SYNLAB

myBIOME

Gut microbiome report

Name:
Sample ID:
Report generated on:

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Laboratory Director

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powered by
MICROBA

Introduction to *myBIOME^{TM}* Report

myBIOME™ 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 substitues 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.

Areas of Action

Patient Name: **Sample II** **Report Date**

Disclaimer: *The following table is intended to inform the practitioner of the analysed parameters that are outside the normal range. Your practitioner will help you in the interpretation of the myBIOME report by assessing the totality of the results included in the report together with your symptoms and medical history.*

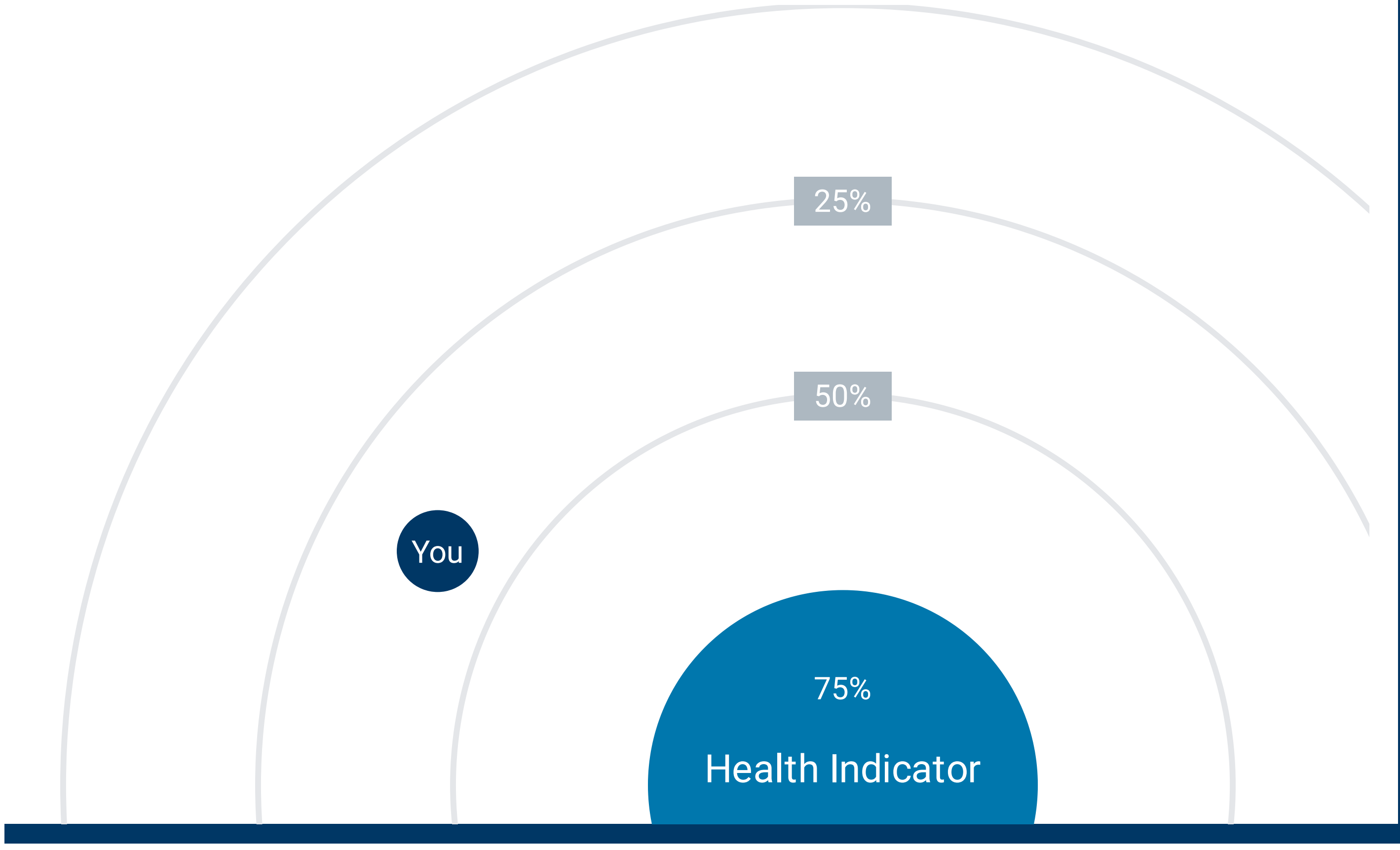
Marker	Suggestion
Pathobiont species	**Further investigation recommended** The following species have been detected in the sample, and some strains can impact health: [Bilophila wadsworthia, Clostridium_M bolteae, Clostridium_M citroniae, Clostridium_Q symbiosum, Coprococcus_B comes, Eggerthella lenta]. Follow-up testing for gut pathogens is recommended, through a pathology provider.
Microbiome Digestive Potential - Protein (High)	**More fibre and less protein** 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 fibre have been observed to increase levels of pro-inflammatory gut metabolites.
Microbiome Digestive Potential - Mucin (High)	**More diverse plant foods** 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 fibre reaching the lower large intestine, allowing gut bacteria that can use mucus as an energy source to multiply.
Diversity (Low)	**More diverse plant foods** A varied diet rich in plant-based foods such as fruits, vegetables, whole grains and nuts can help increase microbiome diversity.
Trimethylamine production (High)	**Increase Broccoli & Cauliflower, reduce red meats** 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. References [1] [2] [3] [4] [5] [6]

Marker	Suggestion
Hydrogen sulphide production (High)	**RS & FOS** 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 sulphide by the microbiome. References [1] [2]
Butyrate production (Low)	**RS & Pectin** 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. References [1] [2] [3] [4] [5] [6] [7] [8]
GABA consumption (High)	**Further investigation** The role of gut bacteria that produce GABA in anxiety and depression is currently not well understood. If you are concerned about your mental health, it is important to seek professional help. References [1] [2] [3]
Ammonia (urease) production (High)	**Consider Fibre/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. Speak with your healthcare practitioner if this result is of concern. References [1] [2]

END OF AREAS OF ACTION

Your report overview

Welcome to the start of your journey to understanding how your microbiome affects your health. Throughout this report, the analysed 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.

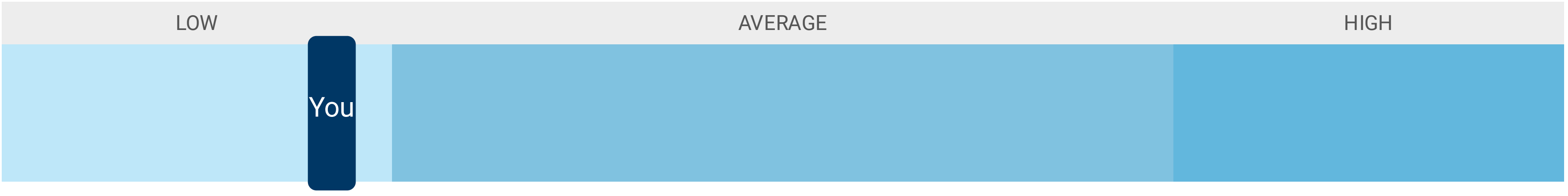


Your gut microbiome score is less than 50%. This measurement is an indication of how well your gut microbiome might be interacting with your overall health. A higher score suggests a more positive interaction.

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

Low

Shannon Index

2.87

Your *key* insights

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

This is not a good level. Your potential to produce butyrate is lower than the healthy group. This is an important gut microbiome function which can be addressed through diet and increased by eating foods high in resistant starch. A similar or high level to produce butyrate is considered beneficial.

A **This sample reported a level lower than 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 a typical level. You have a similar potential to produce hexa-lipopolysaccharides (hexa-LPS) as the healthy group, which means this substance is unlikely to be a major contributor to inflammation in your body. Having diverse sources of fibre can help reduce the levels of microbes that produce hexa-LPS.

A **This sample reported a level similar to 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, icecream, cakes and biscuits.

EVIDENCE RATING ★★★★★

Your *key* insights

Your gut microbiome's ability to break down fibre

This is a good level! Your potential to break down fibre 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 fibre.

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

Fibre-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 fibres—detailed in your food suggestions—will promote the growth of your beneficial, fibre-degrading bacteria. A similar or high proportion of species that can break down fibre compared to the healthy group is considered beneficial.

EVIDENCE RATING ★★★★☆

Your gut microbiome's ability to break down protein

This is not a good level. The proportion of bacteria present in your sample that can break down protein is at a high level, which is not ideal. When protein is broken down by bacteria in the gut microbiome it can lead to the production of substances that promote inflammation. To balance this function, try increasing your consumption of complex fibres such as resistant starch.

