



# Microba *Insight*™

Gut microbiome report

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**Sample ID:** BBD4034

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*New insights. New possibilities*

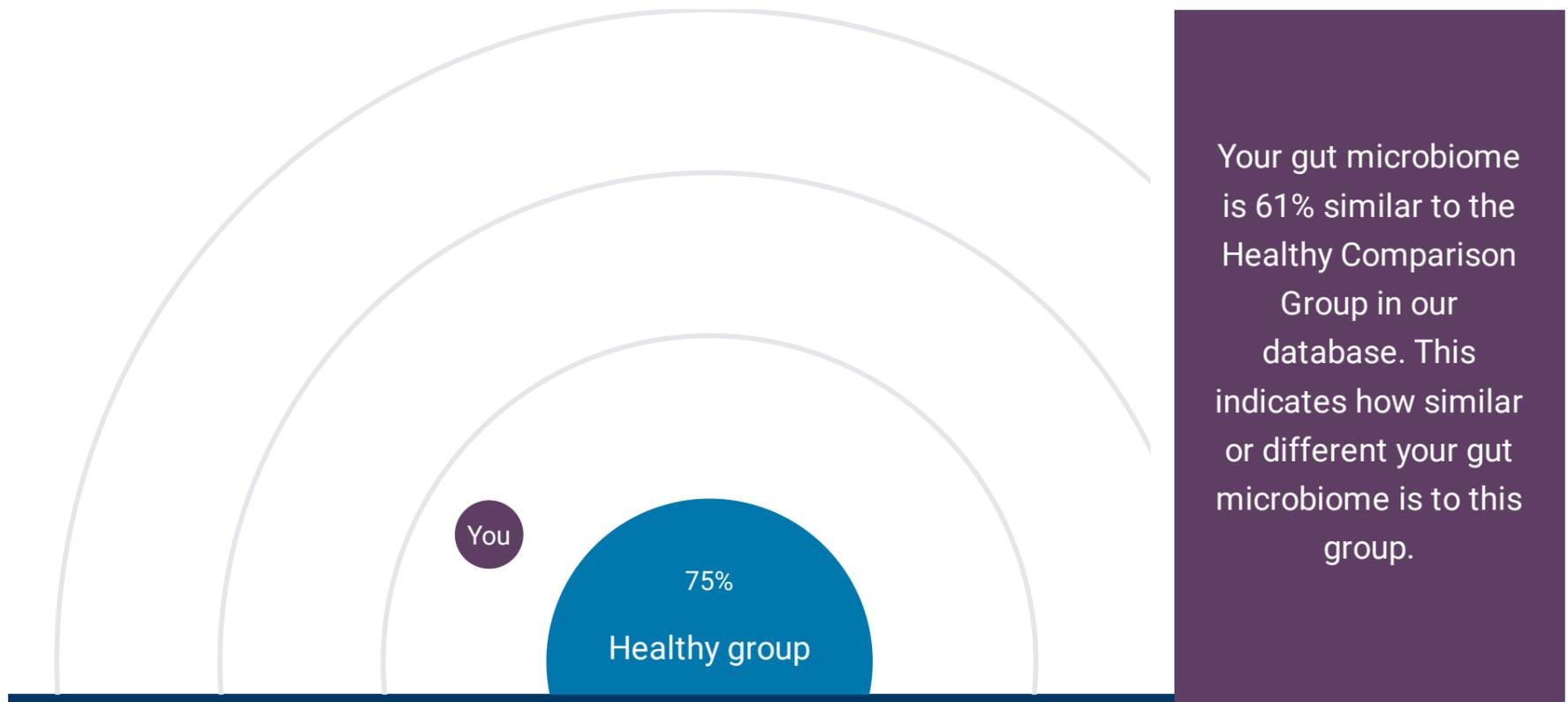
## Introduction to the *Insight*<sup>TM</sup> Report

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

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

# Your report overview

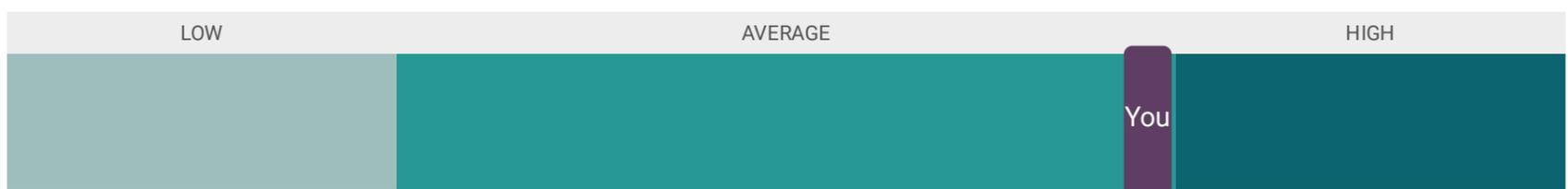
Welcome to the start of your journey to understand how your microbiome affects your health. Throughout this report, the analysed sample is compared to a healthy comparison group. This group is a collection of gut microbiome samples from everyday healthy people, who have not reported any significant health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



## 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

**4.11**

# 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	<i>UBA11524 sp1</i>	6.04%	0.00 - 3.45%	High
Verrucomicrobia	<i>Akkermansia sp1</i>	4.34%	0.00 - 0.00%	High
Firmicutes_A	<i>CAG-83 sp2</i>	3.87%	0.00 - 0.44%	High
Firmicutes_A	<i>CAG-226 MIC3942</i>	3.34%	0.00 - 0.33%	High
Firmicutes_A	<i>CAG-349 sp1</i>	3.16%	0.00 - 0.00%	High

# Your key insights

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

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

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

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

EVIDENCE RATING ★★★★★

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

**This is typical.** You have a similar potential to produce lipopolysaccharides (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 LPS.

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

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

EVIDENCE RATING ★★★★★

# Your key insights

## Your gut microbiome's ability to **break down fibre**

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

**A**

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

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

EVIDENCE RATING ★★★★★☆

## Your gut microbiome's ability to **break down protein**

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

**A**

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

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

EVIDENCE RATING ★★★★★☆

# Your key insights

## Your microbiome's potential to produce **branched chain amino acids**

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

**A**

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

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

EVIDENCE RATING ★★★★★☆

## Your microbiome's potential to contribute to **cardiovascular disease**

**This is 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 cardiometabolic conditions. Plant chemicals known as indoles have been shown to reduce the production on 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 cardiovascular and chronic kidney disease. Diets high in animal protein and low in fibre have been associated with increased trimethylamine production by gut microbes while plant chemicals known as indoles have been shown to reduce the production of TMAO.

EVIDENCE RATING ★★★★★☆

# Your key insights

## Your microbiome's potential to **protect your nervous system**

**This is a good level!** Your potential to produce indolepropionic acid (known as IPA) is at a high level. This is good, because IPA is a strong antioxidant that can protect nerve cells from damage and may help protect against insulin resistance.

