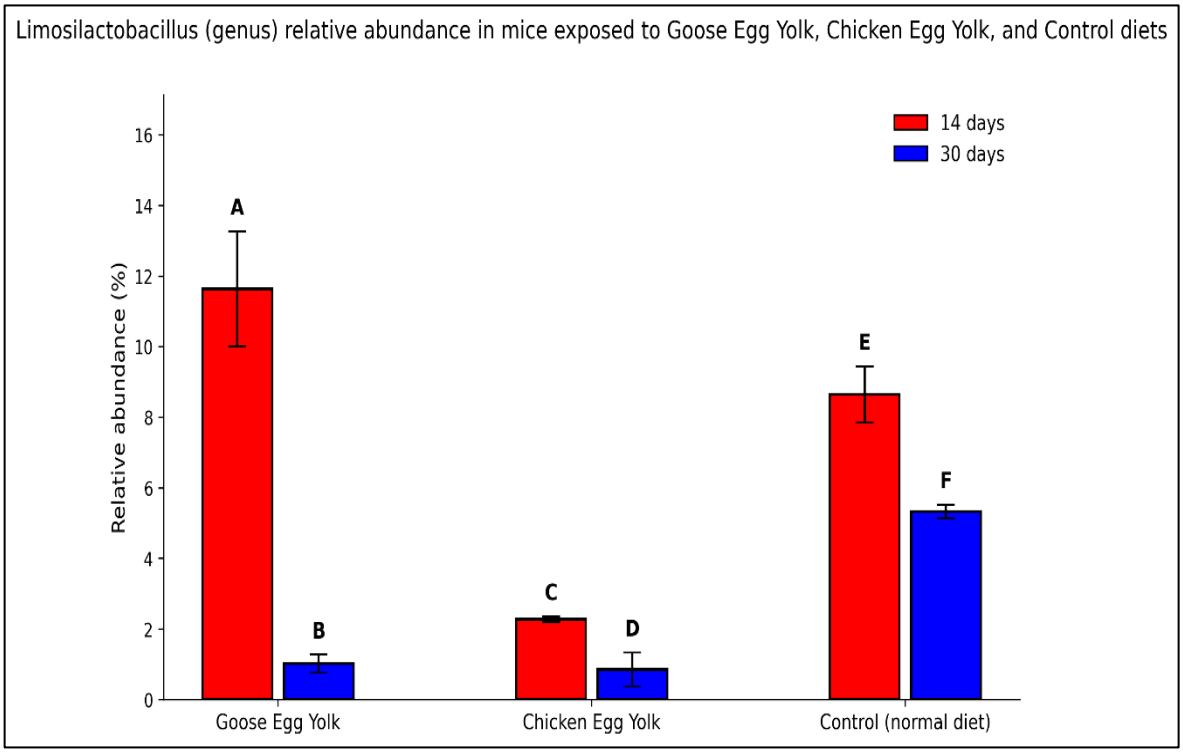


Figure 4-4: Limosilactobacillus (genus) relative abundance in mice exposed to Goose Egg Yolk, Chicken Egg Yolk, and Control diets.

4.1.1.5 Streptococcus

At 14 days, the % of genus Streptococcus relative abundance in the control (normal diet) group was the highest, accounting for 1.6-1.7%, while the goose egg yolk and chicken egg yolk groups had much lower values, 0.1-0.2%. By 30 days, the abundance in the control group had decreased markedly to approx. 0.2-0.3%. The goose egg yolk group had a slight increase in abundance by 30 days compared to 14 days (approx. 0.3%). The chicken egg yolk group had approx. 0.1-0.15% which was a minimal change in abundance from 14 days to 30 days. In total, the control group had the highest abundance which was at 14 days and then had a substantial decline at 30 days (Figure 4-6).

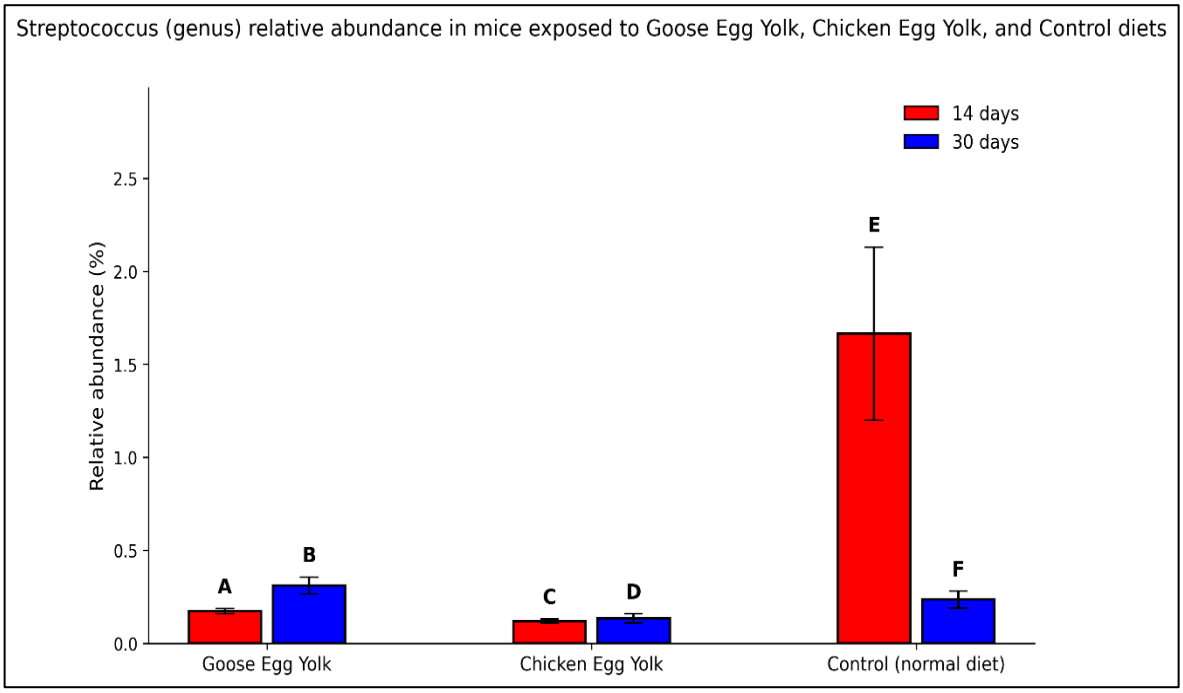


Figure 4-5: Streptococcus (genus) relative abundance in mice exposed to Goose Egg Yolk, Chicken Egg Yolk, and Control diets.

4.1.1.6 Lachnoclostridium

At day 14, the goose egg yolk group had the lowest abundance of Lachnoclostridium (around 0.2%), whereas the chicken egg yolk group and the control group had higher abundance of Lachnoclostridium (around 0.8%-0.9%). The next observation 30 days after egg food yolk inclusion, showed a slight decrease in the abundance of the goose egg yolk group (around 0.1%), and a significant decrease in the abundance of the chicken egg yolk group (around 0.05 – 0.1%). On the other hand, the control group had an abundance increase at day 30 to about 1.2 – 1.3%. The control group had the highest abundance at day 30 whereas the goose egg yolk group had the lowest abundance at both time points (Figure 4-6).

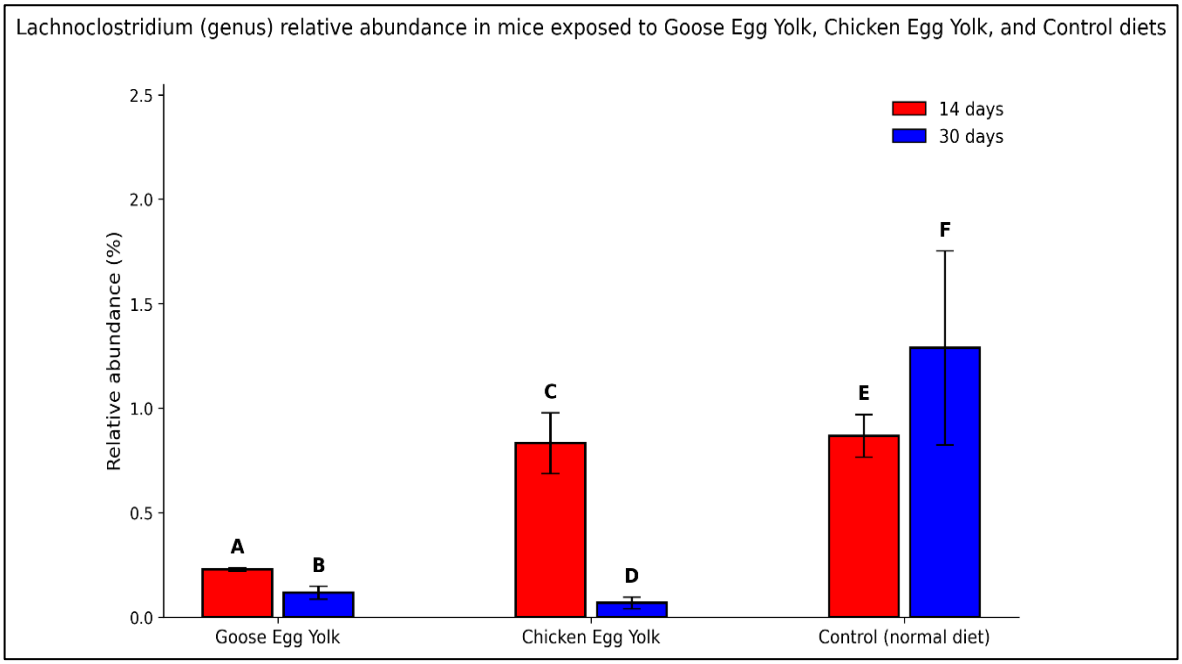


Figure 4-6: Lachnoclostridium (genus) relative abundance in mice exposed to Goose Egg Yolk, Chicken Egg Yolk, and Control diets.

4.1.1.7 Bacteroides

Goose egg yolks had the greatest relative abundance of the genus Bacteroides at 14 days, at about 6%. In the chicken egg yolk and control groups, relative abundance was much lower, at ~0.8-1.0%. By 30 days, there was a decrease in relative abundance for the goose egg yolk group (around 4%), and in the chicken egg yolk group, there was a large increase of relative abundance (about 6-7%), which was the highest at this timepoint. The control group remained at 1% for both time points. The results indicate a shift in the highest abundance from the goose egg yolk group at 14 days to the chicken egg yolk group at 30 days (Figure 4-7).

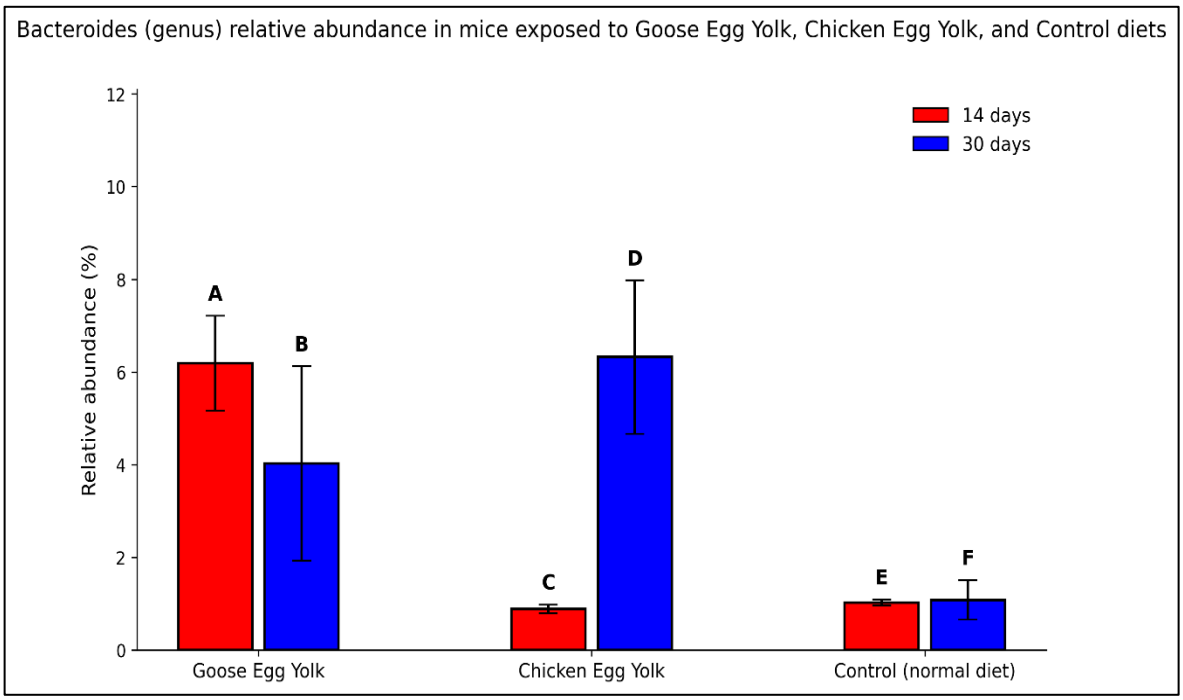


Figure 4-7: Bacteroides (genus) relative abundance in mice exposed to Goose Egg Yolk, Chicken Egg Yolk, and Control diets.

4.1.1.8 Phocaeicola

After the 14 days of exposure to the diet of goose yolk, Phocaeicola displayed a statistically significant ($p < 0.05$) increase in Phocaeicola abundance for both comparison groups. The early period corresponds to the first upward displacement from the baseline extension. Conversely, at the 30-day sampling point, the same genus Phocaeicola showed a significant ($p < 0.05$) increase, which marks a counterbalance to the previous decrement and accounts for the intermediate time frame dip (Figure 4-8).

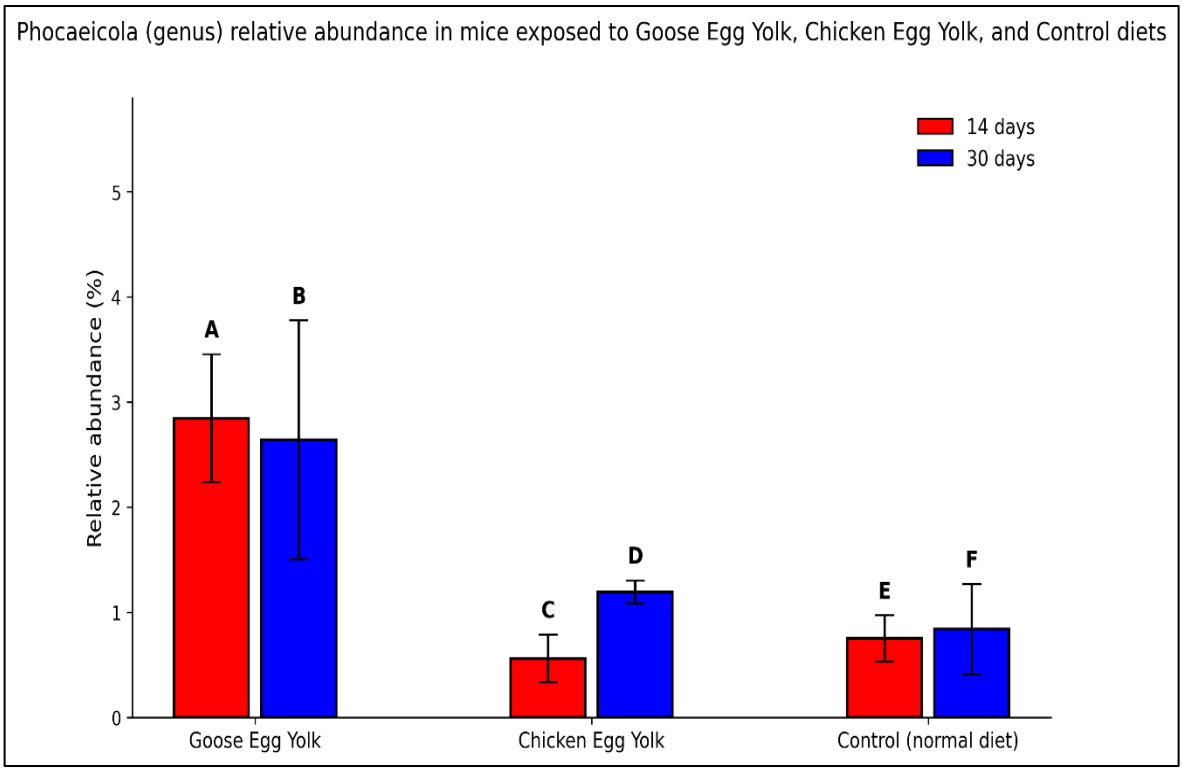


Figure 4-8: Phocaeicola (genus) relative abundance in mice exposed to Goose Egg Yolk, Chicken Egg Yolk, and Control diets.

4.1.1.9 Duncaniella

Zealously Duncaniella's levels were noted to significantly ($p < 0.05$) increase at the 14 day sampling point in the goose yolk group. This behavior portrays an early increase associated with the diet. By the 30 day point in the diet, Phocaeicola abundance significantly ($p < 0.05$) decreased, explaining the previous measurement and showing a decline and short-lived change that was hypothesized to normalize with an extended exposure to the diet (Figure 4-9).

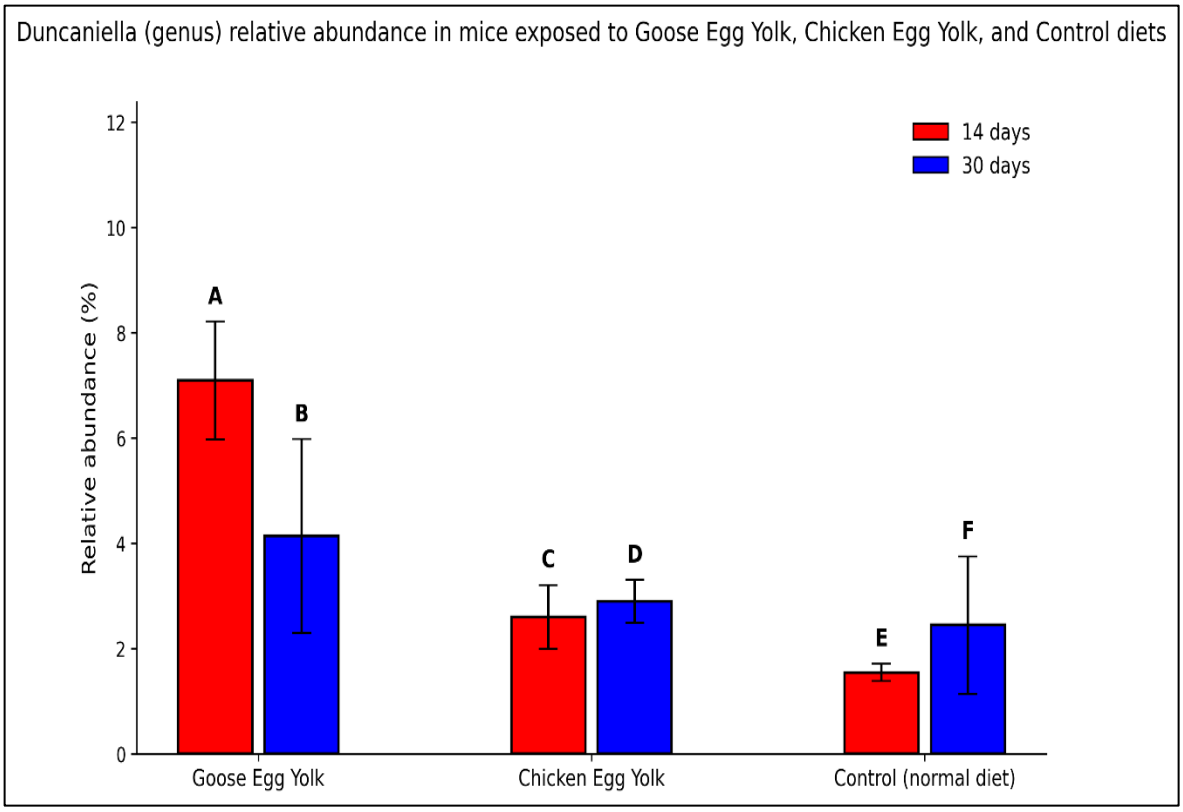


Figure 4-9: Duncaniella (genus) relative abundance in mice exposed to Goose Egg Yolk, Chicken Egg Yolk, and Control diets.

4.1.1.10 Muribaculum

By the time the mice consumed goose yolk for a period of 14 days, Muribaculum abundance had significantly ($p < 0.05$) increased in comparison to the control. The sampling period for this was also increased to 30 days. At this point the mice underwent a significant ($p < 0.05$) decrease, where the control group values had previously increased. The temporal sampling period showed an elevation that was indeed progressive and based on the additional sampling period, was decremental (Figure 4-10).

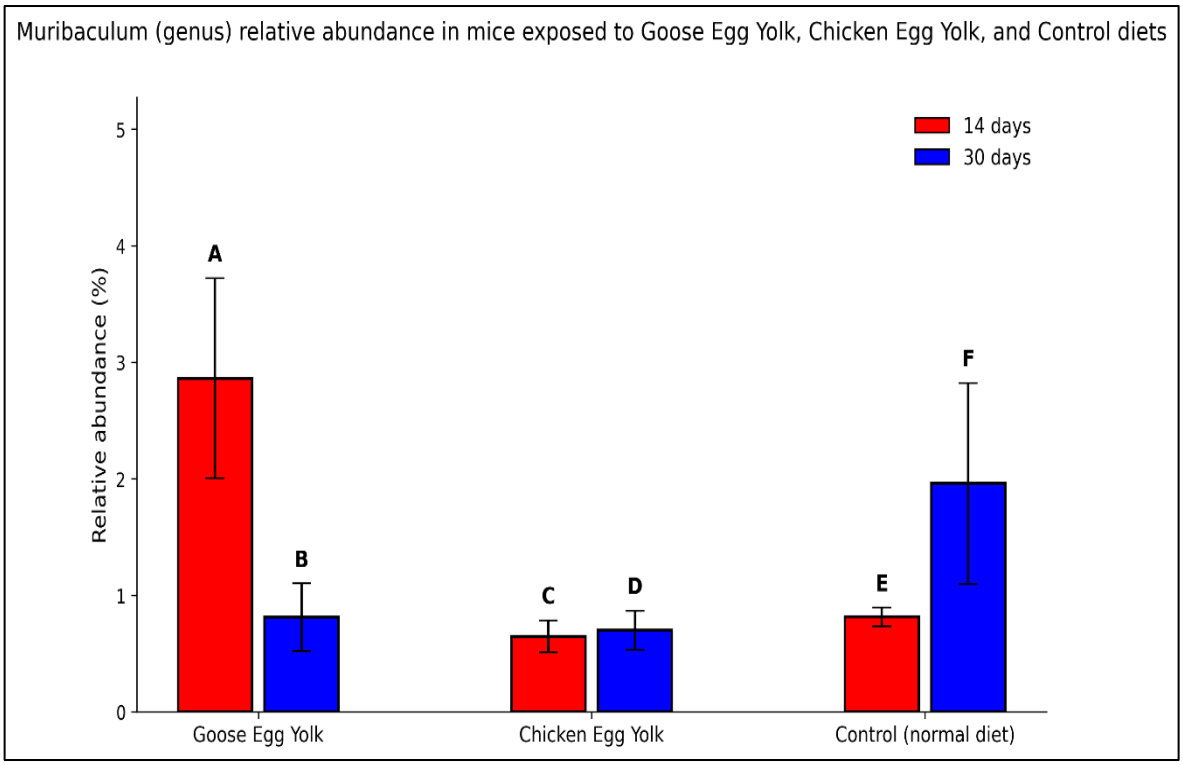


Figure 4-10: Muribaculum (genus) relative abundance in mice exposed to Goose Egg Yolk, Chicken Egg Yolk, and Control diets.

4.1.1.11 Paramuribaculum

The genus Paramuribaculum showed a statistically significant ($p<0.05$) increase in abundance in modified goose-egg-yolk fed mice at the 14-day sampling period compared to the chicken-yolk and control groups. The increase was marked during early adaptation, but did not persist throughout the rest of the experiment. Collection data by day 30 demonstrated a significant ($p<0.05$) decline in abundance, almost reverting to the baseline feeding value, or just below. This pattern suggests early stimulation followed by a late phase decline in abundance (Figure 4-11).

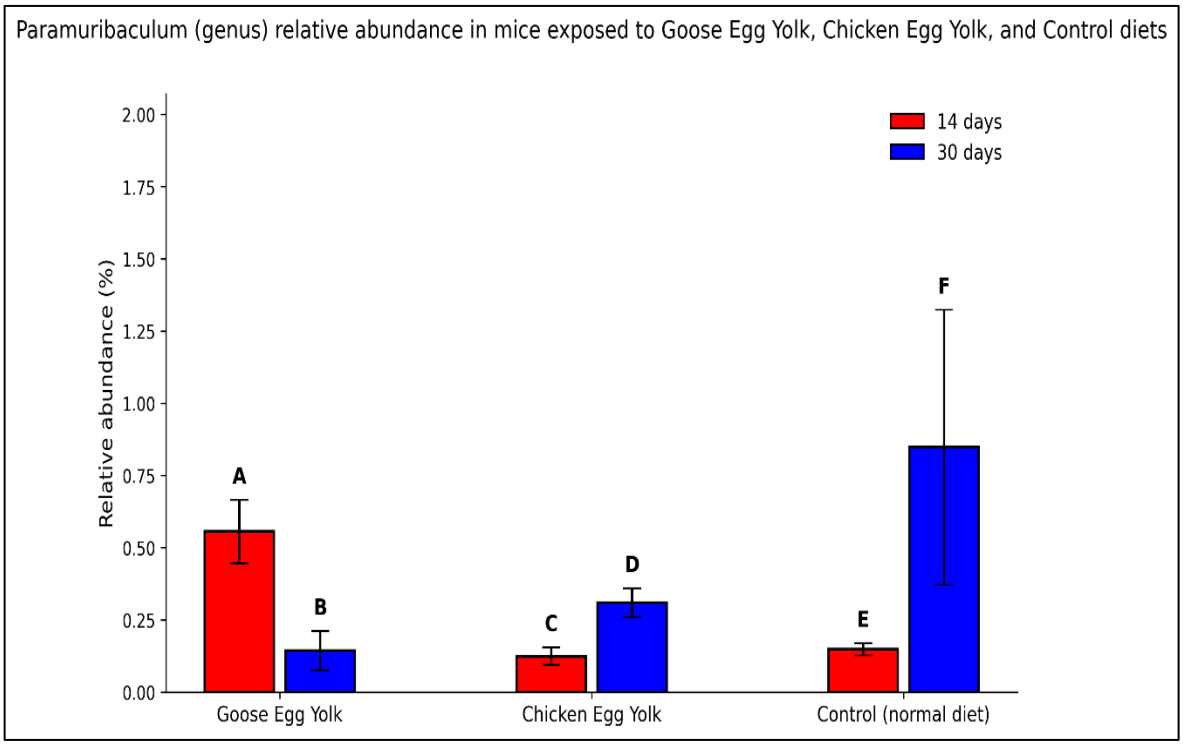


Figure 4-11: Paramuribaculum (genus) relative abundance in mice exposed to Goose Egg Yolk, Chicken Egg Yolk, and Control diets.

4.1.1.12 Sangeribacter

At 14 days, abundance within the genus Sangeribacter was approximately 1.1–1.2% in the goose egg yolk group, followed by 0.9% in the chicken egg yolk group, and was lowest in the control group at approximately 0.25–0.3%. At 30 days, a decrease in abundance was recorded in the goose egg yolk group (approximately 0.8–0.9%), the chicken egg yolk group remained relatively stable (approximately 0.9%), and the control group had an increase (approximately 0.8%). In general, the goose egg yolk group had the highest value at 14 days, while at 30 days the values in the three groups appeared to become more similar (Figure 4-12).

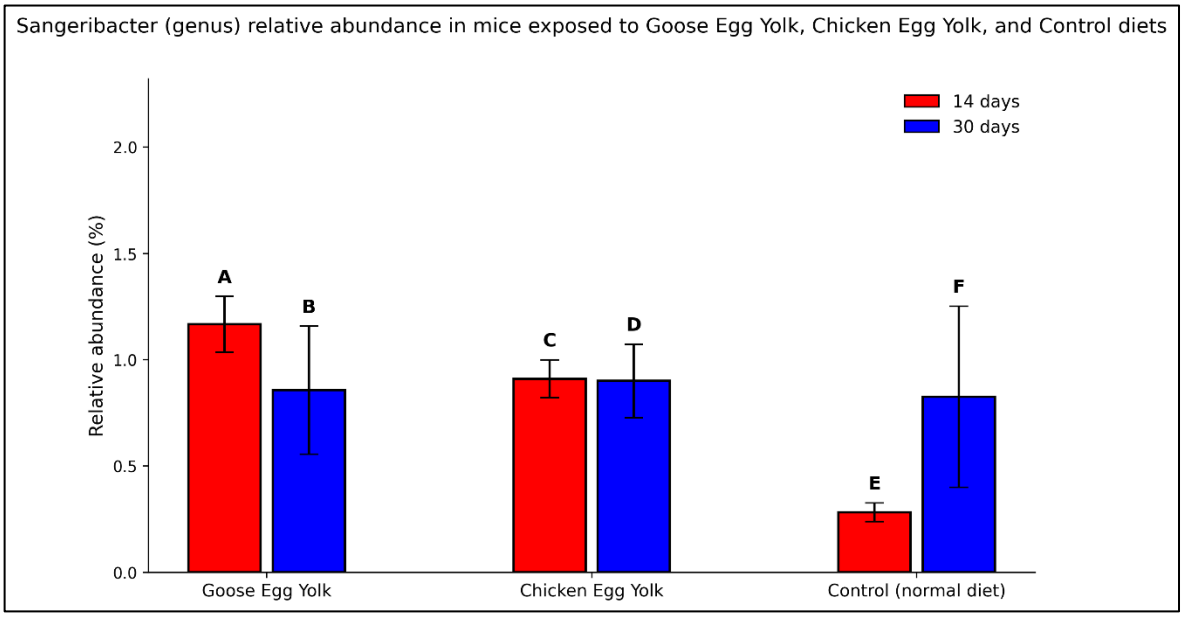


Figure 4-12: Sangeribacter (genus) relative abundance in mice exposed to Goose Egg Yolk, Chicken Egg Yolk, and Control diets.

4.1.1.13 Alloprevotella

The highest relative abundance of the genus Alloprevotella at 14 days was in the goose egg yolk group (about 2.5–2.7%) followed by the control group (about 1.0–1.1%), and the lowest value was seen in the chicken egg yolk group (about 0.2–0.3%). At 30 days, the goose egg yolk group has also seen a decrease in abundance (about 1.5–1.6%). In comparison, the chicken egg yolk group has seen a rise to about 1.0%, and the control group has also experienced an increase to about 1.4–1.6%. While at 14 days the highest value was seen in the goose egg yolk group, by 30 days, the values in all three groups had become more similar (Figure 4-13).

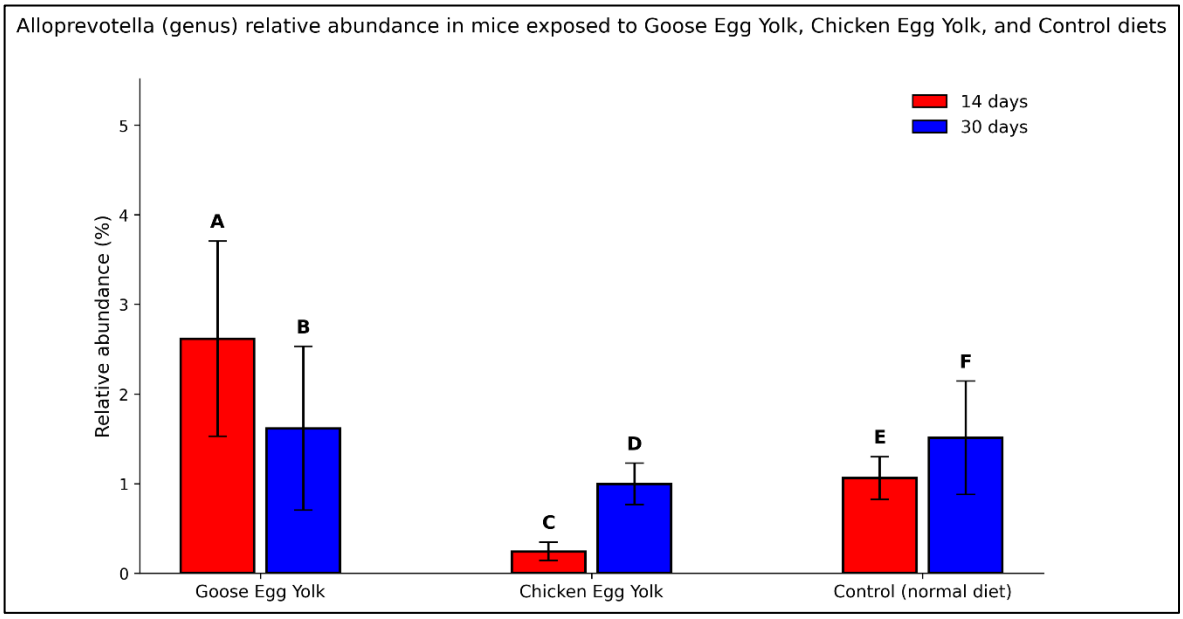


Figure 4-13: Alloprevotella (genus) relative abundance in mice exposed to Goose Egg Yolk, Chicken Egg Yolk, and Control diets.

4.1.1.14 Alistipes

In relative abundance of the genus Alistipes at 14 days, the control group 1.0% and chicken egg yolk group 0.9% both displayed higher percentages, while goose egg yolk group Alistipes had the lowest at 0.7%. However, at 30 days the chicken egg yolk group 1.9% and goose egg yolk group 1.4% had relatively higher abundance, while control group showed a significant relative abundance decrease of Alistipes (0.3 - 0.4%) in comparison to 14 days. Overall, chicken egg yolk group had the most relative abundance of Alistipes at 30 days, while the control group had the least (Figure 4-14).

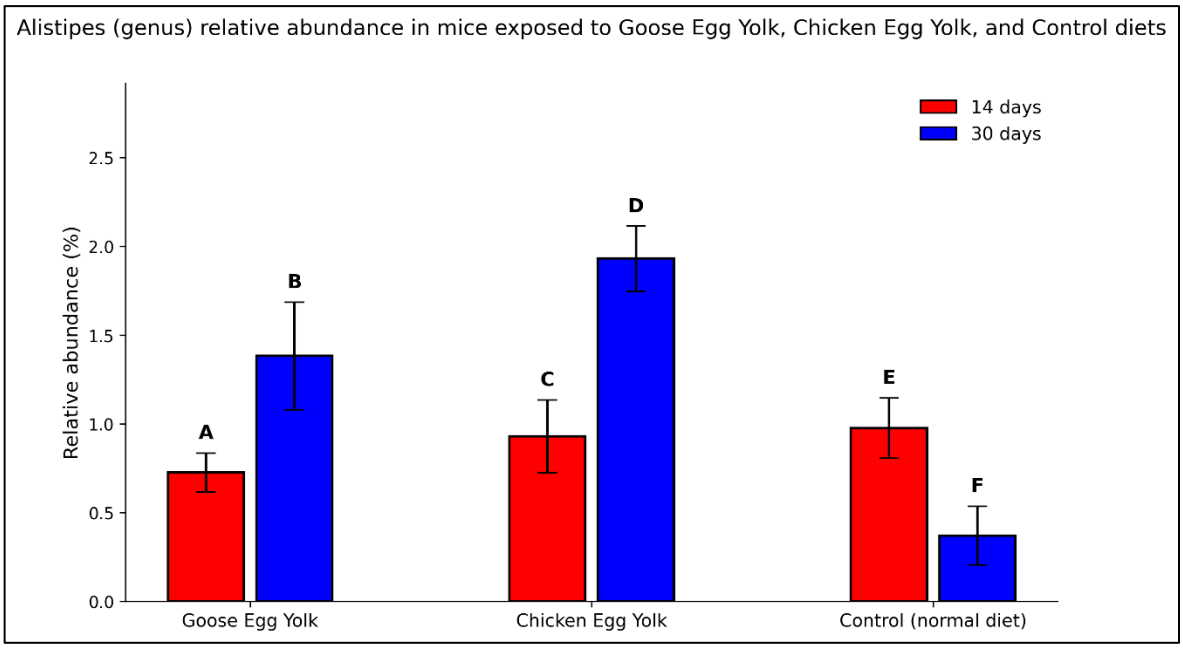


Figure 4-14: Alistipes (genus) relative abundance in mice exposed to Goose Egg Yolk, Chicken Egg Yolk, and Control diets.

4.1.1.15 Escherichia

Fourteen days in, the control group had the highest relative abundance of the genus Escherichia, at about 0.6 percent, while the values for both the goose egg yolk and chicken egg yolk groups were about 0.2 percent. By day 30, there was a marked decrease in abundance for all groups. In the goose egg yolk group abundance decreased to about 0.03 percent, in the chicken egg yolk group to about 0.02 percent, and in the control group to about 0.04-0.05 percent. In the control group, the highest abundance in 14 days was followed by a marked decline in all dietary treatments in 30 days (Figure 4-15).

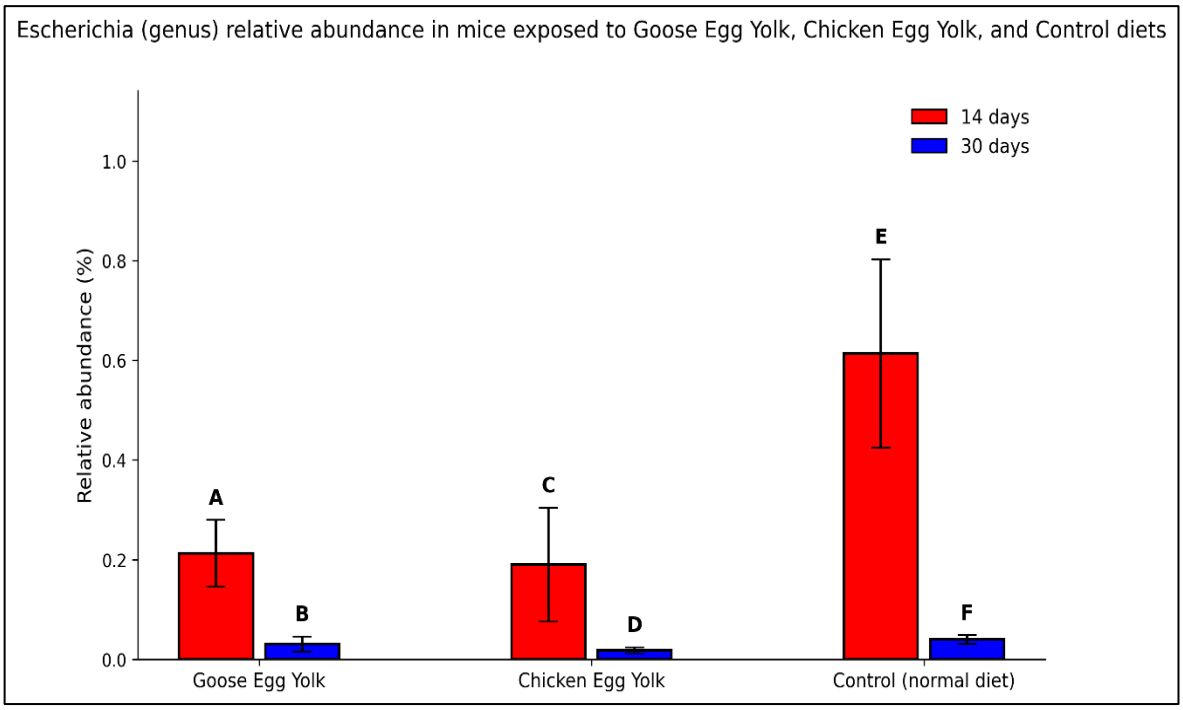


Figure 4-15: Escherichia (genus) relative abundance in mice exposed to Goose Egg Yolk, Chicken Egg Yolk, and Control diets.

4.1.1.16 Desulfovibrio

The relative abundance for the genus Desulfovibrio for the different treatment groups at 14 days were 0.25% for the goose egg yolk group, 0.30% for the chicken egg yolk group, and 0.28% for the control group. At 30 days, the goose egg yolk group experienced an increase in abundance to about 0.65%. The chicken egg yolk group also had an increase in Desulfovibrio to 0.33-0.35% while the control group experienced a decline to about 0.15%. The goose egg yolk group had the highest relative abundance in Desulfovibrio at 30 days and the control group had the lowest relative abundance at 30 days (Figure 4-16).

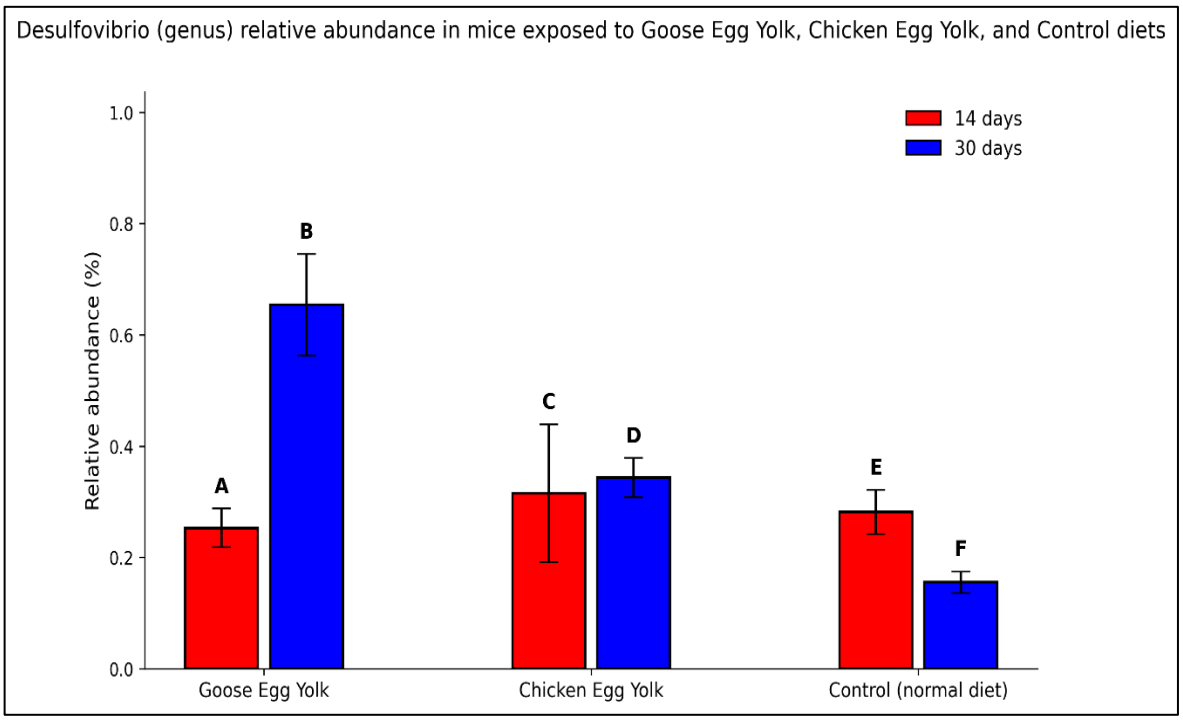


Figure 4-16: Desulfovibrio (genus) relative abundance in mice exposed to Goose Egg Yolk, Chicken Egg Yolk, and Control diets.

4.1.1.17 Lawsonia

The (genus) Lawsonia showed a relative abundance increase in Lawsonia after 14 days of goose-yolk feeding ($p < 0.05$) much (more) than the other (two) groups. During mid-term and long-term sampling intervals, Lawsonia underwent a significant decrease ($p < 0.05$) at 30 days, thereby creating distinct (pas) temporal (Figure 4-17).

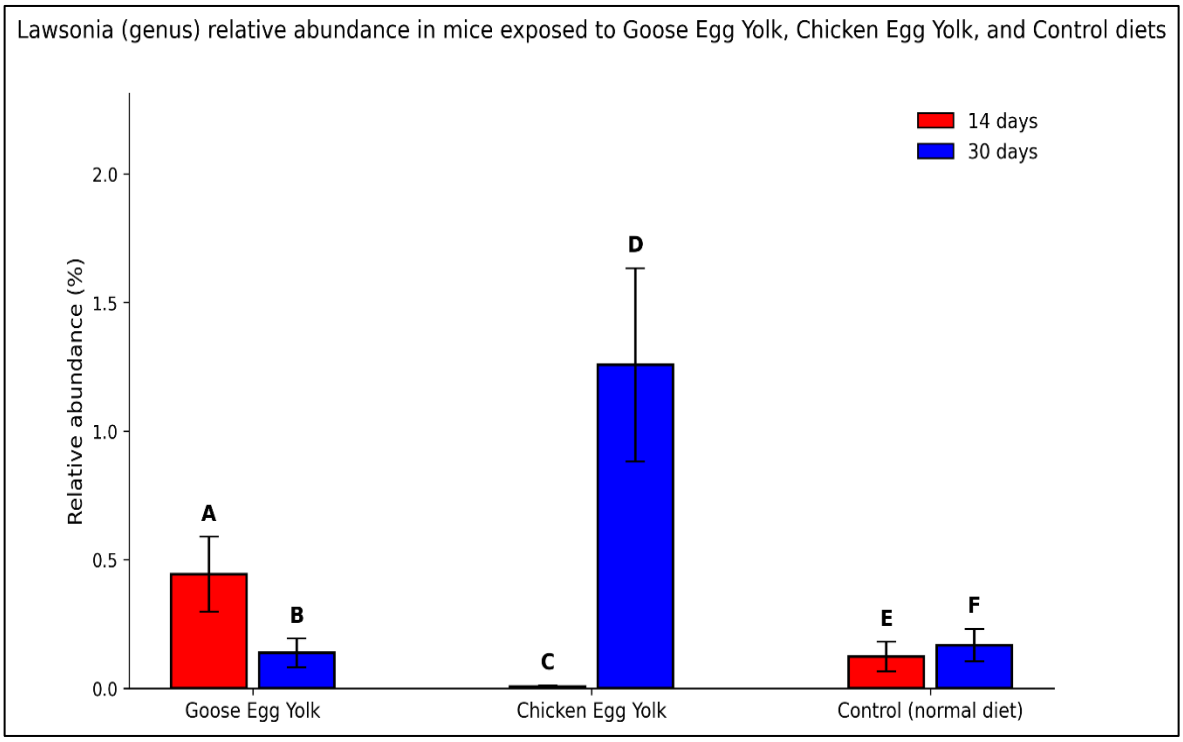


Figure 4-17: Lawsonia (genus) relative abundance in mice exposed to Goose Egg Yolk, Chicken Egg Yolk, and Control diets.

4.1.2. Species level

4.1.2.1. *Adlercreutzia caecimuris*

The control group had a relative abundance of *Adlercreutzia caecimuris* of about 0.12% at day 14, while goose egg yolk and chicken egg yolk groups had comparable and lower relative abundances of about 0.04-0.05%. By day 30, there was a decline in abundance across all groups. The relative abundance of the goose egg yolk group decreased to about 0.01% and the chicken egg yolk group also decreased to about 0.01% while the control group decreased to 0.09-0.10%. In the control, the highest levels at both time points of the study were seen while the goose and chicken egg yolk groups had the lowest levels at day 30 (Figure 4-18).

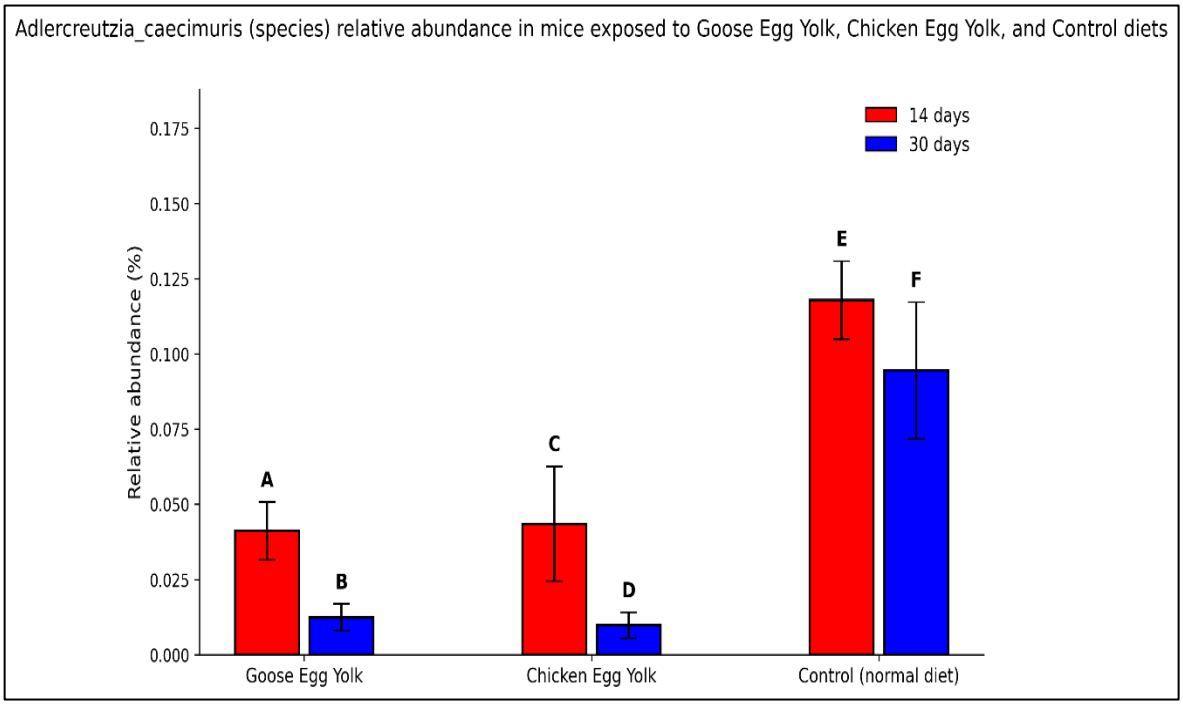


Figure 4-18: *Adlercreutzia_caecimuris* (species) relative abundance in mice exposed to Goose Egg Yolk, Chicken Egg Yolk, and Control diets.

4.1.2.2 *Staphylococcus aureus*

At 14 days, the goose egg yolk group had the highest relative proportion of *Staphylococcus aureus* (about 0.31-0.32%) compared to the control group which had a higher value (about 0.05%) and the chicken egg yolk group which had almost none (about 0%). Then at 30 days, there was a substantial drop in the goose egg yolk group (about 0.05%) and almost none in the control group. The chicken egg yolk group remained approximately zero at both time points. Altogether the highest was in the goose egg yolk group at 14 days and then 30 days had a notable drop after (Figure 4-19).

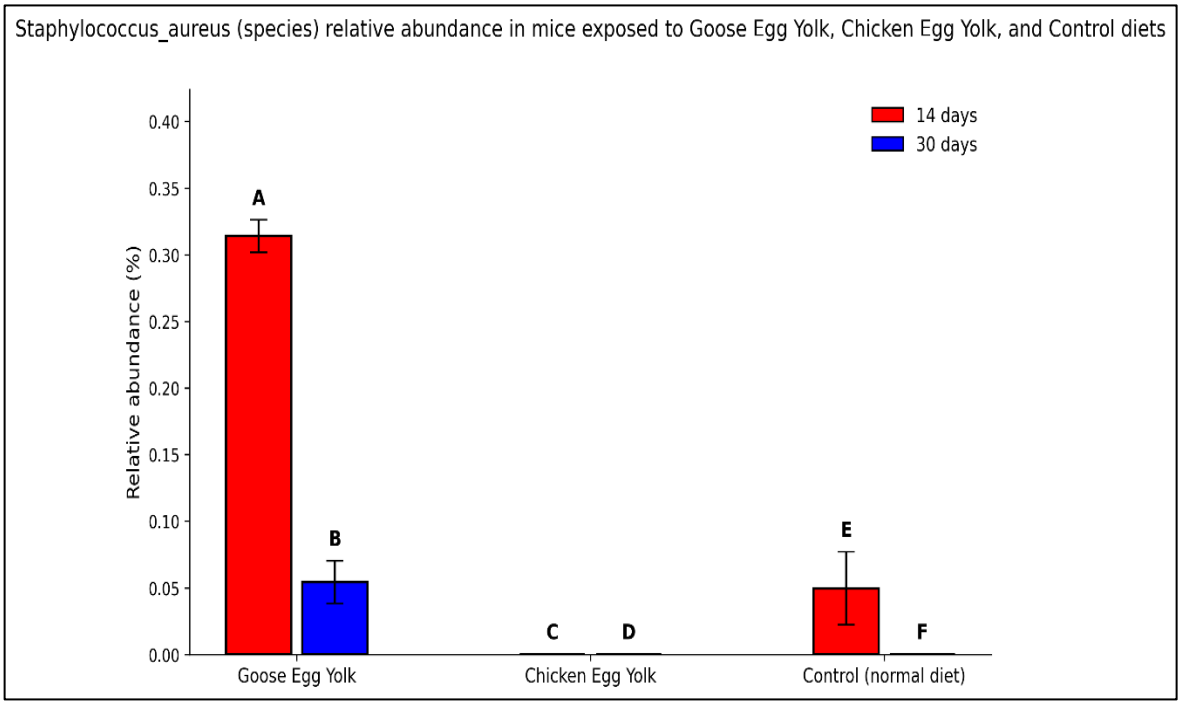


Figure 4-19: *Staphylococcus_aureus* (species) relative abundance in mice exposed to Goose Egg Yolk, Chicken Egg Yolk, and Control diets.

4.1.2.3 *Staphylococcus capitis*

At the 14-day mark, the abundance of *Staphylococcus capitis* relative to the other microorganisms, was highest for the goose egg yolk group (approx. 0.024%) and lowest for the control group (approx. 0.006%) and almost absent for the chicken egg yolk group (approx. 0%). At the 30-day mark, the goose egg yolk group had a further reduced abundance, almost to zero. This was also the case for the control group. In comparison, the chicken egg yolk group showed a small abundance increase at 30 days (approx. 0.004%). The goose egg yolk group had the highest abundance value of all groups at 14 days, followed by a marked decline at 30 days (Figure 4-20).

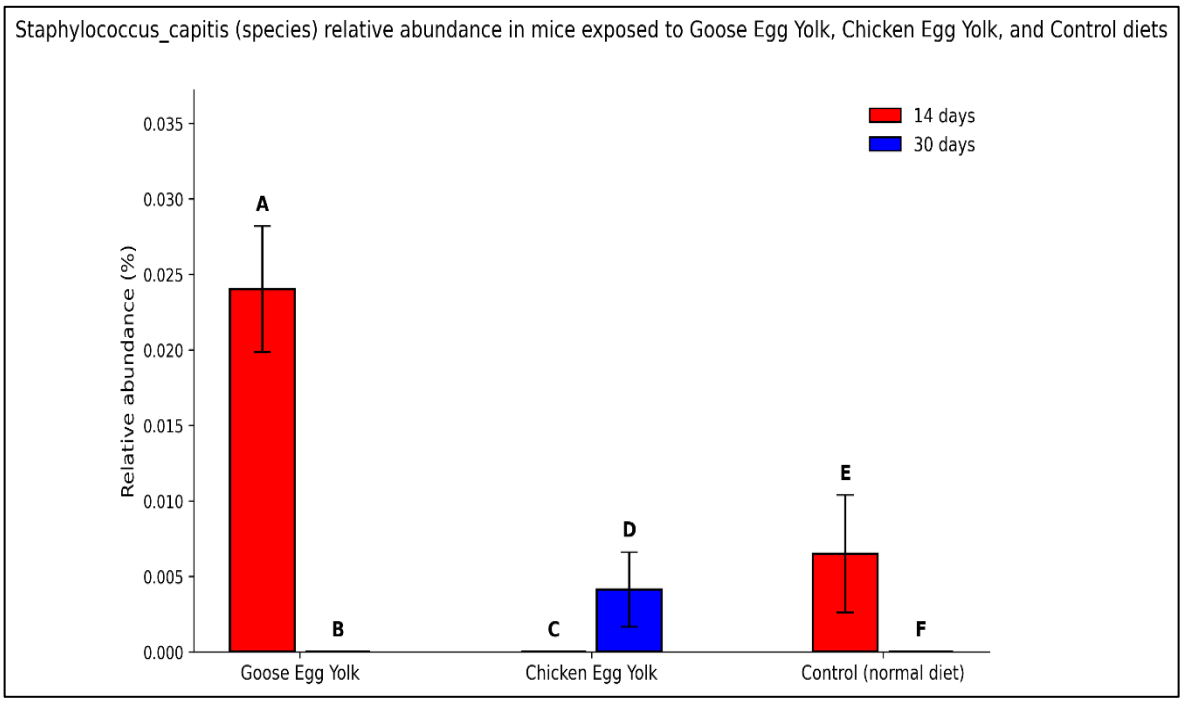


Figure 4-20: *Staphylococcus_capitis* (species) relative abundance in mice exposed to Goose Egg Yolk, Chicken Egg Yolk, and Control diets

4.1.2.4 *Lactobacillus gallinarum*

After 14 days of feeding the Goose-yolk diet, the mice were found to have a significantly greater ($p<0.05$) number of L. gallinarum in comparison to the control and chicken-yolk groups. This same pattern of populations was observed again when a 30 day examination was conducted, marking a significant decline ($p<0.05$). This indicates the presence of a clear 2 phase pattern (Figure 4-21).

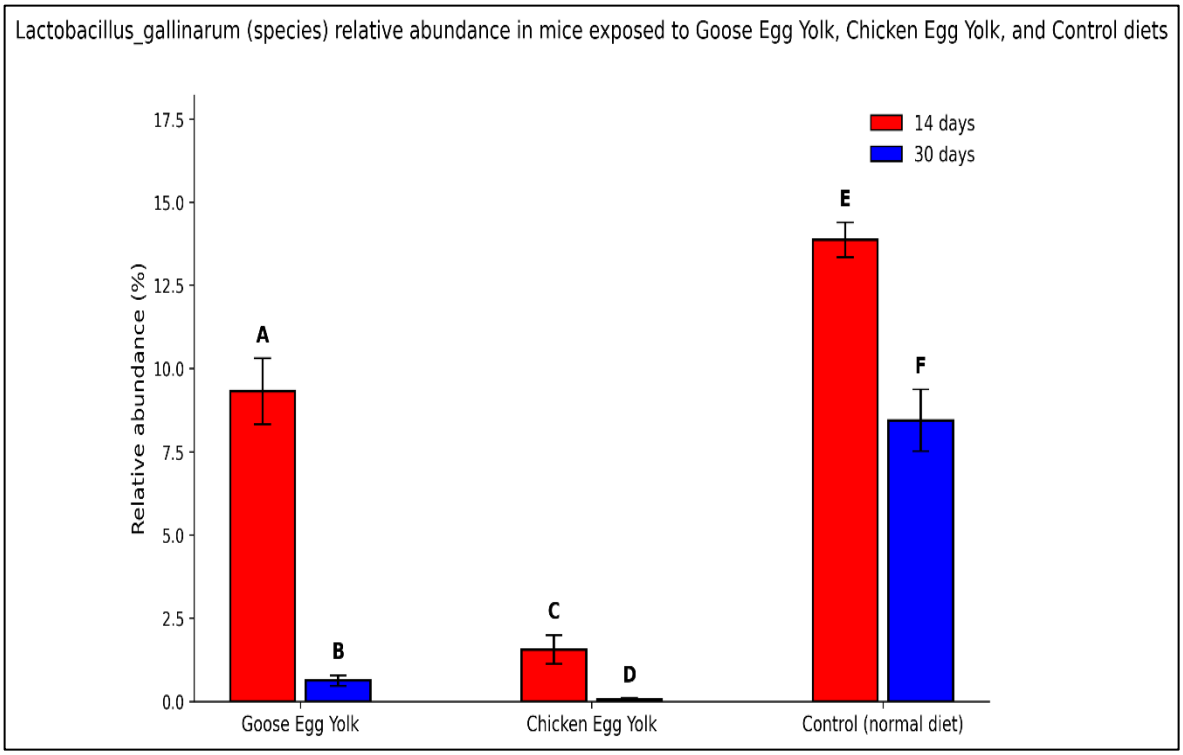


Figure 4-21: *Lactobacillus_gallinarum* (species) relative abundance in mice exposed to Goose Egg Yolk, Chicken Egg Yolk, and Control diets.

4.1.2.5 *Lactobacillus gasseri*

Goose-yolk diet mice were found to have greater ($p<0.05$) levels of L. gasseri after 14 days of feeding. However, after 30 days the same population levels were found, which signifies the levels have drastically decreased ($p<0.05$). This clearly demonstrates that there was a change in population throughout the feeding period and this drop in population appears to be irrevocable (Figure 4-22).

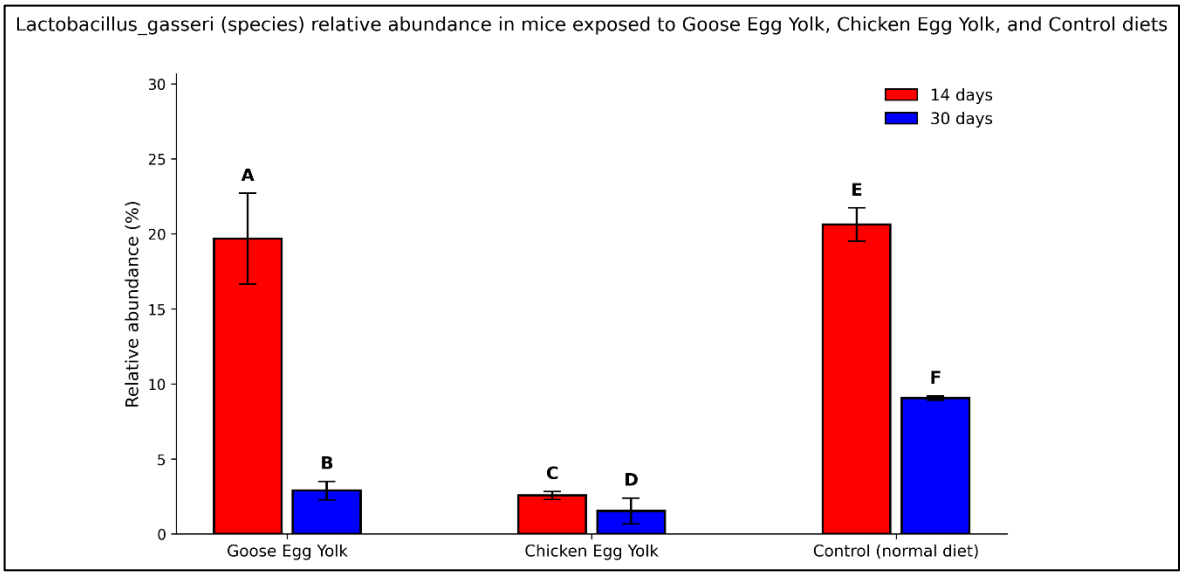


Figure 4-22: *Lactobacillus_gasseri* (species) relative abundance in mice exposed to Goose Egg Yolk, Chicken Egg Yolk, and Control diets.

4.1.2.6 *Ligilactobacillus apodemi*

At 14 days, the relative abundance of *Ligilactobacillus apodemi* was highest in the chicken egg yolk group (approximately 52–55%). The relative abundance of *Ligilactobacillus apodemi* was notably less in the goose egg yolk and control groups, at roughly 5–6%. By 30 days, the relative abundance of *Ligilactobacillus apodemi* in the chicken egg yolk group decreased significantly (approximately 3%). In contrast, the goose egg yolk group

decreased only slightly to 2–3% and the control group remained stable at approximately 5%. The chicken egg yolk group at 14 days still had the highest value overall, and had the largest drop by 30 days (Figure 4-23).

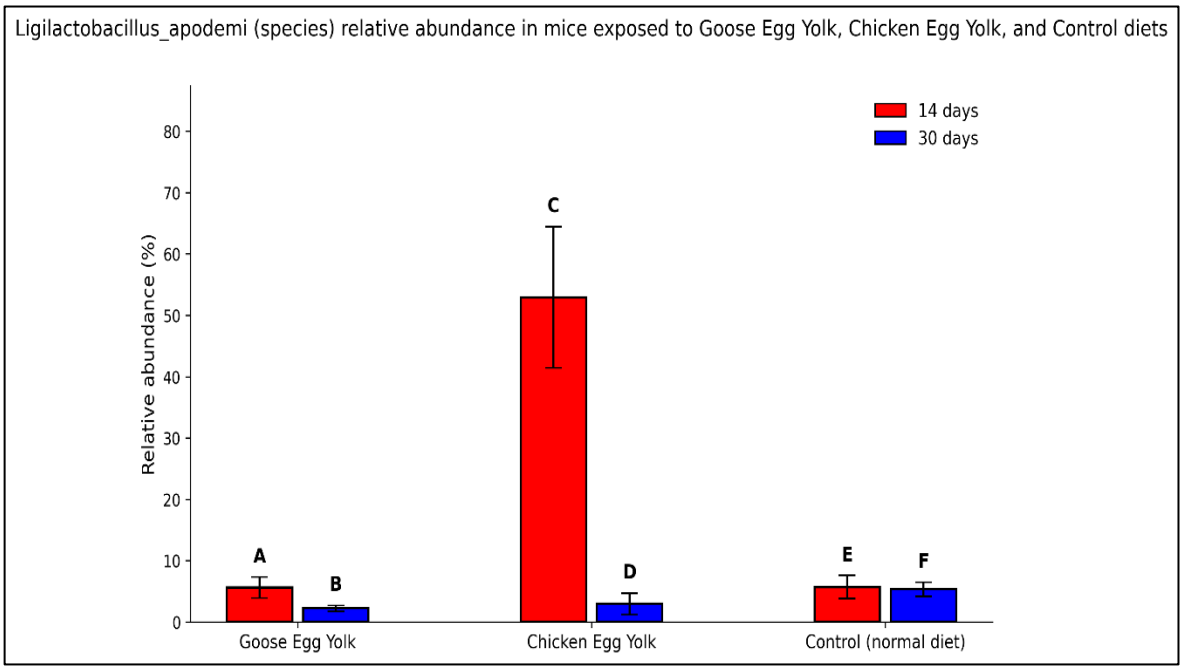


Figure 4-23: *Ligilactobacillus_apodemi* (species) relative abundance in mice exposed to Goose Egg Yolk, Chicken Egg Yolk, and Control diets.

4.1.2.7 *Limosilactobacillus reuteri*

Goose-egg yolk supplementation for 14 days resulted in a significant ($p < 0.05$) increase in L. reuteri counts. During the 30-day period in which the mice were continuously fed, the abundance decreased significantly ($p < 0.05$) which again, followed the previously established cycle of increase and decrease(Figure4-24).

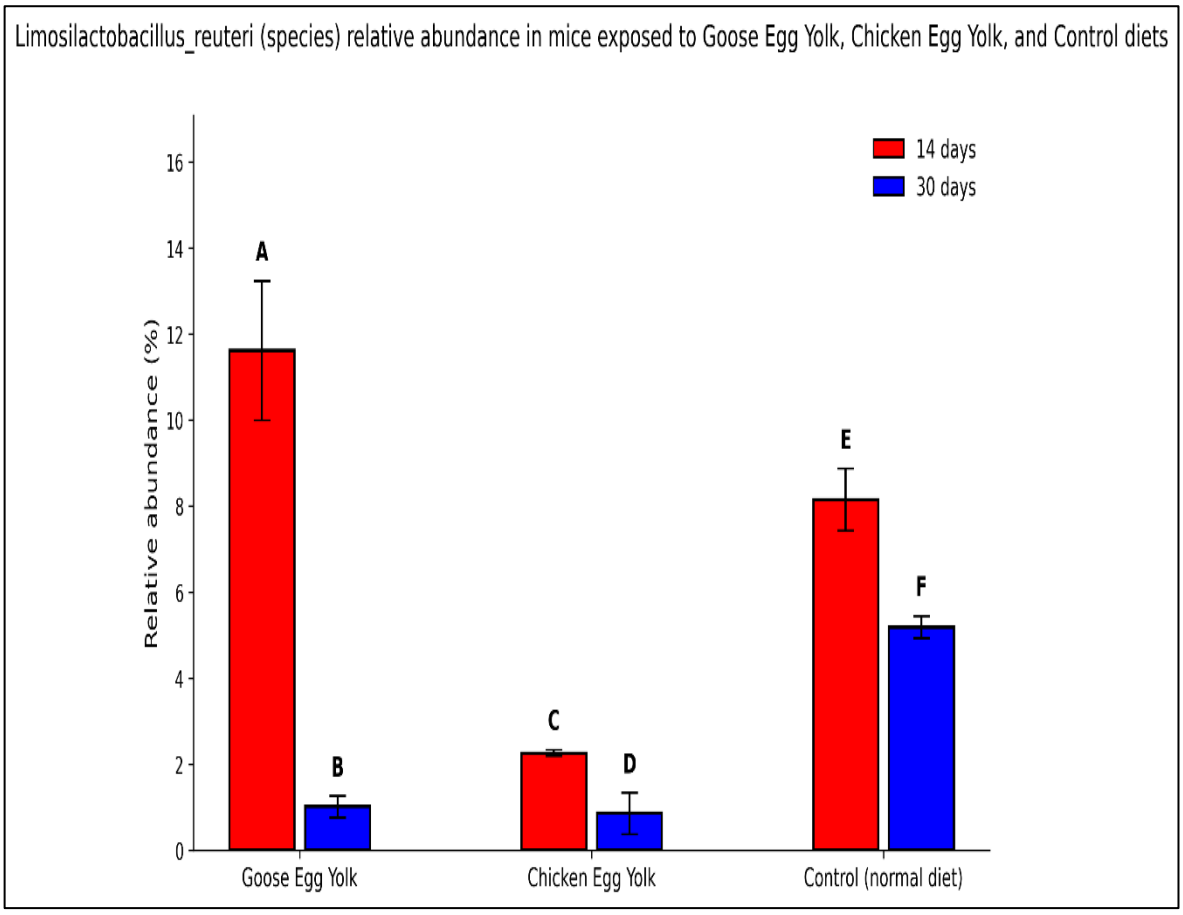


Figure 4-24: *Limosilactobacillus_reuteri* (species) relative abundance in mice exposed to Goose Egg Yolk, Chicken Egg Yolk, and Control diets.

4.1.2.8 *Kineothrix alysoides*

Kineothrix alysoides relative abundance in control group at 14 days was highest at 1.4–1.5%, followed by chicken egg yolk group with 0.6%, while goose egg yolk group was 0.2%. Abundance increased at 30 days in goose egg yolk group and control group to 0.5% and 1.9%, respectively. In comparison, chicken egg yolk group decreased to 0.2% at 30 days. In both time intervals, control group had highest value while goose egg yolk group had lowest value at 14 days (Figure 4-25).

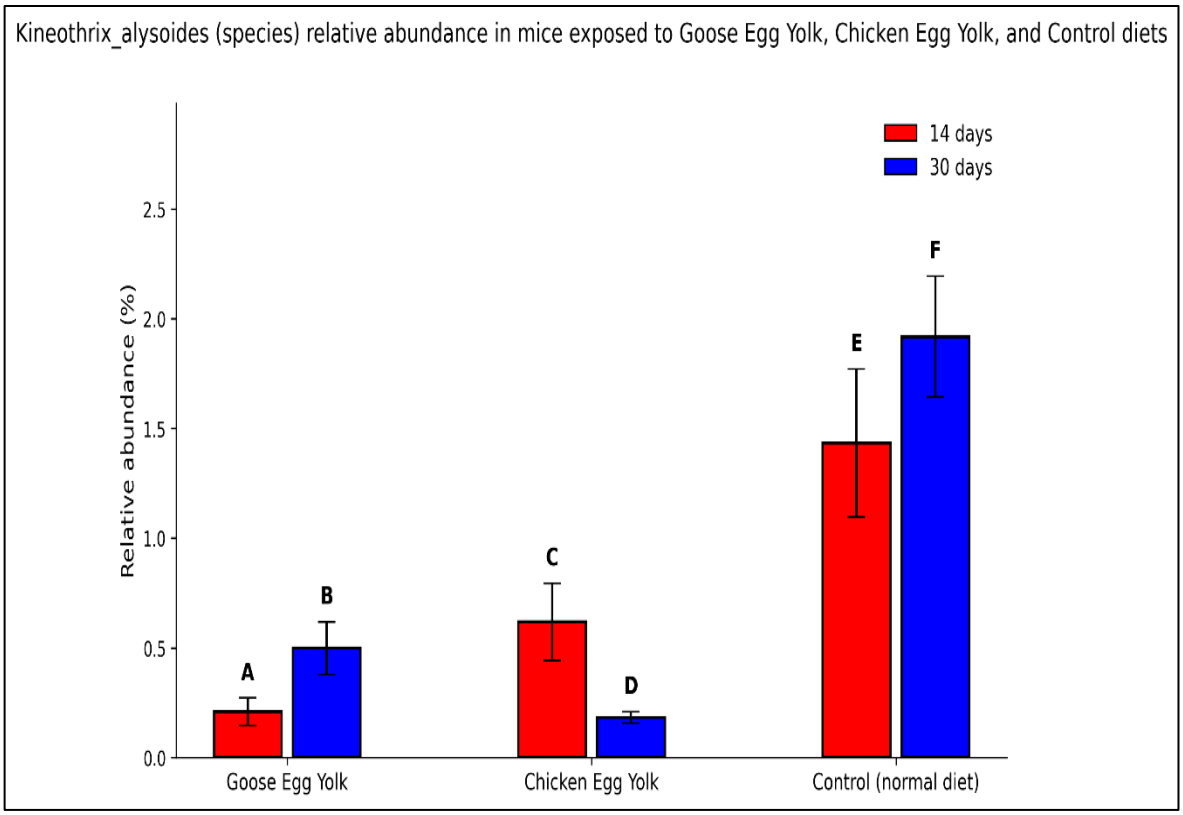


Figure 4-25: *Kineothrix_alysoides* (species) relative abundance in mice exposed to Goose Egg Yolk, Chicken Egg Yolk, and Control diets.

4.1.2.9 *Clostridium scindens*

At 14 days, the relative abundance of *Clostridium scindens* was the lowest among the goose egg yolk group (about 0.2%), and the chicken egg yolk group (about 0.8%) and control group (about 0.85%) had higher values. By 30 days, abundance decreased a little in goose egg yolk group (about 0.1%) and decreased a lot in the chicken egg yolk group (about 0.07%). The control group, however, had a significant increase at 30 days (about 1.3%). Overall, control group had the highest value at 30 days and goose and chicken egg yolk groups had the lowest values (Figure 4-26).

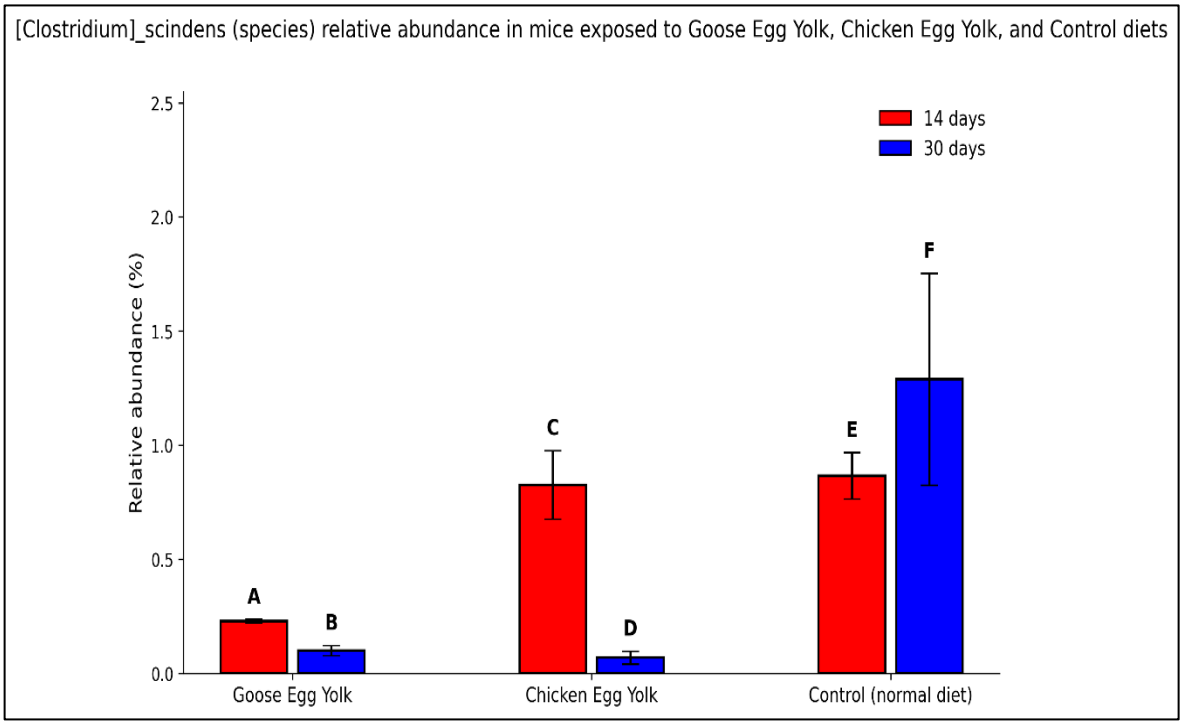


Figure 4-26: *Clostridium scindens* (species) relative abundance in mice exposed to Goose Egg Yolk, Chicken Egg Yolk, and Control diets.

