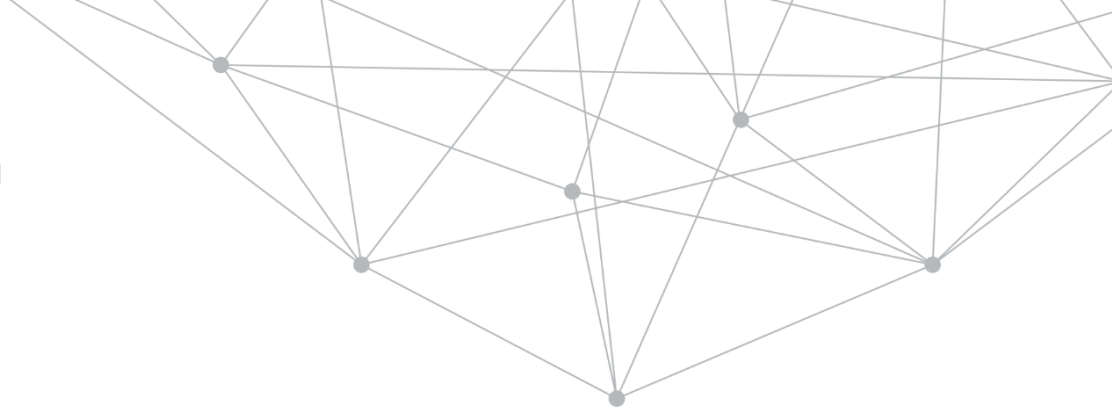




**TFTAK** | CENTER OF FOOD  
AND FERMENTATION  
TECHNOLOGIES



# Gut microbiome analysis report

Thank you for ordering the microbiome analysis kit.

Center of Food and Fermentation Technologies (CFFT) is a research and development institution based on state-of-the-art analytical methods and the principles of systems and synthetic biology, engaged in the development and implementation of novel products in food and biotechnologies. Microbiome studies have been carried out in CFFT since 2012, making them the most experienced provider of microbiome analysis services in Estonia, the Baltics and Scandinavia.

# Introduction

The most abundant microbiota, or microbial community, is located in the colon. Therefore, this analysis was performed based on a stool sample. The development of gut microbial communities is influenced by different factors, such as maternal-derived bacteria, genes, environment including lifestyle, nutrition, illnesses and medications.

A diverse and balanced microbial community protects the body and ensures correct functioning of the digestive tract, as well as affects the human immune system and metabolism. The balanced community is formed mainly by commensal microbes that prevent the overgrowth of pathogens. On the other hand, changes in the gut community are associated with health problems, such as irritable bowel syndrome, inflammation, overweight, diabetes, allergies and other chronic diseases. The state of imbalanced microbial community in the gut is called dysbiosis.

Microorganisms can be classified as potentially beneficial, harmful and disease-causing (intestinal pathogens). Nutrition can alter the balance of potentially beneficial and harmful microorganisms. In order to keep the gut microbial community balanced, healthy lifestyle and nutritional habits need to be persistent. It is important to have a diverse diet rich in fiber, which improves digestion and supports the growth of beneficial bacteria.

Your microbiome report includes the following:

- Overview of the results with the most relevant characteristics.
- Information about the bacterial families in Your gut microbial community.
- Rating with recommendations, if possible, for all the analysed parameters, such as the diversity and richness of Your microbial community, the abundance of bacteria associated with fats and proteins, inflammation and butyric acid production, the abundance of beneficial *Bifidobacterium* and *Lactobacillus* bacteria and enterotypes.
- Appendices. Supplementary tables showing most abundant, commonly found and pro-inflammatory bacteria in Your sample. It is highly recommended to analyse these data tables with a specialist.

## Attention!

- Results presented in the report are based on the published scientific literature and research conducted in Estonia and elsewhere.
- The microbiome analysis includes only the measurements of bacterial community and does not include fungi, parasites and viruses.
- The results presented in the report are for guidance only and are not applicable as a medical diagnosis by a physician.
- This analysis is not suitable for the diagnosis of infectious diarrhea. In case of suspicion of bowel infection, additional analysis are recommended. Information about additional analysis can be requested from SYNLAB customer support.
- In case of dietary changes, a nutritionist consultation is recommended.

# Summary

## Beneficial qualities of Your gut microbiome:

- ☑ The levels of lactic acid bacteria (lactobacilli) are average.

## Unfavorable qualities of Your gut microbiome:

- ☒ The diversity of microbiome is lower than average, which could indicate mild dysbiosis.
- ☒ The species richness is lower than average.
- ☒ The levels of probiotic-like bifidobacteria are lower than average.
- ☒ Gut community is dominated by bacteria, which have been associated with excessive protein and fat consumption.
- ☒ The abundance of intestinal health promoting butyrogenic bacteria are below average.
- ☒ The levels of pro-inflammatory bacteria are above average.