A **This sample reported a level higher than 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 fibre in the diet or an excessive intake of protein. A high proportion of protein-degrading bacteria suggests that not enough fibre is reaching the lower colon to feed the bacteria that specialise in eating fibre.

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 resistant exercise could help regulate BCAA blood levels.

EVIDENCE RATING ★★★★☆

Your microbiome's potential to contribute to cardiovascular disease

This is not a good level. Your potential to produce trimethylamine (TMA) is at a high level in this sample. Trimethylamine is 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 on TMAO. You may wish to consider increasing your consumption of dietary sources of indoles such as broccoli, kale, cabbage and cauliflower.

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

A similar or low potential to produce trimethylamine compared to the healthy group is generally considered beneficial. Trimethylamine is 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 fibre 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 fibre, 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 fibre 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 need 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 sulphide is at a high level. Try adding foods high in prebiotic fibres, 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 sulphide, 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 fibre, protein, mucus and even bile acids, they produce different types of gases as a by-product. Flatulence is primarily made up of odourless gases such as nitrogen, hydrogen, carbon dioxide, and methane. However, a small percent of flatulence can be made up of the gas hydrogen sulphide, which gives flatulence the characteristic rotten eggs smell. A small amount of hydrogen sulphide gas has been found to be protective of the gut, however a high potential to produce hydrogen sulphide has been associated with mitochondrial dysfunction and impaired gut barrier function. Research has found that the production of hydrogen sulphide by gut bacteria can be inhibited by consuming foods high in the prebiotic fibres 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 higher level than 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.

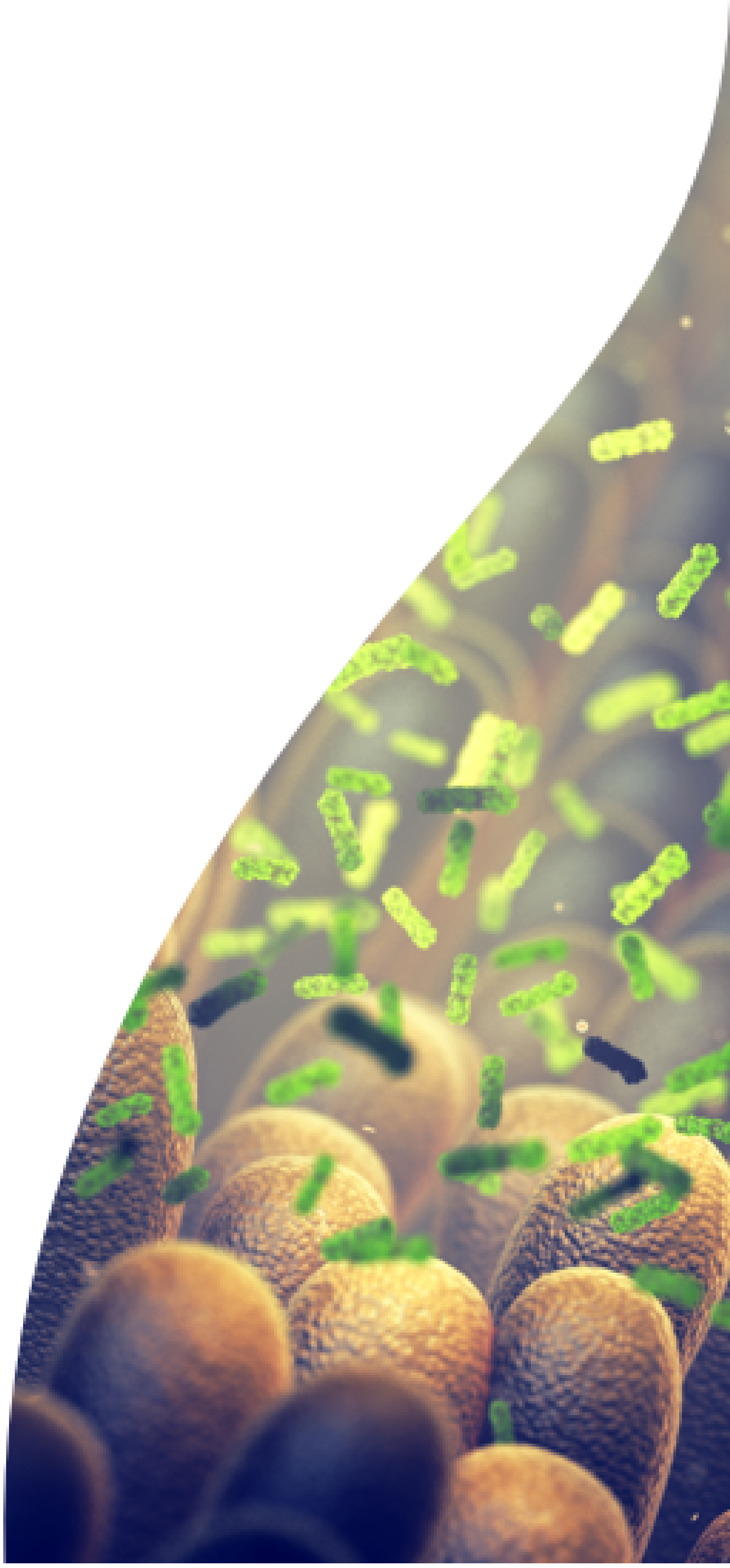
A **This sample reported a level higher than the healthy group**

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



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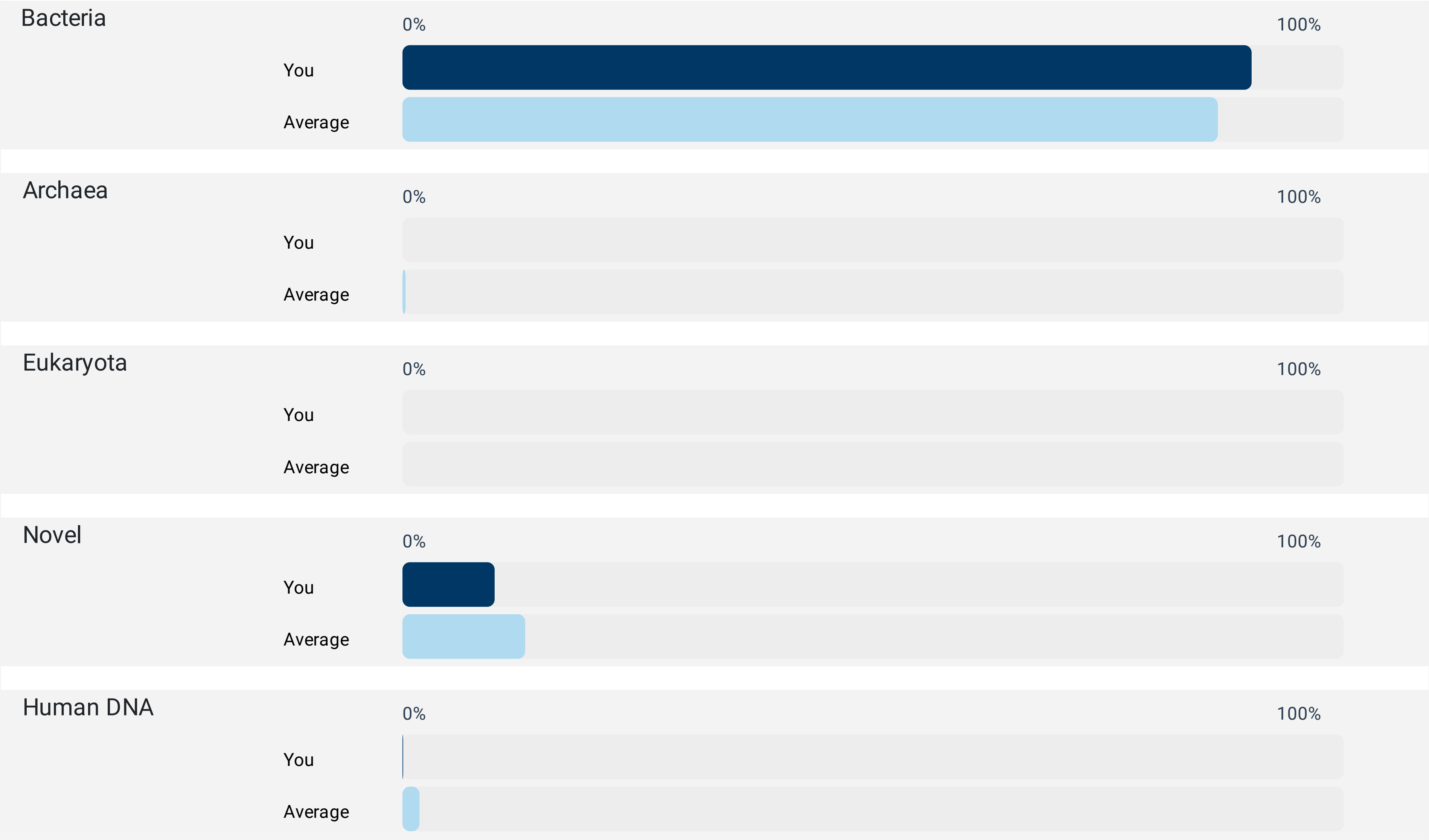
Sample Composition

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.

