63 Zillicoa Street
Asheville, NC 28801

Patient: **SAMPLE PATIENT**
DOB:
Sex:
MRN:

Microbiomix

Improving gut health

Introduction to *Microbiomix*™ Report

Microbiomix is a comprehensive report detailing key information about your personal gut microbiome. As new information about the links between the gut microbiome and health are revealed, we will continue to update your online report to include these new findings.

Any information provided by us (including any information contained on our website or in any microbiome report) is for information purposes only. Such information is not medical advice and must not be taken to be a substitute for a consultation with your healthcare professional or doctor. It is not intended to diagnose conditions nor prescribe the use of any remedy, diet or lifestyle practice. Your health is your responsibility and if you have any concerns related to your health we recommend that you seek the advice of your healthcare professional or doctor.

Any information provided by us (including any information contained on our website or in any microbiome report) is for information purposes only. Such information is not medical advice and must not be taken to be a substitute for a consultation with your health care professional or doctor. It is not intended to diagnose conditions nor prescribe the use of any remedy, diet or lifestyle practice. Your health is your responsibility and if you have any concerns related to your health we recommend that you seek the advice of your health care professional or doctor.

Report Summary

Sample ID: genova-ref-1

Disclaimer: This report summary is provided to assist healthcare practitioners to interpret the Microbiomix report. The report should be used only after the health practitioner (you) has conducted a full client assessment which should include existing medications, allergies & intolerances and full client medical history.

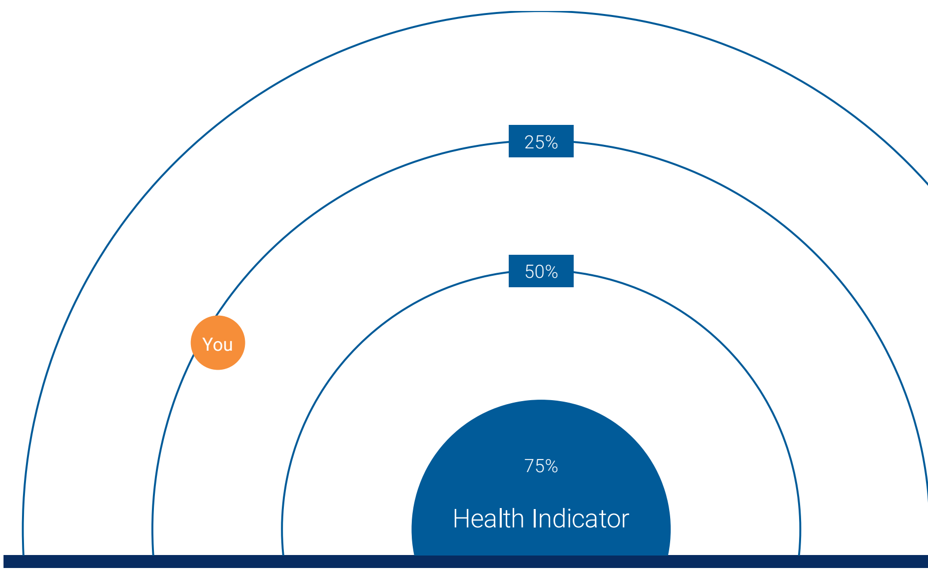
Marker	Suggestion
Pathobiont	**Correlate with clinical symptoms (consider antimicrobials if indicated)** The following species have been detected in the sample, and some strains can impact health: [Clostridium_M bolteae, Escherichia coli (coli_D)]. Investigate whether you have symptoms consistent with GI infection and treat accordingly if infection is suspected.
Hexa-acylated lipopolysaccharide production (High)	**Reduce Saturated Fats** Hexa-lipopolysaccharide (hexa-LPS) is a pro-inflammatory compound produced by certain bacteria. Diets high in fat, especially saturated fat, allow hexa-LPS to cross the intestinal barrier and enter the bloodstream. Avoiding excessive intake of saturated fat can help reduce the ability of hexa-LPS to enter the bloodstream. Common dietary sources of saturated fats include butter, coconut products, palm oil, cheese, fatty meats, biscuit, cakes, chocolate and ice cream. References [1] [2] [3] [4] [5] [6]
Beta-glucuronidase production (High)	**Glucomannan (Konjac root)** Beta-glucuronidase is a bacterial enzyme that may limit the body's ability to excrete compounds such as drugs, hormones, and environmental toxins. One human study has suggested that consuming glucomannan can reduce fecal beta-glucuronidase activity. Glucomannan is a type of prebiotic fiber found in konjac root which is commonly used to make low calorie pasta and noodles. References [1] [2]

Marker	Suggestion
Hydrogen sulfide production (High)	**RS & FOS** Hydrogen sulfide is a gas that some intestinal bacteria produce by breaking down sulfur-containing amino acids. Elevated levels of hydrogen sulfide can inhibit energy production in intestinal cells as well as alter the mucus barrier of the intestine, and this has been associated with inflammatory bowel disease. To prevent elevated production of hydrogen sulfide, ensure intake of the amino acids methionine and cysteine is not excessive. Laboratory based studies have suggested that eating foods high in resistant starch (e.g. lentils, peas, beans, rolled oats and cooked and cooled potatoes) or fructooligosaccharides (FOS) (e.g. onions, garlic, leek, banana, peaches, wheat, barley) can reduce the production of hydrogen sulfide by the microbiome. References [1] [2]
B. fragilis toxin production (High)	**Correlate with clinical symptoms (consider antimicrobials if indicated)** In some people this toxin can cause symptoms such as diarrhea while other people can remain symptom free. There are concerns that this toxin can cause intestinal inflammation. If your patient is experiencing diarrhea and has this toxin present, consider intervention References [1] [2]
Ammonia (urease) production (High)	**Consider Fiber/Protein balance in diet** Ammonia production is a normal way that bacteria recycle protein in the gut. However, high levels of ammonia production have been observed in individuals with impaired gut barrier function and inflammation of the gut. Consider balancing the diet to prevent excessive protein intake and ensure that protein intake is balanced with sufficient fiber intake (fiber to protein ratio). Speak with your healthcare practitioner if this result is of concern. References [1] [2]
Histamine production (High)	**Correlate with clinical symptoms** Gut bacteria that can produce histamine have been observed at increased levels in patients with asthma. Additionally, people with food allergies and irritable bowel syndrome may be more sensitive to histamine in the gut. Speak with your healthcare practitioner if this result is of concern. References [1] [2] [3]

END OF REPORT SUMMARY

Your report overview

Welcome to the start of your journey to understanding how your microbiome affects your health. Throughout this report, the analyzed sample is compared to a healthy comparison group. This group is a collection of gut microbiome samples from everyday healthy people, who have not reported any significant health issues or symptoms. It represents a range of age groups, genders and diets.

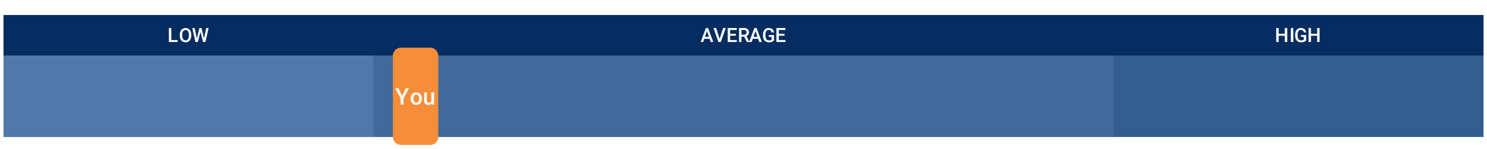


Your gut microbiome score is less than 50%. This measurement is an indication of how well your gut microbiome might be interacting with your overall health. A higher score suggests a more positive interaction.

Microbial Diversity

MICROBIAL DIVERSITY

Microbial diversity is a measure of the number of different microorganisms and the amount of each of these microorganisms in your sample. Average to high microbial diversity is associated with good health. A varied diet rich in plant-based foods such as fruits, vegetables, whole grains and nuts can help increase microbiome diversity. The Shannon Index is a measure of diversity which is used by members of the scientific community to compare results through time.



Your diversity level is
Average

Shannon Index
3.46

Your microbial community

Your top 5 most abundant species

Does your sample have an overly high abundance of any single organism? **Yes**

	Phylum	Species	Abundance	Range	Level
⊖	Bacteroidota	***Bacteroides_B dorei***	10.8%	0.00 - 4.18%	High
	Firmicutes_A	***Blautia_A wexlerae***	10.7%	0.222 - 2.79%	High
	Firmicutes_A	***Faecalibacterium prausnitzii_D***	9.67%	0.099 - 2.11%	High
⊕	Firmicutes_A	***Roseburia inulinivorans***	7.34%	0.00 - 0.636%	High
	Proteobacteria	***Enterobacter himalayensis***	3.92%	0.00 - 0.00%	High

Your *key* insights

Your gut microbiome's potential to produce butyrate, a primary fuel source for gut cells

This is a good level! Your potential to produce butyrate is at a level similar to the healthy group. To benefit from this important gut microbiome function, ensure your diet is rich in dietary sources of resistant starch.

A **This sample reported a level similar to the healthy group**

The production of butyrate is a well-studied function of the gut microbiome. This 'metabolite' is named as one of the primary fuel sources for gut cells and has been shown to reduce inflammation throughout the body and help regulate appetite. A similar or high level to produce butyrate is beneficial for your gut microbiome and helps to maintain a healthy environment in the gut. Foods rich in resistant starch (e.g. lentils, peas, beans, and rolled oats) will encourage microbes in your gut to produce butyrate.

EVIDENCE RATING ★★★★★

Your microbiome's potential to negatively impact your gut through inflammation

This is not a good level. Having a high potential to produce hexa-lipopolysaccharides (hexa-LPS) compared to the healthy group is not ideal. High levels of hexa-LPS can contribute to inflammation throughout the body. Avoiding excessive amounts of saturated fat could help to prevent this substance from spreading to areas outside of the gut. Also try adding foods high in fiber to reduce the levels of bacteria that produce this harmful substance.

A **This sample reported a level higher than the healthy group**

Hexa-lipopolysaccharide (hexa-LPS) is a pro-inflammatory molecule and a component of the cell wall in some bacteria. When these bacteria die, hexa-LPS is released into the gut. Diets high in fat, especially saturated fat, allow hexa-LPS to cross the intestinal barrier and eventually enter the bloodstream. High levels of hexa-LPS in the blood have been observed in individuals with heart disease, type 2 diabetes, obesity, and non-alcoholic fatty liver disease. If you have a high potential to produce hexa-LPS, you may wish to avoid excessive consumption of saturated fat. Dietary sources of saturated fat include butter, coconut oil, cheese, processed meats, chocolate, ice cream, cakes and biscuits.

EVIDENCE RATING ★★★★★

Your *key* insights

Your gut microbiome's ability to break down fiber

This is a good level! Your potential to break down fiber is similar to the healthy group in this sample. This is an important gut microbiome function to maintain because it results in the production of beneficial substances that promote good gut health. To ensure the production of these beneficial compounds ensure your diet contains plenty of fiber.

A **This sample reported a level similar to the healthy group**

Fiber-degrading bacteria are responsible for producing important by-products such as short chain fatty acids which play a critical role in keeping your gut healthy. Specific prebiotic fibers, detailed in your food suggestions, will promote the growth of your beneficial, fiber-degrading bacteria. A similar or high proportion of species that can break down fiber compared to the healthy group is considered beneficial.