## Detailed comments and recommendations:

- Your microbiome composition corresponds to *Bacteroides* enterotype, which is associated with Western diet.
- High abundance of asaccharolytic bacteria indicates potentially low intake of dietary fiber.
- In order to increase the abundance of butyrate-producers, it is recommended to consume more whole grains, boiled and then cooled potatoes and green bananas.
- The abundance of pro-inflammatory bacteria is high. It is recommended to avoid consumption of sweetened beverages and other products enriched with sugars. Instead, eating more vegetables in varied selection and replacing sweets with fruits is highly suggested, as it can reduce Your desire for sugary sweets and snacks.
- The abundance of sulfate-reducing H<sub>2</sub>S producing bacteria is high. As hydrogen sulfide is toxic, avoid consuming excessive amounts food high in sulfur, e.g. fish, poultry.
- *Akkermansia* species were not detected. These bacteria are associated with good bowel health, weight loss and low BMI.
- *Alistipes* species were not detected. These bacteria are associated with good health, weight loss and low BMI. Although mainly associated with animal based diet, abundance can also be increased by consumption of cruciferous vegetables, such as cabbage, swede and broccoli.
- High abundance of *B. vulgatus* may favor inflammatory conditions in the gut. These bacteria are associated with diet rich in meat and low in resistant starch consumption.
- High abundance of *Bilophila* species is associated with diet rich in animal-derived food and the production of toxic compounds.

- Low abundance of *Blautia* species were detected. These bacteria are associated with diet rich in cereals and the abundance can be increased by the consumption of whole grains and brown rice.
- *Christensenellaceae* bacteria were not detected. These bacteria are associated with low body mass index and are considered as one of the most heritable microbes of the gut.
- The abundance of *Dorea formicigenerans* is high, which is associated with overweight and gastrointestinal inflammation.
- The abundance of *R. bicircularans* is high, which is associated with consumption of non-starch polysaccharides (e.g. from cereals).
- Average abundance of *R. bromii* species indicates effective degradation of resistant starch. Intake of boiled and then cooled potatoes and rice, as well as green bananas, could increase the abundance of this bacteria.
- *Alistipes* species were not detected, which is a common bacteria in the gut microbial community of healthy people. On the other hand, there is high abundance of *Mitsuokella jalaludinii*, which is resistant to many antibiotics. Scientific literature suggests that this may indicate frequent use of antibiotics. To balance the microbial community, it is recommended to increase overall fiber intake from both vegetable and legume groups.

# Results

Bacterial family is a taxonomic level, which is comprised of related bacterial genera harboring similar properties. Bacterial genera, in turn, include species with similar properties. There are families, such as *Verrucomicrobiaceae*, which consist of only one described species. Inversely, much more diverse families exist, containing multiple well defined and described species. For example, *Bacteroidaceae* combines tens of species with specific characteristics.

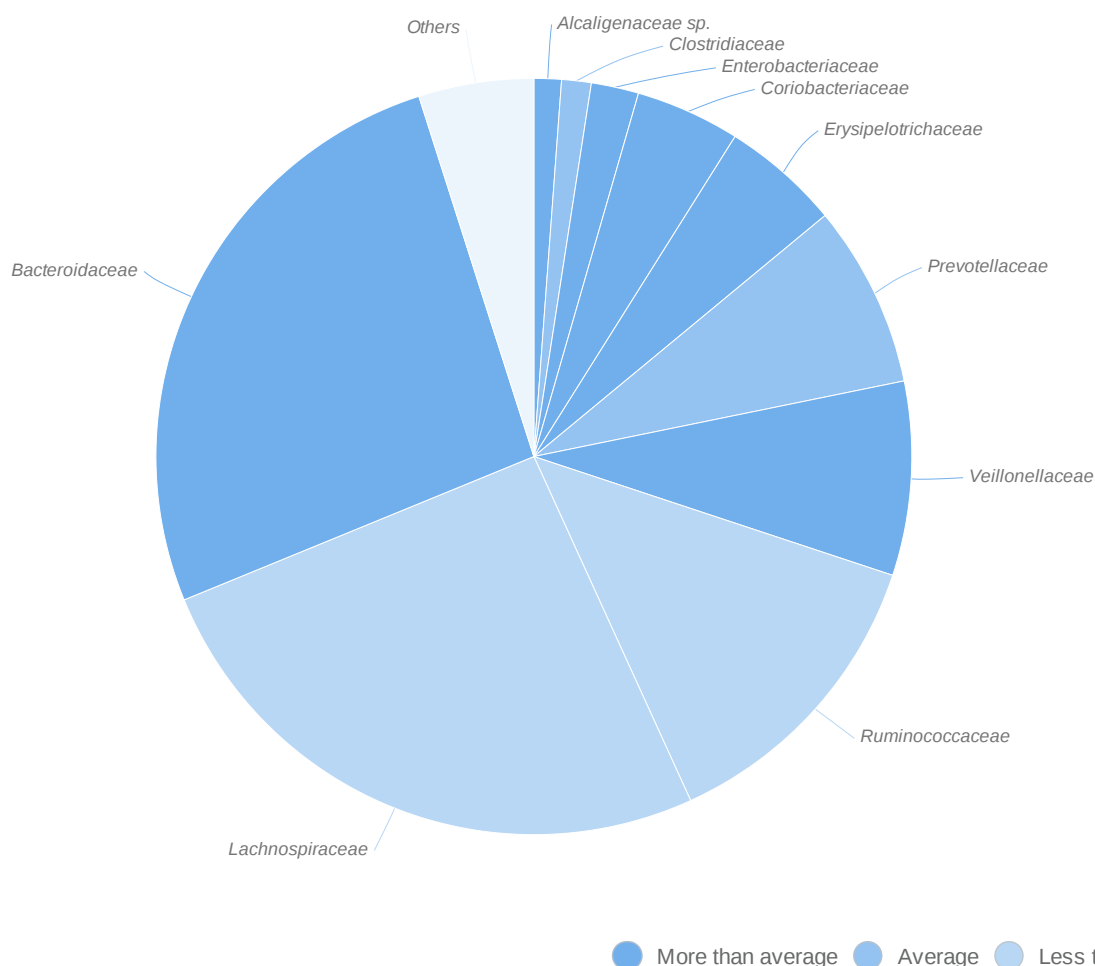


Figure depicts bacteria abundances at family level. Only families with the proportion of more than 1% are shown. Bacterial families with lower abundance are summarized in the sector of "Other".