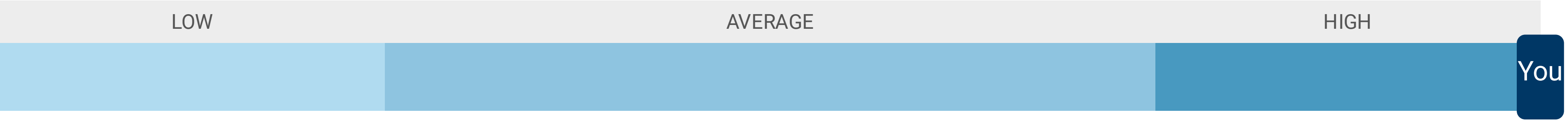


Microbiome Digestion Potential

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 fibre, 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 fibre 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.

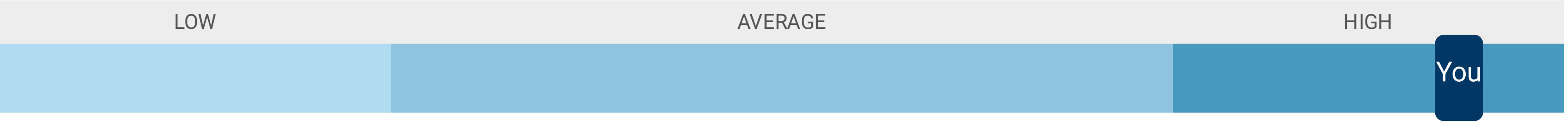
FIBRE

This scale indicates the proportion of species in your gut microbiome that can break down fibre. If you have a low proportion, consider adding more fibre to your diet to improve your gut health. Fibre 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 fibre is an important component of a healthy diet.



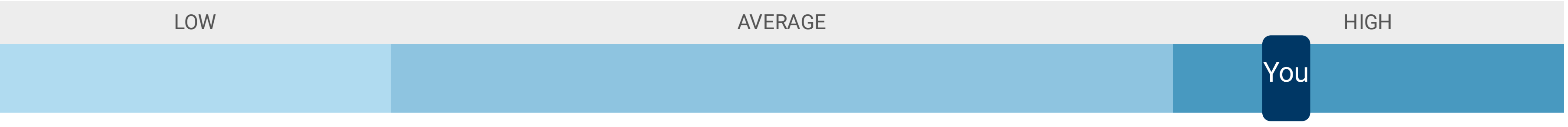
MUCIN

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 fibre 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 fibre 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.

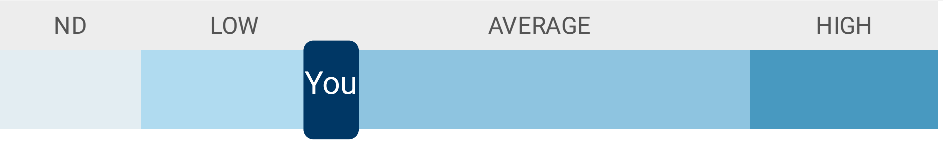
Microbial Metabolites

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

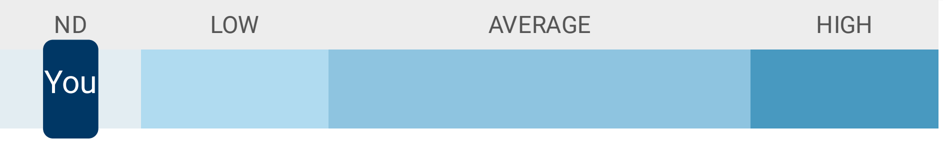
⊖ ***Hexa-acylated lipopolysaccharide production*** **0.023%**



The abundance of this metabolite is about the same as 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]

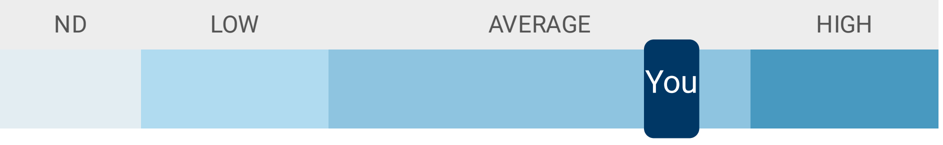
⊖ ***Methane production*** **0.00%**



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]

D-lactic acid production **68.7%**



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

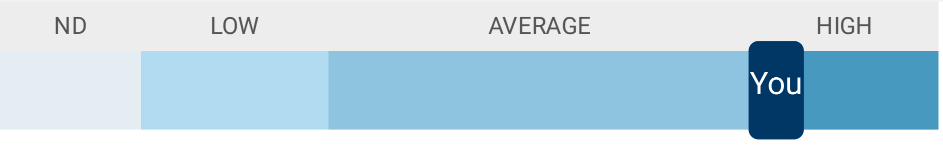
Some lactic acid bacterial species can produce a special form of lactate called D-lactate. As a form of lactate, it has the beneficial properties of being able to reduce inflammation, help maintain the gut cell barrier, and reduce colonisation by pathogens by lowering the pH in the gut. However, this form is not metabolised by our body as quickly and in rare cases in individuals with short bowel syndrome, D-lactate can build up and cause D-lactic acidosis.
[1] [2] [3]

Microbial Metabolites

HEALTH INDICATORS

Produced

⊖ *Trimethylamine production* **8.28%**

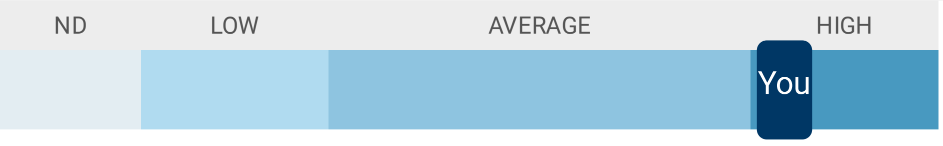


The abundance of this metabolite is higher than the comparison group.

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. The Heart Foundation recommends limiting red meat consumption to less than 350g per week.
[1] [2] [3] [4] [5] [6] [7]

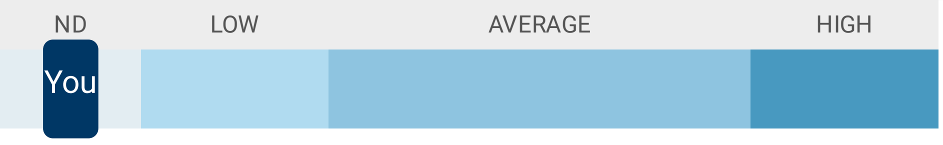
⊖ *Ammonia (urease) production* **11.7%**



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]

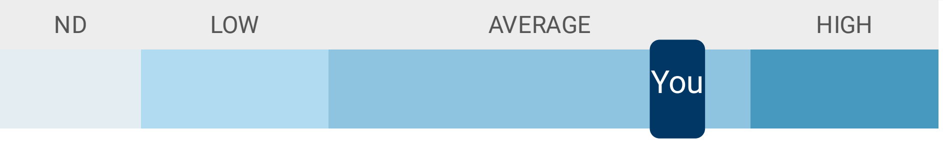
⊖ *B. fragilis toxin production* **0.00%**



This metabolite is not detected in this microbiome.