EVIDENCE RATING ★★★★☆

Your gut microbiome's ability to break down protein

This is a typical level. The proportion of bacteria present in your sample that can break down protein is at level similar to the healthy group. When protein is broken down by bacteria in the gut microbiome it can lead to the production of substances that promote inflammation. To maintain this level, continue eating diverse sources of fiber to encourage the growth of your fiber-degrading bacteria instead of your protein-degrading bacteria.

A **This sample reported a level similar to the healthy group**

Everyone's microbiome contains species that can break down protein into a variety of compounds, including some compounds that promote inflammation. Having a high proportion of these species may reflect an insufficient amount of fiber in the diet or an excessive intake of protein. A high proportion of protein-degrading bacteria suggests that not enough fiber is reaching the lower colon to feed the bacteria that specialize in eating fiber.

EVIDENCE RATING ★★★★☆

Your *key* insights

Your microbiome's potential to produce branched chain amino acids

This is a good level! Your potential to produce branched chain amino acids is at a level similar to the healthy group. This is good, as bacterially produced BCAAs are observed to be associated with obesity and insulin resistance.

A **This sample reported a level similar to the healthy group**

BCAAs play an important role in building muscles and in helping regulate fat and sugar metabolism. However, a high potential to produce BCAAs by your gut microbiome may not be a good thing as high levels of bacterially produced BCAAs have been observed in individuals with obesity and insulin resistance. Having a low or similar potential to produce branched chain amino acids (BCAAs) compared to the healthy group is generally considered beneficial. Maintaining muscle mass through regular resistance exercise could help regulate BCAA blood levels.

EVIDENCE RATING ★★★★☆

Your microbiome's potential to contribute to cardiovascular disease

This is a good level! Your potential to produce trimethylamine (TMA) is at a level similar to the healthy group. Trimethylamine can be converted by the human liver into trimethylamine oxide (TMAO) which has been linked to cardiometabolic conditions. Plant chemicals known as indoles have been shown to reduce the production of TMAO.

A **This sample reported a level similar to the healthy group**

A similar or low potential to produce trimethylamine compared to the healthy group is generally considered beneficial. Trimethylamine can be converted by the human liver into trimethylamine oxide (TMAO) which has been linked to cardiovascular and chronic kidney disease. Diets high in animal protein and low in fiber have been associated with increased trimethylamine production by gut microbes while plant chemicals known as indoles have been shown to reduce the production of TMAO.

EVIDENCE RATING ★★★★☆

Your *key* insights

Your microbiome's potential to protect your nervous system

This is not a good level. Your potential to produce indolepropionic acid (known as IPA) is at a low level. IPA is a strong antioxidant that can protect nerve cells from damage and may help protect against insulin resistance. Try eating a diverse range of foods that are high in fiber, especially foods with rye, to improve this important gut microbiome function.

A **This sample reported a level lower than the healthy group**

IPA is a strong antioxidant produced by our gut bacteria that performs many important functions in our gut. It can protect nerve cells from damage, suppress inflammation and may protect against insulin resistance and type 2 diabetes. Consuming foods high in fiber and in particular rye, has been correlated to increased IPA production in the gut. A similar or high potential to produce indolepropionic acid (IPA) compared to the healthy group is considered beneficial.

EVIDENCE RATING ★★★☆☆

Your microbiome's potential to prevent kidney stones

This is a good level! Your potential to degrade oxalates is similar to the healthy group. This may reduce your risk of developing calcium oxalate kidney stones.

A **This sample reported a level similar to the healthy group**

The gut microbiome of individuals who suffer from frequent kidney stones often have a low potential to degrade oxalate. Oxalate is one of the main components of calcium oxalate kidney stones. If you are prone to kidney stones, you may wish to discuss trialling a low oxalate diet with a health care professional. However, if you do not suffer from kidney stones then your potential to degrade oxalate is not of concern. A similar or high potential to break down oxalate compared to the healthy group is generally considered beneficial.

EVIDENCE RATING ★★★☆☆

Your *key* insights

Your gut microbiome's potential to produce strong-smelling flatulence

This is not a good level. Your potential to produce hydrogen sulfide is at a high level. Try adding foods high in prebiotic fibers, especially those foods containing resistant starch (RS) and fructooligosaccharides (FOS) such as cooked and cooled potatoes/sweet potatoes, rye, slightly green bananas, nectarines, and pears to reduce the production of hydrogen sulfide, which when produced by gut bacteria, has been associated with an impaired gut barrier function.

A **This sample reported a level higher than the healthy group**

As the microbes in your gut digest different fuel sources, such as fiber, protein, mucus and even bile acids, they produce different types of gases as a by-product. Flatulence is primarily made up of odorless gases such as nitrogen, hydrogen, carbon dioxide, and methane. However, a small percent of flatulence can be made up of the gas hydrogen sulfide, which gives flatulence the characteristic rotten eggs smell. A small amount of hydrogen sulfide gas has been found to be protective of the gut, however a high potential to produce hydrogen sulfide has been associated with mitochondrial dysfunction and impaired gut barrier function. Research has found that the production of hydrogen sulfide by gut bacteria can be inhibited by consuming foods high in the prebiotic fibers resistant starch (RS) and fructooligosaccharides (FOS).

EVIDENCE RATING ★★★☆☆

Your microbiome's potential to contribute to cell replication and repair

This is a good level! Your gut microbiome's potential to produce folate is at a level similar to the healthy group. Folate is important for cell replication and repair. Your gut microbiome has the potential to contribute up to 37% of your daily folate requirement.

A **This sample reported a level similar to the healthy group**

Folate plays an important role in cell replication and repair. Deficiencies can result in an increased risk of heart disease, anaemia, and stroke in adults. We cannot produce folate on our own and it is primarily obtained from plants in our diet (e.g. dark green leafy vegetables, fruits and legumes) and bacteria living in our gut. This bacterial production can supplement your body's folate requirements. A similar or high potential to produce folate compared to the healthy group is generally considered beneficial.

EVIDENCE RATING ★★☆☆☆

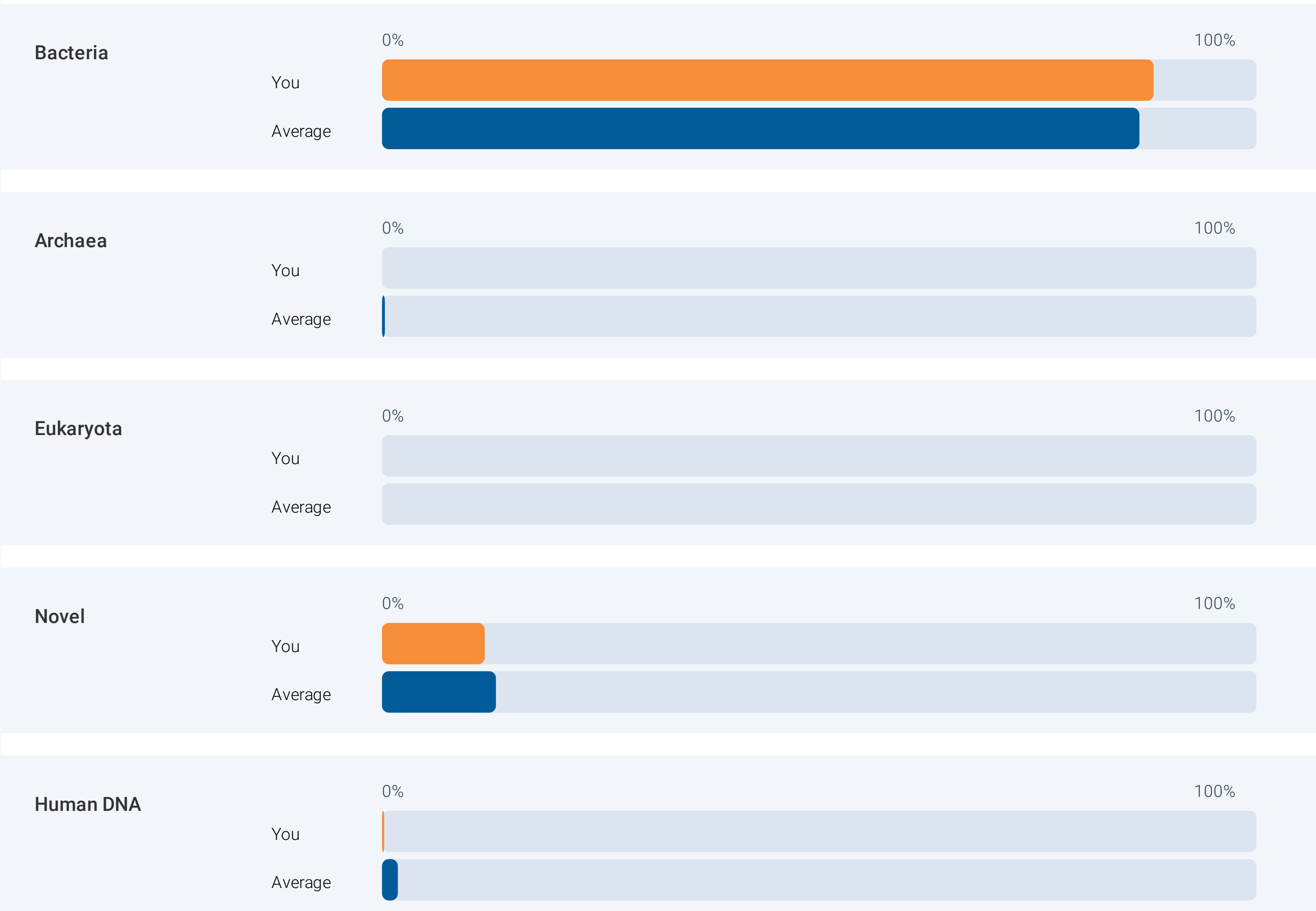
Digging deeper into the detail

Gut microbiome report

Sample Composition

Sample Composition

Most of the DNA in your stool (~99%) is from microorganisms and only a small amount (~1%) is from you. The microorgansims in your gut fall into four main groups: bacteria, archaea (another form of microscopic life), eukaryotes (this includes fungi and parasites) and viruses. Below we show the levels of bacteria, archaea, eukaryotes, and novel (unidentifiable) DNA in your sample. The amount of human DNA in your sample is also shown. A high amount (greater than 4%) of human DNA may indicate gut inflammation. If you have greater than 4% human DNA, and you did not accidentally touch your swab during sampling, you should consult with a health care practitioner.



Microbiome Digestion Potential

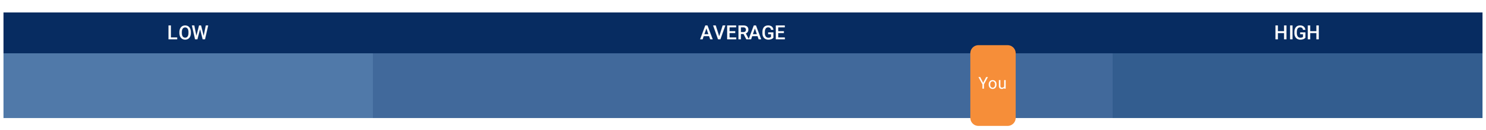
The source of food that bacteria can use varies between different species of gut bacteria. Below we show the proportion of species in your gut microbiome that can break down the fuel sources fiber, protein and mucin (mucus). After you eat a meal, food gets broken down in your stomach and travels to your small intestine, where most nutrients are absorbed. The food components that cannot be absorbed in the small intestine, such as fiber and excess protein, make their way to your large intestine where your gut microbiota transform these components into a variety of products called metabolites. These metabolites can play an important role in your health. Read more about each of the fuel sources and their links to health on each of the tabs below.