4.1.2.10 *Schaedlerella arabinosiphila*

On day 14 of sampling, *S. arabinosiphila* exhibited a significant ($p < 0.05$) increase as compared to controls in the goose-yolk group. Subsequently, 30 days later, its abundance significantly ($p < 0.05$) declined which illustrates a mid-term increase followed by a drop which is transient at the end of the trial (Figure 4-27).

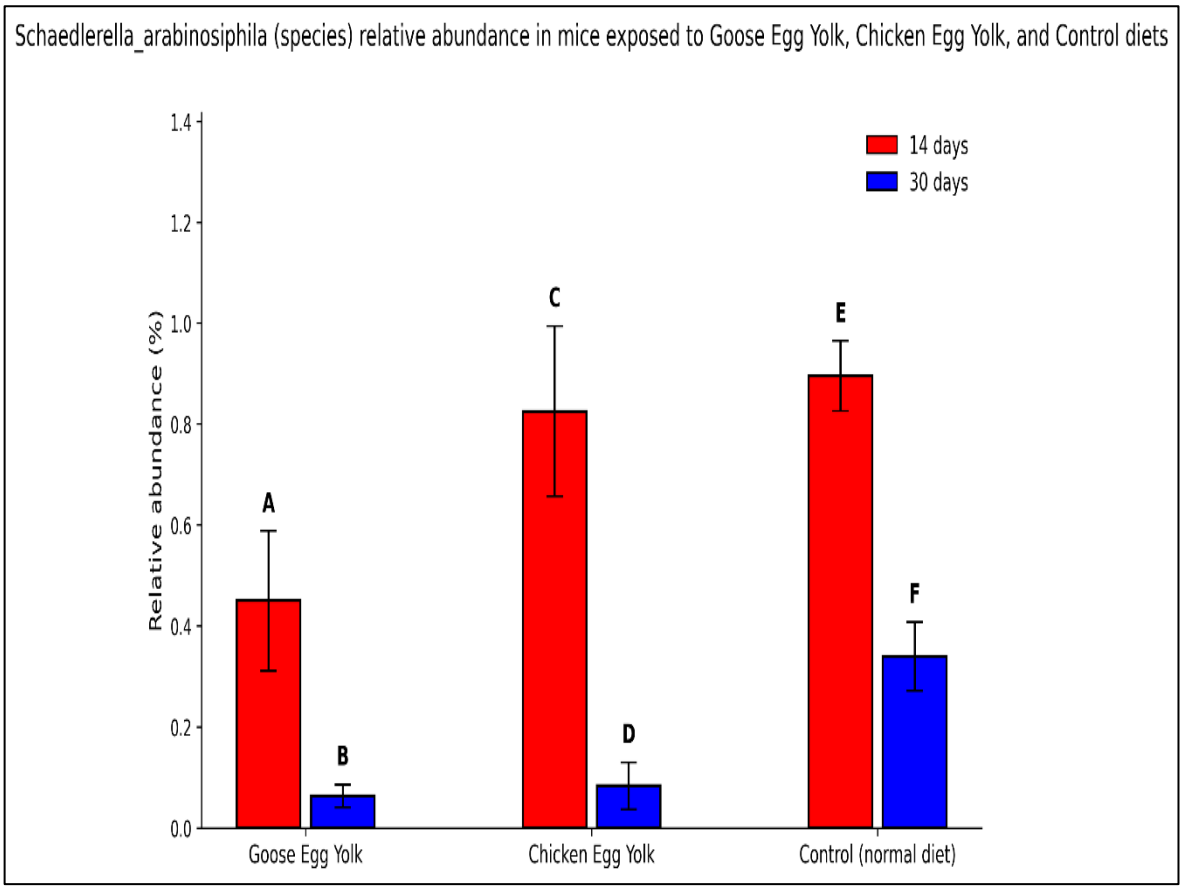


Figure 4-27: *Schaedlerella_arabinosiphila* (species) relative abundance in mice exposed to Goose Egg Yolk, Chicken Egg Yolk, and Control diets.

4.1.2.11 *Bacteroides acidifaciens*

After 14 days, the relative abundance of *Bacteroides acidifaciens* was again the highest for the goose egg yolk group at approximately 4.2–4.5%, while the chicken egg yolk group was at a markedly lesser value of approximately 0.4–0.5%, and the control group was at the lowest value of approximately 0.1–0.2%. After 30 days, there was a decrease in the goose egg yolk group at approximately 3.5%. On the other hand, the chicken egg yolk group exhibited a significant increase at 30 days (approximately 4.8–5.0%), while in the control group there was about a 0.5–0.6% increase. Based on 14 days, the highest value was in the goose egg yolk group, while for 30 days, the highest value was in the chicken egg yolk group (Figure 4-28).

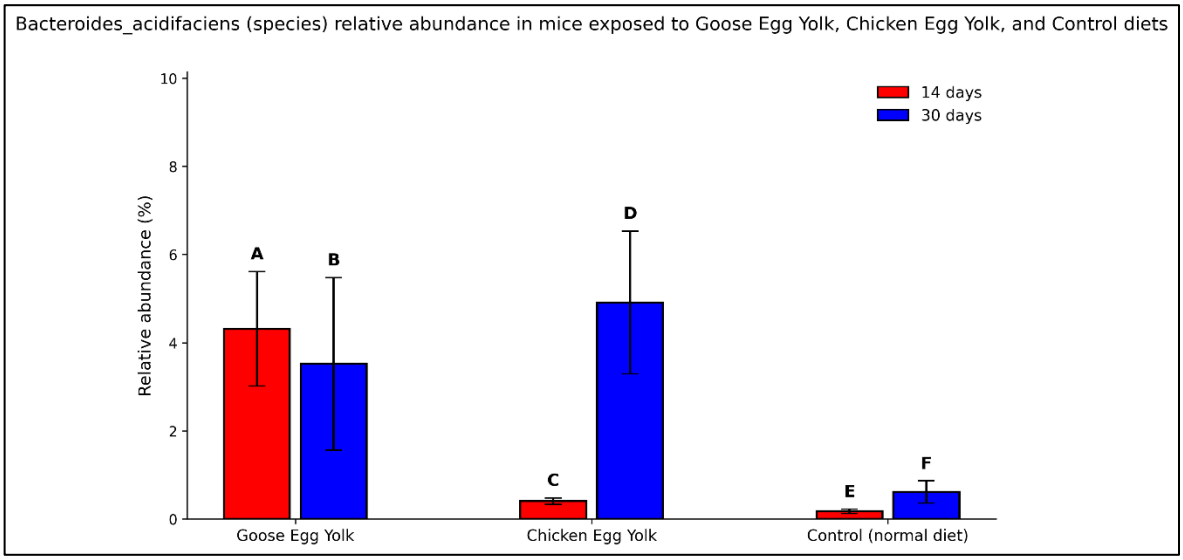


Figure 4-28: *Bacteroides_acidifaciens* (species) relative abundance in mice exposed to Goose Egg Yolk, Chicken Egg Yolk, and Control diets.

4.1.2.12 *Phocaeicola vulgatus*

At 14 days the relative abundance of *Phocaeicola vulgatus* was highest in the goose egg yolk group (approx. 2.8%), followed by chicken egg yolk group (approx. 0.5%) and control group (approx. 0.05%). At 30 days, relative abundance in the goose egg yolk group decreased slightly to approx. 2.6%. However, chicken egg yolk group increased to approx. 1.2% and control group increased to approx. 0.8%. On the whole, goose egg yolk group had the highest values at both time points, and control group had the lowest abundance at 14 days and an increased abundance at 30 days (Figure 4-29).

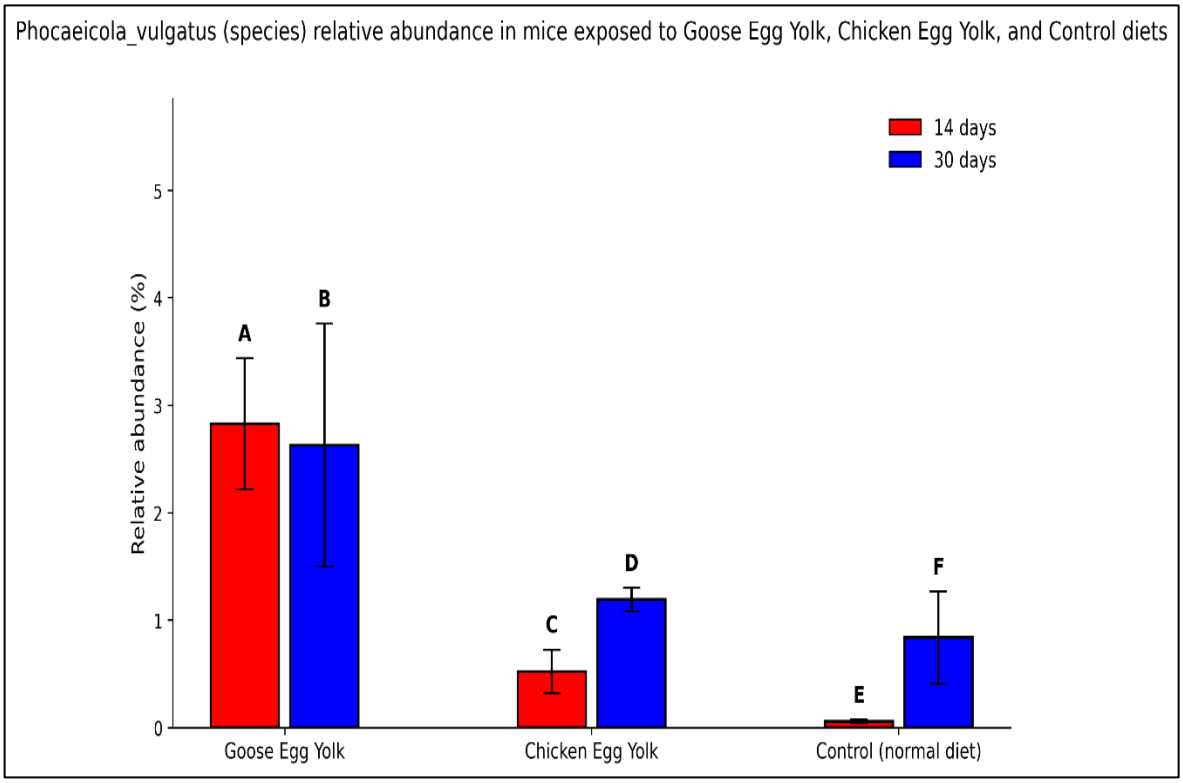


Figure 4-29: *Phocaeicola_vulgatus* (species) relative abundance in mice exposed to Goose Egg Yolk, Chicken Egg Yolk, and Control diets.

4.1.2.13 *Duncaniella muris*

At 14 days, the greatest relative abundance of *Duncaniella muris* (about 3.1%) occurred in the goose egg yolk group, with lower relative abundances in the chicken egg yolk group (about 1.1%) and in the control group (about 0.9%). By 30 days, relative abundances for the goose, chicken, and control egg yolk groups were 1.8%, 1.3%, and 1.1%, respectively. Collectively, the values among the three groups were more comparable at 30 days than at 14 days (Figure 4-30) and the goose egg yolk group was the highest at 14 days.

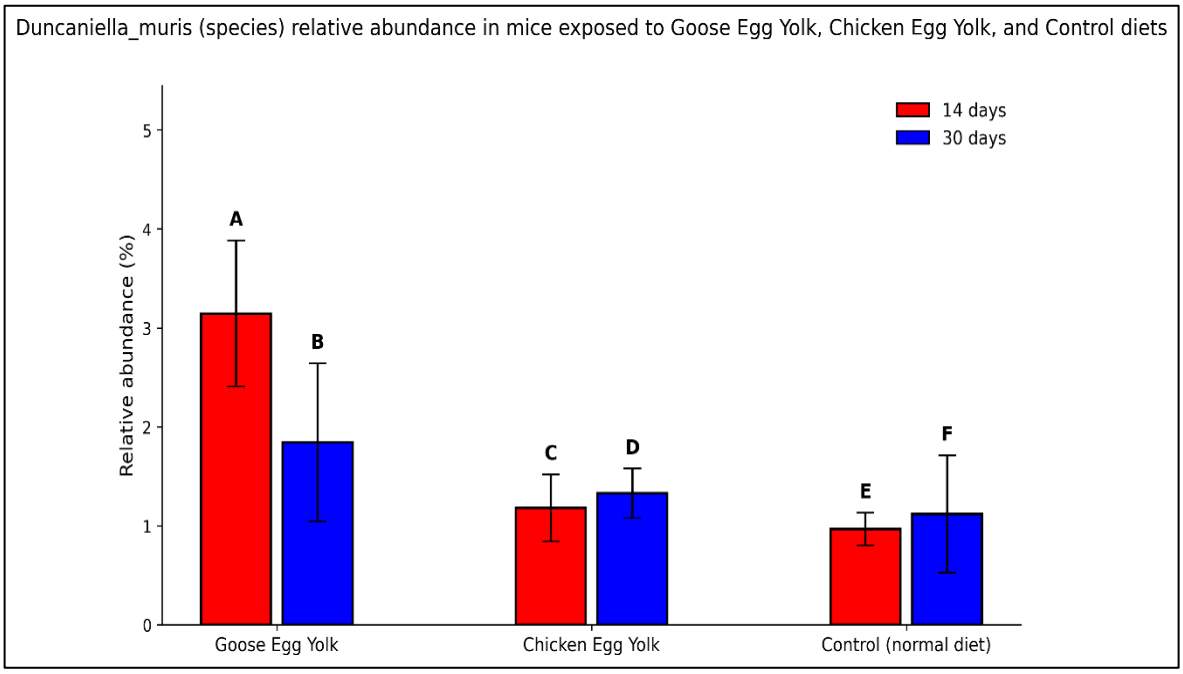


Figure 4-30: *Duncaniella_muris* (species) relative abundance in mice exposed to Goose Egg Yolk, Chicken Egg Yolk, and Control diets.

4.2. Diversity indices

4.2.1. Alph diversity

In index estimation, McDonald argued that, for species richness, the more diverse the species, the higher the value of the index of diversity. Therefore, in this experiment, we noticed that, in mouse gastrointestinal tracts, the more goose yolk wirh chicken diet was added, the higher the index of diversity even though it was initially added as a dietary fiber. In this series of experiments, for each of the eight experimental diets, the starting values are the average values for the indices of diversity. It is indeed very very clear that the values are very low. Even old and latent people with the subjects of the experiment would agree that these values are statistically significantly different than the values obtained for carrying out the experiment with the integrated chicken diet. In these indices of diversity, the distribution richness is much larger, as we can see, than the other one. Moreover, it can be claimed that is even lower than the value of the recurrence of distribution richness of these void s. Hence, it would be accurate to claim that there is larger distribution richness than the other one whereby each infers that lower recurrence of distribution richness results in higher values for wealth of the distribution. In other words, it would be claimed that there indeed is lower recurrent distribution richness in these voids than there is with the value of the recurrence of the distribution of the richness of other voids. Hence, it would be accurate to claim that there is larger distribution richness than the other one such whereby each infers that lower recurrence of distribution richness results in higher values for wealth of the distribution.

4.2.1.1 Chao1 Diversity Index :

From figure 4-31, at 14 days, the control group appeared to have the highest Chao1 index with a value of about 485, followed by chicken egg yolk group with an index of about 440-445, and then the goose egg yolk group with an index of about 400. At 30 days, Chao1 index of goose egg yolk group increased to about 455-460, and chicken egg yolk group increased to an index of about 450-455. Unlike the, control group Chao1 index value decreased to about 470-475 at 30 days. The bars in figure 4-31 illustrate the mean ±SEM.

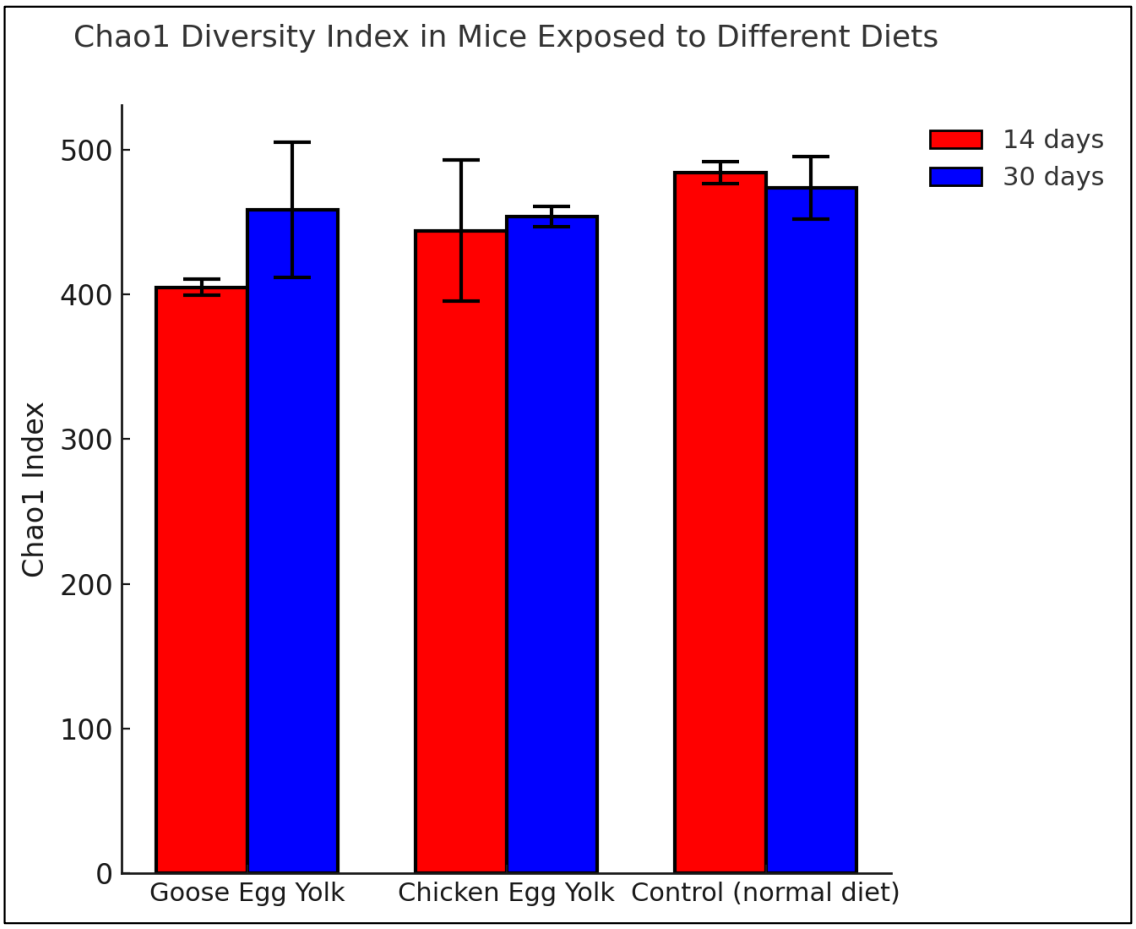


Figure 4-31. Chao1 diversity index results from the control, chicken egg yolk, and goose egg yolk groups at 14 days and 30 days are illustrated in figure 4-31.

4.2.1.2 Shannon Diversity Index :

Of all the mice at 14 days, the control group had the greatest Shannon index (about 5.9-6.0), and the goose egg yolk group had a comparable index (about 5.9) while the chicken egg yolk group index was the least (about 3.8). At 30 days, all groups experienced an increase in Shannon index. The control group is the highest and is at (approx. 6.4-6.5), while the goose egg yolk group is at 6.1 and the chicken egg yolk group increased significantly to (about 5.5-5.6). The mean ± standard error is represented by the bars (Figure 4-32).

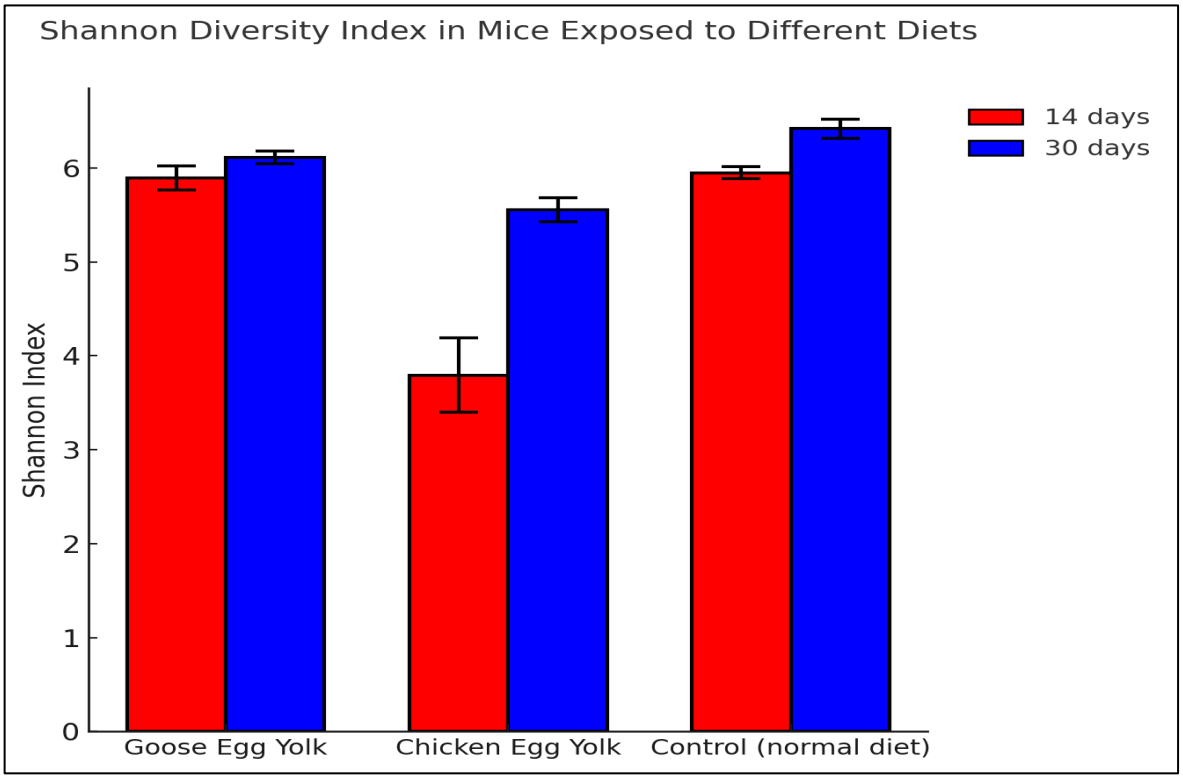


Figure 4-32: Shannon diversity index of mice is illustrated, whose diets consist of goose egg yolk, chicken egg yolk, and a control diet, at 14 and 30 days.

4.2.1.3 Faith's Phylogenetic Diversity Index :

The highest Faith's PD for the control group (about 43) was greater than chicken egg yolk (about 38) and goose egg yolk (about 35) at 14 days. At 30 Days PD index for goose egg yolk group improved to around 41, chicken egg yolk group was similar (37-38) and control group declined to around 34-35. Goose egg yolk group showed the highest value at 30 days and control group declined (Figure 4-33).

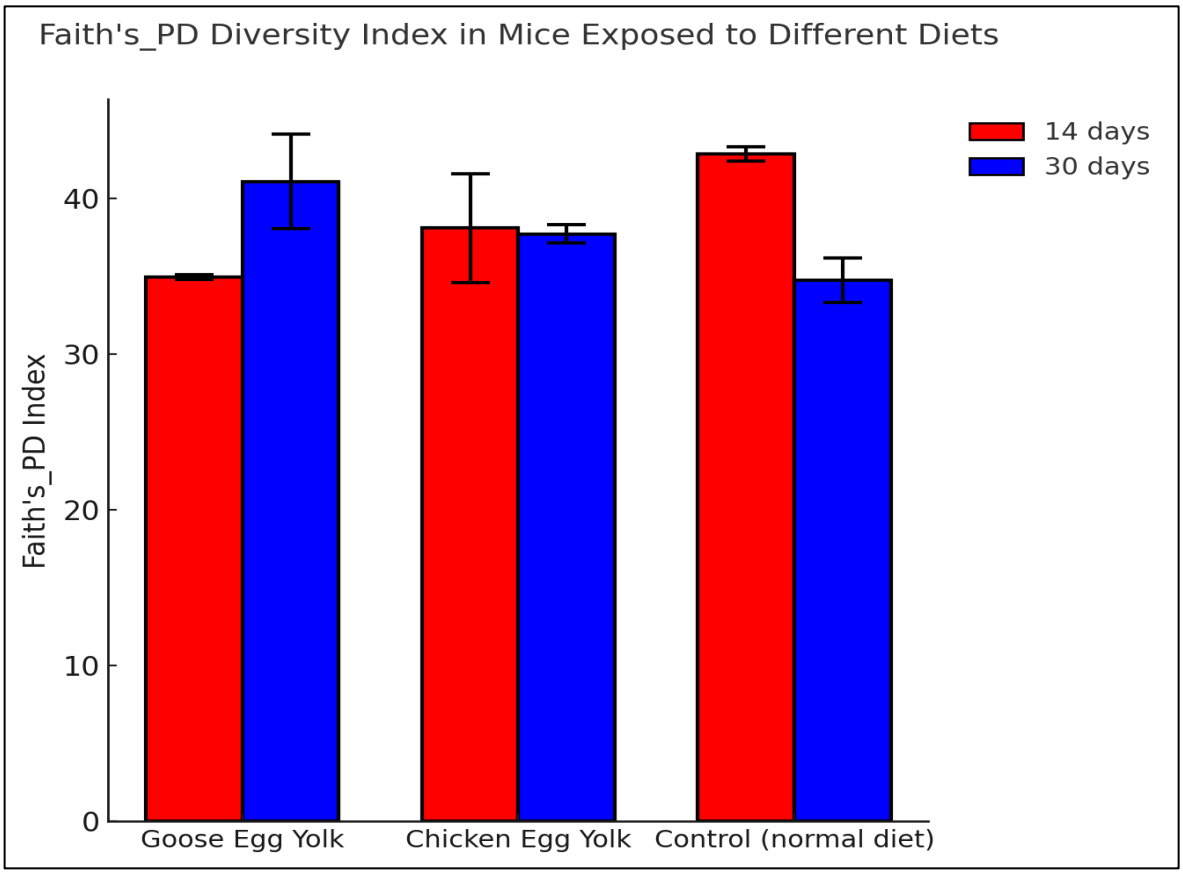


Figure 4-33: Faith's Phylogenetic Diversity (PD) index of mice is presented and described based on diets of goose egg yolk, chicken egg yolk, and control for the ages of 14 and 30 days.

4.2.1. 4 Simpson Diversity Index :

The chicken egg yolk group had the highest Simpson index at 14 days at about 0.38–0.40, whereas the goose egg yolk and control groups had only about 0.05–0.06. The Simpson index for the chicken egg yolk group at 30 days had an even larger decline than that at 14 days at about 0.07. The goose egg yolk group had an even smaller decline than the chicken egg yolk group to about 0.04, and the control group decreased to around 0.03–0.04. To summarize, the chicken egg yolk group had the highest index at 14 days of 30 days Figure 4-34 demonstrates a significant decrease.

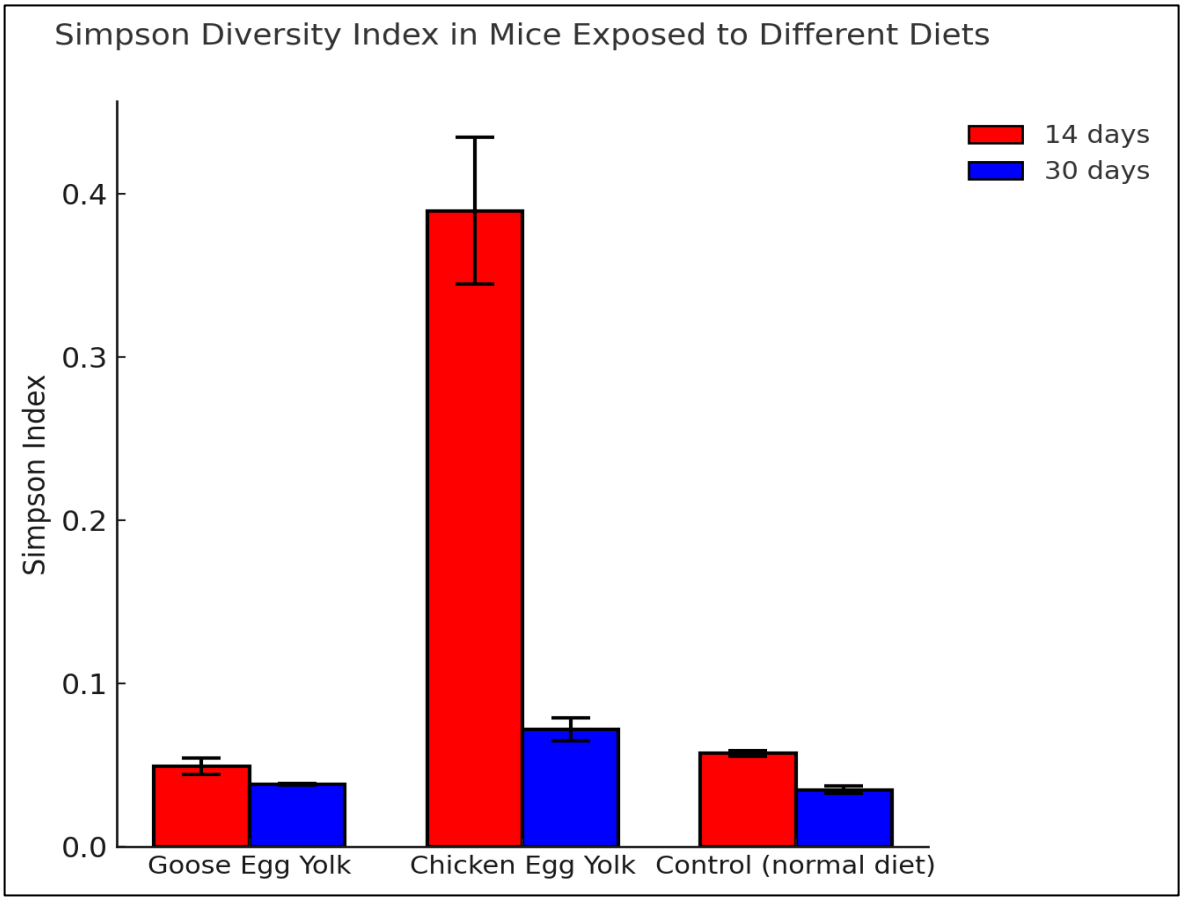


Figure 4-34: Simpson diversity index for the mice fed diets of goose egg and chicken egg yolk as well as control diets for 14 days and 30 days.

4.2.2. Beta diversity

4.2.2.1 Distance matrix

Analysis of beta diversity conducted in this study using the Bray-Curtis method of dissimilarity and represented through Principal Coordinate Analysis (PCoA) showed that the microbial community of mice on goose egg yolk diet changed significantly ($p<0.05$) at day 14 post dietary commencement) relative to both the control and chicken-yolk groups. This change suggests that there was a marked difference in the microbial composition between the dietary treatments at an early stage. However, after 30 days of feeding, the community clustering pattern showed a significant ($p < 0.05$) increase in dissimilarity suggesting that the microbial composition converged closer to the other groups. Thus, the pattern of beta diversity appeared to demonstrate extremely dissimilar values at early stages, followed by convergence at later stages. In this regard, the day 14 data represented the period of greatest variation between groups, and the day 30 data represented a period of compositional stabilization of the gut community Distinct clustering was noted at 14 days ($p < 0.05$), which was reduced significantly ($p < 0.05$) at 30 days, indicating a decrease in inter-group dissimilarity over time, (Figure 4-35).

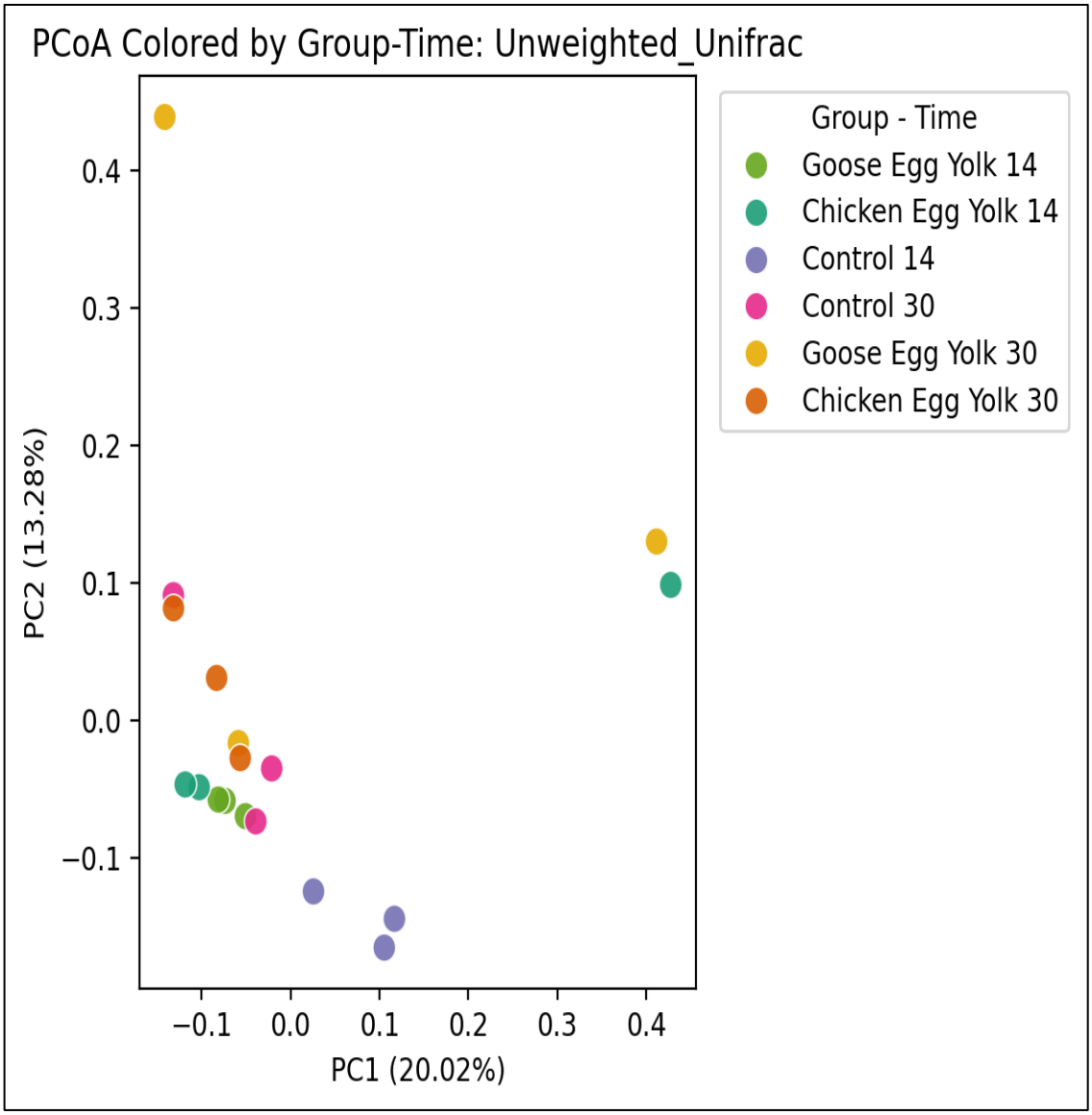


Figure 4-35: Beta diversity analysis based on Bray–Curtis dissimilarity. Bray–Curtis dissimilarity PCoA plot of the gut microbiota from control, chicken-yolk, and goose-yolk groups..

4-3: ELISA:

4-3-1: Concentration of IL-6 in serum

The concentration of serum IL-6 (pg/ML, mean ± SD) was recorded on 14 (day 14) and 30 (day 30) with regard to specific time and diet-related variations. Day 14 had the control group at 85 ± 62, goose egg yolk group at 310 ± 95, and chicken egg yolk group at 190 ± 80. Day 30 had the control group at 210 ± 180, goose yolk group at 150 ± 70, and chicken egg yolk at 410 ± 210. Regarding the goose egg yolk group, higher IL-6 at Day 14 was considered to mean an inflammatory response to the diet, and the chicken egg yolk group was considered to have a marked IL-6 increase at Day 30, and therefore a diet-related inflammation that was delayed or sustained, whereas the control group was considered to have a slight and somewhat random IL-6 response to the diet over time (Fig. 4-36).

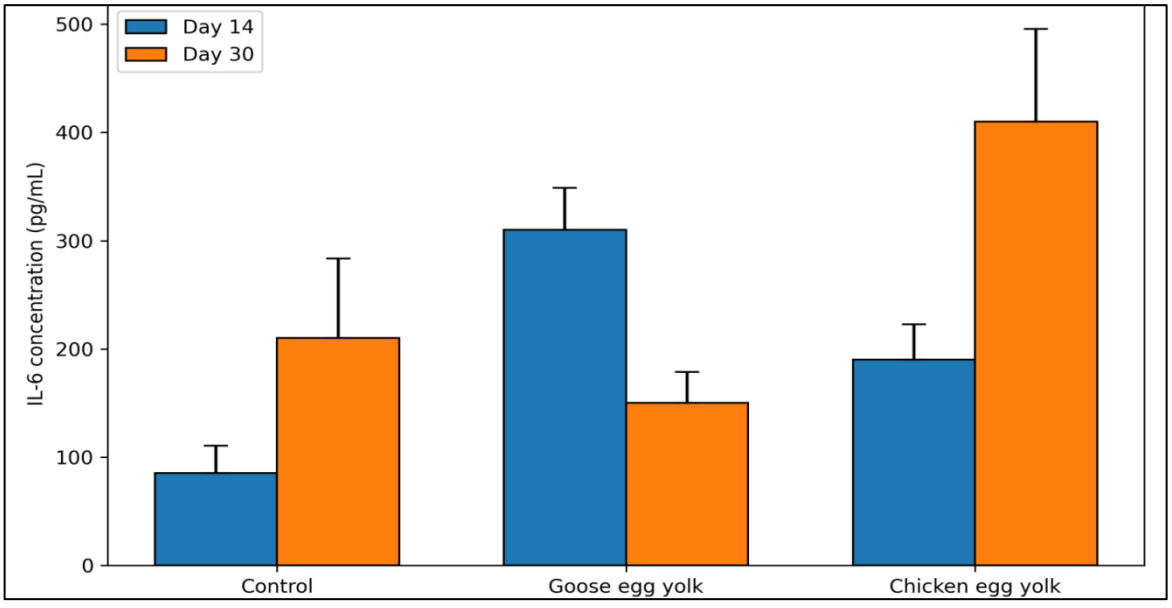


Figure 4-36. Serum interleukin-6 (IL-6) concentrations in mice fed control, goose egg yolk, or chicken egg yolk diets. Blood samples were collected on days 14 and 30. Bars represent mean ± SE (n = 6).

4-3- 2 Concentration of IL-1 in serum

IL-10 in serum (pg/ml, mean ± SD) on day 14 and day 30 in the study reported an overall increase with time across all groups, with the chicken egg yolk group recording the highest value on day 30. On day 14, the control group was 260 ± 90, the goose egg yolk group was 360 ± 110, and the chicken egg yolk group was 310 ± 100. On day 30, the control group was 340 ± 120, the goose egg yolk group was 290 ± 130, and the chicken egg yolk group was 460 ± 150. In the provided interpretation, IL-10 was described as increasing with time across all groups, and with the chicken egg yolk group described as showing the highest IL-10 at day 30 indicating a compensatory anti-inflammatory response, while the goose egg yolk group was reported as showing an earlier IL-10 elevation indicating immune modulation (Fig. 4-37).

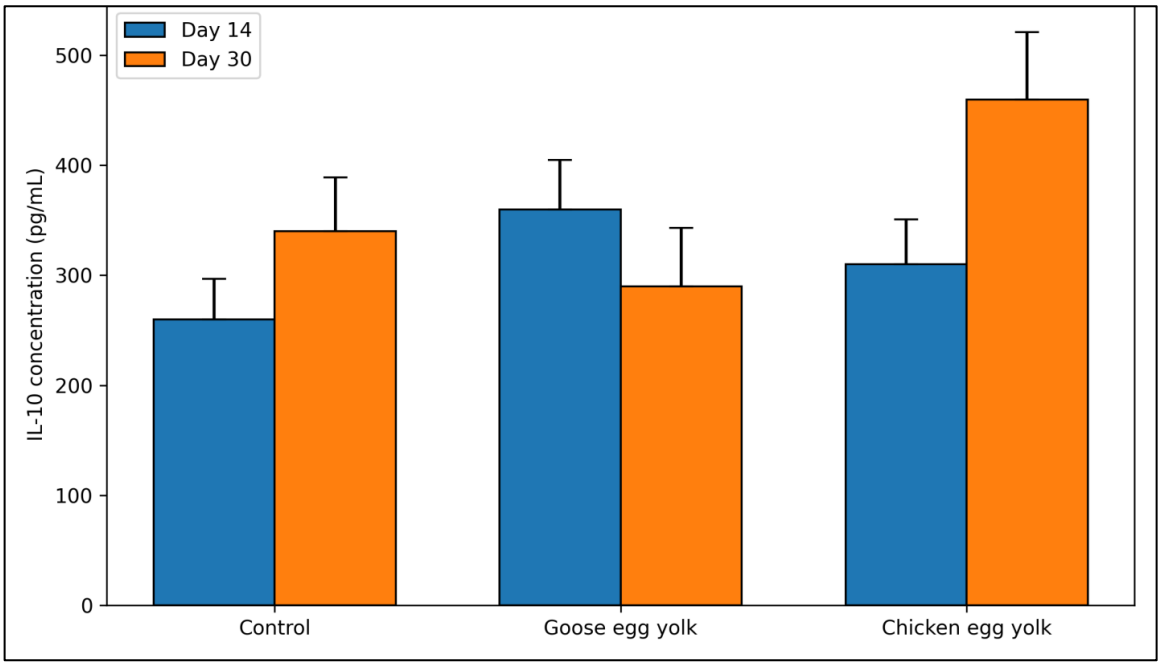


Figure 4-37 . Serum interleukin-10 (IL-10) concentrations in mice fed control, goose egg yolk, or chicken egg yolk diets. Blood samples were collected on days 14 and 30. Bars represent mean ± SE (n = 6).

4.4 : Histomorphometric

4.4.1: Duodenum histomorphometric

All endpoint morphometric illustrated diet-related enlargement of the duodenal villi. Villi length was advanced from 0.4088 mm in the control group to 0.4536 mm in the chicken-yolk group to 0.5183 mm in the goose-yolk group, where control–chicken is recorded as non-significant, and goose-yolk is recorded as significantly greater than chicken-yolk(Fig. 4-38) and greater than control (Fig. 4-38).

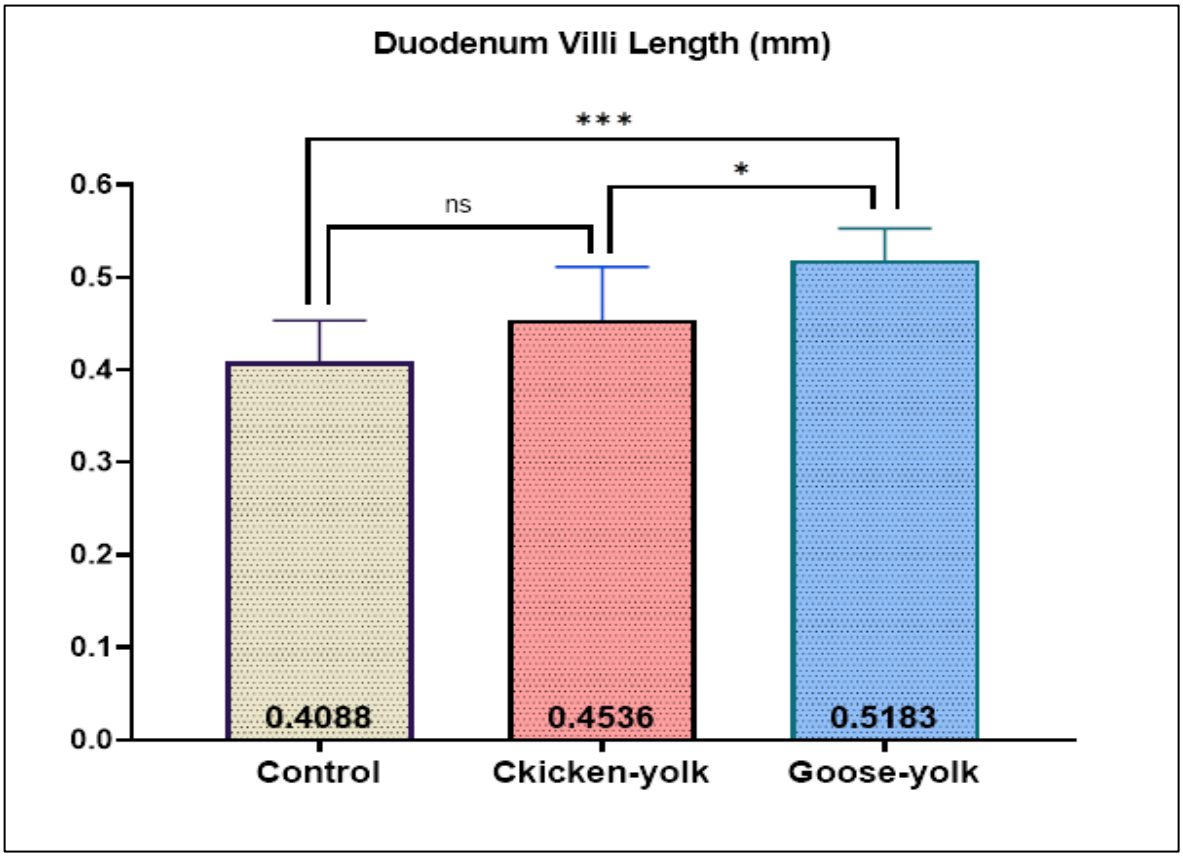


Figure 4-38: illustrates the mean duodenum villi length (mm) measured in the control, chicken yolk, and goose yolk groups.

The control group recorded the smallest mean villi length (0.4088 mm) while the chicken yolk and goose yolk recorded 0.4536 mm and 0.5183 mm respectively with goose yolk showing the highest mean value. The bars show the mean values while the error bars show the mean values and the variability about the mean.

Villi width increased from 0.1098 mm (control) to 0.1451 mm (chicken-yolk) and to 0.1703 mm (goose-yolk), where significance is indicated between control and chicken-yolk (Fig. 4-39) and control and goose-yolk (Fig. 4-39), and where chicken-yolk versus goose-yolk is labeled non-significant.

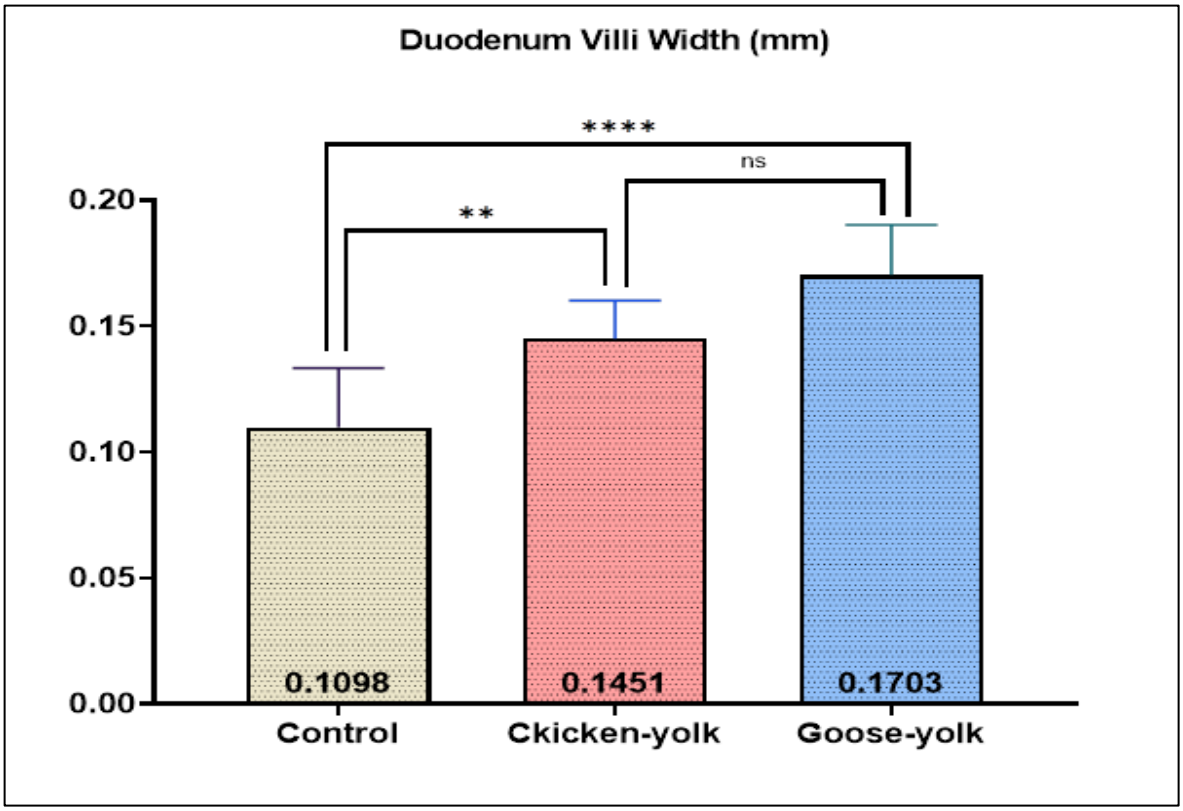


Figure 4-39: Villi width (mm) in the duodenum for control, chicken yolk, and goose yolk groups.

Stepwise increases in villus area from 0.0447 mm² (control) to 0.0659 mm² (chicken-yolk) and to 0.0881 mm² (goose-yolk) demonstrates control vs chicken-yolk (Fig. 4-40) and chicken-yolk vs goose-yolk (Fig. 4-40) significant separations, and control vs goose-yolk (Fig. 4-40) greater separations.

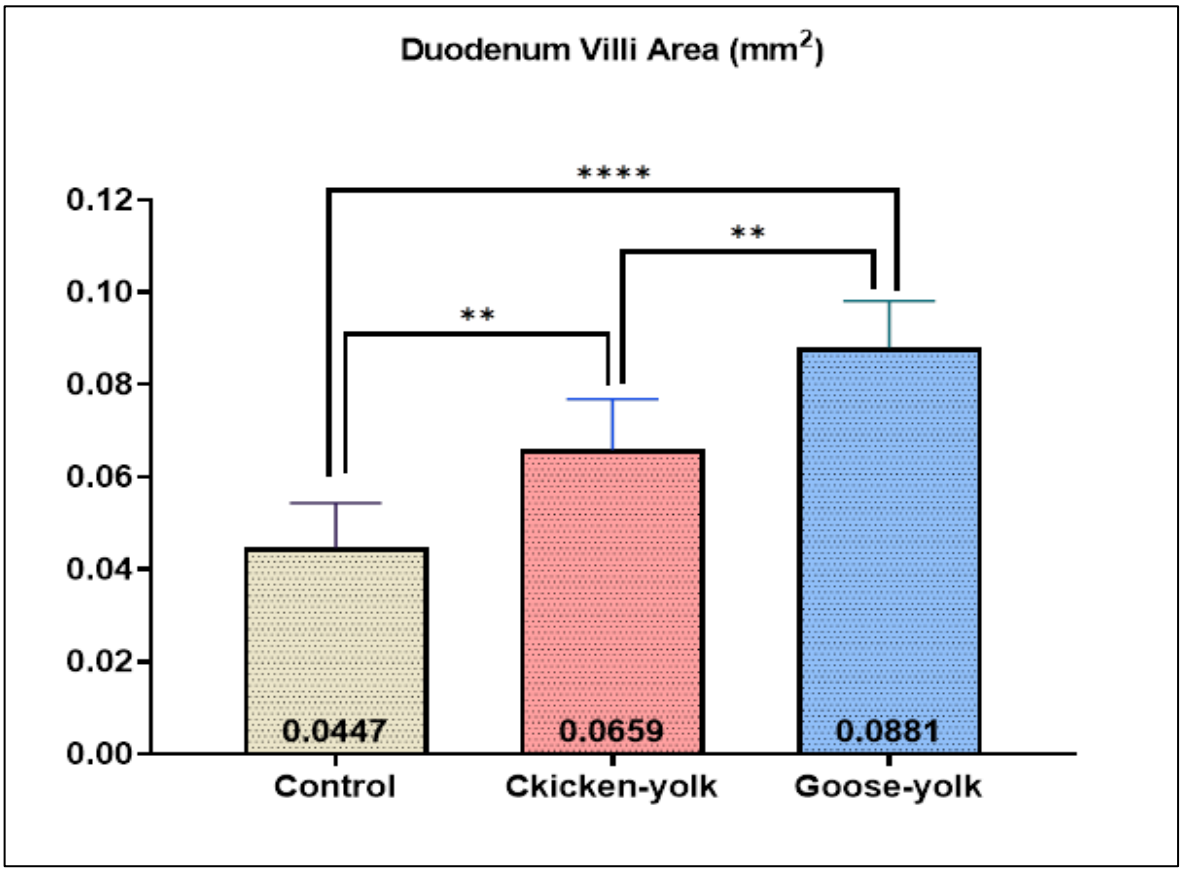


Figure 4-40: Villi area (mm²) in the duodenum for control, chicken yolk, and goose yolk groups.

The mean values are least in the control group and lowest in the average calculation of chicken yolk group with control group reporting 0.0447 mm2 chicken yolk group reporting 0.0659 mm2 and the goose yolk reporting maximum at 0.0881 mm2. The control group had the least mean value of duodenum villi area (mm2) in comparison with chicken yolk and goose yolk

group. The mean value duodenum villi area (mm2) of control group, chicken yolk group and goose yolk group increase progressively. The goose yolk group had the maximum variability around the mean values.

Increased crypt depth was also recorded from 0.1913 mm (control) to 0.2315 mm (chicken-yolk) to 0.2982 mm (goose-yolk), where chicken-yolk vs control is non-significant, but goose-yolk versus chicken-yolk (Fig. 4-41) and goose-yolk versus control (Fig. 4-41) are significant.

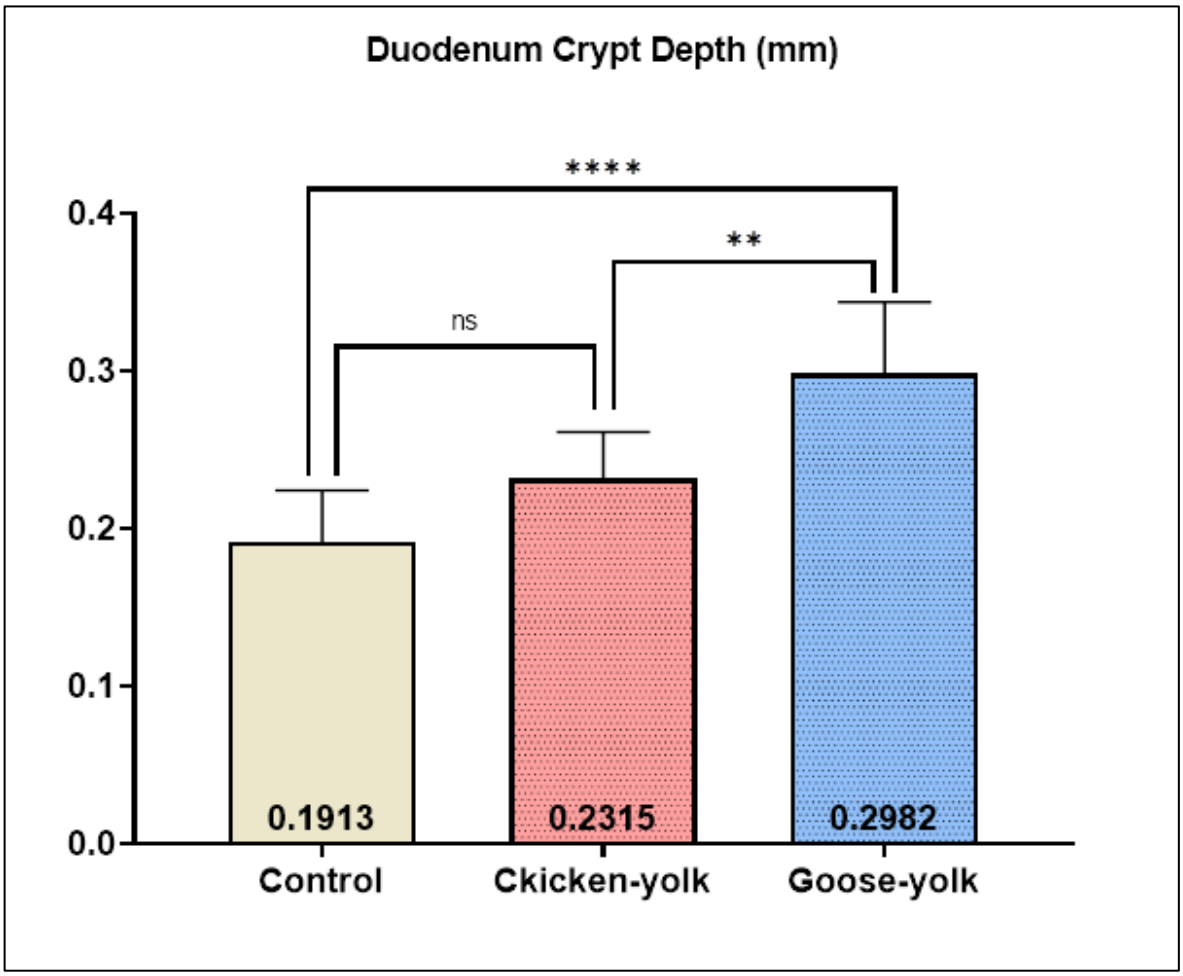


Figure 4-41: Duodenum crypt depth (mm) is shown in control, chicken yolk, and goose yolk groups.

The control group had the least mean crypt depth (0.1913 mm), followed by the chicken yolk group (0.2315 mm), and the goose yolk group had the highest value (0.2982 mm). Error bars show the mean value variability. In all groups, crypt depth increased progressively from control to chicken yolk and finally to goose yolk group, with the highest level noted.

4.4.2: Jejunum histomorphometric

Jejunal villus dimensions illustrated moderate increases, with the strongest statistical support shown for villus width and area as opposed to crypt depth. Villi length increased from 0.3152 mm in the control to 0.3451 mm in chicken-yolk and 0.3866 mm in goose-yolk; comparisons to chicken-yolk were deemed non-significant while control vs. goose-yolk was deemed significant (Fig.4-42).

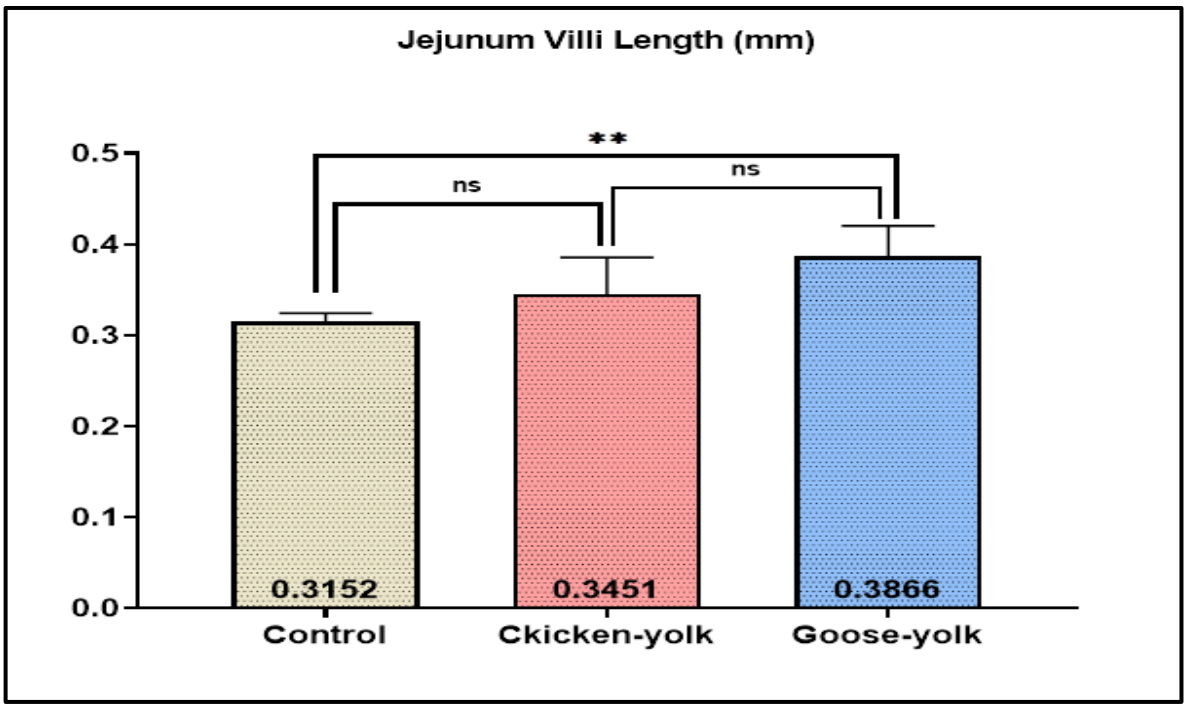


Figure 4-42: Jejunum villi lengths (in mm) are compared across the control, chicken yolk, and goose yolk groups.

The control group had the smallest mean villi length (0.3152 mm) and in the chicken yolk group the mean villi length increased slightly to 0.3451 mm. The goose yolk group showed the greatest mean villi length at 0.3866 mm. Error bars show the mean values variability.

Villi width increased from 0.0785 mm (control) to 0.1090 mm (chicken-yolk) and 0.1225 mm (goose-yolk) with a significant difference noted between control and chicken-yolk and between control and goose-yolk, while the difference between chicken-yolk and goose-yolk was marked non-significant (Fig.4-43).

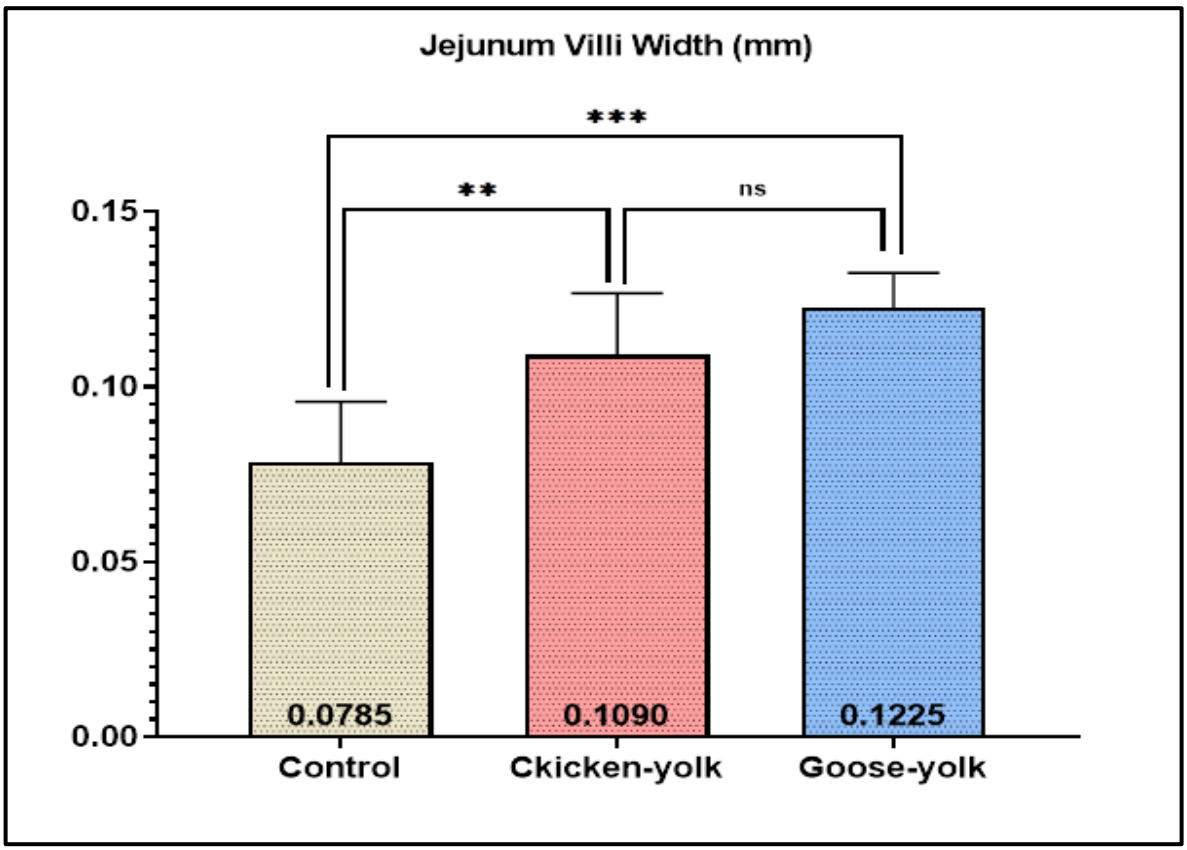


Figure 4-43: Jejunum villi width (mm) in control, chicken yolk, and goose yolk groups is presented.

Control group had the smallest mean villi width (0.0785 mm) and the chicken yolk group had a greater mean (0.1090 mm) while the goose yolk group had the greatest mean (0.1225 mm). The error bars show the spread around the means. Villi width in the control group, chicken yolk group and goose yolk group are increasing in succession.

For villus area, there was a distinct graded increase from 0.0247 mm² (control) to 0.0372 mm² (chicken-yolk) and 0.0473 mm² (goose-yolk) with strong control vs. chicken-yolk significance and chicken-yolk vs goose-yolk significance, and the strongest control vs. goose-yolk separation (Fig.4-44).

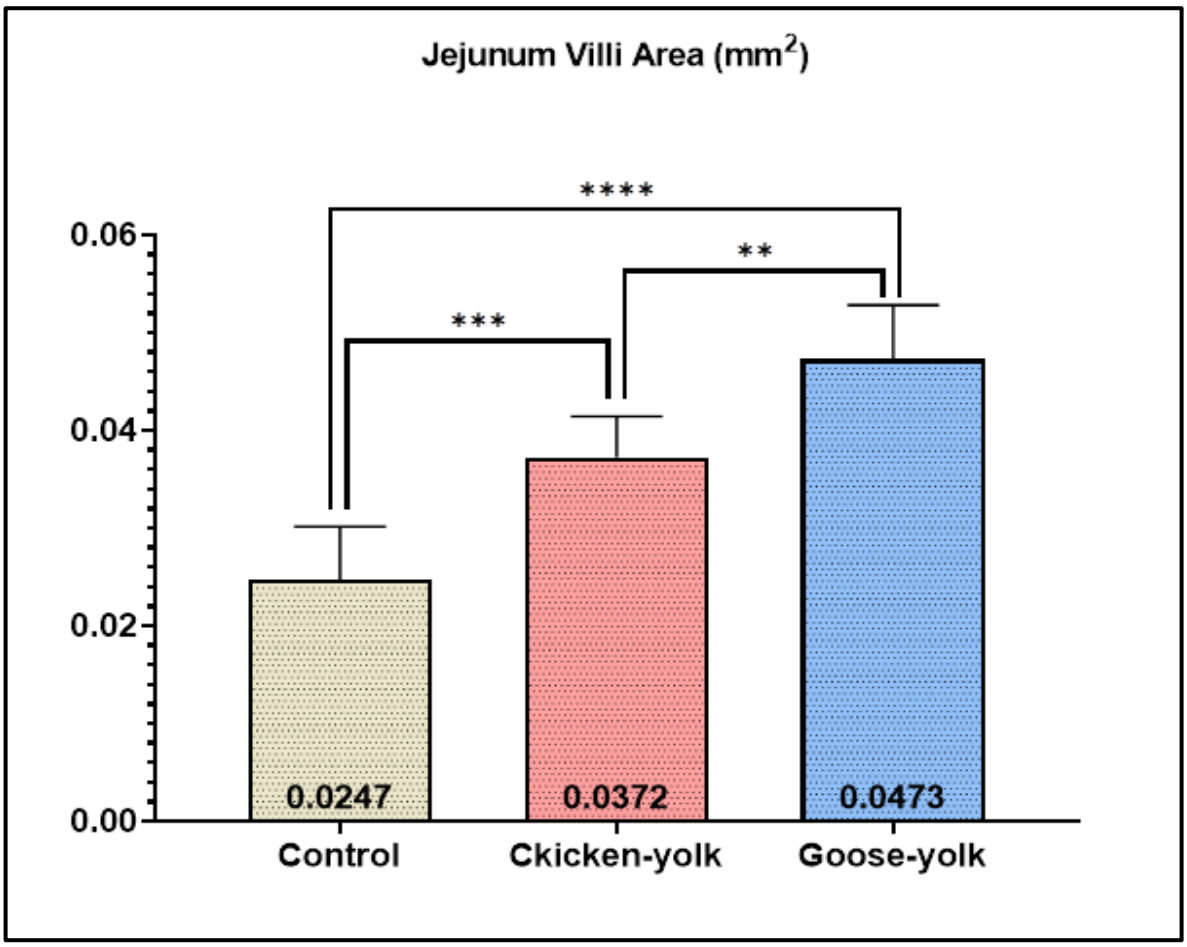


Figure 4-44: The jejunum villi area (mm²) of control, chicken yolk, and goose yolk groups is shown in Figure 4-44.

The mean villi area value is the lowest in the control group (0.0247 mm²), then in the chicken yolk group (0.0372 mm²) and is the highest in the goose yolk group (0.0473 mm²). The error bars show the variability of the mean values.

Conversely, the increase in crypt depth from 0.1452 mm (control) to 0.1618 mm (chicken-yolk) and 0.1747 mm (goose-yolk) was slight and non-significant across all pairwise comparisons, indicating that main jejunal response was focused in villus rather than crypt expansion (Fig.4-45)

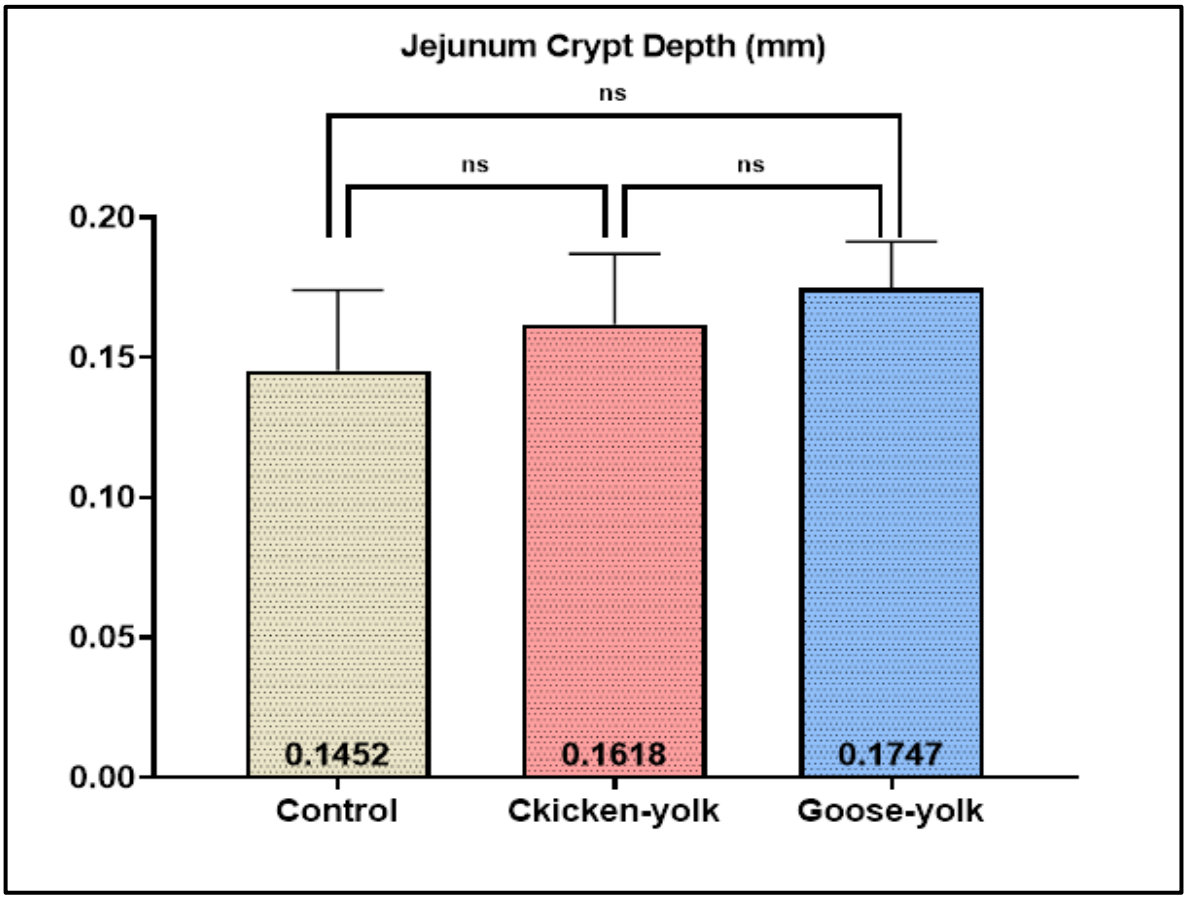


Figure 4-45: The jejunum Mean crypt depth (mm) of control, chicken yolk, and goose yolk groups .

Mean crypt depth was least in the control group (0.1452 mm), then increased in the chicken yolk group (0.1618 mm), and further increased in the goose yolk group (0.1747 mm).

4.4.3: Ileum histomorphometric

Some remodeling was noted in the ileum, but it was more selective, with significant changes noted for villus length, villus area, and crypt depth while villus width was not statistically significant. In controls, the average length of the villi was 0.2365 mm, which increased to 0.2841 mm in chicken-yolk, and 0.3082 mm in goose-yolk, showing a significant increase for chicken-yolk vs controls, and goose-yolk vs controls, while chicken-yolk vs goose-yolk was marked non-significant (Fig.4-46).

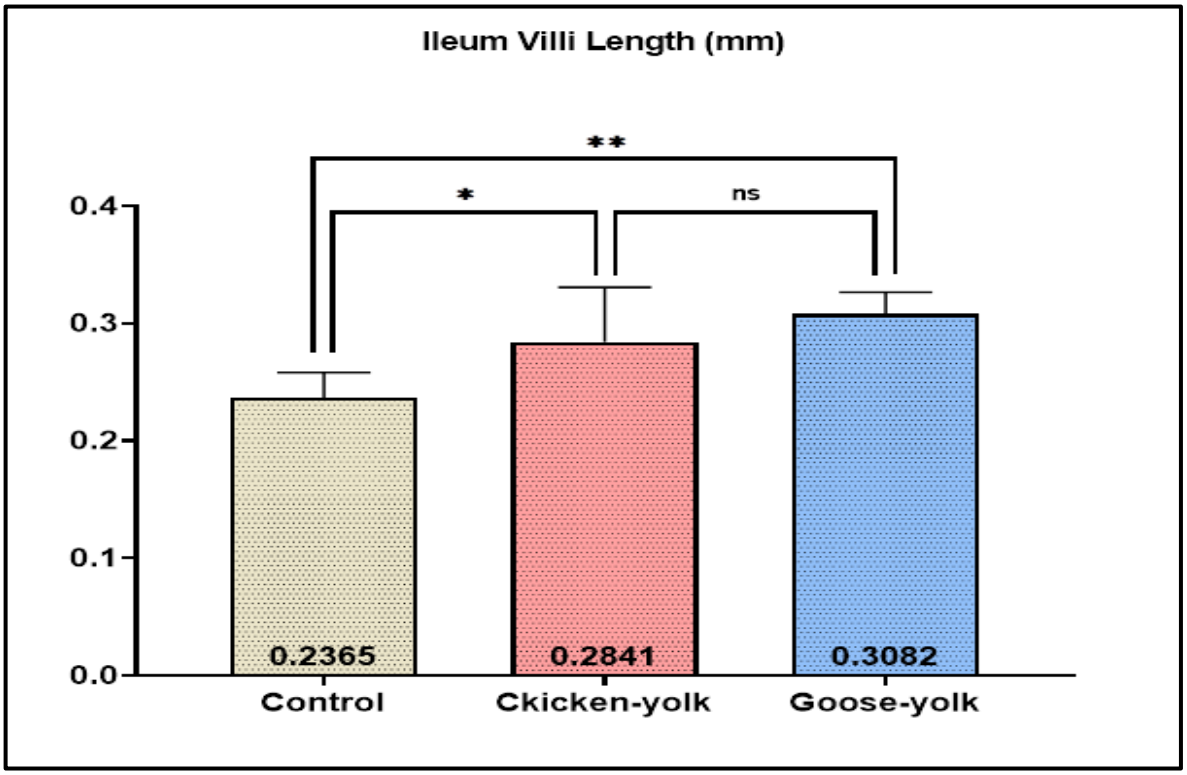


Figure 4-46: Villi length (mm) in the ileum for control, chicken yolk, and goose yolk groups.