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 diarrhoea while other people can remain symptom free. There are concerns that this toxin can cause intestinal inflammation. If you are experiencing diarrhoea and have this toxin, consider seeing a healthcare practitioner.
[1] [2]

Beta-glucuronidase production **23.4%**



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

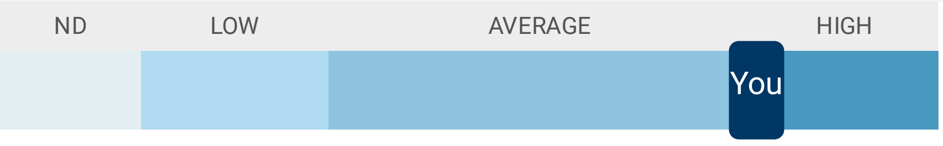
Beta-glucuronidase is a bacterial enzyme which can limit the excretion of compounds from the body such as medications, hormones and environmental toxins. One human study has suggested that consuming glucomannan can reduce faecal beta-glucuronidase activity. Glucomannan is a type of prebiotic fibre found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

Microbial Metabolites

HEALTH INDICATORS

Produced

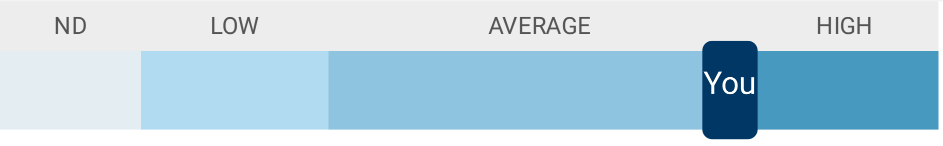
⊖ ***Hydrogen sulphide production*** **13.6%**



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

The gas hydrogen sulphide is produced by bacteria when they break down sulphur-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 sulphide can play a beneficial role by acting as an energy source for gut cells. However at high levels hydrogen sulphide can inhibit energy production in gut cells and disrupt the gut mucus barrier. Elevated levels of hydrogen sulphide 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 sulphide by the microbiome.
[1] [2]

Branched chain amino acids production **69.8%**



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

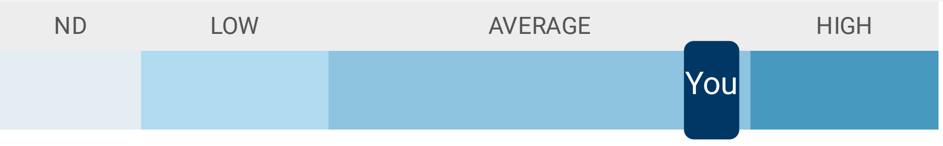
Branch chain amino acids (BCAAs) are involved in the regulation of glucose and fat metabolism and the immune system. High levels of BCAAs have been associated with metabolic diseases, such as obesity and type 2 diabetes. Muscle plays an important role in regulating BCAA levels. A high potential to produce BCAAs has also been associated with people who have a diet that is low in fibre. Maximising muscle mass through regular physical activity can help maintain metabolic balance.
[1] [2]

Microbial Metabolites

HEALTH INDICATORS

Consumed

Oxalate consumption **4.50%**



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

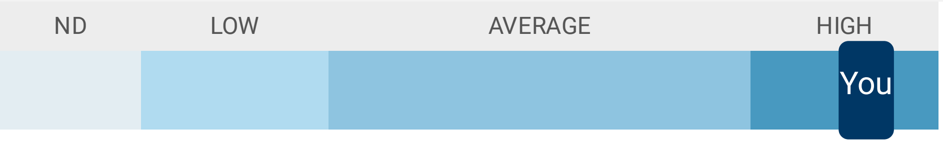
Some bacteria can break down oxalates in the colon, thus reducing the risk of forming calcium oxalate kidney stones. People who suffer from repeated unexplained kidney stones are observed to have a low potential for oxalate degradation in their microbiome compared to non-stone formers. A similar or high 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 **43.8%**

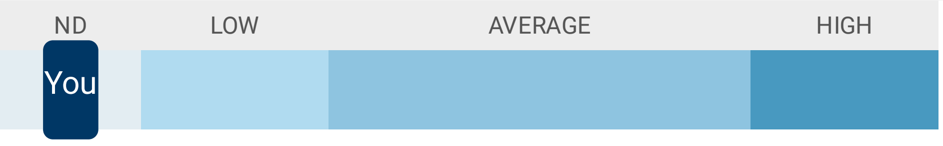


The abundance of this metabolite is higher than the comparison group.

GABA (gamma-aminobutyric acid) plays an important role in regulating mental state by calming the nervous system. Low levels of GABA being 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%**

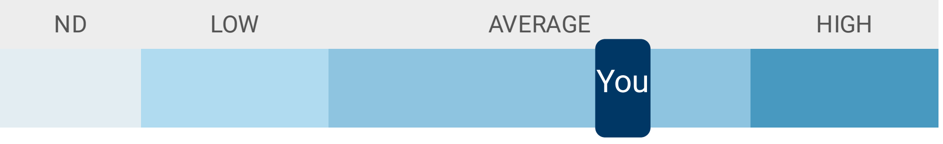


This metabolite is not detected in this microbiome.

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 fibre, and in particular rye, can help increase IPA production.

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

Histamine production **1.35%**



The abundance of this metabolite is about the same as 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.

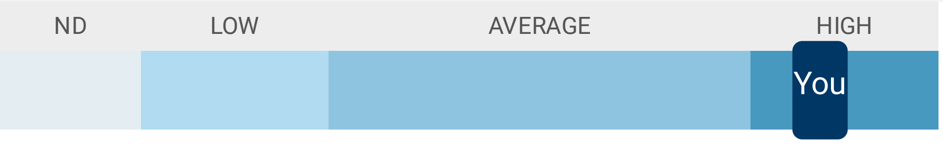
[1] [2] [3]

Microbial Metabolites

NEUROENDOCRINE

Consumed

⊕ ***GABA consumption*** **25.5%**



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

GABA (gamma-aminobutyric acid) plays an important role in regulating mental state by calming the nervous system. Low levels of GABA being 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 consume GABA in anxiety and depression is currently not understood. If you are concerned about your mental health, it is important to seek professional help.

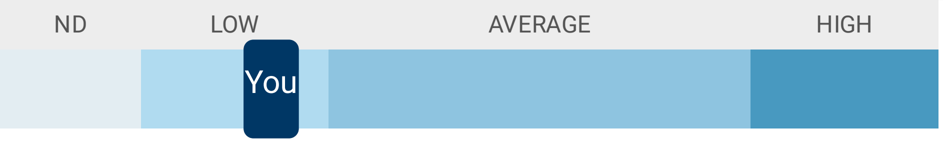
[1] [2] [3]

Microbial Metabolites

SHORT CHAIN FATTY ACIDS

Produced

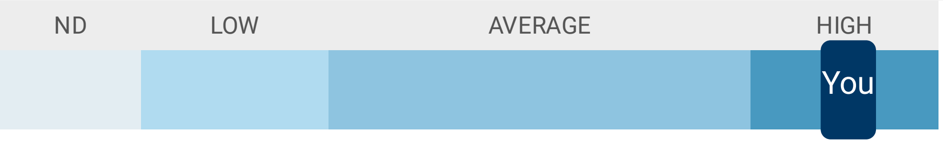
⊕ ***Butyrate production*** **9.22%**



The abundance of this metabolite is lower than 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]

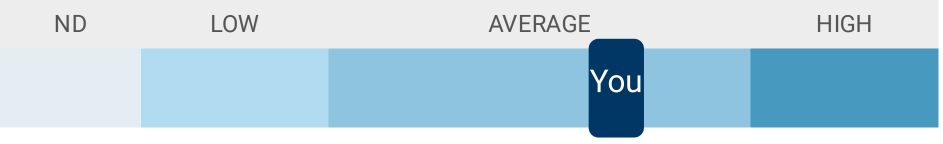
Lactate production **83.2%**



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 yoghurt, kefir, sauerkraut and kimchi.
[1] [2]

⊕ ***Propionate production*** **5.58%**



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

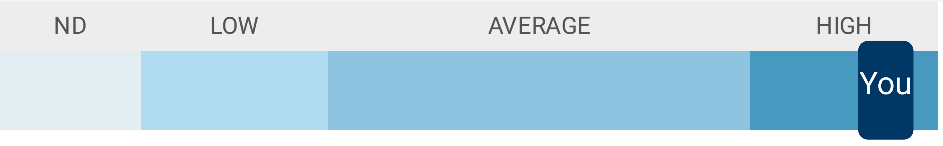
Propionate is a beneficial short chain fatty acid that is important for gut health. It helps maintain blood glucose levels, can reduce inflammation, helps control appetite and promotes the production of serotonin from the gut. The prebiotic fibre beta-glucan, found in oats and barley, has been shown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

Microbial Metabolites

SHORT CHAIN FATTY ACIDS

Produced

Acetate production **83.9%**



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

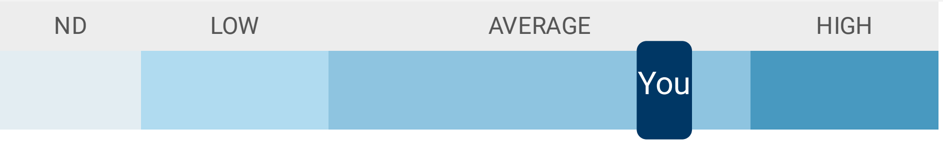
Acetate is the most abundant short chain fatty acid produced by our gut microbiome. It plays a beneficial role by supressing inflammation, regulating appetite, and regulating fat metabolism. Several bacterial species can also convert acetate to the beneficial short chain fatty acid, butyrate. The consumption 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

