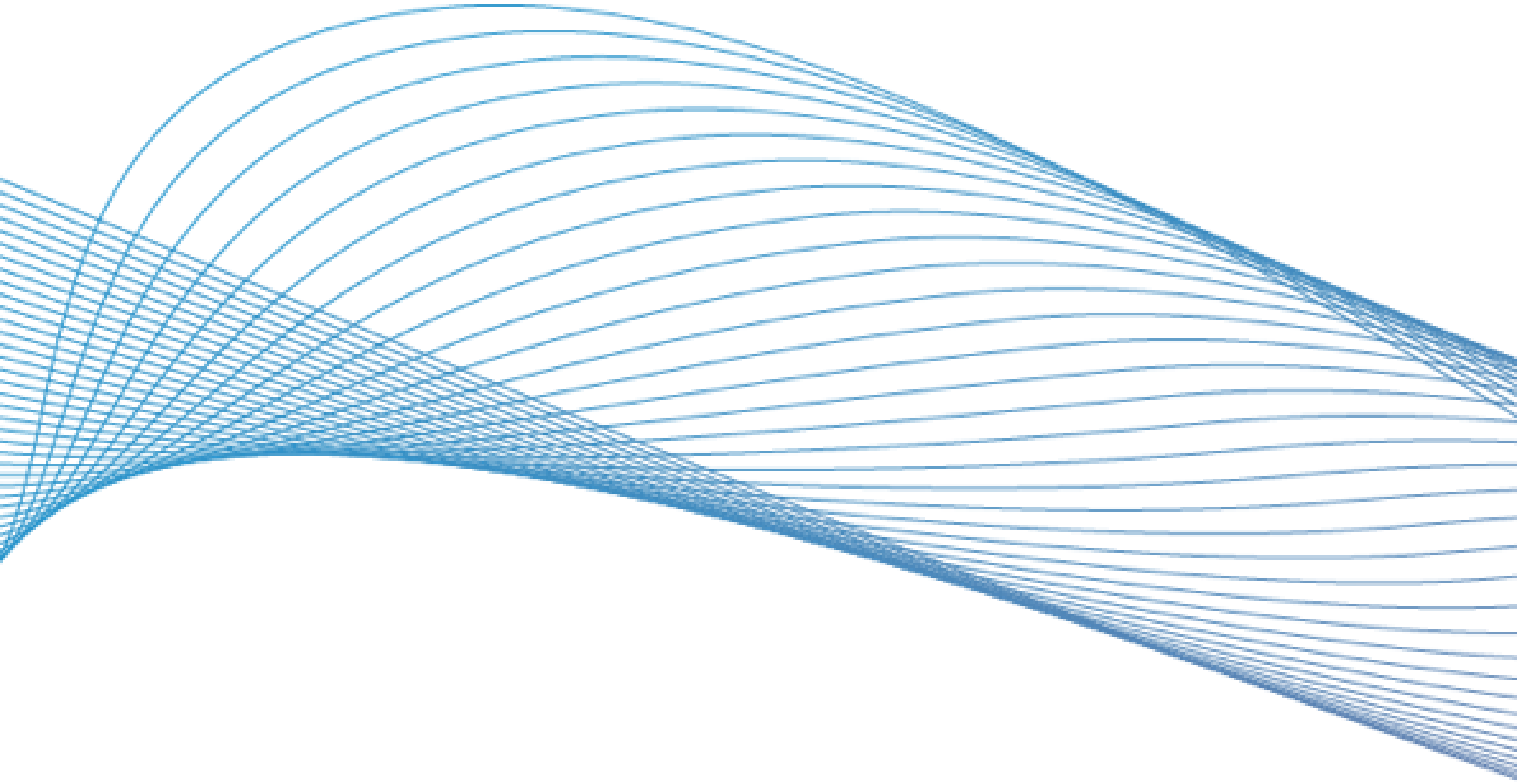
MICROBA

Microba *Insight*™

Gut microbiome report



Name: Kayla Ellery

Sample ID: BBT7764

Report generated on: 12-04-2024

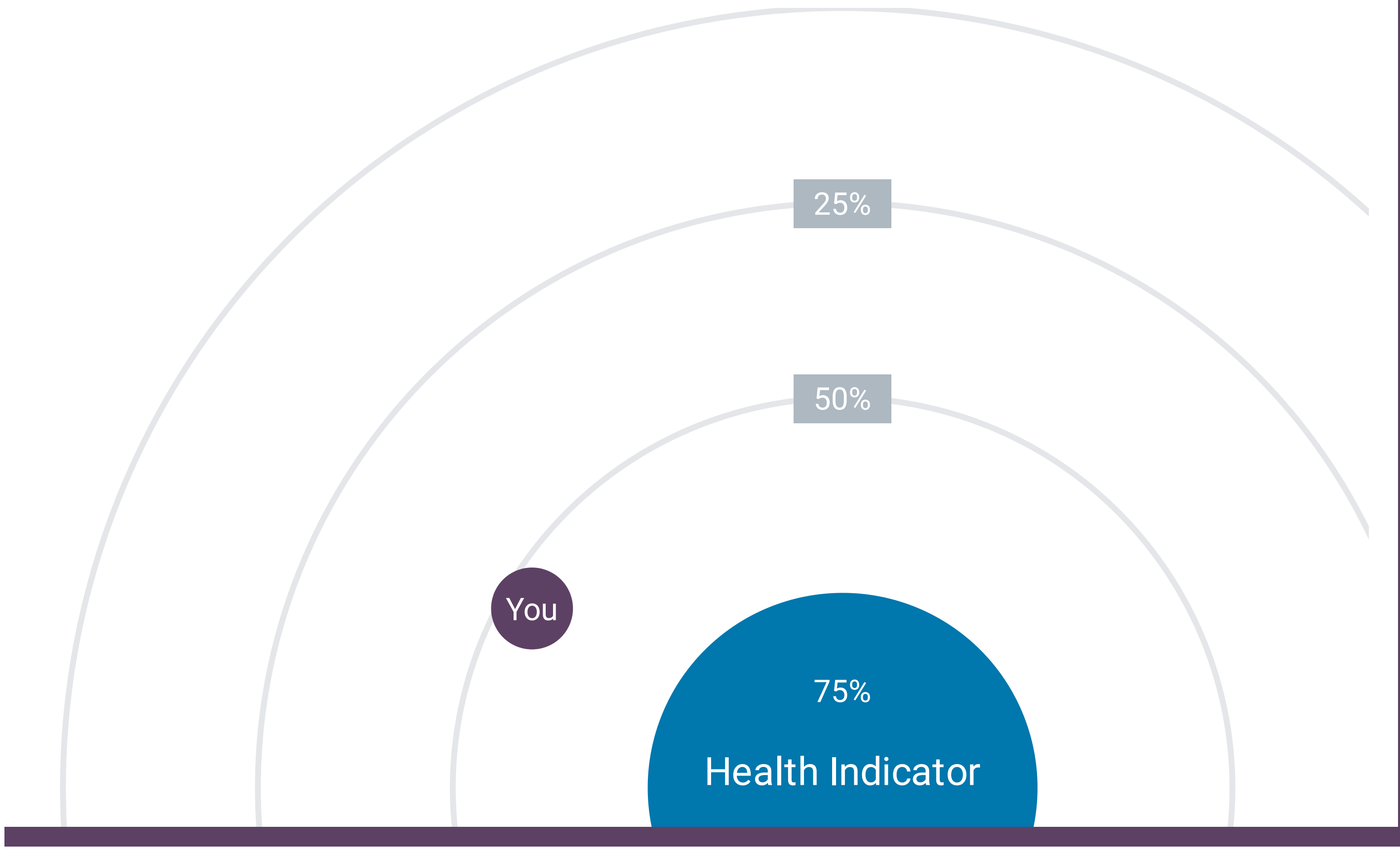
Introduction to *Microba Insight™* Report

Insight™ 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.

2/76 • v0.12.3-gb81b11 • MGDB_v2 • BBT7764 • Kayla Ellery • 12/04/2024
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.

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.

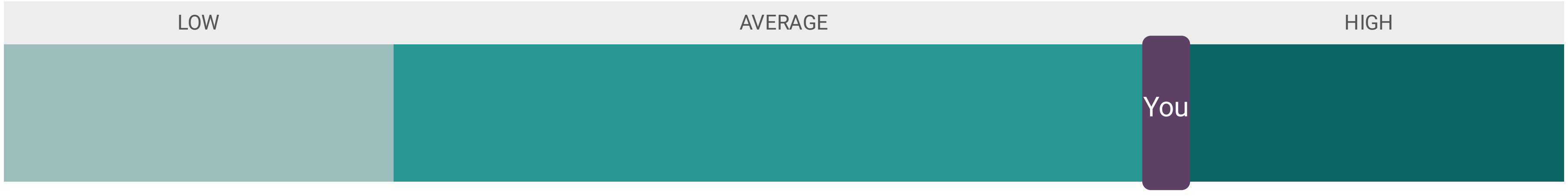


Your gut microbiome score is 54%. This measurement is an indication of how well your gut microbiome might be interacting with your overall health. A higher score suggests a more positive interaction.

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

4.55

Your microbial community

YOUR TOP 5 MOST ABUNDANT SPECIES

Does your sample have an overly high abundance of any single organism? **No**

	Phylum	Species	Abundance	Range	Level
	Firmicutes_A	*UBA1417 sp003531055*	6.60%	0.00 - 0.982%	High
	Firmicutes_A	*Acetatifactor sp900066365*	4.04%	0.00 - 0.817%	High
	Firmicutes_A	*Eisenbergiella sp900066775*	2.74%	0.00 - 0.437%	High
⊖	Bacteroidota	*Bacteroides_B dorei*	2.43%	0.00 - 2.99%	Average
⊕	Firmicutes_A	*Anaerostipes hadrus*	2.34%	0.294 - 5.33%	Average

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. green banana flour, raw oats or high amylose barley) will encourage microbes in your gut to produce butyrate.

EVIDENCE RATING ★★★★★

Your microbiome's potential to contribute to gut 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 reduced heart health, variable glucose regulation, poor weight management, and poor liver health. 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 similar to 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 a good level! The proportion of bacteria present in your sample that can break down protein is at a low level. 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 low level, continue eating diverse sources of fibre to encourage the growth of your fibre-degrading bacteria instead of your protein-degrading bacteria.

A **This sample reported a level lower 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

Your potential to produce branched chain amino acids is at a level similar to the healthy group. Similar or low levels of bacterially produced BCAAs compared to a healthy group is generally considered beneficial, as BCAAs are observed to be associated with poor weight management and variable glucose regulation.

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 poor weight management and variable glucose regulation. 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 influence and support your heart health

This is a good level! Your potential to produce trimethylamine (TMA) is at a level similar to the healthy group. Trimethylamine is converted by the human liver into trimethylamine oxide (TMAO) which has been linked to variable glucose regulation and reduced heart health. Plant compounds 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 is converted by the human liver into trimethylamine oxide (TMAO) which has been linked to poor heart and kidney health. 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 a good level! Your potential to produce indolepropionic acid (known as IPA) is similar to the healthy group. This is good, because IPA is a strong antioxidant that can protect nerve cells from damage and may help support glucose regulation.

A **This sample reported a level similar to 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 improve glucose regulation. Research suggests foods rich in ellagic acid (e.g. chestnuts and ellagic acid enriched pomegranate juice), as well as wholegrain wheat and rye may help support IPA production.

EVIDENCE RATING ★★★☆☆

Your microbiome's potential to contribute to kidney health

This is a good level! Your potential to degrade oxalates is similar to the healthy group. A similar or high potential to break down oxalate compared to the healthy group is generally considered beneficial.

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

The gut microbiome of individuals who suffer from poor kidney health often have a low potential to degrade oxalate. Oxalate is one of the main influences of kidney health. If you have poor kidney health, you may need wish to discuss trialling a low oxalate diet with a health care professional. 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 not a good level. Your gut microbiome's potential to produce folate is at a low level. Folate is important for cell replication and repair. Make sure you are getting enough folate in your diet by consuming foods that are high in folate, such as leafy green vegetables, beans, lentils, and fruits.