In the following section, detailed results of Your microbiome parameters along with illustrative graphs are presented. The blue bar of the circle in the graph shows the value of the result compared to the healthy reference group. The number in the center of the circle indicates the value of the parameter analysed.

### Is my gut community diverse?

#### No, Your gut has low-diversity community.

Microbiota diversity index characterizes gut community balance and is important for disease risk assessment. A diverse microbial community indicates a healthy gut. Microbiota diversity is evaluated by Shannon index, which in Your sample is 3.3 and indicates low diversity (healthy score > 3). Diversity of Your gut is lower than in 87% of healthy reference.

70 species were detected from Your gut (90-130 species in healthy community).

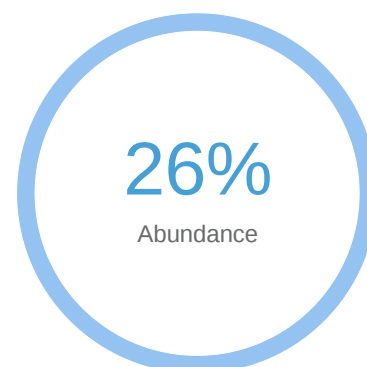


Enrich Your diet with various fiber sources.

### Could my diet be exceedingly rich in protein?

#### Yes, Your gut community contains higher amount of species associated with protein consumption than average.

Proportional abundance of specific species represents current diet and correlates with specific food consumption. High-protein, high-fat diet, which is low in fibers, enhances growth of mucosa-attached species. Excess of such bacteria could cause pro-inflammatory response. Commonly, higher protein and lipid intake is associated with higher abundance of *Bacteroides* species. Your sample contains 26% of these bacteria, which is higher than in 100% of healthy reference and indicates excessive intake of protein or fat.

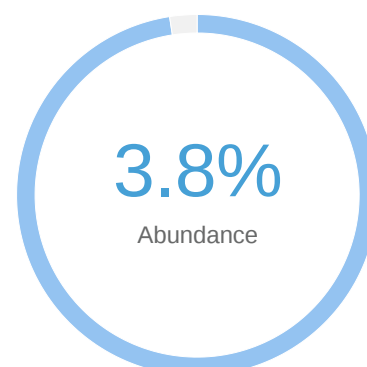


Consume more vegetarian foods and less animal-based products.

## Does my gut microbiota contain elevated levels of pro-inflammatory bacteria?

**Yes, Your gut community contains significantly higher abundance of pro-inflammatory species than average.**

Protection of the host from pro-inflammatory bacteria is facilitated by commensal microbial community through metabolic interactions or induction of immune responses. Commensal bacteria also compete with pro-inflammatory species for gut niches and nutrients. Abundance of pro-inflammatory bacteria in Your sample is 3.8%, which is higher than in 97% of healthy reference.

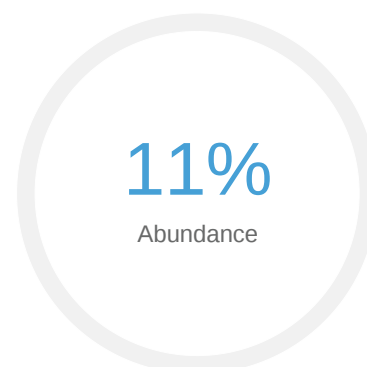


In depth diet analysis and inspection of eating habits is recommended.

## Does my gut microbiota contain sufficient levels of butyrate-producers?

**No, the abundance of butyrate-producers is below average.**

Butyrate, one of the gut microbiota produced metabolites is particularly important for colon health providing anti-inflammatory response. Butyrate is a primary energy resource for intestinal epithelial cells enabling many beneficial features: reduction of toxin accumulation, increase of insulin sensitivity, reinforcement of gut barrier function (reproduction of mucin layer) and protection from diet induced obesity. Abundance of anti-inflammatory butyrogenic bacteria in Your sample is 11%, which is lower than in 100% of healthy reference.



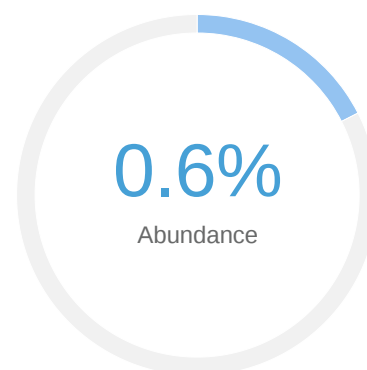
Enrich Your diet with whole grains, Jerusalem artichoke, boiled and then cooled potatoes and green bananas that are rich in fructo-oligosaccharides (FOS) and resistant starch (RS).

## Does my gut microbiota contain sufficient levels of bifidobacteria?

**No, the abundance of bifidobacteria is below average.**

Bifidobacteria are considered as health-promoting bacteria. While they play an important role in infant development, abundance of bifidobacteria is reduced in adults. Various species of this genera can be found in fermented foods, as probiotic strains are added to kefir, yogurt, and other dairy products.