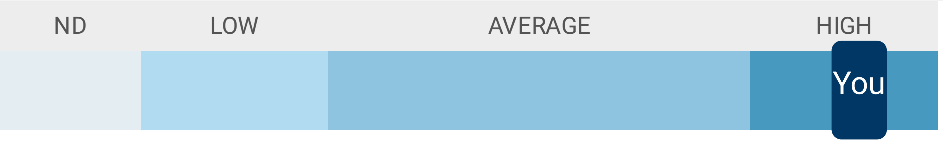
Cobalamin (B12) production **19.5%**



The abundance of this metabolite is about the same as 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]

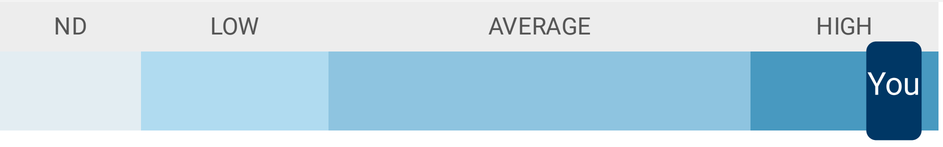
Folate (B9) production **76.4%**



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

Folate or folic acid plays an important role in cell replication and repair. Low folate levels can result in anaemia 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. All non-organic bread in Australia 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 **49.0%**



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

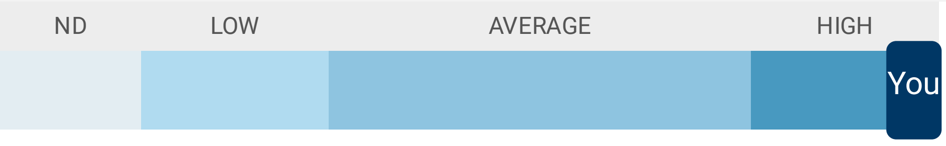
Biotin plays a critical role in metabolism and in the regulation of the immune system. Biotin cannot be produced by human cells and must be obtained through diet or the microbiome. The large intestine has the ability to absorb biotin but it is estimated that the gut microbiome can only provide up to 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

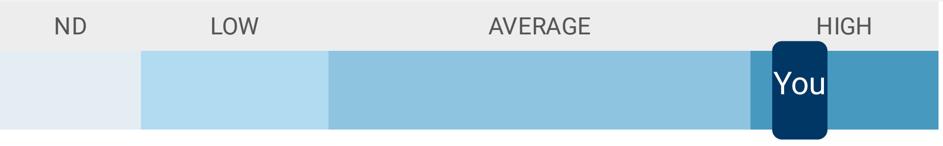
⊕ *Riboflavin (B2) production* **62.2%**



The abundance of this metabolite is higher than 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* **36.3%**



The abundance of this metabolite is higher than 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]

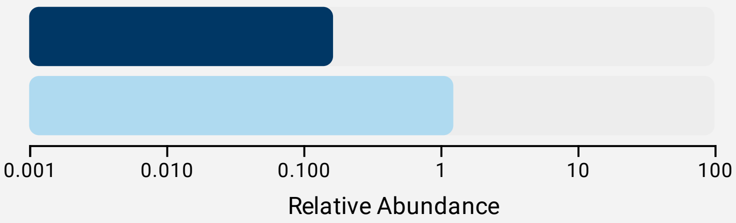
Species of Interest

BACTERIA (PROKARYOTES)