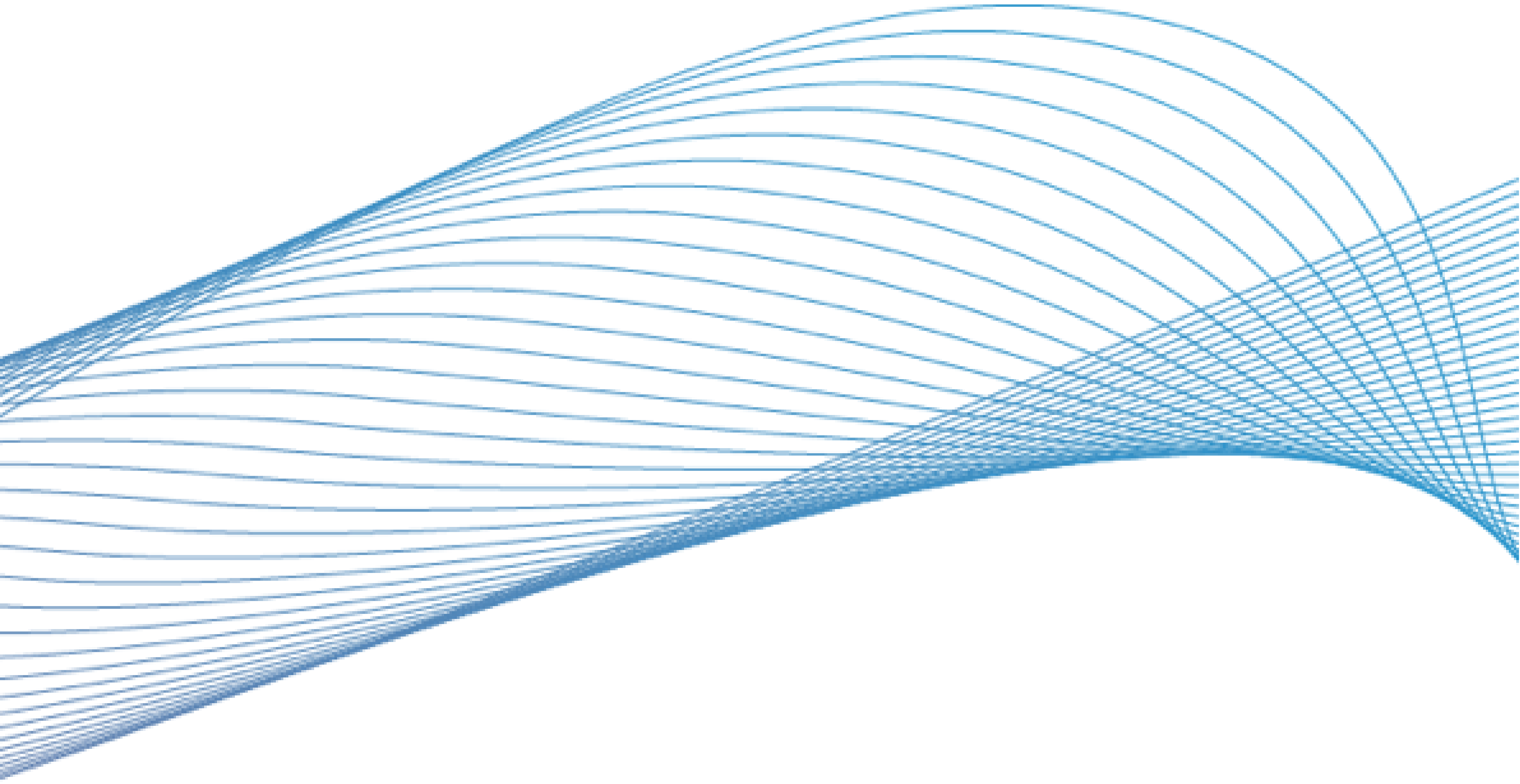
A **This sample reported a level lower than the healthy group**

Folate plays an important role in cell replication and repair. Deficiencies can result in reduced heart and blood health. 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

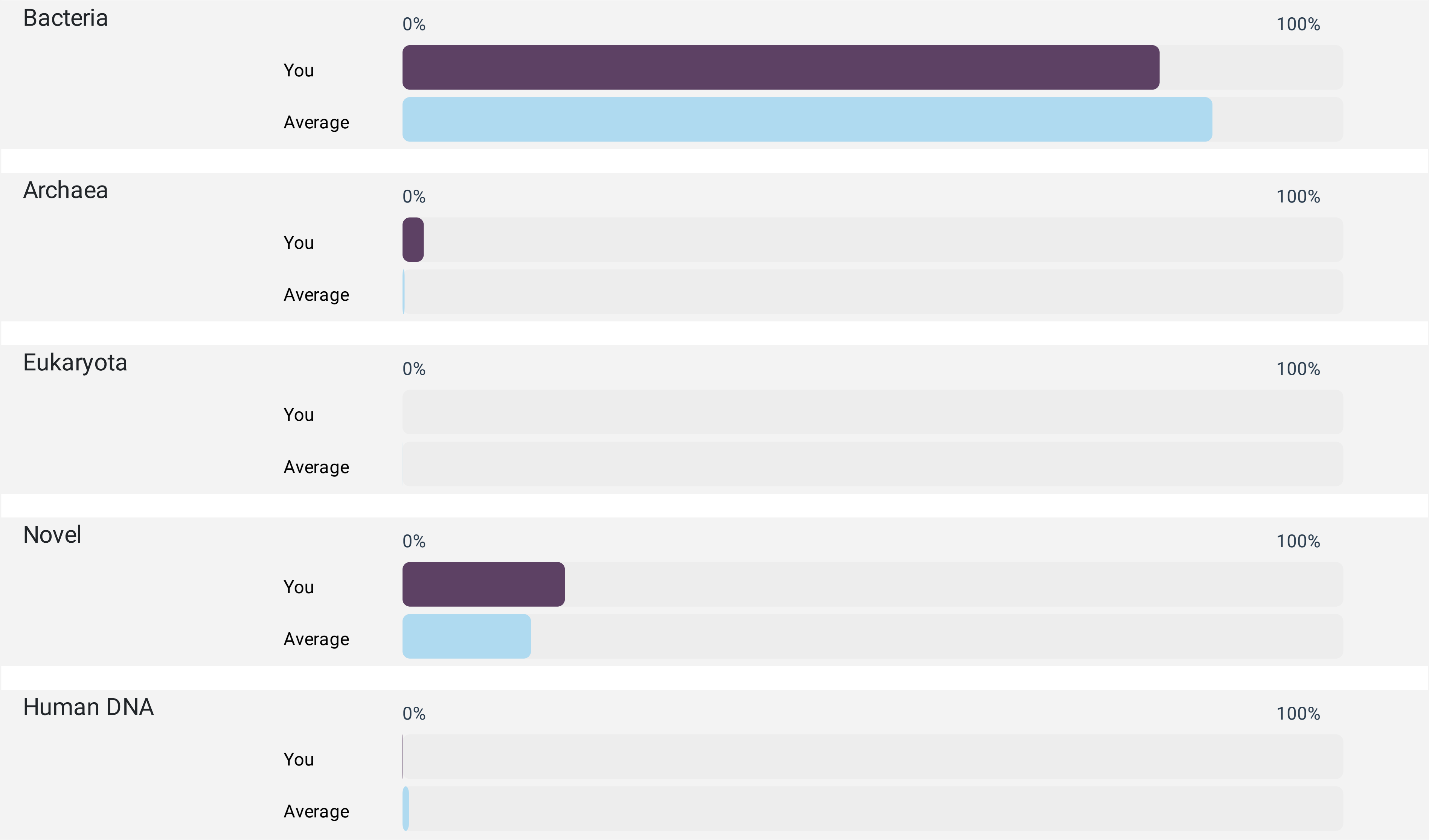
Gut microbiome report



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.

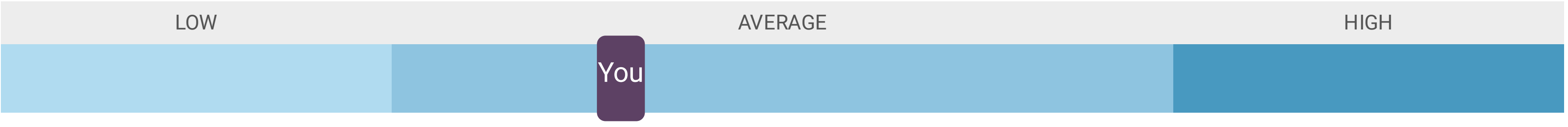


Microbiome Digestion Potential

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 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.

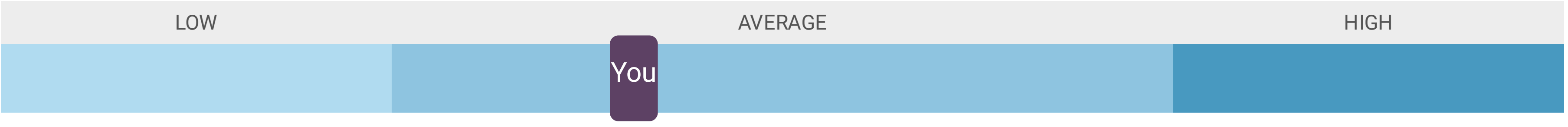
FIBRE

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.



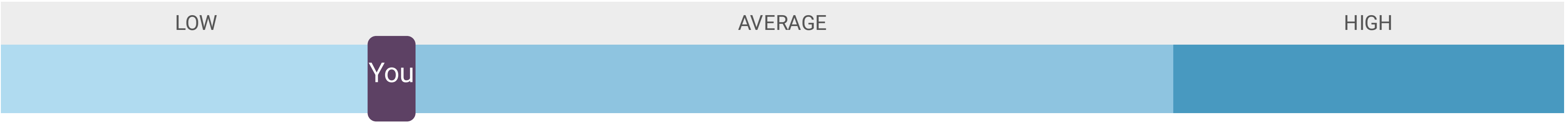
MUCIN

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.



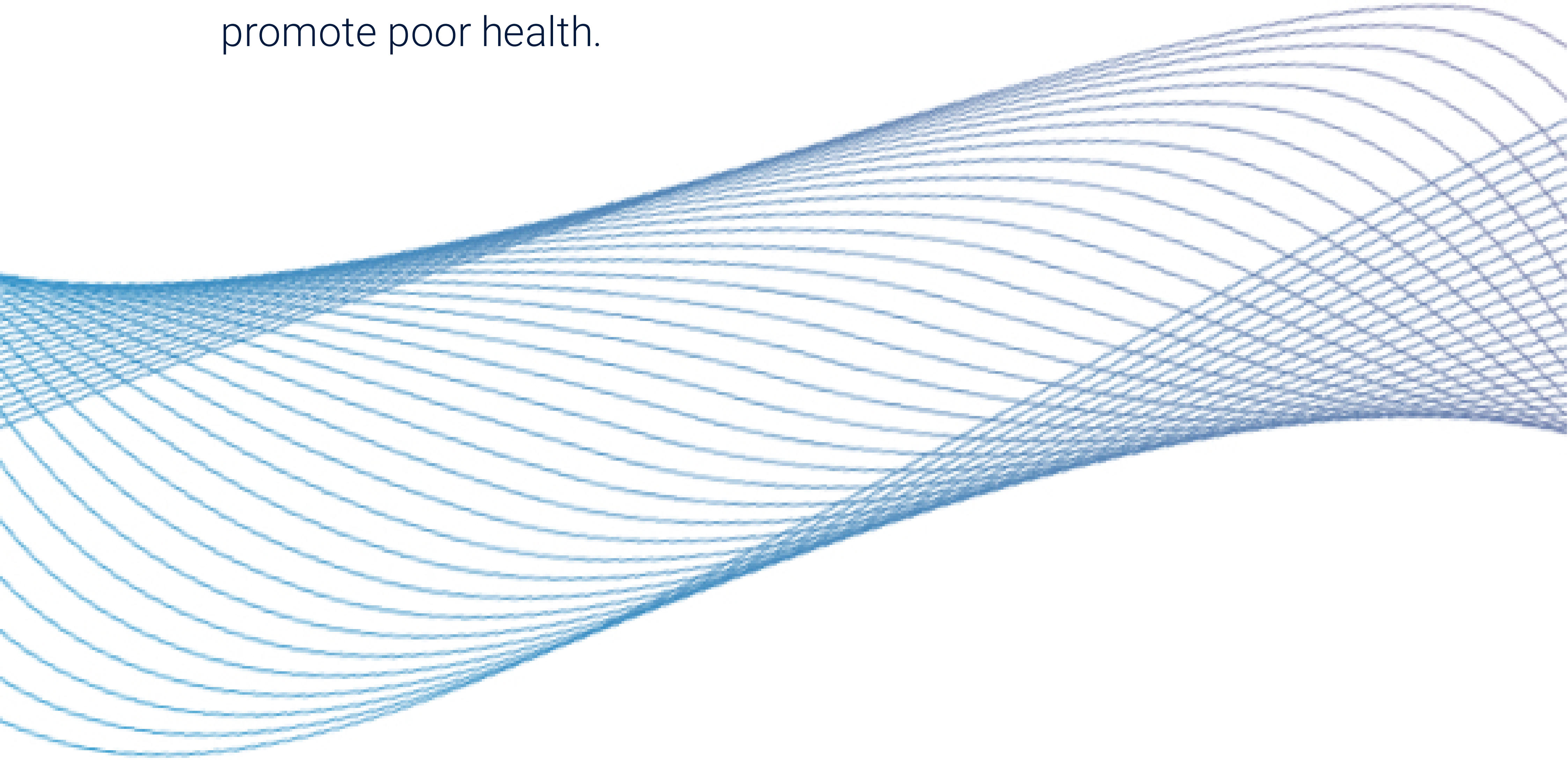
PROTEIN

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.