**A**

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

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

EVIDENCE RATING ★★★★★

## Your microbiome's potential to **prevent kidney stones**

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

**A**

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

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

EVIDENCE RATING ★★★★★

# Your key insights

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

**This is a good level!** Your potential to produce hydrogen sulphide is at a level similar to the healthy group. This is good, because a high potential to produce hydrogen sulphide by gut bacteria has been associated with an impaired gut barrier function.

**A**

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

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

EVIDENCE RATING ★★☆☆☆

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

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

**A**

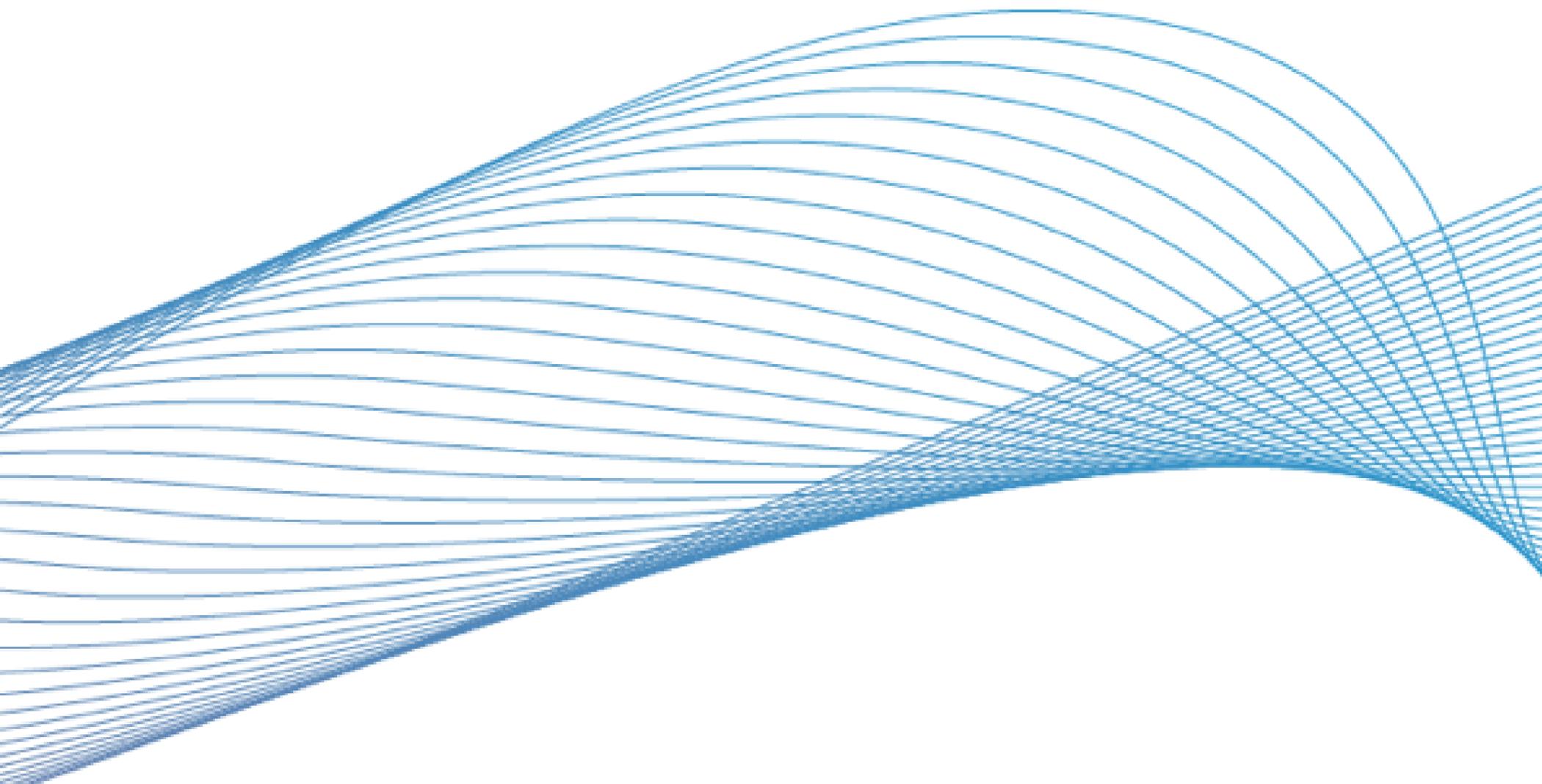
This sample reported a level **similar to the healthy group**