Agathobacter — DETECTED

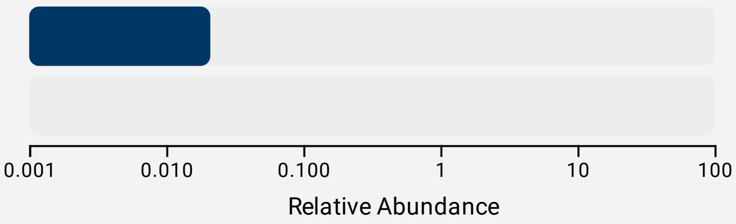
⊕ ***Agathobacter rectale***

You	**0.210%**
Average	**1.74%**



Agathobacter MIC7010

You	**0.024%**
Average	**0.00%**

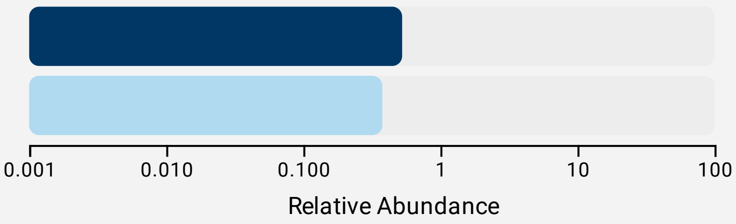


Akkermansia — NOT DETECTED

Bifidobacterium — DETECTED

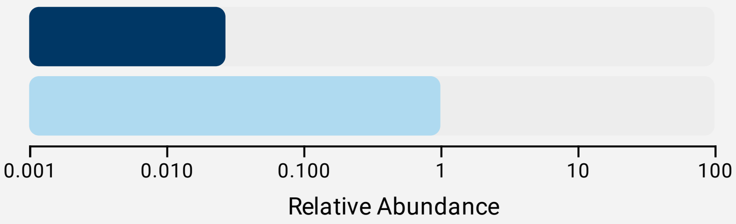
⊕ ***Bifidobacterium longum***

You	**0.707%**
Average	**0.499%**



⊕ ***Bifidobacterium adolescentis***

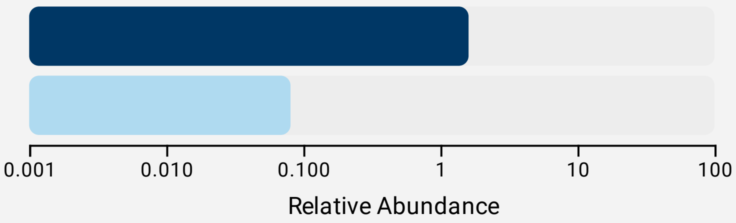
You	**0.032%**
Average	**1.39%**



Bilophila — DETECTED

⊖ ***Bilophila wadsworthia***

You	**2.28%**
Average	**0.099%**



Campylobacter — NOT DETECTED

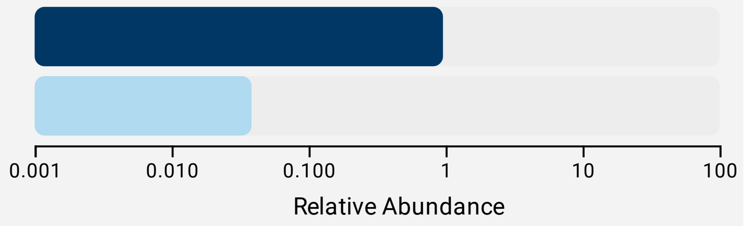
Citrobacter — NOT DETECTED

Clostridioides
NOT DETECTED

Clostridium
DETECTED

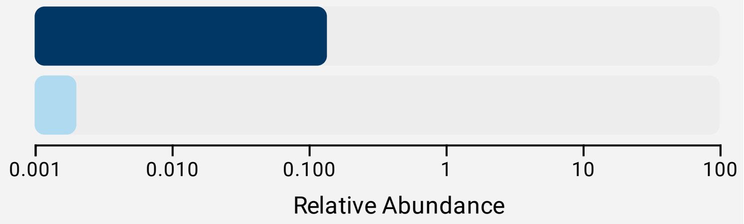
Clostridium_M sp000431375

You	**1.32%**
Average	**0.046%**



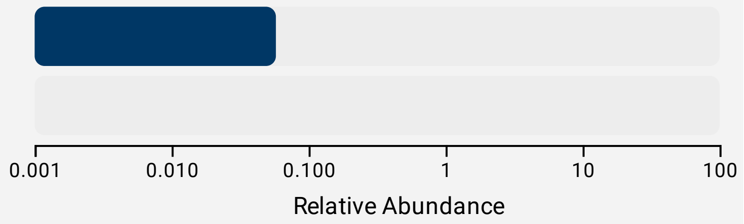
Clostridium_M sp001517625

You	**0.172%**
Average	**0.002%**



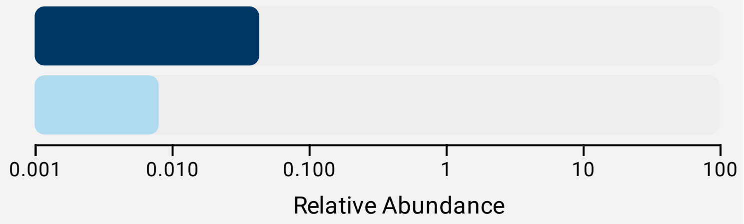
Clostridium_M MIC9612

You	**0.070%**
Average	**0.001%**



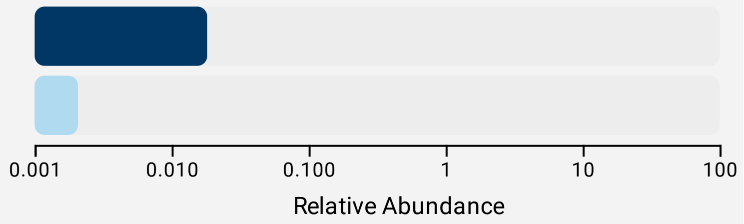
⊖ ***Clostridium_M bolteae***

You	**0.052%**
Average	**0.009%**



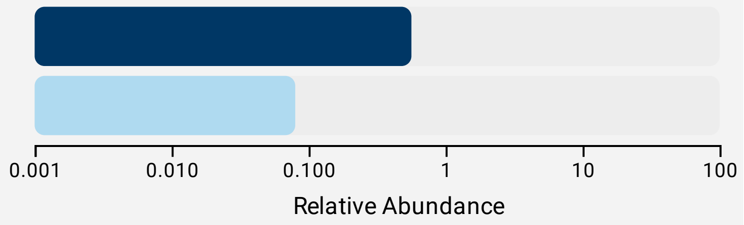
⊖ ***Clostridium_M citroniae***

You	**0.021%**
Average	**0.002%**



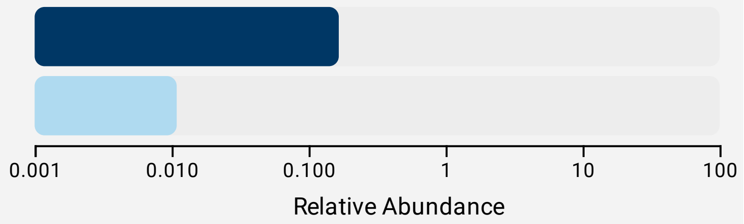
Clostridium_Q sp003024715

You	**0.760%**
Average	**0.098%**



⊖ ***Clostridium_Q symbiosum***

You	**0.211%**
Average	**0.012%**



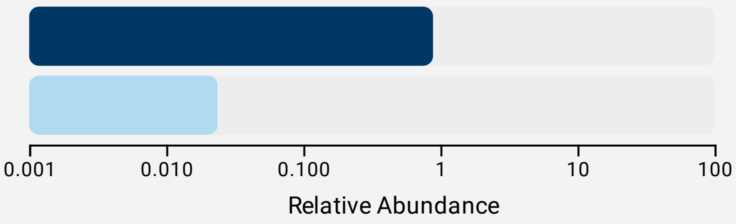
Corynebacterium
NOT DETECTED

NOT DETECTED

Desulfovibrio	**NOT DETECTED**
Eggerthella	**DETECTED**

⊖ ***Eggerthella lenta***

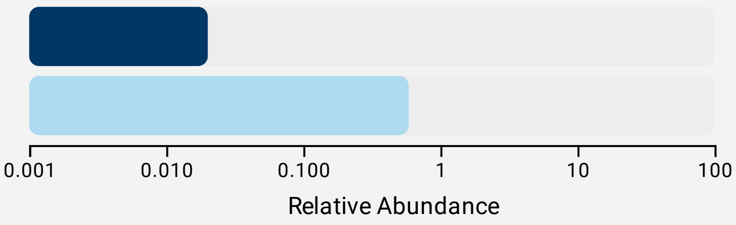
You	**1.22%**
Average	**0.027%**



Enterobacter	**NOT DETECTED**
Enterococcus	**NOT DETECTED**
Escherichia	**DETECTED**

⊖ ***Escherichia coli***

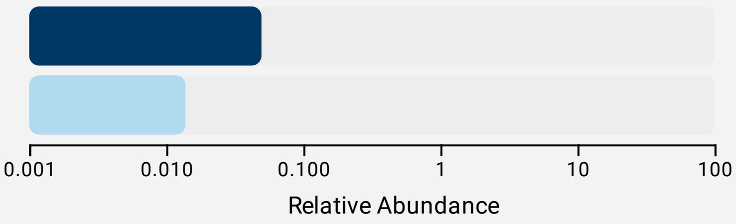
You	**0.023%**
Average	**0.794%**



Faecalibacterium	**NOT DETECTED**
Fusobacterium	**NOT DETECTED**
Helicobacter	**NOT DETECTED**
Klebsiella	**NOT DETECTED**
Lactobacillus	**NOT DETECTED**
Porphyromonas	**DETECTED**

Porphyromonas sp001808555

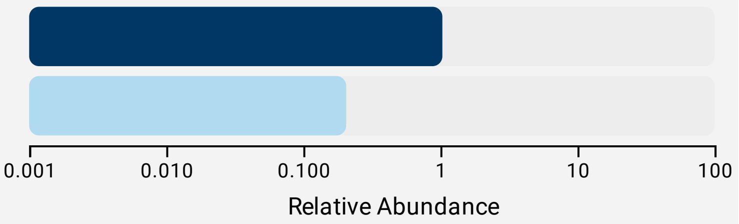
You	**0.060%**
Average	**0.016%**



Prevotella	**NOT DETECTED**
Pseudomonas	**NOT DETECTED**
Roseburia	**DETECTED**

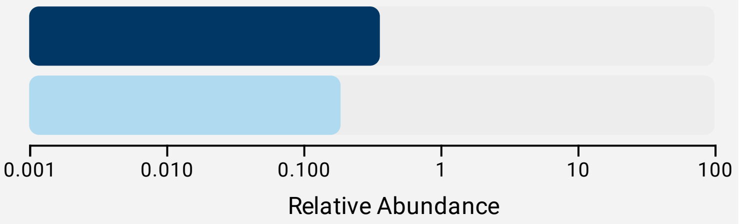
⊕ ***Roseburia intestinalis***

You **1.44%**
Average **0.264%**



⊕ ***Roseburia inulinivorans***

You **0.478%**
Average **0.239%**



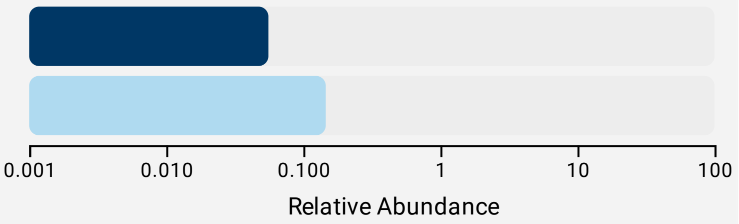
Ruminococcus **NOT DETECTED**

Salmonella **NOT DETECTED**

Streptococcus **DETECTED**

⊖ ***Streptococcus salivarius***

You **0.067%**
Average **0.185%**



Species of Interest

ARCHAEA (PROKARYOTES)