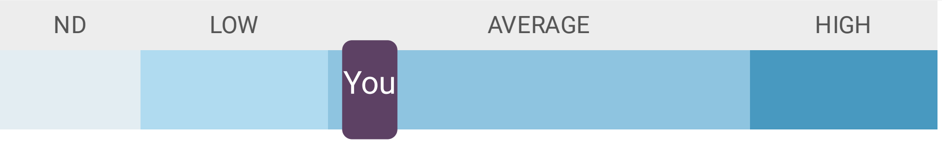
Microbial Metabolites

Below we show the potential of your gut microbiome to produce or consume different metabolites associated with health. 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 poor health. 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 benefits and a ' - ' sign indicates it is associated with poor health.

HEALTH INDICATORS

Produced

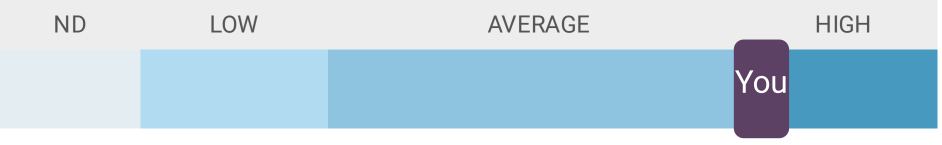
⊖ ***Hexa-acylated lipopolysaccharide production*** **0.036%**



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, poor heart health, poor glucose regulation, and poor liver health. 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]

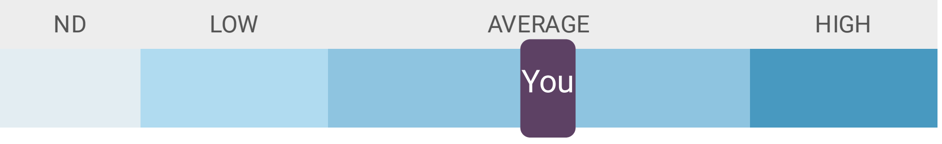
⊖ ***Methane production*** **2.22%**



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

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]

⊖ ***Trimethylamine production*** **3.47%**



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

A high potential to produce trimethylamine has been correlated to poor heart health and poor glucose regulation. 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.

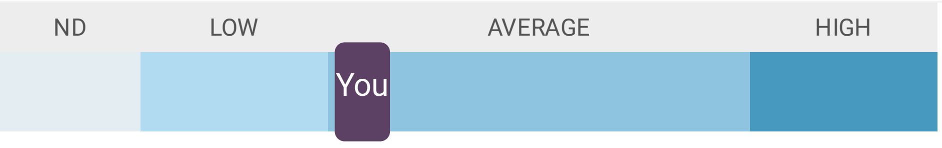
The indoles diindolylmethane (DIM) and indole-3-carbinol (I3C) found in cruciferous vegetables (e.g. broccoli, cauliflower, cabbage, kale) may reduce the amount of trimethylamine that is converted to TMAO in the liver. In addition, excessive red meat consumption is associated with increased levels of 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]

Microbial Metabolites

HEALTH INDICATORS

Produced

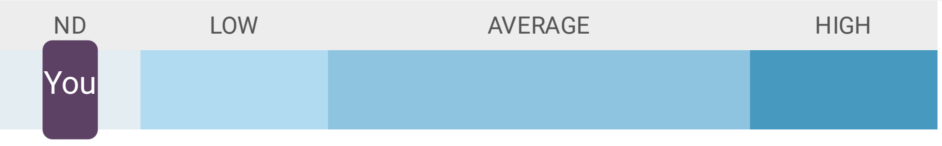
⊖ ***Ammonia (urease) production*** **6.54%**



The abundance of this metabolite is about the same as 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]

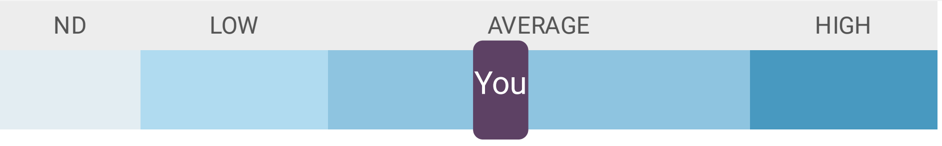
⊖ ***B. fragilis toxin production*** **0.00%**



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]

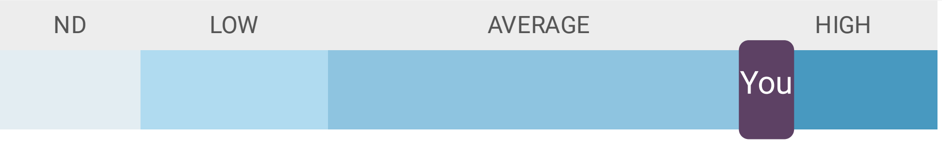
Beta-glucuronidase production **15.1%**



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]

⊖ ***Hydrogen sulphide production*** **16.2%**



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

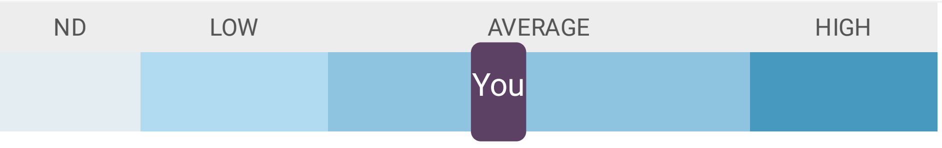
The gas hydrogen sulphide is produced by bacteria when they break down sulphur-containing amino acids found in foods such as eggs, meat, and fish. This gas is responsible for the rotten egg smell of flatulence. At low to average levels, hydrogen sulphide can play a beneficial role by acting as an energy 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 poor intestinal health. 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]

Microbial Metabolites

HEALTH INDICATORS

Produced

Branched chain amino acids production **56.6%**



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

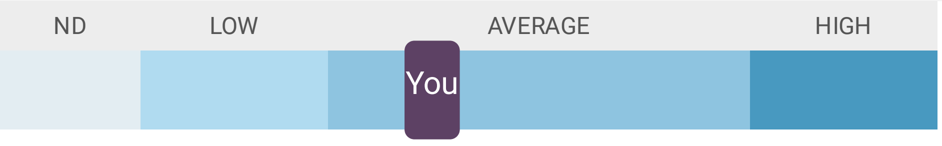
Branch chain amino acids (BCAAs) are involved in the regulation of glucose and fat metabolism and the immune system. High levels of BCAAs have been associated with metabolic diseases, such as obesity and poor glucose regulation. Muscle plays an important role in regulating BCAA levels. A high potential 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 **2.49%**



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

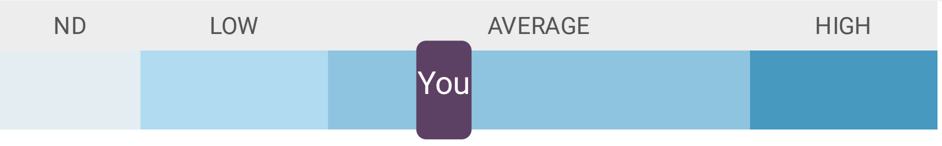
Some bacteria can break down oxalates in the colon, thus reducing the risk of forming calcium oxalate kidney stones. People who suffer from repeated unexplained kidney stones are observed to have a low potential for oxalate degradation in their microbiome compared to non-stone formers. A similar or high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

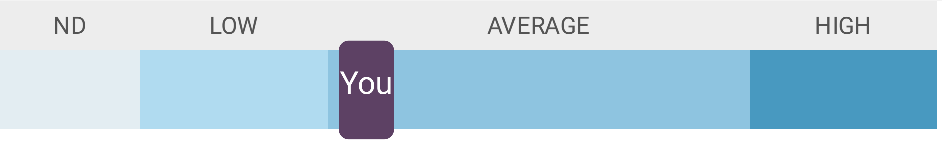
⊕ *GABA production* **9.68%**



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 being associated with poor mental health. 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 mental health is currently not well understood. If you are concerned about your mental health, it is important to seek professional help.
[1] [2] [3]

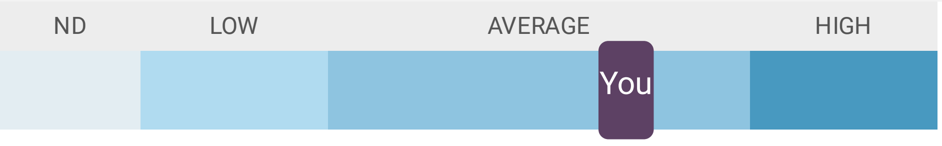
3-indolepropionic acid (IPA) production **0.180%**



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

3-indolepropionic acid (IPA) is a beneficial antioxidant produced by some gut bacteria when they break down the amino acid tryptophan. Research has shown that IPA may play a role in improving glucose regulation and research in animal models suggests that IPA may suppress inflammation and help maintain the gut barrier. Consuming foods rich in ellagic acid (e.g. chestnuts and ellagic acid-enriched pomegranate juice), as well as wholegrain wheat and rye may help support IPA production.
[1] [2] [3] [4] [5]

Histamine production **1.39%**



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

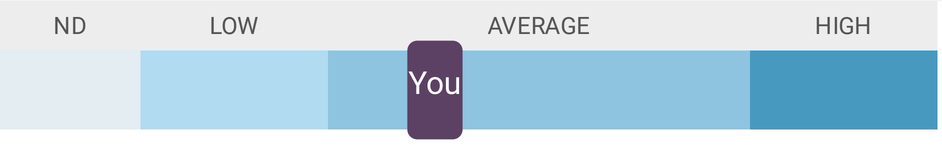
Histamine is a chemical produced by the breakdown of the amino acid histidine. It is produced by human cells and also by some bacterial species in the gut. It plays an important role in immune regulation, gut function and the nervous system. Gut bacteria that can produce histamine have been observed at increased levels in patients with poor lung health. 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* **4.67%**



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

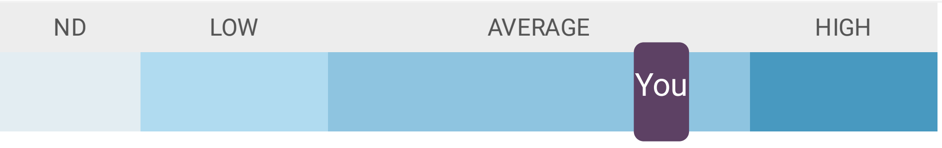
GABA (gamma-aminobutyric acid) plays an important role in regulating mental state by calming the nervous system. Low levels of GABA being associated with poor mental health. Most GABA is produced in the brain however your gut microbiome may contribute to your GABA levels as some bacteria can produce or consume GABA. The role of gut bacteria that produce GABA in mental health is currently not well 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

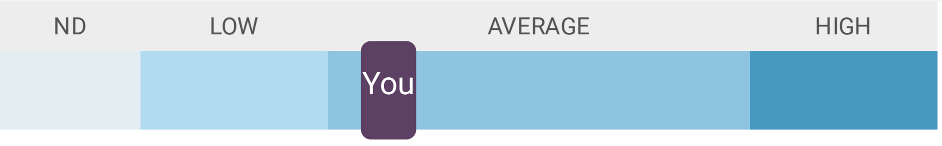
⊕ *Butyrate production* **22.7%**



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 poor intestinal health. Laboratory studies have shown that consuming resistant starch can increase butyrate production. Rich sources of resistant starch include raw banana flour, raw oats, and high amylose barley (e.g. BarleyMax).
[1] [2] [3] [4]