Abundance of bifidobacteria in Your sample is 0.6%, which is lower than in 82% of healthy reference.



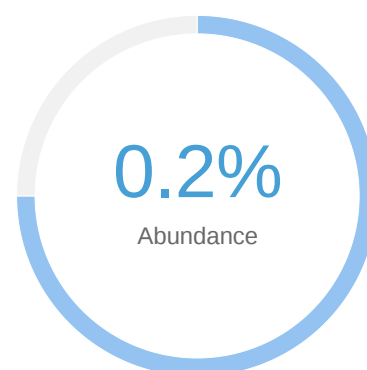
Enrich Your diet with various dietary fiber sources.

## Does my gut microbiota contain lactobacilli?

**Yes, the abundance of lactobacilli is average.**

Lactobacilli are lactic acid producing bacteria, that are considered as health-promoting bacteria. They are used in the production of fermented dairy products (e.g kefir, yogurt) and vegetables (e.g pickles, sauerkraut). Various probiotic strains of this genus are added to kefir, yogurt, and other dairy products.

Abundance of lactobacilli in Your sample is 0.2%, which is similar to healthy reference.

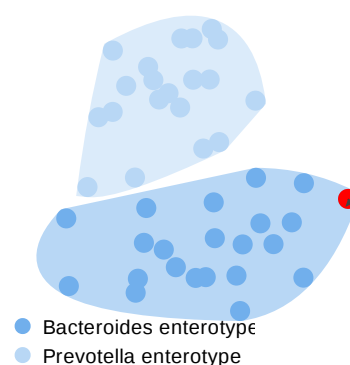




## Which enterotype do I have?

Your microbiome composition corresponds to *Bacteroides* enterotype.

Gut microbial community can be divided into two enterotypes based on the most common genera *Bacteroides* and *Prevotella*. Enterotype development is mainly influenced by long-term dietary habits. *Bacteroides* enterotype is mainly associated with a diet rich in protein and animal fats, but low in fiber, which is characteristic of Western diet. *Prevotella* enterotype, on the other hand, is associated with the consumption of complex carbohydrates and dietary fiber, which is more common in non-industrialized populations. In determining the enterotype, the presence and abundance of *Prevotella* is an important factor, as many people in Western society have a low proportion of *Prevotella* in the gut.



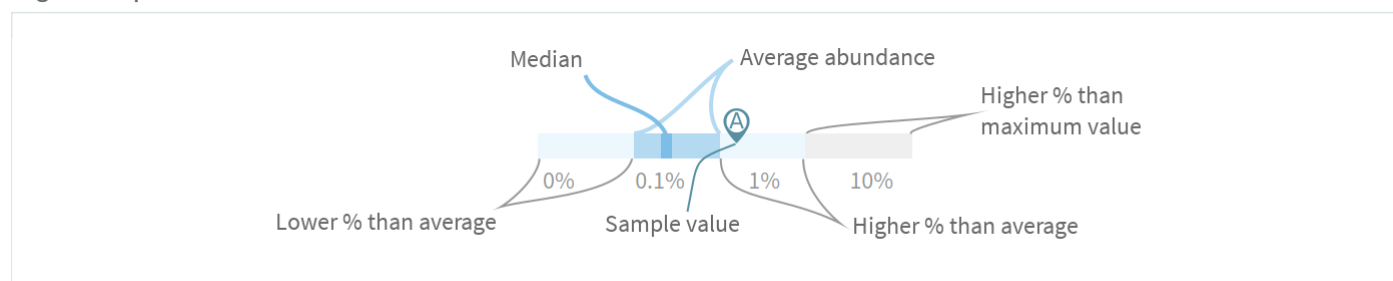
# Appendices

## The most abundant bacteria in Your sample

The following table contains 25 most abundant bacteria in Your gut. Levels of each bacteria are compared to the healthy reference group. Based on the reference group the reference range is calculated and the abundance of the bacteria is assessed accordingly. The rating of the result is statistical and may not reflect the health status. The table is sorted based on Your results in descending order of relative proportion.

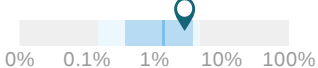
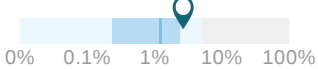
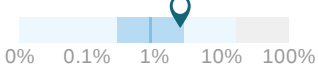
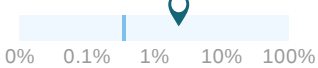
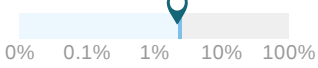
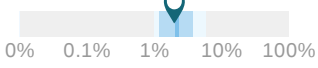
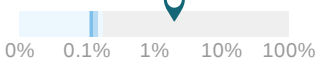
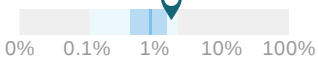
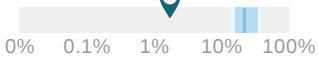
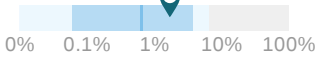
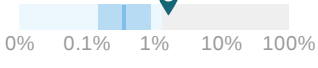
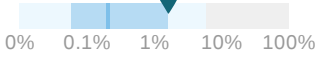
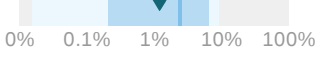
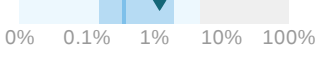
To balance the microbial community of Your gut, the dietary recommendations presented in the summary paragraph of the report should be followed.