Methanogens	**NOT DETECTED**
Other Archea	**NOT DETECTED**

Species of Interest

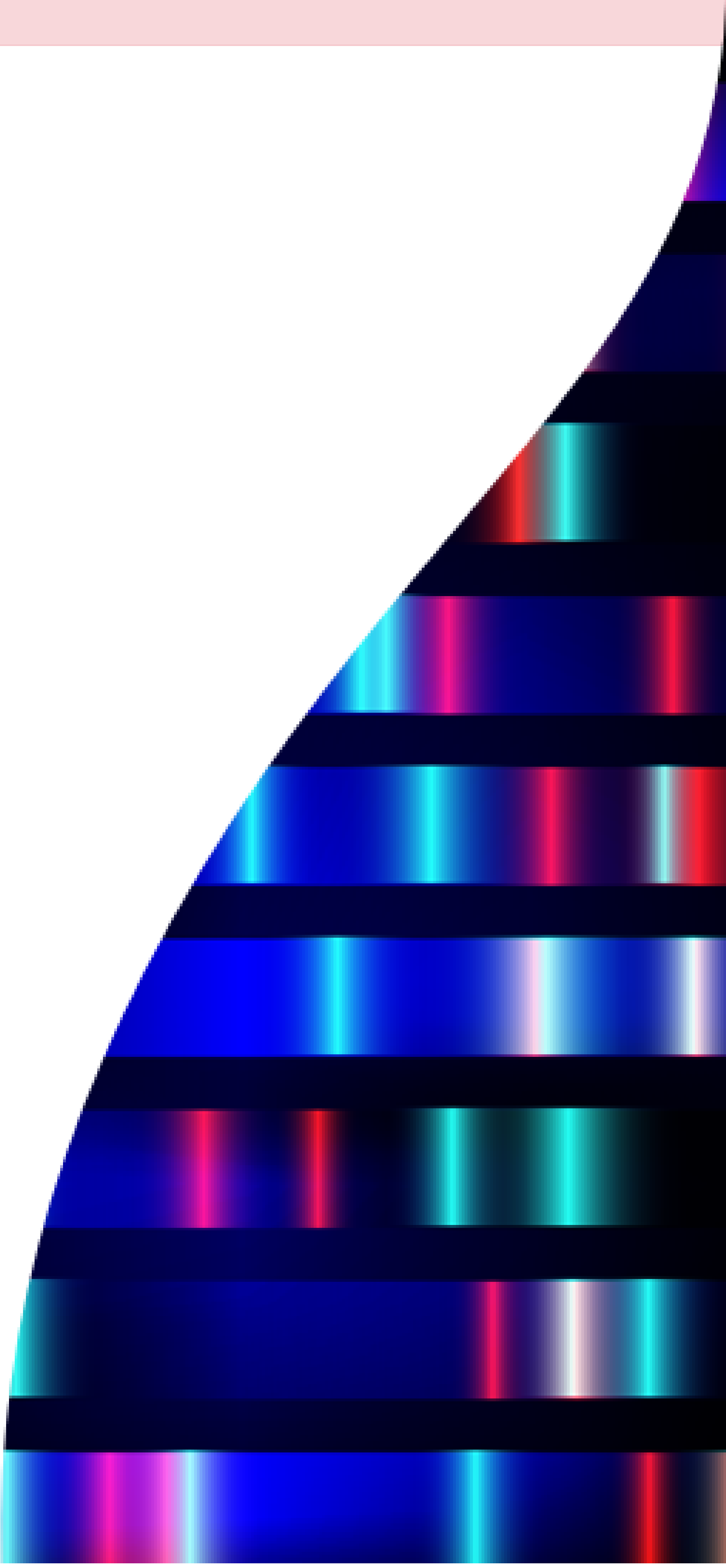
YEASTS/FUNGI & PARASITES (EUKARYOTES)

Blastocystis	**NOT DETECTED**
Candida	**NOT DETECTED**
Saccharomyces	**NOT DETECTED**
Other Eukaryotes	**NOT DETECTED**

Microbial Profile

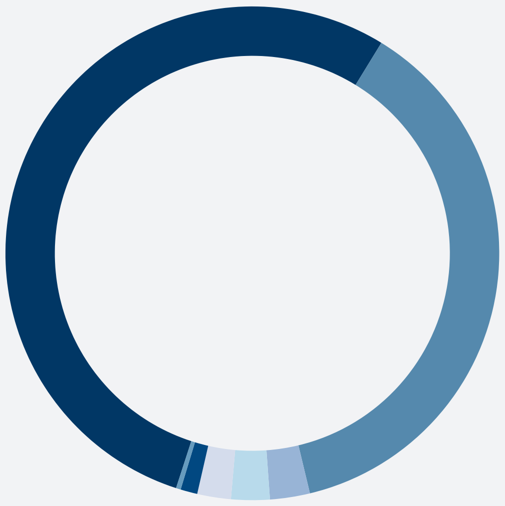
Note: Reports issued in 2022 display updated reference ranges for some species related to an improvement in laboratory processing. For more information contact mybiome@synlab.es.

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
■ Bacteroidota	48.5%	16.5 - 35.0%	High
■ Firmicutes_A	33.8%	32.7 - 58.7%	Average
■ Proteobacteria	2.35%	0.694 - 9.09%	Average
■ Desulfobacterota_A	2.28%	0.074 - 0.501%	High
■ Actinobacteriota	1.99%	1.13 - 10.3%	Average
■ Firmicutes_C	0.996%	0.351 - 2.20%	Average
■ Firmicutes	0.279%	0.743 - 9.80%	Low

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
⊖	Bacteroidota	***Bacteroides_B vulgatus***	24.3%	0.185 - 6.74%	High

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, 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:
High levels of this bacterium have been associated with metabolic and inflammatory conditions. This species has also been associated with a diet high in red meat.

+−	Bacteroidota	***Bacteroides uniformis***	14.6%	0.290 - 3.68%	High

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 inflammatory conditions.

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
	Bacteroidota	***Bacteroides stercoris***	7.41%	0.00 - 1.06%	High

This is a common inhabitant of the gut that can use many different fuel sources.

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, 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:
One study observed this species was at lower levels in individuals with asthma.

	Firmicutes_A	***Blautia_A wexlerae***	5.99%	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	***Fusicatenibacter saccharivorans***	5.38%	0.418 - 4.06%	High

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 sulphide, lactate.

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

⊕	Firmicutes_A	***Anaerostipes hadrus***	3.05%	0.115 - 2.37%	High

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 sulphide, lactate, riboflavin (B2).

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

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
	Proteobacteria	***Sutterella MIC7114***	2.33%	0.00 - 0.00%	High

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, folate (B9), 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 is a newly defined species in the Microba database.

⊖	Desulfobacterota_A	***Bilophila wadsworthia***	2.28%	0.00 - 0.217%	High

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 sulphide, 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:
High levels of this species can promote inflammation in the gut and is associated with a diet high in saturated fats.

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
	Firmicutes_A	***Blautia_A sp900066205***	2.11%	0.00 - 0.211%	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, ammonia (urease), branched chain amino acids, cobalamin (B12), folate (B9), lactate.

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

Emerging research:
This species is named according to the Genome Taxonomy Database (GTDB), a standardised microbial taxonomy based on the genomes of organisms, rather than their phenotype.

⊕	Firmicutes_A	***Roseburia intestinalis***	1.44%	0.00 - 0.540%	High

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

Fuel Sources Used:
This species is a good 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, ammonia (urease), beta-glucuronidase, biotin (B7), branched chain amino acids, butyrate, cobalamin (B12), folate (B9), hydrogen sulphide, 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 reduced levels in individuals with metabolic and inflammatory conditions.

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
	Firmicutes_A	***Clostridium_M sp000431375***	1.32%	0.00 - 0.074%	High
⊖	Firmicutes_A	***Ruminococcus_B gnavus***	1.23%	0.00 - 0.026%	High

This species is one of the earliest colonisers 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 inflammatory conditions.

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
⊖	Actinobacteriota	***Eggerthella lenta***	1.22%	0.00 - 0.080%	High
	Firmicutes_A	***Oscillibacter sp001916835***	1.04%	0.00 - 0.380%	High
	Firmicutes_A	***Lawsonibacter sp900066825***	1.02%	0.00 - 0.00%	High
	Firmicutes_C	***Phascolarctobacterium faecium***	0.996%	0.00 - 0.336%	High

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:
Elevated levels of this species have been associated with cardiovascular and metabolic conditions. 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.

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
⊖	Firmicutes_A	***Dorea longicatena_B***	0.993%	0.00 - 0.277%	High

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), trimethylamine.

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

Emerging research:
Multiple studies have observed this species at higher levels in individuals with obesity comapred to lean controls. However in obese, postmenopausal women, this species was associated with improved insulin sensitivity. This species has also been observed at lower levels in individuals with inflammatory conditions.

	Firmicutes_A	***Agathobaculum butyriciproducens***	0.930%	0.00 - 0.498%	High
	Firmicutes_A	***UBA9502 MIC8595***	0.861%	0.00 - 0.00%	High
	Bacteroidota	***Bacteroides thetaiotaomicron***	0.795%	0.00 - 0.477%	High
	Firmicutes_A	***Clostridium_Q sp003024715***	0.760%	0.00 - 0.214%	High

Species Profile

SPECIES

<table>
<tr><th></th><th>Phylum</th><th>Species</th><th>Abundance</th><th>Range</th><th>Level</th></tr>
<tr><td>⊕</td><td>Actinobacteriota</td><td><i>Bifidobacterium longum</i></td><td>0.707%</td><td>0.031 - 1.44%</td><td>Average</td></tr>
<tr><td colspan="6">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:
<i>B.longum</i> 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.</td></tr>
<tr><td></td><td>Firmicutes_A</td><td><i>CAG-81 sp000435795</i></td><td>0.626%</td><td>0.00 - 0.076%</td><td>High</td></tr>
<tr><td></td><td>Firmicutes_A</td><td><i>Blautia_A sp900066165</i></td><td>0.605%</td><td>0.107 - 1.13%</td><td>Average</td></tr>
<tr><td></td><td>Firmicutes_A</td><td><i>Anaerotignum sp001304995</i></td><td>0.549%</td><td>0.00 - 0.00%</td><td>High</td></tr>
<tr><td></td><td>Firmicutes_A</td><td><i>Lachnospira sp000437735</i></td><td>0.516%</td><td>0.00 - 0.229%</td><td>High</td></tr>
</table>

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
⊕	Bacteroidota	***Alistipes shahii***	0.495%	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, and a study in mice showed this species may improve the efficacy of immunotherapy. However, high levels of this species have also been observed in motorneuron conditions.