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

EVIDENCE RATING ★★☆☆☆

# Digging deeper into the detail

Gut microbiome report

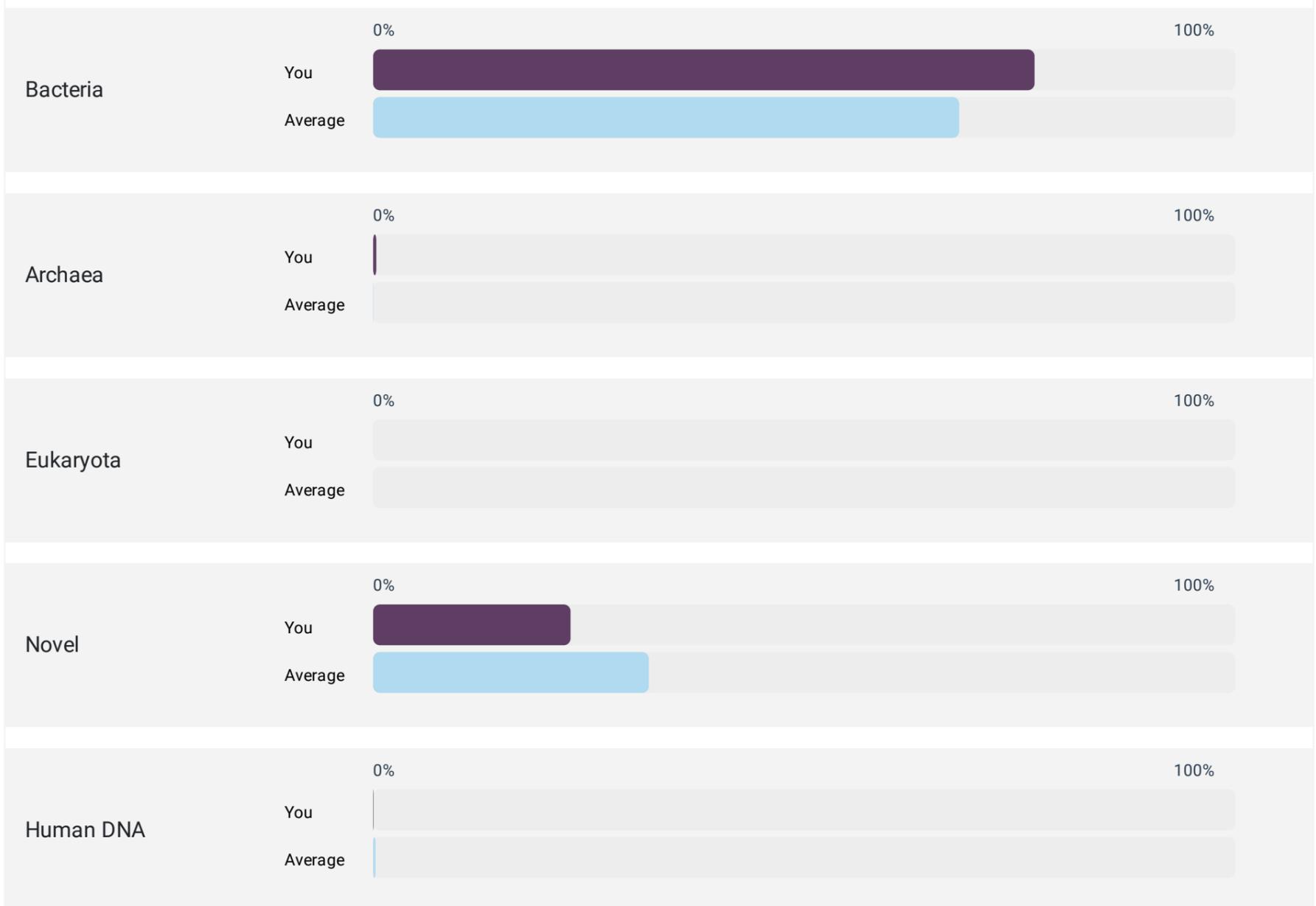


*New insights. New possibilities*

# 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 microorganisms 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.

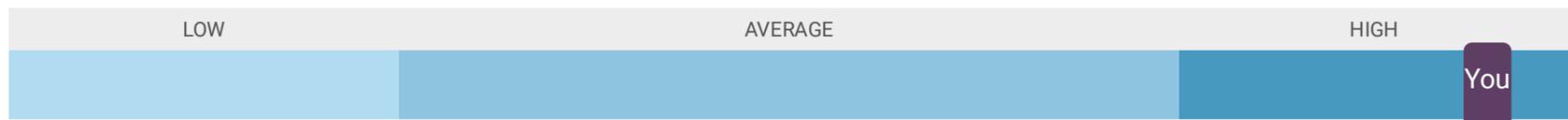


# Microbiome Digestion Potential

Below we show the proportion of species in your gut microbiome that can break down macronutrients, which include fibre, protein, simple sugars and fat. 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 macronutrients and their metabolites on each of the tabs below.

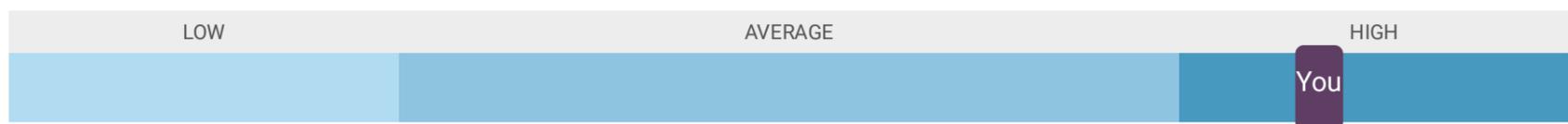
## FAT

This scale indicates the proportion of species in your gut microbiome that can break down fat. Fats are not typically broken down in your lower intestine (where the main population of gut microorganisms reside), instead they just pass through. However, bacteria present in your lower intestine may have the ability to break down fats in addition to fibre and protein.



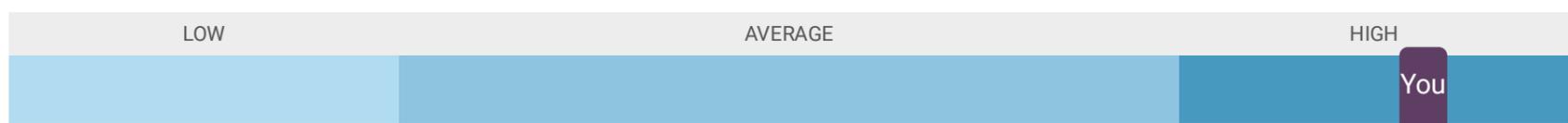
## FIBRE

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.