The error bars show the variability about the mean values. The data shows an incremental improvement in ileum villi length from control to chicken yolk and then to goose yolk.

For control vs chicken-yolk and goose-yolk, villi width changed only slightly from 0.0781 mm to 0.0858 mm and 0.0932 mm, and all comparisons were labeled non-significant (Fig.4-46).

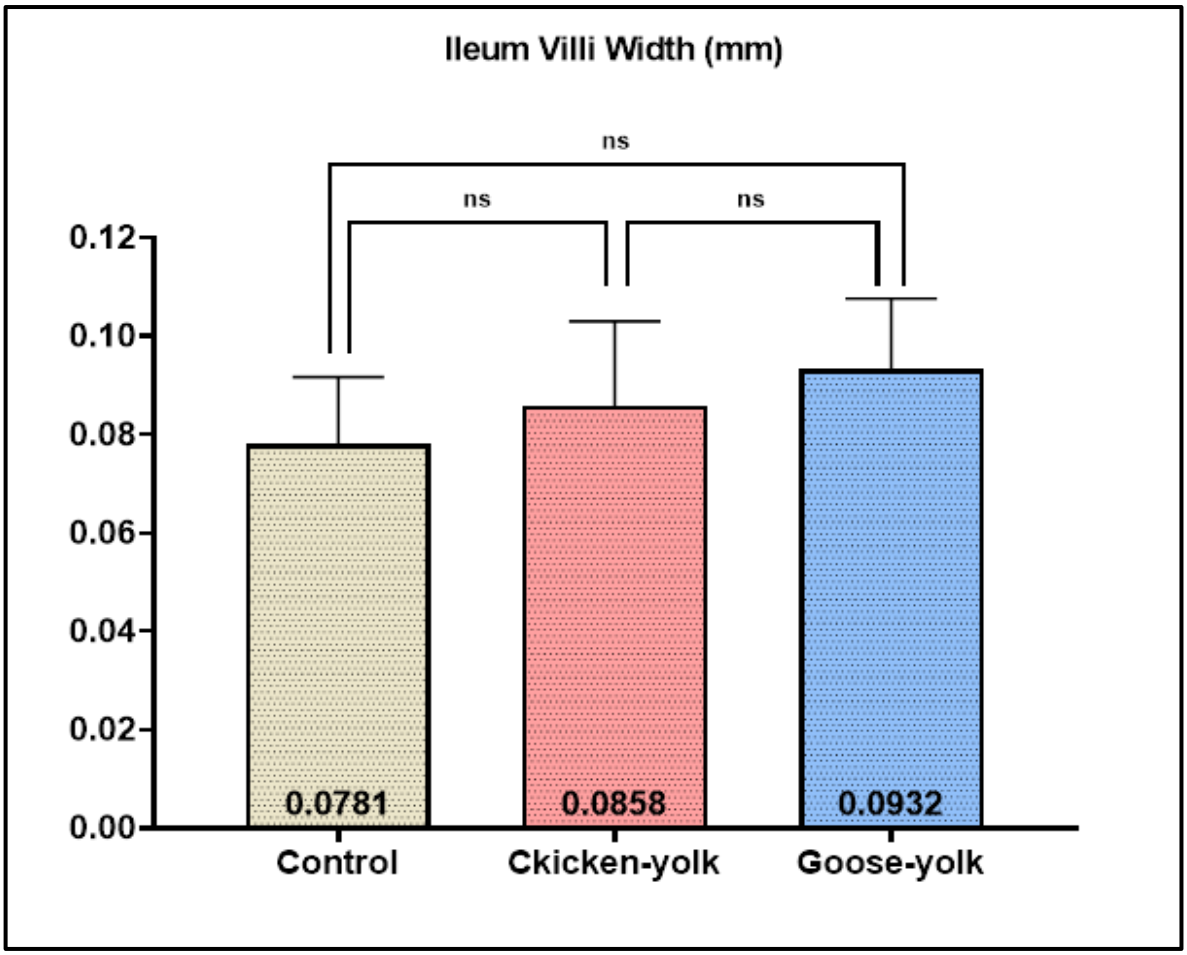


Figure 4-47: Ileum villi width (mm) across the control, chicken yolk, and goose yolk groups.

Mean villi width in control group was 0.0781 mm, which increased to 0.0858 mm in the chicken yolk group and reached the highest at 0.0932 mm

in the goose yolk group. The error bars show the spread of the data around the mean. These data show an increase of ileum villi width from control, chicken yolk to goose yolk groups.

The area of the control villi versus chicken-yolk and goose-yolk increased from 0.0185 mm² to 0.0244 mm² and 0.0287 mm², showing significance for control vs chicken-yolk and for control vs goose-yolk, but not between chicken-yolk and goose-yolk (Fig.4-48).

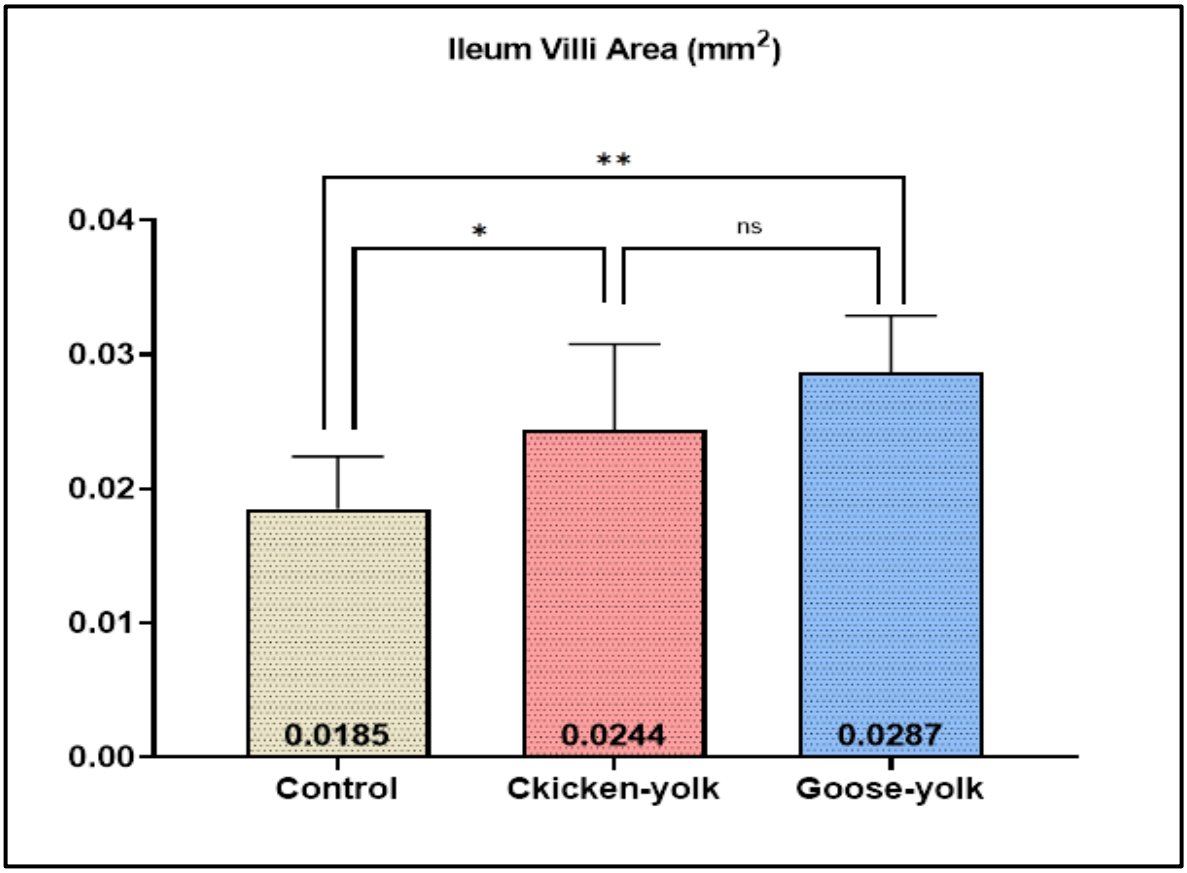


Figure 4-48: Villi area (mm²) of the ileum for control, chicken yolk and goose yolk groups.

The control group had the smallest mean villi area (0.0185 mm²), while the chicken yolk group had a mean of 0.0244 mm² and the goose yolk group had the largest mean of 0.0287 mm². The error bars show the range of the data

compared to the mean. The figure shows that the yolk groups have progressively greater mean villi areas than the control group.

The depth of the controls' crypts increased from 0.0802 mm to 0.1052 mm in chicken-yolk and 0.1202 mm in goose-yolk, with control vs chicken-yolk marked significant, and control vs goose-yolk marked significant, while chicken-yolk vs goose-yolk was labeled non-significant. (Fig. 4-49).

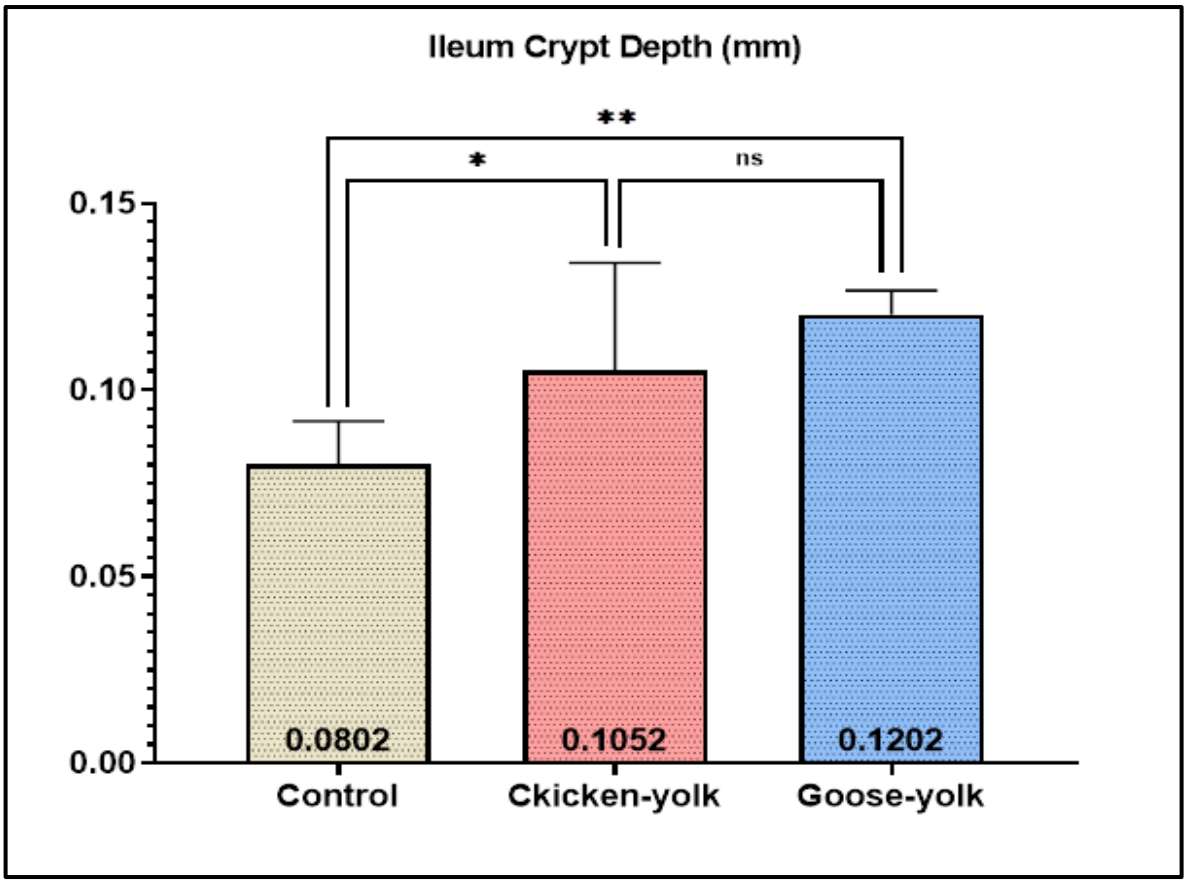


Figure 4-49: Crypt depth of the ileum (in mm) for the control, chicken yolk, and goose yolk groups.

The control group's mean was the lowest at 0.0802 mm, then increased to 0.1052 mm in the chicken yolk group, and then reached its highest at 0.1202 mm in the goose yolk group.

4.5: Photomicrograph:

4.5.1: H&E histology of the duodenum

All groups exhibited normal organization of the duodenum mucosa, but measurable increases of the duodenum villi and crypts were noted in the yolk-fed groups and were consistent with morphometrics plotted. In the control group, well-structured villi and crypts were noted, with villus height measuring 0.410 mm, villus area measuring 0.045 mm^2, and crypt depth measuring 0.190 mm (Fig.4-50). In the chicken-yolk group, similar architecture was noted, however, the villi were taller and wider, with mean values of villus height at 0.450 mm, crypt depth at 0.230 mm, and villus area at 0.065 mm^2 (Fig.4-51). In the goose-yolk group, the same architecture was noted, but with greatest increase in villus height at 0.520 mm, crypt depth at 0.300 mm, and villus area at 0.088 mm^2 (Fig.4-52). This group exhibited greatest trophic response.

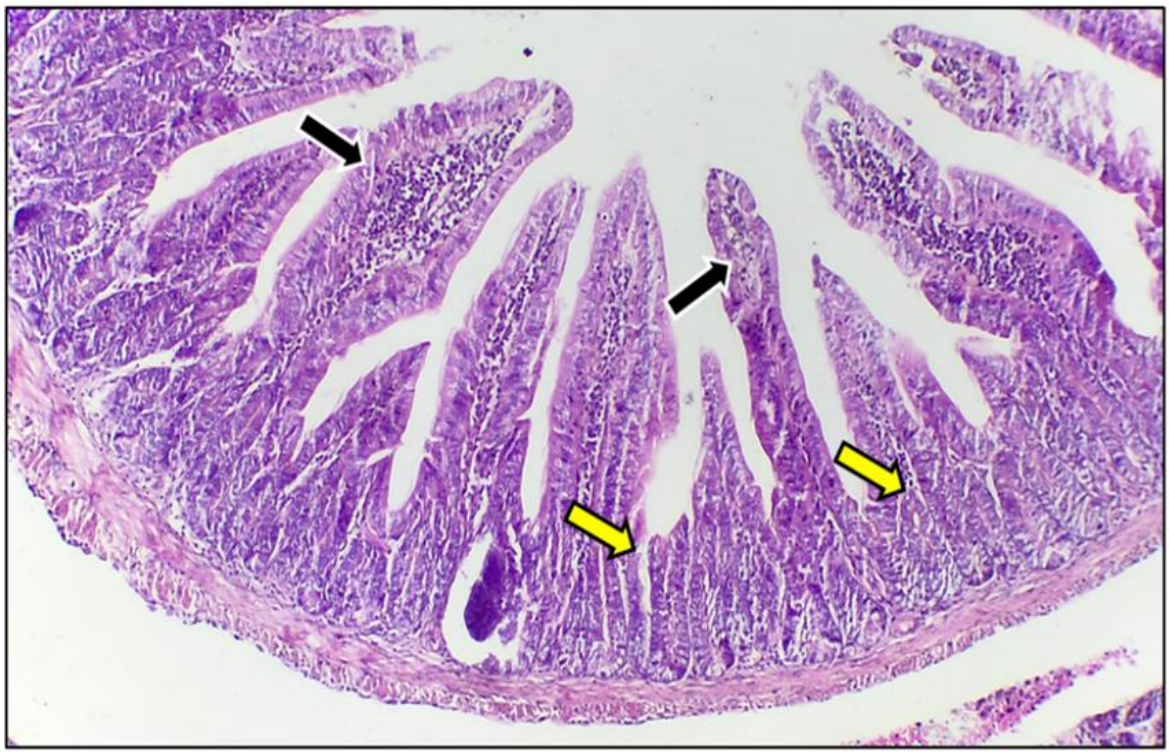


Figure. 4-50: Photomicrograph of Duodenum of control group mouse. Normal histological architecture of the Duodenum was preserved. Well-formed villi (black arrows) were observed, with a mean length of approximately 0.410 mm and a mean villus area of about 0.045 mm². The depth of the Crypts of Lieberkühn (yellow arrows) was approximately 0.190 mm. **H&E. 100x.**



Figure .4-51: Photomicrograph of Duodenum of Chicken-yolk group mouse. Normal histological architecture of the Duodenum was preserved. Well-formed villi (black arrows) were observed, exhibiting a greater mean length (approximately 0.450 mm) and a larger mean villus area (about 0.065 mm^2) compared with the control group. In addition, the Crypts of Lieberkühn (yellow arrows) were deeper, with a mean depth of approximately 0.230 mm relative to controls. **H&E. 100x**

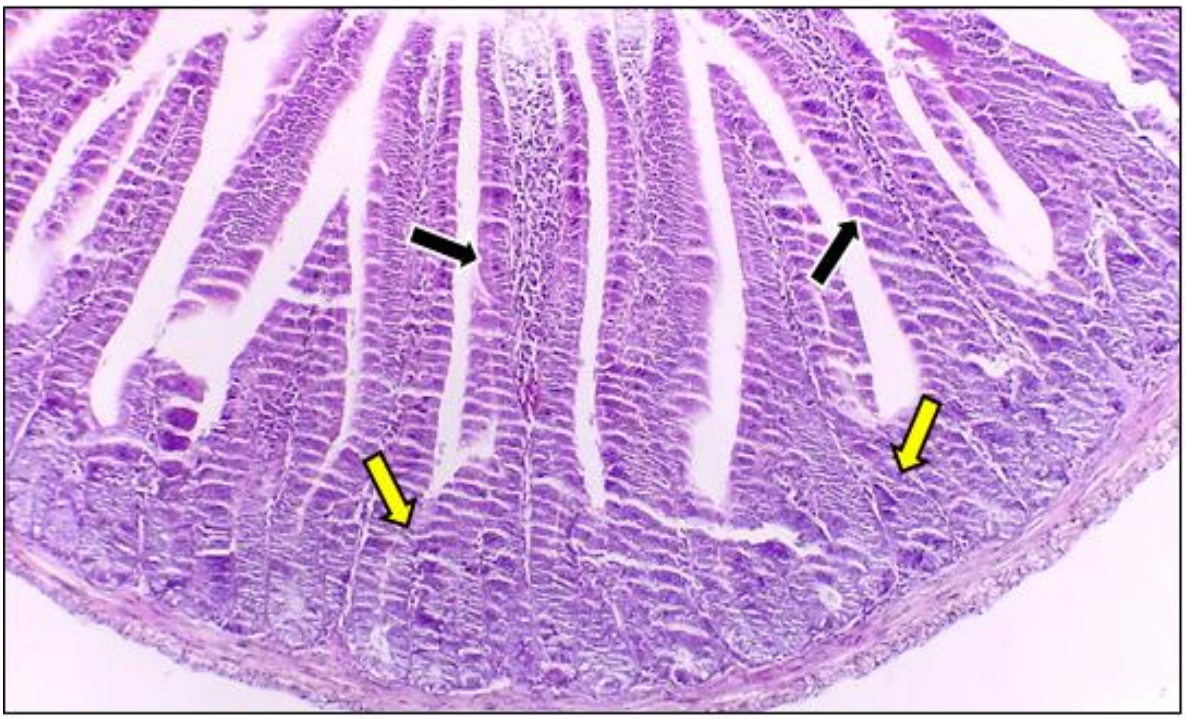


Figure .4-52: Photomicrograph of Duodenum of Goose-yolk group mouse. Normal histological architecture of the Duodenum was preserved. Well-formed villi (black arrows) were observed, exhibiting a greater mean length (approximately 0.520 mm) and a larger mean villus area (about 0.088 mm^2) compared with both the control and chicken-yolk groups. In addition, the Crypts of Lieberkühn (yellow arrows) were deeper, with a mean depth of approximately 0.300 mm relative to both comparison groups. Moreover, villus density increased compared with the control and chicken-yolk groups. **H&E. 100x.**

4-5-2: H&E histology of the jejunum

All groups exhibited the jejunal sections to have normal layering and mucosal continuity, with yolk-fed groups exhibiting increases in villi metrics and comparatively smaller changes in crypt depth. Control jejunum samples exhibited preserved villus alignment and normal crypt organization. Their

measurements averaged 0.315 mm for villus height, 0.024 mm² for villus area, and 0.145 mm for crypt depth, respectively (Fig.4-53). The chicken-yolk group showed similar structural integrity, but their villi were more pronounced, reflecting increased values of 0.350 mm (height), 0.037 mm² (area), and 0.160 mm (crypt depth) (Fig.4-54) . The goose-yolk group had the most developed villi of all the groups, with villus height of 0.386 mm and villus area of 0.047 mm². Only modest increases in crypt depth (0.175 mm), in relation to villus expansion, were recorded in this segment (Fig.4-55).



Figure 4-53: Photomicrograph of Jejunum of control group mouse. Normal histological architecture of the Jejunum was preserved. Well-formed villi (black arrows) were observed, with a mean length of approximately 0.315 mm and a mean villus area of about 0.024 mm². The depth of the Crypts of Lieberkühn (yellow arrows) was approximately 0.145 mm. **H&E. 100x.**

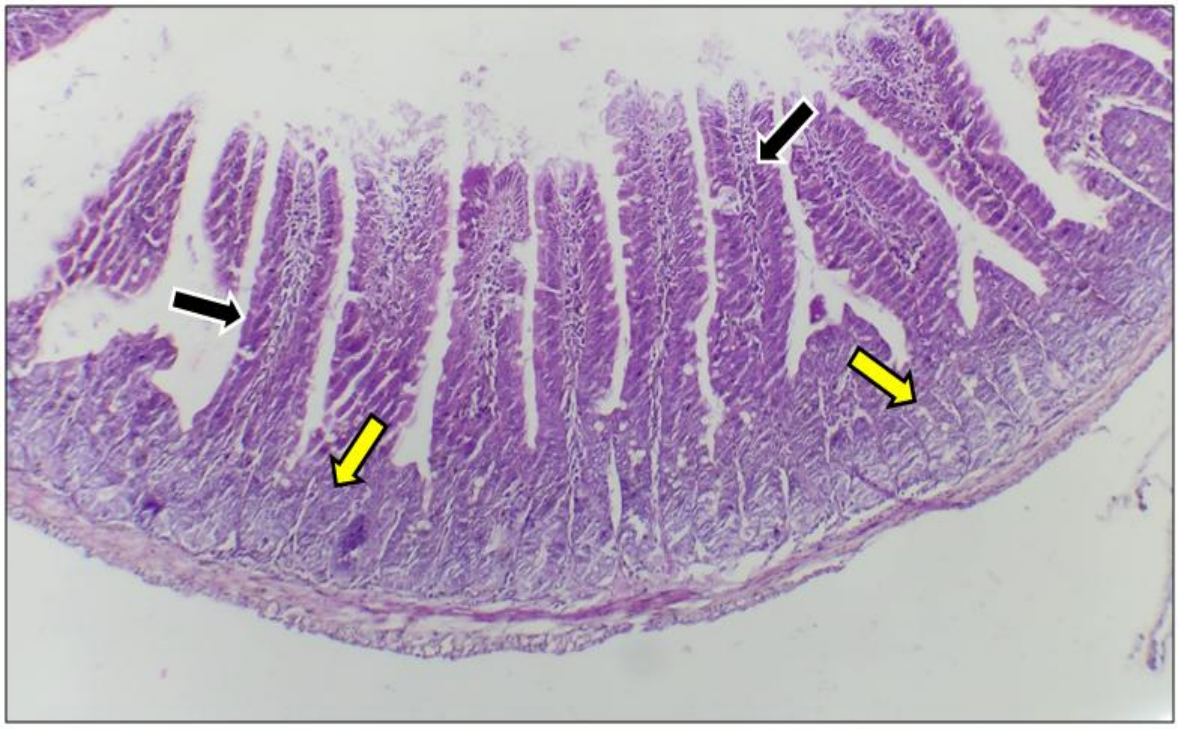


Figure 4-54: Photomicrograph of Jejunum of Chicken-yolk group mouse.

Normal histological architecture of the Jejunum was preserved. Well-formed villi (black arrows) were observed, exhibiting a greater mean length (approximately 0.350 mm) and a larger mean villus area (about 0.037 mm^2) compared with the control group. In addition, the Crypts of Lieberkühn (yellow arrows) were deeper, with a mean depth of approximately 0.160 mm relative to controls. **H&E. 100x.**

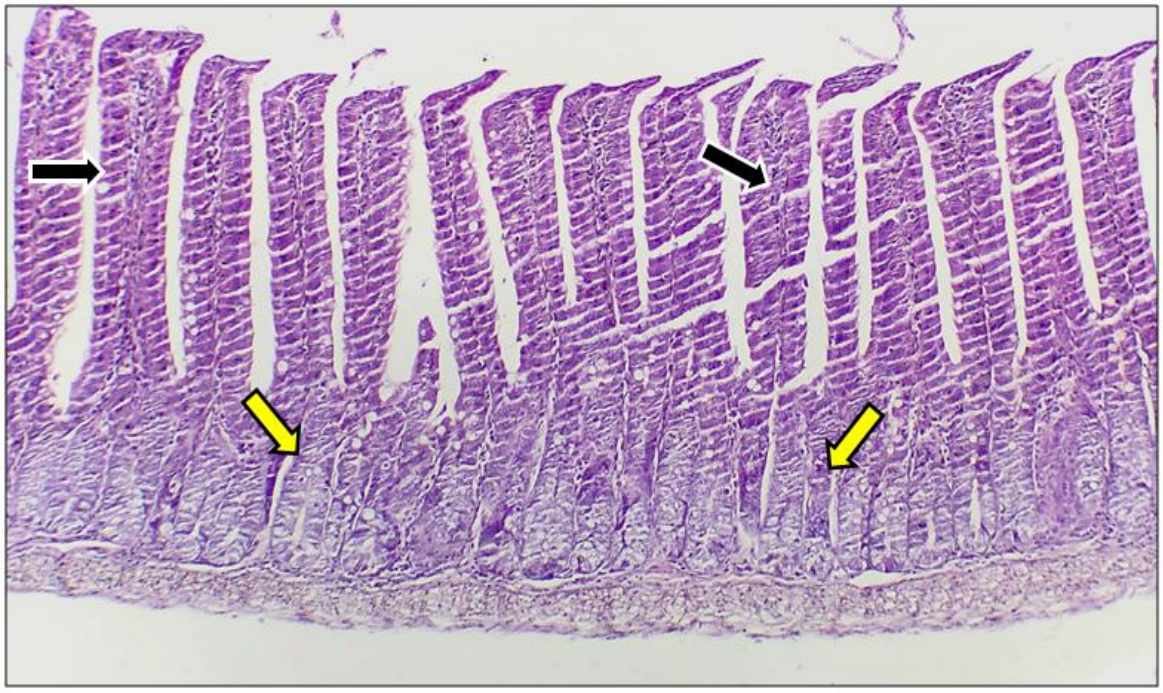


Figure 4-55: Photomicrograph of Jejunum of Goose-yolk group mouse. Normal histological architecture of the Jejunum was preserved. Well-formed villi (black arrows) were observed, exhibiting a greater mean length (approximately 0.386 mm) and a larger mean villus area (about 0.047 mm^2) compared with both the control and chicken-yolk groups. In addition, the Crypts of Lieberkühn (yellow arrows) were deeper, with a mean depth of approximately 0.175 mm relative to both comparison groups. Moreover, villus density was markable increased compared with the control and chicken-yolk groups. **H&E. 100x.**

4.5.3: H&E histology of the ileum :

All groups showed histologically intact ileal mucosa, but increased villus height, villus area, and crypt depth were reported in the yolk-fed groups. In the controls, well-organized sections showed villus height, area, and crypt depth of 0.236 mm, 0.018 mm^2, and 0.080 mm, respectively (Fig.4-56) . For

the chicken-yolk group, data indicated taller villi and a deeper crypt compartment, about 0.284 mm (villus height), 0.024 mm² (villus area), and 0.105 mm (crypt depth) (Fig.4-57) . The highest ileal measurements were recorded in the goose-yolk group with a villus height of about 0.308 mm, a villus area of about 0.028 mm², and a crypt depth of about 0.120 mm (Fig.4-58) . This indicates that the trophic responses reached the distal small intestine, despite the unclear emphasis on the morphometric significance of the changes in villus widths.

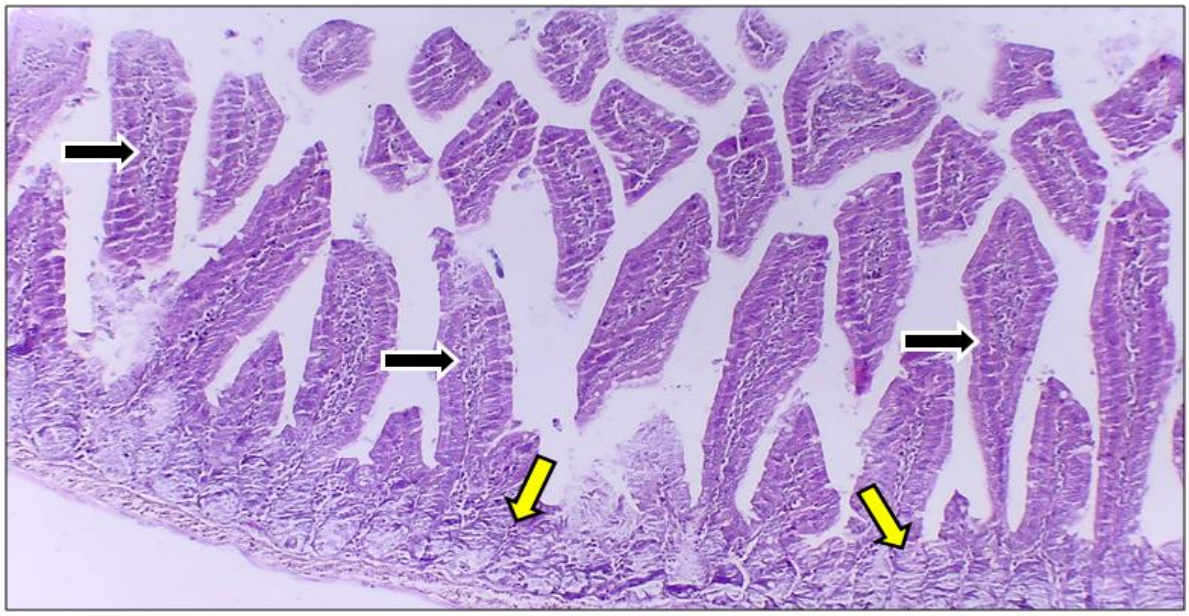


Figure 4-56: Photomicrograph of Ileum of control group mouse. Normal histological architecture of the Ileum was preserved. Well-formed villi (black arrows) were observed, with a mean length of approximately 0.236 mm and a mean villus area of about 0.018 mm². The depth of the Crypts of Lieberkühn (yellow arrows) was approximately 0.080 mm. **H&E. 100x.**

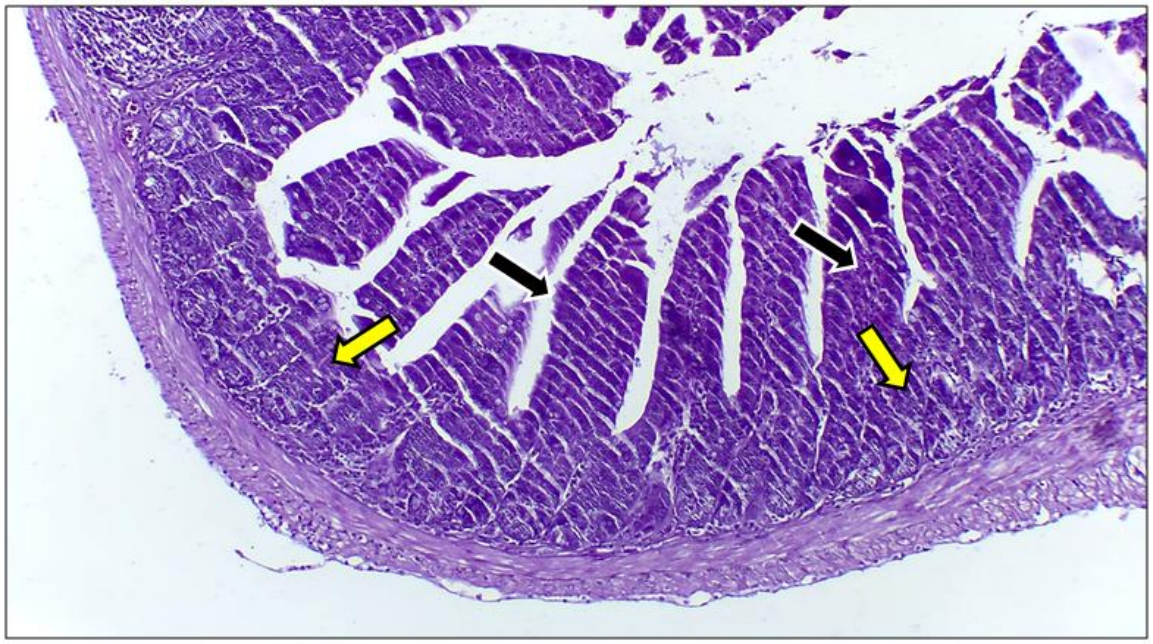


Figure 4-57: Photomicrograph of Ileum of Chicken-yolk group mouse. Normal histological architecture of the Ileum was preserved. Well-formed villi (black arrows) were observed, exhibiting a greater mean length (approximately 0.284 mm) and a larger mean villus area (about 0.018 mm^2) compared with the control group. In addition, the Crypts of Lieberkühn (yellow arrows) were deeper, with a mean depth of approximately 0.105 mm relative to controls. **H&E. 100x.**

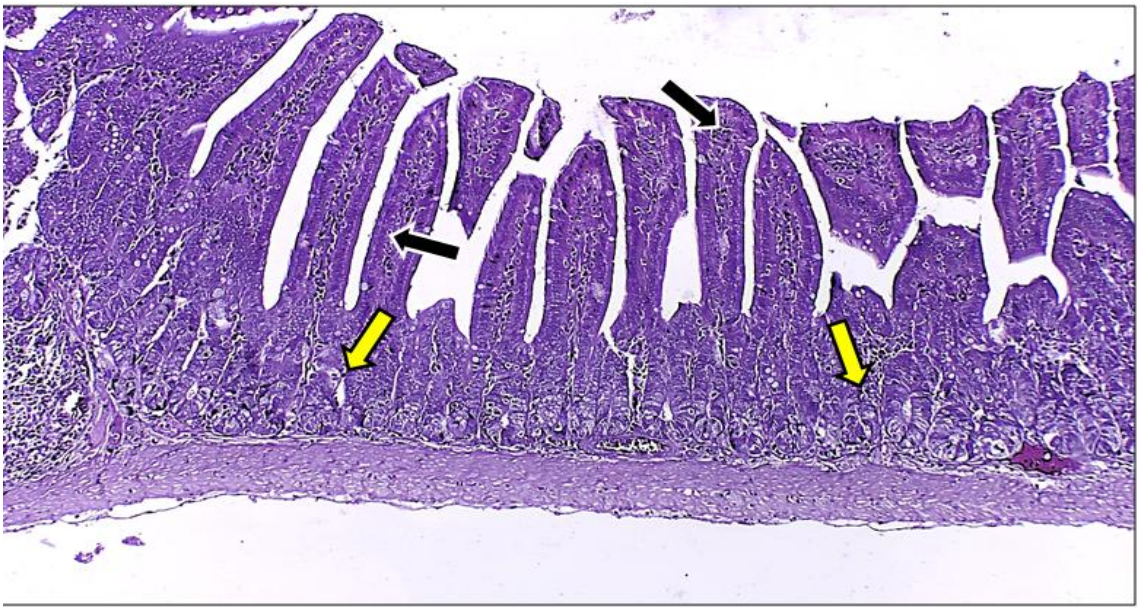


Figure 4-58: Photomicrograph of Ileum of Goose-yolk group mouse. Normal histological architecture of the Ileum was preserved. Well-formed villi (black arrows) were observed, exhibiting a greater mean length (approximately 0.308 mm) and a larger mean villus area (about 0.028 mm^2) compared with both the control and chicken-yolk groups. In addition, the Crypts of Lieberkühn (yellow arrows) were deeper, with a mean depth of approximately 0.120 mm relative to both comparison groups. **H&E. 100x.**

4.5.4: Alcian Blue Staining in Duodenum

All groups showed Acidic Mucin-positive goblet cells of the duodenal region as stained with Alcian Blue, though in yolk groups the density and intensity were observed as increased, with the most notable description for goose-yolk. In control groups, goblet cells in the surface epithelium and crypts were Alcian-positive, creating a baseline for mucin distribution along the villi and openings of the crypts(Fig.4-59) . In the chicken-yolk group, Alcian-positive goblet cells were described as more and the intensity of goblet cells was described as higher, which is consistent with the increased mucin amount in the epithelium(Fig.4-60) .

There was a notable increase in Alcian-positive goblet cells in the goose-yolk group compared to the control and chicken-yolk group. In addition, there was a description of stronger mucin staining across the mucosal surface and crypt regions, indicating an increase in the production of acidic mucin. (Fig. 4-61)



Figure 4-59: Photomicrograph of Duodenum of control group mouse.

A and B: Goblet cells within the surface epithelium and crypts exhibit intense Alcian Blue-positive cytoplasmic staining (black arrow), indicating the presence of acidic mucins. Absorptive enterocytes remain largely unstained with Alcian blue. The lamina propria shows minimal background reactivity. Overall mucosal architecture is preserved, with clearly identifiable villi (in the small intestine) and well-defined crypts of Lieberkühn. **Alcian Blue. A: 100x and B: 400x.**

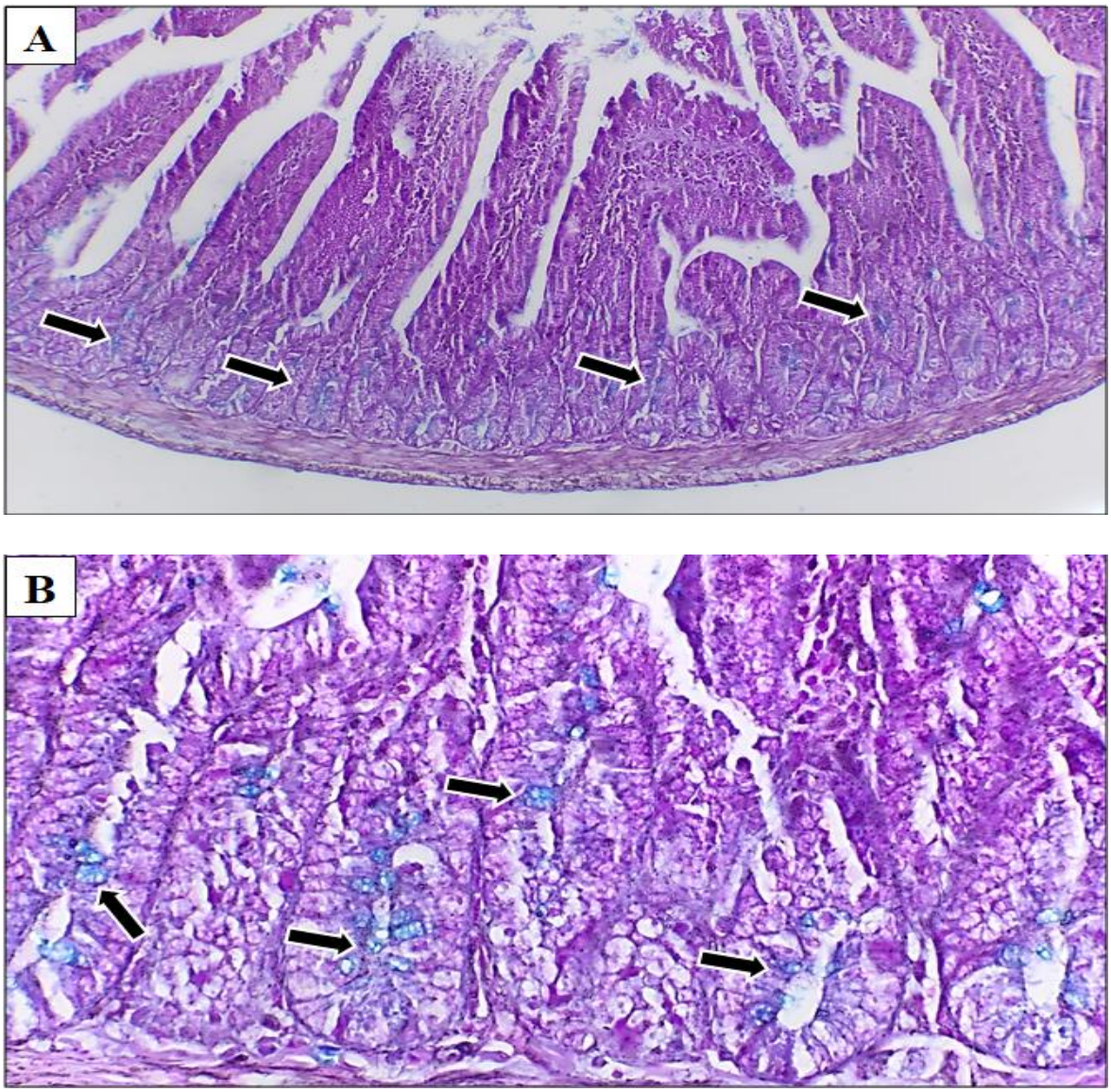


Figure 4-60: Photomicrograph of Duodenum of Chicken-yolk group mouse. A and B: Alcian Blue-positive cytoplasmic staining (black arrow) demonstrates an increased number of positively stained goblet cells and enhanced mucin intensity compared with Control Group. Villous and crypt architecture remains intact. **Alcian Blue. A: 100x and B: 400x.**

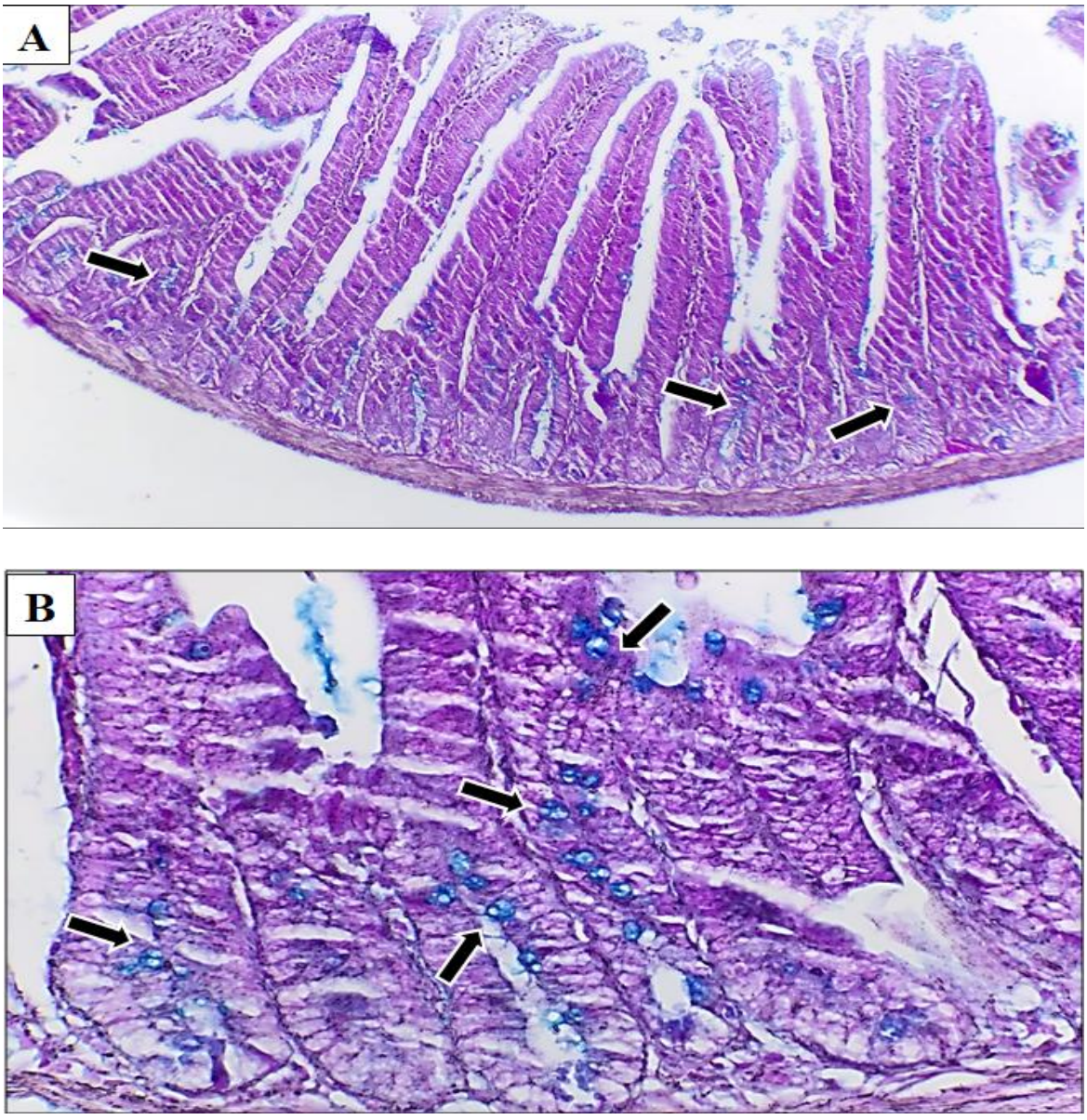


Figure 4-61: Photomicrograph of Duodenum of Goose-yolk group mouse.

A and B: Marked increase in Alcian Blue–positive goblet cells (black arrow) and staining intensity compared with control group, and higher than Chicken-yolk group. Overall mucosal morphology is preserved. **Alcian Blue. A: 100x and B: 400x.**

4.5.5: Alcian Blue Staining in Jejunum

Mucin of goblet cells in the jejunum was demonstrated strongly by Alcian Blue in all of the groups, with yolk-fed groups described to have a greater goblet cell presence and/or stronger staining in the villi and crypt areas. Alcian-positive goblet cells were described in the surface epithelium and crypts of the controls, demonstrating a normal mucin distribution pattern along the mucosa of the jejunum(Fig 4-62) . In the chicken-yolk group, goblet cells were described to be Alcian-positive, with a described increase compared to baseline(Fig 4-63) . In the goose-yolk group, there was a description of intense Alcian positivity, where staining of goblet cells was emphasized in both the villus epithelium and crypts, indicating an overall rise of acidic mucin in relation to yolk feeding (Fig. 4-64) .



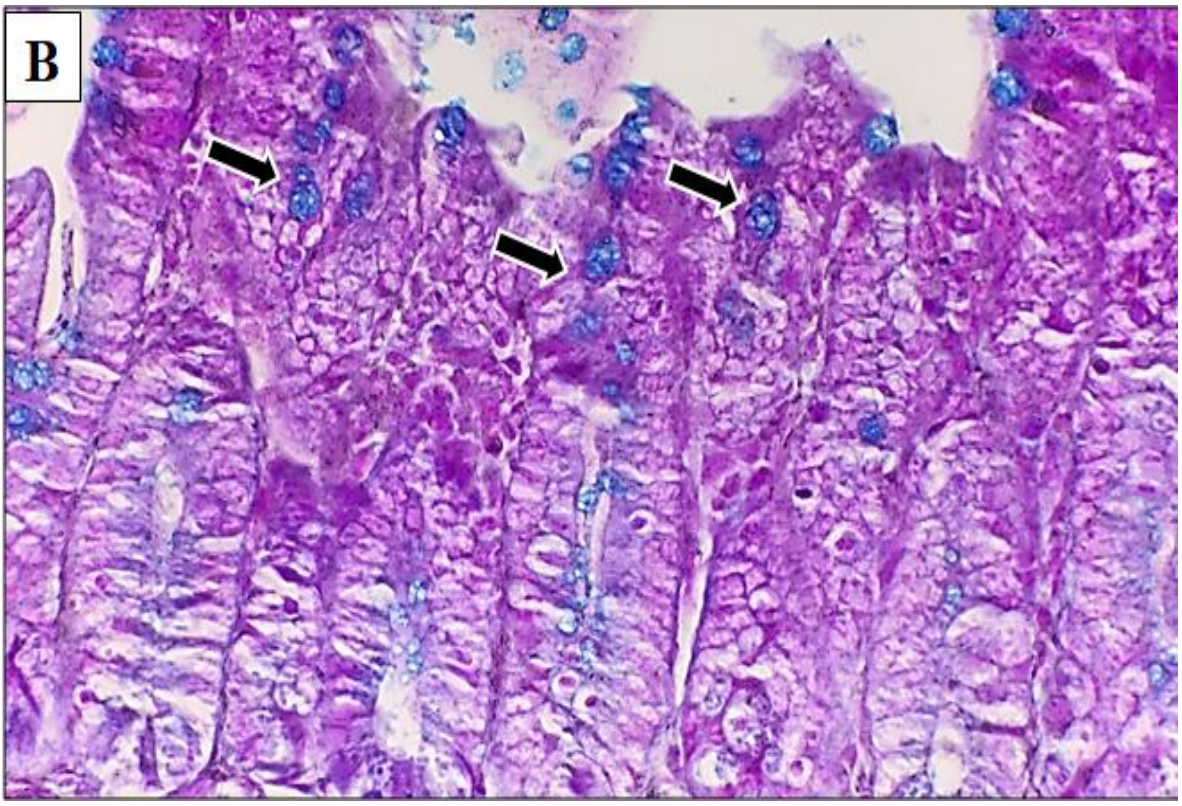


Figure 4-62: Photomicrograph of Jejunum of control group mouse. A and B: Goblet cells within the surface epithelium and crypts exhibit intense Alcian Blue-positive cytoplasmic staining (black arrow), indicating the presence of acidic mucins. Overall mucosal architecture is preserved. **Alcian Blue. A: 100x and B: 400x.**

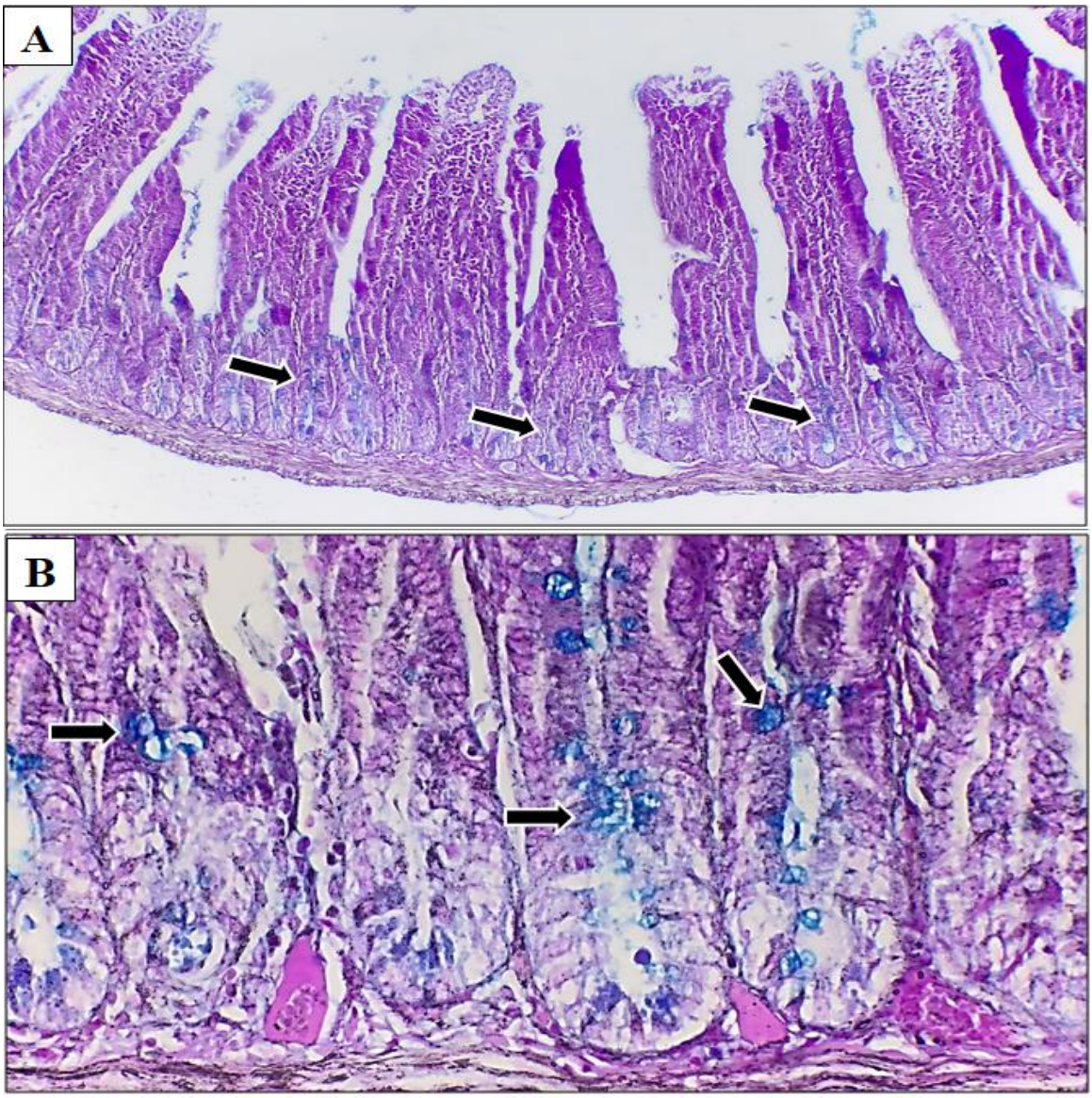


Figure .4-63: Photomicrograph of Jejunum of Chicken-yolk group mouse. A and B: Goblet cells within the surface epithelium and crypts exhibit intense Alcian Blue–positive cytoplasmic staining (black arrow), indicating abundant acidic mucins. The overall mucosal architecture is well preserved. However, the Chicken-yolk group demonstrated a greater density of Alcian Blue–positive goblet cells and stronger mucin staining intensity compared with the control group, suggesting enhanced mucin production and secretory activity. **Alcian Blue. A: 100x and B: 400x.**

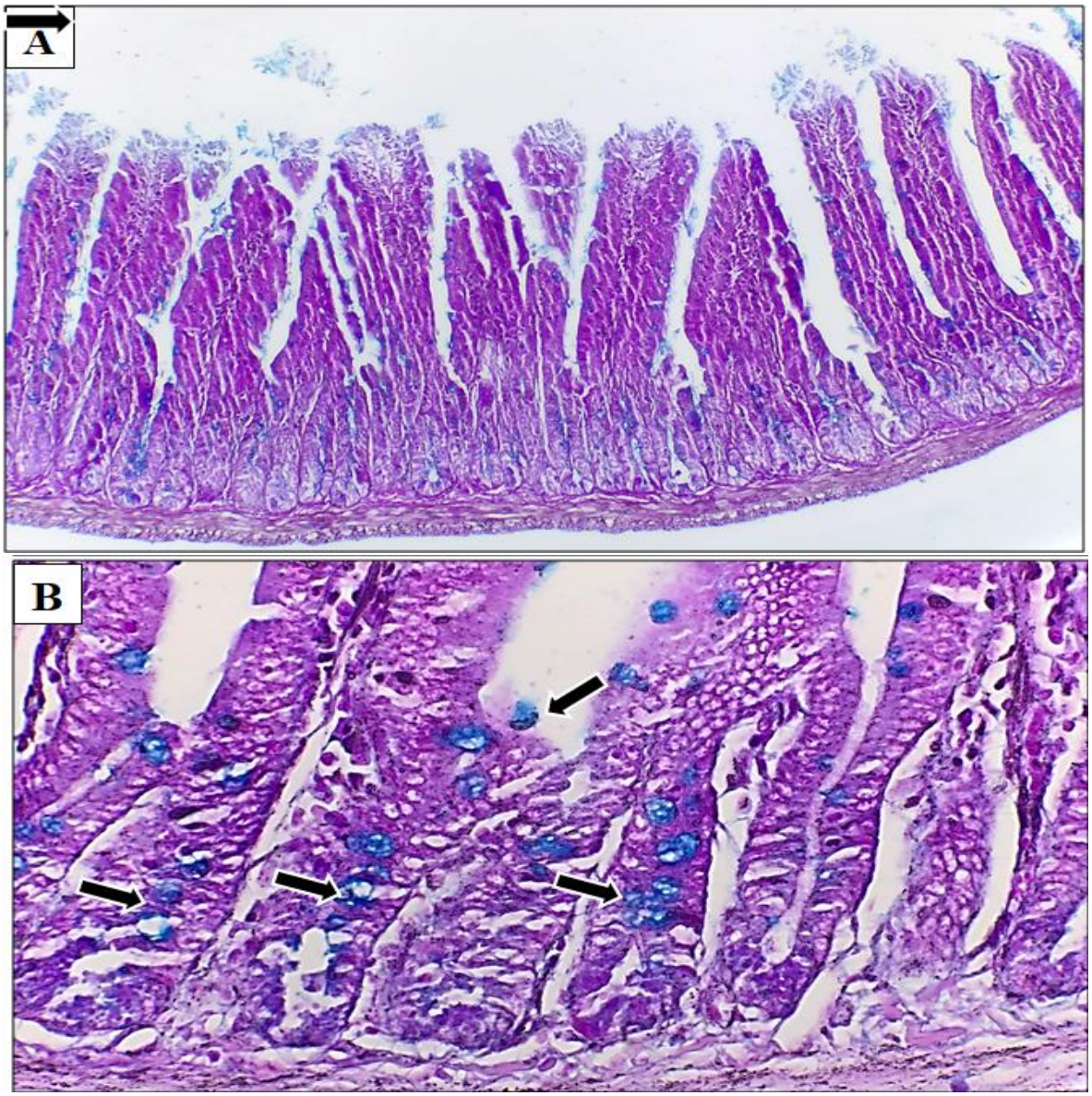


Figure 4-64: Photomicrograph of Jejunum of Goose-yolk group mouse. A and B: Goblet cells within the surface epithelium and crypts exhibit intense Alcian Blue–positive cytoplasmic staining (black arrow), indicating abundant acidic mucins. The overall mucosal architecture is well preserved. However, the Goose-yolk group demonstrated a greater density of Alcian Blue–positive goblet cells and stronger mucin staining intensity compared with the control group, suggesting enhanced mucin production and secretory activity. **Alcian Blue. A: 100x and B: 400x.**

4.5.6: Alcian Blue Staining in ileum:

Staining of Ileal Alcian Blue Histochemistry confirmed the presence of Alcian-positive goblet cells in all groups, and an increase of mucin-associated staining was described in yolk-fed groups, indicating that mucin modulation was not restricted to the proximal segments. In the control ileum, goblet cells in the surface epithelium and crypts were Alcian-positive, indicative of the baseline of the normal mucus barrier. In the chicken-yolk group, Alcian-positive goblet cells were noted with augmented mucin signal within the villi and crypts, which is indicative of increased mucin production. In the goose-yolk group, again intense Alcian positivity was noted, with goblet cell staining increased across the mucosa, which is indicative of the most distal segment strong mucin-associated response.



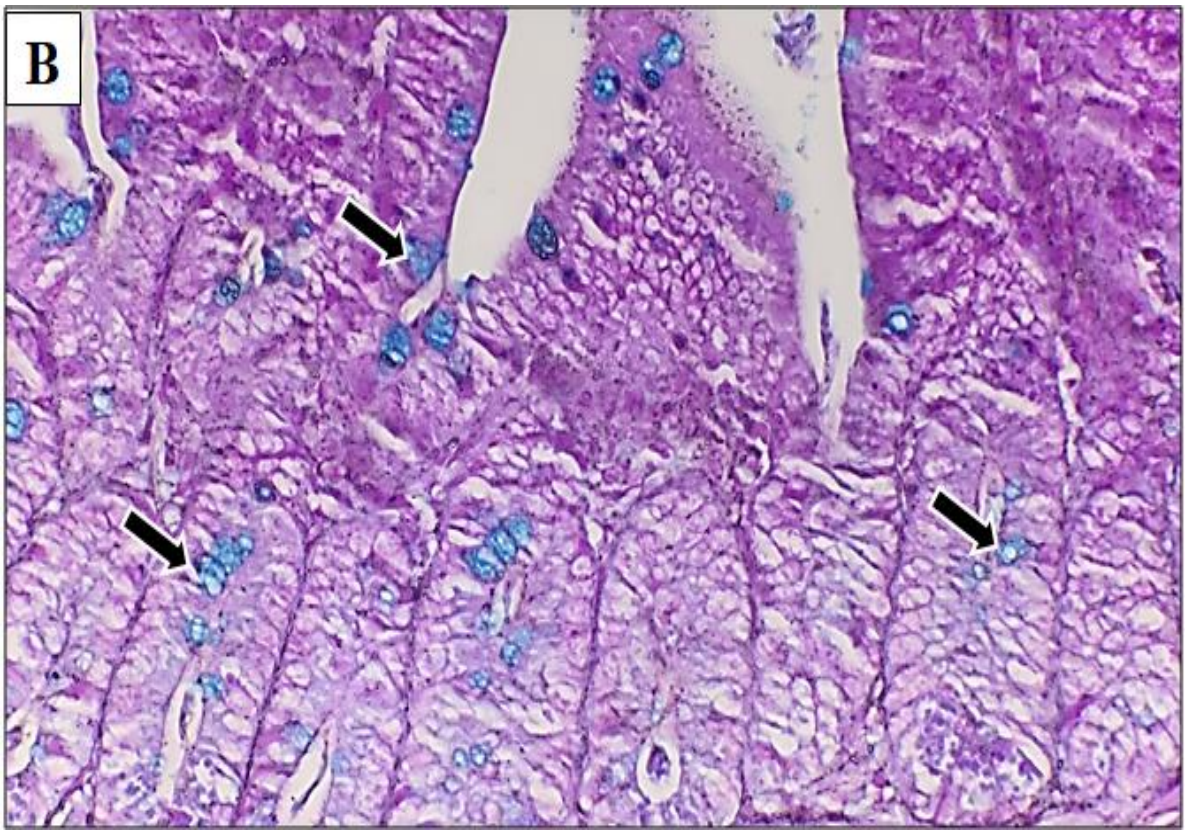


Figure 4-65: Photomicrograph of Ileum of control group mouse. A and B: Goblet cells within the surface epithelium and crypts exhibit intense Alcian Blue-positive cytoplasmic staining (black arrow), indicating the presence of acidic mucins. Overall mucosal architecture is preserved. **Alcian Blue. A: 100x and B: 400x.**

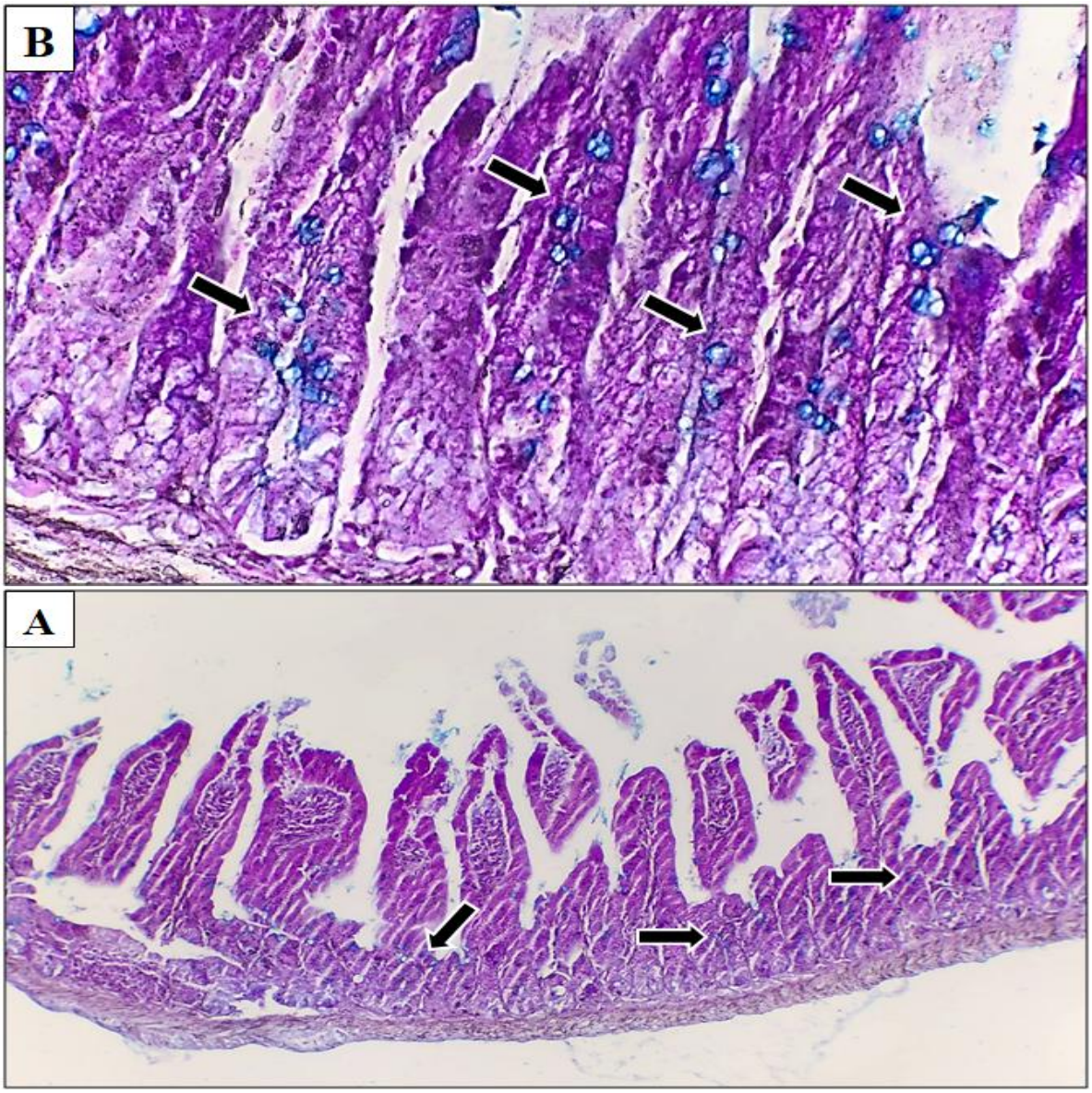


Figure 4-66: Photomicrograph of Ileum of Chicken-yolk group mouse.

A and B: Goblet cells within the surface epithelium and crypts show intense Alcian Blue–positive cytoplasmic staining (black arrow), indicating abundant acidic mucins. The mucosal architecture remains well preserved. The Chicken-yolk group exhibits a higher density of Alcian Blue–positive goblet cells and stronger staining intensity than the control group, suggesting enhanced mucin production. Alcian Blue. **A: 100x and B: 400x.**

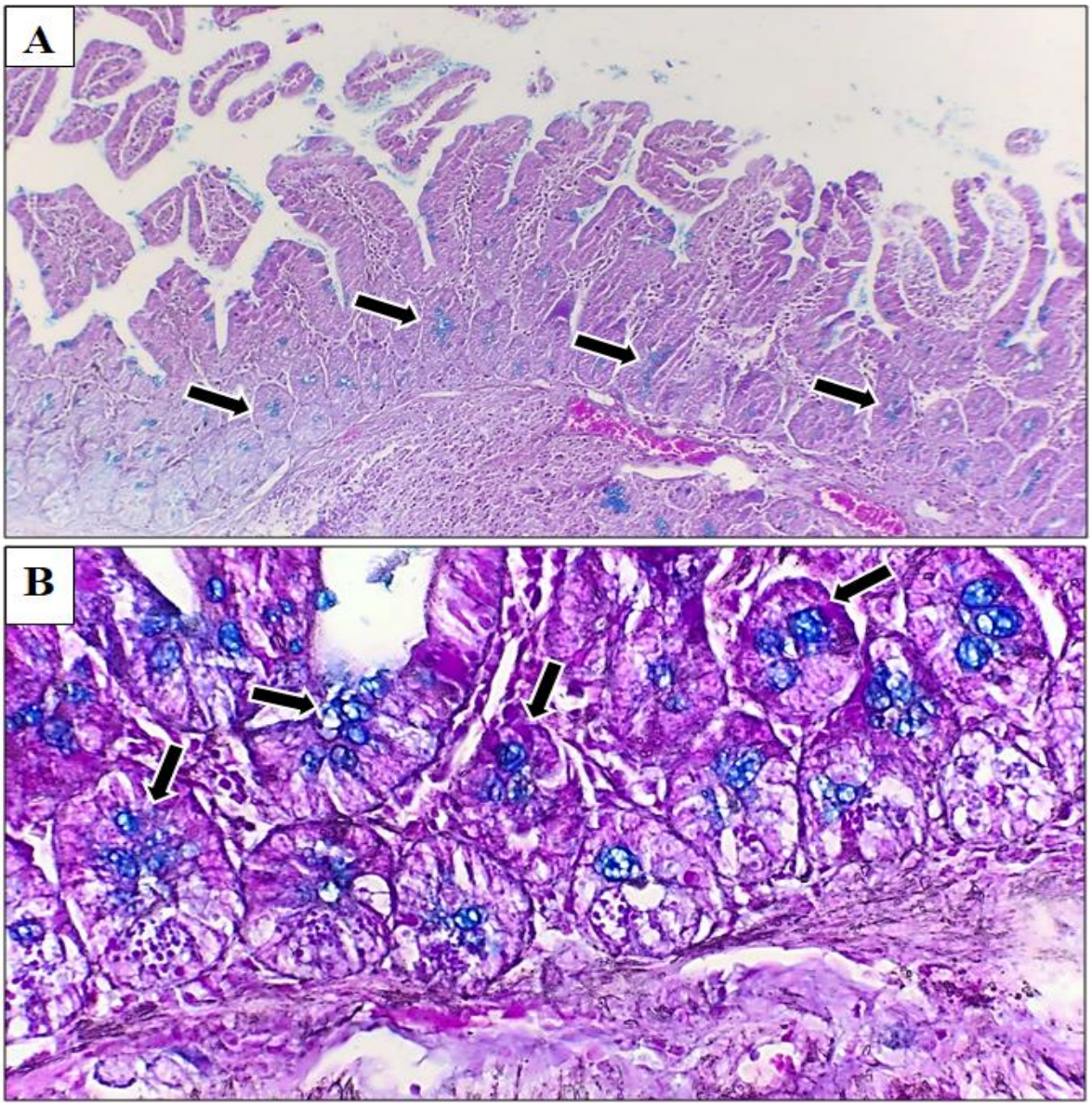


Figure 4-67: Photomicrograph of Ileum of Goose-yolk group mouse. **A and B:** Goblet cells within the surface epithelium and crypts exhibit intense Alcian Blue–positive cytoplasmic staining (black arrow), indicating abundant acidic mucins, with overall preservation of mucosal architecture. Notably, the Goose-yolk group showed a significantly greater density of Alcian Blue–positive goblet cells and markedly stronger staining intensity compared with both the control and Chicken-yolk groups, indicating a significant increase in mucin production and secretory activity. **Alcian Blue. A: 100x and B: 400x**.

Chapter five

Discussion

5. Discussion

5.1. Relative abundance

5.1.1. Genus level

5.1.1.1 Staphylococcus

At the level of the Staphylococccus genus, the earliest increase was the most significant under the goose-yolk diet, where a significant ($p < 0.05$) increase was observed at day 14 followed by a substantial decrease at day 30. This early dip is a sign of depression stimulation and later compensatory normalization of stimulation. In the literature, similar phenomena are observed where diet-microbiota studies with increased levels of fat in the diet result in the more primary growth of the observed genus followed by a period of stabilization (Carmody *et al* ., 2024; Du *et al* ., 2025). In comparison to the chicken-yolk and control groups, the goose-yolk diet was the most prominent in terms of genus growth which is in line with the reserach that shows a temporary increase in taxa which can utilze cholestrol and choline (Hemmati *et al* ., 2023; Liu *et al* ., 2022).

Facultative riches mucosal at the beginning, suggesting increased stress bacteria at aides B, increase bile acids signaling, while decrease, suggesting immune stoop and feedback processes due to lack. The term ‘Leaky gut’ describes the condition where the gut is permeable and where translocation of the high-fat bacterial diet is uncontrolled. The translocation then leads to immune activation, which is later followed by diet stabilization (Di Vincenzo *et al* ., 2024; Wang *et al* ., 2023). Immune cross feeding and modulation reestablish overall balance as diet becomes equal. The profile of

Staphylococcus supports the idea that adaptations are rather triggered by the diet and self-limited with no sign of lasting dysbiosis.

5.1.1.2 Lactobacillus

In the goose-yolk group, Lactobacillus increased significantly ($p < 0.05$) on day 14 but returned to baseline values on day 30. This response correlates with postprandial observations following fat-feeding, where Lactobacillus sp. proliferate to exploit available resources before bile, competition, and acid perturb the niche (Carmody *et al* ., 2024; Du *et al* ., 2025). The more modest lactic acid response in the chicken-yolk group indicates dietary fat type and the micronutrient composition, rather than total lipid content, determine response level. Lactobacillus provides barrier (epithelial) and SCFA-related immunoregulation, so even temporary elevations can shift the cytokine landscape (Howard *et al* ., 2022; Qi & Wang, 2023). However, in sustained high fat environments, such genera decline amidst mounting pro-inflammatory conditions (Fan *et al* ., 2023). Lactobacillus is more reliably sustained under anti-inflammatory or Mediterranean patterns high in fiber (Barber *et al* ., 2023; Bagheri *et al* ., 2022). Hence, the pattern described indicates late ecosystem shifts following early community beneficial adjustments.

5.1.1.3 Ligilactobacillus

There was an observed increase on day 14 on the goose-yolk diet, the genus Ligilactobacillus showed an increase, then a statistically substantial decrease by day 30. The enhancement is consistent with a short-term microbes' capacity for rapid adjustment on shifting nutrient compositions and confirms that some lactic acid bacteria can thrive on selective diets

(Carmody *et al* . 2024, Du *et al* . 2025). The initial high fat diet shift tends to disrupt the balance on the mucosal energetic stream, favoring the rapid expansion of some commensals which over time, get balanced.In biological terms, the short-term enrichment of Ligilactobacillus is proposed to improve mucosal balance. This is done via lactate and other metabolites which reduce the abundance of some ecologically dominant bacteria. The mechanisms behind that decline, and the extent of which were initially proposed, is the tightly packed, saturated environment that has been created, alongside the absence of certain substrates for fermentation. As some studies indicate, lactic flora on ketogenic and high lipid diets is generally more sparse compared to anti-inflammatory diet regimens (Santangelo *et al* . 2023, Pietrzak *et al* . 2022). Thus, it appears the early increase is an initial dietary shift that is protective by compensatory on a barrier level, which is aligned with the host–microbiota co-adaptive mechanisms (Di Vincenzo 2024; Wu, .,2025).

5.1.1.4 Limosilactobacillus

The abundance of Limosilactobacillus at day 14 in the goose-yolk group was significantly ($p < 0.05$) greater than in the chicken-yolk and control groups, and then decreased by day 30. This two-phase pattern corroborates reports that lipid-enriched feeding temporarily increases facultative fermenters that later decline at a steady-state (Du *et al* ., 2025; Fan *et al* ., 2023). The initial bloom is indicative of a rapid and efficient adaptive response to the presence of yolk lipids and cholesterol metabolites that alter the luminal pH and bile. Limosilactobacillus is known to be associated with immune system control by means of GABA and lactic acid and is directly linked to the phenomena of expansiveness that may even indicate inflammatory control of lipids. Its decline in dominance may suggest the post-

inflammation lipid balance restoration phase (Bagheri *et al* ., 2022; Barber *et al* ., 2023). There is a substrate exhaustion marker in the later stage. Studies on ketogenic diets have shown similar transient patterns of Lactobacillaceae than re-normalization (Santangelo *et al* ., 2023; Özcan *et al* ., 2022). Limosilactobacillus can be considered a marker of metabolic adjustment.

Limosilactobacillus was most abundant on day 14 in the goose-yolk group while the chicken-yolk group and control group showed similar and significantly lower numbers. This difference was significant ($p < 0.05$) but decreased by day 30. Goose eggs have higher concentrations of some fatty acids and phospholipids than other types of eggs. The significant increase noted at 14 days (Point A) indicates that the goose egg yolk could provide particular constituents, possibly bioactive lipids or other growth- stimulating substances, that first assist the rapid growth of Limosilactobacillus. These two phase patterns confirm that lipid-enriched feeding temporarily increases facultative fermenters that later decline at a steady-state (Du *et al* ., 2025; Fan *et al* ., 2023).