Fiber

This scale indicates the proportion of species in your gut microbiome that can break down fiber. If you have a low proportion, consider adding more fiber to your diet to improve your gut health. Fiber is the main energy source of gut bacteria, who break it down into beneficial metabolites such as short chain fatty acids and B vitamins. Short chain fatty acids such as butyrate play an important role in keeping us healthy, and is one of the reasons fiber is an important component of a healthy diet.

Mucin

This scale indicates the proportion of species in your gut microbiome that can break down mucin, a component of the protective mucus layer that lines our gut. Some bacteria can use mucin as a fuel source. Mucus turnover is a normal part of our gut function, however when the abundance of bacteria that eat mucus becomes too high, this can result in a thinning of the mucus layer and activation of the immune system. Our mucus layer is important because it serves as a protective barrier between the cells lining our gut and harmful bacteria. Mucus-degrading bacteria may increase in abundance when there is not enough fiber reaching the lower large intestine, allowing gut bacteria that can use mucus as an energy source to multiply.



Protein

This scale indicates the proportion of species in your gut microbiome that can break down protein. If you have a high proportion, consider reducing the amount of protein in your diet to improve gut health. Although most protein is absorbed by your body, excess protein that is not absorbed will pass to your gut microbiome. The metabolites produced from the break down of protein are varied, with some being beneficial and others promoting inflammation. Diets high in animal protein and low in fiber have been observed to increase levels of pro-inflammatory gut metabolites.

Microbial Metabolites

Your gut bacteria can produce thousands of different substances, called metabolites, when they use different fuel sources for energy. These metabolites can interact with our immune, metabolic and nervous systems to influence our health. Some of these metabolites promote good health while others promote poor health.

Microbial Metabolites

Below we show the potential of your gut microbiome to produce or consume different metabolites associated with health and disease. The microorganisms in your gut can transform the food components you eat into thousands of products called metabolites. Some metabolites have been associated with health benefits while others have been associated with disease. Compare your microbiome's potential to produce and consume some of these metabolites with your selected comparison group. A ' + ' sign next to the compound name indicates it is associated with health and a ' - ' sign indicates it is associated with disease.

Health indicators

Produced

		ND	LOW	AVERAGE	HIGH
− *Hexa-acylated lipopolysaccharide production*	**4.41%**				You

The abundance of this metabolite is higher than the comparison group.

Hexa-lipopolysaccharide (hexa-LPS) is a pro-inflammatory compound produced by some species of bacteria within the Proteobacteria phylum. High levels of hexa-LPS in the blood have been observed in individuals with metabolic and inflammatory conditions such as obesity, heart disease, type 2 diabetes and non-alcoholic fatty liver disease. Diets high in fat, especially saturated fat, allow hexa LPS to cross the intestinal barrier and enter the bloodstream. Avoiding excessive intake of saturated fat can help reduce the ability of hexa-LPS to enter the bloodstream.Common dietary sources of saturated fats include butter, coconut products, palm oil, cheese, fatty meats, biscuit, cakes, chocolate and icecream.

[1] [2] [3] [4] [5] [6]

		ND	LOW	AVERAGE	HIGH
− *Methane production*	**0.00%**	You			

This metabolite is not detected in this microbiome.

The gas methane can be produced by some species of the gut microbiome, primarily through the reduction of carbon dioxide and hydrogen. Although methane production is often detected in healthy adult populations, elevated levels of methane production has been associated with slower intestinal transit times and constipation.

[1] [2] [3] [4]

		ND	LOW	AVERAGE	HIGH
− *Trimethylamine production*	**3.44%**			You	

The abundance of this metabolite is about the same as the comparison group.

A high potential to produce trimethylamine has been correlated to heart disease and type 2 diabetes. Once trimethylamine is produced by gut microbes, it is transported to the liver and converted to trimethylamine-n-oxide (TMAO). TMAO has been shown to be involved with blood sugar control, blood clotting and inflammation.

The indoles diindolylmethane (DIM) and indole-3-carbinol (I3C) found in cruciferous vegetables (e.g. broccoli, cauliflower, cabbage, kale) may reduce the amount of trimethylamine that is converted to TMAO in the liver. In addition, excessive red meat consumption is associated with increased levels of TMAO in the blood. If your potential to produce trimethylamine is high, you may wish to increase your consumption of cruciferous vegetables and avoid eating excessive amounts of red meat.

[1] [2] [3] [4] [5] [6] [7]

Microbial Metabolites

Health indicators

Produced

	Metabolite	Value	ND	LOW	AVERAGE	HIGH
⊖	*Ammonia (urease) production*	**11.0%**				You

The abundance of this metabolite is higher than the comparison group.

Ammonia production is a normal way that bacteria recycle protein in the gut. However, high levels of ammonia production have been observed in individuals with impaired gut barrier function and inflammation of the gut.
[1] [2]

	Metabolite	Value	ND	LOW	AVERAGE	HIGH
⊖	*B. fragilis toxin production*	**0.172%**				You

The abundance of this metabolite is higher than the comparison group.

Most people's gut microbiome contain a species of bacteria called *Bacteroides fragilis*. A small proportion of *B. fragilis* strains have the ability to secrete a toxin. In some people this toxin can cause symptoms such as diarrhea while other people can remain symptom free. There are concerns that this toxin can cause intestinal inflammation. If you are experiencing diarrhea and have this toxin,discuss this with your healthcare practitioner.
[1] [2]

	Metabolite	Value	ND	LOW	AVERAGE	HIGH
	Beta-glucuronidase production	**27.3%**				You

The abundance of this metabolite is higher than the comparison group.

Beta-glucuronidase is a bacterial enzyme which can limit the excretion of compounds from the body such as medications, hormones and environmental toxins. One human study has suggested that consuming glucomannan can reduce fecal beta-glucuronidase activity. Glucomannan is a type of prebiotic fiber found in konjac root which is commonly used to make low calorie pasta and noodles.
[1] [2]

	Metabolite	Value	ND	LOW	AVERAGE	HIGH
⊖	*Hydrogen sulfide production*	**17.4%**				You

The abundance of this metabolite is higher than the comparison group.

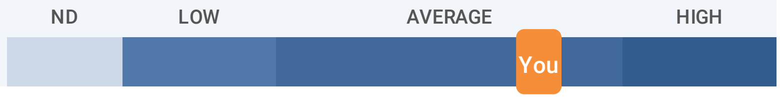
The gas hydrogen sulfide is produced by bacteria when they break down sulfur-containing amino acids found in foods such as eggs, meat, and fish. This gas is responsible for the rotten egg smell of flatulence. At low to average levels, hydrogen sulfide can play a beneficial role by acting as an energy source for gut cells. However at high levels hydrogen sulfide can inhibit energy production in gut cells and disrupt the gut mucus barrier. Elevated levels of hydrogen sulfide have been associated with inflammatory bowel disease (IBD). Laboratory based studies have suggested that eating foods high in resistant starch (e.g. lentils, peas, beans, rolled oats and cooked and cooled potatoes) or fructooligosaccharides (FOS) (e.g. onions, garlic, leek, banana, peaches, wheat, barley) can reduce the production of hydrogen sulfide by the microbiome.
[1] [2]

Microbial Metabolites

Health indicators

Produced

Branched chain amino acids production **65.5%**



The abundance of this metabolite is about the same as the comparison group.

Branch chain amino acids (BCAAs) are involved in the regulation of glucose and fat metabolism and the immune system. High levels of BCAAs have been associated with metabolic diseases, such as obesity and type 2 diabetes. Muscle plays an important role in regulating BCAA levels. A high potential to produce BCAAs has also been associated with people who have a diet that is low in fiber. Maximizing muscle mass through regular physical activity can help maintain metabolic balance.

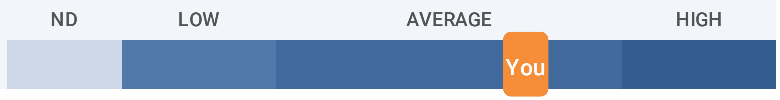
[1] [2]

Microbial Metabolites

Health indicators

Consumed

Oxalate consumption **3.70%**



The abundance of this metabolite is about the same as the comparison group.

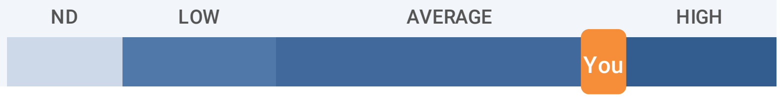
Some bacteria can break down oxalates in the colon, thus reducing the risk of forming calcium oxalate kidney stones. People who suffer from repeated unexplained kidney stones are observed to have a low potential for oxalate degradation in their microbiome compared to non-stone formers. A similar or high level to degrade oxalate compared to the healthy group is considered optimal, however if you do not suffer from kidney stones your gut microbiome's potential to degrade oxalate is not a concern. If your microbiome has a low potential to break down oxalate and you are prone to kidney stones, you may wish to discuss trialling a low oxalate diet with a health care professional.
[1] [2]

Microbial Metabolites

Neuroendocrine

Produced

GABA production **24.1%**

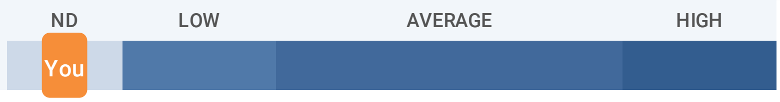


The abundance of this metabolite is about the same as the comparison group.

GABA (gamma-aminobutyric acid) plays an important role in regulating mental state by calming the nervous system. Low levels of GABA have been associated with depression and anxiety. Most GABA is produced in the brain however your gut microbiome may contribute to your GABA levels as some bacteria can produce or consume GABA. The role of gut bacteria that produce GABA in anxiety and depression is currently not understood. If you are concerned about your mental health, it is important to seek professional help.

[1] [2] [3]

3-indolepropionic acid (IPA) production **0.00%**

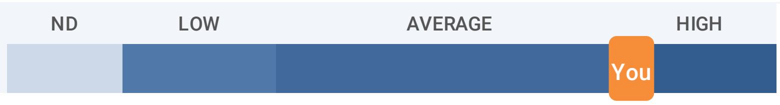


This metabolite is not detected in this microbiome.

3-indolepropionic acid (IPA) is a beneficial substance produced by some gut bacteria when they break down the amino acid tryptophan. It is a strong anti-oxidant that can help protect the nervous system from damage. Research has also shown that IPA may play a role in the prevention of type 2 diabetes and research in animal models suggests that IPA may suppress inflammation and help maintain the gut barrier. Studies have indicated that consuming foods high in dietary fiber, and in particular rye, can help increase IPA production.

[1] [2] [3] [4]

Histamine production **4.52%**



The abundance of this metabolite is higher than the comparison group.