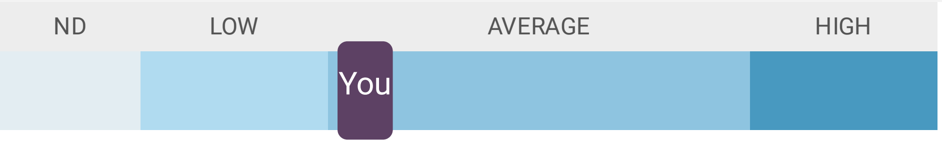
Lactate production **63.7%**



The abundance of this metabolite is about the same as 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* **1.89%**



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

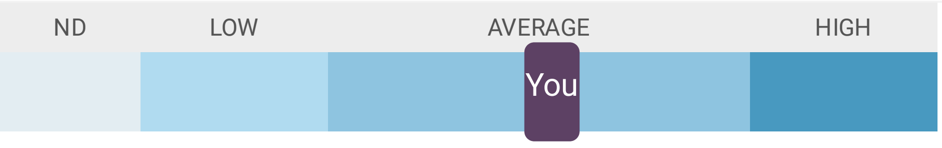
Propionate is a beneficial short chain fatty acid that is important for gut health. It helps maintain blood glucose levels, can reduce inflammation, helps control appetite and promotes the production of serotonin from the gut. The prebiotic fibre beta-glucan, found in oats and barley, has been shown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

Microbial Metabolites

SHORT CHAIN FATTY ACIDS

Produced

⊕ *Acetate production* **71.5%**



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

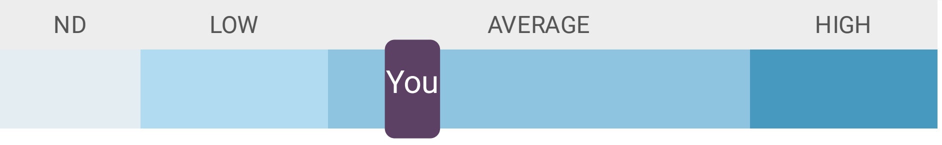
Acetate is the most abundant short chain fatty acid produced by our gut microbiome. It plays a beneficial role by supressing inflammation, regulating appetite, and regulating fat metabolism. Several bacterial species can also convert acetate to the beneficial short chain fatty acid, butyrate. Laboratory studies have shown that consuming pectin can increase acetate production. Pectin rich foods include avocado, berries, kiwi, pumpkin and zucchini.
[1] [2] [3] [4]

Microbial Metabolites

ESSENTIAL VITAMINS

Produced

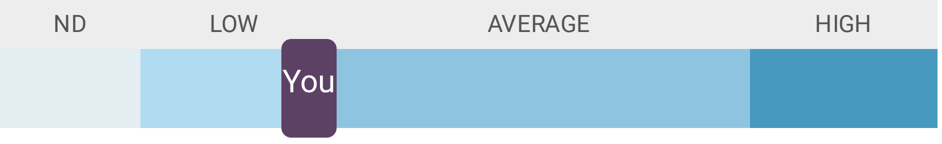
Cobalamin (B12) production **18.8%**



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]

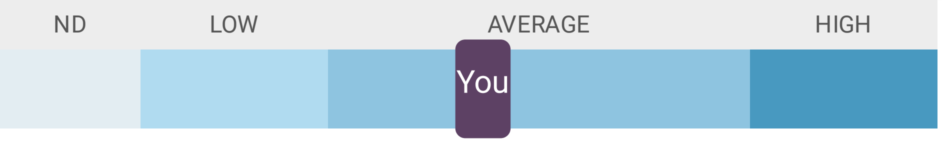
Folate (B9) production **41.1%**



The abundance of this metabolite is lower 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 poor heart health. 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 **15.0%**



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

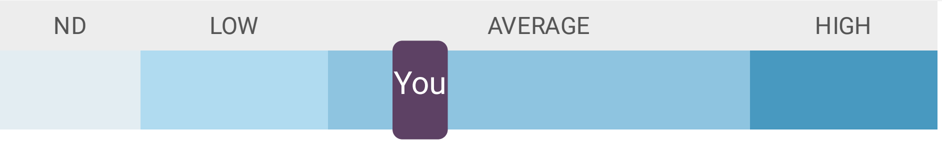
Biotin plays a critical role in metabolism and in the regulation of the immune system. Biotin cannot be produced by human cells and must be obtained through diet or the microbiome. The large intestine has the ability to absorb biotin but it is estimated that the gut microbiome can only provide up to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

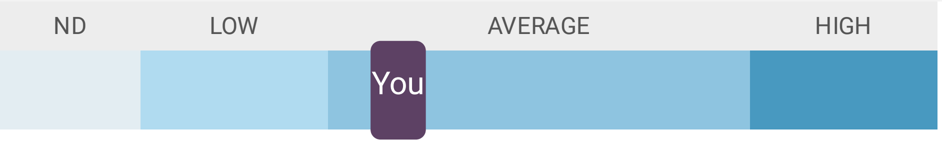
⊕ *Riboflavin (B2) production* **35.8%**



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* **7.75%**



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]

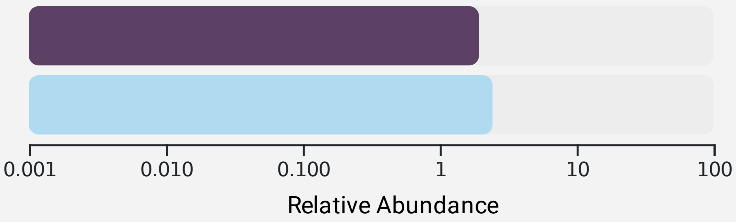
Species of Interest

BACTERIA (PROKARYOTES)