## 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.



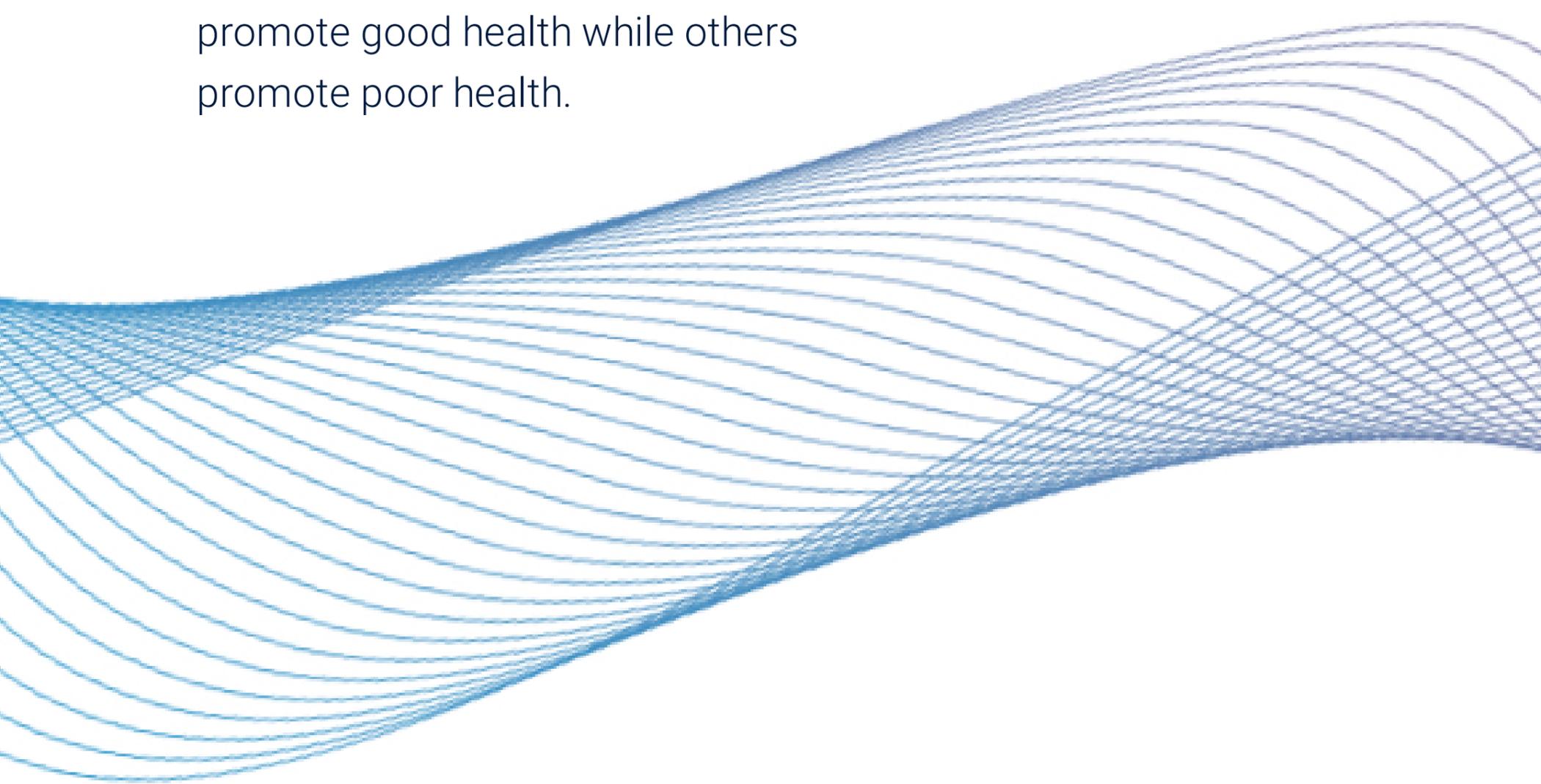
## SUGAR

This scale indicates the proportion of species in your gut microbiome that can break down simple sugars. Simple sugars (e.g. glucose, lactose, fructose, etc.) from your diet will not make it to the large intestine, these are immediately absorbed by your body for quick energy. However, as your gut bacteria break down energy sources such as fibre, this will produce simple sugars that other gut microbes can use.



# 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.



*New insights. New possibilities*

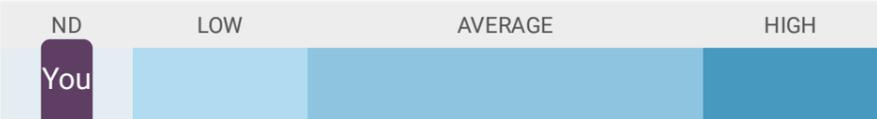
# Microbial Metabolites

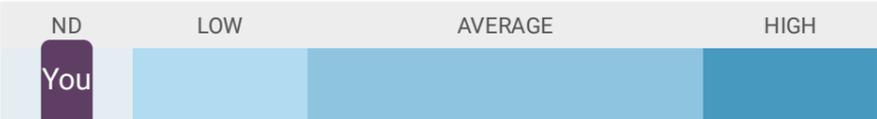
Below we show the potential of your gut microbiome to produce or consume different metabolites associated with health and disease. The microorganisms in your gut can transform the food components you eat into thousands of products called metabolites. Some metabolites have been associated with health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

## HEALTH INDICATORS

### Produced

	ND	LOW	AVERAGE	HIGH
<p><b>- Lipopolysaccharide production</b> <b>10.3%</b></p> 			You	
<p><b>The abundance of this metabolite is about the same as the comparison group.</b></p> <p>Lipopolysaccharides (LPS) are an important component of the cell wall of many bacteria, but when these bacteria die, the LPS is released into the gut where it can be pro-inflammatory. Diets high in fat, especially saturated fat, allow LPS to cross the intestinal barrier and enter the bloodstream. High levels of LPS in the blood have been observed in individuals with metabolic conditions such as heart disease, type 2 diabetes, non-alcoholic fatty liver disease and obesity. Additionally, a high potential to produce LPS has been observed in the gut microbiome of individuals with insulin resistance, colon cancer, and Crohn's disease. Avoiding excessive intake of saturated fat can help reduce the ability of LPS to enter the bloodstream.</p> <p><a href="#">[1]</a> <a href="#">[2]</a> <a href="#">[3]</a> <a href="#">[4]</a> <a href="#">[5]</a> <a href="#">[6]</a></p>				

	ND	LOW	AVERAGE	HIGH
<p><b>- B. fragilis toxin production</b> <b>0.00%</b></p> 	You			
<p><b>This metabolite is not detected in this microbiome.</b></p> <p>Most people's gut microbiome contain a species of bacteria called <i>Bacteroides fragilis</i>. A small proportion of <i>B. fragilis</i> strains have the ability to secrete a toxin. In some people this toxin can cause symptoms such as diarrhea while other people can remain symptom free. There are concerns that this toxin can cause intestinal inflammation. If you are experiencing diarrhea and have this toxin, consider seeing a healthcare practitioner.</p> <p><a href="#">[1]</a> <a href="#">[2]</a></p>				

	ND	LOW	AVERAGE	HIGH
<p><b>- Trimethylamine production</b> <b>0.00%</b></p> 	You			
<p><b>This metabolite is not detected in this microbiome.</b></p> <p>A high potential to produce trimethylamine has been correlated to heart disease and type 2 diabetes. Once trimethylamine is produced by gut microbes, it is transported to the liver and converted to trimethylamine-n-oxide (TMAO). TMAO has been shown to be involved with blood sugar control, blood clotting and inflammation.</p> <p>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.</p> <p><a href="#">[1]</a> <a href="#">[2]</a> <a href="#">[3]</a> <a href="#">[4]</a> <a href="#">[5]</a> <a href="#">[6]</a> <a href="#">[7]</a></p>				

<b>Ammonia (urease) production</b>	<b>3.01%</b>	ND	LOW	AVERAGE	HIGH
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**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>Beta-glucuronidase production</b>	<b>17.0%</b>	ND	LOW	AVERAGE	HIGH
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**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.

[\[1\]](#) [\[2\]](#)

<b>Hydrogen sulphide production</b>	<b>5.22%</b>	ND	LOW	AVERAGE	HIGH
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**The abundance of this metabolite is about the same as the comparison group.**

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

[\[1\]](#) [\[2\]](#)

<b>Branched chain amino acid production</b>	<b>52.3%</b>	ND	LOW	AVERAGE	HIGH
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**The abundance of this metabolite is about the same as the comparison group.**

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

[\[1\]](#) [\[2\]](#)

## Consumed

<b>Trimethylamine consumption</b>	<b>0.31%</b>	ND	LOW	AVERAGE	HIGH
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**The abundance of this metabolite is higher than the comparison group.**

It is considered beneficial if your gut microbiome has the potential to consume trimethylamine. Although several gut microbes can produce trimethylamine, some gut microbes can also use trimethylamine for energy, thus reducing levels of it.

[\[1\]](#) [\[2\]](#) [\[3\]](#) [\[4\]](#) [\[5\]](#)



**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



**This metabolite is not detected in this microbiome.**

Tyramine is a chemical that is produced from the breakdown of the amino acid tyrosine. It occurs naturally in foods such as smoked or aged meats, cheese, and chocolate and is also produced by gut bacteria. Tyramine that you consume in food is absorbed in the small intestine, and foods high in tyramine are thought to trigger migraines in sensitive individuals. In contrast, tyramine produced by your gut microbiota in the large intestine can stimulate serotonin production in the gut. Tyramine is only one of several compounds that can stimulate serotonin production in the gut. Other compounds include butyrate, propionate and vitamin E.