Histamine is a chemical produced by the breakdown of the amino acid histidine. It is produced by human cells and also by some bacterial species in the gut. It plays an important role in immune regulation, gut function and the nervous system. Gut bacteria that can produce histamine have been observed at increased levels in patients with asthma. Additionally, people with food allergies and irritable bowel syndrome may be more sensitive to histamine in the gut.

[1] [2] [3]

Microbial Metabolites

Neuroendocrine

Consumed

			ND	LOW	AVERAGE	HIGH
⊕	*GABA consumption*	**14.9%**				You

The abundance of this metabolite is about the same as the comparison group.

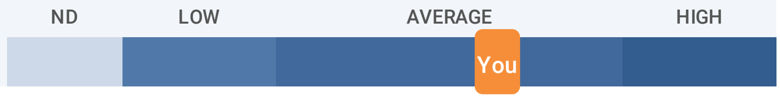
GABA (gamma-aminobutyric acid) plays an important role in regulating mental state by calming the nervous system. Low levels of GABA have been associated with depression and anxiety. Most GABA is produced in the brain however your gut microbiome may contribute to your GABA levels as some bacteria can produce or consume GABA. The role of gut bacteria that produce GABA in anxiety and depression is currently not understood. If you are concerned about your mental health, it is important to seek professional help.
[1] [2] [3]

Microbial Metabolites

Short chain fatty acids

Produced

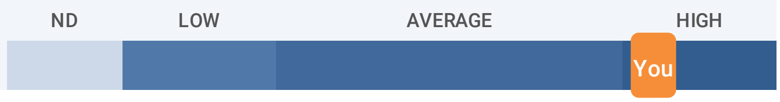
⊕	*Butyrate production*	**20.3%**



The abundance of this metabolite is about the same as the comparison group.

Butyrate is a beneficial short chain fatty acid that is very important for gut health. It is the main fuel source for gut cells, helps keep the gut cell barrier intact, supresses inflammation, helps control appetite, and promotes the production of serotonin in the gut. Low levels of butyrate production have been observed in individuals with inflammatory bowel diseases. Consuming foods high in resistant starch (e.g. lentils, peas, beans, cooked and cooled potatoes, rolled oats) or pectin (e.g. avocado, kiwifruit, berries, citrus fruits, pumpkin, zucchini) have been shown to increase butyrate levels.
[1] [2] [3] [4] [5] [6] [7] [8]

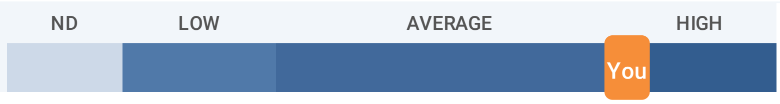
Lactate production	**80.4%**



The abundance of this metabolite is higher than the comparison group.

Lactate, or lactic acid, is a beneficial substance produced by our gut bacteria. It can reduce inflammation, help maintain the gut cell barrier, and protect from gut infections by lowering the pH in the gut. Lactate can also be converted by some bacterial species to beneficial short chain fatty acids. Lactate or lactic-acid producing bacteria have a long tradition of being used to produce fermented foods such as yogurt, kefir, sauerkraut and kimchi.
[1] [2]

⊕	*Propionate production*	**9.24%**



The abundance of this metabolite is higher than the comparison group.

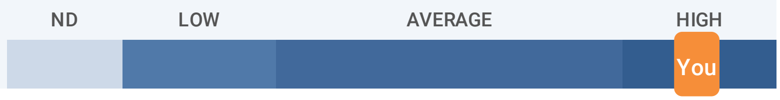
Propionate is a beneficial short chain fatty acid that is important for gut health. It helps maintain blood glucose levels, can reduce inflammation, helps control appetite and promotes the production of serotonin from the gut. The prebiotic fiber beta-glucan, found in oats and barley, has been shown to increase propionate production.
[1] [2] [3] [4] [5] [6]

Microbial Metabolites

Short chain fatty acids

Produced

⊕ *Acetate production* **81.7%**



The abundance of this metabolite is higher than the comparison group.

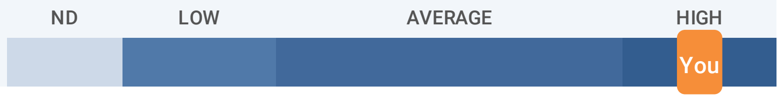
Acetate is the most abundant short chain fatty acid produced by our gut microbiome. It plays a beneficial role by supressing inflammation, regulating appetite, and regulating fat metabolism. Several bacterial species can also convert acetate to the beneficial short chain fatty acid, butyrate. The consumption of wholegrains, fruits, vegetables, legumes, nuts and seeds are associated with increased short chain fatty acids, including acetate. [1] [2] [3]

Microbial Metabolites

Essential vitamins

Produced

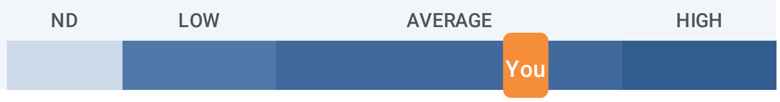
Cobalamin (B12) production **29.3%**



The abundance of this metabolite is higher than the comparison group.

Vitamin B12 is important for ensuring normal functioning of the nervous system and in the development of red blood cells. Although gut bacteria can produce this vitamin, humans are only able to absorb vitamin B12 in the small intestine, thus B12 produced in the large intestine will not be used by our body. However, bacteria also need vitamin B12 to function, so although our gut bacteria are unlikely to provide us with useable vitamin B12, an average to high potential to produce B12 means your bacteria will not compete with you for available vitamin B12. Reduced vitamin B12 production is often seen in the gut microbiome of people as they age and a study in elderly individuals observed that a multistrain probiotic increased plasma B12 levels. The most important dietary sources of vitamin B12 are meat, milk and dairy products.
[1] [2] [3]

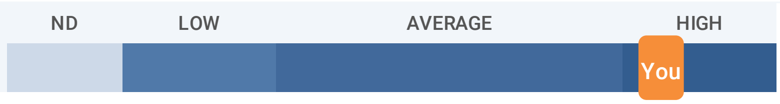
Folate (B9) production **60.2%**



The abundance of this metabolite is about the same as the comparison group.

Folate or folic acid plays an important role in cell replication and repair. Low folate levels can result in anemia and have been linked to an increased risk of heart disease and stroke. Folate cannot be produced by human cells and must be obtained through diet or from the microbiome. The large intestine has the ability to absorb folate produced by the gut microbiome and it is estimated that the human gut microbiome can provide up to 37% of the daily folate requirement. Non-organic bread must be fortified with folic acid while rich dietary sources include dark green leafy vegetables, fruit, legumes, and nuts.
[1] [2] [3]

Biotin (B7) production **35.7%**



The abundance of this metabolite is higher than the comparison group.

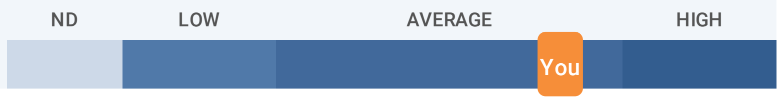
Biotin plays a critical role in metabolism and in the regulation of the immune system. Biotin cannot be produced by human cells and must be obtained through diet or the microbiome. The large intestine has the ability to absorb biotin but it is estimated that the gut microbiome can only provide up to 4.5% of the human daily biotin requirement. Dietary sources of biotin include liver, meat, fish, eggs and nuts.
[1] [2] [3] [4]

Microbial Metabolites

Essential vitamins

Produced

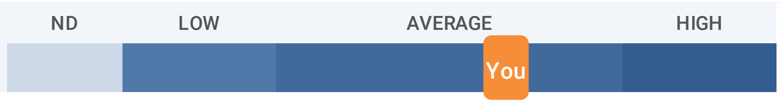
Riboflavin (B2) production **53.3%**



The abundance of this metabolite is about the same as the comparison group.

Riboflavin plays a crucial role in fat, vitamin B6, folate, tryptophan and homocysteine metabolism. Riboflavin cannot be produced by human cells and must be obtained through diet or the microbiome. The large intestine has the ability to absorb riboflavin but it is estimated that the gut microbiome can only provide up to 2.8% of the human daily riboflavin requirement. Dietary sources of riboflavin include milk and milk products, eggs, green vegetables, mushrooms and fortified breads and cereals.
[1] [2] [3]

Vitamin K production **23.3%**



The abundance of this metabolite is about the same as the comparison group.

K vitamins are a family of fat soluble vitamins which play an important role in blood clotting. Vitamin K cannot be produced by human cells and must be obtained through diet or the microbiome. Vitamin K1 (phylloquinone) is found in plants such as dark green leafy vegetables and canola oil, and is the principal form of dietary vitamin K used by the body. Bacterially derived vitamin K (menaquinones) are produced by our gut bacteria and are found in fermented foods, dairy products and meat. The amount of bacterially derived vitamin K (menaquinones) that can be absorbed by the large intestine is still unknown.
[1] [2]

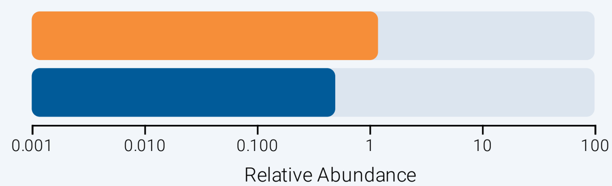
Species of Interest

Bacteria (prokaryotes)

Agathobacter	**NOT DETECTED**
Akkermansia	**NOT DETECTED**
Bifidobacterium	**DETECTED**