Agathobacter DETECTED

⊕ *Agathobacter rectale*

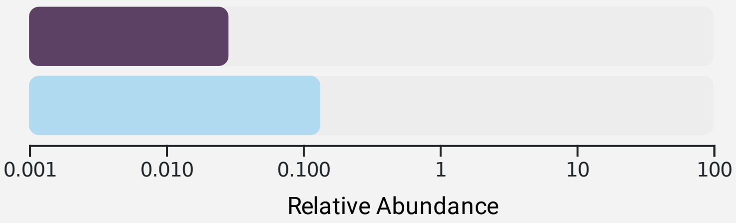
You	**1.93%**
Average	**2.43%**



Akkermansia DETECTED

Akkermansia MIC8757

You	**0.029%**
Average	**0.134%**

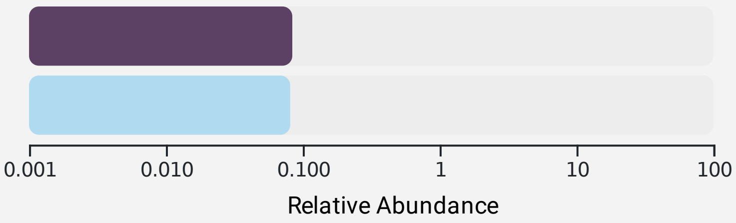


Bifidobacterium NOT DETECTED

Bilophila DETECTED

⊖ *Bilophila wadsworthia*

You	**0.084%**
Average	**0.081%**



Campylobacter NOT DETECTED

Citrobacter NOT DETECTED

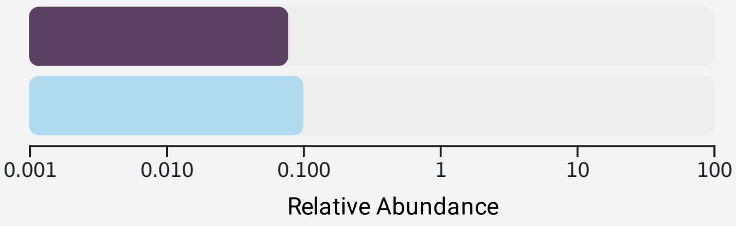
Clostridioides NOT DETECTED

Clostridium

DETECTED

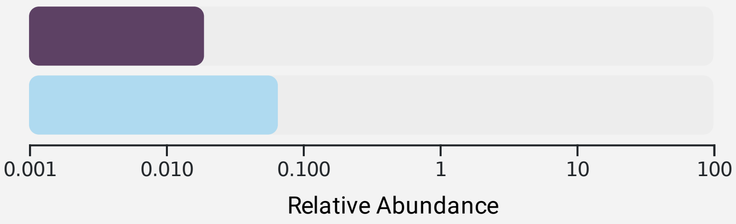
Clostridium MIC8163

You **0.078%**
Average **0.101%**



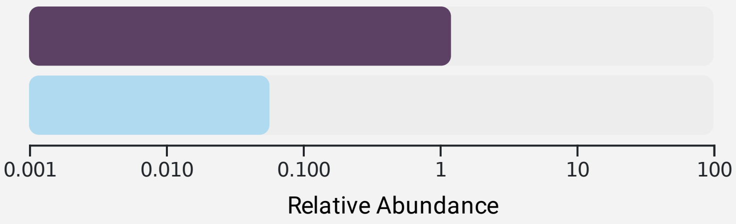
Clostridium MIC8573

You **0.019%**
Average **0.066%**



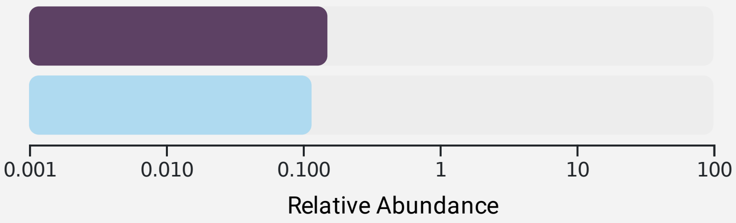
⊕ ***Clostridium_A leptum***

You **1.21%**
Average **0.057%**



Clostridium_Q sp003024715

You **0.151%**
Average **0.116%**

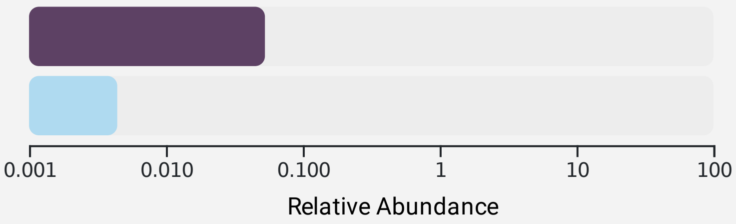


Corynebacterium

DETECTED

Corynebacterium kefirresidentii

You **0.053%**
Average **0.004%**

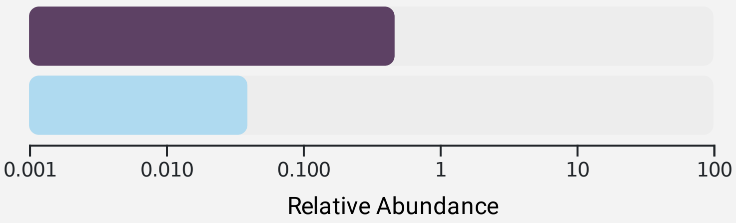


Desulfovibrio

DETECTED

⊖ ***Desulfovibrio piger***

You **0.469%**
Average **0.039%**



Eggerthella

NOT DETECTED

Enterobacter

NOT DETECTED

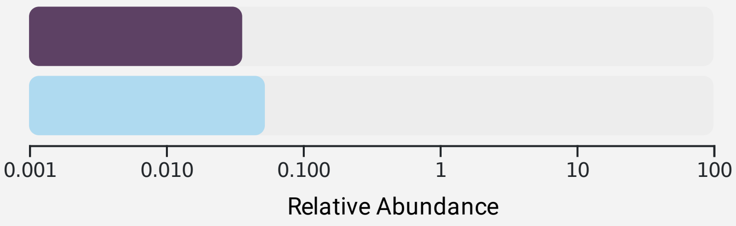
Escherichia

DETECTED

⊖ ***Escherichia coli (coli_D)***

You **0.036%**

Average **0.053%**



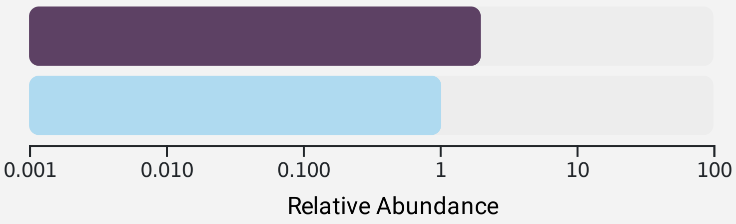
Faecalibacterium

DETECTED

Faecalibacterium prausnitzii_G

You **2.00%**

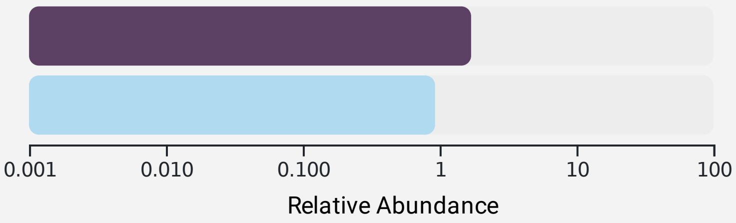
Average **1.03%**



⊕ ***Faecalibacterium prausnitzii_C***

You **1.70%**

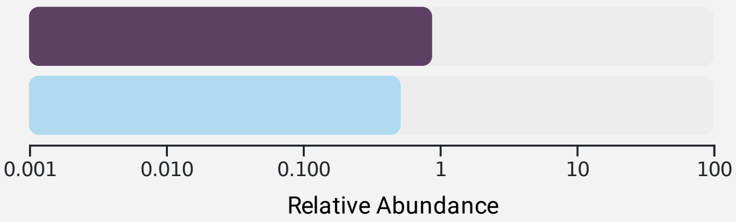
Average **0.926%**



Faecalibacterium prausnitzii_J

You **0.881%**

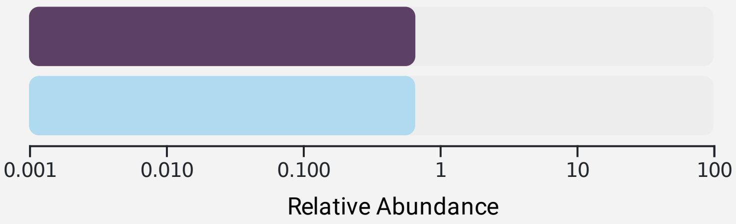
Average **0.519%**



Faecalibacterium MIC7145

You **0.665%**

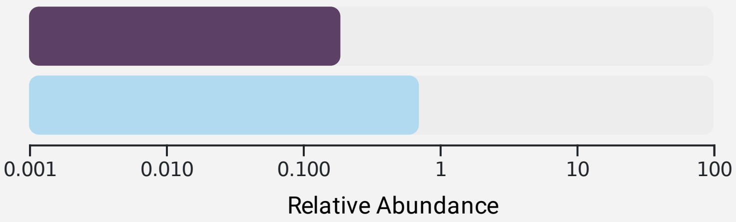
Average **0.662%**



Faecalibacterium prausnitzii_D

You **0.188%**

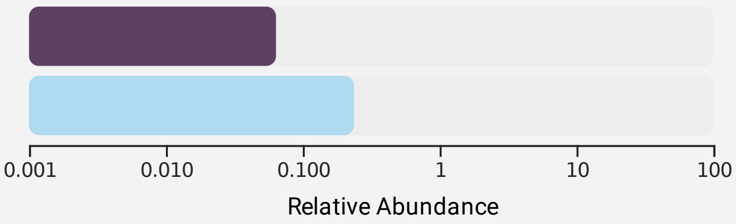
Average **0.705%**



Faecalibacterium prausnitzii_I

You **0.064%**

Average **0.236%**



Fusobacterium

NOT DETECTED

Helicobacter

NOT DETECTED

Klebsiella

NOT DETECTED

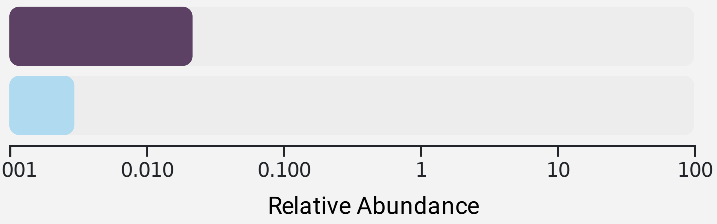
Lactobacillus

DETECTED

Lactobacillus iners

You **0.022%**

Average **0.003%**



Oxalobacter

NOT DETECTED

Porphyromonas

NOT DETECTED

Prevotella

NOT DETECTED

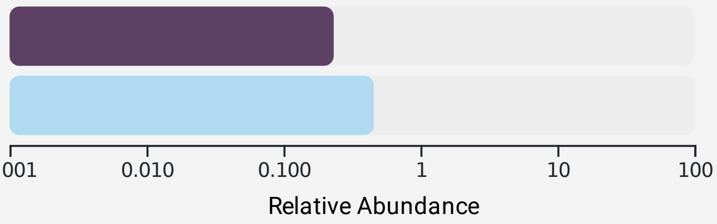
Roseburia

DETECTED

⊕ ***Roseburia intestinalis***

You **0.233%**

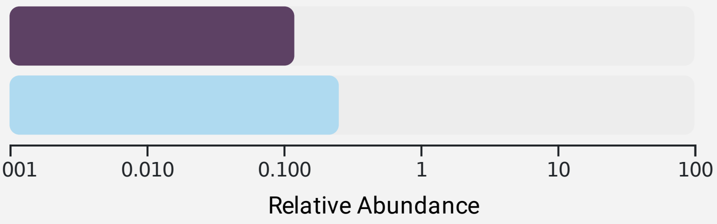
Average **0.457%**



⊕ ***Roseburia inulinivorans***

You **0.120%**

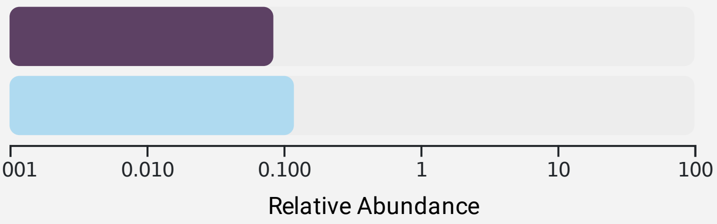
Average **0.253%**



⊕ ***Roseburia hominis***

You **0.084%**

Average **0.119%**



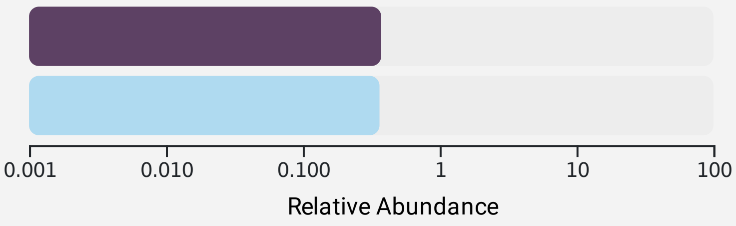
Ruminococcus

DETECTED

Ruminococcus_A sp003011855

You **0.374%**

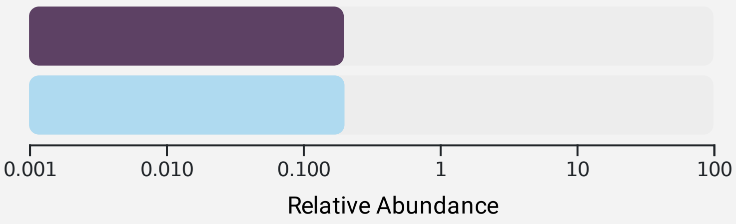
Average **0.364%**



Ruminococcus_C sp000980705

You **0.199%**

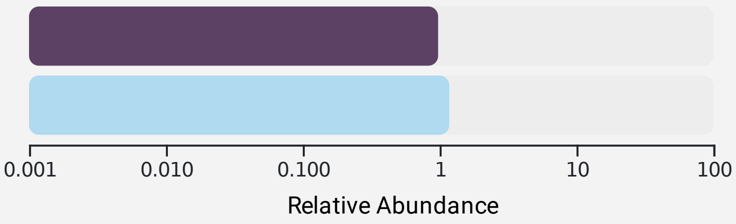
Average **0.202%**



Ruminococcus_D bicirculans

You **0.975%**

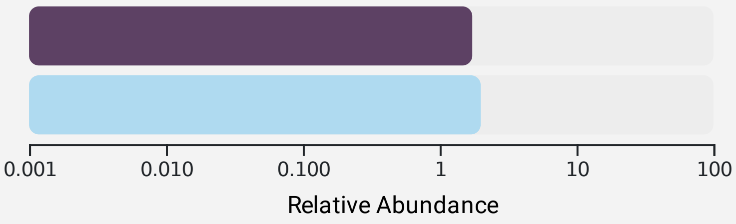
Average **1.18%**



Ruminococcus_E bromii_B

You **1.73%**

Average **2.00%**



Salmonella

NOT DETECTED

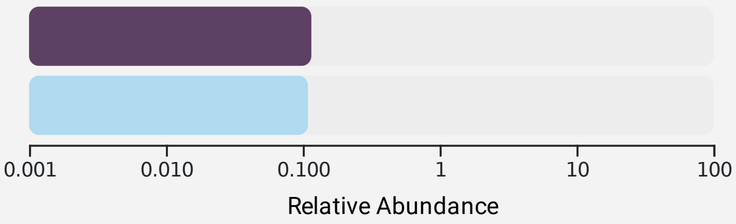
Streptococcus

DETECTED

⊖ ***Streptococcus salivarius***

You **0.116%**

Average **0.109%**

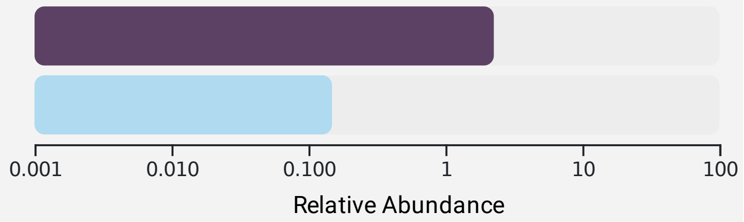


Species of Interest

ARCHAEA (PROKARYOTES)

Methanogens — DETECTED

±	***Methanobrevibacter_A smithii***	You	**2.26%**
		Average	**0.148%**



Other Archea — NOT DETECTED

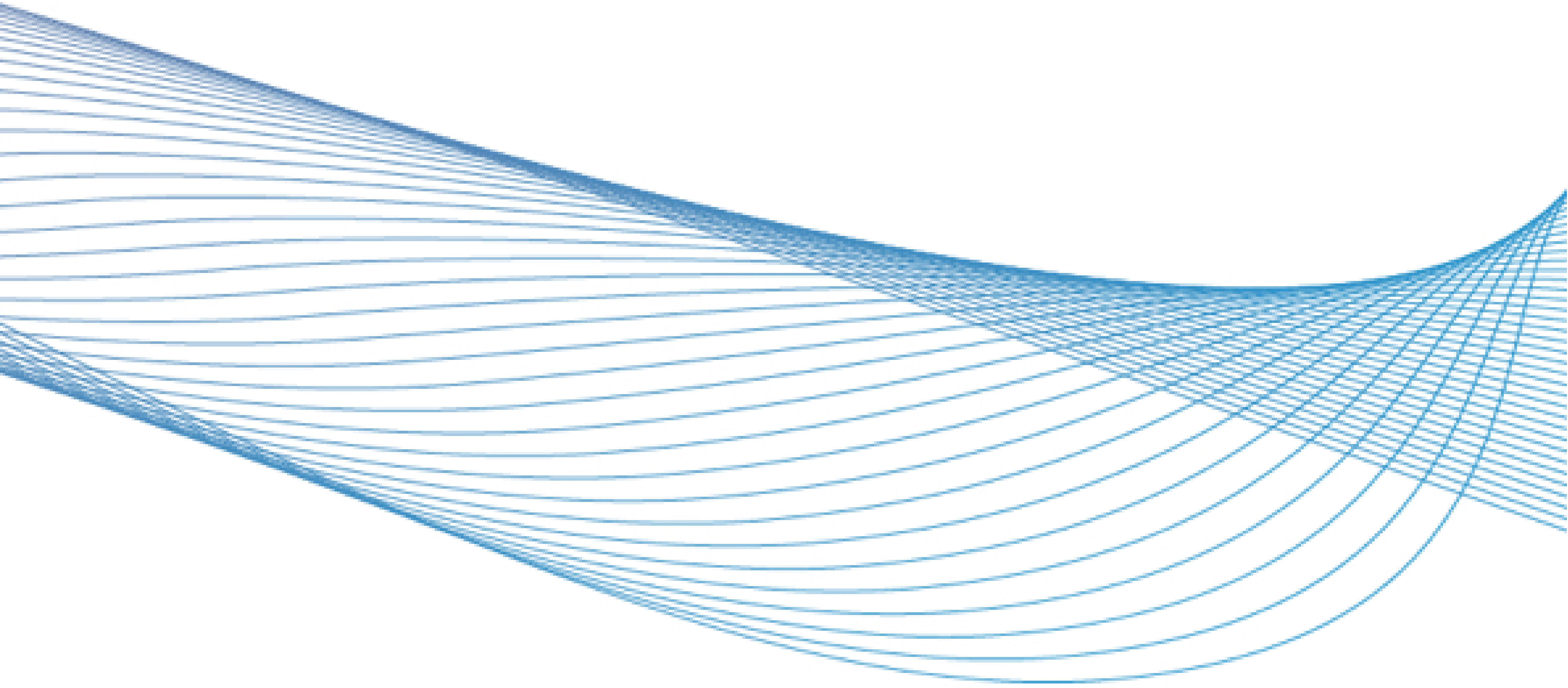
Species of Interest

YEASTS/FUNGI & PROTISTS (EUKARYOTES)