More than 90% of the body's serotonin is produced by cells in the gut, where it plays an important role in many bodily functions such as the immune response, gut motility, bone development, and cardiac function. Only about 10% of the body's serotonin is produced in the brain, where it is used to regulate mood, appetite and sleep. Consuming a sufficient amount of fibre, including fruits and vegetables, can help support serotonin production in your gut.

[\[1\]](#) [\[2\]](#)



**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 depression and anxiety. Most GABA is produced in the brain however your gut microbiome may contribute to your GABA levels as some bacteria can produce or consume GABA. The role of gut bacteria that produce GABA in anxiety and depression is currently not understood. If you are concerned about your mental health, it is important to seek professional help.

[\[1\]](#) [\[2\]](#) [\[3\]](#)



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

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

[\[1\]](#) [\[2\]](#) [\[3\]](#) [\[4\]](#)



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

Histamine is a chemical produced by the breakdown of the amino acid histidine. It is produced by human cells and also by some

bacterial species in the gut. It plays an important role in immune regulation, gut function and the nervous system. Gut bacteria that can produce histamine have been observed at increased levels in patients with asthma. Additionally, people with food allergies and irritable bowel syndrome may be more sensitive to histamine in the gut.

[\[1\]](#) [\[2\]](#) [\[3\]](#)

## Consumed



**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 depression and anxiety. Most GABA is produced in the brain however your gut microbiome may contribute to your GABA levels as some bacteria can produce or consume GABA. The role of gut bacteria that consume GABA in anxiety and depression is currently not understood. If you are concerned about your mental health, it is important to seek professional help.

[\[1\]](#) [\[2\]](#) [\[3\]](#)

# Microbial Metabolites

## SHORT CHAIN FATTY ACIDS

### Produced



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

Succinate is an important compound involved in glucose and protein metabolism and it is also involved in the production of the short chain fatty acid, propionate. It can be produced by both human cells and the gut microbiome. Although succinate plays many beneficial roles in our body, as with many compounds, too much may not be a good thing. High levels of succinate in the blood have been observed in individuals with obesity, heart disease and type 2 diabetes.

[\[1\]](#) [\[2\]](#)



**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, suppresses inflammation, helps control appetite, and promotes the production of serotonin in the gut. Low levels of butyrate production have been observed in individuals with inflammatory bowel diseases. Consuming foods high in resistant starch (e.g. lentils, peas, beans, cooked and cooled potatoes, rolled oats) or pectin (e.g. avocado, kiwifruit, berries, citrus fruits, pumpkin, zucchini) have been shown to increase butyrate levels.

[\[1\]](#) [\[2\]](#) [\[3\]](#) [\[4\]](#) [\[5\]](#) [\[6\]](#) [\[7\]](#) [\[8\]](#)



**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.

[\[1\]](#) [\[2\]](#) [\[3\]](#) [\[4\]](#) [\[5\]](#) [\[6\]](#)



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

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

[\[1\]](#) [\[2\]](#) [\[3\]](#)



**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.

[\[1\]](#) [\[2\]](#)

# Microbial Metabolites

## ESSENTIAL VITAMINS

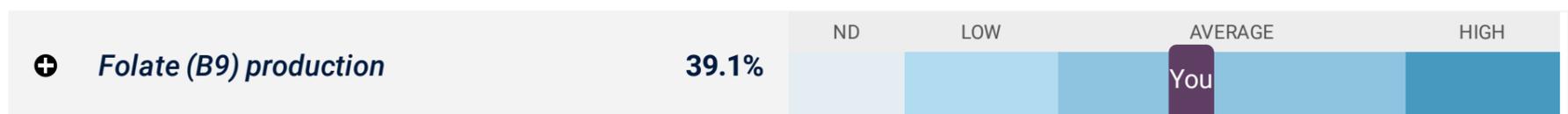
### Produced



**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.

[\[1\]](#) [\[2\]](#) [\[3\]](#)



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

Folate or folic acid plays an important role in cell replication and repair. Low folate levels can result in anemia and have been linked to an increased risk of heart disease and stroke. Folate cannot be produced by human cells and must be obtained through diet or from the microbiome. The large intestine has the ability to absorb folate produced by the gut microbiome and it is estimated that the human gut microbiome can provide up to 37% of the daily folate requirement. 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.

[\[1\]](#) [\[2\]](#) [\[3\]](#)



**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.

[\[1\]](#) [\[2\]](#) [\[3\]](#) [\[4\]](#)



**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.

[\[1\]](#) [\[2\]](#) [\[3\]](#)



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

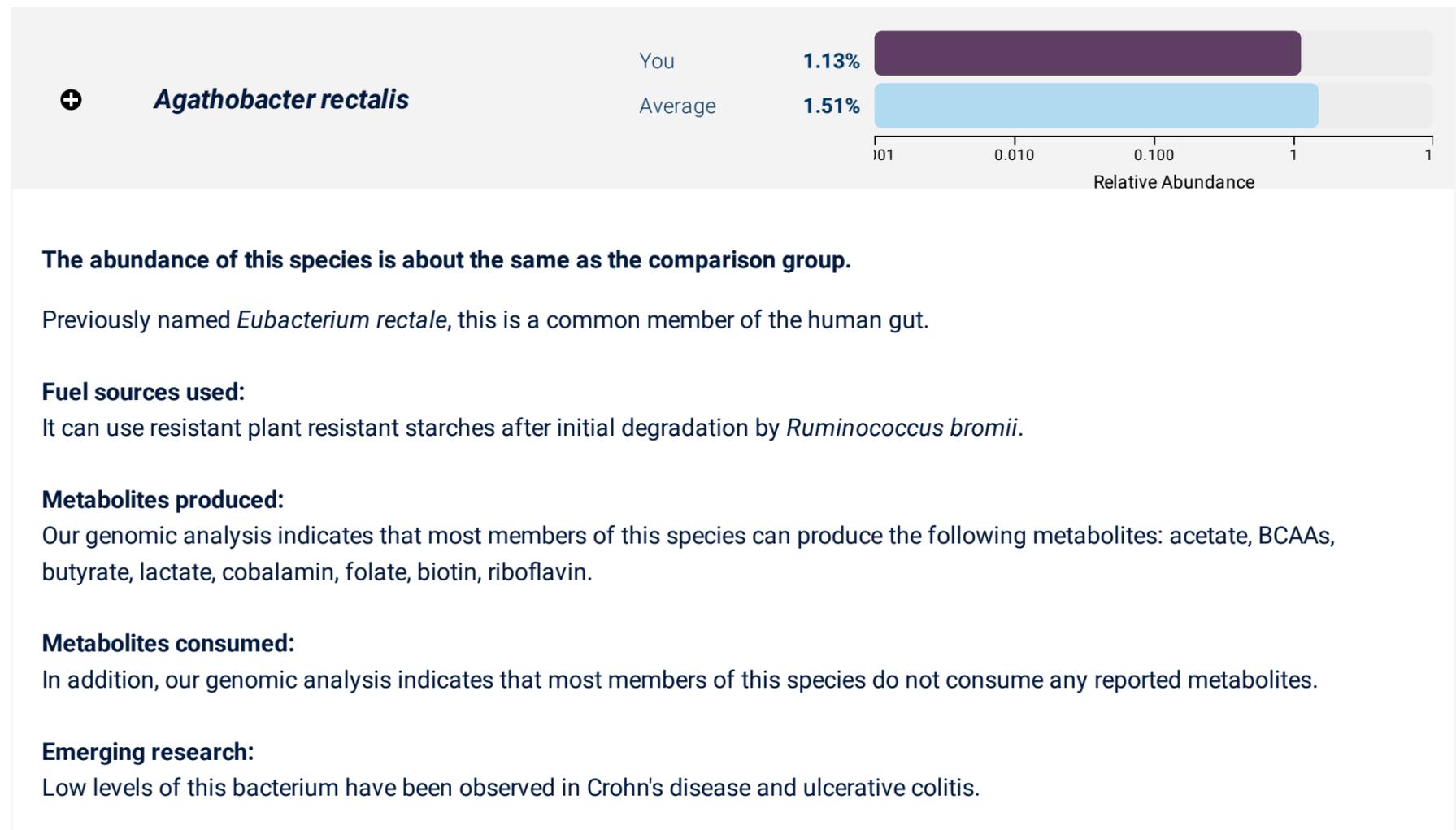
K vitamins are a family of fat soluble vitamins which play an important role in blood clotting. Vitamin K cannot be produced by human cells and must be obtained through diet or the microbiome. Vitamin K1 (phylloquinone) is found in plants such as dark green leafy vegetables and canola oil, and is the 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