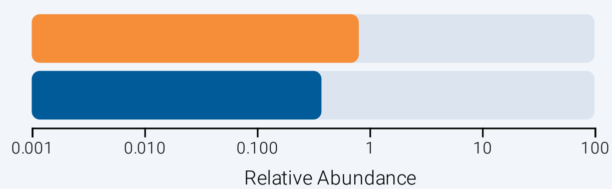
Bifidobacterium longum

You	**1.20%**
Average	**0.499%**



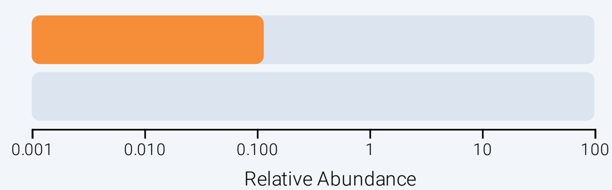
Bifidobacterium bifidum

You	**0.807%**
Average	**0.376%**



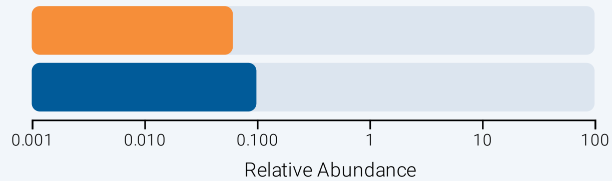
Bifidobacterium dentium

You	**0.115%**
Average	**0.001%**



Bilophila **DETECTED**

⊖ *Bilophila wadsworthia*	You	**0.061%**	
	Average	**0.099%**	



Campylobacter **NOT DETECTED**

Citrobacter **NOT DETECTED**

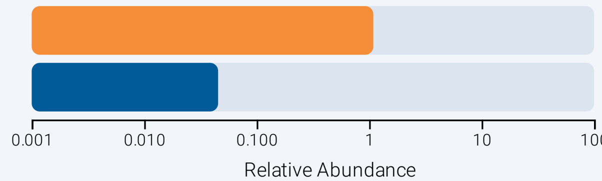
Clostridioides **NOT DETECTED**

Clostridium

DETECTED

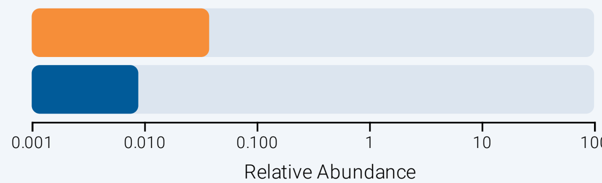
Clostridium_M sp000431375

You	**1.09%**
Average	**0.046%**



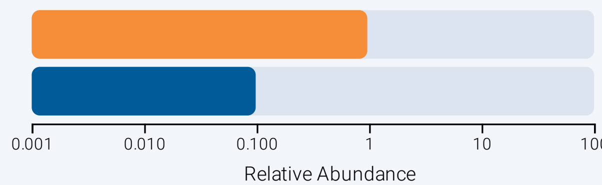
⊖ ***Clostridium_M bolteae***

You	**0.038%**
Average	**0.009%**



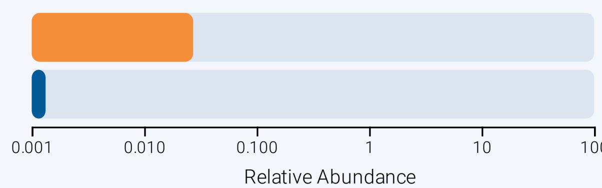
Clostridium_Q sp003024715

You	**0.967%**
Average	**0.098%**



Clostridium_Q saccharolyticum

You	**0.027%**
Average	**0.001%**



Corynebacterium

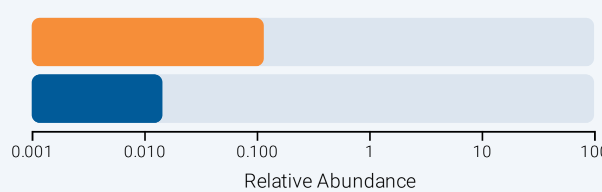
NOT DETECTED

Desulfovibrio

DETECTED

Desulfovibrio piger_A

You	**0.116%**
Average	**0.015%**



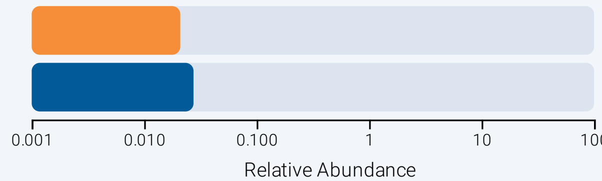
Eggerthella

DETECTED

Eggerthella lenta

You **0.021%**

Average **0.027%**



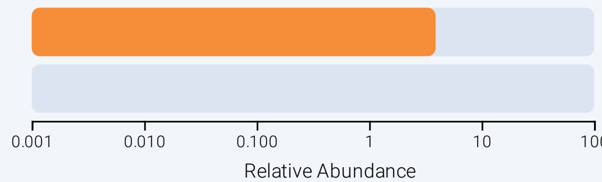
Enterobacter

DETECTED

Enterobacter himalayensis

You **3.92%**

Average **0.001%**



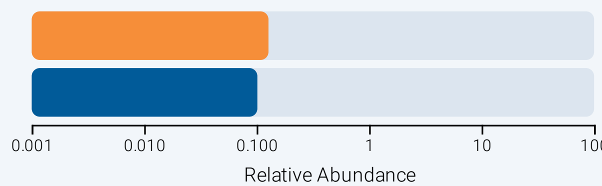
Escherichia

DETECTED

Escherichia coli (coli_D)

You **0.128%**

Average **0.102%**



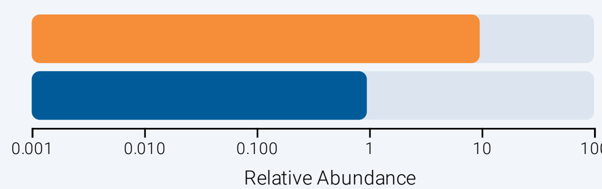
Faecalibacterium

DETECTED

Faecalibacterium prausnitzii_D

You **9.67%**

Average **0.957%**



Fusobacterium

NOT DETECTED

Helicobacter

NOT DETECTED

Klebsiella

NOT DETECTED

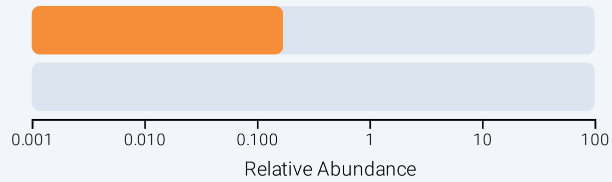
Lactobacillus

DETECTED

⊕ ***Lactobacillus gasseri_A***

You **0.171%**

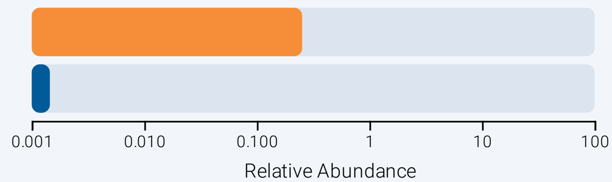
Average **0.00%**



⊕ ***Lactobacillus_C rhamnosus***

You **0.253%**

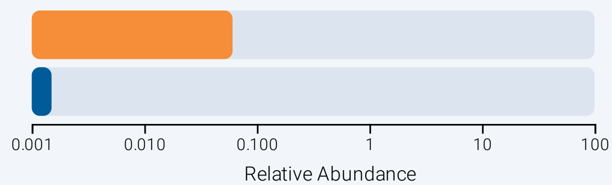
Average **0.001%**



⊕ ***Lactobacillus_C paracasei***

You **0.061%**

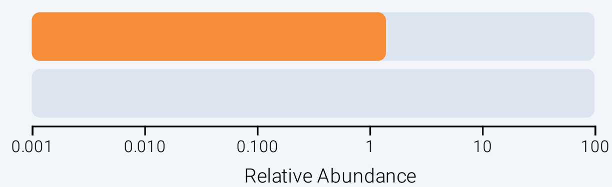
Average **0.002%**



Lactobacillus_H fermentum

You **1.41%**

Average **0.00%**



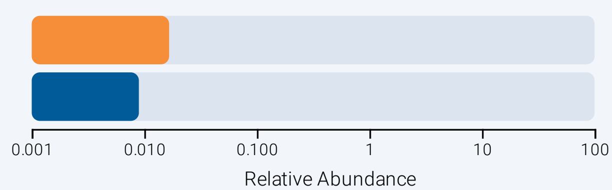
Oxalobacter

DETECTED

Oxalobacter MIC6654

You **0.017%**

Average **0.009%**



Porphyromonas
NOT DETECTED

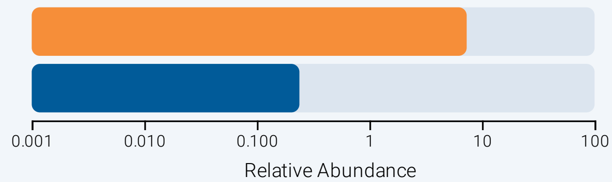
Prevotella
NOT DETECTED

Roseburia
DETECTED

Roseburia inulinivorans

You **7.34%**

Average **0.239%**

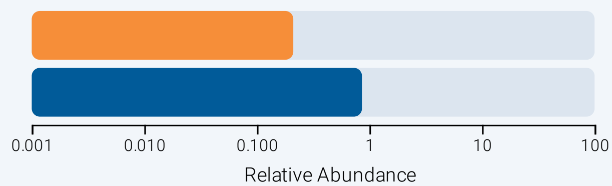


Ruminococcus
DETECTED

Ruminococcus_D bicirculans

You **0.211%**

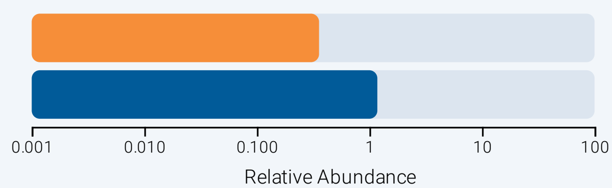
Average **0.861%**



Ruminococcus_E bromii_B

You **0.358%**

Average **1.18%**

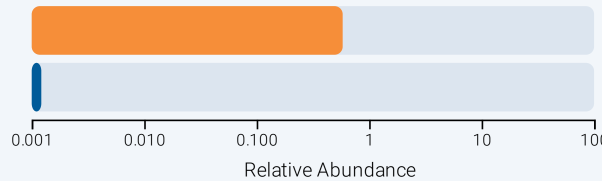


Salmonella
NOT DETECTED

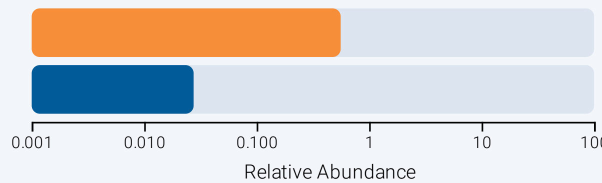
Streptococcus

DETECTED

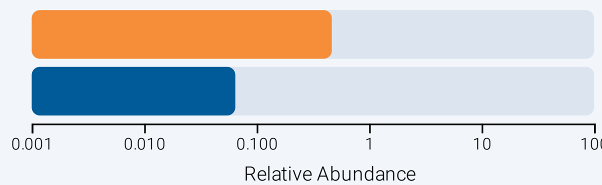
Streptococcus anginosus_C	You	**0.584%**
	Average	**0.001%**



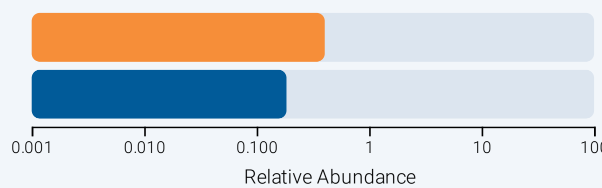
Streptococcus parasanguinis_B	You	**0.561%**
	Average	**0.028%**



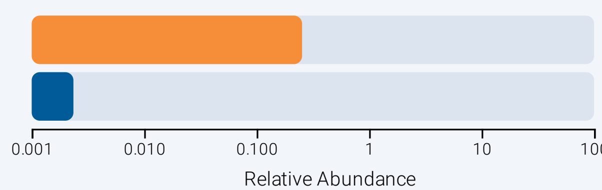
Streptococcus sp001556435	You	**0.467%**
	Average	**0.065%**



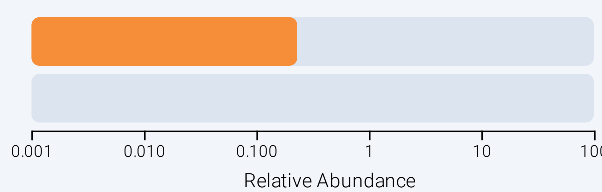
⊖ *Streptococcus salivarius*	You	**0.404%**
	Average	**0.185%**