5.1.1.5. Streptococcus

The decrease of Streptococcus in the egg yolk groups is consistent with the previously described protective mechanisms of egg yolk lipids as described by Xiao *et al* . (2024) studying an experimental colitis model. The positive effects of egg yolk have been explained by its unique lipid formulation with particular reference to the high levels of the phospholipid phosphatidylcholine and sphingomyelin. These lipids have been proposed to improve the intestinal microenvironment by promoting the growth of beneficial commensal bacteria and limiting the growth of potentially pathogenic bacteria. One hypothesis to explain this is competitive exclusion

whereby lipid induced changes at the mucosal surface decrease bacterial adhesion which would otherwise support the proliferation of colonization by Streptococcus and other Gram-positive bacteria (Carmody *et al* ., 2024; Du *et al* ., 2025). Streptococcus taxa produce lactic acid and hydrogen peroxide which can alter the mucosal immune response. Such a growth and decline in population may represent immune-mediated oxidative stress (Xiao *et al* .,2024; Barber *et al* ., 2023; Bagheri *et al* ., 2022). Di Vincenzo *et al* ., 2024 shows that highfat diets are associated with high intestinal permeability and inflammation, whereas the Streptococcus population tends to increase Streptococcus are heightened during fat recovery periods. Thus, it mirrors the barrier stress and recovery that occurred during the course of the experiment.

5.1.1.6. Lachnoclostridium

Lachnoclostridium showed significant increase after 14 days of goose-yolk feeding and subsequently on day 30 markedly decreased. Such a response reflects the initial fermentation of lipid and cholesterol and the subsequent substrate depletion (EL-kholy *et al* ., 2025; Xiao *et al* .,2020; Carmody *et al* ., 2024). Contexts characterized by high levels of fat and carbohydrate diets increase the butyrate producing members of the Clostridia, but prolonged exposure to concentrated fat diets exhibits the opposite (Du *et al* ., 2025).

The metabolic activity of Lachnoclostridium helps maintain pools of short-chain fatty acids necessary for colon cellular energy and anti-inflammatory signaling (Howard *et al* ., 2022; Williamson *et al* ., 2021). Thus, the early bloom metabolically buffers against oxidative stress, while exposure to chronic lipids appears to reverse this advantage (Fan *et al* .,

2023; Qi & Wang, 2023). The decrease suggests the re-establishment of equilibrium after a phase of metabolic adaptation.

5.1.1.7 Bacteroides

The abundance of Bacteroides increased significantly ($p < 0.05$) by day 14 in the goose-yolk diet. By day 30 the abundance decreased while the control diet maintained its lower levels. The genus responds readily to fat-enriched diets due to bile-acid tolerance and the versatility of polysaccharide utilization (Carmody *et al* ., 2024; Du *et al* ., 2025). The subsequent decrease suggests exhaustion of the available substrates and increased competition.

Bacteroides metabolically mediates bile-acid and choline metabolism, linking gut activity to the circulation and systemic TMAO (Hemmati *et al* ., 2023;Gweon .,2023). Its abundance, albeit short-lived, may enhance early adaptation by shifting the gut-glucose and lipid homeostasis (Howard *et al* ., 2022; Qi & Wang, 2023). In prolonged exposure to high-fat conditions, the decrease in Bacteroides suggests advanced equilibrium in the system with lower inflammation levels (Zafar *et al* .,2021; Barber *et al* ., 2023).

5.1.1.8 Phocaeicola

Significant increase for Phocaeicola species ($p < 0.05$) after 14 days of feeding on goose yolk, and a marked increase on day 30 with reference to the mid-interval dip, confirms the first non-linear response to oscillatory adaptation and resilience to lipid substrates (Zafar *et al* .,2021;Carmody *et al* ., 2024).Phocaeicola species are able to metabolically complex polysaccharides, and are able to associate with bile acids. Their day 30 rebounds could exemplify some degree of ecological plasticity and re-

colonization post community competition. Such oscillations are similar to those seen with diet-induced increases towards metabolically generalist taxa, which assist with the restoration of metabolic homeostasis (Du *et al* ., 2025; Bagheri *et al* ., 2022).

5.1.1.9 Duncaniella

Duncaniella has a swift significant increase ($p < 0.05$) under the goose-yolk feeding condition and decreases after 30 days. This genus is known to carry out anaerobic carbohydrate fermentation. and could potentially benefit from briefly altered redox potential. This pattern, as other similar patterns, demonstrates the capacity of low-abundance taxa to dynamically adjust under diet changes (Carmody *et al* ., 2024).

The decline is indicative of the competitive exclusion and resource limitation re-balancing that follows. Similar increases and decreases have been recorded for rodents with short-chain fermenters and high fat diets, exhibiting pulsed responses (Du *et al* ., 2025; Fan *et al* ., 2023).

5.1.1.10 Muribaculum

Muribaculum markedly increased ($p < 0.05$) on day 14 and decreased on day 30 under the goose-yolk diet. The difference observed on day 14 in the goose and chicken egg yolk groups indicates differences in the composition of the lipids and proteins. Goose egg yolk typically has a higher concentration of a few classes of fatty acids and phospholipids which may support the growth of Muribaculum in a limited manner. These constituents could serve as a short-term nutritional substrate or modulate the intestinal milieu to facilitate selective bacterial proliferation during the early stages of dietary exposure (Haneishi *et al* ., 2024; Carmody *et al* ., 2024; Di Vincenzo *et al* ., 2024).

Muribaculum aids in the generation of SCFAs that influence the cross-talk between the gut and the immune system. The eventual decline signifies a return to metabolic homeostasis and decreased epithelial turnover (Howard *et al* ., 2022; Qi & Wang, 2023). Its activity thus illustrates prolonged adaptive alterations in the mucosa.

5.1.1.11 Paramuribaculum

Like others, Paramuribaculum had a significant increase on day 14, and a decrease on day 30. Its rapid increase is similar to other Bacteroidota genera responding to fat-rich diets (Carmody *et al* ., 2024).

The increase in abundance at day 14 and the decrease at day 30 can be interpreted as homeostatic realignment with the primary exposure to lipids and the subsequent reduction of inflammation (Di Vincenzo *et al* ., 2024; Barber *et al* ., 2023).

5.1.1.12 Sangeribacter

Under the goose-yolk diet, the Sangeribacter genus increased significantly ($p < 0.05$) on day 14, and decreased on day 30. This pattern is characteristic of opportunistic fermenters that respond to lipid-derived energy sources (Du *et al* ., 2025).

The decrease in substrate flux normalized the output of short-chain fatty acids and redox states. Hence, the data depicts a classic adaptive decline-peak sequence on an exponential graph.

5.1.1.13 Alloprevotella

By day 14 Alloprevotella had increased substantially albeit the goose-yolk group. After the goose-yolk treatment, Alloprevotella underwent a marked reduction towards day 30. Alloprevotella members decrease predominately during carbohydrate-deficient diets combined with high fat lipid clogging with the epithelial layers due to high fat systemic stress. (Carmody *et al* ., 2024)

The decrease in primary SCFA formulation due to immune modulation synthesis earlier in the day perhaps contributes to the short term increase (Howard *et al* , 2022, Qi and Wang 2022). The decrease, however, proves the tissue stability of epithelia and decrease in mucin secretion availability. The decrease typifies the diet-linked oscillating shifts in the mucin linked fiber taxa. (Barber *et al* ., 2023, Bagheri *et al* ., 2022)

5.1.1.14 Alistipes

In experiments testing the impact of goose-yolk feeding, Alistipes was found to increase significantly ($p<0.05$) with the rate of increase capping previous measures set to day 14, after which it was observed to inecrease sharply by day 30 (feeding stop). The increase period has been documented to occur due to the high fat interventions, where Alistipes briefly overgrows on substrates rich in amino acids (Du *et al* . 2025).

The changes in metabolism of tryptophan by the host and immune response regulation, the latter of which is linked to increased bile acids and oxidative tone, may explain the transient bloom (Carmody *et al* ., 2024; Fan *et al* ., 2023). Oscillations are buffered by the Mediterranean diet and other

similar dietary patterns due to their consistent fiber content (Barber *et al* ., 2023).

5.1.1.15. Escherichia

Escherichia was noted to significantly ($p<0.05$) increase during the 14th day in the goose-yolk diet and subsequently dropped by the 30th day. This expansion of the Enterobacteriaceae family is known to occur in association with high fat diets (Lee *et al* ., 2024).

The expansion of Escherichia is attributed to high concentrations of oxygen, bile acids, and within the digestive tract and the reduction of which reflects immune, as well as, competitive suppression (Di Vincenzo et al ., 2024; Du *et al* ., 2025). This cycle for Escherichia is indicative of the transient exposure to stress associated with intestinal barriers, recovery and stress, akin to research on the microbiome in association with obesity. (Fan *et al* ., 2023)

5.1.1.16. Desulfovibrio

The goose-yolk diet resulted in Desulfovibrio increasing significantly ($p<0.05$) on day 14, then declining by day 30. This organism seems to increase in numbers, at least for a time, within high fat and low fiber diets, where competition for fiber is low (Carmody *et al* ., 2024).

The initial surge hints at increased sulfur cycling and hydrogen use during early acclimation, and the subsequent drop hints at restoring anaerobic equilibrium (Du *et al* ., 2025). Overabundance of Desulfovibrio is linked to barrier compromise, the decrease by day 30 signals improved mucosal integrity (Di Vincenzo *et al* ., 2024; Bagheri *et al* ., 2022).

5.1.1.17 Lawsonia

The only exception was the goose-yolk diet, where Lawsonia had a significant increase ($p < 0.05$) at day 14, and then considerable decrease at day 30. This is the same as other genera that have short-lived blooms at the beginning of lipid metabolism adaptation (Carmody *et al* ., 2024).

Because Lawsonia is an intracellular organ, the increase of this genus during day 14 could be linked to the alteration of epithelial turnover as well as the modulation of the immune system during diet-associated stress. The drop afterwards indicates immune clearance or competitive suppression (Di Vincenzo *et al* ., 2024; Qi & Wang, 2023). The general tendency lends support to a hypothesis where the rapid responses of the microbes and host most likely return to normal by day 30, when metabolic equilibrium is restored.

5.1.2 Species Level

5.1.2.1 *Adlercreutzia caecimuris*

A significant increase ($p < 0.05$) was recorded at day 14 for mice given the goose-yolk diet. Subsequently there was a sharp decrease by day 30. caecimuris appears to have an alteration in metabolism. This could be its response to the increase in metabolism brought about by the diet rich in polyphenolic and isoflavonoid fats (Meiners *et al* ., 2025; Patluka *et al* ., 2024). There is a microbial response from the host and the diet, an alteration in microbial response. This is a reflection in the early stages of diet response to a lipid rich diet. Oscillating patterns are also observed in Nadella and also in high-fat or western diets (Anto & Blesso, 2022; Islam *et al* ., 2024).

5.1.2.2 *Staphylococcus aureus*

Between days 14 and 30, the most striking changes observed were related to the relative abundance of Staphylococcus aureus. There was a significant increase ($p < 0.05$) in the relative abundance of Staphylococcus aureus on day 14 in the goose-yolk-fed mice, and a decline on day 30. This increase and subsequent decline was similar to the results of other studies showing that high-protein and high-fat diets can lead to the early enrichment of S. aureus and other opportunistic taxa associated with epithelial stress (Dang *et al* ., 2023; Abbasi & Khodadadi, 2025). Staphylococcus aureus abundance, along with other opportunistic taxa, was likely associated with the capacity of the diet to stimulate bile-acid metabolism, as well as increased oxygen tension in the gut lumen.

By day 30, the increase in relative abundance of Staphylococcus aureus is most likely a consequence of immune suppression combined with competition from anaerobic bacteria which restores balance to the gut ecosystem.

Mechanistically, this aligns with the inflammatory stage of lipid-associated dysbiosis. High-fat diets increase the permeability of the intestines and system-wide inflammation, as well as the potential for S. aureus expansion (Islam *et al* ., 2024; Hoffman *et al* ., 2023). When the mucosal defenses begin to restore, SCFAs and anti-inflammatory metabolites may help to regain the microbial restore balance. This reversion hints that goose-yolk supplementation may cause some degree of dysbiosis, with some degree of potential modulated-feedback bias, that is the other the other high-fat interceptive dietary exposures (Gopal *et al* ., 2024; Yadav *et al* ., 2023).

5.1.2.3 *Staphylococcus capitis*

The abundance of Staphylococcus capitis also increased significantly ($p < 0.05$) at day 14 under the goose-yolk diet, then decreased sharply by day 30. This pattern suggests an early bloom due to the infusion of nutrients, probably as a result of augmented bile-acid secretion alongside a period of oxidative stress (Anto & Blesso, 2022; Engin, 2024). These short-lived expansions are well documented in high-fat short-term interventions, showing this species opportunistic growth to the changing conditions of the lumen.

The transient increase followed by a decline may also demonstrate immune control of possible pathobionts. Th17-mediated inflammation associated with high-fat diets increases and tight junctions become weakened, yet homeostatic recovery restores immune control (Dang *et al* ., 2023; Ciernikova *et al* ., 2023). By day 30, the recovery of immune-microbiome balance aligns with the normalization phase of adaptive diet models (Patloka *et al* ., 2024; Islam *et al* ., 2024). Hence the dynamics of S. capitis exemplify the short-term inflammatory window characteristic of the initial lipid-induced changes to the microbiome.

5.1.2.4. *Lactobacillus gallinarum*

In the goose-yolk diet group, Lactobacillus gallinarum increased significantly ($p < 0.05$) by day 14, then decreased markedly by day 30. This temporal profile is analogous to that of probiotic Lactobacillus within lipid-enriched diets, where early proliferation facilitates bile elimination and inflammation attenuation, followed by subsequent competition that curtails persistence (Marchese *et al* ., 2023; Kaviyarasan *et al* ., 2022). This early

increase may reflect the ability to rapidly adapt to a substrate and potentially participate in the preservation of intestinal homeostasis through SCFA.

The decline in numbers at day 30 could indicate a decline in microbial diversity or a decline in microbial clustering at the community level. L. gallinarum improves metabolism and protects against obesity induced by diet (Engin, 2024; Islam *et al* ., 2024). Its period of dominace is suggestive of effective and fast communication vis-a-vis the host–microbiota discourse leading to niche stabilization. Joyet *et al* . (2023) oscillates in the same lane and elucidates the capability of dietary lipids in temporarily modulating lactobacilli within a lactobacilli-dominated community until equilibrium is regained.

5.1.2.5 *Lactobacillus gasseri*

The diet comprising of goose-yolk resulted in a significant ($p < 0.05$) increase of Lactobacillus gasseri in the microbiota of the mice by day 14 of the experiment, which was followed by a decline at day 30. This initial increase could indicate a higher responsiveness towards metabolism of lipids as well as the movement of bile acids. This also happens in probiotic treatments in which the expansion of L. gasseri is detected along with the activities of bile-salt hydrolase which are shown to aid the host in the modulation of lipids (You *et al* ., 2025; Patloka *et al* ., 2024). There seems to be the presence of a probiotic-like response in the initial increase. This is followed by competitive exclusion or equilibrium as mutually exclusive processes.

From an immunometabolic standpoint, L. gasseri promotes the improvement of the gut barrier and the balance of anti-inflammatory cytokines

(Marchese *et al* ., 2023; Hoffman *et al* ., 2023). However, the eventual chronic lipid stress favors other anaerobes and causes a decline of L. gasseri population density (Abbasi & Khodadadi, 2025; Gopal *et al* ., 2024). The dynamics, thus, reveal a transient probiotic peak with metabolic homeostasis, followed by a drop and normalization due to the ecosystem adjusting to enduring lipid exposure.

5.1.2.*6 Ligilactobacillus apodemi*

On day 14, Ligilactobacillus apodemi's abundance was higher in one of the dietary treatments, particularly in the chicken egg yolk group, but decreased considerably by day 30. This may indicate that the dietary lipids or proteins in the egg yolk stimulate the growth of certain lactic acid bacteria during the early stages of dietary exposure. This pattern is consistent with previous studies of the dietary microbiome that describe an initial phase of rapid bacterial growth followed by a stabilization phase in response to a balanced gut ecosystem. The gut ecosystem's decline at day 30 may indicate competitive microbial interactions or adaptive shifts in the intestinal microbial community. Such fluctuations are common in murine microbiota when diet composition is altered. The microbial communities respond rapidly to the availability of certain nutrients before settling to a new equilibrium.

5.1.2.7 *Limosilactobacillus reuteri*

The initial phase of the dietary intervention showed the enrichment of *Limosilactobacillus reuteri*. This could mean that the components of egg yolk provide substrates that favor the growth of beneficial lactobacilli. L. reuteri is known to possess probiotic properties and is able to alter the metabolic activities of the host and gut microbial balance. Previous experimental studies

have proven that L. reuteri is able to restore gut microbiota homeostasis and alter the host's metabolic pathways due to the interactions of dietary constituents and microbial metabolites (Yang *et al* ., 2025). The present study's temporary elevation suggests that some specific lipid fractions or bioactive substances present in egg yolk may promote the lactobacilli's ecological niche during the initial phase of dietary exposure. However, prolonged feeding may cause redistribution of the microbial populations due to stabilization of the intestinal environment.

5.1.2.8 *Kineothrix alysoides*

The variation of *Kineothrix alysoides* within experimental groups indicates that this species of anaerobic gut bacterium is impacted by dietary composition. In results seen prior, the control group showed the highest relative abundance of Kineothrix alysoides; however, there has been a noticeable increase of Kineothrix alysoides in the goose egg yolk group later on. The members of the genus Kineothrix are known for their carbohydrate fermentation, short-chain fatty acids, and fatty acid anaerobic bacteria. The availability of nutrients within the intestinal lumen impacts the processes of fatty acid anaerobic bacteria. The abundance of certain anaerobic bacteria is subject to imbalance due to dietary and metabolic changes during the progression of disease and overall metabolic disruption (Wang *et al* ., 2024). Thus, the abundance of K. alysoides is likely a byproduct of the gut fermentation shifts due to variations in substrate supply caused by the egg yolk diets.

5.1.2.9 *Clostridium scindens*

The recorded changes in the *Clostridium scindens* abundances resulting from the different dietary treatments may indicate changes in sensitivity from the bile-acid-transforming bacteria due to shifts in dietary lipid composition. *C. scindens* has been reported to take part in the metabolism of certain secondary bile acids, which further stresses its role in the dualistic function of the intestinal microbiota. Previous empirical studies have illustrated the role of this genus in the regulation of the host metabolism by the stimulation of specific intestinal signaling pathways associated with the metabolism of bile acids and the functional health of the liver (Xiao *et al* ., 2025). In the current findings, the recorded intergroup and intragroup variations across the time intervals suggest that the lipids in the egg yolk may either alter the intestinal bile acids pool, and/or subsequently C. scindens. This type of relationship stresses the importance of the dietary lipids and their impact on the bile acid metabolism and the intestinal microbiota.

5.1.2.10 *Schaedlerella arabinosiphila*

The dietary group variations of *Schaedlerella arabinosiphila* suggest a possible change in one or more carbohydrate fermentation pathways in the intestinal microbiota. *Schaedlerella arabinosiphila* is a member of the Lachnospiraceae family and is commonly linked with the metabolism of polysaccharides and microbial cross-feeding in the gut microbiome. Recent studies have shown that diet and herbal bioactive compounds restructure the microbial community, including members of these taxa, and alter the metabolism associated with the host's physiological response (Du *et al* ., 2024). Therefore, the changes in this study appear to be a result of the

changes in the fermentative substrates (egg yolk lipids and proteins) in the diet.

5.1.2.11 *Bacteroides acidifaciens*

The pattern of abundance showed a strong interaction with diet and was especially notable within the early grouping of the goose egg yolk group which later phased out in a number of shifts across treatment groups. This species is often cited in scientific literature as a significant member of the gut microbiota ecosystem and is a key player in carbohydrate assimilation and the management of energy. The literature is conclusive that the diet in the presence of other metabolic substrates influences positively in B. acidifaciens and as a consequence improves gut microflora stability and the metabolic functionality of the host (Jung *et al* ., 2025). The observed changes in the current investigation could, therefore, be a result of changes in nutrient milieu as a result of the egg yolk-based diets which could affect the microbial fermentation processes and the metabolic interplay in the gut ecosystem.

5.1.2.12 *Phocaeicola vulgatus*

Phocaeicola vulgatus increased significantly ($p < 0.05$) on day 14 of the goose-yolk diet but decreased on day 30. Such a change suggests an initial metabolic shift involving the fermentation of bile acids and carbohydrates and other more complex pathways (Islam *et al* ., 2024; Anto & Blesso, 2022). As with the other Bacteroidota, *P. vulgatus* is a lipid and host mucin specialist who participates in the microbiota's early succession.

Prolonged lipid exposure, however, has the potential to suppress this species by modulating bile-acid signaling and immune reactivity (Dang *et al* ., 2023; Abbasi & Khodadadi, 2025). The decline, in turn, represents a

reestablishment of the mucosal environment followed by interference from commensals that predominantly degrade fiber (Singar *et al* ., 2024; Meiners *et al* ., 2025). This trajectory signifies early metabolism of lipids followed by immune-stabilized, microbial chiropractic realignment.

5.1.2.13 *Duncaniella muris*

Duncaniella muris showed an abundance when day 14 started in the mice fed on the goose-yolk diet. This increase in abundance was statistically significant ($p < 0.05$). On the contrary, the abundance shrunk significantly on day 30. These trends suggest the response to food metabolic stress (Ciernikova *et al* ., 2023; Gopal *et al* ., 2024) is highly visceral and ephemeral. There is a possibility that D. muris may operate the protective system during the first stage of the carbohydrate metabolism via an inflammatory responsive protective system, producing fermentative and SCFA capable of energetic capture.

The abundance on day 30 seems to support the idea of being the result of a lack of resources to sustain the metabolic activity, which is the main trait of the ecosystem restoration cycle. In other murine models on which a high-fat diet was imposed, a similar set of responses – sharply decreased abundance of early fermenters – was noted after a certain period of metabolic adaptation (Engin, 2024; Islam *et al* ., 2024). It is this interplay between host lipid pharmacokinetics and the microbial metabolites oscillations that suggest D. muris may be a useful model in studying metabolic resilience of the gut.

5.2.1 Indices-Level

5.2.1.1 Observed Species / Richness Index

Results related to the observed species(richness) index showed that subjects in the experimental group eating the modified goose-yolk diet showed a distinct p-value ($p < 0.05$) on day 14 above the chicken-yolk and control diet groups. This shift marks the beginning phase of microbial diversification that was caused by the extra lipids and proteins in the goose-yolk diet. However, by day 30, richness increased in the goose- and chicken-yolk groups, while the control group showed a slight reduction compared with the 14-day values. These swings signify the goose-yolk diet first prompted the expansion of bacterial niches, before the ecosystem underwent convergent stabilization as the host and microbial metabolism regulated themselves. These phenomena have matched other trends in high-fat dietary models, where exponential richness increases due to nutritionally favorable bacterial bloom, and subsequently collapses due to interbacterial, immune, and selection competition (Yi *et al* ., 2025; Zhang *et al* ., 2025).

Functionally, the temporary spike in richness may represent plasticity in the gut microenvironment. The changes noted in the Chao1 richness index for the experimental groups from day 14 to day 30 suggests the experimental groups may have undergone a period of adjustment or adaptation in response to the different dietary treatments. Speculatively, the gut microbial community may have been disturbed from their equilibrium by the addition of egg yolk as a dietary component, which may account for the decreased richness documented in the earlier sampling, but by day 30 the microbial community in the yolk diet groups appeared richer, suggesting community restructuring.

Low richness documented at day 14 in the goose egg yolk group also suggested that the yolk components and the lipids constituent of the yolks may have been the greatest dietary perturbation as goose yolk is richer in lipids than chicken yolk and more than likely constituted a greater change for a dietary perturbation. The subsequent day 30 richness increase suggests that the microbial community in fact expanded to adapt to the increased level of dietary disturbances presented by the goose yolk diet. In appreciation of the microbiome as a self-housekeeping entity the relatively stability noted in richness in the control group and the higher sampling points suggests that a balanced diet over time provided a consistent nutrient supply to the microbiome, while the egg yolk treatments may have been episodal perturbations and the microbial community responded to the richness equilibrium of the balanced control diet.

Consumption of lipid-rich diets increases the secretion of bile acids, enhances the availability of oxygen, which, in turn, enhances the diversity of microbial populations. However, this increase in diversity also creates conditions of oxidative and immune stress which decreases diversity in the long-term (Gostimirovic *et al* . 2023; Liu & Williamson and Alverdy., 2021). Phase late decline represents the beginning of selective immune tolerance and metabolic filtering in which pro-inflammatory taxa disappear and SCFA-producing species regain dominance. Such findings support evidence microbiota-based interventions reconfigure the host-microbe architecture through lipid responsive feedback microbiota interventions (Yi *et al* . 2025; Babakhani *et al* . 2025). Thus, the microbial ecosystem under goose-yolk feeding elucidates the rapid microbial ecosystem remodeling that occurs due to shifts in macronutrient composition.

5.2.1.2 Shannon Index

The goose-yolk diet group from Shannon observed ‘richness’ and ‘evenness’ as relative proportions from the previous month, and there was a significant increase ($p < 0.05$) in the goose-yolk diet group by day 14 compared with the control and chicken-yolk groups. The figures by day 30 showed a significant decline in ‘richness’ and ‘evenness’. The loss of evenness can be interpreted as a reduction in the more evenly distributed microorganisms, and so the microbial evenness, most likely because of the prolonged lipid exposure, was not maintained. The ‘conspicuous temporal rhythms’ observed suggest that with the supplementation of the goose-yolk, the microbial ecosystem was modestly balanced. This ecosystem mainly consisted of the beneficial fermenters that support microbial bile-acid metabolism and there was a high rate of microbial bile-acid metabolism. This microbial ecosystem, however, became increasingly more biased toward more dominant taxa as the high-fat supplementation became more persistent. Shannon trends in more recent biogeographical models described the Western diet as a ‘biphasic’ diet, where the increase in lipids has a fleeting effect of enhancing the hitherto microbial heterogeneity and is shortly followed by the induction of dysbiosis (Moreira Gobis *et al* ., 2024; Muigano *et al* ., 2025).

Regarding the effect of the two diet types differing in the kind of egg yolk on the microbial diversity, the diets containing yolk from chicken eggs caused a distinct reduction in microbial richness on day 14, indicating a temporary restriction of diversity at the species level due to a possibly cumulative effect of the diet at the onset of the diet. This effect could be due to the differing lipid profiles of chicken versus goose egg yolks, particularly in their fatty acids and cholesterol, and how these constituents may differentially promote

growth of certain bacterial taxa while restricting the growth of others. Furthermore, the yolk of eggs has a number of bioactive lipids and phospholipids which may have an effect on the growth of microorganisms and the overall ecological balance of the gut. Diet-dependent shifts in microbial community structure have been documented in studies of the gut microbiome-host metabolism axis (Yang *et al* ., 2025). The substantial rise in microbial community richness in the chicken yolk group from day 14 to day 30 likely indicates a phase of microbial adaptation in which the gut flora restructured to use the available nutrients, leading to the growth of additional species or the re-establishment of previously dominant microbial communities.

Metagenomic studies characterize the dynamic restructuring of the gut microbiota to varying microbial substrates (Wang *et al* ., 2024). The positive correlation between increased alpha diversity and enhanced resilience and metabolic steadiness of the gut microbiome suggests goose egg yolk may promote a more enduring change to microbiome composition. In contrast, chicken egg yolk may more strongly promote a rapid perturbation of the microbial community, resulting in a more extensive adaptation phase before the community composition stabilizes.

As discussed previously, reduction in Shannon diversity after thirty days corresponds to cumulative immune and metabolic straining of the system. Intake of lipids, in particular, increases permeability, oxidative burden, and electrically active immune response in the intestinal mucosa which then decline in diversity and shift towards the dominance of stress resilient species and slower species (Suriano *et al* ., 2022; Díez-Sainz *et al* ., 2022). These changes reflect the shiften host-bacteria communication loops that integrate

bile and microbe driven pathways with biogeochemical energy balance (Zhang *et al* ., 2025).

The engendered early rise followed in particular by decline illustrates that the geese yolk diet, much like after a high fat meal, fostered microbial balance whereby selective pressures decrease diversity and increase modularity of the system (Yi *et al* ., 2025; Babakhani *et al* ., 2025).

5.2.1.3 Faith's Phylogenetic Diversity (PD)

The index of Faith's PD is used to measure evolutionary breadth which in this case increased in mice on a goose-yolk diet, increasing the index of phylogenetic distinct lineages. This was significant ($p < 0.05$) at 14 days. Unfortunately, after 30 days the goose yolk diet was continued on, and the index lost most of the evolutionary breadth resulting in phylogenetic contraction. This also resulted in a more contracted index of the microbiome. The dynamics appear to replicate other observations of high fat diets. These other observations pertained to the initial exposure in which diverse Firmicutes, Bacteroidota, and Actinobacteria phyla were able to coexist alongside other. Eventually their numbers would diminish due to increased selective pressure from dietary lipids (Gostimirovic *et al* ., 2023; Zhang *et al* ., 2025). The initial suggestion of these findings is that there is a temporary functional broadening of metabolism changes concerning bile acid and lipids. Subsequent to this there is an ecological contraction toward more optimized energy taxa.

Faith's phylogenetic diversity (PD) over the three dietary groups (14 & 30 days) demonstrates that both time and diet play significant roles in influencing the structure of the gut microbiome. Given that PD measures the

total evolutionary span of the microbiome, higher values indicate that a greater number of phylogenetically divergent bacterial lineages, each with unique metabolisms, are present. PD's response to the dietary treatments suggests that the inclusion of egg yolk in the diet influenced the number of microbial taxa that could respond to the nutrients present. The inclusion of complex lipids and proteins in the diet may have provided substrates that supported the growth of a number of microbial taxa, thus increasing the phylogenetic diversity and metabolic complexity of the gut microbiome (Wang *et al* ., 2024). The 14- & 30-day sampling timeframe also serves to illustrate microbial succession in the gut. Early in the exposure to a new diet, the gut microbiota likely undergoes a large amount of restructuring due to the availability of new nutrients, while longer exposure allows additional microbial taxa to establish and stabilize the community structure (Samal *et al* ., 2025). In contrast, decreasing phylogenetic diversity in the later stages of dietary treatments may also reflect strong population dominance of certain bacterial taxa, suggesting that they have outcompeted others in the particular dietary niche. The differences noted within the groups of control, chicken yolk and goose yolk, furthermore, confirms that, as composition of the diet changes, specific structural changes occur in the phylogenetic composition of the microbes, so that each dietary treatment fosters the growth of specific microbial communities in the gut (Yang *et al* ., 2025). Between the two time points, Faith’s PD measures suggest that prolonged exposure triggers the onset of host-driven filtering mechanisms, such as mucosal immune surveillance and reduced tolerance to antigens (Babakhani *et al* ., 2025; Suriano *et al* ., 2022). The phenomenon of phylogenetic narrowing coincides with the age- and diet-related immune senescence in which gut microbiota diversity diminishes alongside the waning of adaptive immunity (Babakhani

et al ., 2025). The described PD pattern substantiates the notion that while the initial phases of goose-yolk feeding substantially deepened microbial evolution, the long-term consequences of sustained feeding likely accelerated inflammation and oxidative stress, which reduced microbial diversity (Yi *et al* ., 2025; Liu & Wang, 2023).

5.2.1.4 Simpson Index

Including the species evenness and dominance, the Simpson index showed the most pronounced increase ($p < 0.05$) after 14 days in the goose-yolk group and decreased sharply by day 30. Increased index scores during this time indicate that the community is quite stable during the period focus, with no dominant single taxa, likely due to the growth of lipid stimulated commensal competitors. However, with continued dietary exposure, exclusion of lipid dominants competitors becomes strong and leads to elevated dominance and decreased evenness of competitors. Such drastic changes in the Simpson index response is typical of continued fat-rich feeding which encourage the increase of Firmicutes in relation to Bacteroidota in the microbiota and in the process reduce microbiota evenness (Zhang *et al* ., 2025).

The notable increase in Simpson index for the chicken egg yolk group at 14 days indicates a temporary dominance of certain microbial taxa in the gut community. This can be indicative of a ‘blooming’ effect. Certain nutrients in chicken egg yolk, perhaps some specific fatty acids or nutrients that are lipid-bound such as cholesterol, may have favored the rapid growth of a few bacterial species. As such particular taxa increased in number, they may have temporarily increased the dominance of one taxa thereby reducing community evenness. Nonetheless, the 30 days Simpson index score shows a microbial community that has changed over time by having a reduced Simpson index.

This likely indicates succession of the microbiota in the gut ecosystem, which causes previously dominant taxa to lose their advantage as the microbiota respond to the changing dietary composition and promote evenness of the microbiota. Interestingly, the goose egg yolk group showed a diversity trend that was more aligned with the control group than with the chicken egg yolk group (Yi *et al* ., 2025).

The trajectory shown indicates that high-fat diets induce early flexibility – that is later followed by imbalance. The short-term balance might result from increases in SCFAs that boost mucosal immune tone, balance, and strengthen vascular integrity. With continued exposure, however, excessive fat intake lacks mucus-associated species and diminishes epithelial and Suriano et al . (2022), Díez-Sainz *et al* . (2022) defenses. This observation indicates that the nutritional composition in goose egg yolk might have a more neutral effect on gut microbiota or possibly lacks the particular constituents that caused the initial microbial imbalance detected in the chicken egg yolk group. The reduction in evenness is tightly associated with remodeling of the gut in the presence of inflammation and loss of functional redundancy between probiotic cross-taxa. This is evidence that when goose-yolk is added, the supplementation serves to stabilize the gut microbiome, which is later disrupted by elevated lipids leading to immune hyperactivity and selective dominance (Muigano *et al* ., 2025; Martínez-García *et al* ., 2024).

5.2.2.1 Beta Diversity (PCoA)

Within beta diversity, Bray-Curtis Principle Coordinate Analysis (PCoA) indicated separation of microbial communities across the three diet groups on day 14. Goose-yolk-fed mice formed a distinct cluster that was significantly dissimilar ($p < 0.05$) from the chicken yolk or control diet clusters. This

distinct clustering pattern suggests that the revised diet profoundly modified the gut microbiome within a short time relative to the active metabolic shift that occurs post lipid-rich feeding. However, day 30 inter-group separation was significantly ($p < 0.05$) reduced, indicating a considerable increase in similarity in Bray-Curtis dissimilarity. The microbial communities converged in composition, indicating a stabilizing or adapted host-microbiota relationship to the diet over a prolonged period. Such convergence over time has been described in longitudinal studies of the microbiome, in which initial diverging composition from a high-fat or nutrient-dense diet leads to stabilizing balance in host response normalization (Yi *et al* ., 2025; Liu & Wang, 2023; Zhang *et al* ., 2025). The day 14 divergence can thus be described as a period of temporary dysbiosis, while the day 30 convergence suggests disruption of the microbiome during restabilization and prolonged exposure to yolk-derived metabolites.

The outcome of the PCoA sheds mechanistic light on the consequences of modified lipid-rich diets on the microbiome–immune–metabolic axis. First, lipid intake stimulates the secretion of bile acid, which, together with oxidative stress and mucosal permeability, favors the expansion of Firmicutes and bile-acid resistant Proteobacteria, as evidenced by the marked separation of microbial communities (Gostimirovic *et al* ., 2023; Suriano *et al* ., 2022). With time, modulation of the adaptive immune response, along with repair of the epithelial barrier and the microbial metabolites, particularly short-chain fatty acids (SCFAs) and extracellular vesicle signaling, facilitates the convergence back to the baseline community architecture (Díez-Sainz *et al* ., 2022; Babakhani *et al* ., 2025). This late-phase homogenization, likely due to symbiotic remodeling, reflects the host's changes in metabolic pathways to

the new profile of the lipid and amino acid—though still in remodel phase (Muigano *et al* ., 2025; Moreira Gobis *et al* ., 2024). Analogous results are documented in the high-fat and western-diet models, where dissimilarity of composition peaks in the beginning and later decreases as microbial communities adjust to the nutrient and immune milieu (Yi *et al* ., 2025; Martínez-García et al ., 2024). In this regard, the PCoA results further support that goose-yolk supplementation has an active, time-dependent effect on the structure of the gut community—disrupt and, later, stabilize, which aligns with metabolic feedback loops that reconcile dietary intake, immune balance, and microbial ecosystem equilibrium.

5-3 : ELISA:

5-3-1 : ELISA IL-6 concentration :

As discussed, the IL-6 pattern is a time-dependent inflammatory signal that varies by yolk type with an earlier spike under goose yolk and a later, stronger spike under chicken yolk. IL-6 has been used extensively as a systemic inflammatory proxy in murine gut and metabolic models and is often cited as a proxy for barrier restoration and immune regulation in response to diet or microbiota-induced inflammation control.

In several studies of murine colitis, barrier protective compounds have shown a reduction of IL-6 along with improvements to mucus and epithelial integrity, which underlined the interpretation of IL-6 elevations as being a result of inflammatory load as opposed to merely a dietary exposure (Iddrisu *et al* ., 2021; Kase *et al* ., 2024; Kumar *et al* ., 2023). Egg yolk lipid intervention studies with DSS colitis have been documented to decrease inflammatory mediators and offer protection to the intestinal structure, which

served as a useful basis to explain the rationale for why IL-6 may be influenced by yolk composition and microbiota-driven signals over time (Xiao *et al* ., 2024). Given that the microbial mechanisms that weave together diet, bile acids, and systemic inflammation were also shown to modulate the cardiometabolic inflammatory tone, IL-6 may be considered as a result of diet-microbiota-metabolite interactions rather than just isolated cytokine noise (Pathak *et al* ., 2020; Maher *et al* ., 2023)

5-3-2: ELISA IL-10 concentration :

The increases in IL-10 have been characterized as a form of compensatory anti-inflammatory signaling, with the most pronounced late IL-10 under chicken yolk indicating stronger counter-regulation at day 30. IL-10 was often described as a brake on the excessive mucosal inflammation and as a signal that the immune resolution pathways were being actively engaged.

Kumar (2023) noted improved barriers and decreased pro-inflammatory cytokines along with increased anti-inflammatory cytokines (including IL-10) when there was strengthening of mucus and tight-junctions. Similar findings were noted by Yang (2022 and Xiao (2024) when reporting dietary polyphenols and functional-food models. It was observed that when there was an improvement of colitis severity, and an enhancement of barrier proteins and goblet-cell/mucin indices, there were increased IL-10 levels. This linked the increase to variations noted- both mucus and epithelial (biochemical) defenses. In all groups over the relevant times, it was noted that IL-10 had progressively increased. It may suggest an adaptation by the immune system – and it was in response to altered dietary (and microbiomic) exposures. This was noted by Mater(2024) and Xue (2025) when documenting immune systems (systemic and mucosal) progressively altered over time.

5.4: Histomorphometry:

5.4.1 : Histomorphometry of the Duodenum:

Significant expansion of the duodenal villi and deepening of the crypts are suggestive of a trophic mucosal response to facilitated yolk-driven nutrient and lipid delivery. An increase in villus height and area is associated with greater absorption surface, increased epithelial turnover, and especially when coupled with increased crypt depth, because active crypts were presumed to proxy for renewed, robust proliferative activity which under high luminal substrate pressure supported the development of more proximal, taller villi.

This pattern is consistent with the dietary bioactives and lipid fractions that preserve or restore the intestinal structures and barriers in mouse models in which epithelial integrity and goblet cell/mucin indices were improved during inflammatory challenges (Xiao *et al* ., 2024). One of the strongest findings associated with goose yolk was the largest villus area, which may be interpreted as a stronger mucosal “growth” signal, perhaps due to a bile acid–microbiota crosstalk and lipid modulation, as gut microbial pathways have been shown to influence host lipid metabolism and barrier (Pathak *et al* ., 2020; Maher *et al* ., 2023). Considering that the duodenum was also the first site of yolk lipid emulsification, segment-dominant effects were plausible in the <ck>duodenum, and the observed changes were consistent with a diet–microbiota–epithelium framework, where the epithelial response was a result of the available luminal nutrients and not due to a loss of epithelium (Ou *et al* ., 2025; Xiao *et al* ., 2024).

5.4.2: Histomorphometry of the jejunum:

In the jejunum, the emphasis was placed on villus width and area as compared to the depth of the crypt, so the remodeling was seen as surface optimization with the crypt proliferation remaining stable. This profile aligns with dietary interventions aimed at barriers where, in the absence of dominant inflammation, villi and mucosal functioning improved without a notable signature of crypt hyperplasia. Multiple studies on functional foods and microbiota modulation in mice noted improved mucosal functioning and, in many cases, improved barrier indices and decreased inflammation, without reliance on crypt pathology (Mater *et al* ., 2024; Person &Keefer *et al* ., 2021; Xue *et al* ., 2025). The progressive increase in the villus area from control to chicken yolk to goose yolk treatments may reflect a dose/quality response to yolk-derived lipids and micronutrients on the upkeep of the epithelium, with a steady-state support of villus architecture from gut microbial metabolites and immune signals downstream (Ou *et al* ., 2025; Xiao *et al* ., 2024). Diet-induced shifts in microbiota linked to the protective effect on barriers and decreased inflammation in murine models of gut inflammation also support this explanation (Ni Lochlainn *et al* ., 2021; Kumar *et al* ., 2023; Yang *et al* ., 2022).

5.4.3 : Histomorphometry of the Ileum

The selective changes in the ileum were analyzed as a response of the most distal segment, where an increase in villus length and area occurred while the width and crypts moderately increased. This pattern aligns with distal microbial fermentation and immune sampling influencing epithelial response as the ileum was particularly sensitive to microbiota dependent metabolic and

mucosal immune response. Consistently, prebiotic and microbiota focused approaches were documented to reverse barrier dysfunction and systemic inflammation through microbiota stability, with distal segments being emphasized as the microbial community composition was regularly associated with epithelial cohesiveness (Xue *et al* . 2025, Kumar *et al* . 2023). Yolk feeding promoting ileal villus growth can be examined in relation to mucus-barrier biology as increased goblet-cell activity and mucin were often linked to a better villus structure in the dietary modulation studies (Gu *et al* . 2022, Xiao *et al* . 2024, Yang *et al* . 2022). Stronger control-yolk differences in villus length and crypt depth were in line with distal adaptation rather than injury, as barrier-protective substances were shown to minimize inflammatory injury whilst restoring architecture in DSS and similar frameworks (Iddrisu *et al* . 2021, Kase *et al* . 2022, Kumar *et al* . 2023).

5.5: Photomicrograph

5.5.1: Photomicrograph of Duodenum H&E

The loss of duodenal layers coupled with greater villus height and richer crypt population was taken as evidence of adaptive remodeling as opposed to destructive inflammation. In the murine dietary intervention studies where remodeling of the epithelium was described as a form of protective remodeling, the maintenance of villus structure coupled with decreased structural disruption and enhanced mucosal layering, was seen when the microbiome and barrier function were positively modulated (Xiao *et al* ., 2024; Kumar *et al* ., 2023). An increase in the size of the villus was usually described as better absorptive capacity, while a greater population of crypts, was explained as a mechanism for renewal to cope with the stressed increased

lumen exposure to fats and bile-induced stressors which were often attributed to the microbiome (Pathak *et al* ., 2020; Maher *et al* ., 2023). Given that the duodenum was the first segment that received a high dose of lipids, a segment-first remodeling was anticipated, and functional improvement with structural preservation was also seen with microbiota-modulating diets that improved inflammation and barrier function (Mater *et al* ., 2024; Puri *et al* ., 2023).

5.5.2: Photomicrograph of Jejunum H&E

The jejunal H&E findings were characterized as stable mucosal architecture with prominent villi, which was in agreement with the morphometric evidence that villus expansion was the predominant response in this segment.

Functional nutrients have been documented in comparable murine studies to not only modify microbial communities but also reduce injury scores and protect the epithelial structure, which often resulted in the preserved arrangement of villi and diminished inflammatory disruptions (Yang *et al* ., 2022). Compared to the duodenum, the modest crypt response in the jejunum is likely due to the relatively low direct bile-lipid stress and the yolk feeding is suggested to have mucus and tight junction support, rather than crypt hyperplasia, as the primary compensatory mechanism (Gu *et al* ., 2022; Mater *et al* ., 2024). The good villus development associated with goose yolk feeding is probably due to the enhanced bioactive composition and the resulting diet-microbiota interactions, which are known to affect epithelial integrity as well as the immune response (O"Gardy *et al* ., 2019;Markowiak-Kopee &Slizewska., 2020; Xiao *et al* ., 2024).

5.5.3 : Photomicrograph of Ileum H&E

There was discussion on the distal adaptation and microbiota-induced reinforcement of the barrier on the ileum which preserved the tissue layers and resulted in increased villus height and crypt depth.

In models of Murine colitis and barriers, improved epithelial structures often coincided with decreased levels of pro-inflammatory cytokines, and improved features of mucus, tight junctions and other structures. This suggests the possibility of relapse in other inflammatory features when inflammatory drivers are reduced (Korpela *et al* ., 2014). The same phenomenon occurred when the epithelium of the ileum was renewed, where it was suggested that strong immune signaling and microbial metabolites renewed the epithelial structure. Thus, the deepening of the crypts in the ileum could be described as a renewed increased capacity to preserve the integrity of the villi, given the condition of the changing luminal substrates (Xiao *et al* ., 2024). The absence of a strong signal associated with a decrease in the width of a villus in morphometry could correspond to a remodeling pattern that is primarily dominated by increased length and surface elongation as opposed to a circumferential thickening—this was typically the case when remodeling improved constraining barriers without the addition of edema or inflammatory swelling (Rosado *et al* ., 2021).

5.5.4 : Photomicrograph of Duodenum Alcian Blue

Increased Alcian Blue positivity and goblet cell counts were interpreted positively as increased mucin production and enhancement to the mucus barrier. Reinforced mucus barrier was once again posited as a protective mechanism that was improved when a microbiota-diet interaction occurred, as

the mucin barrier reduced the interaction of bacteria to the epithelium and therefore improved immune protection.

Micobiota-directed factors that enhance mucin production have been documented, including the activity of Lactobacillus rhamnosus GG, which is said to boost mucin production via receptor-mediated signaling and modulation of the microbiota (Gu *et al* ., 2022). Interventions that include egg yolk lipids have been shown to Increase goblet cells and MUC2, while preserving barrier function in inflammatory models in mice. This is corroborated by the increased mucin production in the yolk-fed groups (Xiao *et al* ., 2024). the increased response observed in the goose yolk group is likely due to the increased stimulation of the mucus barrier remodeling. This would also concur with the existing literature of bioactive foods where improved mucus production and also reduced inflammatory damage (Lee *et al* ., 2023; Yang *et al* ., 2022).

5.5.5: Photomicrograph of Jejunum Alcian Blue

Increases in the positivity of mucin in the jejunum are indicative of the production of mucus, and suggest that production is occurring beyond the proximal segment of the intestine. This implies that there are adaptations in the defenses of the epithelial cells that are protective.

Multiple studies conducted on mouse models of dietary studies have documented that the strengthening of barriers has been associated with an increased mucous-related endpoints and improved composition of the microbiota, more so when the markers of inflammation were low and the structure of the villi was intact (Ni Lochlainn *et al* ., 2021; Mater *et al* ., 2024; Nordestgaard *et al* ., 2022). Increased mucin output was,

mechanistically, supported by the probiotic activity shown to increase mucin production via host signaling and microbiota, and was, therefore, used to justify increased Alcian under the diet that modified the atmospheric microbial structure (Gu *et al* ., 2022). Similarly, postbiotics and yeast-derived biotherapeutics were shown to maintain intestinal homeostasis and barrier function in DSS models, supporting the hypothesis that microbiota-induced signaling can enhance mucus secreting barriers in various intestinal sections, even the jejunum (Kumar *et al* ., 2023).

5.5.6 : Photomicrograph of Ileum Alcian Blue

Within the ileum, the increase in Alcian Blue positivity was interpreted as a distal strengthening of the mucous barrier and was particularly of interest as the ileum was a central area for microbial-host interaction and immune sampling. Numerous barrier-protective interventions in mice reported increasing goblet-cell/mucin-related endpoints and decreasing pro-inflammatory cytokines which reduced epithelial stress and preserved architecture (Lee *et al* ., 2023; Yang *et al* ., 2022). The prebiotic inulin was shown to reduce barrier dysfunction and systemic inflammation in chronic intermittent hypoxia models, which was attributed to microbiota-related mechanisms, and generally suggested distal mucus and barrier features could be improved by dietary modulation of microbiota ecology (Xue et al ., 2025). Thus, the ileal Alcian response was consistent with a model where yolk diets fostered epithelial defense by mucus reinforcement and microbiota-related immune modulation rather than through overt inflammatory injury (Xiao *et al* ., 2024).

Chapter six

Conclusions

&

Recommendations

6. Conclusions and recommendations

6.1 Conclusions

- Comparative studies involving goose egg yolk, chicken egg yolk and control group ($P < 0.05$) showed that supplementation with both goose egg yolk and chicken egg yolk transformed the composition and diversity of the gut microbiome in mice.
- Supplementation of egg yolks had a broader impact on the systemic immune response, and the result was captured in the differences in the levels of serum IL-6 and IL-10 among the study groups ($P < 0.05$).
- Experimental groups those provided egg yolk diets had a more expressed improvement of the intestinal mucosa (i.e. histomorphometry parameters) compared to the control group, such as the improvement of Intestinal Villus Length, Villus Width, Villus Area, and Crypt Depth, ($P < 0.05$).
- Across the parameters of this study, the impact that goose egg yolk had on the balance of the intestinal microbiome and the intestinal morphology compared to chicken egg yolk was more positive.
- The evidence presented here suggests that egg yolk as a dietary lipid source impacts the microbiome–immune axis and intestinal adaptations of mice.

6.2 Recommendations

- Incorporate Longitudinal Microbiome Monitoring in Nutritional Studies. Future research pertaining to diet should incorporate monitoring immune and microbial responses across longer timeframes to adequately resolve periods of dysbiotic perturbation and recovery.
- Synthesize Functional Metabolomics with Taxonomic Change. Integration of metagenomic data with microbial metabolism (SCFA, bile acid, and oxysterol) profiles will elucidate the mechanisms by which diet-derived microbial products influence host immune and metabolic functions.
- Examine the Anti-inflammatory Potential of Diet–Microbiome Interactions. Further research should target the modulation of cytokine profiles and intestinal permeability to determine the inflammatory pathways of altered microbiota regulation.
- Refine Dietary Targets to Promote Microbiome Stability. Reducing dietary lipid levels and increasing dietary fiber, polyphenol, and probiotic contents can enhance microbial diversity and avoid microbial composition imbalance over time.
- Apply Research Outcomes to Models of Human Nutrition. The observations from murine studies should be cross-validated in controlled human experiments to assess the extent to which intervening with yolk-derived lipids can beneficially modulate the microbiota, immune system, and metabolic derangements.

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Appendix

APPENDIXES

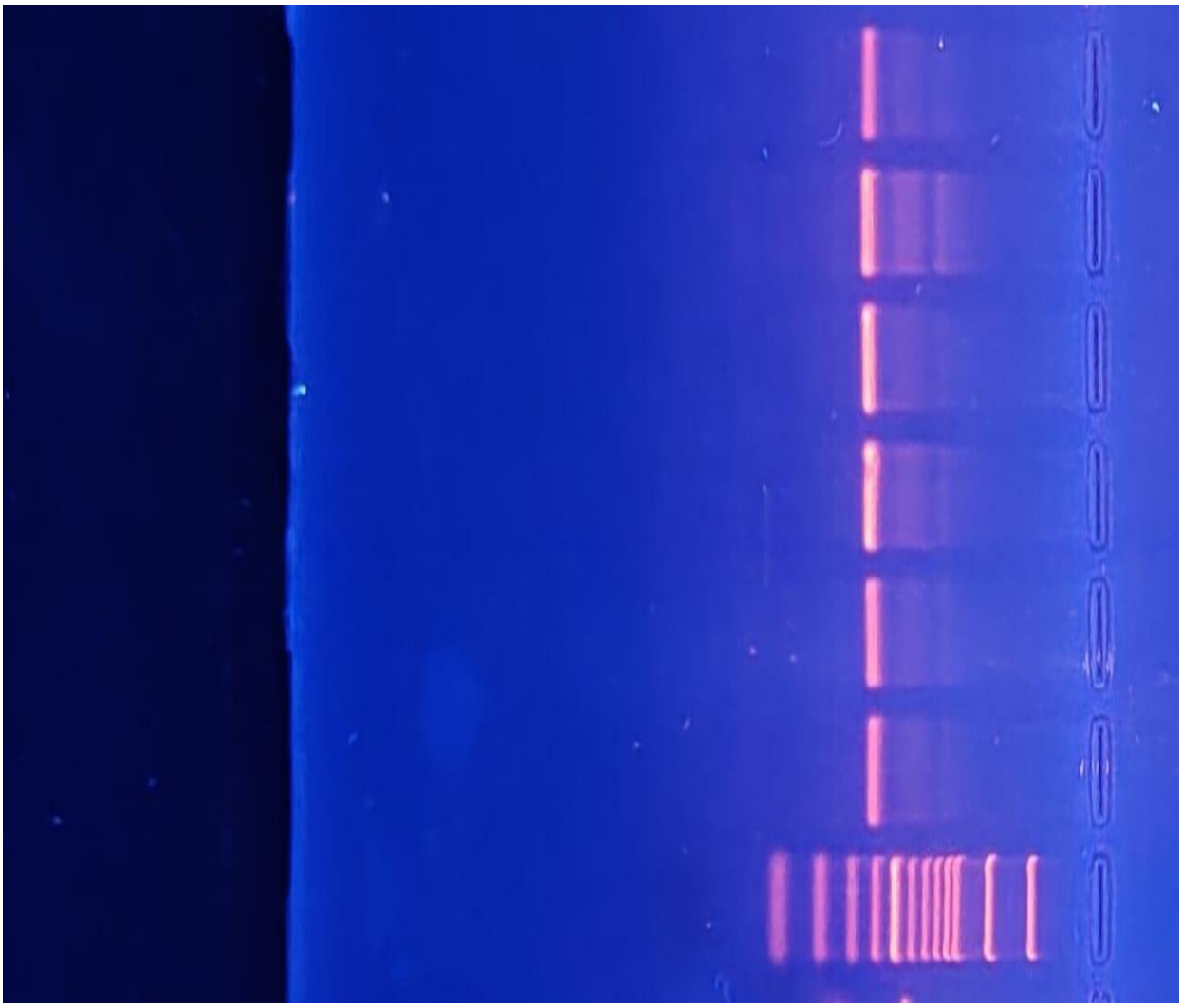


Figure appendix 1: Agarose gel for DNA evaluation after extraction

APPENDIXES

	Sample ID** (<15 letters)	Tube ID
1	DNA of fecal sample from mice	E1 G2/3
2	DNA of fecal sample from mice	E1 G2/4
3	DNA of fecal sample from mice	E1 G2/5
4	DNA of fecal sample from mice	E1 G3/1
5	DNA of fecal sample from mice	E1 G3/5
6	DNA of fecal sample from mice	E1 G3/3
7	DNA of fecal sample from mice	E1 C4
8	DNA of fecal sample from mice	E1 C5
9	DNA of fecal sample from mice	E1 C6
10	DNA of fecal sample from mice	E2 C1
11	DNA of fecal sample from mice	E2 C3
12	DNA of fecal sample from mice	E2 C5
13	DNA of fecal sample from mice	E2 G2/3
14	DNA of fecal sample from mice	E2 G2/4
15	DNA of fecal sample from mice	E2 G2/5
16	DNA of fecal sample from mice	E2 G3/2
17	DNA of fecal sample from mice	E2 G3/4
18	DNA of fecal sample from mice	E2 G3/6
19		

Appenix image 1 for sample sequencing IDs

Sample	Conc. (ng/µl)	260/280 Ratio	Interpretation
G3/1	52	1.76	Good purity, moderate concentration
G2/3	60	1.70	Slightly lower purity, still usable
G2/5	99.8	1.79	High concentration, very good purity
G3/5	60.7	1.73	Good purity, moderate concentration
C4	80	1.76	Good purity, good concentration
C6	142.32	1.84	Very high concentration, excellent purity

APPENDIXES

The Following is the raw data from sequencing and after quantification of sequences

Query	Taxonomy (bootstrap Score)							Taxonomy							Filter
Name	Domain	Phylum	Class	Order	Family	Genus	Species	domain	phylum	class	order	family	genus	species	Filter
ASV1	100	100	100	100	100	100	81	d__Bacteri	p__Bacillot	c__Bacilli	o__Lactob	f__Lactoba	g__Ligilact	s__Ligilactobacillus_apodemi	
ASV2	100	100	100	100	100	100	64	d__Bacteri	p__Bacillot	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	s__Lactobacillus_gallinarum	
ASV3	100	100	100	100	100	100	88	d__Bacteri	p__Bacillot	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	s__Lactobacillus_gasseri	
ASV4	100	13	6	5	5	5	5	d__Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV5	100	100	100	100	91	91	91	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubact	f__Eubacte	g__Eubact	s__Eubacterium_coprostanoligenes	
ASV6	100	97	96	96	96	40	40	d__Bacteri	p__Thermo	c__Desulfo	o__Desulfo	f__Desulfo	NA	NA	Filter: bootstrap Score >= 50
ASV7	100	100	100	100	100	86	84	d__Bacteri	p__Bacillot	c__Bacilli	o__Bacillal	f__Bacillac	g__Niallia	s__Niallia_tiangongensis	
ASV8	100	100	100	100	100	100	100	d__Bacteri	p__Bacillot	c__Bacilli	o__Lactob	f__Lactoba	g__Limosil	s__Limosilactobacillus_reuteri	
ASV9	100	100	100	100	100	100	78	d__Bacteri	p__Bacillot	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	s__Lactobacillus_gasseri	
ASV10	100	97	96	94	64	29	29	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV11	100	100	100	100	100	100	61	d__Bacteri	p__Bacillot	c__Bacilli	o__Bacillal	f__Paeniba	g__Brevib	s__Brevibacillus_borstelensis	
ASV12	100	100	100	100	100	100	100	d__Bacteri	p__Bacteroi	c__Bacteroi	o__Bacteroi	f__Bacteroi	g__Bacteroi	s__Bacteroides_acidifaciens	
ASV13	99	46	9	9	9	3	3	d__Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV14	100	100	100	100	100	100	96	d__Bacteri	p__Bacillot	c__Erysipe	o__Erysipe	f__Turiciba	g__Turicib	s__Turicibacter_bilis	
ASV15	100	100	100	100	100	100	100	d__Bacteri	p__Campyl	c__Epsilon	o__Campyl	f__Helicob	g__Helicob	s__Helicobacter_typhlonius	
ASV16	100	100	100	100	100	29	26	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV17	99	47	26	26	26	5	5	d__Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV18	100	9	7	5	5	5	5	d__Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV19	98	48	8	8	8	6	6	d__Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV20	100	100	100	100	100	100	99	d__Bacteri	p__Bacteroi	c__Bacteroi	o__Bacteroi	f__Bacteroi	g__Bacteroi	s__Bacteroides_acidifaciens	
ASV21	100	100	100	100	100	100	99	d__Bacteri	p__Bacillot	c__Bacilli	o__Bacillal	f__Paeniba	g__Paenib	s__Paenibacillus_glucanolyticus	
ASV22	100	100	100	100	97	86	86	d__Bacteri	p__Bacteroi	c__Bacteroi	o__Bacteroi	f__Prevote	g__Alloprev	s__Alloprevotella_rava	
ASV23	100	100	100	100	99	93	92	d__Bacteri	p__Bacillot	c__Clostrid	o__Peptost	f__Peptost	g__Romboi	s__Romboutsia_timonensis	
ASV24	100	100	100	100	100	100	50	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubact	f__Clostrid	g__Clostrid	s__Clostridium_tertium	
ASV25	100	100	100	100	100	100	73	d__Bacteri	p__Bacillot	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	s__Lactobacillus_gasseri	
ASV26	100	100	100	93	93	31	29	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV27	100	100	100	100	100	100	19	d__Bacteri	p__Bacillot	c__Bacilli	o__Bacillal	f__Paenib	g__Brevib	NA	Filter: bootstrap Score >= 50
ASV28	100	100	100	100	98	63	63	d__Bacteri	p__Bacteroi	c__Bacteroi	o__Bacteroi	f__Prevote	g__Alloprev	s__Alloprevotella_rava	
ASV29	100	100	100	100	100	100	98	d__Bacteri	p__Bacillot	c__Bacilli	o__Bacillal	f__Paenib	g__Paenib	s__Paenibacillus_glucanolyticus	
ASV30	99	98	91	70	70	27	27	d__Bacteri	p__Bacillot	c__Negativ	o__Seleno	f__Seleno	NA	NA	Filter: bootstrap Score >= 50
ASV31	100	100	100	100	100	100	65	d__Bacteri	p__Bacillot	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	s__Lactobacillus_gasseri	
ASV32	100	100	78	62	30	21	21	d__Bacteri	p__Bacteroi	c__Bacteroi	o__Bacteroi	NA	NA	NA	Filter: bootstrap Score >= 50
ASV33	100	100	100	100	100	100	100	d__Bacteri	p__Bacteroi	c__Bacteroi	o__Bacteroi	f__Muriba	g__Dunca	s__Duncaniella_muricolitica	
ASV34	100	100	100	87	87	44	19	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV35	100	100	100	100	100	100	100	d__Bacteri	p__Bacteroi	c__Bacteroi	o__Bacteroi	f__Bacteroi	g__Phoca	s__Phocaeicola_vulgatus	
ASV36	100	100	100	100	100	100	100	d__Bacteri	p__Bacteroi	c__Bacteroi	o__Bacteroi	f__Muriba	g__Dunca	s__Duncaniella_muris	
ASV37	100	100	100	100	100	100	100	d__Bacteri	p__Deferri	c__Deferri	o__Deferri	f__Mucisp	g__Mucisp	s__Mucispirillum_schaedleri	
ASV38	100	100	100	100	100	100	94	d__Bacteri	p__Bacillot	c__Bacilli	o__Lactob	f__Lactoba	g__Limosil	s__Limosilactobacillus_reuteri	
ASV39	100	100	100	100	100	78	20	d__Bacteri	p__Bacillot	c__Clostrid	o__Peptost	f__Peptost	g__Terrisp	NA	Filter: bootstrap Score >= 50
ASV40	100	100	100	100	100	100	100	d__Bacteri	p__Thermo	c__Desulfo	o__Desulfo	f__Desulfo	g__Lawso	s__Lawsonia_intracellularis	
ASV41	100	100	100	100	100	100	55	d__Bacteri	p__Bacteroi	c__Bacteroi	o__Bacteroi	f__Bacteroi	g__Bacteroi	s__Bacteroides_oleiciplenus	
ASV42	100	100	100	100	100	100	98	d__Bacteri	p__Bacteroi	c__Bacteroi	o__Bacteroi	f__Bacteroi	g__Phoca	s__Phocaeicola_vulgatus	
ASV43	100	100	100	100	100	100	100	d__Bacteri	p__Bacteroi	c__Bacteroi	o__Bacteroi	f__Muriba	g__Dunca	s__Duncaniella_muris	
ASV44	100	100	100	100	100	44	43	d__Bacteri	p__Bacteroi	c__Bacteroi	o__Bacteroi	f__Muriba	NA	NA	Filter: bootstrap Score >= 50
ASV45	99	34	8	8	8	4	4	d__Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV46	100	100	100	100	100	100	23	d__Bacteri	p__Bacillot	c__Bacilli	o__Bacillal	f__Staphyl	g__Staphy	NA	Filter: bootstrap Score >= 50
ASV47	100	100	100	100	100	100	98	d__Bacteri	p__Bacillot	c__Bacilli	o__Lactob	f__Lactoba	g__Limosil	s__Limosilactobacillus_reuteri	
ASV48	100	100	100	100	100	94	82	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubact	f__Oscillos	g__Rumin	s__Ruminococcus_callidus	

Taxonomy assignment

APPENDIXES

ASV49	100	100	100	100	100	100	99	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteroi	f_Bacteroi	g_Bacteroi	s_Bacteroides_acidifaciens	
ASV50	100	98	98	98	98	47	47	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachnos	f_Lachnos	NA	NA	Filter: bootstrap Score >= 50
ASV51	100	100	100	100	100	100	100	d_Bacteri	p_Spiroch	c_Spiroch	o_Spiroch	f_Treponi	g_Treponi	s_Treponema_bryantii	
ASV52	100	100	100	100	100	100	100	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteroi	f_Muribac	g_Duncani	s_Duncaniella_dubosii	
ASV53	100	100	100	100	100	100	97	d_Bacteri	p_Bacillo	c_Clostrid	o_Eubacte	f_Clostrid	g_Clostrid	s_Clostridium_butyricum	
ASV54	99	6	2	2	2	2	2	d_Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV55	100	100	100	99	99	61	25	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachnos	f_Lachnos	g_Lacrimi	NA	Filter: bootstrap Score >= 50
ASV56	100	100	100	100	100	100	100	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteroi	f_Muribac	g_Sangeri	s_Sangeribacter_muris	
ASV57	100	100	100	100	100	100	40	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteroi	f_Bacteroi	g_Bacteroi	NA	Filter: bootstrap Score >= 50
ASV58	100	100	100	99	99	99	99	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachnos	f_Lachnos	g_Schaedl	s_Schaedlerella_arabinosiphila	
ASV59	100	100	100	100	100	100	100	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteroi	f_Bacteroi	g_Phocaei	s_Phocaeicola_vulgatus	
ASV60	100	100	100	100	100	100	99	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteroi	f_Tannere	g_Parabac	s_Parabacteroides_distasonis	
ASV61	99	40	17	17	16	1	1	d_Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV62	100	100	100	100	100	100	88	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteroi	f_Rikenel	g_Alistipe	s_Alistipes_finegoldii	
ASV63	100	100	100	11	6	6	1	d_Bacteri	p_Bacillo	c_Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV64	100	100	100	71	71	19	19	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachnos	f_Lachnos	NA	NA	Filter: bootstrap Score >= 50
ASV65	100	100	100	100	100	100	100	d_Bacteri	p_Pseudo	c_Gammap	o_Moraxe	f_Moraxe	g_Moraxe	s_Moraxella_osloensis	
ASV66	100	100	100	100	100	100	87	d_Bacteri	p_Bacillo	c_Bacilli	o_Lactob	f_Lactoba	g_Lactob	s_Lactobacillus_gasseri	
ASV67	100	100	100	100	100	100	100	d_Bacteri	p_Bacillo	c_Bacilli	o_Lactob	f_Lactoba	g_Limosil	s_Limosilactobacillus_reuteri	
ASV68	100	100	100	100	100	100	100	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteroi	f_Muribac	g_Muribac	s_Muribaculum_intestinale	
ASV69	100	100	100	100	100	100	100	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteroi	f_Bacteroi	g_Phocaei	s_Phocaeicola_vulgatus	
ASV70	100	100	100	49	43	43	39	d_Bacteri	p_Bacillo	c_Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV71	100	100	100	100	100	100	95	d_Bacteri	p_Bacillo	c_Bacilli	o_Bacillal	f_Paenib	g_Paenib	s_Paenibacillus_glucanolyticus	
ASV72	100	100	100	100	100	70	61	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteroi	f_Muribac	g_Muribac	s_Muribaculum_intestinale	
ASV73	100	100	100	100	100	100	87	d_Bacteri	p_Bacillo	c_Bacilli	o_Lactob	f_Lactoba	g_Ligilact	s_Ligilactobacillus_faecis	
ASV74	100	100	100	99	99	37	32	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachnos	f_Lachnos	NA	NA	Filter: bootstrap Score >= 50
ASV75	100	100	99	99	94	61	61	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteroi	f_Muribac	g_Muribac	s_Muribaculum_intestinale	
ASV76	100	100	100	100	100	100	69	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteroi	f_Rikenel	g_Alistipe	s_Alistipes_dispar	
ASV77	100	100	100	57	53	53	46	d_Bacteri	p_Bacillo	c_Clostrid	o_Eubacte	f_Clostrid	g_Clostrid	NA	Filter: bootstrap Score >= 50
ASV78	100	100	100	100	100	30	30	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachnos	f_Lachnos	NA	NA	Filter: bootstrap Score >= 50
ASV79	100	100	100	100	100	39	39	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteroi	f_Muribac	NA	NA	Filter: bootstrap Score >= 50
ASV80	100	100	100	100	100	100	39	d_Bacteri	p_Bacillo	c_Bacilli	o_Lactob	f_Lactoba	g_Lactob	NA	Filter: bootstrap Score >= 50
ASV81	100	100	100	100	99	35	34	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteroi	f_Prevote	NA	NA	Filter: bootstrap Score >= 50
ASV82	100	100	100	93	93	19	19	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachnos	f_Lachnos	NA	NA	Filter: bootstrap Score >= 50
ASV83	100	100	100	100	100	77	77	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachnos	f_Lachnos	g_Lachnos	s_[Clostridium]_scindens	
ASV84	100	100	100	94	94	50	19	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachnos	f_Lachnos	g_Lacrimi	NA	Filter: bootstrap Score >= 50
ASV85	100	100	100	100	100	100	85	d_Bacteri	p_Bacillo	c_Erysipe	o_Erysipe	f_Coprob	g_Thomas	s_Thomasclavelia_cocleata	
ASV86	100	45	16	16	12	1	1	d_Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV87	99	12	9	9	9	9	9	d_Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV88	100	100	100	100	100	100	67	d_Bacteri	p_Bacillo	c_Bacilli	o_Lactob	f_Lactoba	g_Limosil	s_Limosilactobacillus_reuteri	
ASV89	100	100	100	100	100	100	97	d_Bacteri	p_Bacillo	c_Bacilli	o_Lactob	f_Strepto	g_Strepto	s_Streptococcus_hyointestinalis	
ASV90	100	99	99	84	84	29	29	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachnos	f_Lachnos	NA	NA	Filter: bootstrap Score >= 50
ASV91	100	100	100	100	100	100	100	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteroi	f_Muribac	g_Duncani	s_Duncaniella_muricolitica	
ASV92	100	100	100	100	100	52	52	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteroi	f_Muribac	g_Duncani	s_Duncaniella_muris	
ASV93	100	100	100	100	100	100	93	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteroi	f_Bacteroi	g_Bacteroi	s_Bacteroides_acidifaciens	
ASV94	100	100	100	100	100	95	86	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteroi	f_Muribac	g_Duncani	s_Duncaniella_dubosii	
ASV95	100	100	100	21	21	20	18	d_Bacteri	p_Bacillo	c_Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV96	100	100	100	100	100	100	36	d_Bacteri	p_Bacillo	c_Bacilli	o_Lactob	f_Lactoba	g_Lactob	NA	Filter: bootstrap Score >= 50
ASV97	100	47	47	47	47	47	47	d_Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV98	100	100	100	100	100	29	10	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteroi	f_Prevote	NA	NA	Filter: bootstrap Score >= 50

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ASV99	100	100	100	100	100	100	100	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	g__Duncar	s__Duncaniella_dubosii		
ASV100	100	100	100	100	100	100	100	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	g__Muriba	s__Muribaculum_intestinale		
ASV101	100	100	92	92	61	33	33	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Prevote	NA	NA	Filter: bootstrap Score >= 50	
ASV102	100	100	100	100	100	100	73	d__Bacteri	p__Campy	c__Epsilon	o__Campy	f__Helicob	g__Helicot	s__Helicobacter_ganmani		
ASV103	100	100	100	100	100	99	95	d__Bacteri	p__Pseudo	c__Gamma	o__Entero	f__Enterob	g__Escher	s__Escherichia_fergusonii		
ASV104	100	100	100	91	91	25	24	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50	
ASV105	100	100	100	100	100	97	67	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Strepto	g__Lactoc	s__Lactococcus_formosensis		
ASV106	100	99	99	98	98	66	33	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Faecal	NA	Filter: bootstrap Score >= 50	
ASV107	100	75	31	31	29	17	12	d__Bacteri	p__Bacillo	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV108	100	100	100	100	100	94	69	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	f__Erysipe	g__Amedi	s__Amedibacillus_hominis		
ASV109	100	100	100	100	100	74	73	d__Bacteri	p__Bacillo	c__Bacilli	o__Bacilla	f__Bacilla	g__Niallia	s__Niallia_tiangongensis		
ASV110	100	100	100	99	99	68	34	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Lacrim	NA	Filter: bootstrap Score >= 50	
ASV111	100	100	99	98	94	33	33	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	NA	NA	Filter: bootstrap Score >= 50	
ASV112	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Limosi	s__Limosilactobacillus_reuteri		
ASV113	100	100	100	100	45	45	45	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV114	100	100	100	98	98	59	26	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Lacrim	NA	Filter: bootstrap Score >= 50	
ASV115	100	100	100	98	98	59	20	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Lacrim	NA	Filter: bootstrap Score >= 50	
ASV116	100	100	100	99	99	50	45	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Dorea	NA	Filter: bootstrap Score >= 50	
ASV117	100	98	98	93	93	12	12	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50	
ASV118	100	99	85	31	24	8	8	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV119	100	100	100	100	100	100	100	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	g__Param	s__Paramuribaculum_intestinale		
ASV120	100	100	100	100	94	55	49	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Odoriba	g__Odorib	NA	Filter: bootstrap Score >= 50	
ASV121	100	100	100	100	100	100	52	d__Bacteri	p__Campy	c__Epsilon	o__Campy	f__Helicob	g__Helicot	s__Helicobacter_ganmani		
ASV122	100	100	100	100	100	60	60	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Lachno	s__[Clostridium]_scindens		
ASV123	100	100	100	88	88	55	27	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Lacrim	NA	Filter: bootstrap Score >= 50	
ASV124	100	100	100	100	100	75	70	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Odoriba	g__Odorib	s__Odoribacter_splanchnicus		
ASV125	100	99	99	99	99	96	92	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Medite	s__Mediterraneibacter_glycyrrhizinilyticus		
ASV126	100	100	100	100	100	100	100	d__Bacteri	p__Deferri	c__Deferri	o__Deferri	f__Mucisp	g__Mucisp	s__Mucispirillum_schaedleri		
ASV127	100	100	100	100	100	94	94	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Lachno	s__[Clostridium]_scindens		
ASV128	100	100	100	100	87	43	43	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	NA	NA	Filter: bootstrap Score >= 50	
ASV129	100	100	100	100	99	45	44	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	NA	NA	Filter: bootstrap Score >= 50	
ASV130	100	100	100	100	100	100	100	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	g__Sanger	s__Sangeribacter_muris		
ASV131	100	100	100	100	100	94	67	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	f__Erysipe	g__Amedi	s__Amedibacillus_hominis		
ASV132	100	100	100	100	100	29	29	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50	
ASV133	100	100	100	92	92	59	15	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Lacrim	NA	Filter: bootstrap Score >= 50	
ASV134	100	100	100	100	100	99	61	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Limosi	s__Limosilactobacillus_reuteri		
ASV135	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	g__Neglec	s__Neglectibacter_caecimuris		
ASV136	100	100	100	100	99	35	35	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	NA	NA	Filter: bootstrap Score >= 50	
ASV137	100	100	100	100	100	100	100	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	g__Duncar	s__Duncaniella_freteri		
ASV138	100	100	100	100	100	88	72	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	f__Erysipe	g__Amedi	s__Amedibacillus_dolichus		
ASV139	100	100	100	100	95	54	54	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	g__Sanger	s__Sangeribacter_muris		
ASV140	100	100	100	100	100	100	39	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Rikene	g__Alistipe	NA	Filter: bootstrap Score >= 50	
ASV141	100	100	100	100	100	42	38	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Butyrici	NA	NA	Filter: bootstrap Score >= 50	
ASV142	100	100	100	100	100	100	100	d__Bacteri	p__Pseudo	c__Gamma	o__Pasteu	f__Pasteu	g__Haemo	s__Haemophilus_parainfluenzae		
ASV143	100	100	100	100	87	37	29	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	NA	NA	Filter: bootstrap Score >= 50	
ASV144	100	100	100	100	100	100	94	d__Bacteri	p__Therm	c__Desulfo	o__Desulfi	f__Desulfo	g__Desulfo	s__Desulfovibrio_porci		
ASV145	100	100	100	100	99	96	96	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	g__Duncar	s__Duncaniella_muris		
ASV146	100	100	100	100	100	100	100	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	g__Sanger	s__Sangeribacter_muris		
ASV147	100	100	100	98	98	57	57	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Kineot	s__Kineothrix_alysoides		
ASV148	100	100	100	100	100	76	76	d__Bacteri	p__Pseudo	c__Betapro	o__Burkho	f__Sutterel	g__Parasu	s__Parasutterella_excrementihominis		