## SPECIES OF INTEREST

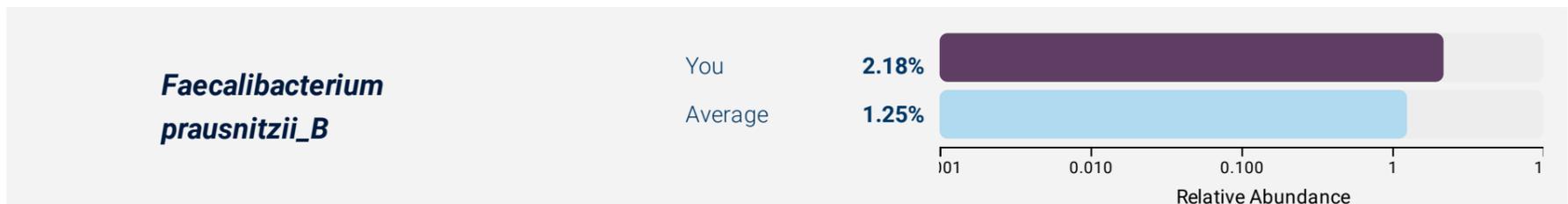
### Detected in you



# Species of Interest

## SPECIES OF INTEREST

### Detected in you



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

*Faecalibacterium prausnitzii\_B* (aka strain L2-6) is a common gut inhabitant.

**Fuel sources used:**

**Fuels sources used:** It can use fibre, simple sugars, acetate and mucus for energy. It can produce ethanol, lactate and the short chain fatty acids acetate and butyrate.

**Metabolites produced:**

Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, BCAAs, butyrate, cobalamin.

**Metabolites consumed:**

In addition, our genomic analysis indicates that most members of this species can consume the following metabolites: oxalate.

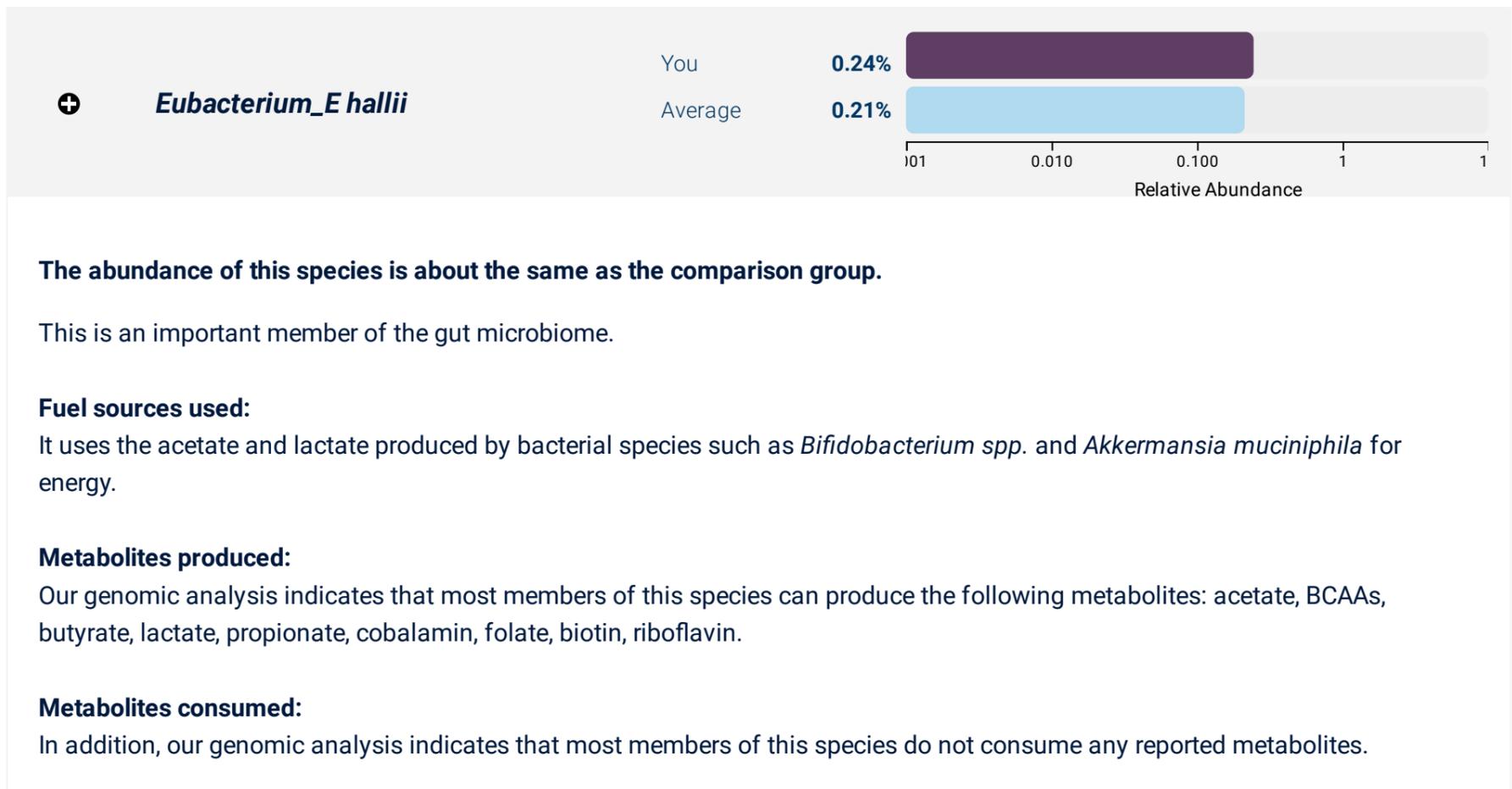
**Disease associations:**

This species has been observed at high levels in individuals with atopic dermatitis.