Streptococcus parasanguinis	You	**0.254%**
	Average	**0.002%**

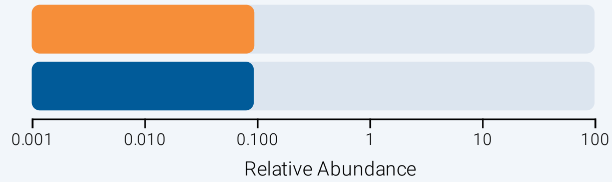


Streptococcus mutans	You	**0.231%**
	Average	**0.00%**



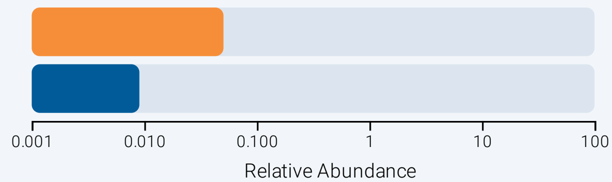
Streptococcus thermophilus

You	**0.095%**	
Average	**0.094%**	



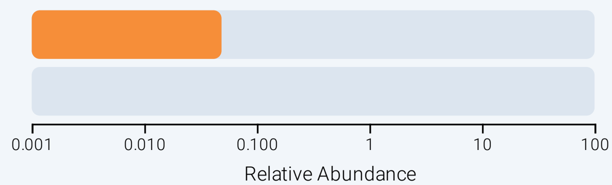
Streptococcus vestibularis

You	**0.051%**	
Average	**0.009%**	



Streptococcus gordonii

You	**0.049%**	
Average	**0.001%**	



Species of Interest

Archaea (prokaryotes)

Methanogens	NOT DETECTED
Other Archea	NOT DETECTED

Species of Interest

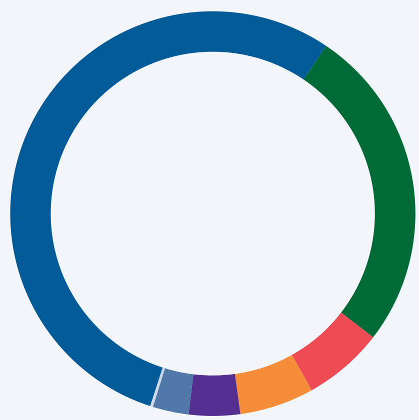
Yeasts/fungi & protists (eukaryotes)	
Blastocystis	NOT DETECTED
Candida	NOT DETECTED
Saccharomyces	NOT DETECTED
Other Eukaryotes	NOT DETECTED

Microbial Profile

This section shows the different bacteria, archaea and eukaryotes present in your gut. A phylum is the highest level of grouping (comprising hundreds to thousands of species), whereas a species is the most detailed view of your gut microbiome

Your Microbiome Profile

Phylum



This Sample

Phylum	Abundance	Range	Level
Firmicutes_A	48.1%	32.7 - 58.7%	Average
Bacteroidota	23.0%	16.5 - 35.0%	Average
Firmicutes	5.67%	0.743 - 9.80%	Average
Proteobacteria	5.24%	0.694 - 9.09%	Average
Actinobacteriota	3.61%	1.13 - 10.3%	Average
Firmicutes_C	2.53%	0.351 - 2.20%	High
Desulfobacterota_A	0.199%	0.074 - 0.501%	Average

Species Profile

Species

	Phylum	Species	Abundance	Range	Level
⊖	Bacteroidota	***Bacteroides_B dorei***	10.8%	0.00 - 4.18%	High

This is a common inhabitant of the gut and is closely related to *Bacteroides vulgatus*.

Fuel Sources Used:
This species is a good degrader of fibre, a good degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, beta-glucuronidase, biotin (B7), branched chain amino acids, folate (B9), GABA, lactate, riboflavin (B2), vitamin K.

Metabolites consumed:
In addition, the genomic analysis shows that most members of this species can consume: GABA.

Emerging Research:
Higher levels of this species have been observed in patients with colon cancer and during the development of type 1 diabetes in children. This species has also been associated with diets high in red meat.

	Phylum	Species	Abundance	Range	Level
	Firmicutes_A	***Blautia_A wexlerae***	10.7%	0.222 - 2.79%	High

This is a recently discovered and common inhabitant of the gut.

Fuel Sources Used:
This species is a moderate degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, ammonia (urease), biotin (B7), branched chain amino acids, cobalamin (B12), folate (B9), lactate, riboflavin (B2).

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Species Profile

Species

	Phylum	Species	Abundance	Range	Level
	Firmicutes_A	***Faecalibacterium prausnitzii_D***	9.67%	0.099 - 2.11%	High

Fuel Sources Used:
This species is a moderate degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, beta-glucuronidase, branched chain amino acids, butyrate, cobalamin (B12), riboflavin (B2).

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

	Phylum	Species	Abundance	Range	Level
⊕	Firmicutes_A	***Roseburia inulinivorans***	7.34%	0.00 - 0.636%	High

This is a common and important member of the human gut microbiome.

Fuel Sources Used:
This species is a moderate degrader of fibre, mucin, and protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, butyrate, folate (B9), hydrogen sulfide, lactate.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging Research:
This is a primary producer of the beneficial short chain fatty acid butyrate. This species has been observed at reduced levels in individuals with type 2 diabetes.

Species Profile

Species

Phylum	Species	Abundance	Range	Level
Proteobacteria	***Enterobacter himalayensis***	3.92%	0.00 - 0.00%	High

Formerly known as *Enterobacter hormaechei.* This species can be found in many areas of the human body including the gut. It can be common in hospital environments.

Fuel Sources Used:
This species is a moderate degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, ammonia (urease), biotin (B7), branched chain amino acids, folate (B9), GABA, hexa-LPS, hydrogen sulfide, lactate, riboflavin (B2), vitamin K.

Metabolites consumed:
In addition, the genomic analysis shows that most members of this species can consume: GABA.

Phylum	Species	Abundance	Range	Level
Bacteroidota	***Bacteroides fragilis***	3.39%	0.00 - 0.119%	High

This is a normal inhabitant of the human gut.

Fuel Sources Used:
This species is a moderate degrader of fibre, a good degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, biotin (B7), branched chain amino acids, folate (B9), GABA, histamine, lactate, propionate, riboflavin (B2), vitamin K.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging Research:
This species has two different forms: a non-toxic form and a toxin-producing form. The majority of *B. fragilis* strains found in the gut microbiome are of the non-toxic form and may even have a beneficial effect on the immune system by promoting the production of anticancer T cells. Additionally, some studies have shown it is depleted in children with autism. The toxin-producing form is much less common, but has been correlated with diarrheal disease, colon cancer and inflammatory bowel disease. You can see if you have the toxin-producing form by checking the levels of "B. fragilis toxin" under the "Microbial metabolites" section of this report.

Species Profile

Species

	Phylum	Species	Abundance	Range	Level
+−	Bacteroidota	***Bacteroides uniformis***	2.84%	0.290 - 3.68%	Average

This is one of the most common inhabitants of the human gut.

Fuel Sources Used:
This species is a good degrader of fibre, a good degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, beta-glucuronidase, biotin (B7), branched chain amino acids, folate (B9), GABA, lactate, riboflavin (B2).

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging Research:
Certain strains have been observed to promote the production of anti-inflammatory compounds, improve immune function, and provide protection against diet induced obesity in mouse models, however this has not yet been validated in humans. One study observed higher levels of this species in patients with ulcerative colitis.

	Phylum	Species	Abundance	Range	Level
	Firmicutes_A	***Agathobaculum butyriciproducens***	2.07%	0.00 - 0.498%	High

This is a recently discovered species from the human gut.

Fuel Sources Used:
This species is a poor degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, butyrate, cobalamin (B12), lactate, riboflavin (B2).

Metabolites consumed:
In addition, the genomic analysis shows that most members of this species can consume: GABA.

Species Profile

Species

	Phylum	Species	Abundance	Range	Level
	Firmicutes_A	***Anaerostipes hadrus***	1.97%	0.115 - 2.37%	Average

Formerly known as *Eubacterium hadrum*. This is a common inhabitant of the human gut.

Fuel Sources Used:
This species is a moderate degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, butyrate, folate (B9), hydrogen sulfide, lactate, riboflavin (B2).

Metabolites consumed:
In addition, the genomic analysis shows that most members of this species can consume: oxalate.

	Phylum	Species	Abundance	Range	Level
⊖	Firmicutes_A	***Ruminococcus_B gnavus***	1.84%	0.00 - 0.026%	High

This is one of the earliest colonizers of the infant human gut, and it persists in the adult human gut.

Fuel Sources Used:
This species is a moderate degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, cobalamin (B12), folate (B9), lactate, propionate.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging Research:
Higher levels of this species have been observed in individuals with irritable bowel syndrome, Crohn's disease, atherosclerosis, and obesity.

Species Profile

Species

	Phylum	Species	Abundance	Range	Level
	Bacteroidota	***Bacteroides xylanisolvens***	1.82%	0.00 - 0.260%	High
	Bacteroidota	***Alistipes putredinis***	1.69%	0.00 - 3.41%	Average

This is a common inhabitant of the gut microbiome.

Fuel Sources Used:
This species is a poor degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: butyrate, folate (B9), GABA, lactate, riboflavin (B2), vitamin K.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging Research:
Studies have observed higher levels of this species in patients with colon cancer. However, other studies associated a low abundance of this species with chronic fatigue syndrome, Crohn's disease and irritable bowel syndrome.

	Phylum	Species	Abundance	Range	Level
	Firmicutes_A	***Blautia_A sp900066165***	1.69%	0.107 - 1.13%	High
	Firmicutes_C	***Veillonella parvula_A***	1.61%	0.00 - 0.00%	High
	Firmicutes	***Lactobacillus_H fermentum***	1.41%	0.00 - 0.00%	High

Species Profile

Species

	Phylum	Species	Abundance	Range	Level
⊕	Firmicutes_A	***Fusicatenibacter saccharivorans***	1.37%	0.418 - 4.06%	Average

This is a recently discovered species and an inhabitant of the human gut.

Fuel Sources Used:
This species is a moderate degrader of fibre, mucin, and protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, ammonia (urease), beta-glucuronidase, branched chain amino acids, cobalamin (B12), folate (B9), hydrogen sulfide, lactate.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging Research:
Lower levels of this species were observed in patients with colon cancer.

	Phylum	Species	Abundance	Range	Level
⊕	Actinobacteriota	***Bifidobacterium longum***	1.20%	0.031 - 1.44%	Average

This is a beneficial inhabitant of the gut in adults and a popular probiotic.

Fuel Sources Used:
This species is a moderate degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, folate (B9), lactate.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging Research:
B.longum has been associated with reductions in harmful bacteria, anti-allergy effects, and anti-obesity effects in mouse models, but further research still needs to be done in humans.

Species Profile

Species

	Phylum	Species	Abundance	Range	Level
	Firmicutes_A	***KLE1615 sp900066985***	1.10%	0.00 - 0.642%	High
	Firmicutes_A	***Clostridium_M sp000431375***	1.09%	0.00 - 0.074%	High
	Firmicutes	***Erysipelatoclostridium MIC9185***	0.988%	0.00 - 0.00%	High
	Firmicutes_A	***Clostridium_Q sp003024715***	0.967%	0.00 - 0.214%	High
	Firmicutes_A	***Blautia_A obeum***	0.919%	0.057 - 0.851%	High
+−	Bacteroidota	***Bacteroides cellulosilyticus***	0.862%	0.00 - 0.326%	High

This is a common gut inhabitant.