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

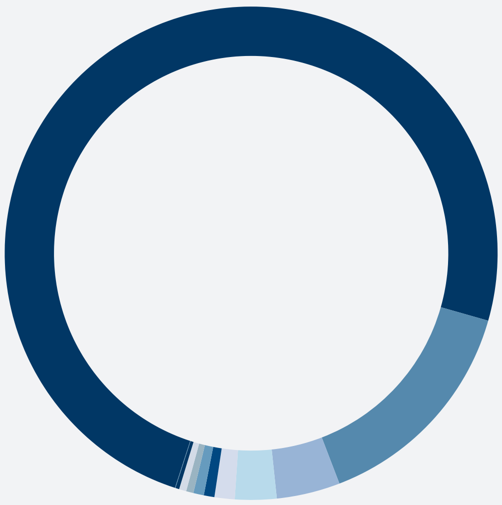
Microbial Profile

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	61.6%	41.8 - 73.1%	Average
■ Bacteroidota	12.2%	10.4 - 26.4%	Average
■ Firmicutes	3.45%	0.741 - 9.75%	Average
■ Euryarchaeota	2.26%	0.00 - 0.717%	High
■ Proteobacteria	1.09%	0.315 - 3.02%	Average
■ Desulfobacterota_A	0.575%	0.020 - 0.385%	High
■ Cyanobacteria	0.569%	0.00 - 0.971%	Average
■ Actinobacteriota	0.396%	1.03 - 7.36%	Low
■ Firmicutes_C	0.393%	0.271 - 1.38%	Average
■ Verrucomicrobiota	0.208%	0.00 - 1.77%	Average
■ Firmicutes_G	0.023%	0.00 - 0.008%	High

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
	Firmicutes_A	***UBA1417 sp003531055***	6.60%	0.00 - 0.982%	High

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

	Phylum	Species	Abundance	Range	Level
	Firmicutes_A	***Acetatifactor sp900066365***	4.04%	0.00 - 0.817%	High

This is a newly discovered genus and species of bacteria from the Lachnospiraceae family that has not been described by scientists yet.

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.

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

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
	Firmicutes_A	***Eisenbergiella sp900066775***	2.74%	0.00 - 0.437%	High

This is a newly discovered genus and species of bacteria from the Lachnospiraceae family that has not been described by scientists yet.

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

⊖	Bacteroidota	***Bacteroides_B dorei***	2.43%	0.00 - 2.99%	Average

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 people with poor intestinal health and poor glucose regulation in children. This species has also been associated with diets high in red meat.

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
⊕	Firmicutes_A	***Anaerostipes hadrus***	2.34%	0.294 - 5.33%	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 sulphide, lactate, riboflavin (B2).

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

±	Euryarchaeota	***Methanobrevibacter_A smithii***	2.26%	0.00 - 0.583%	High

This is a single celled organism belonging to the Archaea domain and is the most common archaeal species 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, branched chain amino acids, histamine, methane.

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 *M. smithii* have been observed with constipation, diverticulosis, and other conditions. However, lower levels have been observed in patients with poor intestinal health. *M. smithii* plays an important role in the gut because it is one of the few species that can remove excess hydrogen.

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
⊕	Firmicutes_A	***Eubacterium_E hallii***	2.13%	0.00 - 1.75%	High

This is an important member 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: 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 can also use the short chain fatty acid acetate, as well as lactate produced by bacterial species such as *Bifidobacterium spp.* for energy.

One study observed lower levels of this species in people with poor intestinal health. Also, a study in mice suggested this species may be effective at improving insulin sensitivity.

	Firmicutes_A	***Faecalibacterium prausnitzii_G***	2.00%	0.00 - 2.39%	Average

Previously called *Faecalibacterium prausnitzii_B* (aka strain L2-6), this is a common gut inhabitant.

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: branched chain amino acids, butyrate, cobalamin (B12).

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 certain skin conditions.

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
⊕	Firmicutes_A	***Agathobacter rectale***	1.93%	0.00 - 7.22%	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 healthier people in research studies. Lower levels of this bacterium have been observed in people with poor intestinal health.

	Phylum	Species	Abundance	Range	Level
	Bacteroidota	***UBA7173 MIC9174***	1.92%	0.00 - 0.00%	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, biotin (B7), 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 is a newly defined species in the Microba database.

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>***Ruminococcus_E bromii_B***</td><td>1.73%</td><td>0.00 - 6.16%</td><td>Average</td></tr>
<tr><td>⊕</td><td>Firmicutes_A</td><td>***Faecalibacterium prausnitzii_C***</td><td>1.70%</td><td>0.00 - 2.02%</td><td>Average</td></tr>
<tr><td colspan="6">

Faecalibacterium prausnitzii_C (aka strain A2-165) is an important member of the human gut microbiome.

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.

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 *F. prausnitzii* have been linked to a range of poor health conditions, including intestinal, metabolic, and mental health.

</td></tr>
<tr><td></td><td>Firmicutes_A</td><td>***CAG-41 sp900066215***</td><td>1.65%</td><td>0.00 - 0.815%</td><td>High</td></tr>
<tr><td></td><td>Firmicutes_A</td><td>***Faecalicatena faecis***</td><td>1.22%</td><td>0.00 - 1.35%</td><td>Average</td></tr>
</table>

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
⊕	Firmicutes_A	***Clostridium_A leptum***	1.21%	0.00 - 0.074%	High

This is an inhabitant of the gut microbiome.

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, 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 have been observed in individuals with poor intestinal health.

	Firmicutes_A	***Blautia_A wexlerae***	1.21%	0.344 - 6.60%	Average
	Bacteroidota	***Bacteroides stercoris***	1.20%	0.00 - 2.66%	Average

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
⊖	Bacteroidota	***Bacteroides cellulosilyticus***	1.06%	0.00 - 0.987%	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 poor heart health. However another study observed lower levels in individuals with irritable bowel syndrome.

	Phylum	Species	Abundance	Range	Level
	Firmicutes_A	***Gemmiger MIC8010***	1.03%	0.00 - 0.228%	High
	Firmicutes_A	***Ruminococcus_D bicirculans***	0.975%	0.00 - 3.46%	Average
	Firmicutes_A	***Phil1 sp001940855***	0.966%	0.00 - 0.369%	High
	Firmicutes	***CAG-313 sp003539625***	0.952%	0.00 - 0.410%	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>Bacteroidota</td><td><i>Parabacteroides distasonis</i></td><td>0.947%</td><td>0.00 - 0.516%</td><td>High</td></tr>
<tr><td colspan="6">
<p>Formerly known as <i>Bacteroides distasonis</i>, this is a common inhabitant of the human gut.</p>
<p>Fuel Sources Used:
This species is a moderate degrader of fibre, a good degrader of mucin, and a moderate degrader of protein.</p>
<p>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.</p>
<p>Metabolites consumed:
In addition, the genomic analysis shows that most members of this species can consume: GABA.</p>
<p>Emerging Research:
Higher levels of this species have been observed in people with poor intestinal health, and with poor glucose regulation during pregnancy.</p>
</td></tr>
<tr><td></td><td>Firmicutes_A</td><td><i>Gemmiger MIC9530</i></td><td>0.918%</td><td>0.00 - 0.443%</td><td>High</td></tr>
<tr><td></td><td>Firmicutes_A</td><td><i>Faecalibacterium prausnitzii_J</i></td><td>0.881%</td><td>0.00 - 1.65%</td><td>Average</td></tr>
</table>

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>Fusicatenibacter saccharivorans</i></td><td>0.878%</td><td>0.518 - 7.34%</td><td>Average</td></tr>
<tr><td colspan="6">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.

Emerging Research:
Lower levels of this species were observed in people with poor intestinal health.</td></tr>
<tr><td></td><td>Firmicutes_A</td><td><i>CAG-273 sp003534295</i></td><td>0.821%</td><td>0.00 - 0.272%</td><td>High</td></tr>
</table>

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
±	Bacteroidota	***Alistipes putredinis***	0.806%	0.00 - 2.61%	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 people with some forms of poor intestinal health. However, other studies associated a low abundance of this species with poor intestinal health, so it's role in health is not yet fully understood.

	Phylum	Species	Abundance	Range	Level
	Firmicutes_A	***CAG-170 sp000432135***	0.794%	0.00 - 0.637%	High

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
⊖	Bacteroidota	***Bacteroides uniformis***	0.791%	0.136 - 4.89%	Average
	Firmicutes_A	***CAG-138 MIC9630***	0.785%	0.00 - 0.479%	High
	Firmicutes_A	***CAG-273 sp000435755***	0.777%	0.00 - 0.037%	High
	Firmicutes_A	***CAG-110 sp000434635***	0.747%	0.00 - 0.560%	High
	Firmicutes_A	***KLE1615 sp900066985***	0.745%	0.172 - 2.22%	Average
	Firmicutes_A	***Blautia_A massiliensis***	0.690%	0.00 - 1.83%	Average
	Firmicutes_A	***Faecalibacterium MIC7145***	0.665%	0.00 - 1.48%	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, and improve health in mouse models, however this has not yet been validated in humans. One study observed higher levels of this species in patients with poor intestinal health.

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
⊕	Bacteroidota	***Alistipes shahii***	0.649%	0.00 - 0.523%	High

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 heart health, and was observed at lower levels in people with poor intestinal health. Additionally, a study in mice showed this species may improve the efficacy of some types of immunotherapy. However, this species was also observed at elevated levels in patients with some neurodegenerative conditions.

	Bacteroidota	***Barnesiella intestinihominis***	0.648%	0.00 - 0.743%	Average
	Firmicutes_A	***UBA1691 MIC9213***	0.627%	0.00 - 0.00%	High
	Proteobacteria	***51-20 sp001917175***	0.545%	0.00 - 0.466%	High
	Firmicutes_A	***CAG-349 sp003539515***	0.518%	0.00 - 0.074%	High
	Firmicutes_A	***CAG-314 sp000437915***	0.503%	0.00 - 0.256%	High
	Firmicutes_A	***UBA5416 MIC7893***	0.501%	0.00 - 0.047%	High

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
	Firmicutes	***CAG-460 sp000437355***	0.491%	0.00 - 0.00%	High
⊖	Desulfobacterota_A	***Desulfovibrio piger***	0.469%	0.00 - 0.182%	High

This species can be 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: acetate, branched chain amino acids, hydrogen sulphide, 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.

One study observed high levels of this species in patients with poor intestinal health.