⊕	Firmicutes_A	***Roseburia inulinivorans***	0.478%	0.00 - 0.636%	Average

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 sulphide, 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
⊖	Firmicutes_A	***Faecalicatena torques***	0.370%	0.00 - 0.188%	High

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 inflammatory conditions.

	Bacteroidota	***Barnesiella intestinihominis***	0.361%	0.00 - 0.524%	Average
	Firmicutes_A	***Gemmiger sp003476825***	0.320%	0.061 - 3.08%	Average

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
⊕	Firmicutes_A	***Dorea formicigenerans***	0.311%	0.069 - 0.301%	High

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 inflammatory conditions, indicating it likely plays a beneficial role in health.

⊖	Firmicutes_A	***Flavonifractor plautii***	0.297%	0.00 - 0.049%	High

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 inflammatory conditions.

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
	Firmicutes_A	***Lachnospiraceae MIC6495***	0.277%	0.00 - 0.085%	High
	Firmicutes_A	***Blautia sp000432195***	0.274%	0.00 - 0.00%	High
⊖	Bacteroidota	***Bacteroides ovatus***	0.249%	0.00 - 0.670%	Average

This is one of the most common inhabitants of the 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, 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:
High levels of this species have been associated with inflammation.

	Phylum	Species	Abundance	Range	Level
	Firmicutes_A	***Tyzzerella sp000411335***	0.213%	0.00 - 0.00%	High

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
⊖	Firmicutes_A	***Clostridium_Q symbiosum***	0.211%	0.00 - 0.00%	High

This is an 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, biotin (B7), branched chain amino acids, butyrate, cobalamin (B12), folate (B9), hydrogen sulphide, lactate, propionate, riboflavin (B2), trimethylamine.

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

Emerging research:
This species has been observed at high levels in individuals with metabolic and poor gut health.

⊕	Firmicutes_A	***Agathobacter rectale***	0.210%	0.00 - 4.44%	Average

Previously named *Eubacterium rectale*, this is a common member 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).

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

Emerging research:
This species is commonly associated with healthy controls in research studies. Low levels of this bacterium have been observed in inflammatory conditions.

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
	Bacteroidota	***Bacteroides MIC7427***	0.194%	0.00 - 0.00%	High
	Firmicutes_A	***Coprococcus_B MIC8649***	0.182%	0.00 - 0.00%	High
⊕	Firmicutes_A	***Coprococcus_A catus***	0.181%	0.00 - 0.269%	Average

This is an 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, propionate, riboflavin (B2).

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

Emerging research:
Its name catus comes from the Latin word for "clever," referring to its unusual property of some strains being able to produce large amounts of butyrate and propionate.

	Firmicutes_A	***Clostridium_M sp001517625***	0.172%	0.00 - 0.00%	High
	Firmicutes_A	***Blautia MIC9227***	0.153%	0.00 - 0.00%	High
	Firmicutes_A	***Blautia_A sp000433815***	0.152%	0.00 - 0.00%	High

Species Profile

SPECIES

<table>
<tr><th></th><th>Phylum</th><th>Species</th><th>Abundance</th><th>Range</th><th>Level</th></tr>
<tr><td>⊕</td><td>Firmicutes_A</td><td><i>Coprococcus_B comes</i></td><td>0.150%</td><td>0.042 - 0.592%</td><td>Average</td></tr>
<tr><td colspan="6">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 decreased levels in individuals with inflammatory conditions.</td></tr>
<tr><td></td><td>Firmicutes_A</td><td><i>Acetatifactor sp900066565</i></td><td>0.136%</td><td>0.00 - 1.00%</td><td>Average</td></tr>
<tr><td></td><td>Firmicutes_A</td><td><i>CAG-41 sp900066215</i></td><td>0.116%</td><td>0.00 - 0.432%</td><td>Average</td></tr>
<tr><td></td><td>Firmicutes_A</td><td><i>Flavonifractor sp000508885</i></td><td>0.115%</td><td>0.00 - 0.020%</td><td>High</td></tr>
<tr><td></td><td>Firmicutes_A</td><td><i>Blautia hansenii</i></td><td>0.113%</td><td>0.00 - 0.00%</td><td>High</td></tr>
<tr><td></td><td>Firmicutes</td><td><i>Erysipelatoclostridium MIC9185</i></td><td>0.112%</td><td>0.00 - 0.00%</td><td>High</td></tr>
<tr><td></td><td>Firmicutes_A</td><td><i>Dorea sp900066555</i></td><td>0.112%</td><td>0.00 - 0.068%</td><td>High</td></tr>
</table>

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
	Firmicutes_A	***Ruthenibacterium MIC9423***	0.110%	0.00 - 0.00%	High
	Firmicutes_A	***GCA-900066135 MIC6659***	0.090%	0.00 - 0.143%	Average
	Firmicutes_A	***Oscillibacter sp900066435***	0.085%	0.00 - 0.136%	Average
	Firmicutes_A	***Lachnospiraceae MIC6885***	0.072%	0.00 - 0.00%	High
	Firmicutes_A	***Faecalicatena glycyrrhizinilyticum***	0.071%	0.00 - 0.00%	High
	Firmicutes_A	***Clostridium_M MIC9612***	0.070%	0.00 - 0.00%	High
⊖	Firmicutes	***Streptococcus salivarius***	0.067%	0.00 - 0.185%	Average

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 associated with poor cardiovascular health.

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
	Bacteroidota	***Porphyromonas sp001808555***	0.060%	0.00 - 0.045%	High
	Firmicutes	***Absiella innocuum***	0.059%	0.00 - 0.020%	High
⊖	Firmicutes_A	***Clostridium_M bolteae***	0.052%	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:
Elevated levels of this species has been associated with metabolic conditions.

	Phylum	Species	Abundance	Range	Level
	Firmicutes_A	***Ruthenibacterium lactatiformans***	0.047%	0.00 - 0.096%	Average
	Firmicutes	***Holdemania massiliensis***	0.041%	0.00 - 0.00%	High
	Bacteroidota	***Parabacteroides MIC6494***	0.036%	0.00 - 0.00%	High
	Firmicutes_A	***Lawsonibacter MIC7082***	0.034%	0.00 - 0.00%	High

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
⊕	Actinobacteriota	***Bifidobacterium adolescentis***	0.032%	0.00 - 3.26%	Average
	Firmicutes_A	***COE1 sp001916965***	0.030%	0.00 - 0.112%	Average
	Actinobacteriota	***Pauljensenia bouchesdurhonensis***	0.029%	0.00 - 0.00%	High
	Firmicutes_A	***Dorea sp000509125***	0.025%	0.00 - 0.00%	High
	Firmicutes_A	***Phocea massiliensis***	0.025%	0.00 - 0.00%	High
	Firmicutes_A	***Agathobacter MIC7010***	0.024%	0.00 - 0.00%	High

This is a common and beneficial inhabitant of the 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, branched chain amino acids, folate (B9), GABA, lactate.

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

Emerging research:
Low levels of this species have been associated with inflammation.

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
⊖	Proteobacteria	***Escherichia coli***	0.023%	0.00 - 0.025%	Average

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, folate (B9), GABA, hexa-LPS, hydrogen sulphide, lactate, propionate, riboflavin (B2), vitamin K.

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

Emerging research:
The harmful strains can produce pro-inflammatory compounds, and toxins that cause infection and diarrhea.

	Phylum	Species	Abundance	Range	Level
	Firmicutes_A	***Acutalibacteraceae MIC8041***	0.022%	0.00 - 0.00%	High

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
⊖	Firmicutes_A	***Clostridium_M citroniae***	0.021%	0.00 - 0.00%	High

This species can 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, branched chain amino acids, cobalamin (B12), folate (B9), hydrogen sulphide, lactate, riboflavin (B2), trimethylamine.

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

Emerging research:
This species has been observed at higher levels in individuals with inflammatory conditions.

	Phylum	Species	Abundance	Range	Level
	Firmicutes_A	***Ruthenibacterium sp003149955***	0.021%	0.00 - 0.00%	High
	Firmicutes_A	***Faecalicatena contorta_B***	0.019%	0.00 - 0.00%	High
	Firmicutes_A	***Eubacterium_G sp000432355***	0.015%	0.00 - 0.030%	Average
	Firmicutes_A	***Oscillospiraceae MIC9672***	0.015%	0.00 - 0.00%	High

SYNLAB

Gut microbiome report

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