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ASV149	100	100	100	95	95	39	36	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV150	100	100	100	100	100	100	96	d_Bacteri	p_Bacillo	c_Bacilli	o_Lactob	f_Lactoba	g_Limosil	s_Limosilactobacillus_reuteri	
ASV151	100	100	100	89	89	10	3	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV152	100	100	100	100	100	100	54	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteri	f_Rikenel	g_Alistipe	s_Alistipes_shahii	
ASV153	100	100	100	100	100	69	62	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteri	f_Muriba	g_Muriba	s_Muribaculum_intestinale	
ASV154	100	100	100	100	100	100	38	d_Bacteri	p_Bacillo	c_Clostrid	o_Eubact	f_Clostrid	g_Clostrid	NA	Filter: bootstrap Score >= 50
ASV155	100	100	100	86	86	31	31	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV156	100	100	100	100	77	56	12	d_Bacteri	p_Therm	c_Desulfo	o_Desulfo	f_Desulfo	g_Desulfo	NA	Filter: bootstrap Score >= 50
ASV157	100	100	100	100	97	31	21	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteri	f_Muriba	NA	NA	Filter: bootstrap Score >= 50
ASV158	100	100	100	100	99	57	57	d_Bacteri	p_Bacillo	c_Clostrid	o_Eubact	f_Oscillos	g_Merdin	s_Merdimmobilis_hominis	
ASV159	100	100	100	99	99	44	8	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV160	100	100	100	100	100	100	100	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteri	f_Muriba	g_Muriba	s_Muribaculum_intestinale	
ASV161	100	100	100	93	93	42	42	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV162	100	100	100	100	87	87	87	d_Bacteri	p_Bacillo	c_Clostrid	o_Eubact	f_Eubacte	g_Eubacte	s_Eubacterium_coprostanoligenes	
ASV163	100	100	100	97	97	7	7	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV164	100	100	100	98	98	64	64	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	g_Kineoth	s_Kineothrix_alysoides	
ASV165	100	100	100	100	100	76	76	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteri	f_Muriba	g_Duncan	s_Duncaniella_muris	
ASV166	100	100	100	100	100	52	52	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteri	f_Rikenel	g_Rikenel	s_Rikenella_microfusus	
ASV167	100	100	100	80	80	29	25	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV168	100	100	100	100	100	67	67	d_Bacteri	p_Bacillo	c_Clostrid	o_Eubact	f_Oscillos	g_Rumin	s_Ruminococcus_bromii	
ASV169	100	100	100	96	96	46	30	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV170	100	100	100	100	100	100	55	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteri	f_Rikenel	g_Alistipe	s_Alistipes_putredinis	
ASV171	100	100	100	100	100	62	62	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	g_Mediter	s_Mediterraneibacter_gnavus	
ASV172	100	100	100	97	97	75	75	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	g_Kineoth	s_Kineothrix_alysoides	
ASV173	100	99	94	47	34	12	12	d_Bacteri	p_Bacillo	c_Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV174	100	100	100	100	100	100	99	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteri	f_Tanner	g_Paraba	s_Parabacteroides_distasonis	
ASV175	100	100	51	42	38	15	15	d_Bacteri	p_Bacteri	c_Bacteroi	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV176	100	100	100	100	100	31	5	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteri	f_Prevote	NA	NA	Filter: bootstrap Score >= 50
ASV177	100	100	100	42	41	41	41	d_Bacteri	p_Bacillo	c_Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV178	100	100	100	100	100	100	96	d_Bacteri	p_Bacillo	c_Bacilli	o_Lactob	f_Strepto	g_Strepto	s_Streptococcus_danieliae	
ASV179	100	100	100	98	98	66	66	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	g_Kineoth	s_Kineothrix_alysoides	
ASV180	100	100	100	100	98	84	49	d_Bacteri	p_Bacillo	c_Clostrid	o_Eubact	f_Oscillos	g_Vescim	NA	Filter: bootstrap Score >= 50
ASV181	100	100	100	100	99	99	99	d_Bacteri	p_Bacillo	c_Clostrid	o_Eubact	f_	g_Flintiba	s_Flintibacter_butyricus	
ASV182	100	100	100	66	66	41	41	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV183	100	100	99	99	99	91	56	d_Bacteri	p_Bacillo	c_Erysipe	o_Erysipe	f_Erysipe	g_Amedi	s_Amedibacillus_dolichus	
ASV184	100	100	100	100	100	100	64	d_Bacteri	p_Bacillo	c_Bacilli	o_Bacilla	f_Staphyl	g_Staphy	s_Staphylococcus_haemolyticus	
ASV185	100	100	96	79	78	75	3	d_Bacteri	p_Bacillo	c_Clostrid	o_Eubact	f_Clostrid	g_Clostrid	NA	Filter: bootstrap Score >= 50
ASV186	100	100	100	100	94	52	52	d_Bacteri	p_Bacillo	c_Erysipe	o_Erysipe	f_Coprob	g_Longib	s_Longibaculum_muris	
ASV187	100	100	98	98	95	56	56	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteri	f_Muriba	g_Sangeri	s_Sangeribacter_muris	
ASV188	100	100	100	100	100	100	86	d_Bacteri	p_Bacillo	c_Clostrid	o_Eubact	f_Oscillos	g_Rumin	s_Ruminococcus_flavefaciens	
ASV189	100	89	88	17	16	16	16	d_Bacteri	p_Bacillo	c_Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV190	100	100	100	100	100	100	100	d_Bacteri	p_Bacillo	c_Bacilli	o_Lactob	f_Aeroco	g_Aeroco	s_Aerococcus_viridans	
ASV191	100	100	100	82	82	21	16	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV192	100	100	100	100	100	100	57	d_Bacteri	p_Bacillo	c_Clostrid	o_Eubact	f_Clostrid	g_Clostrid	s_Clostridium_butyricum	
ASV193	100	96	96	86	86	30	30	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV194	100	100	100	100	100	100	100	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteri	f_Muriba	g_Muriba	s_Muribaculum_gordoncarteri	
ASV195	100	8	3	2	2	2	2	d_Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV196	100	100	100	80	80	23	23	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV197	100	99	99	92	92	47	21	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV198	100	100	100	98	98	15	15	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	NA	NA	Filter: bootstrap Score >= 50

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ASV199	100	100	100	92	92	57	28	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	g__Roseb	NA	Filter: bootstrap Score >= 50
ASV200	100	100	100	28	28	28	21	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV201	100	100	100	100	100	45	45	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV202	100	100	100	90	90	13	3	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV203	100	100	100	100	100	100	63	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Rikene	g__Alistipe	s__Alistipes_dispar	
ASV204	100	100	90	64	52	28	28	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV205	100	100	100	100	94	56	56	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__	g__Colide	s__Colidextribacter_massiliensis	
ASV206	100	100	100	99	99	72	72	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	g__Fusimo	s__Fusimonas_intestini	
ASV207	100	100	100	93	93	61	61	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	g__Kineoth	s__Kineothrix_alysoides	
ASV208	100	100	100	100	100	73	73	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	g__Dunca	s__Duncaniella_muris	
ASV209	100	100	100	100	100	91	73	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	g__Dunca	s__Duncaniella_muris	
ASV210	100	100	100	100	100	100	64	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	s__Lactobacillus_gallinarum	
ASV211	100	99	99	99	99	19	17	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV212	100	90	82	18	13	13	13	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV213	100	100	100	100	100	100	41	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Limosi	NA	Filter: bootstrap Score >= 50
ASV214	100	100	100	100	95	35	9	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Prevote	NA	NA	Filter: bootstrap Score >= 50
ASV215	100	100	100	100	70	49	49	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV216	100	100	100	100	100	100	98	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Limosi	s__Limosilactobacillus_reuteri	
ASV217	100	100	100	100	94	74	44	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	g__Dunca	NA	Filter: bootstrap Score >= 50
ASV218	100	100	100	98	98	8	8	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV219	100	100	100	100	100	100	100	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Bacterd	g__Phoca	s__Phocaeicola_sartorii	
ASV220	100	100	98	91	87	46	46	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	NA	NA	Filter: bootstrap Score >= 50
ASV221	100	100	100	100	100	86	38	d__Bacteri	p__Bacillo	c__Clostrid	o__Peptost	f__Peptost	g__Terrisp	NA	Filter: bootstrap Score >= 50
ASV222	100	100	100	100	100	73	73	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	g__Kineoth	s__Kineothrix_alysoides	
ASV223	100	100	100	100	100	100	100	d__Bacteri	p__Deferri	c__Deferri	o__Deferri	f__Mucisp	g__Mucisp	s__Mucispirillum_schaedleri	
ASV224	100	100	100	100	100	24	24	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	NA	NA	Filter: bootstrap Score >= 50
ASV225	100	100	100	83	83	24	24	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV226	100	100	100	100	100	72	72	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	g__Fusimo	s__Fusimonas_intestini	
ASV227	100	100	100	100	99	49	49	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	NA	NA	Filter: bootstrap Score >= 50
ASV228	100	100	100	74	73	73	65	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Clostrid	g__Clostrid	s__Clostridium_porci	
ASV229	100	100	99	99	99	85	44	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	f__Erysipe	g__Amedi	NA	Filter: bootstrap Score >= 50
ASV230	100	100	100	100	100	100	79	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Bacterd	g__Bacter	s__Bacteroides_caecimuris	
ASV231	100	100	99	99	99	79	53	d__Bacteri	p__Mycopl	c__	o__Mycopl	f__Mycopl	g__Malaco	s__Malacoplasma_micruti	
ASV232	100	100	100	97	96	12	12	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV233	100	100	100	100	86	86	86	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Eubact	g__Eubact	s__Eubacterium_coprostanoligenes	
ASV234	100	100	100	100	100	81	80	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	g__	s__[Eubacterium]_siraeum	
ASV235	100	100	100	100	100	96	95	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Ligilact	s__Ligilactobacillus_ruminis	
ASV236	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Bacilli	o__Bacilla	f__Staphyl	g__Staphyl	s__Staphylococcus_aureus	
ASV237	100	100	100	99	99	68	68	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	g__Oscillib	s__Oscillibacter_valericigenes	
ASV238	100	100	100	99	99	51	51	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	g__Fusimo	s__Fusimonas_intestini	
ASV239	100	100	100	62	62	42	42	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV240	100	98	93	47	17	16	11	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV241	100	100	100	99	99	86	30	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	g__Lacrim	NA	Filter: bootstrap Score >= 50
ASV242	100	99	91	72	64	16	16	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV243	100	100	100	100	93	77	47	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	g__Dunca	NA	Filter: bootstrap Score >= 50
ASV244	100	100	100	72	72	34	29	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV245	100	100	100	100	100	100	32	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Rikene	g__Alistipe	NA	Filter: bootstrap Score >= 50
ASV246	100	100	100	83	83	51	51	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	g__Kineoth	s__Kineothrix_alysoides	
ASV247	100	100	100	100	100	100	82	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Strepto	g__Strepto	s__Streptococcus_danieliae	
ASV248	100	95	86	31	17	14	11	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50

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ASV249	100	74	70	12	12	10	9	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV250	100	100	100	98	98	51	51	d__Bacteri	p__Bacillo	c__Clostrid	o__Christe	f__Christe	g__Guopin	s__Guopingia_tenuis	
ASV251	100	99	99	99	95	95	87	d__Bacteri	p__Spiroch	c__Spiroch	o__Spiroch	f__Trepon	g__Trepon	s__Treponema_succinifaciens	
ASV252	100	100	100	100	100	100	51	d__Bacteri	p__Spiroch	c__Spiroch	o__Spiroch	f__Trepon	g__Trepon	s__Treponema_brennaborense	
ASV253	100	100	99	99	98	97	73	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Muriba	g__Dunca	s__Duncaniella_muris	
ASV254	100	100	100	100	100	34	34	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Muriba	NA	NA	Filter: bootstrap Score >= 50
ASV255	100	100	100	100	72	68	55	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__	g__Intestin	s__Intestinimonas_timonensis	
ASV256	100	100	100	100	100	100	59	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Rikene	g__Alistipe	s__Alistipes_shahii	
ASV257	100	100	95	95	95	73	67	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	f__Erysipe	g__Amedi	s__Amedibacillus_dolichus	
ASV258	100	100	100	97	97	57	56	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Anaero	s__Anaerostipes_butyraticus	
ASV259	100	100	100	100	100	35	35	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Muriba	NA	NA	Filter: bootstrap Score >= 50
ASV260	100	100	100	100	90	56	29	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Muriba	g__Dunca	NA	Filter: bootstrap Score >= 50
ASV261	100	100	100	100	100	100	97	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Limosi	s__Limosilactobacillus_reuteri	
ASV262	100	100	100	100	100	100	100	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Muriba	g__Param	s__Paramuribaculum_intestinale	
ASV263	100	100	100	100	100	100	99	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	s__Lactobacillus_kalixensis	
ASV264	100	100	100	100	87	85	85	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	g__	s__[Clostridium]_viride	
ASV265	100	100	47	42	32	15	15	d__Bacteri	p__Bacter	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV266	100	100	100	100	100	86	43	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	f__Erysipe	g__Amedi	NA	Filter: bootstrap Score >= 50
ASV267	100	100	100	100	100	88	88	d__Bacteri	p__Bacillo	c__Clostrid	o__Peptost	f__Anaero	g__Ihubac	s__Ihubacter_massiliensis	
ASV268	100	99	88	34	14	14	10	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV269	100	89	89	88	88	44	37	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV270	100	100	100	100	100	34	34	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV271	100	100	100	100	100	50	50	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Odorib	g__Culturo	s__Culturomica_massiliensis	
ASV272	100	100	100	100	87	87	87	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Eubact	g__Eubact	s__Eubacterium_coprostanoligenes	
ASV273	100	100	100	100	100	96	91	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Muriba	g__Dunca	s__Duncaniella_dubosii	
ASV274	100	97	87	27	22	4	4	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV275	100	100	100	100	100	100	100	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Muriba	g__Param	s__Paramuribaculum_intestinale	
ASV276	100	100	100	100	100	74	39	d__Bacteri	p__Therm	c__Desulfo	o__Desulfo	f__Desulfo	g__Desulfo	NA	Filter: bootstrap Score >= 50
ASV277	100	100	100	95	68	60	32	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__	g__Intestin	NA	Filter: bootstrap Score >= 50
ASV278	100	100	99	99	99	58	58	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Muriba	g__Sange	s__Sangeribacter_muris	
ASV279	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Ligilact	s__Ligilactobacillus_ruminis	
ASV280	100	99	43	43	34	34	34	d__Bacteri	p__Bacter	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV281	100	100	100	99	99	80	47	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Lacrim	NA	Filter: bootstrap Score >= 50
ASV282	100	100	100	100	100	30	29	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Prevote	NA	NA	Filter: bootstrap Score >= 50
ASV283	100	100	100	100	99	29	29	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Muriba	NA	NA	Filter: bootstrap Score >= 50
ASV284	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Limosi	s__Limosilactobacillus_reuteri	
ASV285	100	100	100	100	100	100	86	d__Bacteri	p__Pseudo	c__Alphap	o__Hyphom	f__Nitroba	g__Bradyr	s__Bradyrhizobium_elkanii	
ASV286	100	100	100	100	100	66	66	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	g__Oscillib	s__Oscillibacter_valericigenes	
ASV287	100	100	94	94	64	24	24	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	f__Coprob	NA	NA	Filter: bootstrap Score >= 50
ASV288	100	99	99	99	99	97	97	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Schae	s__Schaedlerella_arabinosiphila	
ASV289	100	100	100	100	100	24	6	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Prevote	NA	NA	Filter: bootstrap Score >= 50
ASV290	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Acutalit	g__Acutali	s__Acutalibacter_muris	
ASV291	100	100	100	9	6	5	3	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV292	100	100	100	89	89	53	12	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Lacrim	NA	Filter: bootstrap Score >= 50
ASV293	100	100	100	86	86	27	27	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV294	100	100	100	100	98	94	88	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	g__Rumin	s__Ruminococcus_champanellensis	
ASV295	100	100	100	100	73	70	70	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	g__	s__[Clostridium]_viride	
ASV296	100	100	100	100	100	95	91	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Muriba	g__Dunca	s__Duncaniella_muris	
ASV297	100	100	100	100	100	100	38	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Rikene	g__Alistipe	NA	Filter: bootstrap Score >= 50
ASV298	100	100	100	100	53	53	53	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__	g__Flintiba	s__Flintibacter_butyricus	

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ASV299	100	100	100	93	93	41	41	d__Bacteri	p__Actinor	c__Coriobd	o__Eggerth	f__Eggerth	NA	NA	Filter: bootstrap Score >= 50
ASV300	100	100	100	99	99	81	44	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	g__Lacrim	NA	Filter: bootstrap Score >= 50
ASV301	100	93	38	37	17	16	16	d__Bacteri	p__Bacillo	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV302	100	100	100	100	100	100	91	d__Bacteri	p__Therm	c__Desulfo	o__Desulfo	f__Desulfo	g__Desulfo	s__Desulfovibrio_porci	
ASV303	100	100	100	100	100	98	97	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Odoriba	g__Odorib	s__Odoribacter_splanchnicus	
ASV304	100	98	94	25	22	22	22	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV305	100	100	100	100	100	56	53	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	g__Muriba	s__Muribaculum_gordoncarteri	
ASV306	100	100	100	100	98	87	83	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	g__Muriba	s__Muribaculum_gordoncarteri	
ASV307	100	100	100	100	100	41	29	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	NA	NA	Filter: bootstrap Score >= 50
ASV308	100	100	100	96	96	31	16	d__Bacteri	p__Actinor	c__Coriobd	o__Eggerth	f__Eggerth	NA	NA	Filter: bootstrap Score >= 50
ASV309	100	100	100	96	96	25	25	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV310	100	100	100	100	100	100	100	d__Bacteri	p__Actinor	c__Actinob	o__Bifidob	f__Bifidob	g__Bifidob	s__Bifidobacterium_pseudolongum	
ASV311	100	100	100	100	90	89	89	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__	g__Flintiba	s__Flintibacter_butyricus	
ASV312	100	100	100	61	56	56	56	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__	g__	s__[Bacteroides]_pectinophilus	
ASV313	100	99	87	58	38	31	31	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	NA	NA	NA	Filter: bootstrap Score >= 50
ASV314	100	89	86	20	20	18	6	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV315	100	100	100	100	91	55	55	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	g__Param	s__Paramuribaculum_intestinale	
ASV316	100	100	100	100	100	100	49	d__Bacteri	p__Bacillo	c__Bacilli	o__Bacilla	f__Paenib	g__Paenib	NA	Filter: bootstrap Score >= 50
ASV317	100	78	78	78	78	78	78	d__Bacteri	p__Candid	c__Vampir	o__Vampir	f__	g__Vampir	s__Vampirovibrio_chlorellavorus	
ASV318	100	99	94	15	15	15	15	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV319	100	99	99	88	88	12	12	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV320	100	100	100	96	56	48	31	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__	NA	NA	Filter: bootstrap Score >= 50
ASV321	100	100	100	89	89	11	8	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV322	100	100	100	100	100	31	5	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Prevote	NA	NA	Filter: bootstrap Score >= 50
ASV323	100	100	100	100	100	52	50	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	g__Oscillib	s__Oscillibacter_valericigenes	
ASV324	100	100	100	100	96	73	73	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	g__Lawso	s__Lawsonibacter_asaccharolyticus	
ASV325	100	100	100	100	100	79	42	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	g__Blautia	NA	Filter: bootstrap Score >= 50
ASV326	100	100	100	65	65	24	19	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV327	100	100	100	100	100	50	50	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	g__Kineot	s__Kineothrix_alysoides	
ASV328	100	83	77	47	12	10	7	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV329	100	99	98	84	84	47	47	d__Bacteri	p__Bacillo	c__Clostrid	o__Christe	f__Christe	NA	NA	Filter: bootstrap Score >= 50
ASV330	100	100	100	100	100	100	94	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Clostrid	g__Clostrid	s__Clostridium_chartatabidum	
ASV331	100	100	100	100	100	100	100	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	g__Dunca	s__Duncaniella_freteri	
ASV332	100	100	99	99	93	46	46	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	NA	NA	Filter: bootstrap Score >= 50
ASV333	100	100	100	81	81	41	41	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV334	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Clostrid	g__Inconst	s__Inconstantimicrobium_porci	
ASV335	100	100	100	100	100	100	48	d__Bacteri	p__Campy	c__Epsilon	o__Campy	f__Helicob	g__Helicot	NA	Filter: bootstrap Score >= 50
ASV336	100	100	100	100	93	65	65	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	g__Param	s__Paramuribaculum_intestinale	
ASV337	100	100	100	100	100	78	42	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	f__Erysipe	g__Amedi	NA	Filter: bootstrap Score >= 50
ASV338	100	100	99	99	96	46	41	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV339	100	100	100	100	62	36	36	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV340	100	97	90	40	18	18	14	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV341	100	100	100	92	92	49	8	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV342	100	100	100	87	87	17	6	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV343	100	100	100	93	93	45	36	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV344	100	100	100	100	96	74	74	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	g__Sangei	s__Sangeribacter_muris	
ASV345	100	100	100	100	100	60	60	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	g__Lachno	s__[Clostridium]_scindens	
ASV346	100	100	100	99	99	12	10	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV347	100	99	99	99	99	50	41	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	g__Medite	NA	Filter: bootstrap Score >= 50
ASV348	100	100	100	100	100	100	37	d__Bacteri	p__Campy	c__Epsilon	o__Campy	f__Helicob	g__Helicot	NA	Filter: bootstrap Score >= 50

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ASV349	100	100	100	100	100	100	38	d_Bacter	p_Bacter	c_Bacter	o_Bacter	f_Rikene	g_Alistipe	NA	Filter: bootstrap Score >= 50
ASV350	100	100	100	87	87	23	11	d_Bacter	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV351	100	100	100	100	79	57	57	d_Bacter	p_Bacillo	c_Clostrid	o_Eubacte	f_Oscillos	g_Lawso	s_Lawsonibacter_asaccharolyticus	
ASV352	100	100	100	99	99	44	44	d_Bacter	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV353	100	100	100	100	100	99	99	d_Bacter	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	g_Fusimo	s_Fusimonas_intestini	
ASV354	100	97	92	49	16	14	13	d_Bacter	p_Bacillo	c_Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV355	100	100	100	82	82	40	40	d_Bacter	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV356	100	100	100	100	100	100	100	d_Bacter	p_Verruc	c_Verruc	o_Verruc	f_Akkerm	g_Akkerm	s_Akkermansia_muciniphila	
ASV357	100	100	100	100	100	100	94	d_Bacter	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	g_Blautia	s_Blautia_glucerasea	
ASV358	100	100	100	85	85	22	22	d_Bacter	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV359	100	100	100	100	100	79	72	d_Bacter	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	g_Roseb	s_Roseburia_intestinalis	
ASV360	100	100	100	100	100	100	98	d_Bacter	p_Bacter	c_Bacter	o_Bacter	f_Tanner	g_Paraba	s_Parabacteroides_merdae	
ASV361	100	100	100	91	91	23	6	d_Bacter	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV362	100	100	100	100	90	71	66	d_Bacter	p_Bacter	c_Bacter	o_Bacter	f_Muriba	g_Dunca	s_Duncaniella_muris	
ASV363	100	100	100	100	74	74	66	d_Bacter	p_Bacillo	c_Clostrid	o_Eubacte	f_	g_Intestin	s_Intestinimonas_butyriciproducens	
ASV364	100	100	100	100	98	42	40	d_Bacter	p_Bacter	c_Bacter	o_Bacter	f_Muriba	NA	NA	Filter: bootstrap Score >= 50
ASV365	100	100	100	100	100	33	28	d_Bacter	p_Bacter	c_Bacter	o_Bacter	f_Prevote	NA	NA	Filter: bootstrap Score >= 50
ASV366	100	100	100	79	79	37	28	d_Bacter	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV367	100	100	100	99	99	16	16	d_Bacter	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV368	100	100	100	100	100	100	100	d_Bacter	p_Bacillo	c_Bacilli	o_Lactob	f_Lactoba	g_Lactob	s_Lactobacillus_intestinalis	
ASV369	100	100	100	100	95	93	93	d_Bacter	p_Bacter	c_Bacter	o_Bacter	f_Muriba	g_Param	s_Paramuribaculum_intestinale	
ASV370	100	100	100	100	100	91	91	d_Bacter	p_Bacter	c_Bacter	o_Bacter	f_Rikene	g_Rikene	s_Rikenella_microfusus	
ASV371	100	100	100	100	100	100	61	d_Bacter	p_Campy	c_Epsilon	o_Campy	f_Helicob	g_Helicot	s_Helicobacter_bilis	
ASV372	100	100	100	100	100	86	83	d_Bacter	p_Bacter	c_Bacter	o_Bacter	f_Prevote	g_Segate	s_Segatella_copri	
ASV373	100	100	100	100	52	38	38	d_Bacter	p_Bacillo	c_Clostrid	o_Eubacte	f_Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV374	100	100	100	94	94	19	12	d_Bacter	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV375	100	100	100	100	96	96	96	d_Bacter	p_Bacillo	c_Clostrid	o_Eubacte	f_Acutalit	g_Acutali	s_Acutalibacter_muris	
ASV376	100	100	100	100	55	45	35	d_Bacter	p_Bacillo	c_Clostrid	o_Eubacte	f	NA	NA	Filter: bootstrap Score >= 50
ASV377	100	100	100	100	100	81	80	d_Bacter	p_Bacter	c_Bacter	o_Bacter	f_Muriba	g_Dunca	s_Duncaniella_muris	
ASV378	100	100	100	100	100	100	85	d_Bacter	p_Actino	c_Coriob	o_Eggert	f_Eggert	g_Adlerc	s_Adlercreutzia_caecimuris	
ASV379	100	100	100	100	100	100	100	d_Bacter	p_Bacter	c_Bacter	o_Bacter	f_Muriba	g_Dunca	s_Duncaniella_freteri	
ASV380	100	100	100	100	49	35	35	d_Bacter	p_Bacillo	c_Clostrid	o_Eubact	NA	NA	NA	Filter: bootstrap Score >= 50
ASV381	100	100	100	100	100	83	83	d_Bacter	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	g_Kineot	s_Kineothrix_alysoides	
ASV382	100	100	100	100	96	35	24	d_Bacter	p_Bacter	c_Bacter	o_Bacter	f_Muriba	NA	NA	Filter: bootstrap Score >= 50
ASV383	100	100	100	96	96	54	54	d_Bacter	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	g_Kineot	s_Kineothrix_alysoides	
ASV384	100	100	100	97	97	28	25	d_Bacter	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV385	100	100	86	82	31	19	18	d_Bacter	p_Bacter	c_Bacter	o_Bacter	NA	NA	NA	Filter: bootstrap Score >= 50
ASV386	100	91	91	83	61	58	41	d_Bacter	p_Pseudo	c_Alphap	o_Rhodo	f_Kiloniel	g_Aestua	NA	Filter: bootstrap Score >= 50
ASV387	100	100	100	100	100	90	71	d_Bacter	p_Bacter	c_Bacter	o_Bacter	f_Muriba	g_Dunca	s_Duncaniella_muris	
ASV388	100	96	87	51	24	18	13	d_Bacter	p_Bacillo	c_Clostrid	o_Eubact	NA	NA	NA	Filter: bootstrap Score >= 50
ASV389	100	100	100	100	100	48	47	d_Bacter	p_Bacter	c_Bacter	o_Bacter	f_Muriba	NA	NA	Filter: bootstrap Score >= 50
ASV390	100	100	100	100	100	100	90	d_Bacter	p_Spiroc	c_Spiroch	o_Spiroch	f_Trepon	g_Trepon	s_Treponema_bryantii	
ASV391	100	100	100	100	100	100	44	d_Bacter	p_Bacillo	c_Bacilli	o_Lactob	f_Strepto	g_Strepto	NA	Filter: bootstrap Score >= 50
ASV392	100	100	100	100	100	100	82	d_Bacter	p_Bacillo	c_Bacilli	o_Lactob	f_Strepto	g_Strepto	s_Streptococcus_danieliae	
ASV393	100	100	100	97	97	19	19	d_Bacter	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV394	100	100	100	100	90	51	51	d_Bacter	p_Bacillo	c_Clostrid	o_Eubacte	f_Oscillos	g_Lawso	s_Lawsonibacter_asaccharolyticus	
ASV395	100	100	100	100	100	100	82	d_Bacter	p_Actino	c_Coriob	o_Eggert	f_Eggert	g_Adlerc	s_Adlercreutzia_mucosicola	
ASV396	100	100	100	100	100	100	100	d_Bacter	p_Bacillo	c_Clostrid	o_Eubacte	f_	g_Flintiba	s_Flintibacter_butyricus	
ASV397	100	100	100	100	57	52	52	d_Bacter	p_Bacillo	c_Clostrid	o_Eubacte	f	g_Flintiba	s_Flintibacter_butyricus	
ASV398	100	100	100	100	100	42	42	d_Bacter	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	NA	NA	Filter: bootstrap Score >= 50

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ASV399	100	100	100	92	92	37	31	d__Bacteri	p__Actinor	c__Coriobo	o__Eggerth	f__Eggerth	NA	NA	Filter: bootstrap Score >= 50
ASV400	100	100	100	100	100	100	92	d__Bacteri	p__Therm	c__Desulfo	o__Desulfo	f__Desulfo	g__Desulfo	s__Desulfovibrio_porci	
ASV401	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Limosil	s__Limosilactobacillus_reuteri	
ASV402	100	100	100	100	100	99	45	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Lachno	NA	Filter: bootstrap Score >= 50
ASV403	100	100	100	100	99	67	44	d__Bacteri	p__Bacter	c__Bacteroi	o__Bacter	f__Prevote	g__Segate	NA	Filter: bootstrap Score >= 50
ASV404	100	100	100	100	91	71	45	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__	g__Intestin	NA	Filter: bootstrap Score >= 50
ASV405	100	100	100	97	97	61	61	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Kineoth	s__Kineothrix_alysoides	
ASV406	100	100	100	100	100	100	74	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Clostrid	g__Clostrid	s__Clostridium_butyricum	
ASV407	100	100	100	100	100	100	100	d__Bacteri	p__Bacter	c__Bacteroi	o__Bacter	f__Muriba	g__Duncal	s__Duncaniella_muris	
ASV408	100	100	100	100	100	46	46	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV409	100	100	100	100	100	100	54	d__Bacteri	p__Actinor	c__Actinor	o__Mycob	f__Coryne	g__Coryne	s__Corynebacterium_afermentans	
ASV410	100	100	100	100	100	100	99	d__Bacteri	p__Actinor	c__Actinor	o__Actinor	f__Actinor	g__Actinor	s__Actinomyces_denticolens	
ASV411	100	100	100	99	99	51	51	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Kineoth	s__Kineothrix_alysoides	
ASV412	100	100	100	100	100	55	55	d__Bacteri	p__Bacter	c__Bacteroi	o__Bacter	f__Muriba	g__Duncal	s__Duncaniella_muris	
ASV413	100	100	100	100	99	33	10	d__Bacteri	p__Bacter	c__Bacteroi	o__Bacter	f__Prevote	NA	NA	Filter: bootstrap Score >= 50
ASV414	100	96	86	20	15	8	8	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV415	100	100	100	100	64	41	22	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV416	100	100	100	100	90	41	36	d__Bacteri	p__Bacter	c__Bacteroi	o__Bacter	f__Muriba	NA	NA	Filter: bootstrap Score >= 50
ASV417	100	100	98	98	63	63	39	d__Bacteri	p__Bacter	c__Bacteroi	o__Bacter	f__Tanner	g__Paraba	NA	Filter: bootstrap Score >= 50
ASV418	100	99	73	13	6	6	5	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV419	100	100	100	100	100	100	100	d__Bacteri	p__Pseudo	c__Gamma	o__Pasteu	f__Pasteu	g__Haemo	s__Haemophilus_parainfluenzae	
ASV420	100	97	81	28	24	9	9	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV421	100	98	92	50	13	12	9	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	NA	NA	NA	Filter: bootstrap Score >= 50
ASV422	100	74	74	74	59	59	59	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__	g__Flintiba	s__Flintibacter_butyricus	
ASV423	100	100	100	100	100	100	95	d__Bacteri	p__Bacter	c__Bacteroi	o__Bacter	f__Bacteroi	g__Bacteri	s__Bacteroides_uniformis	
ASV424	100	100	100	100	100	100	100	d__Bacteri	p__Pseudo	c__Betapro	o__Burkho	f__Sutterel	g__Turicim	s__Turicimonas_muris	
ASV425	100	100	100	100	100	82	77	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Lachno	s__[Clostridium]_scindens	
ASV426	100	100	100	100	100	100	48	d__Bacteri	p__Bacter	c__Bacteroi	o__Bacter	f__Rikenel	g__Alistipe	NA	Filter: bootstrap Score >= 50
ASV427	100	100	100	100	100	54	54	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Fusimo	s__Fusimonas_intestini	
ASV428	100	98	92	32	31	16	16	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV429	100	100	100	100	100	100	91	d__Bacteri	p__Actinor	c__Coriobo	o__Eggerth	f__Eggerth	g__Adlercr	s__Adlercreutzia_muris	
ASV430	100	99	99	98	83	58	31	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	g__Vescim	NA	Filter: bootstrap Score >= 50
ASV431	100	100	100	100	64	46	46	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV432	100	100	100	100	100	100	86	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Ligilact	s__Ligilactobacillus_apodemi	
ASV433	100	100	100	100	100	100	70	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Strepto	g__Lactoc	s__Lactococcus_taiwanensis	
ASV434	100	100	100	94	94	65	65	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Shuttle	s__Shuttleworthella_satelles	
ASV435	100	100	100	100	100	99	49	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Medite	NA	Filter: bootstrap Score >= 50
ASV436	100	100	100	60	60	27	27	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV437	100	95	78	35	7	6	5	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV438	100	100	100	100	97	96	96	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__	g__Flintiba	s__Flintibacter_butyricus	
ASV439	100	100	100	40	23	23	23	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV440	100	100	100	100	100	100	100	d__Bacteri	p__Bacter	c__Bacteroi	o__Bacter	f__Muriba	g__Duncal	s__Duncaniella_muricolitica	
ASV441	100	100	100	100	99	86	76	d__Bacteri	p__Bacter	c__Bacteroi	o__Bacter	f__Muriba	g__Duncal	s__Duncaniella_muris	
ASV442	100	100	100	100	94	34	34	d__Bacteri	p__Therm	c__Desulfo	o__Desulfo	f__Desulfo	NA	NA	Filter: bootstrap Score >= 50
ASV443	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	f__Erysipe	g__Dubosi	s__Dubosiella_newyorkensis	
ASV444	100	99	92	25	4	2	1	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV445	100	100	100	100	97	70	35	d__Bacteri	p__Bacter	c__Bacteroi	o__Bacter	f__Muriba	g__Dunca	NA	Filter: bootstrap Score >= 50
ASV446	100	96	90	27	18	18	13	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV447	100	67	25	25	25	22	17	d__Bacteri	p__Bacillo	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV448	100	100	100	100	100	52	52	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Lachno	s__[Clostridium]_scindens	

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ASV449	100	100	100	100	100	64	20	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	g__Lacrim	NA	Filter: bootstrap Score >= 50
ASV450	100	100	100	75	75	38	16	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV451	100	100	100	100	100	34	34	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Muriba	NA	NA	Filter: bootstrap Score >= 50
ASV452	100	100	100	100	100	62	62	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	g__Kineoth	s__Kineothrix_alysoides	
ASV453	100	100	100	100	100	100	100	d__Bacteri	p__Pseudo	c__Betapro	o__Burkho	f__Sutterel	g__Turicim	s__Turicimonas_muris	
ASV454	100	100	100	100	99	70	16	d__Bacteri	p__Therm	c__Desulfo	o__Desulf	f__Desulfo	g__Desulfo	NA	Filter: bootstrap Score >= 50
ASV455	100	100	100	100	100	100	69	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Clostrid	g__Clostrid	s__Clostridium_jeddahitimonense	
ASV456	100	100	100	100	100	100	100	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Muriba	g__Muriba	s__Muribaculum_gordoncarteri	
ASV457	100	100	100	100	99	42	39	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Muriba	NA	NA	Filter: bootstrap Score >= 50
ASV458	100	100	100	88	88	16	16	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV459	100	100	100	100	99	88	74	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Butyrici	g__Butyric	s__Butyricicoccus_pullicaecorum	
ASV460	100	100	99	98	88	75	75	d__Bacteri	p__Bacillo	c__Clostrid	o__Peptos	f__Anaero	g__Zhenpi	s__Zhenpiania_hominis	
ASV461	100	100	100	99	99	60	24	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	g__Blautia	NA	Filter: bootstrap Score >= 50
ASV462	100	100	100	81	28	26	14	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	NA	NA	NA	Filter: bootstrap Score >= 50
ASV463	100	100	100	100	100	100	18	d__Bacteri	p__Actinor	c__Actinor	o__Mycob	f__Coryne	g__Coryne	NA	Filter: bootstrap Score >= 50
ASV464	100	100	100	94	94	41	38	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV465	100	100	100	100	100	100	30	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Clostrid	g__Clostrid	NA	Filter: bootstrap Score >= 50
ASV466	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	g__Schaed	s__Schaedlerella_arabinosiphila	
ASV467	100	100	100	100	99	88	87	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Muriba	g__Muriba	s__Muribaculum_gordoncarteri	
ASV468	100	100	100	58	57	57	49	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Clostrid	g__Clostrid	NA	Filter: bootstrap Score >= 50
ASV469	100	86	79	18	18	15	12	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV470	100	99	98	80	70	8	8	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV471	100	100	100	100	100	100	42	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Clostrid	g__Clostrid	NA	Filter: bootstrap Score >= 50
ASV472	100	100	100	95	95	34	34	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV473	100	76	61	61	60	25	14	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	f__Erysipe	NA	NA	Filter: bootstrap Score >= 50
ASV474	100	100	100	100	96	68	41	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Muriba	g__Dunca	NA	Filter: bootstrap Score >= 50
ASV475	100	99	99	4	2	2	2	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV476	100	100	100	94	94	30	30	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV477	100	99	93	76	67	13	13	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV478	100	79	65	31	31	20	16	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV479	100	100	100	95	95	80	80	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	g__Qiania	s__Qiania_dongpingensis	
ASV480	100	77	23	23	23	16	13	d__Bacteri	p__Bacillo	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV481	100	100	100	100	95	93	93	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__	g__Flintiba	s__Flintibacter_butyricus	
ASV482	100	100	100	100	100	100	47	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	g__Anaero	NA	Filter: bootstrap Score >= 50
ASV483	100	100	100	100	100	69	69	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Muriba	g__Param	s__Paramuribaculum_intestinale	
ASV484	100	99	99	74	74	24	13	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV485	100	100	100	100	58	55	49	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	g__Neglec	NA	Filter: bootstrap Score >= 50
ASV486	100	100	100	100	100	93	93	d__Bacteri	p__Actinor	c__Actinor	o__Micron	f__Microm	g__Couch	s__Couchioplanes_caeruleus	
ASV487	100	100	100	100	98	54	47	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Prevote	g__Xylanib	NA	Filter: bootstrap Score >= 50
ASV488	100	100	100	100	100	100	13	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Clostrid	g__Clostrid	NA	Filter: bootstrap Score >= 50
ASV489	100	100	100	96	96	26	16	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV490	100	100	100	100	62	57	57	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	g__	s__[Clostridium]_leptum	
ASV491	100	99	94	89	52	35	35	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV492	100	100	100	24	23	23	16	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV493	100	100	100	100	100	49	49	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV494	100	100	100	100	87	56	56	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	g__Rumin	s__Ruminococcoides_bili	
ASV495	100	84	74	52	16	8	8	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	NA	NA	NA	Filter: bootstrap Score >= 50
ASV496	100	93	88	63	17	14	9	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	NA	NA	NA	Filter: bootstrap Score >= 50
ASV497	100	100	100	100	100	100	94	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Enteroc	g__Enteroc	s__Enterococcus_hirae	
ASV498	100	100	100	94	94	21	21	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50

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ASV499	100	98	95	66	19	19	14	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubact	NA	NA	NA	Filter: bootstrap Score >= 50
ASV500	100	100	100	33	33	33	22	d__Bacteri	p__Bacillot	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV501	100	100	99	84	84	38	38	d__Bacteri	p__Bacillot	c__Clostrid	o__Christe	f__Christe	NA	NA	Filter: bootstrap Score >= 50
ASV502	100	98	98	97	97	23	23	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV503	100	100	100	100	98	52	36	d__Bacteri	p__Bacteroi	c__Bacteroi	o__Bacteroi	f__Muriba	g__Muriba	NA	Filter: bootstrap Score >= 50
ASV504	100	100	100	100	100	100	28	d__Archae	p__Methano	c__Methano	o__Methano	f__Methan	g__Methan	NA	Filter: bootstrap Score >= 50
ASV505	100	100	100	97	97	86	86	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachno	f__Lachno	g__Qiania	s__Qiania_dongpingensis	
ASV506	100	100	100	100	96	51	51	d__Bacteri	p__Bacteroi	c__Bacteroi	o__Bacteroi	f__Muriba	g__Param	s__Paramuribaculum_intestinale	
ASV507	100	100	100	100	96	29	28	d__Bacteri	p__Bacillot	c__Bacilli	o__Bacillal	f__Bacillac	NA	NA	Filter: bootstrap Score >= 50
ASV508	100	51	40	40	39	11	11	d__Bacteri	p__Bacillot	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV509	100	100	100	100	100	67	67	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubact	f__Oscillos	g__Rumin	s__Ruminococcus_bromii	
ASV510	100	100	85	30	19	19	16	d__Bacteri	p__Bacillot	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV511	100	100	100	99	99	99	65	d__Bacteri	p__Mycopl	c__Mollicu	o__Anaero	f__Anaero	g__Anaero	s__Anaeroplasma_bactoclasticum	
ASV512	100	100	100	100	90	32	32	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV513	100	100	100	96	96	17	17	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV514	100	97	80	13	5	5	5	d__Bacteri	p__Bacillot	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV515	100	100	100	100	99	99	72	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachno	f__Anaero	g__Anaero	s__Anaerotignum_lactatifermentans	
ASV516	100	100	100	100	100	100	93	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachno	f__Lachno	g__Roseb	s__Roseburia_intestinalis	
ASV517	100	100	100	100	97	97	91	d__Bacteri	p__Bacteroi	c__Bacteroi	o__Bacteroi	f__Prevote	g__Parapr	s__Paraprevotella_clara	
ASV518	100	83	82	74	68	52	34	d__Bacteri	p__Pseudo	c__Alphapr	o__Rhodo	f__Kiloniel	g__Aestua	NA	Filter: bootstrap Score >= 50
ASV519	100	100	100	100	100	100	27	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubact	f__Clostrid	g__Clostrid	NA	Filter: bootstrap Score >= 50
ASV520	100	100	100	100	99	99	99	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubact	f__Feifani	g__Feifani	s__Feifania_hominis	
ASV521	100	100	100	100	100	100	98	d__Bacteri	p__Pseudo	c__Gamma	o__Moraxe	f__Moraxe	g__Acineto	s__Acinetobacter_radioresistens	
ASV522	100	100	100	90	90	18	16	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV523	100	88	75	24	22	19	12	d__Bacteri	p__Bacillot	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV524	100	100	100	100	86	86	86	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubact	f__Eubact	g__Eubact	s__Eubacterium_coprostanoligenes	
ASV525	100	100	100	100	100	27	26	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV526	100	100	100	71	71	27	27	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV527	100	100	100	100	100	100	100	d__Bacteri	p__Bacteroi	c__Bacteroi	o__Bacteroi	f__Rikene	g__Alistipe	s__Alistipes_okayasuensis	
ASV528	100	100	100	100	100	100	100	d__Bacteri	p__Pseudo	c__Gamma	o__Pasteu	f__Pasteu	g__Haemo	s__Haemophilus_parainfluenzae	
ASV529	100	91	58	58	54	50	46	d__Bacteri	p__Bacillot	c__Erysipe	o__Erysipe	f__Erysipe	g__Brezna	NA	Filter: bootstrap Score >= 50
ASV530	100	100	100	100	100	100	35	d__Bacteri	p__Bacteroi	c__Bacteroi	o__Bacteroi	f__Rikene	g__Alistipe	NA	Filter: bootstrap Score >= 50
ASV531	100	100	100	100	96	96	83	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubact	f__Acutalit	g__Acutalit	s__Acutalibacter_intestini	
ASV532	100	100	100	100	87	61	29	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubact	f__Oscillos	g__Vescim	NA	Filter: bootstrap Score >= 50
ASV533	100	100	100	99	99	82	69	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachno	f__Lachno	g__Catone	s__Catonella_massiliensis	
ASV534	100	100	100	99	99	80	54	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachno	f__Lachno	g__Lacrim	s__Lacrimispora_sphenoides	
ASV535	100	100	100	100	100	100	95	d__Bacteri	p__Bacillot	c__Bacilli	o__Lactob	f__Lactoba	g__Limosil	s__Limosilactobacillus_reuteri	
ASV536	100	100	100	100	100	100	40	d__Bacteri	p__Bacillot	c__Bacilli	o__Lactob	f__Strepto	g__Strepto	NA	Filter: bootstrap Score >= 50
ASV537	100	100	100	97	97	10	10	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV538	100	100	100	95	95	35	18	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV539	100	100	100	96	63	31	31	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubact	f__	NA	NA	Filter: bootstrap Score >= 50
ASV540	100	100	100	100	68	65	34	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubact	f__	g__Intestin	NA	Filter: bootstrap Score >= 50
ASV541	100	100	100	100	99	47	46	d__Bacteri	p__Bacteroi	c__Bacteroi	o__Bacteroi	f__Muriba	NA	NA	Filter: bootstrap Score >= 50
ASV542	100	100	100	99	99	49	47	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV543	100	100	100	97	91	91	55	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubact	f__Aristae	g__Aristae	s__Aristaeella_hokkaidonensis	
ASV544	100	100	100	100	100	88	88	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachno	f__Lachno	g__Lachno	s__[Clostridium]_scindens	
ASV545	100	100	100	100	100	100	74	d__Bacteri	p__Pseudo	c__Gamma	o__Moraxe	f__Moraxe	g__Acineto	s__Acinetobacter_calcoaceticus	
ASV546	100	100	100	97	97	74	3	d__Bacteri	p__Actinob	c__Actinob	o__Pseudo	f__Pseudo	g__Saccha	NA	Filter: bootstrap Score >= 50
ASV547	100	100	100	100	100	100	99	d__Bacteri	p__Actinob	c__Actinob	o__Mycob	f__Corynel	g__Corynes	s__Corynebacterium_tuberculostearicum	
ASV548	100	100	100	93	93	18	11	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50

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ASV549	100	100	100	97	97	5	5	d__Bacteri	p__Bacillo	c__Clostrido	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV550	100	100	100	100	100	99	90	d__Bacteri	p__Bacillo	c__Clostrido	o__Eubact	f__Oscillos	g__Rumino	s__Ruminococcus_callidus	
ASV551	100	100	100	100	100	57	31	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteroi	f__Prevote	g__Segate	NA	Filter: bootstrap Score >= 50
ASV552	100	100	100	99	92	67	60	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteroi	f__Muriba	g__Duncan	s__Duncaniella_muris	
ASV553	100	86	77	23	10	7	7	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV554	100	100	100	100	93	93	85	d__Bacteri	p__Bacillo	c__Clostrido	o__Eubact	f__Acutalib	g__Acutali	s__Acutalibacter_caecimuris	
ASV555	100	100	100	100	100	100	100	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteroi	f__Bacteroi	g__Phocae	s__Phocaeicola_sartorii	
ASV556	100	100	100	100	100	100	43	d__Bacteri	p__Spiroch	c__Spirochi	o__Spirochi	f__Treponi	g__Treponi	NA	Filter: bootstrap Score >= 50
ASV557	100	100	100	99	99	43	43	d__Bacteri	p__Bacillo	c__Clostrido	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV558	100	100	100	100	100	57	57	d__Bacteri	p__Bacillo	c__Clostrido	o__Lachno	f__Lachno	g__Kineoth	s__Kineothrix_alysoides	
ASV559	100	100	100	99	99	39	39	d__Bacteri	p__Bacillo	c__Clostrido	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV560	100	100	100	100	100	26	26	d__Bacteri	p__Bacillo	c__Clostrido	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV561	100	100	100	98	62	32	32	d__Bacteri	p__Bacillo	c__Clostrido	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV562	100	100	100	100	93	90	41	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteroi	f__Muriba	g__Duncan	NA	Filter: bootstrap Score >= 50
ASV563	100	100	100	100	100	100	100	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteroi	f__Rikenel	g__Alistipe	s__Alistipes_okayasuensis	
ASV564	100	100	99	99	95	71	71	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteroi	f__Muriba	g__Sangeri	s__Sangeribacter_muris	
ASV565	100	100	100	100	100	49	49	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteroi	f__Rikenel	NA	NA	Filter: bootstrap Score >= 50
ASV566	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Limosil	s__Limosilactobacillus_reuteri	
ASV567	100	100	100	100	100	100	86	d__Bacteri	p__Actinor	c__Actinor	o__Mycob	f__Gordon	g__Gordon	s__Gordonia_bronchialis	
ASV568	100	100	100	96	96	59	59	d__Bacteri	p__Bacillo	c__Clostrido	o__Lachno	f__Lachno	g__Jingyaa	s__Jingyaoa_shaoxingensis	
ASV569	100	100	100	100	100	100	91	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Ligilact	s__Ligilactobacillus_faecis	
ASV570	100	100	100	100	77	47	41	d__Bacteri	p__Bacillo	c__Clostrido	o__Eubact	f__	NA	NA	Filter: bootstrap Score >= 50
ASV571	100	100	100	100	94	94	87	d__Bacteri	p__Bacillo	c__Clostrido	o__Eubact	f__Oscillos	g__Neglect	s__Neglectibacter_caecimuris	
ASV572	100	100	100	100	100	95	92	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteroi	f__Muriba	g__Duncan	s__Duncaniella_muris	
ASV573	100	85	77	38	35	3	3	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV574	100	100	100	91	90	28	28	d__Bacteri	p__Bacillo	c__Clostrido	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV575	100	100	100	100	100	52	52	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteroi	f__Muriba	g__Paramu	s__Paramuribaculum_intestinale	
ASV576	100	100	100	100	100	100	99	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Limosil	s__Limosilactobacillus_reuteri	
ASV577	100	100	100	40	39	39	32	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV578	100	100	99	99	96	72	72	d__Bacteri	p__Bacillo	c__Clostrido	o__Peptos	f__Anaero	g__Zhenpi	s__Zhenpiania_hominis	
ASV579	100	100	100	25	23	23	19	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV580	100	100	100	99	99	64	60	d__Bacteri	p__Bacillo	c__Negativi	o__Seleno	f__Seleno	g__Mitsuo	s__Mitsuokella_multacida	
ASV581	100	100	100	77	77	17	12	d__Bacteri	p__Bacillo	c__Clostrido	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV582	100	100	100	28	27	27	12	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV583	100	100	100	46	46	46	46	d__Bacteri	p__Actinor	c__Coriob	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV584	100	100	100	85	85	13	13	d__Bacteri	p__Bacillo	c__Clostrido	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV585	100	93	77	31	15	10	5	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV586	100	96	86	48	13	12	8	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV587	100	100	100	100	56	54	48	d__Bacteri	p__Bacillo	c__Clostrido	o__Eubact	f__Oscillos	g__Neglect	NA	Filter: bootstrap Score >= 50
ASV588	100	100	100	100	100	100	100	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteroi	f__Tanner	g__Parabac	s__Parabacteroides_goldsteinii	
ASV589	100	100	99	98	98	56	56	d__Bacteri	p__Bacillo	c__Clostrido	o__Peptos	f__Anaero	g__Emergo	s__Emergencia_timonensis	
ASV590	100	100	100	100	100	100	88	d__Archae	p__Methan	c__Methano	o__Methan	f__Methan	g__Methan	s__Methanosphaera_cuniculi	
ASV591	100	100	100	100	97	38	20	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteroi	f__Prevote	NA	NA	Filter: bootstrap Score >= 50
ASV592	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Clostrido	o__Eubact	f__	g__Flintiba	s__Flintibacter_butyricus	
ASV593	100	100	100	94	94	25	25	d__Bacteri	p__Bacillo	c__Clostrido	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV594	100	92	23	21	19	19	16	d__Bacteri	p__Bacillo	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV595	100	100	100	98	98	22	19	d__Bacteri	p__Bacillo	c__Clostrido	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV596	100	100	100	100	93	77	77	d__Bacteri	p__Bacillo	c__Clostrido	o__Eubact	f__Oscillos	g__Lawson	s__Lawsonibacter_asaccharolyticus	
ASV597	100	100	100	100	99	63	58	d__Bacteri	p__Bacillo	c__Negativi	o__Seleno	f__Seleno	g__Mitsuo	s__Mitsuokella_multacida	
ASV598	100	100	100	100	100	100	32	d__Bacteri	p__Bacillo	c__Bacilli	o__Bacilla	f__Paenib	g__Paenib	NA	Filter: bootstrap Score >= 50

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ASV599	100	100	100	100	100	100	100	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Tanner	g__Paraba	s__Parabacteroides_merdae	
ASV600	100	100	33	33	29	23	23	d__Bacteri	p__Bacter	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV601	100	100	100	100	100	100	88	d__Bacteri	p__Pseud	c__Gamm	o__Entero	f__Enterob	g__Escher	s__Escherichia_fergusonii	
ASV602	100	100	100	100	100	69	59	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	g__Muriba	s__Muribaculum_gordoncarteri	
ASV603	100	100	100	97	97	74	74	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Kineoth	s__Kineothrix_alysoides	
ASV604	100	100	100	42	37	35	24	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV605	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Limosil	s__[Lactobacillus]_timonensis	
ASV606	100	100	100	99	79	79	79	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Eubact	g__Eubact	s__Eubacterium_coprostanoligenes	
ASV607	100	97	97	95	95	34	32	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV608	100	100	100	100	100	100	64	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Bacterd	g__Bacter	s__Bacteroides_caecimuris	
ASV609	100	98	89	34	31	16	16	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV610	100	100	100	100	100	81	58	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	g__Dunca	s__Duncaniella_muris	
ASV611	100	99	83	30	14	14	9	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV612	100	100	100	98	98	7	7	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV613	100	100	100	100	100	100	81	d__Bacteri	p__Spiroch	c__Spiroch	o__Spiroch	f__Treponi	g__Treponi	s__Treponema_bryantii	
ASV614	100	100	100	100	99	57	29	d__Bacteri	p__Therm	c__Desulfo	o__Desulfo	f__Desulfo	g__Desulfo	NA	Filter: bootstrap Score >= 50
ASV615	100	100	94	72	66	29	29	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV616	100	100	100	100	100	100	53	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Strepto	g__Strepto	s__Streptococcus_acidominimus	
ASV617	100	100	100	100	100	100	63	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Rikenel	g__Alistipe	s__Alistipes_indistinctus	
ASV618	100	100	100	100	100	47	47	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV619	100	100	100	100	99	69	12	d__Bacteri	p__Therm	c__Desulfo	o__Desulfo	f__Desulfo	g__Desulfo	NA	Filter: bootstrap Score >= 50
ASV620	100	100	100	84	84	8	4	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV621	100	40	40	40	40	40	40	d__Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV622	100	99	96	34	32	11	11	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV623	100	100	100	37	16	14	6	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV624	100	100	100	100	100	73	33	d__Bacteri	p__Therm	c__Desulfo	o__Desulfo	f__Desulfo	g__Desulfo	NA	Filter: bootstrap Score >= 50
ASV625	100	100	100	100	100	100	42	d__Bacteri	p__Spiroch	c__Spiroch	o__Spiroch	f__Treponi	g__Treponi	NA	Filter: bootstrap Score >= 50
ASV626	100	100	100	85	72	9	4	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV627	100	97	92	24	12	11	8	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV628	100	100	100	100	100	100	100	d__Bacteri	p__Spiroch	c__Spiroch	o__Spiroch	f__Treponi	g__Treponi	s__Treponema_porcinum	
ASV629	100	99	99	75	75	33	23	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV630	100	100	100	100	100	39	39	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV631	100	100	99	91	91	33	12	d__Bacteri	p__Actinor	c__Coriobac	o__Eggerth	f__Eggerth	NA	NA	Filter: bootstrap Score >= 50
ASV632	100	100	100	100	100	85	85	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	g__Sangeri	s__Sangeribacter_muris	
ASV633	100	100	100	81	12	12	12	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	NA	NA	NA	Filter: bootstrap Score >= 50
ASV634	100	100	100	100	100	91	28	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Bacterd	g__Bacter	NA	Filter: bootstrap Score >= 50
ASV635	100	100	100	99	99	54	22	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Lacrim	NA	Filter: bootstrap Score >= 50
ASV636	100	100	100	100	100	100	96	d__Bacteri	p__Therm	c__Desulfo	o__Desulfo	f__Desulfo	g__Desulfo	s__Desulfovibrio_porci	
ASV637	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Kineoth	s__Kineothrix_alysoides	
ASV638	100	69	50	50	50	30	19	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	f__Erysipe	NA	NA	Filter: bootstrap Score >= 50
ASV639	100	100	100	100	62	46	24	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV640	100	100	100	92	66	57	36	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__	g__Intestin	NA	Filter: bootstrap Score >= 50
ASV641	100	100	100	100	99	96	96	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__	g__Flintiba	s__Flintibacter_butyricus	
ASV642	100	100	100	100	98	76	76	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	g__Sangeri	s__Sangeribacter_muris	
ASV643	100	100	100	100	100	51	33	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Jutong	NA	Filter: bootstrap Score >= 50
ASV644	100	100	100	100	100	60	60	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Medite	s__Mediterraneibacter_gnavus	
ASV645	100	100	100	100	100	89	85	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	g__Oscillib	s__Oscillibacter_valericigenes	
ASV646	100	96	75	16	5	2	2	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV647	100	100	100	100	66	57	57	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	g__Flavon	s__Flavonifractor_plautii	
ASV648	100	100	100	100	51	48	48	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50

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ASV649	100	100	100	100	100	100	58	d__Bacteri	p__Actinor	c__Coriobа	o__Eggert	f__Eggerth	g__Adlercr	s__Adlercreutzia_caecimuris		
ASV650	100	100	100	100	100	46	22	d__Bacteri	p__Bacter	c__Bacteroi	o__Bacteroi	f__Prevote	NA	NA	Filter: bootstrap Score >= 50	
ASV651	100	100	100	100	100	100	63	d__Bacteri	p__Actinor	c__Coriobа	o__Eggert	f__Eggerth	g__Adlercr	s__Adlercreutzia_caecimuris		
ASV652	100	100	100	99	99	33	33	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50	
ASV653	100	100	100	100	100	100	71	d__Bacteri	p__Actinor	c__Actinor	o__Geodei	f__Geodei	g__Blastoc	s__Blastococcus_deserti		
ASV654	100	100	100	100	100	100	90	d__Bacteri	p__Bacillo	c__Bacilli	o__Bacillal	f__Staphyl	g__Staphy	s__Staphylococcus_pasteuri		
ASV655	100	100	100	100	99	87	66	d__Bacteri	p__Bacillo	c__Clostrid	o__Peptost	f__Peptost	g__Rombo	s__Romboutsia_timonensis		
ASV656	100	98	88	86	71	7	7	d__Bacteri	p__Bacillo	c__Clostrid	o__Peptost	f__Anaero	NA	NA	Filter: bootstrap Score >= 50	
ASV657	100	100	100	95	95	57	57	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Kineot	s__Kineothrix_alysoides		
ASV658	100	100	100	100	100	100	79	d__Bacteri	p__Bacter	c__Bacteroi	o__Bacteroi	f__Bacteroi	g__Phoca	s__Phocaeicola_faecalis		
ASV659	100	100	100	100	100	75	74	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacti	f__Oscillos	g__Oscillib	s__Oscillibacter_valericigenes		
ASV660	100	100	100	97	97	14	14	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50	
ASV661	100	100	100	100	100	100	42	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacti	f__Clostrid	g__Clostrid	NA	Filter: bootstrap Score >= 50	
ASV662	100	100	100	100	100	100	100	d__Bacteri	p__Bacter	c__Bacteroi	o__Bacteroi	f__Muribac	g__Dunca	s__Duncaniella_muris		
ASV663	100	100	100	99	99	29	29	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50	
ASV664	100	100	100	99	99	94	6	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Blautia	NA	Filter: bootstrap Score >= 50	
ASV665	100	100	100	100	100	41	32	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50	
ASV666	100	100	100	100	100	70	70	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Kineot	s__Kineothrix_alysoides		
ASV667	100	87	70	26	9	9	9	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV668	100	100	100	100	100	100	48	d__Bacteri	p__Bacter	c__Bacteroi	o__Bacteroi	f__Rikenel	g__Alistipe	NA	Filter: bootstrap Score >= 50	
ASV669	100	100	100	93	93	43	29	d__Bacteri	p__Actinor	c__Coriobа	o__Eggert	f__Eggerth	NA	NA	Filter: bootstrap Score >= 50	
ASV670	100	100	100	100	100	89	75	d__Bacteri	p__Bacter	c__Bacteroi	o__Bacteroi	f__Muribac	g__Dunca	s__Duncaniella_muris		
ASV671	100	100	100	100	100	100	58	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	s__Lactobacillus_gallinarum		
ASV672	100	90	43	43	42	18	16	d__Bacteri	p__Bacillo	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV673	100	99	68	60	38	27	27	d__Bacteri	p__Bacter	c__Bacteroi	o__Bacteroi	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV674	100	100	99	99	94	23	23	d__Bacteri	p__Bacter	c__Bacteroi	o__Bacteroi	f__Prevote	NA	NA	Filter: bootstrap Score >= 50	
ASV675	100	100	100	100	100	39	39	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacti	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50	
ASV676	100	98	79	20	5	5	5	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV677	100	100	100	100	99	34	18	d__Bacteri	p__Bacter	c__Bacteroi	o__Bacteroi	f__Prevote	NA	NA	Filter: bootstrap Score >= 50	
ASV678	100	100	100	100	100	100	100	d__Bacteri	p__Actinor	c__Actinor	o__Propior	f__Propior	g__Cutiba	s__Cutibacterium_acnes		
ASV679	100	100	100	98	97	20	4	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50	
ASV680	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacti	f__Clostrid	g__Clostrid	s__Clostridium_bornimense		
ASV681	100	99	99	98	98	24	24	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50	
ASV682	100	100	100	100	97	52	52	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacti	f__Oscillos	g__Pusillib	s__Pusillibacter_faecalis		
ASV683	100	100	100	100	100	100	87	d__Bacteri	p__Spiroch	c__Spiroch	o__Brachy	f__Brachys	g__Brachy	s__Brachyspira_intermedia		
ASV684	100	100	100	100	100	100	34	d__Bacteri	p__Actinor	c__Actinor	o__Mycobа	f__Coryne	g__Coryne	NA	Filter: bootstrap Score >= 50	
ASV685	100	100	100	100	99	99	70	d__Bacteri	p__Therm	c__Desulfo	o__Desulfo	f__Desulfo	g__Desulfa	s__Desulfatiferula_olefinivorans		
ASV686	100	100	100	100	86	56	31	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacti	f__Oscillos	g__Pseudo	NA	Filter: bootstrap Score >= 50	
ASV687	100	100	100	100	100	86	86	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Acetati	s__Acetatifactor_muris		
ASV688	100	100	100	100	100	100	57	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Roseb	s__Roseburia_faecis		
ASV689	100	100	100	100	100	74	60	d__Bacteri	p__Bacillo	c__Clostrid	o__Peptost	f__Peptost	g__Paracl	s__Paraclostridium_tenue		
ASV690	100	100	100	100	100	100	100	d__Bacteri	p__Actinor	c__Actinor	o__Bifidob	f__Bifidob	g__Bifidob	s__Bifidobacterium_animalis		
ASV691	100	100	100	100	100	51	36	d__Bacteri	p__Actinor	c__Actinor	o__Microc	f__Microba	g__Gulosil	NA	Filter: bootstrap Score >= 50	
ASV692	100	100	100	93	93	21	21	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50	
ASV693	100	100	100	96	96	96	96	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacti	f__Eubacte	g__Eubacti	s__Eubacterium_ventriosum		
ASV694	100	98	88	52	37	25	24	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacti	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV695	100	22	22	22	22	22	22	d__Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV696	100	100	100	98	96	67	67	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacti	f__Oscillos	g__Oscillib	s__Oscillibacter_valericigenes		
ASV697	100	100	100	90	90	16	5	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50	
ASV698	100	42	42	42	42	42	42	d__Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50	

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ASV699	100	100	100	84	84	40	40	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV700	100	100	100	100	100	100	100	d__Archae	p__Methan	c__Methan	o__Methan	f__Methan	g__Methan	s__Methanobrevibacter_boviskoreani	
ASV701	100	100	100	100	100	100	100	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	g__Muriba	s__Muribaculum_gordoncarteri	
ASV702	100	100	100	100	100	100	72	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Rikene	g__Alistipe	s__Alistipes_dispar	
ASV703	100	100	100	100	88	88	79	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Acutalit	g__Acutali	s__Acutalibacter_caecimuris	
ASV704	100	100	100	100	98	64	64	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	g__Param	s__Paramuribaculum_intestinale	
ASV705	100	100	100	100	100	49	49	d__Bacteri	p__Mycop	c__	o__Mycop	f__Metam	NA	NA	Filter: bootstrap Score >= 50
ASV706	100	100	100	100	55	37	37	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV707	100	100	100	100	97	71	32	d__Bacteri	p__Bacillo	c__Clostrid	o__Peptos	f__Peptost	g__Paracl	NA	Filter: bootstrap Score >= 50
ASV708	100	100	79	41	33	14	14	d__Bacteri	p__Bacter	c__Bacterd	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV709	100	100	100	100	75	66	37	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	g__Vescim	NA	Filter: bootstrap Score >= 50
ASV710	100	81	77	67	46	45	36	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	NA	NA	NA	Filter: bootstrap Score >= 50
ASV711	100	55	55	55	55	55	55	d__Bacteri	p__Candid	c__Vampiro	o__Vampir	f__	g__Vampir	s__Vampirovibrio_chlorellavorus	
ASV712	100	100	100	100	100	77	77	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	g__	s__[Eubacterium]_siraeum	
ASV713	100	83	83	69	58	50	49	d__Bacteri	p__Pseud	c__Alphap	o__Rhodo	f__Kiloniel	g__Aestua	NA	Filter: bootstrap Score >= 50
ASV714	100	100	99	79	68	5	4	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV715	100	100	100	100	100	48	48	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV716	100	100	100	100	100	100	83	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Strepto	g__Strepto	s__Streptococcus_ovis	
ASV717	100	100	100	100	100	100	100	d__Bacteri	p__Spiroch	c__Spiroch	o__Spiroch	f__Treponi	g__Treponi	s__Treponema_bryantii	
ASV718	100	100	100	100	100	100	58	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Bacterd	g__Phoca	s__Phocaeicola_plebeius	
ASV719	100	76	71	67	37	36	21	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	NA	NA	NA	Filter: bootstrap Score >= 50
ASV720	100	100	100	100	100	79	79	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	g__Qiania	s__Qiania_dongpingensis	
ASV721	100	100	100	100	96	47	47	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV722	100	100	100	100	100	100	80	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	g__Vescim	s__Vescimonas_coprocola	
ASV723	100	100	100	100	100	59	55	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	g__Muriba	s__Muribaculum_intestinale	
ASV724	100	98	34	32	30	30	30	d__Bacteri	p__Bacter	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV725	100	100	100	100	100	89	89	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Rikene	g__Rikene	s__Rikenella_microfusus	
ASV726	100	100	100	100	100	33	33	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	NA	NA	Filter: bootstrap Score >= 50
ASV727	100	100	100	100	100	90	90	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	f__Erysipe	g__Lactim	s__Lactimicrobium_massiliense	
ASV728	100	100	100	99	91	31	31	d__Bacteri	p__Planct	c__Planctc	o__Pirellul	f__Pirellula	NA	NA	Filter: bootstrap Score >= 50
ASV729	100	100	100	93	93	5	5	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV730	100	100	100	93	93	74	74	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	g__Wujia	s__Wujia_chipingensis	
ASV731	100	100	100	100	100	77	77	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	g__Sodalis	s__Sodaliphilus_pleomorphus	
ASV732	100	100	100	100	100	87	60	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	g__Lacrim	s__Lacrimispora_sphenoides	
ASV733	100	100	100	100	100	33	30	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Prevote	NA	NA	Filter: bootstrap Score >= 50
ASV734	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Clostrid	g__Clostri	s__Clostridium_bornimense	
ASV735	100	100	100	93	93	38	18	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV736	100	100	100	100	98	98	40	d__Bacteri	p__Spiroch	c__Spiroch	o__Spiroch	f__Treponi	g__Treponi	NA	Filter: bootstrap Score >= 50
ASV737	100	100	100	100	100	100	87	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Ligilact	s__Ligilactobacillus_faecis	
ASV738	100	100	100	100	100	73	73	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	g__Rumin	s__Ruminococcus_bromii	
ASV739	100	100	100	97	97	74	33	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	g__Eisenb	NA	Filter: bootstrap Score >= 50
ASV740	100	100	100	100	100	98	68	d__Bacteri	p__Therm	c__Desulfo	o__Desulfo	f__Desulfo	g__Desulfa	s__Desulfatiferula_olefinivorans	
ASV741	100	100	100	100	65	36	36	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV742	100	100	100	100	95	45	27	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	NA	NA	Filter: bootstrap Score >= 50
ASV743	100	100	94	80	75	39	39	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV744	100	100	100	100	99	53	51	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	g__Muriba	s__Muribaculum_intestinale	
ASV745	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Negativ	o__Veillon	f__Veillone	g__Megas	s__Megasphaera_elsdenii	
ASV746	100	100	100	92	92	27	27	d__Bacteri	p__Actinor	c__Coriob	o__Eggert	f__Eggerth	NA	NA	Filter: bootstrap Score >= 50
ASV747	100	100	100	100	100	47	31	d__Bacteri	p__Bacillo	c__Bacilli	o__Bacillal	f__Bacillac	NA	NA	Filter: bootstrap Score >= 50
ASV748	100	100	100	100	100	89	89	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	g__Acetati	s__Acetatifactor_muris	

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ASV749	100	100	100	100	87	59	59	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubacte	f__Oscillos	g__Rumino	s__Ruminococcoides_bili		
ASV750	100	100	100	100	100	100	100	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteri	f__Bacteroi	g__Phocae	s__Phocaeicola_massiliensis		
ASV751	100	97	97	96	96	60	29	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachnos	f__Lachnos	g__Faecali	NA	Filter: bootstrap Score >= 50	
ASV752	100	95	82	37	30	11	11	d__Bacteri	p__Bacillot	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV753	100	100	100	100	100	100	100	d__Bacteri	p__Spirocha	c__Spirochi	o__Spirochi	f__Treponi	g__Treponi	s__Treponema_porcinum		
ASV754	100	100	100	100	100	100	43	d__Bacteri	p__Bacillot	c__Bacilli	o__Bacillal	f__Staphyl	g__Staphy	NA	Filter: bootstrap Score >= 50	
ASV755	100	100	100	100	100	100	95	d__Bacteri	p__Pseudo	c__Alphapr	o__Hyphom	f__Boseac	g__Bosea	s__Bosea_thiooxidans		
ASV756	100	100	100	100	96	41	41	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubacte	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50	
ASV757	100	100	99	99	93	24	24	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubacte	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50	
ASV758	100	81	60	60	60	53	52	d__Bacteri	p__Bacillot	c__Erysipel	o__Erysipel	f__Erysipel	g__Breznal	s__Breznakia_pachnodae		
ASV759	100	97	85	35	31	7	7	d__Bacteri	p__Bacillot	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV760	100	100	100	100	100	100	100	d__Bacteri	p__Bacillot	c__Bacilli	o__Lactoba	f__Lactoba	g__Limosil	s__Limosilactobacillus_reuteri		
ASV761	100	100	100	93	93	35	35	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachnos	f__Lachnos	NA	NA	Filter: bootstrap Score >= 50	
ASV762	100	100	100	100	95	85	85	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubacte	f__Oscillos	g__Lawson	s__Lawsonibacter_asaccharolyticus		
ASV763	100	74	54	54	54	4	4	d__Bacteri	p__Bacillot	c__Erysipel	o__Erysipel	f__Erysipel	NA	NA	Filter: bootstrap Score >= 50	
ASV764	100	100	100	94	94	44	44	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachnos	f__Lachnos	NA	NA	Filter: bootstrap Score >= 50	
ASV765	100	100	100	100	100	99	80	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubacte	f__Peptoco	g__Peptoc	s__Peptococcus_niger		
ASV766	100	100	100	100	100	49	49	d__Bacteri	p__Bacteroi	c__Bacteroi	o__Bacteri	f__Muribac	NA	NA	Filter: bootstrap Score >= 50	
ASV767	100	100	100	100	80	41	37	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubacte	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50	
ASV768	100	100	100	100	100	100	100	d__Bacteri	p__Mycopl	c__	o__Mycopl	f__Metamy	g__Metam	s__Metamycoplasma_sualvi		
ASV769	100	100	100	100	100	100	100	d__Bacteri	p__Pseudo	c__Betapro	o__Burkhol	f__Suttere	g__Turicim	s__Turicimonas_muris		
ASV770	100	100	100	100	100	97	97	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubacte	f__Oscillos	g__Fumia	s__Fumia_xinanensis		
ASV771	100	100	100	100	100	100	46	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubacte	f__Clostrid	g__Clostri	NA	Filter: bootstrap Score >= 50	
ASV772	100	100	100	100	100	83	83	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachnos	f__Lachnos	g__Luxiba	s__Luxibacter_massiliensis		
ASV773	100	72	35	35	34	18	17	d__Bacteri	p__Bacillot	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV774	100	97	84	35	17	9	8	d__Bacteri	p__Bacillot	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV775	100	98	79	15	15	14	7	d__Bacteri	p__Bacillot	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV776	100	100	100	100	100	38	38	d__Bacteri	p__Bacillot	c__Clostrid	o__Peptost	f__Anaero	NA	NA	Filter: bootstrap Score >= 50	
ASV777	100	91	83	32	23	23	23	d__Bacteri	p__Bacillot	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV778	100	100	100	100	100	100	98	d__Bacteri	p__Bacillot	c__Bacilli	o__Lactoba	f__Lactoba	g__Limosil	s__Limosilactobacillus_reuteri		
ASV779	100	100	100	100	100	100	91	d__Bacteri	p__Actinob	c__Actinom	o__Mycobac	f__Coryne	g__Coryne	s__Corynebacterium_minutissimum		
ASV780	100	100	100	100	100	100	100	d__Bacteri	p__Bacteroi	c__Flavobac	o__Flavobac	f__Weeksel	g__Apibac	s__Apibacter_mensalis		
ASV781	100	100	100	100	100	94	94	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubacte	f__Oscillos	g__Paludih	s__Paludihabitans_psychrotolerans		
ASV782	100	100	100	24	22	22	13	d__Bacteri	p__Bacillot	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV783	100	100	100	100	100	97	89	d__Bacteri	p__Bacteroi	c__Bacteroi	o__Bacteri	f__Muribac	g__Duncan	s__Duncaniella_muris		
ASV784	100	100	96	78	78	59	59	d__Bacteri	p__Bacillot	c__Clostrid	o__Christe	f__Christe	g__Gehon	s__Gehongia_tenuis		
ASV785	100	100	100	100	100	98	94	d__Bacteri	p__Bacillot	c__Clostrid	o__Peptost	f__Anaero	g__Lentiho	s__Lentihominibacter_faecis		
ASV786	100	93	83	37	32	20	20	d__Bacteri	p__Bacillot	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV787	100	100	100	100	99	72	52	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubacte	f__Butyrici	g__Butyric	s__Butyricicoccus_pullicaecorum		
ASV788	100	100	100	51	51	23	23	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachnos	f__Lachnos	NA	NA	Filter: bootstrap Score >= 50	
ASV789	100	63	63	63	63	63	63	d__Bacteri	p__Candid	c__Vampiri	o__Vampiri	f__	g__Vampir	s__Vampirovibrio_chlorellavorus		
ASV790	100	100	100	98	98	57	57	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachnos	f__Lachnos	g__Kineoth	s__Kineothrix_alysoides		
ASV791	100	100	100	83	83	18	12	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachnos	f__Lachnos	NA	NA	Filter: bootstrap Score >= 50	
ASV792	100	100	100	100	100	100	100	d__Bacteri	p__Spirocha	c__Spirochi	o__Spirochi	f__Treponi	g__Treponi	s__Treponema_succinifaciens		
ASV793	100	100	100	100	100	100	100	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachnos	f__Lachnos	g__Coprod	s__Coprococcus_catus		
ASV794	100	100	100	100	99	27	27	d__Bacteri	p__Bacteroi	c__Bacteroi	o__Bacteri	f__Muribac	NA	NA	Filter: bootstrap Score >= 50	
ASV795	100	99	99	99	99	99	79	d__Bacteri	p__Mycopl	c__Mollicu	o__Anaero	f__Anaero	g__Anaero	s__Anaeroplasma_abactoclasticum		
ASV796	100	100	100	100	100	100	85	d__Bacteri	p__Spirocha	c__Spirochi	o__Spirochi	f__Treponi	g__Treponi	s__Treponema_bryantii		
ASV797	100	100	100	100	100	70	17	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachnos	f__Lachnos	g__Roseb	NA	Filter: bootstrap Score >= 50	
ASV798	100	100	100	100	100	46	32	d__Bacteri	p__Bacteroi	c__Bacteroi	o__Bacteri	f__Muribac	NA	NA	Filter: bootstrap Score >= 50	