	Firmicutes	***Erysipelatoclostridium sp000752095***	0.455%	0.00 - 1.02%	Average
	Firmicutes	***CAG-417 sp000432835***	0.453%	0.00 - 0.056%	High
	Proteobacteria	***Parasutterella excrementihominis***	0.424%	0.00 - 0.389%	High
	Firmicutes_A	***Blautia_A sp900120195***	0.423%	0.00 - 0.125%	High
	Firmicutes_A	***Lachnospira rogosae***	0.415%	0.00 - 1.05%	Average

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
	Cyanobacteria	***QAMI01 MIC9451***	0.412%	0.00 - 0.00%	High
	Firmicutes_A	***CAG-83 sp000435975***	0.408%	0.00 - 0.382%	High
	Firmicutes_A	***TF01-11 sp003529475***	0.393%	0.00 - 0.396%	Average
	Firmicutes_C	***Phascolarctobacterium faecium***	0.393%	0.00 - 0.443%	Average
	Firmicutes_A	***Acutalibacter timonensis***	0.381%	0.00 - 0.00%	High
	Firmicutes_A	***ER4 sp000765235***	0.376%	0.00 - 0.635%	Average
	Firmicutes_A	***Ruminococcus_A sp003011855***	0.374%	0.00 - 0.892%	Average
	Firmicutes_A	***UBA1777 MIC6732***	0.364%	0.00 - 0.343%	High
	Firmicutes_A	***Blautia_A obeum***	0.355%	0.00 - 1.41%	Average
	Bacteroidota	***Parabacteroides goldsteinii***	0.353%	0.00 - 0.056%	High

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
⊖	Firmicutes_A	***Eubacterium_I ramulus***	0.343%	0.00 - 0.428%	Average

This is an inhabitant of the gut microbiome.

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 can also use the plant flavonoid quercetin as an energy source.

This species has been observed at higher levels in postmenopausal, obese women with insulin resistance. However, another study showed lower levels in patients with poor intestinal health.

	Phylum	Species	Abundance	Range	Level
	Firmicutes_A	***Gemmiger sp003476825***	0.294%	0.00 - 2.86%	Average
	Firmicutes	***CAG-710 MIC9574***	0.287%	0.00 - 0.00%	High
	Firmicutes_A	***Ruminiclostridium_C sp000435295***	0.285%	0.00 - 0.302%	Average

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
⊕	Firmicutes_A	***Coprococcus_B comes***	0.278%	0.086 - 0.813%	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 poor intestinal health, poor liver health and chronic fatigue syndrome.

	Firmicutes_A	***Blautia_A sp900066165***	0.276%	0.193 - 2.41%	Average
	Firmicutes_A	***Lachnospira sp003451515***	0.274%	0.00 - 0.400%	Average
	Firmicutes_A	***CAG-127 sp900319515***	0.258%	0.00 - 0.891%	Average
	Firmicutes	***CAG-433 MIC6607***	0.253%	0.00 - 0.00%	High
	Firmicutes_A	***CAG-170 sp002404795***	0.252%	0.00 - 0.301%	Average
	Firmicutes_A	***Lachnospira sp000437735***	0.243%	0.00 - 0.265%	Average

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
	Firmicutes_A	***Eubacterium_F sp003491505***	0.243%	0.00 - 0.477%	Average
⊕	Bacteroidota	***Odoribacter splanchnicus***	0.235%	0.023 - 0.253%	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 women with poor glucose regulation and people with poor intestinal health, indicating it likely plays a beneficial role in health.

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
⊕	Firmicutes_A	***Roseburia intestinalis***	0.233%	0.00 - 1.12%	Average

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 is a primary producer of the beneficial short chain fatty acid butyrate. This species has been observed at lower levels in individuals with poor glucose regulation, as well as younger people with poor intestinal health, suggesting this species likely plays a beneficial role in health.

⊖	Bacteroidota	***Bacteroides_B vulgatus***	0.232%	0.00 - 6.38%	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, 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 bacteria have been associated with a wide range of poor health conditions. This species has been associated with a diet high in red meat.

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
	Firmicutes_A	***Romboutsia timonensis***	0.227%	0.00 - 0.642%	Average
+−	Firmicutes_A	***Dorea longicatena_B***	0.220%	0.00 - 0.747%	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, 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 chronic fatigue syndrome and poor intestinal health.

	Firmicutes_A	***COE1 sp001916965***	0.209%	0.00 - 0.243%	Average
	Firmicutes_A	***UBA1206 sp000433115***	0.209%	0.00 - 0.010%	High
	Firmicutes_A	***Blautia_A sp900066145***	0.202%	0.00 - 0.372%	Average
	Firmicutes_A	***CAG-74 MIC7845***	0.200%	0.00 - 0.00%	High
	Firmicutes_A	***Ruminococcus_C sp000980705***	0.199%	0.00 - 0.695%	Average

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
	Firmicutes_A	***CAG-245 sp000435175***	0.198%	0.00 - 0.220%	Average
	Firmicutes_A	***CAG-74 MIC7649***	0.198%	0.00 - 0.329%	Average
	Firmicutes_A	***ER4 sp900317525***	0.197%	0.00 - 0.375%	Average
	Firmicutes_A	***Oscillibacter sp001916835***	0.192%	0.00 - 0.377%	Average
	Firmicutes_A	***Faecalibacterium prausnitzii_D***	0.188%	0.00 - 1.72%	Average
	Firmicutes_A	***Negativibacillus massiliensis***	0.186%	0.00 - 0.082%	High
	Firmicutes_A	***PeH17 sp000435055***	0.173%	0.00 - 0.834%	Average

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>*Coprococcus eutactus_A*</td><td>0.169%</td><td>0.00 - 1.43%</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, 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), 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 lower levels in individuals with lung conditions and poor intestinal health, and children with poor glucose regulation, indicating it likely plays a beneficial role in health.</td></tr>
<tr><td></td><td>Firmicutes_A</td><td>*UBA7160 MIC6745*</td><td>0.165%</td><td>0.00 - 0.308%</td><td>Average</td></tr>
<tr><td></td><td>Actinobacteriota</td><td>*Adlercreutzia MIC8014*</td><td>0.162%</td><td>0.00 - 0.269%</td><td>Average</td></tr>
<tr><td></td><td>Firmicutes_A</td><td>*CAG-272 MIC8971*</td><td>0.160%</td><td>0.00 - 0.036%</td><td>High</td></tr>
</table>

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
⊕	Firmicutes_A	***Dorea formicigenerans***	0.160%	0.107 - 0.418%	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 poor intestinal health and chronic fatigue syndrome, indicating it likely plays a beneficial role in health.

⊖	Bacteroidota	***Alistipes finegoldii***	0.159%	0.00 - 0.450%	Average

This is a common inhabitant of the gut microbiome.

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: ammonia (urease), 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:
Studies have observed higher levels of this species in people with poor intestinal health. This species has been associated with diets high in red meat and/or low in fruits and vegetables.

Species Profile

SPECIES

Phylum	Species	Abundance	Range	Level
Firmicutes_A	***UBA7102 MIC9705***	0.159%	0.00 - 0.020%	High
Firmicutes_A	***GCA-900066135 MIC6659***	0.158%	0.00 - 0.247%	Average
Firmicutes_A	***TF01-11 sp000436755***	0.158%	0.00 - 0.260%	Average
Firmicutes_A	***CAG-303 sp000437755***	0.157%	0.00 - 0.774%	Average
Firmicutes	***Merdibacter MIC6626***	0.156%	0.00 - 0.066%	High
Firmicutes_A	***CAG-83 sp000435555***	0.154%	0.00 - 1.33%	Average
Firmicutes_A	***Clostridium_Q sp003024715***	0.151%	0.00 - 0.265%	Average
Firmicutes_A	***UBA3818 MIC8425***	0.148%	0.00 - 0.043%	High
Firmicutes_A	***Negativibacillus MIC7916***	0.140%	0.00 - 0.00%	High
Firmicutes_A	***Anaeromassilibacillus sp002159845***	0.139%	0.00 - 0.00%	High
Firmicutes_A	***Gemmiger formicilis***	0.138%	0.00 - 2.51%	Average

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
⊖	Bacteroidota	***Bacteroides caccae***	0.136%	0.00 - 0.482%	Average

This is a common member 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, 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:
A protein produced by this species has been linked to poor intestinal health and elevated levels of this species have been observed in individuals with gout.

	Phylum	Species	Abundance	Range	Level
	Actinobacteriota	***CAG-1427 sp000435675***	0.136%	0.00 - 0.160%	Average

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
⊕	Firmicutes_A	***Coprococcus_A catus***	0.134%	0.00 - 0.431%	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:
Lower levels of this species have been observed in individuals with poor intestinal health and with poor mental health, indicating it likely plays a beneficial role in health.

	Firmicutes_A	***Blautia_A MIC8050***	0.130%	0.00 - 0.327%	Average
	Firmicutes_A	***CAG-448 sp003150135***	0.127%	0.00 - 0.122%	High
	Bacteroidota	***Alistipes onderdonkii***	0.126%	0.00 - 0.680%	Average
	Firmicutes_A	***CAG-170 MIC6396***	0.123%	0.00 - 0.053%	High
	Verrucomicrobiota	***Victivallis vadensis***	0.123%	0.00 - 0.014%	High

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
⊕	Firmicutes_A	***Roseburia inulinivorans***	0.120%	0.00 - 0.648%	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 poor glucose regulation.

	Phylum	Species	Abundance	Range	Level
	Firmicutes_A	***Lachnospiraceae MIC6495***	0.119%	0.00 - 0.142%	Average
	Firmicutes_A	***CAG-56 sp900066615***	0.117%	0.00 - 0.972%	Average

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
⊖	Firmicutes	***Streptococcus salivarius***	0.116%	0.00 - 0.306%	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 observed at higher levels in patients with poor heart health and poor intestinal health, however one study observed it at lower levels in people with a different intestinal health condition.

	Firmicutes_A	***CAG-475 sp000434435***	0.113%	0.00 - 0.111%	High
	Firmicutes_A	***CAG-45 sp900066395***	0.109%	0.00 - 0.290%	Average
	Bacteroidota	***Tidjanibacter inops***	0.106%	0.00 - 0.071%	High
	Firmicutes_A	***Blautia_A sp900066505***	0.106%	0.00 - 0.092%	High
	Firmicutes	***CAG-302 sp000431795***	0.105%	0.00 - 0.165%	Average
	Firmicutes_A	***CAG-452 sp000434035***	0.104%	0.00 - 0.00%	High

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
	Firmicutes_A	***CAG-95 sp900066375***	0.103%	0.00 - 0.122%	Average
	Firmicutes_A	***Oscillibacter sp900066435***	0.101%	0.00 - 0.126%	Average
	Firmicutes_A	***CAG-74 MIC9837***	0.100%	0.00 - 0.067%	High
	Firmicutes_A	***Anaerotignum sp000436415***	0.097%	0.00 - 0.135%	Average
	Firmicutes_A	***Monoglobus pectinilyticus***	0.096%	0.00 - 0.118%	Average
	Firmicutes_A	***NK3B98 sp003150485***	0.095%	0.00 - 0.00%	High
	Firmicutes_A	***UBA1191 MIC6696***	0.091%	0.00 - 0.133%	Average
	Proteobacteria	***CAG-495 sp001917125***	0.090%	0.00 - 0.158%	Average
	Firmicutes	***CAG-1193 MIC7537***	0.086%	0.00 - 0.00%	High
	Firmicutes_A	***UBA11774 sp003507655***	0.086%	0.00 - 0.802%	Average

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
⊕	Firmicutes_A	***Roseburia hominis***	0.084%	0.00 - 0.290%	Average
	Firmicutes_A	***Agathobaculum MIC7900***	0.084%	0.00 - 0.635%	Average
	Firmicutes_A	***CAG-110 sp000435995***	0.084%	0.00 - 0.245%	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, beta-glucuronidase, 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. Lower levels of this species have been observed in patients with poor intestinal health and poor heart health. Another study observed higher levels in active women compared to sedentary women. Laboratory studies suggest this species can help regulate the immune system and help reduce inflammation.

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
⊖	Desulfobacterota_A	***Bilophila wadsworthia***	0.084%	0.00 - 0.200%	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 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:
Higher levels of this species have been observed in people with poor intestinal health 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.

	Firmicutes_A	***UBA7160 MIC9207***	0.083%	0.00 - 0.188%	Average
	Firmicutes_A	***CAG-74 MIC9156***	0.082%	0.00 - 0.00%	High
	Cyanobacteria	***CAG-196 sp002102975***	0.081%	0.00 - 0.414%	Average
	Firmicutes_A	***ER4 sp003522105***	0.080%	0.00 - 0.106%	Average
	Firmicutes_A	***Agathobaculum butyriciproducens***	0.078%	0.00 - 0.621%	Average
	Firmicutes_A	***Clostridium MIC8163***	0.078%	0.00 - 0.305%	Average

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
⊕	Firmicutes_A	***Ruminiclostridium_E siraeum***	0.078%	0.00 - 1.58%	Average

Formerly known as *Eubacterium siraeum*. 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, branched chain amino acids, folate (B9).