# Species of Interest

## SPECIES OF INTEREST

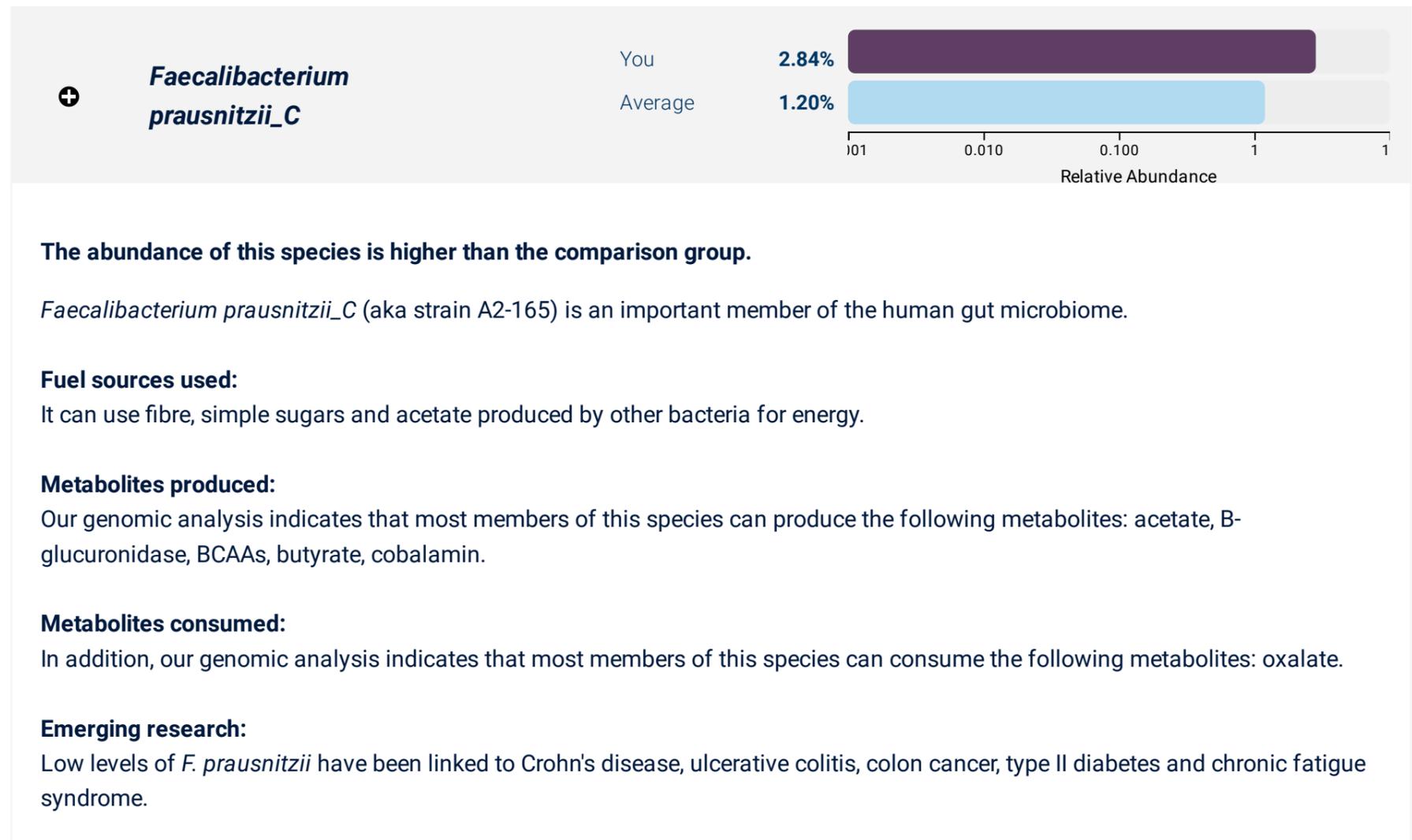
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# Species of Interest

## SPECIES OF INTEREST

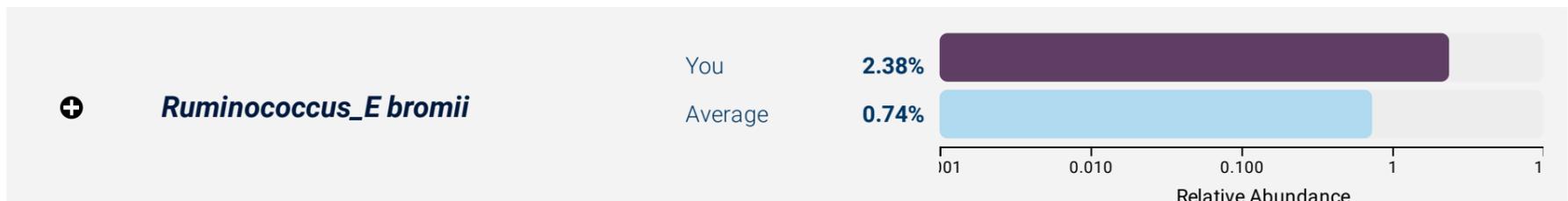
### Detected in you



# Species of Interest

## SPECIES OF INTEREST

### Detected in you



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

This is a common member of the human gut and is considered a keystone species of the gut microbiome for its ability to break down resistant starch.

#### Fuel sources used:

*Ruminococcus bromii* uses resistant starch for energy.

#### Metabolites produced:

Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, BCAAs, lactate, biotin.

#### Metabolites consumed:

In addition, our genomic analysis indicates that most members of this species do not consume any reported metabolites.