Fuel Sources Used:
This species is a good degrader of fibre, a good degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, beta-glucuronidase, biotin (B7), branched chain amino acids, folate (B9), GABA, lactate, riboflavin (B2).

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging Research:
Higher levels of this species have been observed in patients with hypertension. However another study observed lower levels in individuals with irritable bowel syndrome.

	Phylum	Species	Abundance	Range	Level
	Firmicutes_A	***Tyzzerella sp000411335***	0.839%	0.00 - 0.00%	High

Species Profile

Species

	Phylum	Species	Abundance	Range	Level
	Firmicutes_A	***Blautia hansenii***	0.832%	0.00 - 0.00%	High
	Firmicutes_A	***Lachnospira eligens_B***	0.820%	0.00 - 1.24%	Average
⊕	Actinobacteriota	***Bifidobacterium bifidum***	0.807%	0.00 - 0.911%	Average

This is a naturally occurring human gut bacterium and a probiotic. This is one of the first colonizers of the human gut, and is important in the development of the infant immune system.

Fuel Sources Used:
This species is a moderate degrader of fibre, mucin, and protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, folate (B9), lactate.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

	Phylum	Species	Abundance	Range	Level
	Firmicutes_A	***Romboutsia timonensis***	0.727%	0.026 - 0.358%	High
	Actinobacteriota	***Collinsella aerofaciens_F***	0.692%	0.00 - 0.195%	High
	Firmicutes	***Streptococcus anginosus_C***	0.584%	0.00 - 0.00%	High
	Firmicutes	***Streptococcus parasanguinis_B***	0.561%	0.00 - 0.00%	High

Species Profile

Species

	Phylum	Species	Abundance	Range	Level
	Bacteroidota	***Bacteroides thetaiotaomicron***	0.550%	0.00 - 0.477%	High
⊖	Firmicutes_C	***Veillonella dispar_A***	0.548%	0.00 - 0.00%	High

This is a common inhabitant of the oral microbiome but can also be found in the human gut.

Fuel Sources Used:
This species is a poor degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, biotin (B7), branched chain amino acids, cobalamin (B12), folate (B9), hydrogen sulfide, lactate, propionate, riboflavin (B2), vitamin K.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging Research:
This species can also use lactate as an energy source.

This species has been observed at elevated levels in individuals with hepatitis B liver cirrhosis.

	Phylum	Species	Abundance	Range	Level
	Firmicutes_A	***CAG-41 sp900066215***	0.521%	0.00 - 0.432%	High
	Firmicutes_A	***Dorea sp000433535***	0.520%	0.00 - 0.00%	High
	Firmicutes	***Streptococcus sp001556435***	0.467%	0.00 - 0.006%	High
	Proteobacteria	***CAG-495 sp000436375***	0.455%	0.00 - 0.173%	High

Species Profile

Species

	Phylum	Species	Abundance	Range	Level
⊖	Firmicutes	***Streptococcus salivarius***	0.404%	0.00 - 0.185%	High

This is a common inhabitant of the human oral microbiota and is also found in the human gut.

Fuel Sources Used:
This species is a moderate degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, ammonia (urease), branched chain amino acids, folate (B9), lactate.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging Research:
This species has been observed at higher levels in patients with hypertension, Crohn's disease and atherosclerosis, however one study observed it at lower levels in patients with colon cancer.

	Phylum	Species	Abundance	Range	Level
⊖	Bacteroidota	***Parabacteroides merdae***	0.366%	0.00 - 0.524%	Average

Formerly known as *Bacteroides merdae*. This is a common inhabitant of the human gut.

Fuel Sources Used:
This species is a moderate degrader of fibre, a good degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, beta-glucuronidase, biotin (B7), branched chain amino acids, folate (B9), GABA, lactate, riboflavin (B2), vitamin K.

Metabolites consumed:
In addition, the genomic analysis shows that most members of this species can consume: GABA.

Emerging Research:
Higher levels of this species have been observed in individuals with hypertension and colon cancer. This species has been associated with a diet low in fruits and vegetables.

Species Profile

Species

	Phylum	Species	Abundance	Range	Level
⊕	Firmicutes_A	***Ruminococcus_E bromii_B***	0.358%	0.00 - 4.21%	Average

Fuel Sources Used:
This species is a poor degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, lactate.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

	Phylum	Species	Abundance	Range	Level
	Actinobacteriota	***Collinsella MIC8209***	0.324%	0.00 - 0.00%	High
	Proteobacteria	***Parasutterella excrementihominis***	0.318%	0.00 - 0.201%	High
	Firmicutes	***Streptococcus parasanguinis***	0.254%	0.00 - 0.00%	High

Species Profile

Species

	Phylum	Species	Abundance	Range	Level
⊕	Firmicutes	***Lactobacillus_C rhamnosus***	0.253%	0.00 - 0.00%	High

This species is commonly found in fermented dairy products but can also be found in the human gut.

Fuel Sources Used:
This species is a moderate degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, beta-glucuronidase, folate (B9), lactate.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging Research:
Studies in children have shown some strains may help reduce diarrhea, respiratory infections, and abdominal pain associated with irritable bowel syndrome. In general, Lactobacillus species do not colonize the adult human gut and are only transient.

	Phylum	Species	Abundance	Range	Level
	Firmicutes_A	***CAG-81 sp900066535***	0.252%	0.00 - 0.162%	High
	Firmicutes_A	***CAG-217 sp000436335***	0.251%	0.00 - 0.323%	Average
	Firmicutes	***Streptococcus mutans***	0.231%	0.00 - 0.00%	High

Species Profile

Species

	Phylum	Species	Abundance	Range	Level
⊕	Firmicutes_A	***Dorea formicigenerans***	0.220%	0.069 - 0.301%	Average

Formerly known as *Eubacterium formicgenerans*. This is a common inhabitant of the human gut.

Fuel Sources Used:
This species is a poor degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, cobalamin (B12), folate (B9), lactate, riboflavin (B2).

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging Research:
This species has been observed at decreased levels in individuals with colon cancer, inflammatory bowel disease and chronic fatigue syndrome, indicating it likely plays a beneficial role in health.

	Phylum	Species	Abundance	Range	Level
	Proteobacteria	***Haemophilus_D parainfluenzae_K***	0.216%	0.00 - 0.00%	High
	Firmicutes_A	***Ruminococcus_D bicirculans***	0.211%	0.00 - 2.88%	Average
	Firmicutes_A	***Blautia_A sp000433815***	0.208%	0.00 - 0.00%	High
	Firmicutes_A	***Eisenbergiella sp900066775***	0.192%	0.00 - 0.312%	Average
	Firmicutes_A	***TF01-11 sp000436755***	0.187%	0.00 - 0.140%	High
	Proteobacteria	***Haemophilus_D sp001815355***	0.184%	0.00 - 0.046%	High

Species Profile

Species

	Phylum	Species	Abundance	Range	Level
⊖	Firmicutes_C	***Veillonella parvula***	0.184%	0.00 - 0.00%	High

This is a common member of the oral microbiome and is also found in the gut.

Fuel Sources Used:
This species is a poor degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, biotin (B7), branched chain amino acids, cobalamin (B12), folate (B9), hydrogen sulfide, lactate, riboflavin (B2), vitamin K.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging Research:
This species can also use lactate for energy.

This species has been observed at higher levels in individuals with hepatitis B liver cirrhosis, and in children with cystic fibrosis.

	Phylum	Species	Abundance	Range	Level
⊖	Firmicutes_C	***Dialister invisus***	0.180%	0.00 - 0.997%	Average

This is a common inhabitant of the oral microbiome and is also found in the gut microbiome.

Fuel Sources Used:
This species is a poor degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: biotin (B7), cobalamin (B12), folate (B9), lactate, riboflavin (B2).

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging Research:
In the mouth, this species is associated with periodontal infections. In the gut, higher levels of this species have been observed in patients with atherosclerosis.

Species Profile

Species

	Phylum	Species	Abundance	Range	Level
⊕	Firmicutes	***Lactobacillus gasseri_A***	0.171%	0.00 - 0.00%	High

This lactic acid bacterium can be found in several fermented foods.

Fuel Sources Used:
This species is a moderate degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, beta-glucuronidase, folate (B9), lactate.

Metabolites consumed:
In addition, the genomic analysis shows that most members of this species can consume: oxalate.

Emerging Research:
Research suggests some strains of this species can improve immune function, especially in the elderly. However one study found increased levels of this species in individuals with type 2 diabetes. In general, Lactobacillus species do not colonize the adult human gut and are only transient.

	Phylum	Species	Abundance	Range	Level
	Firmicutes_A	***Coprococcus_B MIC8649***	0.152%	0.00 - 0.00%	High
	Firmicutes_A	***Blautia_A sp900066145***	0.128%	0.00 - 0.138%	Average

Species Profile

Species

	Phylum	Species	Abundance	Range	Level
⊖	Proteobacteria	***Escherichia coli (coli_D)***	0.128%	0.00 - 0.048%	High

This species is a common inhabitant of the gut, although it is usually present at a low abundance compared to other gut microbiome species.

Fuel Sources Used:
This species is a moderate degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, beta-glucuronidase, biotin (B7), branched chain amino acids, butyrate, folate (B9), GABA, hexa-LPS, hydrogen sulfide, lactate, propionate, riboflavin (B2), trimethylamine, vitamin K.

Metabolites consumed:
In addition, the genomic analysis shows that most members of this species can consume: GABA, oxalate.

Emerging Research:
This species encompasses a large number of strains with diverse properties; a few well-known strains are a common cause of gastrointestinal disease. However, most strains will not cause gastrointestinal symptoms. Studies have observed this species at higher levels in individuals with Crohn's Disease and advanced liver fibrosis. Additionally, a recent study identified several strains from this species as being able to produce a toxin called colibactin which can damage DNA.

	Phylum	Species	Abundance	Range	Level
⊕	Firmicutes_A	***Coprococcus_B comes***	0.127%	0.042 - 0.592%	Average

This is a common inhabitant of the human gut.

Fuel Sources Used:
This species is a moderate degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, butyrate, cobalamin (B12), folate (B9), lactate, riboflavin (B2), trimethylamine.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging Research:
This species likely plays a beneficial role in health as it has been observed at lower levels in individuals with Crohn's disease, liver cirrhosis and chronic fatigue syndrome.

Species Profile

Species

	Phylum	Species	Abundance	Range	Level
	Firmicutes_A	***ER4 sp900317525***	0.120%	0.00 - 0.496%	Average
	Desulfobacterota_A	***Desulfovibrio piger_A***	0.116%	0.00 - 0.00%	High
	Actinobacteriota	***Bifidobacterium dentium***	0.115%	0.00 - 0.00%	High

This is the only *Bifidobacterium* member that is a common inhabitant of the mouth, as well as the gut.

Fuel Sources Used:
This species is a moderate degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, beta-glucuronidase, branched chain amino acids, folate (B9), GABA, lactate.

Metabolites consumed:
In addition, the genomic analysis shows that most members of this species can consume: oxalate.