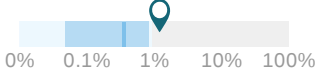
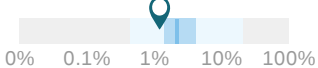
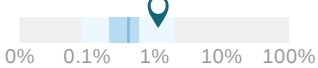
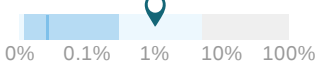
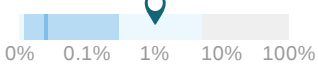
Figure explanation:



Bacterium	Abundance Percentage	Group limits	Prevalence	Status
<i>Bacteroides vulgatus</i>	23%	0–10%	Abundant	● ● ●
<i>Lachnospiraceae unclassified</i>	11%	19–52%	Abundant	● ● ●
<i>Mitsuokella jalaludinii</i>	3.7%	0–0.5%	Rare	● ● ●
<i>Catenibacterium mitsuokai</i>	3.2%	0–2.4%	Frequent	● ● ●
<i>Faecalibacterium prausnitzii</i>	2.9%	2.1–13%	Abundant	● ● ●
<i>Alloprevotella unclassified</i>	2.7%	0–5.7%	Occasional	● ● ●

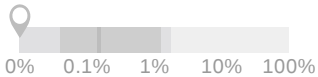

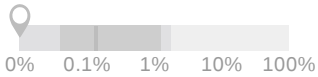

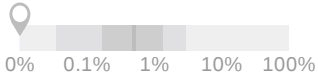

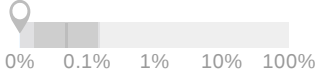

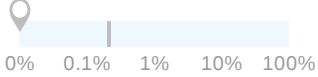

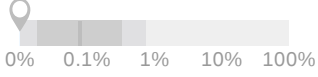

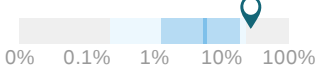

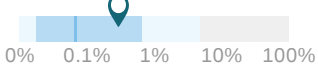

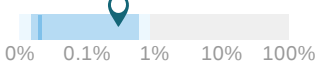

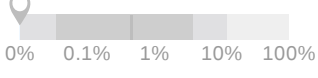

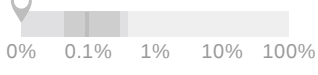

● Average levels ● Above/below average ● Above/below limits  
 Prevalence: rare <5/100, occasional <25/100, frequent <75/100, abundant ≥75/100

Bacterium	Abundance Percentage	Group limits	Prevalence	Status
<i>Subdoligranulum formicilis</i>	2.7% 	0.1–5.0%	Abundant	<span style="color: green;">●</span> <span style="color: gray;">●</span> <span style="color: gray;">●</span>
<i>Dialister invisus</i>	2.6% 	0–5.0%	Frequent	<span style="color: gray;">●</span> <span style="color: yellow;">●</span> <span style="color: gray;">●</span>
<i>Collinsella aerofaciens</i>	2.3% 	0–16%	Abundant	<span style="color: green;">●</span> <span style="color: gray;">●</span> <span style="color: gray;">●</span>
<i>Ruminococcus bicirculans</i>	2.2% 	0–2.7%	Abundant	<span style="color: gray;">●</span> <span style="color: yellow;">●</span> <span style="color: gray;">●</span>
<i>Prevotella_1 unclassified</i>	2.2% 	0–2.3%	Rare	<span style="color: gray;">●</span> <span style="color: gray;">●</span> <span style="color: gray;">●</span>
<i>Blautia wexlerae</i>	2.0% 	1.0–5.9%	Abundant	<span style="color: green;">●</span> <span style="color: gray;">●</span> <span style="color: gray;">●</span>
<i>Prevotella stercorea</i>	1.9% 	0–0.2%	Occasional	<span style="color: gray;">●</span> <span style="color: gray;">●</span> <span style="color: red;">●</span>
<i>Dorea longicatena</i>	1.8% 	0.1–2.3%	Abundant	<span style="color: gray;">●</span> <span style="color: yellow;">●</span> <span style="color: gray;">●</span>
<i>Ruminococcaceae unclassified</i>	1.7% 	13–38%	Abundant	<span style="color: gray;">●</span> <span style="color: gray;">●</span> <span style="color: gray;">●</span>
<i>Ruminococcus bromii</i>	1.7% 	0–6.6%	Frequent	<span style="color: green;">●</span> <span style="color: gray;">●</span> <span style="color: gray;">●</span>
<i>Lachnoclostridium faecis</i>	1.6% 	0–1.3%	Abundant	<span style="color: gray;">●</span> <span style="color: gray;">●</span> <span style="color: red;">●</span>
<i>Bacteroides uniformis</i>	1.6% 	0–6.1%	Abundant	<span style="color: green;">●</span> <span style="color: gray;">●</span> <span style="color: gray;">●</span>
<i>Eubacterium rectale</i>	1.2% 	0.02–9.1%	Abundant	<span style="color: green;">●</span> <span style="color: gray;">●</span> <span style="color: gray;">●</span>
<i>Clostridium sensu stricto unclassified</i>	1.2% 	0–5.0%	Frequent	<span style="color: green;">●</span> <span style="color: gray;">●</span> <span style="color: gray;">●</span>