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ASV799	100	100	100	100	98	81	56	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteroi	f_Prevotel	g_Segatel	s_Segatella_copri		
ASV800	100	100	100	100	100	100	55	d_Bacteri	p_Bacillo	c_Bacilli	o_Lactoba	f_Strepto	g_Streptoc	s_Streptococcus_danieliae		
ASV801	100	100	99	99	97	51	51	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteroi	f_Muribac	g_Sangeri	s_Sangeribacter_muris		
ASV802	100	96	92	62	27	23	22	d_Bacteri	p_Bacillo	c_Clostrid	o_Eubacte	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV803	100	100	100	100	100	100	98	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachnos	f_Anaerot	g_Anaerot	s_Anaerotignum_aminivorans		
ASV804	100	100	100	100	100	100	100	d_Bacteri	p_Bacillo	c_Bacilli	o_Lactoba	f_Lactoba	g_Ligilact	s_Ligilactobacillus_ruminis		
ASV805	100	100	100	97	97	70	70	d_Bacteri	p_Bacillo	c_Clostrid	o_Christe	f_Christe	g_Guopin	s_Guopingia_tenuis		
ASV806	100	100	100	100	100	66	66	d_Bacteri	p_Bacillo	c_Clostrid	o_Eubacte	f_Oscillos	g_Anaerot	s_Anaerotruncus_rubiinfantis		
ASV807	100	100	100	100	50	50	40	d_Bacteri	p_Bacillo	c_Clostrid	o_Eubacte	f_Acutalib	g_Acutalib	NA	Filter: bootstrap Score >= 50	
ASV808	100	100	100	98	98	32	32	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachnos	f_Lachnos	NA	NA	Filter: bootstrap Score >= 50	
ASV809	100	100	99	98	95	57	57	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteroi	f_Muribac	g_Sangeri	s_Sangeribacter_muris		
ASV810	100	100	100	100	100	77	75	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteroi	f_Prevotel	g_Segatel	s_Segatella_copri		
ASV811	100	100	100	98	98	62	62	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachnos	f_Lachnos	g_Kineoth	s_Kineothrix_alysoides		
ASV812	100	100	100	100	100	100	100	d_Bacteri	p_Bacillo	c_Bacilli	o_Lactoba	f_Lactoba	g_Limosil	s_Limosilactobacillus_reuteri		
ASV813	100	100	100	100	48	28	28	d_Bacteri	p_Bacillo	c_Clostrid	o_Eubacte	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV814	100	100	100	100	52	52	45	d_Bacteri	p_Bacillo	c_Clostrid	o_Eubacte	f_Oscillos	g_Neglect	NA	Filter: bootstrap Score >= 50	
ASV815	100	100	100	100	100	50	33	d_Bacteri	p_Bacillo	c_Clostrid	o_Eubacte	f_Oscillos	g_Oscillib	NA	Filter: bootstrap Score >= 50	
ASV816	100	100	100	100	100	37	27	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachnos	f_Lachnos	NA	NA	Filter: bootstrap Score >= 50	
ASV817	100	99	99	97	97	12	3	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachnos	f_Lachnos	NA	NA	Filter: bootstrap Score >= 50	
ASV818	100	100	100	100	100	100	95	d_Bacteri	p_Bacillo	c_Bacilli	o_Bacillal	f_Caryoph	g_Kurthia	s_Kurthia_zopfii		
ASV819	100	100	100	100	100	100	42	d_Bacteri	p_Bacillo	c_Clostrid	o_Eubacte	f_Clostrid	g_Clostrid	NA	Filter: bootstrap Score >= 50	
ASV820	100	99	93	38	28	10	10	d_Bacteri	p_Bacillo	c_Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV821	100	100	100	100	100	100	100	d_Bacteri	p_Bacillo	c_Erysipel	o_Erysipel	f_Erysipel	g_Faecalib	s_Faecalibaculum_rodentium		
ASV822	100	100	100	100	72	47	30	d_Bacteri	p_Bacillo	c_Clostrid	o_Eubacte	f_Oscillos	NA	NA	Filter: bootstrap Score >= 50	
ASV823	100	100	100	100	100	100	40	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachnos	f_Lachnos	g_Blautia	NA	Filter: bootstrap Score >= 50	
ASV824	100	100	100	100	100	100	60	d_Bacteri	p_Pseudo	c_Gamma	o_Moraxel	f_Moraxel	g_Acineto	s_Acinetobacter_variabilis		
ASV825	100	100	100	100	100	100	51	d_Bacteri	p_Pseudo	c_Gamma	o_Moraxel	f_Moraxel	g_Acineto	s_Acinetobacter_tjernbergiae		
ASV826	100	100	100	96	96	60	60	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachnos	f_Lachnos	g_Kineoth	s_Kineothrix_alysoides		
ASV827	100	100	100	100	100	100	82	d_Bacteri	p_Bacillo	c_Clostrid	o_Eubacte	f_Oscillos	g_Vescimo	s_Vescimonas_fastidiosa		
ASV828	100	100	99	81	80	80	67	d_Bacteri	p_Bacillo	c_Clostrid	o_Eubacte	f_Aristaer	g_Aristaer	s_Aristaella_hokkaidonensis		
ASV829	100	100	100	100	100	100	100	d_Bacteri	p_Bacillo	c_Negativi	o_Selenom	f_Selenom	g_Schwart	s_Schwartzia_succinivorans		
ASV830	100	100	100	99	99	38	38	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachnos	f_Lachnos	NA	NA	Filter: bootstrap Score >= 50	
ASV831	100	100	100	100	100	35	13	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteroi	f_Prevotel	NA	NA	Filter: bootstrap Score >= 50	
ASV832	100	92	87	11	11	11	5	d_Bacteri	p_Bacillo	c_Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV833	100	100	100	100	97	46	25	d_Bacteri	p_Bacillo	c_Clostrid	o_Eubacte	f_Oscillos	NA	NA	Filter: bootstrap Score >= 50	
ASV834	100	100	100	100	100	85	34	d_Bacteri	p_Bacillo	c_Clostrid	o_Peptost	f_Peptost	g_Terrisp	NA	Filter: bootstrap Score >= 50	
ASV835	100	100	100	94	94	19	17	d_Bacteri	p_Actinob	c_Coriobac	o_Eggerth	f_Eggerth	NA	NA	Filter: bootstrap Score >= 50	
ASV836	100	94	78	48	37	8	8	d_Bacteri	p_Bacillo	c_Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV837	100	100	100	100	100	100	100	d_Bacteri	p_Bacillo	c_Erysipel	o_Erysipel	f_Erysipel	g_Floccifex	s_Floccifex_porci		
ASV838	100	100	100	98	98	66	66	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachnos	f_Lachnos	g_Acetatif	s_Acetatifactor_muris		
ASV839	100	100	100	100	97	58	58	d_Bacteri	p_Bacillo	c_Clostrid	o_Eubacte	f_Oscillos	g_Lawsone	s_Lawsonibacter_asaccharolyticus		
ASV840	100	100	100	100	100	100	100	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteroi	f_Muribac	g_Duncani	s_Duncaniella_freteri		
ASV841	100	100	100	100	68	55	55	d_Bacteri	p_Bacillo	c_Clostrid	o_Eubacte	f_Oscillos	g__	s_[Clostridium]_viride		
ASV842	100	100	100	100	100	100	48	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachnos	f_Lachnos	g_Blautia	NA	Filter: bootstrap Score >= 50	
ASV843	100	100	100	100	100	92	92	d_Bacteri	p_Bacillo	c_Clostrid	o_Eubacte	f_Oscillos	g_Angelak	s_Angelakisella_massiliensis		
ASV844	100	100	100	78	78	50	22	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachnos	f_Lachnos	g_Roseb	NA	Filter: bootstrap Score >= 50	
ASV845	100	99	68	38	21	10	10	d_Bacteri	p_Bacteri	c_Bacteroi	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV846	100	100	100	100	100	100	100	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteroi	f_Muribac	g_Sangeri	s_Sangeribacter_muris		
ASV847	100	100	100	100	100	100	91	d_Bacteri	p_Bacillo	c_Clostrid	o_Eubacte	f_Clostrid	g_Clostrid	s_Clostridium_paraputrificum		
ASV848	100	100	91	37	37	37	37	d_Bacteri	p_Bacillo	c_Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50	

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ASV849	100	99	99	99	66	33	33	d_Bacteri	p_Bacillo	c_Clostrid	o_Eubact	f_Acutalit	NA	NA	Filter: bootstrap Score >= 50
ASV850	100	73	73	73	73	73	73	d_Bacteri	p_Candid	c_Vampiri	o_Vampir	f_	g_Vampir	s_Vampirovibrio_chlorellavorus	
ASV851	100	100	100	100	100	100	100	d_Bacteri	p_Bacillo	c_Bacilli	o_Lactob	f_Lactoba	g_Limosil	s_Limosilactobacillus_reuteri	
ASV852	100	100	100	100	100	49	49	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV853	100	100	100	100	100	100	64	d_Bacteri	p_Bacillo	c_Clostrid	o_Eubact	f_Clostrid	g_Clostrid	s_Clostridium_tertium	
ASV854	100	100	100	100	98	82	82	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteroi	f_Muriba	g_Sodalip	s_Sodaliphilus_pleomorphus	
ASV855	100	100	100	100	100	100	86	d_Bacteri	p_Bacillo	c_Clostrid	o_Eubact	f_Oscillos	g_Vescim	s_Vescimonas_fastidiosa	
ASV856	100	98	98	94	77	48	27	d_Bacteri	p_Bacillo	c_Clostrid	o_Eubact	f_Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV857	100	11	6	5	5	5	5	d_Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV858	100	100	100	100	100	100	99	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteroi	f_Tanner	g_Parabac	s_Parabacteroides_gordonii	
ASV859	100	100	100	100	100	100	54	d_Bacteri	p_Bacillo	c_Bacilli	o_Lactob	f_Lactoba	g_Pediocc	s_Pediococcus_pentosaceus	
ASV860	100	100	100	100	100	52	52	d_Bacteri	p_Bacillo	c_Clostrid	o_Peptost	f_Anaero	g_Mogiba	s_Mogibacterium_kristiansenii	
ASV861	100	100	100	100	100	91	91	d_Bacteri	p_Bacillo	c_Clostrid	o_Eubact	f_Clostrid	g_Inconst	s_Inconstantimicrobium_porci	
ASV862	100	100	100	100	100	100	100	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteroi	f_Muriba	g_Muriba	s_Muribaculum_gordoncarteri	
ASV863	100	100	100	100	100	100	93	d_Bacteri	p_Bacillo	c_Bacilli	o_Bacillal	f_Staphyl	g_Staphy	s_Staphylococcus_capitis	
ASV864	100	100	100	100	100	100	100	d_Bacteri	p_Bacillo	c_Clostrid	o_Eubact	f_Eubact	g_Anaero	s_Anaerofustis_stercorihominis	
ASV865	100	97	94	19	19	17	17	d_Bacteri	p_Bacillo	c_Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV866	100	100	100	31	28	28	28	d_Bacteri	p_Bacillo	c_Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV867	100	100	100	33	14	14	14	d_Bacteri	p_Bacillo	c_Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV868	100	100	100	100	87	30	23	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteroi	f_Muriba	NA	NA	Filter: bootstrap Score >= 50
ASV869	100	100	100	100	100	100	32	d_Bacteri	p_Bacillo	c_Bacilli	o_Bacillal	f_Staphyl	g_Staphy	NA	Filter: bootstrap Score >= 50
ASV870	100	100	100	100	100	100	51	d_Bacteri	p_Bacillo	c_Clostrid	o_Eubact	f_Clostrid	g_Clostrid	s_Clostridium_tertium	
ASV871	99	7	2	2	2	2	2	d_Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV872	100	99	98	78	61	47	17	d_Bacteri	p_Actinor	c_Coriobac	o_Coriobac	f_Coriobac	NA	NA	Filter: bootstrap Score >= 50
ASV873	100	100	100	100	100	96	96	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteroi	f_Odoriba	g_Odorib	s_Odoribacter_splanchnicus	
ASV874	100	99	99	98	91	41	41	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteroi	f_Muriba	NA	NA	Filter: bootstrap Score >= 50
ASV875	100	100	100	100	92	92	71	d_Bacteri	p_Bacillo	c_Clostrid	o_Eubact	f_Acutalit	g_Acutali	s_Acutalibacter_caecimuris	
ASV876	100	100	100	100	100	71	68	d_Bacteri	p_Bacillo	c_Negativi	o_Selenor	f_Selenor	g_Mitsuo	s_Mitsuokella_jalaludinii	
ASV877	100	100	100	98	94	44	44	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteroi	f_Muriba	NA	NA	Filter: bootstrap Score >= 50
ASV878	100	100	100	100	100	100	76	d_Bacteri	p_Spirocl	c_Spirochi	o_Spirochi	f_Treponi	g_Treponi	s_Treponema_bryantii	
ASV879	100	100	100	100	100	100	98	d_Bacteri	p_Pseudo	c_Gammap	o_Enterob	f_Enterob	g_Escheri	s_Escherichia_fergusonii	
ASV880	100	100	100	99	70	43	32	d_Bacteri	p_Bacillo	c_Clostrid	o_Eubact	f_Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV881	100	100	100	75	75	4	4	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV882	100	89	86	84	79	63	37	d_Bacteri	p_Pseudo	c_Alphapr	o_Rhodob	f_Kiloniell	g_Aestua	NA	Filter: bootstrap Score >= 50
ASV883	100	100	100	100	100	71	60	d_Bacteri	p_Actinor	c_Coriobac	o_Eggertl	f_Eggertl	g_Adlercr	s_Adlercreutzia_muris	
ASV884	100	100	100	100	100	44	44	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV885	100	100	99	99	93	68	68	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteroi	f_Muriba	g_Paramu	s_Paramuribaculum_intestinale	
ASV886	100	100	100	95	95	21	21	d_Bacteri	p_Actinor	c_Coriobac	o_Eggertl	f_Eggertl	NA	NA	Filter: bootstrap Score >= 50
ASV887	100	100	100	100	98	78	78	d_Bacteri	p_Bacillo	c_Clostrid	o_Eubact	f_Oscillos	g_Fumia	s_Fumia_xinanensis	
ASV888	100	67	39	39	38	29	24	d_Bacteri	p_Bacillo	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV889	100	100	100	100	100	100	93	d_Bacteri	p_Bacillo	c_Clostrid	o_Eubact	f_Clostrid	g_Clostrid	s_Clostridium_butyricum	
ASV890	100	88	80	44	42	9	3	d_Bacteri	p_Bacillo	c_Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV891	100	100	100	100	100	100	9	d_Bacteri	p_Actinor	c_Actinob	o_Actinor	f_Actinor	g_Actinor	NA	Filter: bootstrap Score >= 50
ASV892	100	98	95	95	37	16	16	d_Bacteri	p_Bacillo	c_Erysipe	o_Erysipe	NA	NA	NA	Filter: bootstrap Score >= 50
ASV893	100	97	97	95	95	44	44	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV894	100	100	100	100	100	100	98	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	g_Anaero	s_Anaerobutyricum_soehngenii	
ASV895	100	100	100	100	100	100	100	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteroi	f_Prevote	g_Segate	s_Segatella_copri	
ASV896	100	100	100	100	100	69	57	d_Bacteri	p_Bacillo	c_Negativi	o_Selenor	f_Selenor	g_Mitsuo	s_Mitsuokella_multacida	
ASV897	100	100	100	100	100	98	33	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteroi	f_Bacteroi	g_Bacteroi	NA	Filter: bootstrap Score >= 50
ASV898	100	96	96	32	31	29	14	d_Bacteri	p_Bacillo	c_Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50

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ASV899	100	100	100	99	99	61	61	d__Bacteri	p__Bacillo	c__Clostrido	o__Lachnc	f__Lachno	g__Kineoth	s__Kineothrix_alysoides		
ASV900	100	100	100	100	100	100	46	d__Bacteri	p__Bacillo	c__Bacilli	o__Bacilla	f__Paenib	g__Paenib	NA	Filter: bootstrap Score >= 50	
ASV901	100	100	100	100	100	100	84	d__Bacteri	p__Actinor	c__Actinor	o__Bifidob	f__Bifidoba	g__Bifidob	s__Bifidobacterium_boum		
ASV902	100	100	100	100	100	100	100	d__Bacteri	p__Pseudo	c__Betapro	o__Burkho	f__Sutterel	g__Turicim	s__Turicimonas_muris		
ASV903	100	100	100	100	100	100	97	d__Bacteri	p__Actinor	c__Coriobo	o__Coriob	f__Coriobac	g__Collins	s__Collinsella_aerofaciens		
ASV904	100	100	100	100	100	91	91	d__Bacteri	p__Bacter	c__Bacterc	o__Bacter	f__Muribac	g__Sodalis	s__Sodaliphilus_pleomorphus		
ASV905	100	100	100	100	100	100	99	d__Bacteri	p__Campy	c__Epsilon	o__Campy	f__Helicob	g__Helicob	s__Helicobacter_mastomyrinus		
ASV906	100	100	100	100	100	100	100	d__Bacteri	p__Chlamy	c__Chlamy	o__Chlamy	f__Chlamy	g__Chlamy	s__Chlamydia_muridarum		
ASV907	100	100	100	92	92	54	18	d__Bacteri	p__Bacillo	c__Clostrido	o__Lachnc	f__Lachno	g__Lacrim	NA	Filter: bootstrap Score >= 50	
ASV908	100	100	100	100	98	46	46	d__Bacteri	p__Bacter	c__Bacterc	o__Bacter	f__Muribac	NA	NA	Filter: bootstrap Score >= 50	
ASV909	100	100	100	27	16	16	16	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV910	100	100	100	100	94	65	40	d__Bacteri	p__Bacillo	c__Clostrido	o__Eubact	f__Oscillos	g__Vescin	NA	Filter: bootstrap Score >= 50	
ASV911	100	96	83	83	82	22	15	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	f__Erysipe	NA	NA	Filter: bootstrap Score >= 50	
ASV912	100	100	100	100	100	100	100	d__Bacteri	p__Spiroch	c__Spiroch	o__Spiroch	f__Treponi	g__Treponi	s__Treponema_berlinense		
ASV913	100	100	100	97	97	47	47	d__Bacteri	p__Bacillo	c__Clostrido	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50	
ASV914	100	100	100	56	37	33	33	d__Bacteri	p__Bacillo	c__Clostrido	o__Eubact	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV915	100	100	100	100	100	47	47	d__Bacteri	p__Bacillo	c__Clostrido	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50	
ASV916	100	100	100	100	100	29	11	d__Bacteri	p__Bacter	c__Bacterc	o__Bacter	f__Prevote	NA	NA	Filter: bootstrap Score >= 50	
ASV917	100	100	100	100	100	100	73	d__Bacteri	p__Spiroch	c__Spiroch	o__Spiroch	f__Treponi	g__Treponi	s__Treponema_brennaborense		
ASV918	100	100	100	100	100	100	84	d__Bacteri	p__Bacillo	c__Clostrido	o__Lachnc	f__Anaero	g__Anaero	s__Anaerotignum_aminivorans		
ASV919	100	100	96	96	96	45	45	d__Bacteri	p__Bacillo	c__Clostrido	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50	
ASV920	100	100	100	100	100	60	29	d__Bacteri	p__Bacter	c__Bacterc	o__Bacter	f__Prevote	g__Segate	NA	Filter: bootstrap Score >= 50	
ASV921	100	100	100	100	100	87	51	d__Bacteri	p__Bacillo	c__Clostrido	o__Eubact	f__Oscillos	g__Vescin	s__Vescimonas_coprocola		
ASV922	100	100	100	83	83	52	30	d__Bacteri	p__Bacillo	c__Clostrido	o__Lachnc	f__Lachno	g__Lacrim	NA	Filter: bootstrap Score >= 50	
ASV923	100	100	100	100	100	27	12	d__Bacteri	p__Bacillo	c__Clostrido	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50	
ASV924	100	100	100	100	66	50	50	d__Bacteri	p__Bacillo	c__Clostrido	o__Eubact	f__Oscillos	g__	s__[Clostridium]_viride		
ASV925	100	100	100	96	96	20	20	d__Bacteri	p__Bacillo	c__Clostrido	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50	
ASV926	100	78	75	28	14	10	4	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV927	100	100	100	100	89	89	89	d__Bacteri	p__Bacillo	c__Clostrido	o__Eubact	f__	g__Gemm	s__Gemmiger_formicilis		
ASV928	100	97	91	53	16	14	12	d__Bacteri	p__Bacillo	c__Clostrido	o__Eubact	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV929	100	100	100	100	74	74	74	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	f__Coprob	g__Longib	s__Longibaculum_muris		
ASV930	100	100	100	100	100	100	40	d__Bacteri	p__Bacillo	c__Clostrido	o__Eubact	f__Clostrid	g__Clostrid	NA	Filter: bootstrap Score >= 50	
ASV931	100	91	68	29	20	20	20	d__Bacteri	p__Pseudo	c__Alphap	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV932	100	87	84	32	32	30	11	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV933	100	100	100	100	77	50	17	d__Bacteri	p__Bacillo	c__Clostrido	o__Eubact	f__Oscillos	g__Vescin	NA	Filter: bootstrap Score >= 50	
ASV934	100	100	100	100	100	100	95	d__Bacteri	p__Bacter	c__Bacterc	o__Bacter	f__Rikenel	g__Alistipe	s__Alistipes_communis		
ASV935	100	100	100	100	100	28	28	d__Bacteri	p__Bacillo	c__Clostrido	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50	
ASV936	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Clostrido	o__Eubact	f__Oscillos	g__Ruther	s__Ruthenibacterium_lactatiformans		
ASV937	100	100	100	100	66	21	21	d__Bacteri	p__Bacillo	c__Clostrido	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50	
ASV938	100	100	100	99	72	61	22	d__Bacteri	p__Bacillo	c__Clostrido	o__Eubact	f__Oscillos	g__Vescin	NA	Filter: bootstrap Score >= 50	
ASV939	100	100	100	100	100	100	47	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Limosil	NA	Filter: bootstrap Score >= 50	
ASV940	100	100	100	92	92	27	27	d__Bacteri	p__Bacillo	c__Clostrido	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50	
ASV941	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Clostrido	o__Eubact	f__	g__Flintiba	s__Flintibacter_butyricus		
ASV942	100	100	100	100	100	100	67	d__Bacteri	p__Bacillo	c__Clostrido	o__Eubact	f__Clostrid	g__Clostrid	s__Clostridium_moniliforme		
ASV943	100	100	100	100	100	54	26	d__Bacteri	p__Bacter	c__Bacterc	o__Bacter	f__Prevote	g__Segate	NA	Filter: bootstrap Score >= 50	
ASV944	100	100	100	100	100	69	55	d__Bacteri	p__Bacter	c__Bacterc	o__Bacter	f__Prevote	g__Segate	s__Segatella_copri		
ASV945	100	100	100	100	100	100	61	d__Bacteri	p__Pseudo	c__Gammo	o__Moraxe	f__Moraxe	g__Psychr	s__Psychrobacter_pasteurii		
ASV946	100	100	100	99	99	78	78	d__Bacteri	p__Bacillo	c__Clostrido	o__Lachnc	f__Lachno	g__Acetati	s__Acetatifactor_muris		
ASV947	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Limosil	s__Limosilactobacillus_reuteri		
ASV948	100	100	100	100	100	43	28	d__Bacteri	p__Bacter	c__Bacterc	o__Bacter	f__Prevote	NA	NA	Filter: bootstrap Score >= 50	

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ASV949	100	100	100	100	100	45	45	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnd	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV950	100	100	100	100	100	49	40	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnd	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV951	100	100	100	99	99	37	17	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnd	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV952	100	100	100	100	100	84	84	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacf	f__Oscillos	g__Angela	s__Angelakisella_massiliensis	
ASV953	100	99	99	98	96	96	61	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacf	f__Aristaec	g__Aristae	s__Aristaeella_lactis	
ASV954	100	100	100	100	96	28	22	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteri	f__Muribac	NA	NA	Filter: bootstrap Score >= 50
ASV955	100	100	100	100	100	100	88	d__Bacteri	p__Spirocl	c__Spirocl	o__Spirocl	f__Treponi	g__Treponi	s__Treponema_bryantii	
ASV956	100	100	100	100	100	38	27	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteri	f__Prevote	NA	NA	Filter: bootstrap Score >= 50
ASV957	100	100	100	100	100	92	91	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacf	f__Oscillos	g__Oscillib	s__Oscillibacter_valericigenes	
ASV958	100	100	100	100	100	100	100	d__Bacteri	p__Pseudo	c__Gammo	o__Enterob	f__Enterob	g__Klebsie	s__Klebsiella_pneumoniae	
ASV959	100	100	100	100	93	93	61	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnd	f__Cellulos	g__Cellulo	s__Cellulosilyticum_lentocellum	
ASV960	100	10	4	3	3	3	3	d__Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV961	100	100	100	24	14	14	13	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV962	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacf	f__Oscillos	g__Vescim	s__Vescimonas_fastidiosa	
ASV963	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Negativ	o__Selend	f__Selenol	g__Schwa	s__Schwartzia_succinivorans	
ASV964	100	100	100	100	85	85	51	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnd	f__Cellulos	g__Cellulo	s__Cellulosilyticum_ruminicola	
ASV965	100	100	100	81	81	42	42	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnd	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV966	100	97	95	53	11	10	7	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacf	NA	NA	NA	Filter: bootstrap Score >= 50
ASV967	100	100	100	100	100	57	57	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnd	f__Lachno	g__Wansu	s__Wansuia_hejianensis	
ASV968	100	86	86	86	63	28	27	d__Bacteri	p__Deferri	c__Deferri	o__Deferri	f__Geovib	NA	NA	Filter: bootstrap Score >= 50
ASV969	100	100	100	100	100	62	59	d__Bacteri	p__Bacillo	c__Negativ	o__Selend	f__Selenol	g__Mitsuo	s__Mitsuokella_multacida	
ASV970	100	100	100	100	100	39	24	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnd	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV971	100	100	92	91	40	40	40	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacf	NA	NA	NA	Filter: bootstrap Score >= 50
ASV972	100	100	100	100	88	64	41	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacf	f__	g__Intestin	NA	Filter: bootstrap Score >= 50
ASV973	100	71	52	52	49	18	13	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	NA	NA	NA	Filter: bootstrap Score >= 50
ASV974	100	100	100	93	93	42	20	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnd	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV975	100	86	85	51	50	6	6	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnd	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV976	100	100	100	92	92	20	14	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnd	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV977	100	100	100	100	100	79	76	d__Bacteri	p__Pseudo	c__Gammo	o__Enterob	f__Enterob	g__Escher	s__Escherichia_fergusonii	
ASV978	100	100	100	100	97	59	59	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteri	f__Muribac	g__Param	s__Paramuribaculum_intestinale	
ASV979	100	100	100	100	100	100	42	d__Archae	p__Methan	c__Methano	o__Methan	f__Methan	g__Methan	NA	Filter: bootstrap Score >= 50
ASV980	100	81	76	67	29	29	25	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacf	NA	NA	NA	Filter: bootstrap Score >= 50
ASV981	100	100	100	100	100	100	92	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacf	f__Aristaec	g__Aristae	s__Aristaeella_hokkaidonensis	
ASV982	100	100	100	98	98	54	36	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnd	f__Lachno	g__Lacrim	NA	Filter: bootstrap Score >= 50
ASV983	100	100	100	100	100	84	71	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteri	f__Prevote	g__Segate	s__Segatella_baroniae	
ASV984	100	100	100	100	100	44	37	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteri	f__Prevote	NA	NA	Filter: bootstrap Score >= 50
ASV985	100	100	100	100	100	64	25	d__Bacteri	p__Bacillo	c__Clostrid	o__Peptost	f__Peptost	g__Terrisp	NA	Filter: bootstrap Score >= 50
ASV986	100	100	100	100	100	78	53	d__Bacteri	p__Thermi	c__Desulfo	o__Desulfo	f__Desulfo	g__Desulfo	s__Desulfovibrio_litoralis	
ASV987	100	100	100	100	100	100	87	d__Bacteri	p__Spirocl	c__Spirocl	o__Spirocl	f__Treponi	g__Treponi	s__Treponema_bryantii	
ASV988	100	97	79	21	18	11	11	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV989	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacf	f__	g__Flintiba	s__Flintibacter_butyricus	
ASV990	100	100	100	27	14	12	10	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV991	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Limosil	s__Limosilactobacillus_reuteri	
ASV992	100	91	73	73	73	60	60	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	f__Erysipe	g__Brezna	s__Breznakia_blatticola	
ASV993	100	100	100	100	100	100	84	d__Bacteri	p__Actinob	c__Actinom	o__Microc	f__Microc	g__Rothia	s__Rothia_terrae	
ASV994	100	100	100	100	99	98	69	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteri	f__Muribac	g__Duncan	s__Duncaniella_muris	
ASV995	100	100	100	96	96	96	80	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacf	f__Aristaec	g__Aristae	s__Aristaeella_hokkaidonensis	
ASV996	100	100	100	100	100	59	46	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnd	f__Lachno	g__Blautia	NA	Filter: bootstrap Score >= 50
ASV997	100	100	100	100	100	92	83	d__Bacteri	p__Bacillo	c__Clostrid	o__Peptost	f__Anaerol	g__Lentiho	s__Lentihominibacter_faecis	
ASV998	100	100	100	100	95	45	45	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteri	f__Prevote	NA	NA	Filter: bootstrap Score >= 50

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ASV999	100	100	100	100	100	60	18	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachnos	f__Lachnos	g__Jutongi	NA	Filter: bootstrap Score >= 50
ASV1000	100	100	100	96	96	12	9	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachnos	f__Lachnos	NA	NA	Filter: bootstrap Score >= 50
ASV1001	100	100	100	100	100	100	43	d__Bacteri	p__Actinom	c__Actinom	o__Mycobac	f__Corynet	g__Corynet	NA	Filter: bootstrap Score >= 50
ASV1002	100	100	100	98	98	20	20	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachnos	f__Lachnos	NA	NA	Filter: bootstrap Score >= 50
ASV1003	100	99	95	95	66	23	23	d__Bacteri	p__Bacillot	c__Erysipel	o__Erysipel	f__Coprobi	NA	NA	Filter: bootstrap Score >= 50
ASV1004	100	99	99	94	94	42	42	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachnos	f__Lachnos	NA	NA	Filter: bootstrap Score >= 50
ASV1005	100	100	100	100	100	100	100	d__Bacteri	p__Bacteroi	c__Bacteroi	o__Bacteroi	f__Prevotel	g__Segatel	s__Segatella_copri	
ASV1006	100	100	100	100	99	86	86	d__Bacteri	p__Bacteroi	c__Bacteroi	o__Bacteroi	f__Muribac	g__Sodalis	s__Sodaliphilus_pleomorphus	
ASV1007	100	93	82	40	20	20	10	d__Bacteri	p__Bacillot	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1008	100	100	100	100	100	100	76	d__Bacteri	p__Actinom	c__Actinom	o__Mycobac	f__Dietziac	g__Dietzia	s__Dietzia_cinnamea	
ASV1009	100	100	99	83	82	82	71	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubacte	f__Aristaee	g__Aristaee	s__Aristaeella_hokkaidonensis	
ASV1010	100	100	100	100	100	100	80	d__Bacteri	p__Bacillot	c__Bacilli	o__Lactoba	f__Aerococ	g__Ruoffia	s__Ruoffia_tabacinasalis	
ASV1011	100	100	100	94	94	27	20	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachnos	f__Lachnos	NA	NA	Filter: bootstrap Score >= 50
ASV1012	100	100	100	99	99	70	70	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachnos	f__Lachnos	g__Lachnos	s__[Clostridium]_scindens	
ASV1013	100	100	100	100	99	32	32	d__Bacteri	p__Bacteroi	c__Bacteroi	o__Bacteroi	f__Muribac	NA	NA	Filter: bootstrap Score >= 50
ASV1014	100	94	85	22	22	17	16	d__Bacteri	p__Bacillot	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1015	100	100	100	100	100	77	77	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubacte	f__Oscillos	g__Ruminic	s__Ruminococcus_bromii	
ASV1016	100	100	100	100	96	57	43	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubacte	f__	g__Intestin	NA	Filter: bootstrap Score >= 50
ASV1017	100	100	100	94	94	19	19	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachnos	f__Lachnos	NA	NA	Filter: bootstrap Score >= 50
ASV1018	100	87	78	8	8	8	5	d__Bacteri	p__Bacillot	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1019	100	90	90	90	88	14	14	d__Bacteri	p__Bacillot	c__Bacilli	o__Bacillal	f__Bacillac	NA	NA	Filter: bootstrap Score >= 50
ASV1020	100	100	100	100	71	60	60	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubacte	f__Oscillos	g__	s__[Clostridium]_leptum	
ASV1021	100	100	100	100	88	34	34	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubacte	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV1022	100	35	35	35	35	35	35	d__Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1023	100	100	100	100	100	100	100	d__Bacteri	p__Bacillot	c__Bacilli	o__Lactoba	f__Lactoba	g__Limosil	s__Limosilactobacillus_reuteri	
ASV1024	100	88	68	10	6	6	6	d__Bacteri	p__Bacillot	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1025	100	100	100	100	100	100	70	d__Bacteri	p__Spirocha	c__Spirocha	o__Spirocha	f__Treponi	g__Treponi	s__Treponema_peruense	
ASV1026	100	100	100	100	92	50	50	d__Bacteri	p__Bacteroi	c__Bacteroi	o__Bacteroi	f__Muribac	g__Sangeri	s__Sangeribacter_muris	
ASV1027	100	100	100	100	100	61	61	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubacte	f__Oscillos	g__Oscillib	s__Oscillibacter_valericigenes	
ASV1028	100	100	100	96	96	45	45	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachnos	f__Lachnos	NA	NA	Filter: bootstrap Score >= 50
ASV1029	100	100	100	100	94	31	31	d__Bacteri	p__Bacteroi	c__Bacteroi	o__Bacteroi	f__Muribac	NA	NA	Filter: bootstrap Score >= 50
ASV1030	100	100	100	100	100	100	68	d__Bacteri	p__Bacteroi	c__Chitinop	o__Chitinop	f__Chitinop	g__Sediminic	s__Sediminibacterium_salmoneum	
ASV1031	100	100	100	100	100	100	55	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachnos	f__Lachnos	g__Roseburi	s__Roseburia_intestinalis	
ASV1032	100	77	38	38	37	21	18	d__Bacteri	p__Bacillot	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1033	100	100	100	100	100	100	45	d__Bacteri	p__Bacteroi	c__Bacteroi	o__Bacteroi	f__Odoribac	g__Butyricic	NA	Filter: bootstrap Score >= 50
ASV1034	100	100	99	99	99	87	65	d__Bacteri	p__Bacillot	c__Erysipel	o__Erysipel	f__Erysipel	g__Amedibi	s__Amedibacillus_hominis	
ASV1035	100	100	100	100	100	45	45	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachnos	f__Lachnos	NA	NA	Filter: bootstrap Score >= 50
ASV1036	100	100	100	97	97	25	16	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachnos	f__Lachnos	NA	NA	Filter: bootstrap Score >= 50
ASV1037	100	100	100	99	99	61	18	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachnos	f__Lachnos	g__Blautia	NA	Filter: bootstrap Score >= 50
ASV1038	100	100	100	100	100	99	99	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachnos	f__Lachnos	g__Coprocc	s__Coprococcus_catus	
ASV1039	100	100	100	100	100	96	96	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachnos	f__Lachnos	g__Kineoth	s__Kineothrix_alysoides	
ASV1040	100	100	100	95	95	9	7	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachnos	f__Lachnos	NA	NA	Filter: bootstrap Score >= 50
ASV1041	100	82	74	16	16	15	4	d__Bacteri	p__Bacillot	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1042	100	100	100	100	100	64	64	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachnos	f__Lachnos	g__Luxibac	s__Luxibacter_massiliensis	
ASV1043	100	100	100	100	100	83	5	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachnos	f__Lachnos	g__Blautia	NA	Filter: bootstrap Score >= 50
ASV1044	100	100	100	100	100	41	41	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachnos	f__Lachnos	NA	NA	Filter: bootstrap Score >= 50
ASV1045	100	100	100	100	100	100	99	d__Bacteri	p__Bacteroi	c__Bacteroi	o__Bacteroi	f__Rikenel	g__Alistipe	s__Alistipes_okayasuensis	
ASV1046	100	100	100	100	100	94	94	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachnos	f__Lachnos	g__Coprocc	s__Coprococcus_comes	
ASV1047	100	100	100	100	100	100	100	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachnos	f__Lachnos	g__Jingyaoa	s__Jingyaoa_shaoxingensis	
ASV1048	100	100	100	100	100	100	100	d__Bacteri	p__Bacillot	c__Negativi	o__Veillon	f__Veillone	g__Megasp	s__Megasphaera_elsdenii	

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ASV1049	100	100	100	100	85	61	61	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__	g__Intestin	s__Intestinimonas_timonensis		
ASV1050	100	100	100	100	96	93	93	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	g__Lawso	s__Lawsonibacter_asaccharolyticus		
ASV1051	100	100	100	95	95	74	73	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Anaero	s__Anaerostipes_butyraticus		
ASV1052	100	100	100	98	71	22	22	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__	NA	NA	Filter: bootstrap Score >= 50	
ASV1053	100	100	96	96	95	28	28	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50	
ASV1054	100	100	100	92	92	60	17	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Lacrim	NA	Filter: bootstrap Score >= 50	
ASV1055	100	100	100	100	100	100	100	d__Bacteri	p__Actinor	c__Coriobac	o__Coriob	f__Kribbib	g__Granul	s__Granulimonas_faecalis		
ASV1056	100	92	92	92	92	89	47	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Ligilact	NA	Filter: bootstrap Score >= 50	
ASV1057	100	100	100	100	18	11	9	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV1058	100	100	100	100	100	100	45	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Rikene	g__Alistipe	NA	Filter: bootstrap Score >= 50	
ASV1059	100	100	100	100	100	100	47	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Limosi	NA	Filter: bootstrap Score >= 50	
ASV1060	100	100	100	100	100	100	50	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Limosi	s__Limosilactobacillus_oris		
ASV1061	100	100	100	100	100	84	37	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Bacter	g__Bacter	NA	Filter: bootstrap Score >= 50	
ASV1062	100	100	100	100	100	100	30	d__Bacteri	p__Actinor	c__Actinor	o__Mycob	f__Coryne	g__Coryne	NA	Filter: bootstrap Score >= 50	
ASV1063	100	100	100	100	100	100	92	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	s__Lactobacillus_kalixensis		
ASV1064	100	100	100	98	98	39	39	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50	
ASV1065	100	100	100	100	100	71	71	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Kineoth	s__Kineothrix_alysoides		
ASV1066	100	100	69	29	27	9	9	d__Bacteri	p__Bacter	c__Bacter	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV1067	100	100	100	100	100	100	83	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Anaero	s__Anaerobutyricum_soehngenii		
ASV1068	100	100	100	100	94	38	38	d__Bacteri	p__Actinor	c__Actinor	o__Microc	f__Intrasp	NA	NA	Filter: bootstrap Score >= 50	
ASV1069	100	100	100	100	91	27	24	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Muriba	NA	NA	Filter: bootstrap Score >= 50	
ASV1070	100	100	100	100	100	94	94	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Sporof	s__Sporofaciens_musculi		
ASV1071	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Acutalit	g__Acutali	s__Acutalibacter_intestini		
ASV1072	100	100	100	97	97	33	33	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50	
ASV1073	100	100	100	100	74	67	39	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__	g__Intestin	NA	Filter: bootstrap Score >= 50	
ASV1074	100	100	100	99	99	26	26	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50	
ASV1075	100	100	100	100	99	61	61	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Muriba	g__Param	s__Paramuribaculum_intestinale		
ASV1076	100	100	100	85	85	32	32	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50	
ASV1077	100	99	95	52	14	8	8	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV1078	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	f__Erysipe	g__Holden	s__Holdemanella_porci		
ASV1079	100	100	99	99	86	46	46	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50	
ASV1080	100	100	100	100	100	100	68	d__Bacteri	p__Bacillo	c__Negativi	o__Veillon	f__Veillone	g__Veillon	s__Veillonella_parvula		
ASV1081	100	100	100	76	76	21	21	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50	
ASV1082	100	100	100	39	17	16	16	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV1083	100	100	100	100	76	25	25	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50	
ASV1084	100	94	94	91	54	32	32	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Acutalit	NA	NA	Filter: bootstrap Score >= 50	
ASV1085	100	100	100	98	98	98	98	d__Bacteri	p__Actinor	c__Coriobac	o__Coriob	f__Coriobac	g__Parviba	s__Parvibacter_caecicola		
ASV1086	100	100	100	98	98	98	98	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Lachno	s__[Clostridium]_aminophilum		
ASV1087	100	100	98	72	43	42	36	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV1088	100	100	100	100	95	65	51	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Muriba	g__Dunca	s__Duncaniella_dubosii		
ASV1089	100	100	100	100	100	44	44	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50	
ASV1090	100	100	100	100	100	78	78	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Coprod	s__Coprococcus_comes		
ASV1091	100	100	100	94	94	21	21	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50	
ASV1092	100	100	100	100	100	100	100	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Bacter	g__Phoca	s__Phocaeicola_vulgatus		
ASV1093	100	73	52	52	52	5	5	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	f__Erysipe	NA	NA	Filter: bootstrap Score >= 50	
ASV1094	100	100	100	98	98	15	4	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50	
ASV1095	100	100	100	96	96	59	27	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Lacrim	NA	Filter: bootstrap Score >= 50	
ASV1096	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Negativi	o__Acidam	f__Acidam	g__Phasco	s__Phascolarctobacterium_succinatutens		
ASV1097	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Negativi	o__Acidam	f__Acidam	g__Phasco	s__Phascolarctobacterium_succinatutens		
ASV1098	100	100	100	100	100	100	87	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Bacter	g__Phoca	s__Phocaeicola_faecalis		

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ASV1099	100	100	22	22	22	14	8	d__Bacteri	p__Bacteri	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1100	100	68	23	23	23	4	3	d__Bacteri	p__Bacillo	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1101	100	100	100	100	67	67	34	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Acutalib	g__Acutalib	NA	Filter: bootstrap Score >= 50
ASV1102	100	100	100	100	99	99	78	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Anaerot	g__Anaerot	s__Anaerotignum_aminivorans	
ASV1103	100	100	100	100	100	100	98	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Clostrid	g__Clostrid	s__Clostridium_chartatabidum	
ASV1104	100	100	100	100	100	100	82	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Anaerot	g__Anaerot	s__Anaerotignum_aminivorans	
ASV1105	100	100	100	100	100	100	94	d__Bacteri	p__Spirocl	c__Spirocl	o__Spirocl	f__Treponi	g__Treponi	s__Treponema_parvum	
ASV1106	100	96	74	71	10	9	8	d__Bacteri	p__Bacteri	c__Bacteri	o__Bacteri	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1107	100	98	98	97	97	20	20	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachnos	NA	NA	Filter: bootstrap Score >= 50
ASV1108	100	100	100	92	92	25	11	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachnos	NA	NA	Filter: bootstrap Score >= 50
ASV1109	100	100	100	100	100	100	62	d__Bacteri	p__Bacteri	c__Bacteri	o__Bacteri	f__Rikenel	g__Alistipe	s__Alistipes_shahii	
ASV1110	100	100	100	98	98	27	27	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachnos	NA	NA	Filter: bootstrap Score >= 50
ASV1111	100	100	100	97	96	7	7	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachnos	NA	NA	Filter: bootstrap Score >= 50
ASV1112	100	100	100	100	52	52	50	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Acutalib	g__Acutalib	s__Acutalibacter_caecimuris	
ASV1113	100	100	100	100	100	100	74	d__Bacteri	p__Bacillo	c__Bacilli	o__Bacillal	f__Paenibac	g__Brevibac	s__Brevibacillus_reuszeri	
ASV1114	100	79	79	79	79	67	52	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachnos	g__Faecalis	s__Faecalicatena_orotica	
ASV1115	100	100	100	100	100	99	71	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachnos	g__Roseb	s__Roseburia_inulinivorans	
ASV1116	100	100	99	99	99	80	75	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Oscillos	g__Anaerot	s__Anaerotruncus_colihominis	
ASV1117	100	96	81	26	16	16	12	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1118	100	100	100	100	98	74	74	d__Bacteri	p__Bacillo	c__Clostrid	o__Peptost	f__Anaerov	g__Sinana	s__Sinanaerobacter_chloroacetimidivorans	
ASV1119	100	100	100	100	100	25	16	d__Bacteri	p__Bacteri	c__Bacteri	o__Bacteri	f__Prevote	NA	NA	Filter: bootstrap Score >= 50
ASV1120	100	100	100	100	100	42	9	d__Bacteri	p__Bacteri	c__Bacteri	o__Bacteri	f__Prevote	NA	NA	Filter: bootstrap Score >= 50
ASV1121	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Aerococ	g__Aerococ	s__Aerococcus_viridans	
ASV1122	100	97	97	90	90	21	21	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachnos	NA	NA	Filter: bootstrap Score >= 50
ASV1123	100	41	33	25	24	24	18	d__Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1124	100	100	65	64	8	8	4	d__Bacteri	p__Bacteri	c__Bacteri	o__Bacteri	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1125	100	94	93	22	18	18	18	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1126	100	98	90	26	26	11	11	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1127	100	100	100	92	92	17	17	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachnos	NA	NA	Filter: bootstrap Score >= 50
ASV1128	100	100	100	100	97	97	97	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__	g__Colidex	s__Colidextribacter_massiliensis	
ASV1129	100	100	100	100	100	100	98	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Limosil	s__Limosilactobacillus_mucosae	
ASV1130	100	100	100	100	88	88	71	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Oscillos	g__Neglect	s__Neglectibacter_timonensis	
ASV1131	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Oscillos	g__	s__[Eubacterium]_siraeum	
ASV1132	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__	g__Flintiba	s__Flintibacter_butyricus	
ASV1133	100	97	97	65	55	4	4	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachnos	NA	NA	Filter: bootstrap Score >= 50
ASV1134	100	100	100	100	100	35	24	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachnos	NA	NA	Filter: bootstrap Score >= 50
ASV1135	100	75	59	59	58	3	3	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	f__Erysipe	NA	NA	Filter: bootstrap Score >= 50
ASV1136	100	100	100	100	98	61	61	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Oscillos	g__Lawsoni	s__Lawsonibacter_asaccharolyticus	
ASV1137	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Oscillos	g__Rumino	s__Ruminococcus_champanellensis	
ASV1138	100	97	61	17	2	1	0	d__Bacteri	p__Bacteri	c__Bacteri	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1139	100	100	99	91	88	88	71	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Aristaee	g__Aristaee	s__Aristaeella_hokkaidonensis	
ASV1140	100	100	100	100	100	100	100	d__Bacteri	p__Bacteri	c__Bacteri	o__Bacteri	f__Prevote	g__Hallella	s__Hallella_mizrahii	
ASV1141	100	100	95	95	44	44	44	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1142	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	f__Erysipe	g__Holdem	s__Holdemanella_porci	
ASV1143	100	100	100	100	100	100	75	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Aristaee	g__Aristaee	s__Aristaeella_hokkaidonensis	
ASV1144	100	86	77	31	25	10	8	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1145	100	100	100	99	99	75	31	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachnos	g__Eisenb	NA	Filter: bootstrap Score >= 50
ASV1146	100	100	100	99	99	3	3	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachnos	NA	NA	Filter: bootstrap Score >= 50
ASV1147	100	100	100	100	100	54	27	d__Bacteri	p__Bacteri	c__Bacteri	o__Bacteri	f__Prevote	g__Segate	NA	Filter: bootstrap Score >= 50
ASV1148	100	97	84	7	7	7	7	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50

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ASV1149	100	100	100	98	98	37	23	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1150	100	100	100	100	100	66	56	d__Bacteri	p__Bacillo	c__Negativi	o__Seleno	f__Seleno	g__Mitsuo	s__Mitsuokella_multacida	
ASV1151	100	100	99	98	49	37	23	d__Bacteri	p__Bacteri	c__Bacteri	o__Bacteri	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1152	100	100	100	95	95	35	33	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1153	100	100	100	90	90	84	43	d__Bacteri	p__Actinot	c__Coriobac	o__Eggerth	f__Eggerth	g__Adlerc	NA	Filter: bootstrap Score >= 50
ASV1154	100	94	89	38	11	8	5	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1155	100	100	100	98	98	79	79	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	g__Acetatif	s__Acetatifactor_muris	
ASV1156	100	100	100	94	94	36	36	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1157	100	100	100	96	96	44	44	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1158	100	100	98	98	95	41	39	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacti	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV1159	100	99	96	92	91	89	8	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacti	f__Clostrid	g__Clostri	NA	Filter: bootstrap Score >= 50
ASV1160	100	100	100	84	84	68	68	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	g__Medite	s__Mediterraneibacter_faecis	
ASV1161	100	100	99	95	94	94	80	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacti	f__Aristae	g__Aristae	s__Aristaeella_lactis	
ASV1162	100	100	100	82	82	21	21	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1163	100	100	44	38	24	16	16	d__Bacteri	p__Bacteri	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1164	100	100	100	36	36	36	36	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1165	100	100	100	76	76	6	5	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1166	100	100	100	100	84	68	38	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacti	f__Oscillos	g__Vescin	NA	Filter: bootstrap Score >= 50
ASV1167	100	100	99	99	96	77	77	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacti	f__Oscillos	g__Fumia	s__Fumia_xinanensis	
ASV1168	100	100	100	100	100	72	66	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	g__Roseb	s__Roseburia_intestinalis	
ASV1169	100	100	100	100	97	28	27	d__Bacteri	p__Bacillo	c__Bacilli	o__Bacillal	f__Bacillac	NA	NA	Filter: bootstrap Score >= 50
ASV1170	100	100	100	100	100	100	94	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacti	f__Clostrid	g__Clostri	s__Clostridium_chartatabidum	
ASV1171	100	94	89	49	16	16	12	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1172	100	100	100	100	77	53	53	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacti	f__Oscillos	g__	s__[Clostridium]_viride	
ASV1173	100	100	100	100	100	65	42	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	f__Erysipe	g__Amedi	NA	Filter: bootstrap Score >= 50
ASV1174	100	100	100	100	78	45	45	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacti	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV1175	100	100	100	98	54	38	6	d__Bacteri	p__Bacteri	c__Bacteri	o__Bacteri	f__Tanneri	NA	NA	Filter: bootstrap Score >= 50
ASV1176	100	100	100	100	100	81	81	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacti	f__Oscillos	g__Rumin	s__Ruminococcoides_bili	
ASV1177	100	100	100	100	100	100	81	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Ligilact	s__Ligilactobacillus_apodemi	
ASV1178	100	100	100	100	93	93	93	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacti	f__	g__Colide	s__Colidextribacter_massiliensis	
ASV1179	100	100	100	65	65	18	18	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1180	100	100	100	100	85	79	58	d__Bacteri	p__Bacteri	c__Bacteri	o__Bacteri	f__Bacter	g__Bacter	s__Bacteroides_ndongoniae	
ASV1181	100	100	100	100	100	40	16	d__Bacteri	p__Bacteri	c__Bacteri	o__Bacteri	f__Prevote	NA	NA	Filter: bootstrap Score >= 50
ASV1182	100	22	22	22	22	22	22	d__Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1183	100	100	100	100	100	100	76	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	s__Lactobacillus_gasseri	
ASV1184	100	100	100	100	96	54	53	d__Bacteri	p__Bacillo	c__Bacilli	o__Bacillal	f__Bacillac	g__Bacillu	s__Bacillus_caccae	
ASV1185	100	100	100	97	97	43	38	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1186	100	100	99	99	98	32	32	d__Bacteri	p__Bacteri	c__Bacteri	o__Bacteri	f__Muriba	NA	NA	Filter: bootstrap Score >= 50
ASV1187	100	99	97	97	66	19	19	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacti	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV1188	100	100	100	95	95	44	42	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1189	100	100	100	100	100	53	45	d__Bacteri	p__Bacteri	c__Bacteri	o__Bacteri	f__Muriba	g__Dunca	NA	Filter: bootstrap Score >= 50
ASV1190	100	100	100	100	100	100	98	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacti	f__Clostrid	g__Clostri	s__Clostridium_massiliamazoniense	
ASV1191	100	100	100	99	99	58	58	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	g__Kineot	s__Kineothrix_alysoides	
ASV1192	100	100	100	100	100	100	78	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacti	f__Oscillos	g__Vescin	s__Vescimonas_fastidiosa	
ASV1193	100	100	100	100	100	72	72	d__Bacteri	p__Bacillo	c__Negativi	o__Seleno	f__Seleno	g__Mitsuo	s__Mitsuokella_jalaludinii	
ASV1194	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Negativi	o__Acidam	f__Acidam	g__Phasc	s__Phascolarctobacterium_succinatutens	
ASV1195	100	87	87	87	85	71	71	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	f__Erysipe	g__Lactim	s__Lactimicrobium_massiliense	
ASV1196	100	100	100	100	100	72	72	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	g__Kineot	s__Kineothrix_alysoides	
ASV1197	100	100	100	100	63	43	43	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacti	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV1198	100	100	100	100	100	100	95	d__Bacteri	p__Therm	c__Desulfo	o__Desulfo	f__Desulfo	g__Desulfo	s__Desulfovibrio_porci	

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ASV1199	100	100	100	99	99	16	16	d__Bacter	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1200	100	100	100	93	93	22	11	d__Bacter	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1201	100	100	100	98	98	11	11	d__Bacter	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1202	100	100	100	100	100	100	34	d__Archae	p__Methan	c__Methano	o__Methan	f__Methan	g__Methan	NA	Filter: bootstrap Score >= 50
ASV1203	100	100	100	100	100	100	100	d__Bacter	p__Bacter	c__Bacteroi	o__Bacter	f__Muriba	g__Sangeri	s__Sangeribacter_muris	
ASV1204	100	100	100	98	98	25	24	d__Bacter	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1205	100	100	100	100	100	100	100	d__Bacter	p__Bacillo	c__Negativi	o__Selenc	f__Selenor	g__Selenc	s__Selenomonas_bovis	
ASV1206	100	100	100	100	100	71	62	d__Bacter	p__Bacillo	c__Negativi	o__Selenc	f__Selenor	g__Mitsuo	s__Mitsuokella_multacida	
ASV1207	100	98	98	98	98	87	87	d__Bacter	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Lachno	s__[Clostridium]_hylemonae	
ASV1208	100	95	84	70	47	20	15	d__Bacter	p__Bacillo	c__Clostrid	o__Eubact	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1209	100	100	100	100	100	100	21	d__Bacter	p__Actinor	c__Actinor	o__Mycob	f__Coryne	g__Coryne	NA	Filter: bootstrap Score >= 50
ASV1210	100	99	99	62	62	25	22	d__Bacter	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1211	100	78	31	31	31	10	2	d__Bacter	p__Bacillo	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1212	100	100	99	93	54	35	35	d__Bacter	p__Bacillo	c__Clostrid	o__Eubact	f__	NA	NA	Filter: bootstrap Score >= 50
ASV1213	100	100	99	99	99	67	67	d__Bacter	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	g__Angela	s__Angelakisella_massiliensis	
ASV1214	100	100	100	100	99	41	41	d__Bacter	p__Bacillo	c__Negativi	o__Selenc	f__Selenor	NA	NA	Filter: bootstrap Score >= 50
ASV1215	100	100	100	100	100	100	46	d__Bacter	p__Bacillo	c__Clostrid	o__Eubact	f__Aristae	g__Aristae	NA	Filter: bootstrap Score >= 50
ASV1216	100	100	100	100	99	83	83	d__Bacter	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	g__Anaero	s__Anaerotruncus_colihominis	
ASV1217	100	100	100	100	100	23	8	d__Bacter	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1218	100	100	100	100	100	98	98	d__Bacter	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Agatho	s__Agathobacter_rectalis	
ASV1219	100	89	84	36	12	11	11	d__Bacter	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1220	100	95	84	50	16	15	13	d__Bacter	p__Bacillo	c__Clostrid	o__Eubact	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1221	100	100	96	96	96	96	56	d__Bacter	p__Bacillo	c__Bacilli	o__Bacilla	f__Staphyl	g__Staphy	s__Staphylococcus_pasteuri	
ASV1222	100	100	100	100	100	100	94	d__Bacter	p__Therm	c__Desulfo	o__Desulfo	f__Desulfo	g__Desulfo	s__Desulfovibrio_porci	
ASV1223	100	100	100	100	95	58	58	d__Bacter	p__Bacter	c__Bacteroi	o__Bacter	f__Prevote	g__Marseil	s__Marseilla_massiliensis	
ASV1224	100	100	100	100	100	95	77	d__Bacter	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Roseb	s__Roseburia_intestinalis	
ASV1225	100	100	100	100	100	100	100	d__Archae	p__Methan	c__Methano	o__Methan	f__Methan	g__Methan	s__Methanobrevibacter_boviskoreani	
ASV1226	100	100	100	93	93	24	18	d__Bacter	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1227	100	100	100	92	91	30	30	d__Bacter	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1228	100	66	62	40	40	34	26	d__Bacter	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1229	100	100	100	97	97	61	61	d__Bacter	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Acetati	s__Acetatifactor_muris	
ASV1230	100	100	100	100	100	100	57	d__Bacter	p__Bacillo	c__Bacilli	o__Bacilla	f__Paenib	g__Brevib	s__Brevibacillus_brevis	
ASV1231	100	100	100	100	99	49	49	d__Bacter	p__Bacter	c__Bacteroi	o__Bacter	f__Muriba	NA	NA	Filter: bootstrap Score >= 50
ASV1232	100	100	100	100	100	83	33	d__Bacter	p__Bacillo	c__Clostrid	o__Peptos	f__Peptos	g__Terrisp	NA	Filter: bootstrap Score >= 50
ASV1233	100	67	9	9	9	9	9	d__Bacter	p__Bacillo	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1234	100	100	100	100	100	100	46	d__Bacter	p__Bacillo	c__Clostrid	o__Eubact	f__Clostrid	g__Clostri	NA	Filter: bootstrap Score >= 50
ASV1235	100	100	100	61	61	61	61	d__Bacter	p__Bacillo	c__Clostrid	o__Eubact	f__Eubacte	g__Eubacte	s__Eubacterium_xylanophilum	
ASV1236	100	100	100	82	82	32	19	d__Bacter	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1237	100	100	42	32	19	10	10	d__Bacter	p__Bacter	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1238	100	100	100	99	51	34	34	d__Bacter	p__Bacter	c__Bacteroi	o__Bacter	f__Prevote	NA	NA	Filter: bootstrap Score >= 50
ASV1239	100	100	100	100	97	75	59	d__Bacter	p__Bacter	c__Bacteroi	o__Bacter	f__Muriba	g__Duncan	s__Duncaniella_dubosii	
ASV1240	100	100	100	100	100	100	100	d__Bacter	p__Bacter	c__Bacteroi	o__Bacter	f__Bacteroi	g__Phoca	s__Phocaeicola_massiliensis	
ASV1241	100	100	100	100	100	100	31	d__Bacter	p__Bacillo	c__Bacilli	o__Lactob	f__Strepto	g__Strepto	NA	Filter: bootstrap Score >= 50
ASV1242	100	100	100	100	97	73	39	d__Bacter	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	g__Vescim	NA	Filter: bootstrap Score >= 50
ASV1243	100	100	100	100	100	100	57	d__Bacter	p__Bacillo	c__Negativi	o__Veillon	f__Veillone	g__Veillon	s__Veillonella_parvula	
ASV1244	100	100	100	100	100	29	27	d__Bacter	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1245	100	100	100	97	97	11	11	d__Bacter	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1246	100	100	100	100	100	96	96	d__Bacter	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	g__Ruther	s__Ruthenibacterium_lactatiformans	
ASV1247	100	100	100	100	98	34	34	d__Bacter	p__Bacillo	c__Bacilli	o__Bacilla	f__Bacillac	NA	NA	Filter: bootstrap Score >= 50
ASV1248	100	52	51	41	41	41	18	d__Bacter	p__Mycop	c__Mollicu	NA	NA	NA	NA	Filter: bootstrap Score >= 50

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ASV1249	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Bacilli	o__Bacillal	f__Bacillac	g__Bacillus	s__Bacillus_cereus		
ASV1250	100	100	100	100	100	42	33	d__Bacteri	p__Bacteroi	c__Bacteroi	o__Bacteroi	f__Prevotel	NA	NA	Filter: bootstrap Score >= 50	
ASV1251	100	100	100	100	100	100	80	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachnos	f__Anaerot	g__Anaerot	s__Anaerotignum_aminivorans		
ASV1252	100	100	100	100	100	72	72	d__Bacteri	p__Bacteroi	c__Bacteroi	o__Bacteroi	f__Muribac	g__Duncan	s__Duncaniella_muris		
ASV1253	100	64	52	20	20	9	9	d__Bacteri	p__Bacillot	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV1254	100	100	100	100	100	75	74	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachnos	f__Lachnos	g__Lachno	s__[Clostridium]_scindens		
ASV1255	100	95	95	95	95	40	40	d__Bacteri	p__Thermo	c__Desulfo	o__Desulfo	f__Desulfo	NA	NA	Filter: bootstrap Score >= 50	
ASV1256	100	100	98	98	97	27	27	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubacte	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50	
ASV1257	100	100	100	100	100	100	100	d__Bacteri	p__Bacteroi	c__Bacteroi	o__Bacteroi	f__Prevotel	g__Segatel	s__Segatella_copri		
ASV1258	100	100	100	100	98	66	66	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubacte	f__Oscillos	g__Lawsoni	s__Lawsonibacter_asaccharolyticus		
ASV1259	100	100	100	73	73	19	16	d__Bacteri	p__Actinob	c__Coriobac	o__Eggerth	f__Eggerth	NA	NA	Filter: bootstrap Score >= 50	
ASV1260	100	100	100	100	100	100	81	d__Bacteri	p__Pseudo	c__Gammap	o__Lysobac	f__Lysobac	g__Stenotr	s__Stenotrophomonas_maltophilia		
ASV1261	100	100	100	100	100	89	88	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubacte	f__Oscillos	g__Oscillib	s__Oscillibacter_valericigenes		
ASV1262	100	100	95	95	64	21	21	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubacte	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50	
ASV1263	100	100	100	100	100	100	40	d__Bacteri	p__Actinob	c__Actinob	o__Bifidob	f__Bifidob	g__Bifidob	NA	Filter: bootstrap Score >= 50	
ASV1264	100	100	100	100	100	64	64	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachnos	f__Lachnos	g__Stomat	s__Stomatobaculum_longum		
ASV1265	100	100	100	100	98	98	98	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubacte	f__	g__Gemmi	s__Gemmiger_formicilis		
ASV1266	100	100	100	100	100	30	29	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubacte	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50	
ASV1267	100	100	100	96	96	60	60	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachnos	f__Lachnos	g__Acetati	s__Acetatifactor_muris		
ASV1268	100	100	100	100	100	98	98	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubacte	f__	g__Flintiba	s__Flintibacter_butyricus		
ASV1269	100	100	100	100	100	46	46	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachnos	f__Lachnos	NA	NA	Filter: bootstrap Score >= 50	
ASV1270	100	100	100	100	98	19	18	d__Bacteri	p__Bacillot	c__Bacilli	o__Bacillal	f__Bacillac	NA	NA	Filter: bootstrap Score >= 50	
ASV1271	100	100	100	100	93	68	32	d__Bacteri	p__Bacteroi	c__Bacteroi	o__Bacteroi	f__Muribac	g__Duncan	NA	Filter: bootstrap Score >= 50	
ASV1272	100	100	97	80	77	77	60	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubacte	f__Aristae	g__Aristae	s__Aristaeella_hokkaidonensis		
ASV1273	100	100	100	100	100	78	77	d__Bacteri	p__Bacteroi	c__Bacteroi	o__Bacteroi	f__Prevotel	g__Hoylesi	s__Hoylesella_oralis		
ASV1274	100	46	46	46	46	46	46	d__Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV1275	100	100	100	100	100	64	63	d__Bacteri	p__Bacteroi	c__Bacteroi	o__Bacteroi	f__Muribac	g__Duncan	s__Duncaniella_muris		
ASV1276	100	81	62	62	61	53	53	d__Bacteri	p__Bacillot	c__Erysipe	o__Erysipe	f__Erysipe	g__Breznak	s__Breznakia_blatticola		
ASV1277	100	91	75	19	19	14	5	d__Bacteri	p__Bacillot	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV1278	100	92	80	43	13	13	10	d__Bacteri	p__Bacillot	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV1279	100	100	100	100	99	99	99	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubacte	f__	g__Flintiba	s__Flintibacter_butyricus		
ASV1280	100	100	100	100	87	70	36	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubacte	f__	g__Intestin	NA	Filter: bootstrap Score >= 50	
ASV1281	100	100	100	100	100	84	35	d__Bacteri	p__Bacillot	c__Clostrid	o__Peptost	f__Peptost	g__Terrisp	NA	Filter: bootstrap Score >= 50	
ASV1282	100	100	100	100	100	90	90	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachnos	f__Lachnos	g__Kineoth	s__Kineothrix_alysoides		
ASV1283	100	95	87	16	16	16	5	d__Bacteri	p__Bacillot	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV1284	100	100	100	99	99	32	32	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubacte	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50	
ASV1285	100	100	100	100	99	99	99	d__Bacteri	p__Bacteroi	c__Bacteroi	o__Bacteroi	f__Prevotel	g__Paraprv	s__Paraprevotella_clara		
ASV1286	100	77	63	63	63	14	14	d__Bacteri	p__Bacillot	c__Erysipe	o__Erysipe	f__Erysipe	NA	NA	Filter: bootstrap Score >= 50	
ASV1287	100	100	100	99	99	94	43	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachnos	f__Lachnos	g__Roseb	NA	Filter: bootstrap Score >= 50	
ASV1288	100	100	100	100	100	47	47	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachnos	f__Lachnos	NA	NA	Filter: bootstrap Score >= 50	
ASV1289	100	25	19	16	16	9	8	d__Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV1290	100	100	100	91	91	51	34	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachnos	f__Lachnos	g__Lacrim	NA	Filter: bootstrap Score >= 50	
ASV1291	100	100	99	99	98	81	77	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubacte	f__Oscillos	g__Anaero	s__Anaerotruncus_colihominis		
ASV1292	100	100	100	100	100	80	74	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachnos	f__Lachnos	g__Roseb	s__Roseburia_intestinalis		
ASV1293	100	100	100	100	80	40	30	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubacte	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50	
ASV1294	100	100	100	100	100	100	79	d__Bacteri	p__Bacillot	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	s__Lactobacillus_delbrueckii		
ASV1295	100	100	100	100	100	93	84	d__Bacteri	p__Bacillot	c__Clostrid	o__Peptost	f__Anaero	g__Lentiho	s__Lentihominibacter_faecis		
ASV1296	100	100	100	100	100	100	99	d__Bacteri	p__Bacillot	c__Bacilli	o__Lactob	f__Lactoba	g__Ligilact	s__Ligilactobacillus_ruminis		
ASV1297	100	100	100	100	100	100	100	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubacte	f__Butyrici	g__Butyric	s__Butyricicoccus_porcorum		
ASV1298	100	100	100	100	100	36	21	d__Bacteri	p__Bacteroi	c__Bacteroi	o__Bacteroi	f__Prevotel	NA	NA	Filter: bootstrap Score >= 50	

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ASV1299	100	99	97	97	97	62	33	d__Bacteri	p__Therm	c__Desulfo	o__Desulfo	f__Desulfo	g__Desulfo	NA		Filter: bootstrap Score >= 50
ASV1300	100	100	100	100	100	99	99	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Fusimo	s__Fusimonas_intestini		
ASV1301	100	100	100	99	99	90	58	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Oscillos	g__Rumino	s__Ruminococcus_flavefaciens		
ASV1302	100	100	100	31	14	14	14	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA		Filter: bootstrap Score >= 50
ASV1303	100	100	100	100	100	100	80	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Anaero	s__Anaerobutyricum_soehngenii		
ASV1304	100	100	100	100	100	100	91	d__Bacteri	p__Actinor	c__Actinor	o__Mycob	f__Coryne	g__Coryne	s__Corynebacterium_casei		
ASV1305	100	100	100	100	100	94	88	d__Bacteri	p__Pseudo	c__Gamma	o__Entero	f__Enterob	g__Escheri	s__Escherichia_fergusonii		
ASV1306	100	100	100	100	69	52	52	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Oscillos	g__Lawson	s__Lawsonibacter_asaccharolyticus		
ASV1307	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__	g__Flintiba	s__Flintibacter_butyricus		
ASV1308	100	100	100	100	100	100	61	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Oscillos	g__Vescim	s__Vescimonas_coprocola		
ASV1309	100	99	99	93	85	85	54	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Aristaee	g__Aristae	s__Aristaella_hokkaidonensis		
ASV1310	100	100	100	100	100	100	70	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	s__Lactobacillus_delbrueckii		
ASV1311	100	100	100	99	78	11	11	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Oscillos	NA	NA		Filter: bootstrap Score >= 50
ASV1312	100	100	100	100	55	45	45	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Oscillos	NA	NA		Filter: bootstrap Score >= 50
ASV1313	100	100	100	100	99	95	67	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteroi	f__Muriba	g__Dunca	s__Duncaniella_muris		
ASV1314	100	100	100	100	99	70	70	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteroi	f__Muriba	g__Param	s__Paramuribaculum_intestinale		
ASV1315	100	100	100	61	36	34	33	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	NA	NA	NA		Filter: bootstrap Score >= 50
ASV1316	100	97	97	91	90	19	19	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA		Filter: bootstrap Score >= 50
ASV1317	100	100	100	96	96	75	50	d__Bacteri	p__Actinor	c__Actinor	o__Pseudo	f__Pseudo	g__Sacchas	s__Saccharopolyspora_griseoalba		
ASV1318	100	100	100	100	95	53	52	d__Bacteri	p__Bacillo	c__Bacilli	o__Bacilla	f__Bacillac	g__Bacillus	s__Bacillus_caccae		
ASV1319	100	100	100	100	100	100	97	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteroi	f__Prevote	g__Segate	s__Segatella_copri		
ASV1320	100	100	100	99	99	42	22	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA		Filter: bootstrap Score >= 50
ASV1321	100	100	100	100	100	97	28	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Blautia	NA		Filter: bootstrap Score >= 50
ASV1322	100	100	91	38	32	11	11	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA		Filter: bootstrap Score >= 50
ASV1323	100	100	100	100	100	100	66	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteroi	f__Rikenel	g__Alistipe	s__Alistipes_shahii		
ASV1324	100	100	100	100	100	85	85	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Qiania	s__Qiania_dongpingensis		
ASV1325	100	100	100	100	100	83	66	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteroi	f__Prevote	g__Segate	s__Segatella_baroniae		
ASV1326	100	100	77	42	32	17	14	d__Bacteri	p__Bacteri	c__Bacteroi	NA	NA	NA	NA		Filter: bootstrap Score >= 50
ASV1327	100	100	100	100	100	30	18	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA		Filter: bootstrap Score >= 50
ASV1328	100	100	100	100	94	76	74	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__	g__Intestin	s__Intestinimonas_massiliensis		
ASV1329	100	21	16	9	8	7	7	d__Bacteri	NA	NA	NA	NA	NA	NA		Filter: bootstrap Score >= 50
ASV1330	100	100	57	57	31	24	17	d__Bacteri	p__Bacteri	c__Flavobi	o__Flavob	NA	NA	NA		Filter: bootstrap Score >= 50
ASV1331	100	80	33	33	33	21	18	d__Bacteri	p__Bacillo	NA	NA	NA	NA	NA		Filter: bootstrap Score >= 50
ASV1332	100	100	100	100	100	100	99	d__Bacteri	p__Actinor	c__Actinor	o__Bifidob	f__Bifidoba	g__Bifidob	s__Bifidobacterium_animalis		
ASV1333	100	47	22	22	22	7	4	d__Bacteri	NA	NA	NA	NA	NA	NA		Filter: bootstrap Score >= 50
ASV1334	100	100	100	92	92	23	16	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA		Filter: bootstrap Score >= 50
ASV1335	100	73	58	58	56	7	7	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	f__Erysipe	NA	NA		Filter: bootstrap Score >= 50
ASV1336	100	100	100	100	98	35	33	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteroi	f__Muriba	NA	NA		Filter: bootstrap Score >= 50
ASV1337	100	100	100	98	88	71	53	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Oscillos	g__Vescim	s__Vescimonas_fastidiosa		
ASV1338	100	100	100	100	100	47	45	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteroi	f__Prevote	NA	NA		Filter: bootstrap Score >= 50
ASV1339	100	100	100	100	100	46	34	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteroi	f__Prevote	NA	NA		Filter: bootstrap Score >= 50
ASV1340	100	100	100	100	100	61	61	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Acetati	s__Acetatifactor_muris		
ASV1341	100	100	100	100	99	46	46	d__Bacteri	p__Pseudo	c__Gamma	o__Entero	f__Enterob	NA	NA		Filter: bootstrap Score >= 50
ASV1342	100	100	89	89	89	87	33	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	NA		Filter: bootstrap Score >= 50
ASV1343	100	100	100	100	100	99	99	d__Bacteri	p__Bacillo	c__Clostrid	o__Christe	f__Christe	g__Guopin	s__Guopingia_tenuis		
ASV1344	100	100	100	99	99	50	50	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Hominis	s__Hominisplanchenecus_faecis		
ASV1345	100	100	97	95	95	79	79	d__Bacteri	p__Bacillo	c__Clostrid	o__Christe	f__Christe	g__Gehon	s__Gehongia_tenuis		
ASV1346	100	100	100	100	100	54	54	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Medite	s__Mediterraneibacter_gnavus		
ASV1347	100	100	100	100	90	81	81	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Oscillos	g__Lawson	s__Lawsonibacter_asaccharolyticus		
ASV1348	100	100	100	100	98	69	33	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteroi	f__Prevote	g__Segate	NA		Filter: bootstrap Score >= 50