Emerging Research:
Mice models have shown this species can stimulate mucus production (which is important for a healthy gut) and it was a common species observed in elderly Chinese over 100 years old. However higher levels of this species were also observed in patients with rheumatoid arthritis.

	Phylum	Species	Abundance	Range	Level
	Bacteroidota	***Bacteroides nordii***	0.107%	0.00 - 0.00%	High

Species Profile

Species

	Phylum	Species	Abundance	Range	Level
⊕	Bacteroidota	***Odoribacter splanchnicus***	0.106%	0.079 - 0.440%	Average

Formerly known as *Bacteroides splanchnicus*. This a common inhabitant of the human gut.

Fuel Sources Used:
This species is a moderate degrader of fibre, a good degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, ammonia (urease), biotin (B7), branched chain amino acids, butyrate, folate (B9), GABA, lactate, riboflavin (B2), vitamin K.

Metabolites consumed:
In addition, the genomic analysis shows that most members of this species can consume: GABA.

Emerging Research:
Lower levels of this species have been observed in postmenopausal obese women with insulin resistance, patients with irritable bowel syndrome and in women with bladder pain syndrome, indicating it likely plays a beneficial role in health.

	Phylum	Species	Abundance	Range	Level
	Firmicutes_A	***Anaerotignum lactatifermentans***	0.100%	0.00 - 0.00%	High
	Actinobacteriota	***Actinomyces viscosus***	0.099%	0.00 - 0.00%	High

Species Profile

Species

	Phylum	Species	Abundance	Range	Level
⊕	Firmicutes	***Streptococcus thermophilus***	0.095%	0.00 - 0.154%	Average

This is the most widely used lactate bacteria in the dairy industry for producing cheese and yogurt (it is considered the safest *Streptococcus* species by the dairy industry). It helps make reduced-fat cheese with similar characteristics to full-fat cheese.

Fuel Sources Used:
This species is a poor degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, ammonia (urease), branched chain amino acids, folate (B9), lactate.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging Research:
Because of its superior ability to use lactose, this species is often used by lactose-intolerant individuals to help them digest milk products. This bacterium also shows good potential for reducing inflammation, although more research needs to be conducted in humans.

	Phylum	Species	Abundance	Range	Level
	Actinobacteriota	***Collinsella MIC9024***	0.085%	0.00 - 0.00%	High
	Bacteroidota	***Bacteroides MIC8726***	0.081%	0.00 - 0.001%	High
	Actinobacteriota	***Pauljensenia sp000278725***	0.078%	0.00 - 0.00%	High
	Firmicutes_A	***Dorea sp900066555***	0.070%	0.00 - 0.068%	High
	Firmicutes_A	***GCA-900066135 sp900066135***	0.070%	0.00 - 0.052%	High
	Bacteroidota	***Coprobacter fastidiosus***	0.065%	0.00 - 0.093%	Average

Species Profile

Species

	Phylum	Species	Abundance	Range	Level
⊖	Desulfobacterota_A	***Bilophila wadsworthia***	0.061%	0.00 - 0.217%	Average

This is a common inhabitant of the human gut, but can become problematic at high levels.

Fuel Sources Used:
This species is a poor degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, ammonia (urease), branched chain amino acids, hydrogen sulfide, lactate, riboflavin (B2), trimethylamine.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging Research:
Higher levels of this species have been observed in patients with colon cancer and in people that have a diet high in saturated fats. Mice studies have also suggested this species can promote increased inflammation in the gut and increased barrier dysfunction, though more research needs to be conducted in humans to confirm these results.

	Phylum	Species	Abundance	Range	Level
⊕	Firmicutes	***Lactobacillus_C paracasei***	0.061%	0.00 - 0.00%	High

This lactic acid bacteria is naturally found in low numbers on all plant surfaces. It is commonly found in fermented foods such as sauerkraut, kimchi and pickles.

Fuel Sources Used:
This species is a moderate degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, folate (B9), lactate.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging Research:
Clinical trials have observed some strains of this species can be effective at improving symptoms of diverticulitis and diarrhea. In general, Lactobacillus species do not colonize the adult human gut and are only transient.

Species Profile

Species

Phylum	Species	Abundance	Range	Level
Firmicutes_A	***Ruminiclostridium_C sp000435295***	0.057%	0.00 - 0.252%	Average
Bacteroidota	***Alistipes_A ihumii***	0.052%	0.00 - 0.158%	Average
Firmicutes_A	***CAG-74 MIC9837***	0.051%	0.00 - 0.060%	Average
Firmicutes	***Streptococcus vestibularis***	0.051%	0.00 - 0.00%	High
Actinobacteriota	***CAG-1427 sp000435475***	0.050%	0.00 - 0.113%	Average
Firmicutes	***Streptococcus gordonii***	0.049%	0.00 - 0.00%	High
Bacteroidota	***Odoribacter laneus***	0.047%	0.00 - 0.00%	High
Bacteroidota	***Alistipes obesi***	0.045%	0.00 - 0.422%	Average

Species Profile

Species

	Phylum	Species	Abundance	Range	Level
⊕	Bacteroidota	***Alistipes shahii***	0.045%	0.00 - 0.497%	Average

This is a common inhabitant of the human gut.

Fuel Sources Used:
This species is a moderate degrader of fibre, a good degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: beta-glucuronidase, branched chain amino acids, folate (B9), GABA, lactate, riboflavin (B2).

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging Research:
This species appears to have mostly beneficial effects. It has been associated with beneficial markers of cardiac health (low triglycerides, high beneficial cholesterol HDL levels), and was observed as depleted in patients with atherosclerotic heart disease and Crohn's disease. Additionally, a study in mice showed this species may improve the efficacy of cancer immunotherapy. However, this species was also observed at elevated levels in patients with Parkinson's Disease.

	Phylum	Species	Abundance	Range	Level
	Bacteroidota	***UBA11471 sp000434215***	0.041%	0.00 - 0.357%	Average
	Firmicutes_A	***Blautia sp001304935***	0.041%	0.00 - 0.00%	High
	Actinobacteriota	***Pauljensenia sp000411415***	0.039%	0.00 - 0.00%	High
	Actinobacteriota	***Adlercreutzia MIC8014***	0.039%	0.00 - 0.056%	Average
	Firmicutes_A	***Acutalibacteraceae MIC7795***	0.038%	0.00 - 0.052%	Average

Species Profile

Species

	Phylum	Species	Abundance	Range	Level
⊖	Firmicutes_A	***Clostridium_M bolteae***	0.038%	0.00 - 0.00%	High

This is an inhabitant of the human gut.

Fuel Sources Used:
This species is a moderate degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, cobalamin (B12), folate (B9), lactate, riboflavin (B2), trimethylamine.

Metabolites consumed:
In addition, the genomic analysis shows that most members of this species can consume: GABA.

Emerging Research:
This species has been observed at higher levels in individuals with type II diabetes, asthma, inflammatory bowel disease, colon cancer, diarrhea, on the autism spectrum, and in postmenopausal, obese women with insulin resistance.

	Phylum	Species	Abundance	Range	Level
⊖	Firmicutes_A	***Flavonifractor plautii***	0.037%	0.00 - 0.049%	Average

Formerly known as *Clostridium orbiscindens* and *Eubacterium plautii*.

Fuel Sources Used:
This species is a poor degrader of fibre, a moderate degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, butyrate, cobalamin (B12), lactate, propionate.

Metabolites consumed:
In addition, the genomic analysis shows that most members of this species can consume: GABA.

Emerging Research:
Higher levels of this species have been observed in patients with Crohn's disease, ulcerative colitis and in children with irritable bowel syndrome.

Species Profile

Species

	Phylum	Species	Abundance	Range	Level
⊖	Firmicutes	***Erysipelatoclostridium ramosum***	0.037%	0.00 - 0.00%	High

Formerly known as *Clostridium ramosum*. This is an inhabitant of the human gut.

Fuel Sources Used:
This species is a moderate degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, folate (B9), hydrogen sulfide, lactate.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging Research:
Elevated levels of this species have been observed in individuals with with obesity, type II diabetes, Crohn's disease and asthma. This species has been associated with a high fat diet. A mouse study observed that glucose and fat transporters are more active when this species is present, suggesting a possible way this species is involved in metabolic disorders.

	Phylum	Species	Abundance	Range	Level
	Actinobacteriota	***Collinsella MIC6458***	0.037%	0.00 - 0.00%	High
	Firmicutes_A	***CAG-145 sp000435715***	0.032%	0.00 - 0.001%	High
	Firmicutes_A	***Oscillibacter MIC7169***	0.031%	0.00 - 0.015%	High

Species Profile

Species

	Phylum	Species	Abundance	Range	Level
⊖	Firmicutes_A	***Faecalicatena torques***	0.029%	0.00 - 0.188%	Average

Previously called *Ruminococcus torques.* This is a common inhabitant of the human gut.

Fuel Sources Used:
This species is a moderate degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, cobalamin (B12), folate (B9), lactate, riboflavin (B2).

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging Research:
This species has been observed at higher levels in individuals with obesity, colon cancer, insulin resistance and high triglyceride levels.

	Phylum	Species	Abundance	Range	Level
	Firmicutes	***Erysipelatoclostridium spiroforme***	0.029%	0.00 - 0.033%	Average
	Firmicutes_A	***Clostridium_Q saccharolyticum***	0.027%	0.00 - 0.00%	High
	Actinobacteriota	***Rothia mucilaginosa_A***	0.027%	0.00 - 0.00%	High
	Firmicutes_A	***CAG-110 sp000435995***	0.027%	0.00 - 0.230%	Average
	Firmicutes_A	***UBA1777 sp002320035***	0.025%	0.00 - 0.00%	High
	Desulfobacterota_A	***Mailhella sp003150275***	0.021%	0.00 - 0.020%	High

Species Profile

Species

	Phylum	Species	Abundance	Range	Level
⊖	Actinobacteriota	***Eggerthella lenta***	0.021%	0.00 - 0.080%	Average

This is an inhabitant of the gut microbiota, but has also been associated with gastrointestinal infections.

Fuel Sources Used:
This species is a poor degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, GABA, histamine, lactate, vitamin K.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging Research:
This species can also use some steroids such as the stress hormone cortisol, and the neurotransmitter dopamine, for energy.

Elevated levels of *E. lenta* have been associated with frailty, atherosclerosis, chronic fatigue syndrome, type II diabetes, irritable bowel syndrome and inflammatory bowel disease. This species can also inactivate the cardiac drug digoxin by breaking it down. Interestingly, this species prefers the amino acid arginine for growth. When arginine is present, this inhibits *E. lenta* from breaking down digoxin.

	Phylum	Species	Abundance	Range	Level
	Bacteroidota	***Barnesiella intestinihominis***	0.017%	0.00 - 0.524%	Average
	Proteobacteria	***Oxalobacter MIC6654***	0.017%	0.00 - 0.036%	Average
	Firmicutes	***Holdemania sp900120005***	0.015%	0.00 - 0.00%	High
	Bacteroidota	***Gabonibacter MIC7641***	0.013%	0.00 - 0.00%	High
	Firmicutes_A	***Lachnoclostridium_A edouardi***	0.013%	0.00 - 0.00%	High
	Firmicutes	***Absiella MIC9514***	0.012%	0.00 - 0.00%	High

Gut microbiome report