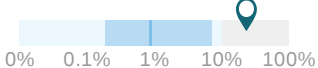
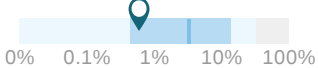

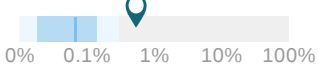
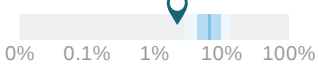
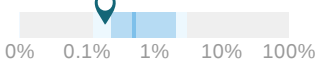
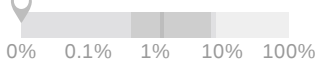
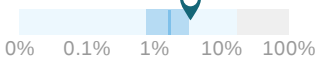
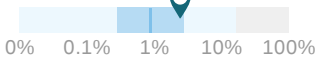
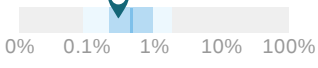
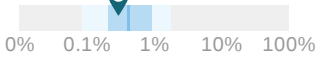
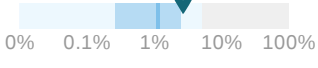
Bacterium	Abundance Percentage	Group limits	Prevalence	Status
<i>Sutterella wadsworthensis</i>	1.2% 	0–0.9%	Frequent	<input type="radio"/> <input type="radio"/> <input checked="" type="radio"/>
<i>Coriobacteriaceae unclassified</i>	1.2% 	0.4–21%	Abundant	<input type="radio"/> <input type="radio"/> <input type="radio"/>
<i>Dorea formicigenerans</i>	1.1% 	0.08–2.1%	Abundant	<input type="radio"/> <input checked="" type="radio"/> <input type="radio"/>
<i>Escherichia unclassified</i>	1.0% 	0–5.1%	Frequent	<input type="radio"/> <input checked="" type="radio"/> <input type="radio"/>
<i>Escherichia coli</i>	1.0% 	0–5.0%	Frequent	<input type="radio"/> <input checked="" type="radio"/> <input type="radio"/>

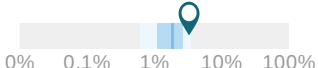
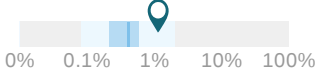
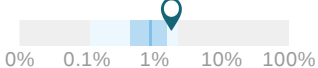

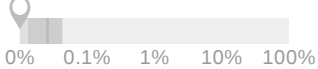
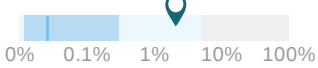
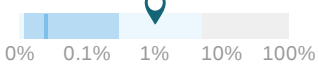
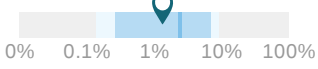
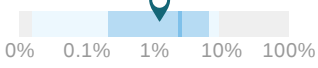
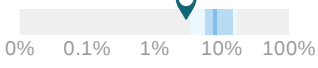
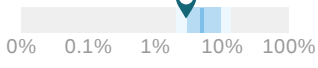
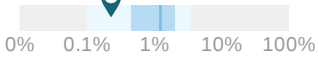
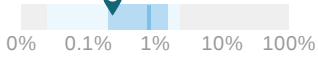
## Abundance of common bacteria in Your gut

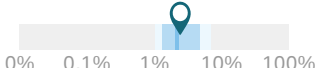
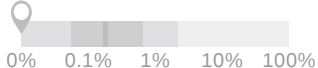
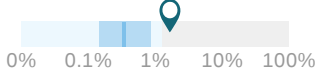

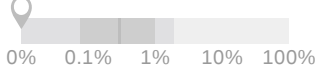
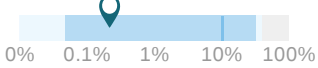
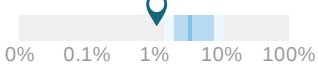
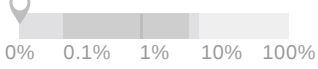
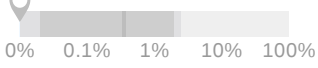
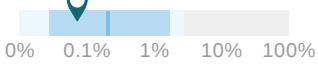
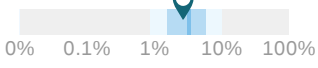
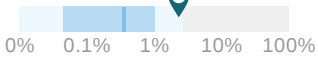
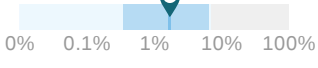
In the following table, common bacterial taxa detected in average gut are presented with the proportion of the bacteria in Your sample. Levels of each bacterium are compared to the healthy reference group to give a rating to the result. The rating of the result is statistical and may not reflect the health status. This table is sorted in alphabetical order, in which the general (higher) level is genus (**bold**) and the specific (lower) level is species (table: genus name + species name). If bacterial genera include lots of species, only the most common are shown.