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ASV1349	100	100	100	100	100	71	71	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachnos	g__Kineoth	s__Kineothrix_alysoides		
ASV1350	100	100	100	99	99	20	19	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachnos	NA	NA	Filter: bootstrap Score >= 50	
ASV1351	100	100	99	94	86	86	72	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Aristaee	g__Aristae	s__Aristaeella_lactis		
ASV1352	100	100	100	100	100	82	57	d__Bacteri	p__Thermo	c__Desulfo	o__Desulfo	f__Desulfo	g__Nitratid	s__Nitratidesulfovibrio_oxamicus		
ASV1353	100	93	83	30	14	12	11	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV1354	100	100	100	100	100	68	65	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	f__Erysipe	g__Amedib	s__Amedibacillus_hominis		
ASV1355	100	81	68	40	27	9	9	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV1356	100	99	99	90	90	12	12	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachnos	NA	NA	Filter: bootstrap Score >= 50	
ASV1357	100	100	100	100	69	22	22	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50	
ASV1358	100	100	100	100	99	96	76	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Oscillos	g__Rumino	s__Ruminococcus_albus		
ASV1359	100	100	100	100	100	100	100	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteroi	f__Prevotel	g__Segatel	s__Segatella_copri		
ASV1360	100	100	100	100	100	29	29	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteroi	f__Muribac	NA	NA	Filter: bootstrap Score >= 50	
ASV1361	100	100	97	93	51	36	36	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50	
ASV1362	100	100	100	100	99	82	82	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteroi	f__Muribac	g__Paramu	s__Paramuribaculum_intestinale		
ASV1363	100	100	100	100	100	44	44	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50	
ASV1364	100	100	100	93	93	43	43	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachnos	NA	NA	Filter: bootstrap Score >= 50	
ASV1365	100	100	100	100	95	38	33	d__Bacteri	p__Bacillo	c__Bacilli	o__Bacillal	f__Bacillac	NA	NA	Filter: bootstrap Score >= 50	
ASV1366	100	100	100	100	100	100	87	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachnos	g__Blautia	s__Blautia_luti		
ASV1367	100	100	99	99	99	21	21	d__Bacteri	p__Bacillo	c__Clostrid	o__Peptost	f__Anaerov	NA	NA	Filter: bootstrap Score >= 50	
ASV1368	100	100	100	100	100	100	46	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachnos	g__Anaerov	NA	Filter: bootstrap Score >= 50	
ASV1369	100	100	98	98	72	25	25	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50	
ASV1370	100	100	100	96	96	36	36	d__Bacteri	p__Actinor	c__Coriobac	o__Eggerth	f__Eggerth	NA	NA	Filter: bootstrap Score >= 50	
ASV1371	100	100	100	100	100	60	60	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachnos	g__Fusimo	s__Fusimonas_intestini		
ASV1372	100	100	100	100	100	100	98	d__Bacteri	p__Pseudo	c__Gammap	o__Enterob	f__Enterob	g__Klebsie	s__Klebsiella_pneumoniae		
ASV1373	100	100	76	70	69	3	3	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachnos	NA	NA	Filter: bootstrap Score >= 50	
ASV1374	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__	g__Flintiba	s__Flintibacter_butyricus		
ASV1375	100	100	100	91	91	37	37	d__Bacteri	p__Actinor	c__Coriobac	o__Eggerth	f__Eggerth	NA	NA	Filter: bootstrap Score >= 50	
ASV1376	100	95	86	80	75	75	37	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Aristaee	g__Aristae	NA	Filter: bootstrap Score >= 50	
ASV1377	100	100	100	100	100	100	53	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachnos	g__Blautia	s__Blautia_glucerasea		
ASV1378	100	100	100	100	99	98	57	d__Bacteri	p__Spiroch	c__Spirochi	o__Spirochi	f__Treponer	g__Treponi	s__Treponema_bryantii		
ASV1379	100	97	94	79	77	77	53	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Aristaee	g__Aristae	s__Aristaeella_lactis		
ASV1380	100	100	100	100	76	31	31	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50	
ASV1381	100	100	100	100	100	100	100	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteroi	f__Prevotel	g__Segatel	s__Segatella_copri		
ASV1382	100	100	100	100	100	100	95	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactoba	f__Strepto	g__Strepto	s__Streptococcus_danieliae		
ASV1383	100	100	100	100	100	100	49	d__Bacteri	p__Campy	c__Epsilon	o__Campy	f__Helicob	g__Helicob	NA	Filter: bootstrap Score >= 50	
ASV1384	100	100	100	100	99	60	60	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteroi	f__Muribac	g__Sangeri	s__Sangeribacter_muris		
ASV1385	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__	g__Flintiba	s__Flintibacter_butyricus		
ASV1386	100	100	100	99	99	84	63	d__Bacteri	p__Actinor	c__Coriobac	o__Eggerth	f__Eggerth	g__Raoultil	s__Raoultibacter_timonensis		
ASV1387	100	100	99	99	99	96	96	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Oscillos	g__	s__[Eubacterium]_siraeum		
ASV1388	100	100	100	100	100	87	87	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachnos	g__Kineoth	s__Kineothrix_alysoides		
ASV1389	100	100	100	93	93	11	11	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachnos	NA	NA	Filter: bootstrap Score >= 50	
ASV1390	100	100	100	100	84	31	9	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactoba	f__Enteroc	NA	NA	Filter: bootstrap Score >= 50	
ASV1391	100	100	78	77	55	33	33	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Peptoc	NA	NA	Filter: bootstrap Score >= 50	
ASV1392	100	100	100	100	100	41	25	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteroi	f__Prevotel	NA	NA	Filter: bootstrap Score >= 50	
ASV1393	100	96	96	96	96	96	96	d__Bacteri	p__Thermo	c__Desulfo	o__Desulfo	f__Desulfo	g__Lawsoni	s__Lawsonia_intracellularis		
ASV1394	100	99	99	74	74	30	30	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachnos	NA	NA	Filter: bootstrap Score >= 50	
ASV1395	100	97	86	70	46	46	46	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV1396	100	100	100	100	76	41	41	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__	NA	NA	Filter: bootstrap Score >= 50	
ASV1397	100	100	100	95	95	75	64	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachnos	g__Oribact	s__Oribacterium_sinus		
ASV1398	100	100	99	96	96	71	71	d__Bacteri	p__Bacillo	c__Clostrid	o__Christe	f__Christe	g__Guopin	s__Guopingia_tenuis		

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ASV1399	100	100	100	32	32	32	32	d_Bacter	p_Actinor	c_Coriob	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1400	100	92	92	41	19	18	16	d_Bacter	p_Bacillo	c_Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1401	100	100	100	100	100	97	97	d_Bacter	p_Bacillo	c_Clostrid	o_Eubact	f_Oscillos	g_Ruther	s_Ruthenibacterium_lactatiformans	
ASV1402	100	100	100	100	100	40	40	d_Bacter	p_Bacillo	c_Clostrid	o_Eubact	f_Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV1403	100	100	100	100	100	86	64	d_Bacter	p_Bacter	c_Bacter	o_Bacter	f_Muriba	g_Dunca	s_Duncaniella_muris	
ASV1404	100	100	87	87	87	85	25	d_Bacter	p_Bacillo	c_Bacilli	o_Lactob	f_Lactoba	g_Lactob	NA	Filter: bootstrap Score >= 50
ASV1405	100	100	100	100	100	100	100	d_Bacter	p_Elusim	c_Elusim	o_Elusim	f_Elusimi	g_Elusim	s_Elusimicrobium_minutum	
ASV1406	100	100	100	98	98	38	38	d_Bacter	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1407	100	100	100	100	100	99	30	d_Bacter	p_Pseudo	c_Alphap	o_Rhodo	f_Paraco	g_Paraco	NA	Filter: bootstrap Score >= 50
ASV1408	100	100	100	100	100	100	100	d_Bacter	p_Bacillo	c_Erysipe	o_Erysipe	f_Erysipe	g_Dubos	s_Dubosiella_newyorkensis	
ASV1409	100	100	100	100	100	56	56	d_Bacter	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	g_Medite	s_Mediterraneibacter_gnavus	
ASV1410	100	100	100	100	100	88	88	d_Bacter	p_Bacillo	c_Clostrid	o_Eubact	f_Oscillos	g_Paludi	s_Paludihabitans_psychrotolerans	
ASV1411	100	100	100	94	94	62	42	d_Bacter	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	g_Lacrim	NA	Filter: bootstrap Score >= 50
ASV1412	100	100	60	29	18	16	15	d_Bacter	p_Bacter	c_Bacter	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1413	100	98	93	76	66	39	39	d_Bacter	p_Bacillo	c_Clostrid	o_Eubact	f_Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV1414	100	67	40	40	40	17	9	d_Bacter	p_Bacillo	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1415	100	94	77	23	16	15	15	d_Bacter	p_Bacillo	c_Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1416	100	100	100	100	100	100	100	d_Bacter	p_Pseudo	c_Gamm	o_Aerom	f_Succini	g_Succin	s_Succinivibrio_dextrinosolvens	
ASV1417	100	99	95	76	76	26	26	d_Bacter	p_Bacillo	c_Clostrid	o_Christe	f_Christe	NA	NA	Filter: bootstrap Score >= 50
ASV1418	100	100	100	100	100	100	94	d_Bacter	p_Bacillo	c_Bacilli	o_Lactob	f_Enteroc	g_Entero	s_Enterococcus_faecalis	
ASV1419	100	100	74	74	74	74	18	d_Bacter	p_Bacillo	c_Bacilli	o_Lactob	f_Lactoba	g_Limosi	NA	Filter: bootstrap Score >= 50
ASV1420	100	47	47	47	47	47	47	d_Bacter	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1421	100	100	74	68	68	24	20	d_Bacter	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1422	100	100	100	100	100	47	12	d_Bacter	p_Bacter	c_Bacter	o_Bacter	f_Prevote	NA	NA	Filter: bootstrap Score >= 50
ASV1423	100	100	63	45	28	7	7	d_Bacter	p_Bacter	c_Bacter	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1424	100	100	70	47	26	14	13	d_Bacter	p_Bacter	c_Bacter	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1425	100	100	100	100	100	100	98	d_Bacter	p_Bacter	c_Bacter	o_Bacter	f_Prevote	g_Segate	s_Segatella_hominis	
ASV1426	100	100	100	100	100	100	98	d_Bacter	p_Bacillo	c_Negativ	o_Seleno	f_Seleno	g_Seleno	s_Selenomonas_bovis	
ASV1427	100	100	100	100	100	99	61	d_Bacter	p_Bacillo	c_Clostrid	o_Peptos	f_Anaero	g_Lentiho	s_Lentihominibacter_faecis	
ASV1428	100	98	80	42	25	13	13	d_Bacter	p_Bacillo	c_Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1429	100	100	100	100	100	100	94	d_Bacter	p_Actinor	c_Actinor	o_Mycob	f_Coryne	g_Coryne	s_Corynebacterium_glutamicum	
ASV1430	100	99	99	99	99	99	99	d_Bacter	p_Bacter	c_Bacter	o_Bacter	f_Muriba	g_Dunca	s_Duncaniella_muris	
ASV1431	100	100	100	100	57	47	47	d_Bacter	p_Bacillo	c_Clostrid	o_Eubact	f_Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV1432	100	96	86	33	16	12	7	d_Bacter	p_Bacillo	c_Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1433	100	100	100	89	89	33	32	d_Bacter	p_Actinor	c_Coriob	o_Eggerth	f_Eggerth	NA	NA	Filter: bootstrap Score >= 50
ASV1434	100	100	100	100	100	99	60	d_Bacter	p_Bacillo	c_Erysipe	o_Erysipe	f_Coprob	g_Faecal	s_Faecalibacillus_intestinalis	
ASV1435	100	100	100	100	100	83	83	d_Bacter	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	g_Dorea	s_Dorea_longicatena	
ASV1436	100	98	93	57	41	35	31	d_Bacter	p_Bacillo	c_Clostrid	o_Eubact	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1437	100	97	91	55	55	39	39	d_Bacter	p_Bacillo	c_Clostrid	o_Christe	f_Christe	NA	NA	Filter: bootstrap Score >= 50
ASV1438	100	97	86	61	23	22	19	d_Bacter	p_Bacillo	c_Clostrid	o_Eubact	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1439	100	100	100	100	100	100	85	d_Bacter	p_Bacillo	c_Bacilli	o_Lactob	f_Strepto	g_Strepto	s_Streptococcus_ovis	
ASV1440	100	100	100	100	100	100	86	d_Bacter	p_Bacter	c_Bacter	o_Bacter	f_Prevote	g_Segate	s_Segatella_copri	
ASV1441	100	100	85	85	85	84	25	d_Bacter	p_Bacillo	c_Bacilli	o_Lactob	f_Lactoba	g_Lactob	NA	Filter: bootstrap Score >= 50
ASV1442	100	100	100	100	100	100	100	d_Bacter	p_Bacillo	c_Clostrid	o_Eubact	f	g_Flintiba	s_Flintibacter_butyricus	
ASV1443	100	100	100	98	98	27	25	d_Bacter	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1444	100	100	99	99	99	86	54	d_Bacter	p_Bacillo	c_Erysipe	o_Erysipe	f_Erysipe	g_Amedi	s_Amedibacillus_hominis	
ASV1445	100	100	59	44	19	14	14	d_Bacter	p_Bacter	c_Bacter	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1446	100	99	98	92	86	86	61	d_Bacter	p_Bacillo	c_Clostrid	o_Eubact	f_Aristae	g_Aristae	s_Aristaeella_hokkaidonensis	
ASV1447	100	100	99	95	89	55	35	d_Bacter	p_Bacillo	c_Clostrid	o_Eubact	f_Oscillos	g_Vescim	NA	Filter: bootstrap Score >= 50
ASV1448	100	100	100	100	100	100	57	d_Bacter	p_Pseudo	c_Gamm	o_Moraxe	f_Moraxe	g_Acineto	s_Acinetobacter_johnsonii	

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ASV1449	100	100	100	100	74	74	61	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__	g__Intestin	s__Intestinimonas_butyriciproducens		
ASV1450	100	100	99	99	99	52	52	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Oscillos	g__Angelak	s__Angelakisella_massiliensis		
ASV1451	100	100	100	100	100	100	99	d__Bacteri	p__Bacillo	c__Negativi	o__Selenor	f__Selenor	g__Selenor	s__Selenomonas_bovis		
ASV1452	100	100	100	100	100	100	78	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachno	g__Blautia	s__Blautia_luti		
ASV1453	100	100	100	97	76	28	17	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50	
ASV1454	100	100	100	100	100	55	55	d__Bacteri	p__Bacillo	c__Negativi	o__Selenor	f__Selenor	g__Mitsuok	s__Mitsuokella_jalaludinii		
ASV1455	100	100	100	98	98	29	16	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachno	NA	NA	Filter: bootstrap Score >= 50	
ASV1456	100	98	98	82	82	30	30	d__Bacteri	p__Actinor	c__Coriobac	o__Eggerth	f__Eggerth	NA	NA	Filter: bootstrap Score >= 50	
ASV1457	100	100	100	100	98	57	57	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Oscillos	g__Allofou	s__Allofournierella_massiliensis		
ASV1458	100	100	100	97	95	95	79	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Aristaee	g__Aristaee	s__Aristaeella_hokkaidonensis		
ASV1459	100	100	100	100	91	37	37	d__Bacteri	p__Bacter	c__Bacteroi	o__Bacteroi	f__Prevote	NA	NA	Filter: bootstrap Score >= 50	
ASV1460	100	100	100	100	91	32	32	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50	
ASV1461	100	99	91	61	26	25	18	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV1462	100	91	58	15	15	3	3	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV1463	100	98	98	94	92	25	25	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachno	NA	NA	Filter: bootstrap Score >= 50	
ASV1464	100	100	96	96	96	24	24	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50	
ASV1465	100	100	100	100	100	100	100	d__Bacteri	p__Actinor	c__Coriobac	o__Eggerth	f__Eggerth	g__Ellagibi	s__Ellagibacter_isourolithinifaciens		
ASV1466	100	100	100	100	96	59	26	d__Bacteri	p__Bacter	c__Bacteroi	o__Bacteroi	f__Muriba	g__Muriba	NA	Filter: bootstrap Score >= 50	
ASV1467	100	100	100	100	100	64	62	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachno	g__Roseb	s__Roseburia_intestinalis		
ASV1468	100	100	100	97	27	15	15	d__Bacteri	p__Bacter	c__Bacteroi	o__Bacteroi	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV1469	100	100	100	100	100	86	86	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Oscillos	g__Rumino	s__Ruminococcus_bromii		
ASV1470	100	99	95	76	62	11	8	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachno	NA	NA	Filter: bootstrap Score >= 50	
ASV1471	100	100	100	100	100	66	52	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Oscillos	g__Oscillib	s__Oscillibacter_valericigenes		
ASV1472	100	93	88	43	16	15	15	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV1473	100	100	100	100	100	100	100	d__Bacteri	p__Bacter	c__Bacteroi	o__Bacteroi	f__Rikenel	g__Alistipe	s__Alistipes_okayasuensis		
ASV1474	100	100	100	94	94	52	51	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachno	g__Diplocl	s__Diplocloster_agilis		
ASV1475	100	99	90	72	53	51	51	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Peptoc	g__Dehalo	s__Dehalobacterium_formicoaceticum		
ASV1476	100	100	100	99	99	37	36	d__Bacteri	p__Actinor	c__Coriobac	o__Eggerth	f__Eggerth	NA	NA	Filter: bootstrap Score >= 50	
ASV1477	100	100	100	100	100	23	16	d__Bacteri	p__Bacter	c__Bacteroi	o__Bacteroi	f__Prevote	NA	NA	Filter: bootstrap Score >= 50	
ASV1478	100	86	85	41	7	7	6	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV1479	100	100	100	100	100	100	99	d__Bacteri	p__Bacillo	c__Clostrid	o__Peptost	f__Peptost	g__Paracl	s__Paraclostridium_bifermentans		
ASV1480	100	100	100	99	99	47	47	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachno	NA	NA	Filter: bootstrap Score >= 50	
ASV1481	100	77	58	20	20	16	16	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV1482	100	100	100	85	85	21	21	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachno	NA	NA	Filter: bootstrap Score >= 50	
ASV1483	100	99	99	98	98	28	28	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachno	NA	NA	Filter: bootstrap Score >= 50	
ASV1484	100	78	34	34	34	30	22	d__Bacteri	p__Bacillo	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV1485	100	100	100	35	24	24	24	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV1486	100	96	73	12	6	6	6	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV1487	100	100	100	11	9	9	8	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV1488	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Negativi	o__Selenor	f__Selenor	g__Selenor	s__Selenomonas_bovis		
ASV1489	100	100	100	69	58	58	53	d__Bacteri	p__Actinor	c__Actinom	o__Micrococ	f__Bogorie	g__Georgei	s__Georgenia_deserti		
ASV1490	100	84	80	17	17	13	10	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV1491	100	100	100	99	99	29	9	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachno	NA	NA	Filter: bootstrap Score >= 50	
ASV1492	100	100	100	98	98	81	81	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachno	g__Kineoth	s__Kineothrix_alysoides		
ASV1493	100	100	100	100	100	59	59	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Oscillos	g__Angelak	s__Angelakisella_massiliensis		
ASV1494	100	100	100	93	93	35	35	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachno	NA	NA	Filter: bootstrap Score >= 50	
ASV1495	100	100	92	92	92	87	30	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Ligilact	NA	Filter: bootstrap Score >= 50	
ASV1496	100	100	100	100	96	55	55	d__Bacteri	p__Bacter	c__Bacteroi	o__Bacteroi	f__Muriba	g__Param	s__Paramuribaculum_intestinale		
ASV1497	100	100	100	100	91	91	75	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Acutalib	g__Acutalib	s__Acutalibacter_caecimuris		
ASV1498	100	100	100	100	100	40	40	d__Bacteri	p__Bacillo	c__Clostrid	o__Peptost	f__Anaerov	NA	NA	Filter: bootstrap Score >= 50	

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ASV1499	100	100	100	100	98	25	25	d__Bacteri	p__Bacter	c__Bacteroi	o__Bacteri	f__Muribac	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1500	100	97	97	76	47	11	3	d__Bacteri	p__Planct	c__Planctc	o__Pirellul	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1501	100	100	100	91	74	56	37	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Oscillos	g__Vescim	NA	NA	Filter: bootstrap Score >= 50
ASV1502	100	100	99	98	16	11	11	d__Bacteri	p__Bacter	c__Bacteroi	o__Bacteri	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1503	100	100	100	100	100	100	100	d__Bacteri	p__Bacter	c__Bacteroi	o__Bacteri	f__Prevote	g__Segate	s__Segatella_copri		
ASV1504	100	100	96	90	89	89	77	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Aristaeu	g__Aristae	s__Aristaeella_hokkaidonensis		
ASV1505	100	100	100	100	100	60	60	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachno	g__Chordi	s__Chordicoccus_furentiruminis		
ASV1506	100	100	100	24	24	24	24	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1507	100	100	100	100	60	60	60	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__	g__Flintiba	s__Flintibacter_butyricus		
ASV1508	100	98	98	98	98	68	44	d__Bacteri	p__Thermi	c__Desulfo	o__Desulfo	f__Desulfo	g__Desulfo	NA	NA	Filter: bootstrap Score >= 50
ASV1509	100	99	51	51	51	48	17	d__Bacteri	p__Bacter	c__Sphingo	o__Sphingo	f__Sphingo	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1510	100	100	46	41	24	13	5	d__Bacteri	p__Bacter	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1511	100	63	20	20	20	8	4	d__Bacteri	p__Bacillo	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1512	100	88	87	67	35	27	27	d__Bacteri	p__Pseudo	c__Alphap	o__Rhodo	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1513	100	100	100	98	98	79	79	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachno	g__Acetati	s__Acetatifactor_muris		
ASV1514	100	100	100	96	96	13	13	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachno	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1515	100	100	100	100	100	49	29	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachno	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1516	100	100	100	100	100	100	81	d__Bacteri	p__Bacter	c__Bacteroi	o__Bacteri	f__Prevote	g__Segate	s__Segatella_copri		
ASV1517	100	100	100	98	56	54	54	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Acutalib	g__Caproi	s__Caproicibacter_fermentans		
ASV1518	100	100	100	96	84	49	35	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Oscillos	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1519	100	100	100	100	100	100	87	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachno	g__Blautia	s__Blautia_luti		
ASV1520	100	100	100	100	99	44	7	d__Bacteri	p__Bacter	c__Bacteroi	o__Bacteri	f__Prevote	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1521	100	100	100	99	72	51	34	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Oscillos	g__Vescim	NA	NA	Filter: bootstrap Score >= 50
ASV1522	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Bacilli	o__Bacillal	f__Caryop	g__Kurthia	s__Kurthia_gibsonii		
ASV1523	100	100	100	88	81	77	77	d__Bacteri	p__Pseudo	c__Alphap	o__Rhodo	f__Rhodos	g__Defluvi	s__Defluviicoccus_vanus		
ASV1524	100	100	100	99	99	71	24	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachno	g__Blautia	NA	NA	Filter: bootstrap Score >= 50
ASV1525	100	100	100	99	92	68	62	d__Bacteri	p__Bacter	c__Bacteroi	o__Bacteri	f__Odoriba	g__Odorib	s__Odoribacter_splanchnicus		
ASV1526	100	100	100	100	96	83	83	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Oscillos	g__Fumia	s__Fumia_xinanensis		
ASV1527	100	100	100	65	65	17	17	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachno	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1528	100	100	100	100	89	89	89	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Oscillos	g__Dysosm	s__Dysosmobacter_acutus		
ASV1529	100	100	59	59	58	45	43	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	f__Erysipe	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1530	100	100	100	100	100	98	54	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Ligilact	s__Ligilactobacillus_apodemi		
ASV1531	100	89	84	36	36	32	17	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1532	100	100	100	100	100	79	78	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Oscillos	g__Oscillib	s__Oscillibacter_valericigenes		
ASV1533	100	100	100	100	100	100	100	d__Bacteri	p__Actinor	c__Coriobac	o__Coriobac	f__Atopobi	g__Paratra	s__Paratractidigestivibacter_faecalis		
ASV1534	100	100	100	100	76	45	25	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Oscillos	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1535	100	100	100	100	100	70	36	d__Bacteri	p__Bacter	c__Bacteroi	o__Bacteri	f__Prevote	g__Segate	NA	NA	Filter: bootstrap Score >= 50
ASV1536	100	100	27	27	27	13	10	d__Bacteri	p__Bacter	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1537	100	100	100	97	51	51	51	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Yeguia	g__Yeguia	s__Yeguia_hominis		
ASV1538	100	48	48	48	48	48	48	d__Bacteri	NA	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1539	100	100	100	100	100	73	28	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	f__Erysipe	g__Erysipe	NA	NA	Filter: bootstrap Score >= 50
ASV1540	100	100	100	100	100	100	100	d__Bacteri	p__Bacter	c__Bacteroi	o__Bacteri	f__Bacteroi	g__Bacteroi	s__Bacteroides_caecigallinarum		
ASV1541	100	100	100	25	22	21	8	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1542	100	100	100	97	97	25	25	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachno	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1543	100	100	100	94	94	44	44	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachno	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1544	100	100	100	97	97	41	41	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachno	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1545	100	100	99	99	99	94	94	d__Bacteri	p__Bacter	c__Bacteroi	o__Bacteri	f__Prevote	g__Prevot	s__Prevotellamassilia_timonensis		
ASV1546	100	100	100	99	99	41	41	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachno	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1547	100	75	13	13	13	6	5	d__Bacteri	p__Bacillo	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1548	100	100	100	100	100	71	68	d__Bacteri	p__Bacillo	c__Negativi	o__Selenc	f__Seleno	g__Mitsuo	s__Mitsuokella_jalaludinii		

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ASV1549	100	100	100	86	86	31	31	d__Bacter	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1550	100	100	100	100	81	28	28	d__Bacter	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV1551	100	100	100	100	100	76	76	d__Bacter	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	g__Kineoth	s__Kineothrix_alysoides	
ASV1552	100	100	100	100	100	100	100	d__Bacter	p__Pseudc	c__Gamm	o__Pseudc	f__Pseudc	g__Pseudc	s__Pseudomonas_putida	
ASV1553	100	100	100	100	100	63	63	d__Bacter	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	g__Lawsor	s__Lawsonibacter_asaccharolyticus	
ASV1554	100	100	100	100	100	100	63	d__Bacter	p__Bacillo	c__Bacilli	o__Bacillal	f__Paenib	g__Paenib	s__Paenibacillus_peoriae	
ASV1555	100	100	100	100	100	100	88	d__Bacter	p__Bacillo	c__Clostrid	o__Lachnc	f__Anaero	g__Anaero	s__Anaerotignum_aminivorans	
ASV1556	100	76	69	30	24	24	24	d__Bacter	p__Pseudc	c__Alphap	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1557	100	100	100	97	97	39	39	d__Bacter	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1558	100	100	100	46	36	35	35	d__Bacter	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1559	100	94	75	46	14	14	9	d__Bacter	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1560	100	100	100	97	97	65	4	d__Bacter	p__Actinor	c__Actinor	o__Pseudc	f__Pseudc	g__Saccha	NA	Filter: bootstrap Score >= 50
ASV1561	100	100	100	100	100	100	100	d__Bacter	p__Bacter	c__Bacter	o__Bacter	f__Muriba	g__Param	s__Paramuribaculum_intestinale	
ASV1562	100	100	100	100	76	76	76	d__Bacter	p__Bacillo	c__Clostrid	o__Eubact	f__	g__Gemm	s__Gemmiger_formicilis	
ASV1563	100	63	22	19	13	13	13	d__Bacter	p__Bacillo	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1564	100	100	100	100	83	57	47	d__Bacter	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	g__Anaero	NA	Filter: bootstrap Score >= 50
ASV1565	100	99	99	94	92	57	57	d__Bacter	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	g__Ructiba	s__Ructibacterium_gallinarum	
ASV1566	100	100	100	100	66	33	33	d__Bacter	p__Bacillo	c__Clostrid	o__Eubact	f__Acutalit	NA	NA	Filter: bootstrap Score >= 50
ASV1567	100	100	100	98	95	80	80	d__Bacter	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	g__	s__[Eubacterium]_siraeum	
ASV1568	100	100	100	99	99	74	74	d__Bacter	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	g__Kineoth	s__Kineothrix_alysoides	
ASV1569	100	100	100	97	97	20	20	d__Bacter	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1570	100	100	100	96	53	53	27	d__Bacter	p__Bacter	c__Bacter	o__Bacter	f__Tanner	g__Paraba	NA	Filter: bootstrap Score >= 50
ASV1571	100	100	46	36	23	20	20	d__Bacter	p__Bacter	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1572	100	100	100	100	100	45	22	d__Bacter	p__Bacter	c__Bacter	o__Bacter	f__Prevote	NA	NA	Filter: bootstrap Score >= 50
ASV1573	100	98	98	46	46	46	46	d__Bacter	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1574	100	100	100	100	99	83	83	d__Bacter	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	g__	s__[Eubacterium]_siraeum	
ASV1575	100	98	98	84	39	5	0	d__Bacter	p__Planct	c__Planct	o__Pirellul	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1576	100	100	100	100	100	72	52	d__Bacter	p__Bacter	c__Bacter	o__Bacter	f__Prevote	g__Segate	s__Segatella_copri	
ASV1577	100	100	61	43	32	9	9	d__Bacter	p__Bacter	c__Bacter	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1578	100	85	64	64	64	63	58	d__Bacter	p__Bacillo	c__Erysipe	o__Erysipe	f__Erysipe	g__Breznal	s__Breznakia_pachnodae	
ASV1579	100	89	80	33	24	10	10	d__Bacter	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1580	100	100	99	99	96	63	63	d__Bacter	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	g__	s__[Clostridium]_methylpentosum	
ASV1581	100	95	95	95	95	94	38	d__Bacter	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Ligilact	NA	Filter: bootstrap Score >= 50
ASV1582	100	100	100	100	93	89	89	d__Bacter	p__Bacter	c__Bacter	o__Bacter	f__Muriba	g__Param	s__Paramuribaculum_intestinale	
ASV1583	100	100	100	91	91	91	91	d__Bacter	p__Bacillo	c__Clostrid	o__Monoc	f__Monogl	g__Monog	s__Monoglobus_pectinilyticus	
ASV1584	100	100	100	100	96	96	96	d__Bacter	p__Bacillo	c__Clostrid	o__Eubact	f__	g__Colidex	s__Colidextribacter_massiliensis	
ASV1585	100	56	56	56	51	49	43	d__Bacter	p__Bacter	c__Bacter	o__Bacter	f__Muriba	NA	NA	Filter: bootstrap Score >= 50
ASV1586	100	100	100	100	100	100	100	d__Bacter	p__Bacillo	c__Negativ	o__Acidam	f__Acidam	g__Phasc	s__Phascolarctobacterium_succinatutens	
ASV1587	100	100	99	99	99	99	74	d__Bacter	p__Bacillo	c__Erysipe	o__Erysipe	f__Turicib	g__Turicib	s__Turicibacter_bilis	
ASV1588	100	100	100	100	100	96	82	d__Bacter	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	g__Roseb	s__Roseburia_intestinalis	
ASV1589	100	100	99	36	36	36	36	d__Bacter	p__Actinor	c__Coriob	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1590	100	13	13	13	13	13	13	d__Bacter	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1591	100	100	100	100	100	94	88	d__Bacter	p__Bacter	c__Bacter	o__Bacter	f__Odorib	g__Odorib	s__Odoribacter_splanchnicus	
ASV1592	100	100	100	100	100	100	68	d__Bacter	p__Bacter	c__Bacter	o__Bacter	f__Rikene	g__Alistipe	s__Alistipes_shahii	
ASV1593	100	74	57	57	52	20	15	d__Bacter	p__Bacillo	c__Erysipe	o__Erysipe	f__Erysipe	NA	NA	Filter: bootstrap Score >= 50
ASV1594	100	100	100	95	95	42	41	d__Bacter	p__Bacillo	c__Clostrid	o__Lachnc	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1595	100	100	100	100	100	69	69	d__Bacter	p__Bacillo	c__Clostrid	o__Eubact	f__Butyrici	g__Intestin	s__Intestinibacillus_massiliensis	
ASV1596	100	72	69	34	21	13	13	d__Bacter	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1597	100	99	96	89	88	88	60	d__Bacter	p__Bacillo	c__Clostrid	o__Eubact	f__Aristae	g__Aristae	s__Aristaeella_hokkaidonensis	
ASV1598	100	100	100	100	100	81	43	d__Bacter	p__Bacillo	c__Negativ	o__Seleno	f__Seleno	g__Seleno	NA	Filter: bootstrap Score >= 50

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ASV1599	100	100	100	99	84	50	32	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	g__Vescim	NA	Filter: bootstrap Score >= 50
ASV1600	100	49	49	49	49	49	49	d__Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1601	100	100	100	100	100	63	44	d__Bacteri	p__Pseudo	c__Alphap	o__Hyphor	f__Hyphor	g__Hyphor	NA	Filter: bootstrap Score >= 50
ASV1602	100	99	95	80	72	20	20	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1603	100	39	39	39	39	39	37	d__Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1604	100	100	100	100	100	100	94	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Bacterd	g__Bacter	s__Bacteroides_xylanisolvens	
ASV1605	100	98	97	96	78	78	78	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Eubacte	g__Eubacte	s__Eubacterium_coprostanoligenes	
ASV1606	100	71	27	27	27	5	5	d__Bacteri	p__Bacillo	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1607	100	99	87	38	17	17	10	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1608	100	80	67	67	63	36	18	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	f__Erysipe	NA	NA	Filter: bootstrap Score >= 50
ASV1609	100	100	100	100	100	99	99	d__Bacteri	p__Pseudo	c__Gamm	o__Entero	f__Erwinia	g__Pantoe	s__Pantoea_agglomerans	
ASV1610	100	100	100	100	74	47	47	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV1611	100	100	100	95	95	23	23	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1612	100	100	100	99	94	94	78	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Aristae	g__Aristae	s__Aristaeella_lactis	
ASV1613	100	100	100	100	95	43	39	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV1614	100	100	100	100	100	100	91	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Prevote	g__Segate	s__Segatella_hominis	
ASV1615	100	100	66	65	11	11	9	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1616	100	78	57	46	15	15	15	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1617	100	100	100	100	100	17	17	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1618	100	100	100	67	67	58	36	d__Bacteri	p__Actinor	c__Coriob	o__Coriob	f__Coriob	g__Seneg	NA	Filter: bootstrap Score >= 50
ASV1619	100	97	97	97	97	97	97	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Maliiba	g__Maliiba	s__Maliibacterium_massiliense	
ASV1620	100	100	100	100	100	100	91	d__Bacteri	p__Spiroch	c__Spiroch	o__Spiroch	f__Treponi	g__Treponi	s__Treponema_porcinum	
ASV1621	100	100	100	100	100	100	99	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Tanner	g__Paraba	s__Parabacteroides_gordonii	
ASV1622	100	100	100	99	99	76	6	d__Bacteri	p__Actinor	c__Actinor	o__Pseudo	f__Pseudo	g__Saccha	NA	Filter: bootstrap Score >= 50
ASV1623	100	100	100	100	100	100	61	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Rikene	g__Alistipe	s__Alistipes_finegoldii	
ASV1624	100	100	100	100	100	100	81	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Rikene	g__Alistipe	s__Alistipes_putredinis	
ASV1625	100	100	100	100	100	50	49	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Diplod	NA	Filter: bootstrap Score >= 50
ASV1626	100	100	100	100	54	48	48	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV1627	100	100	100	32	31	18	8	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1628	100	100	100	98	89	89	28	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Anaero	g__Anaero	NA	Filter: bootstrap Score >= 50
ASV1629	100	100	99	99	86	12	12	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV1630	100	99	33	33	33	8	5	d__Bacteri	p__Bacter	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1631	100	100	40	40	40	19	9	d__Bacteri	p__Bacter	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1632	100	100	100	96	91	71	35	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	g__Vescim	NA	Filter: bootstrap Score >= 50
ASV1633	100	99	90	85	77	77	41	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Aristae	g__Aristae	NA	Filter: bootstrap Score >= 50
ASV1634	100	100	100	98	31	30	21	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1635	100	100	100	100	100	100	77	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Bacterd	g__Bacter	s__Bacteroides_acidifaciens	
ASV1636	100	100	100	100	100	100	80	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Anaero	g__Anaero	s__Anaerotignum_lactatifermentans	
ASV1637	100	100	100	95	95	9	9	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1638	100	41	23	23	23	5	4	d__Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1639	100	100	100	100	90	90	83	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	g__Neglec	s__Neglectibacter_caecimuris	
ASV1640	100	100	100	96	77	20	10	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV1641	100	100	96	73	73	56	28	d__Bacteri	p__Bacillo	c__Clostrid	o__Christe	f__Christe	g__Christe	NA	Filter: bootstrap Score >= 50
ASV1642	100	69	55	55	52	27	21	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	f__Erysipe	NA	NA	Filter: bootstrap Score >= 50
ASV1643	100	100	100	98	28	28	28	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1644	100	100	80	80	79	25	16	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV1645	100	96	82	24	10	9	8	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1646	100	68	65	61	35	12	6	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1647	100	99	98	83	83	77	77	d__Bacteri	p__Bacillo	c__Clostrid	o__Christe	f__Christe	g__Gehon	s__Gehongia_tenuis	
ASV1648	100	99	97	75	66	9	9	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50

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ASV1649	100	100	100	100	100	100	99	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Butyrici	g__Butyric	s__Butyricicoccus_intestinisimiae		
ASV1650	100	100	100	100	100	97	67	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Anaero	s__Anaerostipes_butyraticus		
ASV1651	100	97	87	10	10	6	6	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV1652	100	100	100	100	100	46	14	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Prevote	NA	NA	Filter: bootstrap Score >= 50	
ASV1653	100	100	100	100	100	88	88	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Prevote	g__Prevot	s__Prevotellamassilia_timonensis		
ASV1654	100	100	100	100	100	90	89	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Oscillos	g__Dysosm	s__Dysosmobacter_acutus		
ASV1655	100	100	99	92	86	86	58	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Aristaee	g__Aristae	s__Aristaeella_hokkaidonensis		
ASV1656	100	100	100	96	95	42	42	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50	
ASV1657	100	100	100	100	100	100	19	d__Bacteri	p__Bacillo	c__Bacilli	o__Bacilla	f__Staphyl	g__Staphy	NA	Filter: bootstrap Score >= 50	
ASV1658	100	100	100	100	100	54	14	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Prevote	g__Segate	NA	Filter: bootstrap Score >= 50	
ASV1659	100	100	100	100	100	100	70	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Tanner	g__Parabа	s__Parabacteroides_merdae		
ASV1660	100	100	100	100	96	53	53	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Oscillos	g__Lawso	s__Lawsonibacter_asaccharolyticus		
ASV1661	100	100	100	96	96	23	23	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50	
ASV1662	100	99	99	91	91	19	19	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50	
ASV1663	100	99	96	45	45	36	36	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV1664	100	100	100	64	54	54	54	d__Bacteri	p__Actinor	c__Actinor	o__Microc	f__Bogorie	g__George	s__Georgenia_deserti		
ASV1665	100	100	100	100	100	77	77	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	f__Erysipe	g__Lactim	s__Lactimicrobium_massiliense		
ASV1666	100	100	100	100	100	93	93	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Kineot	s__Kineothrix_alysoides		
ASV1667	100	100	100	100	100	100	100	d__Bacteri	p__Fibroba	c__Fibroba	o__Fibroba	f__Fibroba	g__Fibrob	s__Fibrobacter_succinogenes		
ASV1668	100	100	100	97	89	65	34	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Oscillos	g__Vescim	NA	Filter: bootstrap Score >= 50	
ASV1669	100	100	100	99	64	63	50	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Tanner	g__Parabа	s__Parabacteroides_distasonis		
ASV1670	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__	g__Howar	s__Howardella_ureilytica		
ASV1671	100	100	100	100	83	83	82	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__	g__Gemm	s__Gemmiger_formicilis		
ASV1672	100	100	99	99	57	57	57	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Clostrid	g__Massili	s__Massilioclostridium_coli		
ASV1673	100	100	100	100	91	49	27	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50	
ASV1674	100	100	99	84	34	34	23	d__Bacteri	p__Actinor	c__Thermo	o__Solirub	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV1675	100	100	100	100	80	79	79	d__Bacteri	p__Actinor	c__Actinor	o__Mycob	f__Nocard	g__Smara	s__Smaragdicoccus_niigatensis		
ASV1676	100	99	93	90	87	74	29	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Eubacte	g__Acetob	NA	Filter: bootstrap Score >= 50	
ASV1677	100	93	78	14	12	11	11	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV1678	100	100	100	100	100	100	99	d__Bacteri	p__Pseudo	c__Betapro	o__Burkho	f__Alcalige	g__Paenal	s__Paenalcaligenes_hominis		
ASV1679	100	100	100	100	100	100	36	d__Bacteri	p__Pseudo	c__Alphapr	o__Rhodo	f__Paracoc	g__Paracc	NA	Filter: bootstrap Score >= 50	
ASV1680	100	100	100	100	100	100	66	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Rikene	g__Alistipe	s__Alistipes_putredinis		
ASV1681	100	100	100	100	100	100	96	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Roseb	s__Roseburia_porci		
ASV1682	100	100	100	100	100	100	100	d__Bacteri	p__Mycop	c__	o__Mycop	f__Metamy	g__Metam	s__Metamycoplasma_sualvi		
ASV1683	100	100	100	100	69	50	50	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Oscillos	g__	s__[Clostridium]_leptum		
ASV1684	100	95	95	76	7	7	7	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV1685	100	100	100	98	98	40	40	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50	
ASV1686	100	100	100	96	59	30	29	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__	NA	NA	Filter: bootstrap Score >= 50	
ASV1687	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Eubacte	g__Eubacte	s__Eubacterium_pyruvativorans		
ASV1688	100	100	100	100	100	89	43	d__Bacteri	p__Bacillo	c__Negativi	o__Seleno	f__Seleno	g__Seleno	NA	Filter: bootstrap Score >= 50	
ASV1689	100	100	100	100	100	100	92	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Prevote	g__Segate	s__Segatella_copri		
ASV1690	100	74	74	74	74	74	24	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	NA	Filter: bootstrap Score >= 50	
ASV1691	100	99	99	99	69	20	20	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	f__Coprob	NA	NA	Filter: bootstrap Score >= 50	
ASV1692	100	100	100	100	100	71	23	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Ligilact	NA	Filter: bootstrap Score >= 50	
ASV1693	100	87	87	87	87	49	49	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Prevote	NA	NA	Filter: bootstrap Score >= 50	
ASV1694	100	100	100	99	99	59	58	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Entero	s__Enterocloster_aldenensis		
ASV1695	100	100	27	27	27	12	12	d__Bacteri	p__Bacter	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV1696	100	51	51	51	50	50	38	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Ligilact	NA	Filter: bootstrap Score >= 50	
ASV1697	100	100	100	100	100	100	100	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Tanner	g__Parabа	s__Parabacteroides_distasonis		
ASV1698	100	100	94	90	86	86	86	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Peptoc	g__Dehalo	s__Dehalobacterium_formicoaceticum		

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ASV1699	100	76	74	30	4	4	4	d_Bacteri	p_Bacillo	c_Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1700	100	100	100	96	96	15	7	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1701	100	100	100	100	100	100	85	d_Bacteri	p_Spiroch	c_Spiroch	o_Spiroch	f_Treponi	g_Treponi	s_Treponema_bryantii	
ASV1702	100	100	100	100	100	92	85	d_Bacteri	p_Bacillo	c_Negativ	o_Selenc	f_Seleno	g_Selenc	s_Selenomonas_ruminantium	
ASV1703	100	100	100	100	100	98	53	d_Bacteri	p_Bacillo	c_Bacilli	o_Lactob	f_Lactoba	g_Lactob	s_Lactobacillus_paragasseri	
ASV1704	100	46	8	8	7	4	4	d_Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1705	100	99	98	92	83	83	71	d_Bacteri	p_Bacillo	c_Clostrid	o_Eubact	f_Aristae	g_Aristae	s_Aristaeella_lactis	
ASV1706	100	100	99	99	71	34	15	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteri	f_Prevote	NA	NA	Filter: bootstrap Score >= 50
ASV1707	100	100	100	100	100	100	42	d_Bacteri	p_Spiroch	c_Spiroch	o_Spiroch	f_Treponi	g_Treponi	NA	Filter: bootstrap Score >= 50
ASV1708	100	100	100	99	99	62	12	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	g_Blautia	NA	Filter: bootstrap Score >= 50
ASV1709	100	100	100	99	81	33	33	d_Bacteri	p_Bacillo	c_Clostrid	o_Eubact	f_Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV1710	100	100	100	100	100	96	96	d_Bacteri	p_Bacillo	c_Erysipe	o_Erysipe	f_Coprob	g_Longib	s_Longibaculum_muris	
ASV1711	100	75	66	32	32	17	13	d_Bacteri	p_Bacillo	c_Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1712	100	100	100	100	100	96	42	d_Bacteri	p_Acidob	c_Blastoc	o_Blastoc	f_Blastoc	g_Stenot	NA	Filter: bootstrap Score >= 50
ASV1713	100	84	59	59	59	28	28	d_Bacteri	p_Bacillo	c_Erysipe	o_Erysipe	f_Erysipe	NA	NA	Filter: bootstrap Score >= 50
ASV1714	100	100	100	98	98	34	33	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1715	100	100	100	95	95	44	44	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1716	100	93	85	20	20	17	7	d_Bacteri	p_Bacillo	c_Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1717	100	100	100	100	100	100	65	d_Bacteri	p_Actinor	c_Actinor	o_Mycob	f_Coryne	g_Coryne	s_Corynebacterium_oculi	
ASV1718	100	89	72	63	42	12	12	d_Bacteri	p_Bacillo	c_Clostrid	o_Eubact	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1719	100	89	83	22	22	18	12	d_Bacteri	p_Bacillo	c_Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1720	100	90	90	90	85	78	78	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteri	f_Prevote	g_Alloprev	s_Alloprevotella_rava	
ASV1721	100	100	100	68	68	37	35	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1722	100	100	98	98	39	35	35	d_Bacteri	p_Bacillo	c_Clostrid	o_Eubact	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1723	100	100	100	100	95	94	64	d_Bacteri	p_Bacillo	c_Clostrid	o_Eubact	f_Clostrid	g_Clostrid	s_Clostridium_jeddahitimonense	
ASV1724	100	97	94	37	19	16	16	d_Bacteri	p_Bacillo	c_Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1725	100	100	100	100	100	99	96	d_Bacteri	p_Actinor	c_Coriobac	o_Coriobac	f_Atopobi	g_Olsenel	s_Olsenella_congonensis	
ASV1726	100	100	100	100	100	73	73	d_Bacteri	p_Bacillo	c_Clostrid	o_Eubact	f_Oscillos	g_Angela	s_Angelakisella_massiliensis	
ASV1727	100	80	80	80	80	80	66	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteri	f_Rikenel	g_Alistipe	s_Alistipes_dispar	
ASV1728	100	100	100	100	100	70	35	d_Bacteri	p_Bacillo	c_Bacilli	o_Lactob	f_Lactoba	g_Ligilact	NA	Filter: bootstrap Score >= 50
ASV1729	100	100	100	100	100	100	44	d_Bacteri	p_Bacillo	c_Bacilli	o_Lactob	f_Lactoba	g_Lactob	NA	Filter: bootstrap Score >= 50
ASV1730	100	93	93	92	90	73	73	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteri	f_Odoriba	g_Culturo	s_Culturomica_massiliensis	
ASV1731	100	90	90	90	87	87	75	d_Bacteri	p_Spiroch	c_Spiroch	o_Spiroch	f_Treponi	g_Treponi	s_Treponema_succinifaciens	
ASV1732	100	100	100	100	100	100	99	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteri	f_Odoriba	g_Butyricl	s_Butyricimonas_synergistica	
ASV1733	100	100	100	100	83	76	76	d_Bacteri	p_Bacillo	c_Clostrid	o_Eubact	f_Oscillos	g_Dysosm	s_Dysosmobacter_acutus	
ASV1734	100	96	79	25	12	8	8	d_Bacteri	p_Bacillo	c_Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1735	100	100	100	100	100	100	94	d_Bacteri	p_Bacillo	c_Bacilli	o_Lactob	f_Lactoba	g_Weisse	s_Weissella_confusa	
ASV1736	100	100	100	95	90	90	58	d_Bacteri	p_Bacillo	c_Clostrid	o_Eubact	f_Aristae	g_Aristae	s_Aristaeella_hokkaidonensis	
ASV1737	100	100	100	100	98	30	20	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteri	f_Muriba	NA	NA	Filter: bootstrap Score >= 50
ASV1738	100	100	100	97	97	60	39	d_Bacteri	p_Actinor	c_Coriobac	o_Eggerth	f_Eggerth	g_Adlerc	NA	Filter: bootstrap Score >= 50
ASV1739	100	99	99	99	99	31	31	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1740	100	100	100	100	100	36	36	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteri	f_Muriba	NA	NA	Filter: bootstrap Score >= 50
ASV1741	100	100	100	100	100	100	89	d_Bacteri	p_Bacillo	c_Clostrid	o_Eubact	f_Oscillos	g_Oscillib	s_Oscillibacter_valericigenes	
ASV1742	100	100	100	94	94	83	83	d_Bacteri	p_Bacillo	c_Clostrid	o_Eubact	f_Oscillos	g_Ructiba	s_Ructibacterium_gallinarum	
ASV1743	100	100	100	79	62	60	30	d_Bacteri	p_Actinor	c_Coriobac	o_Coriobac	f_Atopobi	g_Olsenel	NA	Filter: bootstrap Score >= 50
ASV1744	100	100	100	100	100	60	58	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	g_Mediter	s_Mediterraneibacter_gnavus	
ASV1745	100	100	100	100	100	12	12	d_Bacteri	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1746	100	99	99	99	98	60	23	d_Bacteri	p_Bacillo	c_Clostrid	o_Peptos	f_Peptost	g_Terrisp	NA	Filter: bootstrap Score >= 50
ASV1747	100	100	22	22	22	10	7	d_Bacteri	p_Bacteri	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1748	100	100	100	100	100	35	23	d_Bacteri	p_Bacteri	c_Bacteroi	o_Bacteri	f_Prevote	NA	NA	Filter: bootstrap Score >= 50

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ASV1749	100	100	31	31	31	4	3	d__Bacteri	p__Bacteri	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1750	100	100	100	100	100	89	50	d__Bacteri	p__Acidob	c__Blastoc	o__Blastoc	f__Blastoc	g__Stenotr	s__Stenotrophobacter_roseus	
ASV1751	100	51	31	18	13	12	12	d__Bacteri	p__Bacillo	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1752	100	100	100	98	98	80	3	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Blautia	NA	Filter: bootstrap Score >= 50
ASV1753	100	100	100	100	100	100	100	d__Bacteri	p__Pseudo	c__Gamma	o__Pseudo	f__Pseudo	g__Stutzer	s__Stutzerimonas_stutzeri	
ASV1754	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Clostrid	g__Clostrid	s__[Clostridium]_innocuum	
ASV1755	100	100	100	98	98	10	10	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1756	100	100	100	100	100	100	97	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Weisse	s__Weissella_confusa	
ASV1757	100	100	100	100	100	99	99	d__Bacteri	p__Bacteri	c__Cytophi	o__Cytophi	f__Cesirib	g__Nafulse	s__Nafulsella_turpanensis	
ASV1758	100	100	100	100	100	41	41	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV1759	100	100	100	100	100	75	36	d__Bacteri	p__Bacillo	c__Bacilli	o__Bacillal	f__Gemell	g__Gemell	NA	Filter: bootstrap Score >= 50
ASV1760	100	75	46	46	46	20	15	d__Bacteri	p__Bacillo	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1761	100	89	55	46	42	19	0	d__Bacteri	p__Bacteri	c__Bacteri	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1762	100	100	100	69	69	44	12	d__Bacteri	p__Actinor	c__Actinor	o__Pseudo	f__Pseudo	NA	NA	Filter: bootstrap Score >= 50
ASV1763	100	98	98	98	98	82	82	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Coprod	s__Coprococcus_comes	
ASV1764	100	100	100	100	100	100	89	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Anaero	g__Anaero	s__Anaerotignum_aminivorans	
ASV1765	100	100	100	100	100	100	32	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Strepto	g__Strepto	NA	Filter: bootstrap Score >= 50
ASV1766	100	100	50	49	47	26	26	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1767	100	100	100	100	100	36	36	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Butyrici	NA	NA	Filter: bootstrap Score >= 50
ASV1768	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	g__Owarii	s__Owariibacterium_komagatae	
ASV1769	100	99	92	78	78	35	16	d__Bacteri	p__Bacillo	c__Negativ	o__Seleno	f__Seleno	NA	NA	Filter: bootstrap Score >= 50
ASV1770	100	47	47	47	47	47	47	d__Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1771	100	100	100	100	76	26	26	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV1772	100	100	97	91	57	57	30	d__Bacteri	p__Bacteri	c__Bacteri	o__Bacteri	f__Tanneri	g__Paraba	NA	Filter: bootstrap Score >= 50
ASV1773	100	100	100	100	99	90	84	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	g__Rumino	s__Ruminococcus_callidus	
ASV1774	100	100	100	99	97	30	30	d__Bacteri	p__Bacillo	c__Clostrid	o__Peptos	f__Anaero	NA	NA	Filter: bootstrap Score >= 50
ASV1775	100	100	100	99	91	38	33	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV1776	100	99	97	66	66	29	29	d__Bacteri	p__Bacillo	c__Clostrid	o__Christe	f__Christe	NA	NA	Filter: bootstrap Score >= 50
ASV1777	100	100	100	100	100	83	20	d__Bacteri	p__Bacteri	c__Bacteri	o__Bacteri	f__Bacteri	g__Bacteri	NA	Filter: bootstrap Score >= 50
ASV1778	100	100	100	100	67	45	45	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV1779	100	100	100	92	92	48	48	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1780	100	51	51	50	50	30	30	d__Bacteri	p__Bacteri	c__Bacteri	o__Bacteri	f__Prevote	NA	NA	Filter: bootstrap Score >= 50
ASV1781	100	100	100	100	100	74	74	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Coprod	s__Coprococcus_comes	
ASV1782	100	100	89	36	6	6	3	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1783	100	84	59	59	59	49	48	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	f__Erysipe	NA	NA	Filter: bootstrap Score >= 50
ASV1784	100	100	100	100	98	98	87	d__Bacteri	p__Bacteri	c__Bacteri	o__Bacteri	f__Bacteri	g__Bacteri	s__Bacteroides_acidifaciens	
ASV1785	100	90	85	52	10	10	7	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1786	100	100	100	100	100	45	45	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1787	100	98	98	97	66	37	37	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Acutalit	NA	NA	Filter: bootstrap Score >= 50
ASV1788	100	99	78	64	6	6	2	d__Bacteri	p__Bacteri	c__Bacteri	o__Bacteri	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1789	100	73	55	32	17	17	17	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1790	100	100	100	100	100	96	6	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Limosil	NA	Filter: bootstrap Score >= 50
ASV1791	100	100	45	37	25	16	16	d__Bacteri	p__Bacteri	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1792	100	100	100	99	99	98	76	d__Bacteri	p__Bacteri	c__Bacteri	o__Bacteri	f__Muriba	g__Duncan	s__Duncaniella_dubosii	
ASV1793	100	100	100	100	100	100	98	d__Bacteri	p__Actinor	c__Coriob	o__Coriob	f__Coriob	g__Collins	s__Collinsella_bouchesdurhonensis	
ASV1794	100	100	100	100	100	100	90	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	s__Lactobacillus_porci	
ASV1795	100	66	46	46	23	20	18	d__Bacteri	p__Bacillo	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1796	100	100	52	38	26	23	23	d__Bacteri	p__Bacteri	c__Bacteri	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1797	100	100	100	29	29	29	29	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1798	100	100	100	100	100	100	100	d__Bacteri	p__Bacteri	c__Sphingo	o__Sphingo	f__Sphingo	g__Sphingo	s__Sphingobacterium_multivorum	

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ASV1799	100	100	100	47	45	45	36	d__Bacteri	p__Bacillot	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1800	100	100	100	100	100	100	100	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Tanner	g__Paraba	s__Parabacteroides_merdae	
ASV1801	100	100	100	100	100	51	51	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubact	f__	g__Evtepia	s__Evtepia_gabavorous	
ASV1802	100	99	81	27	9	8	8	d__Bacteri	p__Bacillot	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1803	100	99	99	99	99	95	30	d__Bacteri	p__Bacillot	c__Bacilli	o__Lactob	f__Lactoba	g__Ligilact	NA	Filter: bootstrap Score >= 50
ASV1804	100	37	37	37	37	37	37	d__Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1805	100	96	85	22	22	10	10	d__Bacteri	p__Bacillot	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1806	99	47	29	29	29	15	10	d__Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1807	100	100	100	100	100	48	48	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Muriba	NA	NA	Filter: bootstrap Score >= 50
ASV1808	100	82	81	74	25	23	20	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubact	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1809	100	100	100	100	80	32	26	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV1810	100	64	64	64	63	40	30	d__Bacteri	p__Therm	c__Desulfo	o__Desulfo	f__Desulfo	NA	NA	Filter: bootstrap Score >= 50
ASV1811	100	100	100	100	61	57	38	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Tanner	g__Paraba	NA	Filter: bootstrap Score >= 50
ASV1812	100	100	100	100	97	37	37	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Muriba	NA	NA	Filter: bootstrap Score >= 50
ASV1813	100	99	98	83	83	43	16	d__Bacteri	p__Bacillot	c__Negativi	o__Selenc	f__Selenor	NA	NA	Filter: bootstrap Score >= 50
ASV1814	100	100	100	100	99	99	80	d__Bacteri	p__Bacillot	c__Clostrid	o__Peptos	f__Anaero	g__Lentiho	s__Lentihominibacter_faecis	
ASV1815	100	86	29	29	29	9	6	d__Bacteri	p__Bacillot	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1816	100	100	100	62	62	9	8	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1817	100	100	99	70	62	16	8	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1818	100	93	85	74	55	35	35	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubact	f__Eubact	NA	NA	Filter: bootstrap Score >= 50
ASV1819	100	100	100	100	100	100	38	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubact	f__Clostrid	g__Clostrid	NA	Filter: bootstrap Score >= 50
ASV1820	100	100	100	99	99	78	78	d__Bacteri	p__Bacillot	c__Clostrid	o__Christe	f__Christe	g__Guopin	s__Guopingia_tenuis	
ASV1821	100	100	100	100	100	100	57	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Odoriba	g__Butyric	s__Butyricimonas_faecihominis	
ASV1822	100	100	100	100	100	100	89	d__Bacteri	p__Bacillot	c__Bacilli	o__Lactob	f__Strepto	g__Strepto	s__Streptococcus_thoraltensis	
ASV1823	100	100	99	99	99	83	43	d__Bacteri	p__Bacillot	c__Bacilli	o__Lactob	f__Lactoba	g__Ligilact	NA	Filter: bootstrap Score >= 50
ASV1824	100	100	100	100	100	100	100	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Bacter	g__Bacter	s__Bacteroides_eggerthii	
ASV1825	100	100	100	100	100	100	77	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubact	f__Aristae	g__Aristae	s__Aristaeella_hokkaidonensis	
ASV1826	100	100	100	100	100	68	68	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Muriba	g__Sangei	s__Sangeribacter_muris	
ASV1827	100	100	100	98	98	27	16	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1828	100	93	73	73	73	70	69	d__Bacteri	p__Bacillot	c__Erysipe	o__Erysipe	f__Erysipe	g__Breznа	s__Breznakia_pachnodae	
ASV1829	100	100	100	100	100	56	56	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachno	f__Lachno	g__Jutong	s__Jutongia_hominis	
ASV1830	100	79	69	69	65	31	12	d__Bacteri	p__Bacillot	c__Erysipe	o__Erysipe	f__Erysipe	NA	NA	Filter: bootstrap Score >= 50
ASV1831	100	17	17	17	17	17	17	d__Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1832	100	100	100	100	100	98	29	d__Bacteri	p__Pseudo	c__Betapro	o__Burkho	f__Oxalob	g__Massili	NA	Filter: bootstrap Score >= 50
ASV1833	100	79	58	58	58	54	48	d__Bacteri	p__Bacillot	c__Erysipe	o__Erysipe	f__Erysipe	g__Brezna	NA	Filter: bootstrap Score >= 50
ASV1834	100	100	100	100	95	51	29	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Prevote	g__Segate	NA	Filter: bootstrap Score >= 50
ASV1835	100	54	54	54	54	54	54	d__Bacteri	p__Candid	c__Vampiri	o__Vampiri	f__	g__Vampir	s__Vampirovibrio_chlorellavorus	
ASV1836	100	100	100	98	98	98	98	d__Bacteri	p__Bacillot	c__Clostrid	o__Monog	f__Monogl	g__Monog	s__Monoglobus_pectinilyticus	
ASV1837	100	100	66	40	12	12	12	d__Bacteri	p__Bacter	c__Bacter	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1838	100	100	100	100	100	94	70	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Muriba	g__Duncan	s__Duncaniella_muris	
ASV1839	100	100	100	100	100	100	69	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachno	f__Lachno	g__Blautia	s__Blautia_luti	
ASV1840	100	100	100	97	73	17	17	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV1841	100	97	95	89	89	66	66	d__Bacteri	p__Bacillot	c__Clostrid	o__Christe	f__Christe	g__Gehon	s__Gehongia_tenuis	
ASV1842	100	100	100	100	100	15	14	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1843	100	100	100	98	98	42	31	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1844	100	100	100	100	99	31	6	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Prevote	NA	NA	Filter: bootstrap Score >= 50
ASV1845	100	100	100	100	66	46	35	d__Bacteri	p__Bacillot	c__Clostrid	o__Eubact	f__	NA	NA	Filter: bootstrap Score >= 50
ASV1846	100	100	41	37	19	15	15	d__Bacteri	p__Bacter	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1847	100	100	100	100	100	100	54	d__Bacteri	p__Bacillot	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	s__Lactobacillus_paragasseri	
ASV1848	100	100	100	92	92	27	27	d__Bacteri	p__Bacillot	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50

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ASV1849	100	99	99	97	95	95	78	d_Bacter	p_Bacillo	c_Clostrid	o_Eubact	f_Aristae	g_Aristae	s_Aristaeella_hokkaidonensis			
ASV1850	100	100	100	100	41	8	7	d_Bacter	p_Planct	c_Planct	o_Pirellul	NA	NA	NA	Filter: bootstrap Score >= 50		
ASV1851	100	100	100	98	98	55	55	d_Bacter	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	g_Jutong	s_Jutongia_hominis			
ASV1852	100	100	100	100	100	100	97	d_Bacter	p_Campy	c_Epsilon	o_Campy	f_Helicob	g_Helicob	s_Helicobacter_typhlonius			
ASV1853	100	100	100	100	100	100	100	d_Bacter	p_Bacillo	c_Bacilli	o_Bacillal	f_Staphy	g_Jeotga	s_Jeotgalicoccus_aerolatus			
ASV1854	100	77	39	39	39	14	11	d_Bacter	p_Bacillo	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50		
ASV1855	100	100	100	100	99	97	97	d_Bacter	p_Bacillo	c_Clostrid	o_Peptost	f_Peptost	g_Rombo	s_Romboutsia_timonensis			
ASV1856	100	100	100	100	100	99	87	d_Bacter	p_Actinor	c_Actinor	o_Geodel	f_Geodel	g_Geodel	s_Geodermatophilus_obscurus			
ASV1857	100	100	100	100	47	33	33	d_Bacter	p_Bacillo	c_Clostrid	o_Eubact	NA	NA	NA	Filter: bootstrap Score >= 50		
ASV1858	100	100	100	100	100	99	77	d_Bacter	p_Bacillo	c_Bacilli	o_Bacillal	f_Bacillac	g_Aeriba	s_Aeribacillus_composti			
ASV1859	100	100	100	100	100	99	76	d_Bacter	p_Bacter	c_Bacter	o_Bacter	f_Bacterd	g_Bacter	s_Bacteroides_acidifaciens			
ASV1860	100	100	100	85	85	43	43	d_Bacter	p_Actinor	c_Coriob	o_Eggert	f_Eggerth	NA	NA	Filter: bootstrap Score >= 50		
ASV1861	100	98	85	41	32	32	23	d_Bacter	p_Bacillo	c_Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50		
ASV1862	100	70	52	52	49	20	15	d_Bacter	p_Bacillo	c_Erysipe	o_Erysipe	NA	NA	NA	Filter: bootstrap Score >= 50		
ASV1863	100	100	100	100	99	78	69	d_Bacter	p_Bacter	c_Bacter	o_Bacter	f_Muriba	g_Muriba	s_Muribaculum_intestinale			
ASV1864	100	62	62	62	53	31	26	d_Bacter	p_Bacter	c_Bacter	o_Bacter	f_Muriba	NA	NA	Filter: bootstrap Score >= 50		
ASV1865	100	97	97	97	97	97	86	d_Bacter	p_Bacter	c_Bacter	o_Bacter	f_Rikene	g_Alistipe	s_Alistipes_dispar			
ASV1866	100	99	82	82	79	78	69	d_Bacter	p_Bacillo	c_Bacilli	o_Lactob	f_Lactoba	g_Ligilact	s_Ligilactobacillus_apodemi			
ASV1867	100	100	100	91	91	16	16	d_Bacter	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	NA	NA	Filter: bootstrap Score >= 50		
ASV1868	100	100	100	100	91	85	85	d_Bacter	p_Bacillo	c_Clostrid	o_Eubact	f_	g_Flintiba	s_Flintibacter_butyricus			
ASV1869	100	100	100	99	99	24	24	d_Bacter	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	NA	NA	Filter: bootstrap Score >= 50		
ASV1870	100	100	100	100	100	50	50	d_Bacter	p_Bacillo	c_Erysipe	o_Erysipe	f_Erysipe	g_Lactim	s_Lactimicrobium_massiliense			
ASV1871	100	100	100	100	99	53	31	d_Bacter	p_Bacter	c_Bacter	o_Bacter	f_Prevote	g_Segate	NA	Filter: bootstrap Score >= 50		
ASV1872	100	99	99	99	99	98	42	d_Bacter	p_Bacillo	c_Bacilli	o_Lactob	f_Lactoba	g_Lactob	NA	Filter: bootstrap Score >= 50		
ASV1873	100	99	97	88	53	53	37	d_Bacter	p_Bacillo	c_Clostrid	o_Eubact	f_Aristae	g_Aristae	NA	Filter: bootstrap Score >= 50		
ASV1874	100	99	67	60	21	19	19	d_Bacter	p_Bacter	c_Bacter	o_Bacter	NA	NA	NA	Filter: bootstrap Score >= 50		
ASV1875	100	100	99	93	92	31	23	d_Bacter	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	NA	NA	Filter: bootstrap Score >= 50		
ASV1876	100	100	100	100	100	100	95	d_Bacter	p_Bacillo	c_Clostrid	o_Eubact	f_Butyrici	g_Butyrici	s_Butyricicoccus_intestinisimiae			
ASV1877	100	100	100	100	91	56	46	d_Bacter	p_Bacillo	c_Clostrid	o_Eubact	f_Oscillos	g_Anaero	NA	Filter: bootstrap Score >= 50		
ASV1878	100	100	100	40	31	30	22	d_Bacter	p_Bacillo	c_Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50		
ASV1879	100	100	100	100	99	99	67	d_Bacter	p_Bacillo	c_Clostrid	o_Eubact	f_Aristae	g_Aristae	s_Aristaeella_lactis			
ASV1880	100	100	100	100	100	100	100	d_Bacter	p_Bacter	c_Bacter	o_Bacter	f_Prevote	g_Segate	s_Segatella_copri			
ASV1881	100	88	87	84	53	27	11	d_Bacter	p_Bacillo	c_Clostrid	o_Eubact	f_	NA	NA	Filter: bootstrap Score >= 50		
ASV1882	100	100	100	98	97	97	83	d_Bacter	p_Bacillo	c_Clostrid	o_Eubact	f_Aristae	g_Aristae	s_Aristaeella_hokkaidonensis			
ASV1883	100	100	100	100	100	100	61	d_Bacter	p_Actinor	c_Actinor	o_Mycob	f_Corynel	g_Corynes	s_Corynebacterium_variabile			
ASV1884	100	100	100	99	14	14	11	d_Bacter	p_Bacillo	c_Clostrid	o_Eubact	NA	NA	NA	Filter: bootstrap Score >= 50		
ASV1885	100	100	100	100	99	66	66	d_Bacter	p_Bacillo	c_Clostrid	o_Eubact	f_Oscillos	g_Flavon	s_Flavonifractor_plautii			
ASV1886	100	93	91	64	64	28	28	d_Bacter	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	NA	NA	Filter: bootstrap Score >= 50		
ASV1887	100	84	83	12	12	12	5	d_Bacter	p_Bacillo	c_Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50		
ASV1888	100	100	100	71	69	5	5	d_Bacter	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	NA	NA	Filter: bootstrap Score >= 50		
ASV1889	100	100	100	100	100	84	84	d_Bacter	p_Bacillo	c_Clostrid	o_Eubact	f_Oscillos	g_	s_[Eubacterium]_siraeum			
ASV1890	100	100	100	100	29	29	29	d_Bacter	p_Bacillo	c_Clostrid	o_Eubact	NA	NA	NA	Filter: bootstrap Score >= 50		
ASV1891	100	100	100	100	100	100	85	d_Bacter	p_Bacillo	c_Bacilli	o_Lactob	f_Lactoba	g_Limosil	s_Limosilactobacillus_coleohominis			
ASV1892	100	100	100	98	92	32	32	d_Bacter	p_Bacillo	c_Clostrid	o_Eubact	f_Oscillos	NA	NA	Filter: bootstrap Score >= 50		
ASV1893	100	100	100	100	100	87	28	d_Bacter	p_Bacillo	c_Bacilli	o_Lactob	f_Lactoba	g_Ligilact	NA	Filter: bootstrap Score >= 50		
ASV1894	100	100	100	100	100	100	70	d_Bacter	p_Bacillo	c_Bacilli	o_Lactob	f_Lactoba	g_Lactob	s_Lactobacillus_gasseri			
ASV1895	100	99	99	84	31	28	24	d_Bacter	p_Pseudo	c_Alphap	o_Rhodo	NA	NA	NA	Filter: bootstrap Score >= 50		
ASV1896	100	60	60	52	50	15	15	d_Bacter	p_Bacillo	c_Clostrid	o_Lachno	f_Lachno	NA	NA	Filter: bootstrap Score >= 50		
ASV1897	100	100	99	99	98	29	27	d_Bacter	p_Bacter	c_Bacter	o_Bacter	f_Muriba	NA	NA	Filter: bootstrap Score >= 50		
ASV1898	100	100	100	100	100	100	52	d_Bacter	p_Spiroch	c_Spiroch	o_Spiroch	f_Trepon	g_Trepon	s_Treponema_peruense			

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ASV1899	100	100	100	98	98	98	98	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Eubacte	g__Anaerof	s__Anaerofustis_stercorihominis		
ASV1900	100	100	100	89	89	42	42	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50	
ASV1901	100	76	70	47	47	15	15	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV1902	100	71	55	52	51	14	14	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50	
ASV1903	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Bacilli	o__Bacillal	f__Thermo	g__Novibac	s__Novibacillus_thermophilus		
ASV1904	100	100	100	100	100	44	44	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50	
ASV1905	100	100	100	96	93	5	5	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50	
ASV1906	100	78	46	46	46	41	24	d__Bacteri	p__Bacillo	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV1907	100	83	83	83	83	79	75	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Bacter	g__Phocae	s__Phocaeicola_dorei		
ASV1908	100	86	68	38	23	11	1	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV1909	100	93	93	16	16	10	8	d__Bacteri	p__Cyanob	c__Cyanob	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV1910	100	100	100	87	87	18	10	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50	
ASV1911	100	100	100	100	97	82	15	d__Bacteri	p__Pseudo	c__Alphap	o__Hyphom	f__Brucella	g__Brucell	NA	Filter: bootstrap Score >= 50	
ASV1912	100	88	81	19	19	18	13	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV1913	100	100	100	100	72	25	25	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50	
ASV1914	100	78	78	71	38	35	5	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV1915	100	100	100	56	56	17	9	d__Bacteri	p__Actinob	c__Coriobac	o__Eggerth	f__Eggerth	NA	NA	Filter: bootstrap Score >= 50	
ASV1916	100	100	100	100	99	68	56	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Muriba	g__Duncan	s__Duncaniella_muris		
ASV1917	100	98	98	78	78	9	6	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50	
ASV1918	100	100	100	100	100	46	46	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50	
ASV1919	100	100	100	100	100	100	83	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Aristae	g__Aristae	s__Aristaeella_hokkaidonensis		
ASV1920	100	100	100	100	100	100	92	d__Bacteri	p__Spiroch	c__Spiroch	o__Spiroch	f__Treponi	g__Treponi	s__Treponema_porcinum		
ASV1921	100	100	99	99	72	72	72	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Eubacte	g__Eubacte	s__Eubacterium_coprostanoligenes		
ASV1922	100	100	100	100	100	100	95	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	f__Coprob	g__Sharpea	s__Sharpea_porci		
ASV1923	100	97	95	95	92	37	28	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	f__Erysipe	NA	NA	Filter: bootstrap Score >= 50	
ASV1924	100	99	98	89	89	53	48	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Dorea	NA	Filter: bootstrap Score >= 50	
ASV1925	100	100	100	100	100	52	52	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	g__Dysosm	s__Dysosmobacter_acutus		
ASV1926	100	100	100	100	100	100	44	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	g__Faecali	NA	Filter: bootstrap Score >= 50	
ASV1927	100	100	100	100	98	73	73	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	g__Merdim	s__Merdimmobilis_hominis		
ASV1928	100	100	99	94	84	84	84	d__Bacteri	p__Verruco	c__Verruco	o__Limisp	f__Fontisp	g__Fontisp	s__Fontisphaera_persica		
ASV1929	100	100	98	98	96	39	39	d__Bacteri	p__Actinob	c__Acidimi	o__Acidimi	f__Iamiace	NA	NA	Filter: bootstrap Score >= 50	
ASV1930	100	100	100	98	98	42	16	d__Bacteri	p__Planctd	c__Planctd	o__Planctd	f__Planctd	NA	NA	Filter: bootstrap Score >= 50	
ASV1931	100	63	63	63	63	63	50	d__Bacteri	p__Campyl	c__Epsilon	o__Campyl	f__Helicob	g__Helicob	s__Helicobacter_japonicus		
ASV1932	100	100	100	100	54	37	37	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50	
ASV1933	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Clostrid	g__Clostrid	s__Clostridium_perfringens		
ASV1934	100	99	99	95	78	34	34	d__Bacteri	p__Pseudo	c__Betapro	o__Burkho	f__Sutterel	NA	NA	Filter: bootstrap Score >= 50	
ASV1935	100	100	100	100	100	93	61	d__Bacteri	p__Actinob	c__Actinob	o__Microc	f__Microc	g__Glutam	s__Glutamicibacter_creatinolyticus		
ASV1936	100	100	100	100	100	87	87	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Acetati	s__Acetatifactor_muris		
ASV1937	100	100	100	100	100	90	84	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Butyrici	g__Butyrici	s__Butyricicoccus_pullicaecorum		
ASV1938	100	100	100	100	100	100	84	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Anaerot	g__Anaerot	s__Anaerotignum_lactatifermentans		
ASV1939	100	100	100	100	100	100	100	d__Bacteri	p__Actinob	c__Actinob	o__Microc	f__Microc	g__Kocuria	s__Kocuria_rosea		
ASV1940	100	100	100	100	100	83	80	d__Bacteri	p__Pseudo	c__Betapro	o__Burkho	f__Oxalob	g__Janthin	s__Janthinobacterium_lividum		
ASV1941	100	99	97	97	97	80	39	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Ligilact	NA	Filter: bootstrap Score >= 50	
ASV1942	100	99	99	99	98	97	40	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	NA	Filter: bootstrap Score >= 50	
ASV1943	100	83	83	83	83	9	9	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50	
ASV1944	100	98	77	68	16	8	8	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV1945	100	100	100	100	100	100	100	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Bacter	g__Phocae	s__Phocaeicola_vulgatus		
ASV1946	100	96	96	96	95	69	59	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Muriba	g__Muriba	s__Muribaculum_intestinale		
ASV1948	100	90	90	90	90	90	88	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Muriba	g__Duncan	s__Duncaniella_dubosii		
ASV1949	100	100	100	100	100	100	100	d__Bacteri	p__Actinob	c__Coriobac	o__Coriob	f__Coriobac	g__Collinsi	s__Collinsella_tanakaei		