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

Emerging Research:
This species was observed at lower levels in individuals with poor metabolic and intestinal health, suggesting it likely plays a role in promoting good health.

	Phylum	Species	Abundance	Range	Level
	Firmicutes_A	***Acutalibacter sp000435395***	0.076%	0.00 - 0.048%	High
	Firmicutes_A	***Ruthenibacterium lactatiformans***	0.073%	0.00 - 0.079%	Average

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
⊖	Firmicutes_A	***Faecalicatena lactaris***	0.072%	0.00 - 0.879%	Average

Previously called *Ruminococcus lactaris,* this is a common inhabitant of the human gut.

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, cobalamin (B12), 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 lower levels in individuals with insulin resistance and poor intestinal health. However, despite the likely beneficial role of this species, one study did observe this species at higher levels in patients with autoimmune conditions of the joints.

	Firmicutes_A	***Lawsonibacter MIC8046***	0.072%	0.00 - 0.046%	High
	Firmicutes_A	***CAG-45 sp000438375***	0.071%	0.00 - 0.113%	Average
	Firmicutes_A	***CAG-81 sp900066535***	0.071%	0.00 - 0.164%	Average
	Bacteroidota	***Bacteroides faecis***	0.071%	0.00 - 0.248%	Average
	Firmicutes_A	***CAG-81 sp000435795***	0.070%	0.00 - 0.104%	Average
	Firmicutes_A	***CAG-727 MIC7825***	0.070%	0.00 - 0.052%	High

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
	Bacteroidota	***Alistipes obesi***	0.069%	0.00 - 0.430%	Average
	Firmicutes_A	***Eubacterium_G sp000432355***	0.066%	0.00 - 0.057%	High
	Firmicutes_A	***Faecalicatena sp900120155***	0.065%	0.00 - 0.00%	High
	Firmicutes_A	***Lawsonibacter asaccharolyticus***	0.064%	0.00 - 0.127%	Average
	Firmicutes_A	***Faecalibacterium prausnitzii_I***	0.064%	0.00 - 0.535%	Average
	Firmicutes_A	***CAG-272 sp000433515***	0.061%	0.00 - 0.033%	High
	Firmicutes_A	***UBA5446 MIC7134***	0.060%	0.00 - 0.00%	High
	Firmicutes_A	***Dorea sp900066555***	0.059%	0.00 - 0.130%	Average
	Cyanobacteria	***QAMI01 MIC7050***	0.058%	0.00 - 0.00%	High

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
⊕	Bacteroidota	***Alistipes senegalensis***	0.058%	0.00 - 0.109%	Average

This is a newly discovered 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: ammonia (urease), 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:
A high BMI has been associated with a low abundance of this species. Lower levels of this species have also been observed in individuals with poor intestinal health, suggesting it may play a beneficial role in health.

	Firmicutes_A	***GCA-900066575 sp900066385***	0.057%	0.00 - 0.031%	High
	Firmicutes_A	***Ruminococcaceae MIC8623***	0.055%	0.00 - 0.031%	High
	Firmicutes_A	***Anaerovoracaceae MIC7161***	0.054%	0.00 - 0.011%	High
	Firmicutes_A	***CAG-170 sp003516765***	0.054%	0.00 - 0.087%	Average
	Actinobacteriota	***Corynebacterium kefirresidentii***	0.053%	0.00 - 0.00%	High
	Firmicutes_A	***CAG-81 sp900066055***	0.053%	0.00 - 0.035%	High

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
	Firmicutes_A	***QAND01 MIC7514***	0.052%	0.00 - 0.015%	High
	Bacteroidota	***Bacteroides xylanisolvens***	0.052%	0.00 - 0.429%	Average
	Firmicutes_A	***CAG-145 MIC8493***	0.051%	0.00 - 0.029%	High
	Firmicutes_A	***Dorea sp000433215***	0.051%	0.00 - 0.077%	Average
	Firmicutes_A	***Lachnospiraceae MIC7543***	0.050%	0.00 - 0.036%	High
	Bacteroidota	***Coprobacter fastidiosus***	0.047%	0.00 - 0.096%	Average
	Firmicutes_A	***CAG-177 sp003514385***	0.047%	0.00 - 0.619%	Average
	Firmicutes_A	***UBA7182 MIC8422***	0.047%	0.00 - 0.090%	Average
	Firmicutes_A	***CAG-145 MIC9666***	0.046%	0.00 - 0.053%	Average
	Actinobacteriota	***Gordonibacter pamelaeae***	0.045%	0.00 - 0.037%	High
	Firmicutes_A	***Flavonifractor MIC8104***	0.043%	0.00 - 0.031%	High
	Firmicutes_A	***CAG-81 sp900066785***	0.041%	0.00 - 0.146%	Average
	Firmicutes_A	***Blautia_A sp000436615***	0.041%	0.00 - 1.55%	Average

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
	Firmicutes_A	***Ruthenibacterium MIC9855***	0.040%	0.00 - 0.00%	High
	Firmicutes_A	***Eubacterium_G sp000434315***	0.040%	0.00 - 0.086%	Average
	Firmicutes_A	***CAG-83 MIC7830***	0.039%	0.00 - 0.082%	Average
	Firmicutes	***Absiella sp000165065***	0.038%	0.00 - 0.00%	High
	Firmicutes_A	***UBA5446 MIC9241***	0.038%	0.00 - 0.00%	High
	Firmicutes_A	***Lachnospiraceae MIC6612***	0.038%	0.00 - 0.061%	Average
	Firmicutes_A	***UBA9475 MIC7490***	0.037%	0.00 - 0.025%	High
	Firmicutes_A	***Butyricicoccaceae MIC8222***	0.037%	0.00 - 0.023%	High
	Bacteroidota	***UBA1820 sp003150615***	0.037%	0.00 - 0.00%	High
	Firmicutes_A	***Blautia_A sp900066335***	0.036%	0.00 - 0.967%	Average

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
⊖	Proteobacteria	***Escherichia coli (coli_D)***	0.036%	0.00 - 0.012%	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 sulphide, 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 poor intestinal health and poor liver health. Additionally, a recent study identified several strains from this species as being able to produce a toxin called colibactin which can damage DNA.

	Firmicutes_A	***Lachnospiraceae MIC9331***	0.034%	0.00 - 0.00%	High
	Firmicutes_A	***Oscillibacter MIC6596***	0.034%	0.00 - 0.014%	High
	Bacteroidota	***Bacteroides finegoldii***	0.033%	0.00 - 0.271%	Average
	Firmicutes_A	***Oscillospiraceae MIC9672***	0.033%	0.00 - 0.00%	High
	Firmicutes_A	***CAG-272 MIC8323***	0.032%	0.00 - 0.00%	High
	Firmicutes_A	***Marvinbryantia MIC9792***	0.032%	0.00 - 0.077%	Average

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
	Firmicutes_A	***CAG-882 sp003486385***	0.031%	0.00 - 0.376%	Average
	Firmicutes_A	***UBA5394 sp003150565***	0.030%	0.00 - 0.00%	High
	Firmicutes_A	***CAG-74 MIC6989***	0.030%	0.00 - 0.065%	Average
	Verrucomicrobiota	***Victivallis sp002998355***	0.029%	0.00 - 0.046%	Average
	Firmicutes_A	***Anaerovoracaceae MIC7478***	0.029%	0.00 - 0.046%	Average
	Firmicutes_A	***Acutalibacteraceae MIC8814***	0.029%	0.00 - 0.00%	High
	Firmicutes_A	***Oscillibacter MIC6950***	0.029%	0.00 - 0.00%	High
	Verrucomicrobiota	***Akkermansia MIC8757***	0.029%	0.00 - 0.00%	High
	Firmicutes_A	***UBA2856 MIC8224***	0.028%	0.00 - 0.00%	High
	Firmicutes_A	***QAND01 sp003150225***	0.028%	0.00 - 0.009%	High
	Verrucomicrobiota	***CAG-312 MIC7338***	0.027%	0.00 - 0.00%	High
	Firmicutes_A	***CAG-272 MIC9439***	0.027%	0.00 - 0.00%	High
	Firmicutes_A	***CAG-83 MIC8731***	0.025%	0.00 - 0.211%	Average

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
⊕	Firmicutes_A	***Intestinimonas butyriciproducens***	0.025%	0.00 - 0.007%	High

This is a recently discovered species that can 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, branched chain amino acids, butyrate, cobalamin (B12), lactate, propionate.

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

Emerging Research:
Reduced levels have been observed in individuals with poor intestinal health, suggesting it likely plays a beneficial role in health.

	Firmicutes_A	***Coprococcus_A MIC9199***	0.025%	0.00 - 0.274%	Average
	Bacteroidota	***Butyricimonas sp900258545***	0.024%	0.00 - 0.00%	High
	Firmicutes_A	***Lachnospiraceae MIC6593***	0.024%	0.00 - 0.036%	Average
	Firmicutes_A	***CAG-74 MIC9650***	0.023%	0.00 - 0.022%	High
	Firmicutes_A	***Acutalibacteraceae MIC6990***	0.023%	0.00 - 0.015%	High
	Firmicutes_G	***DTU025 MIC9102***	0.023%	0.00 - 0.008%	High

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
	Firmicutes_A	***ER4 MIC9395***	0.022%	0.00 - 0.00%	High
	Firmicutes_A	***UBA5446 MIC7746***	0.022%	0.00 - 0.00%	High
	Desulfobacterota_A	***Mailhella MIC8103***	0.022%	0.00 - 0.015%	High
	Firmicutes_A	***UBA644 MIC9235***	0.022%	0.00 - 0.015%	High
	Firmicutes	***Lactobacillus iners***	0.022%	0.00 - 0.00%	High
	Firmicutes_A	***CAG-552 MIC9697***	0.022%	0.00 - 0.00%	High
	Firmicutes	***CAG-288 sp000437395***	0.021%	0.00 - 0.203%	Average
	Firmicutes_A	***GCA-900066135 sp900066135***	0.021%	0.00 - 0.086%	Average
	Firmicutes_A	***CAG-552 MIC7772***	0.020%	0.00 - 0.00%	High
	Firmicutes_A	***Acutalibacteraceae MIC7229***	0.019%	0.00 - 0.00%	High
	Firmicutes_A	***Clostridium MIC8573***	0.019%	0.00 - 0.067%	Average
	Firmicutes_A	***Lachnospirales MIC7715***	0.019%	0.00 - 0.00%	High
	Firmicutes_A	***Provencibacterium massiliense***	0.018%	0.00 - 0.00%	High

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
	Firmicutes_A	***Acutalibacteraceae MIC9774***	0.018%	0.00 - 0.00%	High
	Bacteroidota	***UBA11471 sp000434215***	0.018%	0.00 - 0.285%	Average
	Cyanobacteria	***CAG-306 sp000980375***	0.018%	0.00 - 0.019%	Average
	Firmicutes_A	***CAG-110 MIC9052***	0.018%	0.00 - 0.094%	Average
	Firmicutes_A	***Anaerovoracaceae MIC8502***	0.017%	0.00 - 0.061%	Average
	Bacteroidota	***Alistipes_A sp900240235***	0.016%	0.00 - 0.069%	Average
	Firmicutes_A	***QALS01 MIC9566***	0.016%	0.00 - 0.035%	Average
	Firmicutes	***Staphylococcus haemolyticus***	0.013%	0.00 - 0.00%	High
	Firmicutes_A	***Lachnospiraceae MIC9747***	0.013%	0.00 - 0.00%	High
	Firmicutes_A	***Blautia_A sp000285855***	0.013%	0.00 - 0.129%	Average
	Firmicutes_A	***Oscillibacter MIC7446***	0.013%	0.00 - 0.033%	Average
	Firmicutes_A	***Lachnospiraceae MIC7157***	0.013%	0.00 - 0.00%	High
	Firmicutes_A	***Gemmiger MIC8926***	0.012%	0.00 - 0.00%	High

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
	Firmicutes_A	***UBA1191 sp900066305***	0.011%	0.00 - 0.022%	Average
	Firmicutes_A	***Christensenellaceae MIC8561***	0.011%	0.00 - 0.00%	High
	Firmicutes_A	***Phocea massiliensis***	0.011%	0.00 - 0.00%	High
	Firmicutes_A	***UBA644 MIC9596***	0.011%	0.00 - 0.00%	High
	Firmicutes_A	***Lachnospiraceae MIC9183***	0.010%	0.00 - 0.00%	High

MICROBA

Gut microbiome report