Bacterium	Abundance Percentage	Group limits	Prevalence	Status
<b>Akkermansia sp.</b>	<0.01% 	0–1.8%	Frequent	
<i>Akkermansia muciniphila</i>	<0.01% 	0–1.8%	Frequent	
<b>Alistipes sp.</b>	<0.01% 	0.04–3.0%	Abundant	
<i>Alistipes finegoldii</i>	<0.01% 	0–0.2%	Frequent	
<i>Alistipes putredinis</i>	<0.01% 	0–0.8%	Abundant	
<i>Alistipes shahii</i>	<0.01% 	0–0.7%	Abundant	
<b>Bacteroides sp.</b>	26% 	0.2–23%	Abundant	
<i>Bacteroides cellulosilyticus</i>	0.3% 	0–4.9%	Frequent	
<i>Bacteroides eggerthii</i>	0.3% 	0–0.9%	Occasional	
<i>Bacteroides plebeius</i>	<0.01% 	0–11%	Frequent	
<i>Bacteroides thetaiotaomicron</i>	<0.01% 	0–0.4%	Frequent	

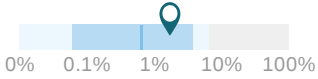
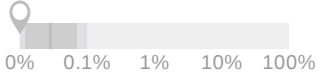
 Average levels  
  Above/below average  
  Above/below limits  
 Prevalence: rare <5/100, occasional <25/100, frequent <75/100, abundant ≥75/100

Bacterium	Abundance Percentage	Group limits	Prevalence	Status
<i>Bacteroides uniformis</i>	1.6% 	0–6.1%	Abundant	<span style="color: green;">●</span> <span style="color: gray;">●</span> <span style="color: gray;">●</span>
<i>Bacteroides vulgatus</i>	23% 	0–10%	Abundant	<span style="color: gray;">●</span> <span style="color: gray;">●</span> <span style="color: red;">●</span>
<b><i>Bifidobacterium sp.</i></b>	0.6% 	0–32%	Abundant	<span style="color: green;">●</span> <span style="color: gray;">●</span> <span style="color: gray;">●</span>
<b><i>Bilophila sp.</i></b>	0.5% 	0–0.3%	Abundant	<span style="color: gray;">●</span> <span style="color: gray;">●</span> <span style="color: red;">●</span>
<i>Bilophila wadsworthia</i>	0.5% 	0–0.3%	Frequent	<span style="color: gray;">●</span> <span style="color: gray;">●</span> <span style="color: red;">●</span>
<b><i>Blautia sp.</i></b>	2.2% 	2.7–13%	Abundant	<span style="color: gray;">●</span> <span style="color: gray;">●</span> <span style="color: red;">●</span>
<i>Blautia faecis</i>	0.2% 	0.1–3.1%	Abundant	<span style="color: gray;">●</span> <span style="color: yellow;">●</span> <span style="color: gray;">●</span>
<b><i>Christensenellaceae</i></b>	<0.01% 	0–8.3%	Frequent	<span style="color: gray;">●</span> <span style="color: gray;">●</span> <span style="color: gray;">●</span>
<b><i>Collinsella sp.</i></b>	3.3% 	0–17%	Abundant	<span style="color: gray;">●</span> <span style="color: yellow;">●</span> <span style="color: gray;">●</span>
<i>Collinsella aerofaciens</i>	2.3% 	0–16%	Abundant	<span style="color: green;">●</span> <span style="color: gray;">●</span> <span style="color: gray;">●</span>
<b><i>Coprococcus sp.</i></b>	0.3% 	0.09–1.9%	Abundant	<span style="color: green;">●</span> <span style="color: gray;">●</span> <span style="color: gray;">●</span>
<i>Coprococcus comes</i>	0.3% 	0.09–1.8%	Abundant	<span style="color: green;">●</span> <span style="color: gray;">●</span> <span style="color: gray;">●</span>
<b><i>Dialister sp.</i></b>	2.6% 	0–5.1%	Frequent	<span style="color: gray;">●</span> <span style="color: yellow;">●</span> <span style="color: gray;">●</span>

Bacterium	Abundance Percentage	Group limits	Prevalence	Status
<b><i>Dorea sp.</i></b>	3.2% 	0.6–3.6%	Abundant	<input type="radio"/> <input checked="" type="radio"/> <input type="radio"/>
<i>Dorea formicigenerans</i>	1.1% 	0.08–2.1%	Abundant	<input type="radio"/> <input checked="" type="radio"/> <input type="radio"/>
<i>Dorea longicatena</i>	1.8% 	0.1–2.3%	Abundant	<input type="radio"/> <input checked="" type="radio"/> <input type="radio"/>
<b><i>Eggerthella</i></b>	<0.01% 	0–0.05%	Occasional	<input type="radio"/> <input type="radio"/> <input type="radio"/>
<i>Eggerthella lenta</i>	<0.01% 	0–0.05%	Occasional	<input type="radio"/> <input type="radio"/> <input type="radio"/>
<b><i>Escherichia sp.</i></b>	2.0% 	0–5.1%	Frequent	<input type="radio"/> <input checked="" type="radio"/> <input type="radio"/>
<i>Escherichia coli</i>	1.0% 	0–5.0%	Frequent	<input type="radio"/> <input checked="" type="radio"/> <input type="radio"/>
<b><i>Eubacterium sp.</i></b>	1.3% 	0.1–9.3%	Abundant	<input checked="" type="radio"/> <input type="radio"/> <input type="radio"/>
<i>Eubacterium rectale</i>	1.2% 	0.02–9.1%	Abundant	<input checked="" type="radio"/> <input type="radio"/> <input type="radio"/>
<b><i>Faecalibacterium sp.</i></b>	2.9% 	3.4–16%	Abundant	<input type="radio"/> <input type="radio"/> <input checked="" type="radio"/>
<i>Faecalibacterium prausnitzii</i>	2.9% 	2.1–13%	Abundant	<input type="radio"/> <input checked="" type="radio"/> <input type="radio"/>
<b><i>Fusicatenibacter sp.</i></b>	0.2% 	0.1–3.7%	Abundant	<input type="radio"/> <input checked="" type="radio"/> <input type="radio"/>
<i>Fusicatenibacter saccharivorans</i>	0.2% 	0.02–2.4%	Abundant	<input checked="" type="radio"/> <input type="radio"/> <input type="radio"/>