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ASV1950	100	100	100	100	100	96	26	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	NA	Filter: bootstrap Score >= 50
ASV1951	100	45	45	45	45	45	45	d__Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1952	100	96	96	90	72	39	39	d__Bacteri	p__Pseudo	c__Betapr	o__Burkho	f__Sutterel	NA	NA	Filter: bootstrap Score >= 50
ASV1953	100	92	90	90	84	75	75	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Prevote	g__Alloprev	s__Alloprevotella_rava	
ASV1954	100	83	32	32	17	17	4	d__Bacteri	p__Bacter	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1955	100	72	64	62	55	34	18	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	NA	NA	Filter: bootstrap Score >= 50
ASV1956	100	100	100	100	100	100	100	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Muriba	g__Dunca	s__Duncaniella_muricolitica	
ASV1957	100	100	100	100	100	100	100	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Prevote	g__Segate	s__Segatella_copri	
ASV1958	100	95	92	77	65	48	48	d__Bacteri	p__Bacillo	c__Clostri	o__Eubact	f__	NA	NA	Filter: bootstrap Score >= 50
ASV1959	100	100	39	39	39	5	4	d__Bacteri	p__Bacter	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1960	100	100	90	57	57	44	44	d__Bacteri	p__Bacillo	c__Clostri	o__Christe	f__Christe	NA	NA	Filter: bootstrap Score >= 50
ASV1961	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Clostri	o__Eubact	f__Oscillos	g__Congzl	s__Congzhengia_minquanensis	
ASV1962	100	78	42	42	41	23	12	d__Bacteri	p__Bacillo	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1963	100	100	100	100	100	100	100	d__Bacteri	p__Spiroch	c__Spiroch	o__Spiroch	f__Treponi	g__Treponi	s__Treponema_berlinense	
ASV1964	100	100	100	100	100	45	36	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Prevote	NA	NA	Filter: bootstrap Score >= 50
ASV1965	100	100	100	100	100	87	75	d__Bacteri	p__Actinor	c__Coriob	o__Eggerth	f__Eggerth	g__Paraeg	s__Paraeggerthella_hominis	
ASV1966	100	100	100	97	97	83	83	d__Bacteri	p__Bacillo	c__Clostri	o__Lachno	f__Lachno	g__Acetati	s__Acetatifactor_muris	
ASV1967	100	100	100	100	100	49	37	d__Bacteri	p__Actinor	c__Coriob	o__Eggerth	f__Eggerth	NA	NA	Filter: bootstrap Score >= 50
ASV1968	100	100	100	100	100	54	54	d__Bacteri	p__Bacillo	c__Negativ	o__Selenor	f__Selenor	g__Mitsuo	s__Mitsuokella_jalaludinii	
ASV1969	100	100	100	100	100	100	100	d__Bacteri	p__Spiroch	c__Spiroch	o__Spiroch	f__Treponi	g__Treponi	s__Treponema_saccharophilum	
ASV1970	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Negativ	o__Veillon	f__Veillone	g__Allison	s__Allisonella_histaminiformans	
ASV1971	100	86	85	69	21	15	15	d__Bacteri	p__Pseudo	c__Alphap	o__Rhodo	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1972	100	100	92	67	55	18	18	d__Bacteri	p__Bacillo	c__Clostri	o__Peptos	f__Peptost	NA	NA	Filter: bootstrap Score >= 50
ASV1973	100	93	93	83	83	20	20	d__Bacteri	p__Bacillo	c__Clostri	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1974	100	100	100	100	100	81	81	d__Bacteri	p__Bacillo	c__Clostri	o__Eubact	f__Oscillos	g__Dysosm	s__Dysosmobacter_acutus	
ASV1975	100	100	99	97	61	38	38	d__Bacteri	p__Bacillo	c__Clostri	o__Eubact	f__Acutalit	NA	NA	Filter: bootstrap Score >= 50
ASV1976	100	100	100	99	98	98	73	d__Bacteri	p__Bacillo	c__Clostri	o__Eubact	f__Clostri	g__Clostri	s__Clostridium_jeddahitimonense	
ASV1977	100	100	100	100	99	98	59	d__Bacteri	p__Therm	c__Desulfo	o__Desulfo	f__Desulfo	g__Desulfo	s__Desulfovibrio_simplex	
ASV1978	100	100	100	100	100	97	33	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Ligilact	NA	Filter: bootstrap Score >= 50
ASV1979	100	94	83	70	45	21	21	d__Bacteri	p__Bacillo	c__Clostri	o__Eubact	NA	NA	NA	Filter: bootstrap Score >= 50
ASV1980	100	98	98	98	97	55	55	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Prevote	g__Marseil	s__Marseilla_massiliensis	
ASV1981	100	93	93	93	93	81	60	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Muriba	g__Dunca	s__Duncaniella_dubosii	
ASV1982	100	76	76	76	76	35	19	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Prevote	NA	NA	Filter: bootstrap Score >= 50
ASV1983	100	100	100	100	100	99	99	d__Bacteri	p__Bacillo	c__Clostri	o__Lachno	f__Lachno	g__Fusimo	s__Fusimonas_intestini	
ASV1984	100	100	98	97	97	96	40	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	NA	Filter: bootstrap Score >= 50
ASV1985	100	100	100	100	99	98	39	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	NA	Filter: bootstrap Score >= 50
ASV1986	100	100	100	100	100	100	26	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Bacter	g__Bacter	NA	Filter: bootstrap Score >= 50
ASV1987	100	100	100	100	100	100	100	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Muriba	g__Dunca	s__Duncaniella_freteri	
ASV1988	100	96	96	94	94	61	60	d__Bacteri	p__Bacillo	c__Clostri	o__Lachno	f__Lachno	g__Lachno	s__[Clostridium]_hylemonae	
ASV1989	100	100	100	100	100	100	39	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	NA	Filter: bootstrap Score >= 50
ASV1990	100	100	100	100	100	95	51	d__Bacteri	p__Bacillo	c__Bacilli	o__Bacillal	f__Gemell	g__Gemell	s__Gemella_parahaemolysans	
ASV1991	100	99	99	93	93	5	4	d__Bacteri	p__Bacillo	c__Clostri	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1992	100	93	93	93	93	92	55	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Bacter	g__Bacter	s__Bacteroides_rodentium	
ASV1993	100	100	100	92	92	21	21	d__Bacteri	p__Bacillo	c__Clostri	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1994	100	98	98	98	98	84	4	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Limosil	NA	Filter: bootstrap Score >= 50
ASV1995	100	100	100	100	100	100	36	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Tanner	g__Paraba	NA	Filter: bootstrap Score >= 50
ASV1996	100	100	100	100	95	65	36	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Prevote	g__Segate	NA	Filter: bootstrap Score >= 50
ASV1997	100	100	100	86	86	40	40	d__Bacteri	p__Bacillo	c__Clostri	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV1998	100	98	98	98	98	98	88	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Rikene	g__Alistipe	s__Alistipes_dispar	
ASV1999	100	100	100	100	100	99	99	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Muriba	g__Muriba	s__Muribaculum_gordoncarteri	

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ASV2000	100	100	100	100	100	99	47	d__Bacteri	p__Bacillo	c__Bacilli	o__Bacilla	f__Thermo	g__Therm	NA	Filter: bootstrap Score >= 50
ASV2001	100	99	99	99	99	98	98	d__Bacteri	p__Pseudo	c__Betapro	o__Burkho	f__Sutterel	g__Turicim	s__Turicimonas_muris	
ASV2002	100	80	79	68	68	35	31	d__Bacteri	p__Actinor	c__Coriobac	o__Eggerth	f__Eggerth	NA	NA	Filter: bootstrap Score >= 50
ASV2004	100	100	100	62	45	44	44	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2006	100	100	100	100	100	100	80	d__Bacteri	p__Spiroch	c__Spiroch	o__Spiroch	f__Treponi	g__Treponi	s__Treponema_rectale	
ASV2007	100	100	100	96	96	55	47	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Pseudo	NA	Filter: bootstrap Score >= 50
ASV2008	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Maliibac	g__Maliiba	s__Maliibacterium_massiliense	
ASV2009	100	100	83	83	83	82	82	d__Bacteri	p__Bacillo	c__Negativi	o__Selenc	f__Selenor	g__Schwa	s__Schwartzia_succinivorans	
ASV2010	100	83	83	83	83	83	83	d__Bacteri	p__Spiroch	c__Spiroch	o__Spiroch	f__Treponi	g__Treponi	s__Treponema_bryantii	
ASV2011	100	99	90	90	28	22	22	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2012	100	100	100	98	98	15	15	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV2013	100	100	100	100	100	100	100	d__Bacteri	p__Actinor	c__Coriobac	o__Coriobac	f__Atopobi	g__Parafa	s__Parafannyhessea_umbonata	
ASV2014	100	100	100	99	59	57	42	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteroi	f__Tannere	g__Paraba	NA	Filter: bootstrap Score >= 50
ASV2015	100	100	100	100	100	100	90	d__Bacteri	p__Verruco	c__Verrucc	o__Verrucc	f__Akkerm	g__Akkerm	s__Akkermansia_glycaniphila	
ASV2016	100	100	100	100	100	92	91	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	g__Oscillib	s__Oscillibacter_valericigenes	
ASV2017	100	100	100	100	100	100	38	d__Bacteri	p__Actinor	c__Coriobac	o__Coriobac	f__Atopobi	g__Olsene	NA	Filter: bootstrap Score >= 50
ASV2018	100	100	100	100	100	99	89	d__Bacteri	p__Spiroch	c__Spiroch	o__Spiroch	f__Treponi	g__Treponi	s__Treponema_bryantii	
ASV2019	100	100	99	95	51	48	25	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteroi	f__Tannere	NA	NA	Filter: bootstrap Score >= 50
ASV2020	100	100	100	100	100	70	70	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteroi	f__Muribac	g__Duncan	s__Duncaniella_muris	
ASV2021	100	100	100	100	98	50	46	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteroi	f__Prevote	g__Prevot	NA	Filter: bootstrap Score >= 50
ASV2022	100	100	100	100	100	71	71	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	g__Dysosm	s__Dysosmobacter_acutus	
ASV2023	100	88	87	87	87	87	74	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	f__Turicib	g__Turicib	s__Turicibacter_bilis	
ASV2024	100	99	66	56	40	39	33	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2025	100	100	100	100	100	100	30	d__Bacteri	p__Spiroch	c__Spiroch	o__Spiroch	f__Treponi	g__Treponi	NA	Filter: bootstrap Score >= 50
ASV2026	100	100	100	100	100	100	100	d__Bacteri	p__Fibroba	c__Fibroba	o__Fibroba	f__Fibroba	g__Hallere	s__Hallerella_porci	
ASV2027	100	100	100	99	93	93	93	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Clostrid	g__Clostri	s__Clostridium_bornimense	
ASV2028	100	94	91	89	33	33	33	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2029	100	100	100	97	97	45	44	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV2030	100	100	100	100	95	52	52	d__Bacteri	p__Pseudo	c__Alphapr	o__Hyphor	f__Methyl	g__Methyl	s__Methylosinus_trichosporium	
ASV2031	100	42	42	38	38	38	38	d__Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2032	100	9	8	8	8	8	8	d__Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2033	100	99	99	99	92	72	54	d__Bacteri	p__Verruco	c__Verrucc	o__Verrucc	f__Verrucc	g__Roseib	s__Roseibacillus_ponti	
ASV2035	100	100	100	100	100	100	100	d__Bacteri	p__Chloro	c__Tepidifi	o__Tepidifi	f__Tepidifo	g__Tepidifi	s__Tepidiforma_bonchosmolovskayae	
ASV2036	100	100	100	100	98	15	14	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteroi	f__Prevote	NA	NA	Filter: bootstrap Score >= 50
ASV2037	100	100	100	100	100	64	64	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Butyricic	g__Intestin	s__Intestinibacillus_massiliensis	
ASV2038	100	92	88	88	86	24	24	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	f__Erysipe	NA	NA	Filter: bootstrap Score >= 50
ASV2039	100	99	99	96	90	23	23	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV2040	100	100	100	100	100	100	99	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteroi	f__Muribac	g__Duncan	s__Duncaniella_muris	
ASV2041	100	95	95	95	95	95	87	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteroi	f__Rikenel	g__Alistipe	s__Alistipes_dispar	
ASV2042	100	99	99	91	91	20	20	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV2043	100	68	68	68	68	68	68	d__Bacteri	p__Pseudo	c__Betapro	o__Burkho	f__Sutterel	g__Turicim	s__Turicimonas_muris	
ASV2044	100	100	100	100	100	93	93	d__Bacteri	p__Pseudo	c__Betapro	o__Burkho	f__Comam	g__Comam	s__Comamonas_antarctica	
ASV2045	100	100	100	100	100	100	47	d__Bacteri	p__Pseudo	c__Gammo	o__Lysoba	f__Lysoba	g__Stenot	NA	Filter: bootstrap Score >= 50
ASV2046	100	100	100	100	100	100	49	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	NA	Filter: bootstrap Score >= 50
ASV2047	100	100	100	100	100	100	57	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	s__Lactobacillus_gasseri	
ASV2048	100	87	87	87	87	87	38	d__Bacteri	p__Campy	c__Epsilon	o__Campy	f__Helicob	g__Helicob	NA	Filter: bootstrap Score >= 50
ASV2049	100	100	100	98	98	62	62	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Lachno	s__[Clostridium]_scindens	
ASV2050	100	97	97	97	97	97	52	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteroi	f__Bacteroi	g__Bacter	s__Bacteroides_acidifaciens	
ASV2051	100	20	20	20	20	20	20	d__Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2052	100	99	99	99	98	64	41	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteroi	f__Muribac	g__Duncan	NA	Filter: bootstrap Score >= 50

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ASV2053	100	82	82	80	74	13	13	d_Bacteri	p_Bacillot	c_Clostrid	o_Eubacte	f_Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV2054	100	76	72	67	59	9	9	d_Bacteri	p_Bacillot	c_Clostrid	o_Eubacte	f_Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV2055	100	97	97	97	97	97	97	d_Bacteri	p_Bacteroi	c_Bacteroi	o_Bacteroi	f_Muribac	g_Duncan	s_Duncaniella_dubosii	
ASV2056	100	97	97	97	97	60	56	d_Bacteri	p_Bacteroi	c_Bacteroi	o_Bacteroi	f_Bacteroi	g_Phocae	s_Phocaeicola_massiliensis	
ASV2057	100	100	100	100	98	50	50	d_Bacteri	p_Bacillot	c_Clostrid	o_Eubacte	f_Oscillos	g_Ethanoli	s_Ethanoligenens_harbinense	
ASV2058	100	100	100	100	100	77	77	d_Bacteri	p_Bacillot	c_Clostrid	o_Eubacte	f_Oscillos	g_Angelak	s_Angelakisella_massiliensis	
ASV2059	100	87	87	87	60	60	38	d_Bacteri	p_Actinom	c_Actinom	o_Propioni	f_Propioni	g_Microlu	NA	Filter: bootstrap Score >= 50
ASV2060	100	90	90	90	90	90	58	d_Bacteri	p_Campyl	c_Epsilon	o_Campyl	f_Helicob	g_Helicob	s_Helicobacter_ganmani	
ASV2061	100	100	100	100	100	100	83	d_Bacteri	p_Bacillot	c_Bacilli	o_Lactoba	f_Lactoba	g_Limosil	s_Limosilactobacillus_reuteri	
ASV2062	100	100	100	100	99	99	99	d_Bacteri	p_Bacteroi	c_Bacteroi	o_Bacteroi	f_Muribac	g_Muribac	s_Muribaculum_intestinale	
ASV2063	100	54	54	54	54	54	53	d_Bacteri	p_Bacillot	c_Erysipel	o_Erysipel	f_Coprobi	g_Thomas	s_Thomasclavelia_cocleata	
ASV2064	100	100	100	100	100	100	57	d_Bacteri	p_Bacillot	c_Erysipel	o_Erysipel	f_Coprobi	g_Thomas	s_Thomasclavelia_saccharogumia	
ASV2065	100	96	96	96	96	96	63	d_Bacteri	p_Campyl	c_Epsilon	o_Campyl	f_Helicob	g_Helicob	s_Helicobacter_ganmani	
ASV2066	100	100	100	100	100	100	33	d_Bacteri	p_Bacillot	c_Bacilli	o_Lactoba	f_Lactoba	g_Lactob	NA	Filter: bootstrap Score >= 50
ASV2067	100	100	71	71	66	23	23	d_Bacteri	p_Bacillot	c_Erysipel	o_Erysipel	f_Coprobi	NA	NA	Filter: bootstrap Score >= 50
ASV2068	100	75	66	66	62	9	5	d_Bacteri	p_Thermo	c_Desulfo	o_Desulfo	f_Desulfo	NA	NA	Filter: bootstrap Score >= 50
ASV2069	100	100	100	100	100	100	28	d_Bacteri	p_Bacillot	c_Bacilli	o_Lactoba	f_Lactoba	g_Lactob	NA	Filter: bootstrap Score >= 50
ASV2070	100	80	78	72	44	12	11	d_Bacteri	p_Bacteroi	c_Bacteroi	o_Bacteroi	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2071	100	100	100	100	100	96	60	d_Bacteri	p_Bacillot	c_Bacilli	o_Bacillal	f_Bacillac	g_Lederb	s_Lederbergia_ruris	
ASV2072	100	98	85	28	18	15	3	d_Bacteri	p_Bacillot	c_Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2073	100	100	100	100	100	100	64	d_Bacteri	p_Bacillot	c_Bacilli	o_Lactoba	f_Lactoba	g_Ligilact	s_Ligilactobacillus_apodemi	
ASV2074	100	100	88	86	34	18	18	d_Bacteri	p_Bacteroi	c_Bacteroi	o_Bacteroi	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2075	100	53	53	50	50	24	20	d_Bacteri	p_Bacillot	c_Clostrid	o_Lachnos	f_Lachnos	NA	NA	Filter: bootstrap Score >= 50
ASV2076	100	100	100	100	100	35	35	d_Bacteri	p_Actinom	c_Actinom	o_Mycobac	f_Mycoba	NA	NA	Filter: bootstrap Score >= 50
ASV2077	100	100	97	79	79	53	53	d_Bacteri	p_Bacillot	c_Clostrid	o_Lachnos	f_Lachnos	g_Marvini	s_Marvinbryantia_formatexigens	
ASV2078	100	100	100	34	34	34	27	d_Bacteri	p_Bacillot	c_Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2079	100	100	100	100	100	100	89	d_Bacteri	p_Pseudo	c_Gammap	o_Lysobac	f_Lysoba	g_Stenotr	s_Stenotrophomonas_maltophilia	
ASV2080	100	95	90	65	65	57	57	d_Bacteri	p_Bacillot	c_Clostrid	o_Christe	f_Christe	g_Guopin	s_Guopingia_tenuis	
ASV2081	100	100	52	52	52	22	1	d_Bacteri	p_Bacillot	c_Bacilli	o_Lactoba	f_Lactoba	NA	NA	Filter: bootstrap Score >= 50
ASV2083	100	100	100	100	100	100	61	d_Bacteri	p_Bacteroi	c_Bacteroi	o_Bacteroi	f_Bacteroi	g_Bacteroi	s_Bacteroides_acidifaciens	
ASV2084	100	98	94	17	17	14	14	d_Bacteri	p_Bacillot	c_Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2085	100	100	96	83	80	77	72	d_Bacteri	p_Bacillot	c_Clostrid	o_Peptostr	f_Peptostr	g_Romboi	s_Romboutsia_timonensis	
ASV2086	100	100	100	100	99	96	30	d_Bacteri	p_Bacillot	c_Clostrid	o_Peptostr	f_Peptostr	g_Terrisp	NA	Filter: bootstrap Score >= 50
ASV2087	100	69	49	49	48	4	4	d_Bacteri	p_Bacillot	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2088	100	98	98	98	98	98	95	d_Bacteri	p_Bacteroi	c_Bacteroi	o_Bacteroi	f_Prevotel	g_Segatel	s_Segatella_hominis	
ASV2089	100	100	100	100	100	100	100	d_Bacteri	p_Actinom	c_Coriobac	o_Coriobac	f_Atopobi	g_Tractid	s_Tractidigestivibacter_scatoligenes	
ASV2090	100	100	100	85	85	30	30	d_Bacteri	p_Bacillot	c_Clostrid	o_Lachnos	f_Lachnos	NA	NA	Filter: bootstrap Score >= 50
ASV2091	100	100	100	100	100	57	57	d_Bacteri	p_Bacillot	c_Negativi	o_Selenom	f_Selenom	g_Mitsuok	s_Mitsuokella_jalaludinii	
ASV2092	100	70	67	67	67	67	60	d_Bacteri	p_Bacillot	c_Erysipel	o_Erysipel	f_Turiciba	g_Turicib	s_Turicibacter_bilis	
ASV2093	100	93	88	82	71	35	35	d_Bacteri	p_Bacillot	c_Clostrid	o_Eubacte	f_Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV2094	100	100	100	100	100	100	100	d_Bacteri	p_Bacteroi	c_Bacteroi	o_Bacteroi	f_Bacteroi	g_Bacteroi	s_Bacteroides_togonis	
ASV2095	100	100	100	100	89	59	59	d_Bacteri	p_Bacteroi	c_Bacteroi	o_Bacteroi	f_Muribac	g_Paramu	s_Paramuribaculum_intestinale	
ASV2097	100	80	80	80	80	77	48	d_Bacteri	p_Bacillot	c_Bacilli	o_Lactoba	f_Lactoba	g_Ligilact	NA	Filter: bootstrap Score >= 50
ASV2098	100	93	93	93	87	74	64	d_Bacteri	p_Bacteroi	c_Bacteroi	o_Bacteroi	f_Muribac	g_Duncan	s_Duncaniella_dubosii	
ASV2099	100	100	99	70	70	12	12	d_Bacteri	p_Bacillot	c_Clostrid	o_Lachnos	f_Lachnos	NA	NA	Filter: bootstrap Score >= 50
ASV2100	100	98	54	54	54	28	28	d_Bacteri	p_Bacillot	c_Clostrid	o_Lachnos	f_Lachnos	NA	NA	Filter: bootstrap Score >= 50
ASV2101	100	98	97	69	69	4	4	d_Bacteri	p_Bacillot	c_Clostrid	o_Lachnos	f_Lachnos	NA	NA	Filter: bootstrap Score >= 50
ASV2102	100	100	100	100	100	99	31	d_Bacteri	p_Bacillot	c_Bacilli	o_Lactoba	f_Lactoba	g_Lactob	NA	Filter: bootstrap Score >= 50
ASV2103	100	100	100	100	100	91	60	d_Bacteri	p_Pseudo	c_Betapro	o_Neisser	f_Neisser	g_Neisse	s_Neisseria_dentiae	
ASV2104	100	99	99	99	99	99	99	d_Bacteri	p_Deferri	c_Deferri	o_Deferri	f_Mucisp	g_Mucisp	s_Mucispirillum_schaedleri	

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ASV2105	100	100	100	100	100	96	69	d__Bacteri	p__Pseudo	c__Gamm	o__Pasteu	f__Pasteu	g__Roden	s__Rodentibacter_ratti		
ASV2106	100	100	100	100	100	100	49	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Bacter	g__Phoca	NA	Filter: bootstrap Score >= 50	
ASV2107	100	100	100	100	100	100	96	d__Bacteri	p__Pseudo	c__Gamm	o__Aerom	f__Succini	g__Anaero	s__Anaerobiospirillum_succiniciproducens		
ASV2108	100	92	92	92	92	92	86	d__Bacteri	p__Therm	c__Desulfo	o__Desulfo	f__Desulfo	g__Desulfo	s__Desulfovibrio_porci		
ASV2109	100	100	99	99	76	52	52	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Muriba	g__Hemin	s__Heminiphilus_faecis		
ASV2110	100	98	94	24	24	24	24	d__Bacteri	p__Bacillo	c__Clostri	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV2111	100	99	99	99	99	95	39	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Ligilact	NA	Filter: bootstrap Score >= 50	
ASV2112	100	95	88	10	10	8	8	d__Bacteri	p__Bacillo	c__Clostri	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV2113	100	100	99	99	99	98	44	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	NA	Filter: bootstrap Score >= 50	
ASV2114	100	54	54	54	54	54	35	d__Bacteri	p__Campy	c__Epsilon	o__Campy	f__Helicob	g__Helicot	NA	Filter: bootstrap Score >= 50	
ASV2115	100	100	100	100	100	98	16	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Limosil	NA	Filter: bootstrap Score >= 50	
ASV2116	100	100	100	100	99	31	20	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Prevote	NA	NA	Filter: bootstrap Score >= 50	
ASV2117	100	100	100	100	96	92	52	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Bacter	g__Bacter	s__Bacteroides_clarus		
ASV2118	100	100	100	100	100	100	59	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	s__Lactobacillus_taiwanensis		
ASV2119	100	100	100	77	77	13	10	d__Bacteri	p__Bacillo	c__Clostri	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50	
ASV2120	100	100	99	99	99	99	46	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	NA	Filter: bootstrap Score >= 50	
ASV2121	100	100	100	100	73	30	30	d__Bacteri	p__Bacillo	c__Clostri	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50	
ASV2122	100	100	100	100	100	100	93	d__Bacteri	p__Bacillo	c__Bacilli	o__Bacilla	f__Staphyl	g__Staphy	s__Staphylococcus_aureus		
ASV2123	100	100	100	100	63	37	31	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Prevote	NA	NA	Filter: bootstrap Score >= 50	
ASV2124	100	100	54	54	54	52	12	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Limosil	NA	Filter: bootstrap Score >= 50	
ASV2125	100	100	100	83	83	32	32	d__Bacteri	p__Bacillo	c__Clostri	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50	
ASV2126	100	100	98	92	92	11	11	d__Bacteri	p__Bacillo	c__Clostri	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50	
ASV2127	100	100	100	100	78	78	45	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Tanner	g__Paraba	NA	Filter: bootstrap Score >= 50	
ASV2128	100	70	15	14	6	5	5	d__Bacteri	p__Bacillo	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV2129	100	84	81	48	45	7	7	d__Bacteri	p__Bacillo	c__Clostri	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV2131	100	100	100	100	100	100	100	d__Bacteri	p__Deferri	c__Deferri	o__Deferri	f__Mucisp	g__Mucisp	s__Mucispirillum_schaedleri		
ASV2132	100	100	100	100	100	62	34	d__Bacteri	p__Pseudo	c__Gamm	o__Pseudo	f__Pseudo	g__Pseud	NA	Filter: bootstrap Score >= 50	
ASV2133	100	100	100	36	30	27	27	d__Bacteri	p__Pseudo	c__Alphap	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV2134	100	95	76	62	35	22	22	d__Bacteri	p__Bacillo	c__Clostri	o__Eubact	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV2135	100	100	100	100	91	91	91	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Muriba	g__Muriba	s__Muribaculum_intestinale		
ASV2136	100	80	80	80	80	76	19	d__Bacteri	p__Bacillo	c__Bacilli	o__Bacilla	f__Paenib	g__Brevib	NA	Filter: bootstrap Score >= 50	
ASV2137	100	100	100	100	100	100	100	d__Bacteri	p__Therm	c__Desulfo	o__Desulfo	f__Desulfo	g__Lawso	s__Lawsonia_intracellularis		
ASV2138	100	81	44	44	42	33	26	d__Bacteri	p__Bacillo	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV2139	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Bacilli	o__Bacilla	f__Thermo	g__Kroppe	s__Kroppenstedtia_sanguinis		
ASV2140	100	100	100	100	68	42	40	d__Bacteri	p__Bacillo	c__Clostri	o__Eubact	f__	NA	NA	Filter: bootstrap Score >= 50	
ASV2141	100	100	100	99	99	49	49	d__Bacteri	p__Bacillo	c__Clostri	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50	
ASV2142	100	100	99	70	70	40	35	d__Bacteri	p__Bacillo	c__Clostri	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50	
ASV2143	100	94	81	30	14	14	11	d__Bacteri	p__Bacillo	c__Clostri	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV2144	100	100	86	86	86	86	24	d__Bacteri	p__Bacillo	c__Bacilli	o__Bacilla	f__Staphyl	g__Staphy	NA	Filter: bootstrap Score >= 50	
ASV2145	100	100	100	100	100	98	95	d__Bacteri	p__Pseudo	c__Gamm	o__Pseudo	f__Pseudo	g__Pseud	s__Pseudomonas_putida		
ASV2146	100	100	100	100	98	98	98	d__Bacteri	p__Bacillo	c__Bacilli	o__Bacilla	f__Bacilla	g__Lysinib	s__Lysinibacillus_sphaericus		
ASV2147	100	100	100	100	100	100	63	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	f__Coprob	g__Thoma	s__Thomasclavelia_saccharogumia		
ASV2148	100	94	94	94	94	94	17	d__Bacteri	p__Campy	c__Epsilon	o__Campy	f__Helicob	g__Helicot	NA	Filter: bootstrap Score >= 50	
ASV2149	100	100	100	100	100	100	45	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Rikene	g__Alistipe	NA	Filter: bootstrap Score >= 50	
ASV2150	100	100	100	100	98	70	55	d__Bacteri	p__Actino	c__Actino	o__Microc	f__Ornithin	g__Ornithi	s__Ornithinimicrobium_kibberense		
ASV2151	100	98	98	98	96	19	19	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Prevote	NA	NA	Filter: bootstrap Score >= 50	
ASV2153	100	100	95	95	25	25	25	d__Bacteri	p__Bacillo	c__Clostri	o__Eubact	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV2154	100	100	99	99	96	75	75	d__Bacteri	p__Bacillo	c__Clostri	o__Eubact	f__Oscillos	g__Bittarel	s__Bittarella_massiliensis		
ASV2155	100	97	97	96	96	95	76	d__Bacteri	p__Actino	c__Coriob	o__Eggert	f__Eggerth	g__Raoult	s__Raoultibacter_timonensis		
ASV2156	100	100	100	67	52	14	5	d__Bacteri	p__Bacillo	c__Clostri	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50	

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ASV2157	100	100	100	99	95	95	57	d_Bacteri	p_Bacillot	c_Clostrid	o_Lachnc	f_Anaero	g_Anaero	s_Anaerotignum_faecicola		
ASV2158	100	100	100	100	100	100	74	d_Bacteri	p_Actinor	c_Coriobi	o_Coriob	f_Coriobа	g_Senegi	s_Senegalimassilia_anaerobia		
ASV2160	100	100	89	85	33	27	24	d_Bacteri	p_Bacteri	c_Bacteri	o_Bacteri	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV2161	100	100	99	99	57	57	50	d_Bacteri	p_Bacillot	c_Clostrid	o_Eubact	f_Aristae	g_Aristae	s_Aristaeella_lactis		
ASV2162	100	32	15	14	6	6	4	d_Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV2163	100	91	91	91	91	91	74	d_Bacteri	p_Bacillot	c_Erysipe	o_Erysipe	f_Turiciba	g_Turicib	s_Turicibacter_bilis		
ASV2166	100	100	100	100	89	72	72	d_Bacteri	p_Bacteri	c_Bacteri	o_Bacteri	f_Muribac	g_Paramu	s_Paramuribaculum_intestinale		
ASV2167	100	95	95	95	95	95	44	d_Bacteri	p_Bacillot	c_Bacilli	o_Lactob	f_Lactoba	g_Lactob	NA	Filter: bootstrap Score >= 50	
ASV2168	100	100	100	100	99	98	92	d_Bacteri	p_Bacillot	c_Clostrid	o_Peptos	f_Peptost	g_Rombo	s_Romboutsia_timonensis		
ASV2169	100	67	41	41	15	8	6	d_Bacteri	p_Bacillot	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV2170	100	100	100	100	71	47	43	d_Bacteri	p_Bacteri	c_Bacteri	o_Bacteri	f_Prevote	NA	NA	Filter: bootstrap Score >= 50	
ASV2171	100	98	98	98	98	98	98	d_Bacteri	p_Spirocl	c_Spirocl	o_Spirocl	f_Treponi	g_Treponi	s_Treponema_bryantii		
ASV2172	100	100	100	100	44	25	21	d_Bacteri	p_Bacillot	c_Clostrid	o_Eubact	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV2173	100	100	100	92	89	9	9	d_Bacteri	p_Bacillot	c_Clostrid	o_Lachnc	f_Lachno	NA	NA	Filter: bootstrap Score >= 50	
ASV2174	100	51	50	50	50	50	13	d_Bacteri	p_Bacillot	c_Bacilli	o_Lactob	f_Lactoba	g_Limosil	NA	Filter: bootstrap Score >= 50	
ASV2175	100	100	99	99	99	63	34	d_Bacteri	p_Actinor	c_Acidimi	o_Acidim	f_Iamiace	g_Rhabd	NA	Filter: bootstrap Score >= 50	
ASV2176	100	12	12	12	11	9	4	d_Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV2177	100	100	100	100	100	76	76	d_Bacteri	p_Acidob	c_Vicinan	o_Vicinan	f_Vicinan	g_Luteita	s_Luteitalea_pratensis		
ASV2178	100	100	100	100	100	100	100	d_Bacteri	p_Actinor	c_Actinor	o_Propior	f_Propior	g_Microlu	s_Microlunatus_phosphovorus		
ASV2179	100	100	100	95	95	65	65	d_Bacteri	p_Pseudo	c_Betapro	o_Rhodo	f_Rhodoc	g_Rhodo	s_Rhodocyclus_gracilis		
ASV2180	100	100	100	100	100	53	53	d_Bacteri	p_Planctc	c_Planctc	o_Planctc	f_Planctc	g_Planctc	s_Planctomicrobium_piriforme		
ASV2181	100	100	100	100	92	63	38	d_Bacteri	p_Pseudo	c_Alphapi	o_Rhodo	f_Paracc	g_Gemm	NA	Filter: bootstrap Score >= 50	
ASV2184	100	9	8	8	8	5	4	d_Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV2185	100	38	16	9	8	7	7	d_Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV2187	100	100	100	98	48	24	15	d_Bacteri	p_Bacteri	c_Bacteri	o_Bacteri	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV2188	100	90	90	90	90	90	90	d_Bacteri	p_Bacteri	c_Bacteri	o_Bacteri	f_Muribac	g_Sangei	s_Sangeribacter_muris		
ASV2189	100	94	94	94	94	94	94	d_Bacteri	p_Bacteri	c_Bacteri	o_Bacteri	f_Muribac	g_Sangei	s_Sangeribacter_muris		
ASV2190	100	100	100	100	100	99	25	d_Bacteri	p_Actinor	c_Actinor	o_Microc	f_Micrоc	g_Kocuri	NA	Filter: bootstrap Score >= 50	
ASV2191	100	99	93	38	17	17	5	d_Bacteri	p_Bacillot	c_Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV2192	100	100	100	100	100	100	99	d_Bacteri	p_Bacteri	c_Bacteri	o_Bacteri	f_Rikene	g_Alistipe	s_Alistipes_communis		
ASV2193	100	79	78	74	62	56	56	d_Bacteri	p_Bacillot	c_Clostrid	o_Eubact	f	g_Colidex	s_Colidextribacter_massiliensis		
ASV2194	100	100	100	100	100	100	49	d_Bacteri	p_Bacteri	c_Cytophi	o_Cytoph	f_Hymen	g_Rufiba	NA	Filter: bootstrap Score >= 50	
ASV2195	100	100	100	100	100	88	65	d_Bacteri	p_Bacteri	c_Cytophi	o_Cytoph	f_Hymen	g_Rufiba	s_Rufibacter_glacialis		
ASV2196	100	89	66	66	64	13	13	d_Bacteri	p_Bacillot	c_Erysipe	o_Erysipe	f_Erysipe	NA	NA	Filter: bootstrap Score >= 50	
ASV2197	100	100	100	100	100	98	67	d_Bacteri	p_Pseudo	c_Alphapi	o_Hyphor	f_Methyl	g_Microv	s_Microvirga_antarctica		
ASV2198	100	100	100	100	100	100	79	d_Bacteri	p_Pseudo	c_Alphapi	o_Sphing	f_Sphing	g_Sphing	s_Sphingomonas_ginsengisoli		
ASV2199	100	99	99	98	98	53	34	d_Bacteri	p_Bacillot	c_Bacilli	o_Lactob	f_Lactoba	g_Ligilact	NA	Filter: bootstrap Score >= 50	
ASV2200	100	100	100	100	75	74	28	d_Bacteri	p_Bacteri	c_Bacteri	o_Bacteri	f_Bacteri	g_Bacteri	NA	Filter: bootstrap Score >= 50	
ASV2201	100	59	58	58	55	26	26	d_Bacteri	p_Bacteri	c_Bacteri	o_Bacteri	f_Muribac	NA	NA	Filter: bootstrap Score >= 50	
ASV2202	100	98	98	98	98	79	51	d_Bacteri	p_Bacteri	c_Bacteri	o_Bacteri	f_Bacteri	g_Phoca	s_Phocaeicola_dorei		
ASV2203	100	93	93	93	93	93	19	d_Bacteri	p_Campyl	c_Epsilon	o_Campyl	f_Helicob	g_Helicob	NA	Filter: bootstrap Score >= 50	
ASV2204	100	100	100	100	100	99	59	d_Bacteri	p_Bacteri	c_Bacteri	o_Bacteri	f_Bacteri	g_Phoca	s_Phocaeicola_vulgatus		
ASV2205	100	67	66	66	60	27	27	d_Bacteri	p_Bacteri	c_Bacteri	o_Bacteri	f_Muribac	NA	NA	Filter: bootstrap Score >= 50	
ASV2206	100	99	91	91	89	85	63	d_Bacteri	p_Bacillot	c_Bacilli	o_Lactob	f_Lactoba	g_Ligilact	s_Ligilactobacillus_apodemi		
ASV2207	100	100	100	100	100	81	40	d_Bacteri	p_Bacillot	c_Bacilli	o_Lactob	f_Lactoba	g_Lactob	NA	Filter: bootstrap Score >= 50	
ASV2208	100	98	98	98	98	98	98	d_Bacteri	p_Bacteri	c_Bacteri	o_Bacteri	f_Muribac	g_Dunca	s_Duncaniella_freteri		
ASV2209	100	100	46	45	44	25	25	d_Bacteri	p_Bacillot	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50	
ASV2210	100	61	61	61	61	60	24	d_Bacteri	p_Bacillot	c_Bacilli	o_Lactob	f_Lactoba	g_Lactob	NA	Filter: bootstrap Score >= 50	
ASV2211	100	100	86	86	86	86	35	d_Bacteri	p_Bacillot	c_Bacilli	o_Lactob	f_Lactoba	g_Lactob	NA	Filter: bootstrap Score >= 50	
ASV2212	100	69	69	69	69	69	32	d_Bacteri	p_Bacillot	c_Bacilli	o_Lactob	f_Lactoba	g_Lactob	NA	Filter: bootstrap Score >= 50	

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ASV2213	100	100	100	92	80	29	28	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV2214	100	100	99	99	99	98	43	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	NA	Filter: bootstrap Score >= 50
ASV2215	100	100	100	100	100	100	100	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	g__Dunca	s__Duncaniella_muricolitica	
ASV2216	100	100	100	100	100	100	66	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Bacterd	g__Bacter	s__Bacteroides_acidifaciens	
ASV2217	100	100	100	79	79	60	59	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Lachno	s__[Clostridium]_scindens	
ASV2218	100	100	100	100	100	100	100	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	g__Dunca	s__Duncaniella_muris	
ASV2219	100	100	100	100	100	100	100	d__Bacteri	p__Chlamy	c__Chlamy	o__Chlamy	f__Chlamy	g__Chlamy	s__Chlamydia_muridarum	
ASV2220	100	99	99	99	99	99	38	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	NA	Filter: bootstrap Score >= 50
ASV2221	100	100	100	73	58	54	54	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__	g__Flintiba	s__Flintibacter_butyricus	
ASV2222	100	100	99	99	97	34	25	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	NA	NA	Filter: bootstrap Score >= 50
ASV2224	100	72	71	71	71	67	67	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	g__Muriba	s__Muribaculum_gordoncarteri	
ASV2225	100	88	73	73	73	62	59	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	f__Erysipe	g__Breznia	s__Breznakia_blatticola	
ASV2227	100	100	99	99	99	99	26	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	NA	Filter: bootstrap Score >= 50
ASV2228	100	32	25	21	21	21	18	d__Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2229	100	100	98	98	98	74	37	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	f__Erysipe	g__Amedil	NA	Filter: bootstrap Score >= 50
ASV2230	100	100	100	100	99	93	84	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	g__Dunca	s__Duncaniella_dubosii	
ASV2231	100	86	85	83	83	32	32	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV2232	100	64	64	61	59	53	45	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Oscillos	g__Anaero	NA	Filter: bootstrap Score >= 50
ASV2233	100	50	50	50	49	11	9	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2234	100	77	77	77	77	77	69	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Rikenel	g__Alistipe	s__Alistipes_dispar	
ASV2235	100	100	100	100	100	99	46	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Ligilact	NA	Filter: bootstrap Score >= 50
ASV2236	100	97	97	96	96	38	38	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV2237	100	91	37	37	36	24	23	d__Bacteri	p__Bacillo	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2238	100	100	100	100	100	97	51	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	s__Lactobacillus_paragasseri	
ASV2239	100	96	95	79	79	47	37	d__Bacteri	p__Actinor	c__Coriobac	o__Eggerth	f__Eggerth	NA	NA	Filter: bootstrap Score >= 50
ASV2240	100	100	100	100	100	100	63	d__Bacteri	p__Actinor	c__Actinom	o__Mycobc	f__Corynet	g__Corynet	s__Corynebacterium_mastitidis	
ASV2241	100	100	100	100	100	95	95	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	g__Muriba	s__Muribaculum_intestinale	
ASV2242	100	90	88	87	87	76	24	d__Bacteri	p__Actinor	c__Coriobac	o__Eggerth	f__Eggerth	g__Adlercr	NA	Filter: bootstrap Score >= 50
ASV2243	100	97	81	81	79	77	77	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Oscillos	g__	s__[Clostridium]_viride	
ASV2244	100	100	100	100	99	86	86	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	g__Dunca	s__Duncaniella_freteri	
ASV2245	100	100	97	90	90	31	31	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV2246	100	100	100	100	100	56	56	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Murico	s__Muricomes_intestini	
ASV2247	100	100	100	100	100	61	13	d__Bacteri	p__Pseudo	c__Betapro	o__Burkho	f__Oxalob	g__Pseudo	NA	Filter: bootstrap Score >= 50
ASV2248	100	70	69	69	52	48	48	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Prevote	NA	NA	Filter: bootstrap Score >= 50
ASV2249	100	81	81	80	55	40	40	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Prevote	NA	NA	Filter: bootstrap Score >= 50
ASV2250	100	96	96	96	94	94	6	d__Bacteri	p__Bacillo	c__Bacilli	o__Bacilla	f__Staphyl	g__Staphy	NA	Filter: bootstrap Score >= 50
ASV2252	100	100	100	100	100	100	97	d__Bacteri	p__Campy	c__Epsilon	o__Campy	f__Helicob	g__Helicot	s__Helicobacter_typhlonius	
ASV2253	100	100	100	100	100	100	58	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Rikenel	g__Alistipe	s__Alistipes_dispar	
ASV2255	100	100	97	97	97	91	28	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Limosil	NA	Filter: bootstrap Score >= 50
ASV2256	100	90	90	81	73	7	5	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV2257	100	100	92	76	76	29	29	d__Bacteri	p__Bacillo	c__Clostrid	o__Christe	f__Christe	NA	NA	Filter: bootstrap Score >= 50
ASV2258	100	100	100	100	100	72	34	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	g__Dunca	NA	Filter: bootstrap Score >= 50
ASV2259	100	90	86	86	86	85	55	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Ligilact	s__Ligilactobacillus_apodemi	
ASV2260	100	100	100	99	99	99	99	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Schaed	s__Schaedlerella_arabinosiphila	
ASV2261	100	100	100	100	65	65	65	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	g__Dunca	s__Duncaniella_muricolitica	
ASV2263	100	96	96	96	96	95	8	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Limosil	NA	Filter: bootstrap Score >= 50
ASV2264	100	100	100	100	100	100	98	d__Bacteri	p__Campy	c__Epsilon	o__Campy	f__Helicob	g__Helicot	s__Helicobacter_typhlonius	
ASV2266	100	100	100	100	99	91	29	d__Bacteri	p__Actinor	c__Actinom	o__Microc	f__Cellulo	g__Cellulo	NA	Filter: bootstrap Score >= 50
ASV2267	100	95	95	86	86	17	17	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV2268	100	100	100	100	100	100	90	d__Bacteri	p__Pseudo	c__Alphapr	o__Hyphom	f__Boseac	g__Bosea	s__Bosea_thiooxidans	

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ASV2269	100	90	90	82	80	31	31	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV2271	100	45	45	45	45	45	45	d__Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2272	100	100	100	100	100	100	77	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Ligilact	s__Ligilactobacillus_apodemi	
ASV2273	100	97	87	30	30	14	14	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2274	100	100	100	78	69	3	3	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV2275	100	100	100	95	95	38	38	d__Bacteri	p__Bacillo	c__Clostrid	o__Christe	f__Christe	NA	NA	Filter: bootstrap Score >= 50
ASV2276	100	90	76	76	76	76	66	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	f__Turiciba	g__Turicib	s__Turicibacter_bilis	
ASV2277	100	96	74	60	29	14	14	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2278	100	100	100	100	100	100	39	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Bacterd	g__Bacter	NA	Filter: bootstrap Score >= 50
ASV2279	100	100	100	100	100	97	55	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachno	g__Anaero	s__Anaerobutyricum_hallii	
ASV2280	100	100	86	86	86	86	75	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	f__Turiciba	g__Turicib	s__Turicibacter_bilis	
ASV2281	100	100	97	97	94	94	78	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	f__Turiciba	g__Turicib	s__Turicibacter_bilis	
ASV2282	100	100	98	83	83	34	5	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV2283	100	100	100	100	99	97	96	d__Bacteri	p__Bacillo	c__Clostrid	o__Peptost	f__Peptost	g__Rombo	s__Romboutsia_timonensis	
ASV2284	100	100	81	79	29	17	17	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2285	100	100	95	95	95	95	36	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	NA	Filter: bootstrap Score >= 50
ASV2286	100	90	90	88	85	81	61	d__Bacteri	p__Bacillo	c__Clostrid	o__Peptost	f__Peptost	g__Rombo	s__Romboutsia_timonensis	
ASV2287	100	87	87	43	21	11	10	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2288	100	100	95	95	95	90	40	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Clostrid	g__Clostrid	NA	Filter: bootstrap Score >= 50
ASV2289	100	49	18	18	18	12	12	d__Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2290	100	95	95	95	93	39	39	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	NA	NA	Filter: bootstrap Score >= 50
ASV2291	100	95	95	95	94	33	33	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Prevote	NA	NA	Filter: bootstrap Score >= 50
ASV2292	100	91	87	87	81	64	63	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	g__Muriba	s__Muribaculum_intestinale	
ASV2293	100	100	100	100	100	96	2	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Limosil	NA	Filter: bootstrap Score >= 50
ASV2294	100	98	95	91	55	24	23	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__	NA	NA	Filter: bootstrap Score >= 50
ASV2295	100	100	100	100	100	100	69	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Bacterd	g__Phoca	s__Phocaeicola_vulgatus	
ASV2297	100	77	77	68	67	67	20	d__Bacteri	p__Bacillo	c__Clostrid	o__Peptost	f__Peptost	g__Terrisp	NA	Filter: bootstrap Score >= 50
ASV2299	100	100	100	100	71	34	28	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	NA	NA	Filter: bootstrap Score >= 50
ASV2300	100	41	41	41	41	39	35	d__Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2301	100	100	100	100	100	100	87	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Rikene	g__Alistipe	s__Alistipes_dispar	
ASV2302	100	100	99	98	84	80	80	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__	g__Colidex	s__Colidextribacter_massiliensis	
ASV2303	100	96	91	91	82	82	54	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Tanner	g__Paraba	s__Parabacteroides_gordonii	
ASV2304	100	71	71	71	71	71	71	d__Bacteri	p__Spiroc	c__Spiroch	o__Spiroch	f__Trepon	g__Trepon	s__Treponema_succinifaciens	
ASV2305	100	100	100	100	79	38	38	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Acutalit	NA	NA	Filter: bootstrap Score >= 50
ASV2307	100	46	18	16	16	8	8	d__Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2308	100	100	100	100	100	99	70	d__Bacteri	p__Actino	c__Actino	o__Propio	f__Nocard	g__Nocard	s__Nocardioides_marmoriterrae	
ASV2309	100	99	98	97	97	96	94	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	g__Rumino	s__Ruminococcus_callidus	
ASV2310	100	100	100	64	46	29	20	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2311	100	98	98	97	93	63	29	d__Bacteri	p__Pseudo	c__Gamma	o__Entero	f__Enterob	g__Shigell	NA	Filter: bootstrap Score >= 50
ASV2312	100	100	100	100	100	100	49	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	g__Faecal	NA	Filter: bootstrap Score >= 50
ASV2313	100	78	52	44	40	39	39	d__Bacteri	p__Therm	c__Desulfu	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2314	100	99	97	95	93	89	70	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	g__Duncan	s__Duncaniella_muris	
ASV2316	100	93	93	93	93	90	34	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	NA	Filter: bootstrap Score >= 50
ASV2317	100	94	92	92	74	30	30	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Muriba	NA	NA	Filter: bootstrap Score >= 50
ASV2318	100	100	99	99	97	94	27	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	NA	Filter: bootstrap Score >= 50
ASV2319	100	98	98	98	98	98	88	d__Bacteri	p__Bacter	c__Bacterd	o__Bacter	f__Tanner	g__Paraba	s__Parabacteroides_goldsteinii	
ASV2320	100	100	100	100	100	100	96	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Strepto	g__Strepto	s__Streptococcus_danieliae	
ASV2321	100	86	82	63	55	55	38	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Anaero	g__Anaero	NA	Filter: bootstrap Score >= 50
ASV2322	100	58	58	50	39	39	38	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2323	100	98	93	71	60	4	4	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachno	NA	NA	Filter: bootstrap Score >= 50

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ASV2324	100	100	100	97	86	43	34	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV2325	100	100	85	85	83	81	40	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	NA	Filter: bootstrap Score >= 50
ASV2326	100	100	100	100	78	42	15	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteri	f__Prevote	NA	NA	Filter: bootstrap Score >= 50
ASV2327	100	100	100	100	100	100	100	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteri	f__Muriba	g__Dunca	s__Duncaniella_muris	
ASV2328	100	48	48	48	43	27	17	d__Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2329	100	100	100	100	100	100	97	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteri	f__Odoriba	g__Butyric	s__Butyricimonas_synergistica	
ASV2330	100	100	100	100	100	100	100	d__Bacteri	p__Actinor	c__Coriobo	o__Coriob	f__Kribbiba	g__Granul	s__Granulimonas_faecalis	
ASV2331	100	100	100	100	100	100	90	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	s__Lactobacillus_hominis	
ASV2332	100	64	57	28	18	18	16	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2333	100	100	100	99	99	26	26	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV2334	100	97	97	89	89	22	21	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV2335	100	98	87	54	12	10	6	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2336	100	85	85	84	84	56	52	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Dorea	s__Dorea_phocaeensis	
ASV2337	100	95	95	95	95	56	52	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteri	f__Muriba	g__Muriba	s__Muribaculum_gordoncarteri	
ASV2338	100	100	100	57	32	32	27	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2339	100	57	54	31	24	12	12	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2340	100	86	86	86	86	86	18	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Limosi	NA	Filter: bootstrap Score >= 50
ASV2341	100	100	100	100	100	100	71	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	s__Lactobacillus_taiwanensis	
ASV2342	100	100	100	100	95	50	50	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteri	f__Muriba	g__Dunca	s__Duncaniella_muris	
ASV2344	100	78	78	78	78	7	7	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteri	f__Prevote	NA	NA	Filter: bootstrap Score >= 50
ASV2346	100	100	100	100	100	100	51	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Limosi	s__Limosilactobacillus_albertensis	
ASV2347	100	100	69	69	69	47	45	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	f__Erysipe	NA	NA	Filter: bootstrap Score >= 50
ASV2348	100	71	71	68	61	13	13	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV2349	100	100	100	100	100	100	30	d__Bacteri	p__Campy	c__Epsilon	o__Campy	f__Helicob	g__Helicob	NA	Filter: bootstrap Score >= 50
ASV2350	100	100	85	85	84	83	77	d__Bacteri	p__Bacillo	c__Bacilli	o__Bacillal	f__Staphyl	g__Staphy	s__Staphylococcus_warneri	
ASV2351	100	65	43	43	43	27	15	d__Bacteri	p__Bacillo	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2352	100	100	99	99	95	95	84	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Strepto	g__Strepto	s__Streptococcus_hyointestinalis	
ASV2353	100	69	67	52	30	30	21	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2354	100	94	94	79	79	62	44	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Entero	NA	Filter: bootstrap Score >= 50
ASV2356	100	100	100	100	100	100	57	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteri	f__Bacteroi	g__Phoca	s__Phocaeicola_plebeius	
ASV2357	100	93	93	93	93	74	27	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	NA	Filter: bootstrap Score >= 50
ASV2358	100	100	100	100	100	83	18	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Ligilact	NA	Filter: bootstrap Score >= 50
ASV2359	100	87	86	86	86	62	62	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteri	f__Odoriba	g__Culturo	s__Culturomica_massiliensis	
ASV2360	100	98	98	97	83	17	17	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV2361	100	100	100	100	73	41	41	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteri	f__Prevote	NA	NA	Filter: bootstrap Score >= 50
ASV2362	100	100	67	67	67	67	55	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	s__Lactobacillus_taiwanensis	
ASV2363	100	99	99	99	99	20	20	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteri	f__Muriba	NA	NA	Filter: bootstrap Score >= 50
ASV2364	100	100	69	69	53	52	36	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Ligilact	NA	Filter: bootstrap Score >= 50
ASV2365	100	100	96	96	95	66	29	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	NA	Filter: bootstrap Score >= 50
ASV2366	100	100	100	100	100	89	58	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Ligilact	s__Ligilactobacillus_apodemi	
ASV2367	100	99	98	97	95	90	49	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	NA	Filter: bootstrap Score >= 50
ASV2368	100	100	97	97	91	40	27	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteri	f__Muriba	NA	NA	Filter: bootstrap Score >= 50
ASV2369	100	78	78	78	78	13	13	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteri	f__Bacteroi	NA	NA	Filter: bootstrap Score >= 50
ASV2370	100	97	97	67	67	17	17	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV2371	100	100	100	100	35	35	16	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2372	100	100	100	25	22	21	21	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2373	100	100	99	98	98	85	85	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Qiania	s__Qiania_dongpingensis	
ASV2374	100	100	100	99	99	99	72	d__Bacteri	p__Actinor	c__Coriobo	o__Eggerth	f__Eggerth	g__Adlercr	s__Adlercreutzia_equolifaciens	
ASV2375	100	100	100	100	61	57	57	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	g__	s__[Clostridium]_leptum	
ASV2376	100	100	100	100	97	92	90	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteri	f__Muriba	g__Dunca	s__Duncaniella_freteri	

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ASV2377	100	98	98	98	97	23	21	d__Bacteri	p__Bacteri	c__Bacteroi	o__Bacteroi	f__Prevotel	NA	NA	Filter: bootstrap Score >= 50
ASV2378	100	81	81	81	81	81	71	d__Bacteri	p__Actinob	c__Actinobi	o__Actinom	f__Actinom	g__Actinom	s__Actinomyces_denticolens	
ASV2379	100	99	98	79	73	17	17	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachnos	NA	NA	Filter: bootstrap Score >= 50
ASV2380	100	52	52	44	44	40	35	d__Bacteri	p__Actinob	c__Coriobac	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2381	100	72	72	69	69	27	27	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachnos	NA	NA	Filter: bootstrap Score >= 50
ASV2382	100	100	100	100	100	100	67	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactoba	f__Lactoba	g__Lactob	s__Lactobacillus_crispatus	
ASV2383	100	82	82	60	60	17	17	d__Bacteri	p__Actinob	c__Coriobac	o__Eggerth	f__Eggerth	NA	NA	Filter: bootstrap Score >= 50
ASV2384	100	98	98	67	67	23	23	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachnos	NA	NA	Filter: bootstrap Score >= 50
ASV2386	100	47	45	45	36	21	20	d__Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2387	100	99	98	62	61	42	40	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Butyricic	NA	NA	Filter: bootstrap Score >= 50
ASV2388	100	79	78	76	42	42	33	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2389	100	76	76	64	40	32	0	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2390	100	99	99	99	99	78	78	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachnos	g__Qiania	s__Qiania_dongpingensis	
ASV2391	100	50	50	49	49	8	8	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2392	100	90	90	83	83	5	5	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachnos	NA	NA	Filter: bootstrap Score >= 50
ASV2393	100	100	90	51	42	24	24	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2394	100	100	100	100	90	20	20	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV2395	100	77	76	76	74	74	9	d__Bacteri	p__Campyl	c__Epsilon	o__Campyl	f__Helicob	g__Helicob	NA	Filter: bootstrap Score >= 50
ASV2396	100	100	100	100	100	100	99	d__Bacteri	p__Actinob	c__Actinobi	o__Mycobac	f__Corynet	g__Corynet	s__Corynebacterium_flavescens	
ASV2397	100	100	100	100	100	100	58	d__Bacteri	p__Bacteroi	c__Bacteroi	o__Bacteroi	f__Bacteroi	g__Bacteroi	s__Bacteroides_acidifaciens	
ASV2398	100	100	98	89	79	20	20	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV2400	100	100	100	100	100	100	37	d__Bacteri	p__Actinob	c__Actinobi	o__Propioni	f__Propioni	g__Tessari	NA	Filter: bootstrap Score >= 50
ASV2401	100	100	100	100	100	100	100	d__Bacteri	p__Bacteroi	c__Bacteroi	o__Bacteroi	f__Muribac	g__Duncan	s__Duncaniella_dubosii	
ASV2402	100	92	92	92	92	87	16	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Limosil	NA	Filter: bootstrap Score >= 50
ASV2403	100	100	97	93	91	19	19	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachnos	f__Lachnos	NA	NA	Filter: bootstrap Score >= 50
ASV2404	100	100	98	89	89	60	60	d__Bacteri	p__Bacillo	c__Clostrid	o__Peptost	f__Anaerov	g__Emergo	s__Emergencia_timonensis	
ASV2405	100	92	84	19	19	13	13	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2406	100	100	48	48	40	40	40	d__Bacteri	p__Bacillo	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2407	100	95	95	52	52	52	52	d__Bacteri	p__Actinob	c__Coriobac	o__Coriobac	f__Coriobac	g__Parvibac	s__Parvibacter_caecicola	
ASV2408	100	99	99	99	99	99	99	d__Bacteri	p__Campyl	c__Epsilon	o__Campyl	f__Helicob	g__Helicob	s__Helicobacter_typhlonius	
ASV2409	100	100	100	100	99	99	99	d__Bacteri	p__Bacteroi	c__Bacteroi	o__Bacteroi	f__Muribac	g__Duncan	s__Duncaniella_muris	
ASV2410	100	100	98	76	76	75	27	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	NA	Filter: bootstrap Score >= 50
ASV2412	100	100	97	97	95	95	95	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__	g__Flintiba	s__Flintibacter_butyricus	
ASV2414	100	100	59	59	59	59	13	d__Bacteri	p__Bacillo	c__Bacilli	o__Bacillal	f__Paeniba	g__Brevib	NA	Filter: bootstrap Score >= 50
ASV2415	100	99	56	55	55	55	25	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	NA	Filter: bootstrap Score >= 50
ASV2417	100	98	98	98	97	41	28	d__Bacteri	p__Bacteroi	c__Bacteroi	o__Bacteroi	f__Muribac	NA	NA	Filter: bootstrap Score >= 50
ASV2418	100	100	100	100	94	64	64	d__Bacteri	p__Bacillo	c__Erysipel	o__Erysipel	f__Coprob	g__Longib	s__Longibaculum_muris	
ASV2419	100	89	89	85	80	64	50	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubacte	f__Oscillos	g__Rumin	s__Ruminococcus_champanellensis	
ASV2420	100	63	63	57	57	18	18	d__Bacteri	p__Actinob	c__Coriobac	o__Eggerth	f__Eggerth	NA	NA	Filter: bootstrap Score >= 50
ASV2421	100	100	100	100	100	100	67	d__Bacteri	p__Actinob	c__Actinobi	o__Micrococ	f__Dermat	g__Brachy	s__Brachybacterium_faecium	
ASV2422	100	21	21	21	21	21	21	d__Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2423	100	98	88	81	64	30	30	d__Bacteri	p__Bacteroi	c__Bacteroi	o__Bacteroi	f__Porphyr	NA	NA	Filter: bootstrap Score >= 50
ASV2424	100	100	100	100	100	100	99	d__Bacteri	p__Actinob	c__Actinobi	o__Mycobac	f__Corynet	g__Corynet	s__Corynebacterium_durum	
ASV2425	100	100	100	100	100	100	88	d__Bacteri	p__Bacteroi	c__Bacteroi	o__Bacteroi	f__Bacteroi	g__Bacteroi	s__Bacteroides_acidifaciens	
ASV2426	100	99	99	99	91	38	38	d__Bacteri	p__Bacillo	c__Erysipel	o__Erysipel	f__Coprob	NA	NA	Filter: bootstrap Score >= 50
ASV2427	100	45	38	38	38	38	29	d__Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2428	100	57	54	52	38	33	28	d__Bacteri	p__Bacteroi	c__Bacteroi	o__Bacteroi	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2429	100	100	100	100	94	64	46	d__Bacteri	p__Pseudo	c__Betapro	o__Burkhol	f__Comam	g__Curvib	NA	Filter: bootstrap Score >= 50
ASV2431	100	100	100	37	37	37	37	d__Bacteri	p__Actinob	c__Actinobi	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2432	100	100	58	58	57	32	31	d__Bacteri	p__Bacillo	c__Erysipel	o__Erysipel	f__Erysipel	NA	NA	Filter: bootstrap Score >= 50

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ASV2434	100	95	95	95	95	95	7	d__Bacteri	p__Pseudo	c__Alphap	o__Hyphor	f__Boseac	g__Bosea	NA	Filter: bootstrap Score >= 50
ASV2435	100	100	100	100	100	100	100	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Muriba	g__Dunca	s__Duncaniella_muris	
ASV2437	100	100	100	100	100	100	91	d__Bacteri	p__Pseudo	c__Gamma	o__Lysoba	f__Lysoba	g__Pseudo	s__Pseudoxanthomonas_japonensis	
ASV2440	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	f__Erysipe	g__Intestin	s__Intestinibaculum_porci	
ASV2443	100	84	68	20	15	15	15	d__Bacteri	p__Pseudo	c__Alphap	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2444	100	73	73	73	73	72	71	d__Bacteri	p__Spiroch	c__Spiroch	o__Spiroch	f__Treponi	g__Treponi	s__Treponema_bryantii	
ASV2445	100	88	88	83	83	12	12	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV2446	100	100	99	99	99	99	38	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	NA	Filter: bootstrap Score >= 50
ASV2447	100	90	89	89	89	38	18	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Prevote	NA	NA	Filter: bootstrap Score >= 50
ASV2448	100	56	56	50	49	27	25	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2449	100	100	100	100	100	100	92	d__Bacteri	p__Chlamy	c__Chlamy	o__Chlamy	f__Chlamy	g__Chlamy	s__Chlamydia_muridarum	
ASV2450	100	98	94	74	20	11	11	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2451	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Tissier	o__Tissier	f__Peptoni	g__Anaero	s__Anaerococcus_prevotii	
ASV2452	100	100	100	79	48	48	47	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2453	100	100	100	99	97	88	88	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	g__Congzh	s__Congzhengia_minquanensis	
ASV2455	100	96	73	64	63	22	14	d__Bacteri	p__Bacillo	c__Negativ	o__Selenc	f__Seleno	NA	NA	Filter: bootstrap Score >= 50
ASV2456	100	100	100	100	100	73	73	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Muriba	g__Param	s__Paramuribaculum_intestinale	
ASV2457	100	92	30	30	30	25	24	d__Bacteri	p__Bacillo	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2458	100	100	100	85	84	24	15	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV2459	100	100	99	99	99	99	76	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	f__Turicib	g__Turicib	s__Turicibacter_bilis	
ASV2460	100	100	100	100	53	36	26	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Bacter	NA	NA	Filter: bootstrap Score >= 50
ASV2461	100	100	100	100	100	100	100	d__Bacteri	p__Chlamy	c__Chlamy	o__Chlamy	f__Chlamy	g__Chlamy	s__Chlamydia_muridarum	
ASV2462	100	98	78	78	77	77	72	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	f__Turicib	g__Turicib	s__Turicibacter_bilis	
ASV2463	100	100	98	91	89	41	20	d__Bacteri	p__Bacillo	c__Clostrid	o__Peptos	f__Peptost	NA	NA	Filter: bootstrap Score >= 50
ASV2464	100	100	96	80	80	47	14	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV2466	100	77	59	52	24	22	22	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2467	100	84	84	84	83	56	30	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Prevote	g__Prevot	NA	Filter: bootstrap Score >= 50
ASV2468	100	100	100	100	52	40	40	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV2469	100	100	100	100	100	100	100	d__Bacteri	p__Spiroch	c__Spiroch	o__Spiroch	f__Treponi	g__Treponi	s__Treponema_berlinense	
ASV2470	100	100	100	100	80	64	37	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Muriba	g__Dunca	NA	Filter: bootstrap Score >= 50
ASV2471	100	97	97	97	97	97	50	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	s__Lactobacillus_crispatus	
ASV2472	100	97	97	97	91	43	43	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Muriba	NA	NA	Filter: bootstrap Score >= 50
ASV2473	100	96	96	96	96	96	45	d__Bacteri	p__Spiroch	c__Spiroch	o__Spiroch	f__Treponi	g__Treponi	NA	Filter: bootstrap Score >= 50
ASV2478	100	100	100	77	19	19	10	d__Bacteri	p__Pseudo	c__Alphap	o__Rhodo	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2482	100	100	100	66	66	12	12	d__Bacteri	p__Planct	c__Planct	o__Gemm	f__Gemma	NA	NA	Filter: bootstrap Score >= 50
ASV2483	100	100	99	99	93	93	63	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Rikene	g__Alistipe	s__Alistipes_montrealensis	
ASV2484	100	100	100	100	100	99	29	d__Bacteri	p__Actino	c__Coriob	o__Eggerth	f__Eggerth	g__Adlerc	NA	Filter: bootstrap Score >= 50
ASV2485	100	100	86	86	86	85	45	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	NA	Filter: bootstrap Score >= 50
ASV2486	100	100	100	100	100	100	100	d__Bacteri	p__Deferri	c__Deferri	o__Deferri	f__Mucisp	g__Mucisp	s__Mucispirillum_schaedleri	
ASV2490	100	75	73	73	54	50	32	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Muriba	g__Dunca	NA	Filter: bootstrap Score >= 50
ASV2492	100	99	99	97	97	96	96	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	g__Schaed	s__Schaedlerella_arabinosiphila	
ASV2493	100	98	98	98	98	90	28	d__Bacteri	p__Pseudo	c__Gamma	o__Pseudo	f__Pseudo	g__Pseudo	NA	Filter: bootstrap Score >= 50
ASV2494	100	100	100	100	100	100	100	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	f__Erysipe	g__Dubosi	s__Dubosiella_newyorkensis	
ASV2495	100	100	100	100	100	100	96	d__Bacteri	p__Campy	c__Epsilon	o__Campy	f__Helicob	g__Helicot	s__Helicobacter_typhlonius	
ASV2497	100	100	100	100	100	98	94	d__Bacteri	p__Pseudo	c__Gamma	o__Pasteu	f__Pasteu	g__Roden	s__Rodentibacter_pneumotropicus	
ASV2499	100	85	69	18	5	5	1	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2500	100	100	100	98	98	80	80	d__Bacteri	p__Pseudo	c__Alphap	o__Gemin	f__Gemini	g__Arboric	s__Arboricoccus_pini	
ASV2501	100	35	29	29	27	24	24	d__Bacteri	NA	NA	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2502	100	97	97	97	96	94	58	d__Bacteri	p__Bacillo	c__Bacilli	o__Bacilla	f__Staphyl	g__Jeotga	s__Jeotgalicoccus_nanhaiensis	
ASV2503	100	100	100	100	100	98	72	d__Bacteri	p__Pseudo	c__Alphap	o__Rhodo	f__Roseob	g__Rubelli	s__Rubellimicrobium_rubrum	

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ASV2505	100	96	96	96	96	96	23	d__Bacteri	p__Campy	c__Epsilon	o__Campy	f__Helicob	g__Helicot	NA	Filter: bootstrap Score >= 50
ASV2506	100	98	67	67	67	43	43	d__Bacteri	p__Bacillo	c__Erysipe	o__Erysipe	f__Erysipe	NA	NA	Filter: bootstrap Score >= 50
ASV2508	100	99	98	98	92	57	57	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Muriba	g__Paramı	s__Paramuribaculum_intestinale	
ASV2509	100	90	90	90	90	90	68	d__Bacteri	p__Campy	c__Epsilon	o__Campy	f__Helicob	g__Helicot	s__Helicobacter_japonicus	
ASV2510	100	100	100	100	100	99	37	d__Bacteri	p__Pseudo	c__Alphap	o__Rhodo	f__Azospir	g__Skerm	NA	Filter: bootstrap Score >= 50
ASV2511	100	97	97	97	97	74	10	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Limosil	NA	Filter: bootstrap Score >= 50
ASV2513	100	99	99	99	99	97	11	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Limosil	NA	Filter: bootstrap Score >= 50
ASV2514	100	100	65	65	65	42	14	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV2515	100	100	100	100	85	24	12	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV2516	100	100	100	100	88	23	12	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__Oscillos	NA	NA	Filter: bootstrap Score >= 50
ASV2517	100	100	100	100	100	100	81	d__Bacteri	p__Spiroch	c__Spiroch	o__Spiroch	f__Treponı	g__Treponı	s__Treponema_bryantii	
ASV2518	100	51	51	51	51	42	28	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Rikenel	NA	NA	Filter: bootstrap Score >= 50
ASV2519	100	95	95	77	76	3	3	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV2520	100	100	100	100	100	41	41	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV2521	100	100	100	100	100	95	60	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	s__Lactobacillus_kitasatonis	
ASV2522	100	99	99	98	98	96	29	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	NA	Filter: bootstrap Score >= 50
ASV2525	100	100	100	100	100	99	99	d__Bacteri	p__Bacter	c__Bacter	o__Bacter	f__Muriba	g__Muriba	s__Muribaculum_gordoncarteri	
ASV2526	100	100	100	100	100	100	94	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Strepto	g__Strepto	s__Streptococcus_hyointestinalis	
ASV2527	100	100	61	61	61	61	61	d__Bacteri	p__Bacillo	c__Clostrid	o__Eubact	f__	g__Flintiba	s__Flintibacter_butyricus	
ASV2528	100	98	98	98	98	71	11	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Limosil	NA	Filter: bootstrap Score >= 50
ASV2529	100	99	99	99	99	92	8	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Limosil	NA	Filter: bootstrap Score >= 50
ASV2530	100	98	98	98	98	85	10	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Limosil	NA	Filter: bootstrap Score >= 50
ASV2531	100	100	63	63	63	62	14	d__Bacteri	p__Bacillo	c__Bacilli	o__Lactob	f__Lactoba	g__Lactob	NA	Filter: bootstrap Score >= 50
ASV2532	100	100	100	89	86	32	17	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV2533	100	100	88	36	30	25	25	d__Bacteri	p__Bacillo	c__Clostrid	NA	NA	NA	NA	Filter: bootstrap Score >= 50
ASV2534	100	81	81	79	79	17	17	d__Bacteri	p__Bacillo	c__Clostrid	o__Lachno	f__Lachno	NA	NA	Filter: bootstrap Score >= 50
ASV2538	100	100	100	100	53	40	17	d__Bacteri	p__Bacillo	c__Bacilli	o__Bacillal	f__Caryop	NA	NA	Filter: bootstrap Score >= 50

الخلاصة

تؤثر الأنظمة الغذائية بشكل كبير على الميكروبيوم المعوي (البكتيريا النافعة) والاستجابات المناعية للمضيف. فالأطعمة الغنية بالدهون، مثل تلك التي تحتوي على صفار البيض، تشتمل على الفوسفوليبيدات، والكوليسترول، والفيتامينات القابلة للذوبان في الدهون، والأحماض الدهنية الأساسية، والتي تؤثر جميعها على نشاط الميكروبيوم، وفسيولوجيا الأمعاء، والوظائف المناعية. ومع ذلك، فإن الاختلافات في تأثير بيض الإوز مقابل بيض الدجاج على محور (الميكروبيوم-المناعة) لا تزال قيد الدراسة المحدودة. لهذا السبب، هدفت الدراسة الحالية إلى فحص التأثير الذي أحدثه تدعيم النظام الغذائي بصفار بيض الإوز مقابل صفار بيض الدجاج على الميكروبيوم المعوي، واستجابات السيتوكينات، والتحليل المورفولوجي النسجي للأمعاء.

تحت نفس الظروف البيئية والرقابة التجريبية، تم تقسيم ثلاثين من فئران التجارب المختبرية إلى واحدة من ثلاث مجموعات؛ حيث كانت إحداها بمثابة مجموعة ضابطة، بينما تم تدعيم المجموعتين الأخريين بصفار بيض الدجاج أو صفار بيض الإوز. وبعد فترات زمنية متفاوتة بلغت أسبوعين وشهر واحد، تم تقييم الميكروبيوم المعوي باستخدام تقنية تسلسل (S rRNA amplicon sequencing16). كما تم فحص الدم لتقييم الاستجابات المناعية عن طريق قياس اثنين من السيتوكينات (IL-6 وIL-10)، وتقييم اضطرابات الميكروبيوم المعوي من خلال الصور المورفومترية النسيجية. حُللت البيانات باستخدام اختبار (ANOVA) أحادي الاتجاه، وتحددت قيمة ($p < 0.05$) كعتبة للدلالة الإحصائية.

في هذه الدراسة، تبيّن أن جزءاً كبيراً من تخصيص الموارد قد استُخدم لصالح الميكروبيوم المعوي. وكشفت تقييمات المجتمعات الميكروبية عن تعزيز كبير في الأصناف البكتيرية النافعة بين المجموعات المدعمة بالصفار مقارنة بالمجموعات الضابطة من خلال تحليل الوفرة النسبية. وتشمل الأمثلة البارزة لهذا التأثير الأصناف التابعة لأجناس Ligilactobacillus، وLimosilactobacillus، وBacteroides ($P < 0.05$)، فيما يتعلق بالإثراء المعنوي. وفي مجموعة صفار بيض الدجاج، أظهرت بكتيريا Ligilactobacillus apodemi زيادة مؤقتة معنوية في اليوم الرابع عشر. أما بكتيريا Bacteroides، فقد وصلت وفرتها النسبية إلى 53-55%، ثم شهدت انخفاضاً وصولاً إلى اليوم الثلاثين بنسبة وفرة بلغت 3%، مما يجسد نموذجاً للتعاقب المبكر السريع وإعادة هيكلة المجتمع الميكروبي.

وفي المقابل، أظهرت مجموعة صفار بيض الإوز درجة أكبر من الاستقرار الميكروبي المستدام، وتميزت بإثراء مستمر للأصناف النافعة وتقلب زمني أقل للميكروبات السائدة. وكما يتضح من مؤشري (Chao1) و(Bray Curtis)، أظهر التحليل اللاحق للتنوع من نوع (ألفا وبيتا) إعادة تنظيم معنوية للمجتمعات الميكروبية بالنسبة للمجموعات الضابطة نتيجة للتدعيم بالصفار. ولوحظ ضمن كلتا مجموعتي العلاج بالصفار تحسن في المجتمع الميكروبي وإعادة هيكلته، بما في ذلك زيادة في الغنى الميكروبي خلال فترة التغذية المبكرة ($P < 0.05$)، جنباً إلى جنب مع زيادة في تنوع شانون (Shannon)، ومؤشر سيمبسون (Simpson)، والتنوع التطوري (Phylogenetic diversity).

أثّرت التغييرات الغذائية بقوة على تركيز السيتوكينات في الدم. فقد بلغ تركيز (IL-6) في دم مجموعة صفار بيض الإوز (310 ± 95 بيكوغرام/مل) في اليوم الرابع عشر، مقارنة بالمجموعة الضابطة التي سجلت (85 ± 62 بيكوغرام/مل) ($P < 0.05$).

من ناحية أخرى، أظهرت مجموعة صفار بيض الدجاج أعلى مستوى من (IL-6) في اليوم الثلاثين (410 ± 210 بيكوغرام/مل)، وهو ما كان معنوياً مقارنة بالمجموعتين الضابطة وصفار بيض الإوز ($P < 0.05$)، مما يُظهر نمطاً متأخراً من الاستجابة الالتهابية. كما كان هناك أيضاً فرق معنوي بين المعالجات في إشارات مضادات الالتهاب؛ فعلى الرغم من ارتفاع مستوى (IL-10) في المصل لدى جميع المجموعات بمرور الوقت، إلا أن مجموعة صفار بيض الدجاج سجلت أعلى مستوى من (IL-10) في اليوم الثلاثين (460 ± 150 بيكوغرام/مل)، وهو ما كان معنوياً مقارنة بالمجموعة الضابطة ($P < 0.05$)، مما يؤكد تفعيل المسارات التنظيمية التعويضية المضادة للالتهاب التي نجمت عن التكيف الميكروبي والتمثيلي الناجم عن النظام الغذائي.

أظهر التقييم المورفومتري النسجي للأنسجة المعوية تحسناً هيكلياً معنوياً عند التدعيم بصفار البيض. ففي الاثني عشر، أظهرت مجموعة صفار بيض الدجاج زيادة معنوية في متوسط طول الزغابات المعوية حيث بلغت 0.4536 مم مقارنة بـ 0.4088 مم في المجموعة الضابطة و0.5183 مم في مجموعة صفار بيض الإوز ($P < 0.05$). وتم إثبات اتجاه مماثل في الصائم، حيث بلغت القياسات في المجموعة الضابطة 0.3156 مم، وفي مجموعة صفار الدجاج 0.3451 مم، وفي مجموعة صفار الإوز 0.3866 مم ($P < 0.05$). وفي لفائفي المجموعة الضابطة، بلغ طول الزغابات 0.2365 مم، بينما سجلت

مجموعة صفار الدجاج 0.2841 مم، ومجموعة صفار الإوز 0.3082 مم ($P < 0.05$). كما أظهرت مجموعات الصفار زيادة معنوية في عرض الزغابات، ومساحة الزغابات، وعمق الغدد (Crypt depth) مقارنة بالمجموعة الضابطة في جميع أقسام الأمعاء ($P < 0.05$)، وهو ما يعد انعكاساً لتحسن التجديد الظهاري، وتوسع السطح الامتصاصي، والقدرة الوظيفية للمخاطية.

تحت الظروف التجريبية لهذه الدراسة، أظهرت جميع المعايير الموصوفة أن التدعيم بكلا نوعي صفار البيض أدى إلى تغيير ميكروبيوتا الأمعاء، والاستجابة المناعية، وبنية الأنسجة المعوية. ومع ذلك، أظهر التدعيم بصفار بيض الإوز ميكروبيوتا معوية نافعة أكثر وضوحاً، واستجابة مناعية أكثر توازناً، وتحسناً أكثر عمقاً في بنية الأنسجة المعوية مقارنة بالتدعيم بصفار بيض الدجاج، في هذه الدراسة.

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دور النظام الغذائي المعدل في تعديل سلامة الأمعاء ومحور الميكروبيوم المناعي في الفئران.

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وهي جزء من متطلبات نيل شهادة دكتوراه فلسفة في الأحياء المجهرية البيطرية

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