Bacterium	Abundance Percentage	Group limits	Prevalence	Status
<b><i>Lachnoclostridium sp.</i></b>	2.3% 	1.0–6.9%	Abundant	<span style="color: green;">●</span> <span style="color: gray;">●</span> <span style="color: gray;">●</span>
<i>Lachnoclostridium torques</i>	<0.01% 	0–2.3%	Abundant	<span style="color: gray;">●</span> <span style="color: gray;">●</span> <span style="color: gray;">●</span>
<i>Lachnoclostridium faecis</i>	1.6% 	0–1.3%	Abundant	<span style="color: gray;">●</span> <span style="color: gray;">●</span> <span style="color: red;">●</span>
<i>Lachnoclostridium gnavus</i>	<0.01% 	0–0.3%	Occasional	<span style="color: gray;">●</span> <span style="color: gray;">●</span> <span style="color: gray;">●</span>
<i>Lachnoclostridium lactaris</i>	<0.01% 	0–2.0%	Frequent	<span style="color: gray;">●</span> <span style="color: gray;">●</span> <span style="color: gray;">●</span>
<b><i>Prevotella sp.</i></b>	0.2% 	0–40%	Abundant	<span style="color: green;">●</span> <span style="color: gray;">●</span> <span style="color: gray;">●</span>
<b><i>Roseburia sp.</i></b>	1.1% 	1.4–10%	Abundant	<span style="color: gray;">●</span> <span style="color: gray;">●</span> <span style="color: red;">●</span>
<i>Roseburia faecis</i>	<0.01% 	0–4.6%	Abundant	<span style="color: gray;">●</span> <span style="color: gray;">●</span> <span style="color: gray;">●</span>
<i>Roseburia intestinalis</i>	<0.01% 	0–2.5%	Abundant	<span style="color: gray;">●</span> <span style="color: gray;">●</span> <span style="color: gray;">●</span>
<i>Roseburia inulinivorans</i>	0.07% 	0–2.7%	Abundant	<span style="color: green;">●</span> <span style="color: gray;">●</span> <span style="color: gray;">●</span>
<b><i>Ruminococcus_1 sp.</i></b>	2.7% 	0.9–10%	Abundant	<span style="color: green;">●</span> <span style="color: gray;">●</span> <span style="color: gray;">●</span>
<i>Ruminococcus bicirculans</i>	2.2% 	0–2.7%	Abundant	<span style="color: gray;">●</span> <span style="color: orange;">●</span> <span style="color: gray;">●</span>
<b><i>Ruminococcus_2 sp.</i></b>	1.7% 	0–6.9%	Abundant	<span style="color: green;">●</span> <span style="color: gray;">●</span> <span style="color: gray;">●</span>


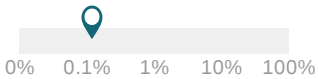
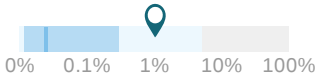
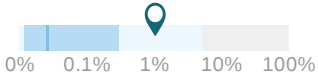
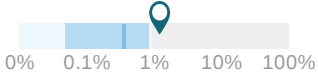


Bacterium	Abundance Percentage	Group limits	Prevalence	Status
<i>Ruminococcus bromii</i>	1.7% 	0–6.6%	Frequent	<span style="color: green;">●</span> <span style="color: gray;">●</span> <span style="color: gray;">●</span>
<i>Veillonella sp.</i>	<0.01% 	0–0.1%	Frequent	<span style="color: gray;">●</span> <span style="color: gray;">●</span> <span style="color: gray;">●</span>

## Abundance of pro-inflammatory bacteria in Your gut

This table contains up to 7 most abundant pro-inflammatory bacteria in Your gut. Levels of each bacteria are compared to the healthy reference group and assessed accordingly. The table is sorted in alphabetical order.

Several pro-inflammatory bacteria are commonly found in the gut microbial community of healthy people, but in low abundance. Attention is needed in case these pro-inflammatory bacteria are detected in higher abundance than average.

Bacterium	Abundance Percentage	Group limits	Prevalence	Status
<i>Bilophila wadsworthia</i>	0.5% 	0–0.3%	Frequent	<span style="color: grey;">●</span> <span style="color: grey;">●</span> <span style="color: red;">●</span>
<i>Campylobacter showae</i>	0.1% 	<0.01%	–	<span style="color: grey;">●</span> <span style="color: grey;">●</span> <span style="color: red;">●</span>
<i>Escherichia coli</i>	1.0% 	0–5.0%	Frequent	<span style="color: grey;">●</span> <span style="color: yellow;">●</span> <span style="color: grey;">●</span>
<i>Escherichia unclassified</i>	1.0% 	0–5.1%	Frequent	<span style="color: grey;">●</span> <span style="color: yellow;">●</span> <span style="color: grey;">●</span>
<i>Sutterella wadsworthensis</i>	1.2% 	0–0.9%	Frequent	<span style="color: grey;">●</span> <span style="color: grey;">●</span> <span style="color: red;">●</span>

● Average levels   
 ● Above/below average   
 ● Above/below limits  
 Prevalence: rare <5/100, occasional <25/100, frequent <75/100, abundant ≥75/100