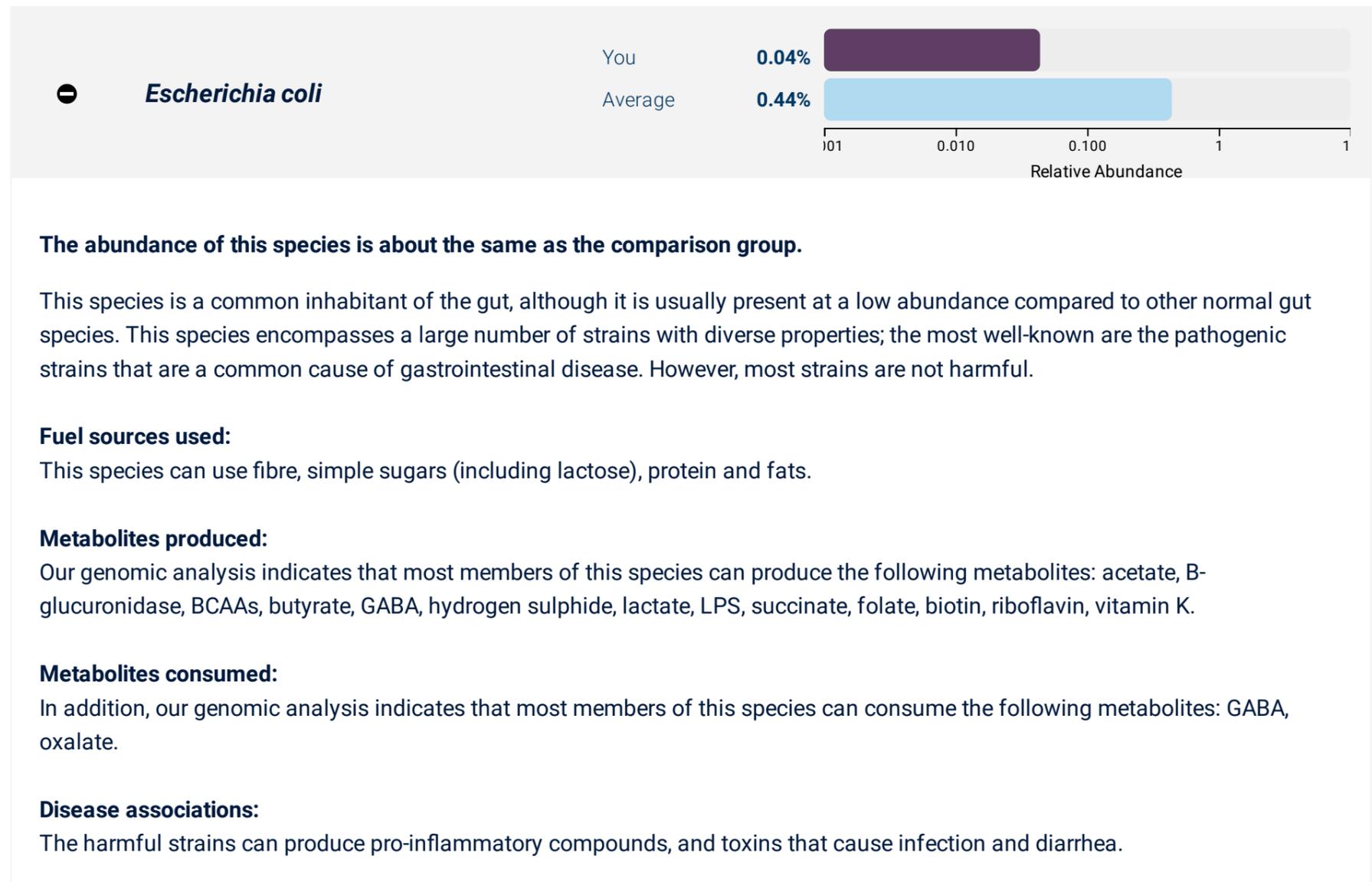
#### Emerging research:

Studies suggest the role of *R. bromii* as a primary starch degrader helps stimulate the growth of butyrate-producing bacterial species.

# Species of Interest

## SPECIES OF INTEREST

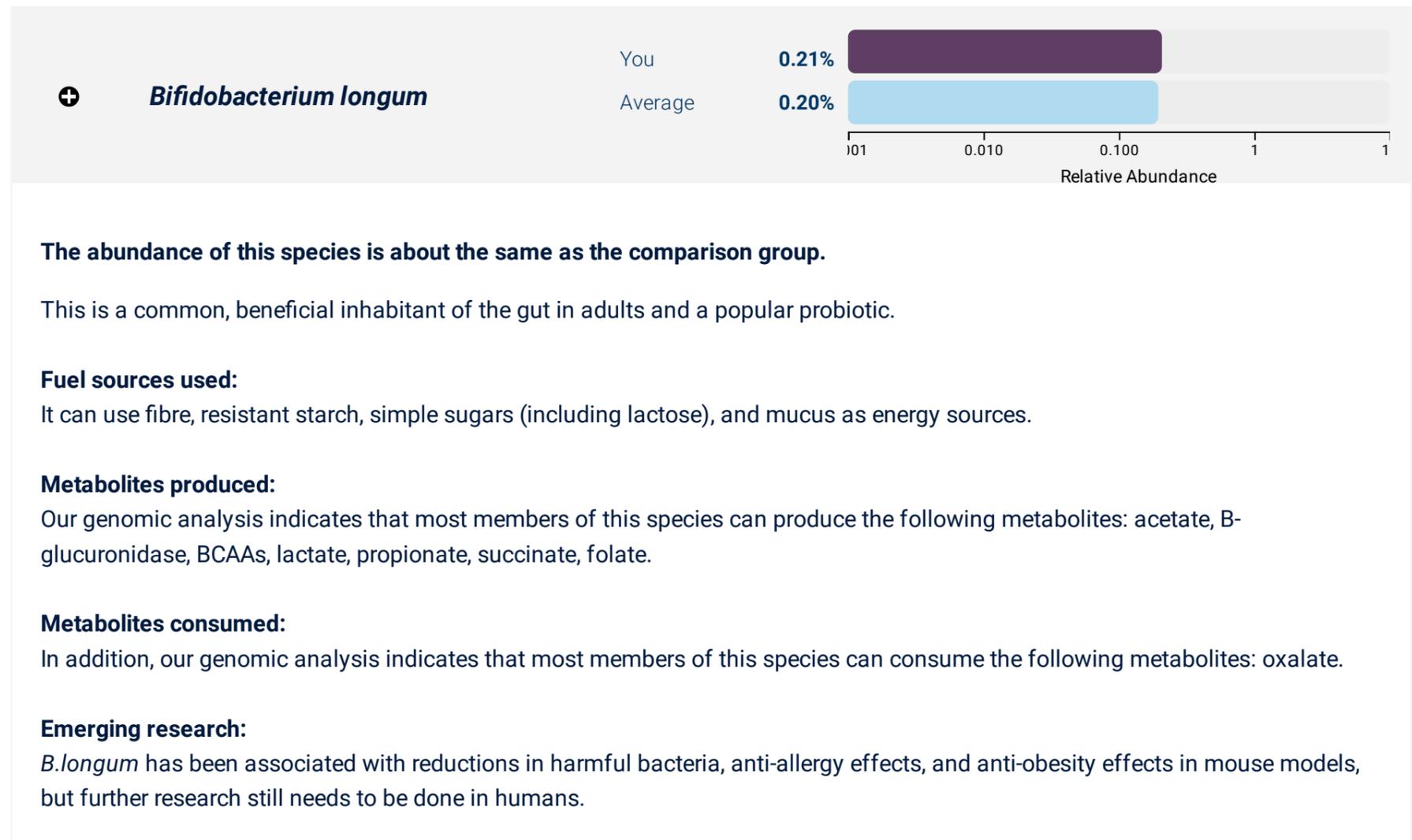
### Detected in you



# Species of Interest

## SPECIES OF INTEREST

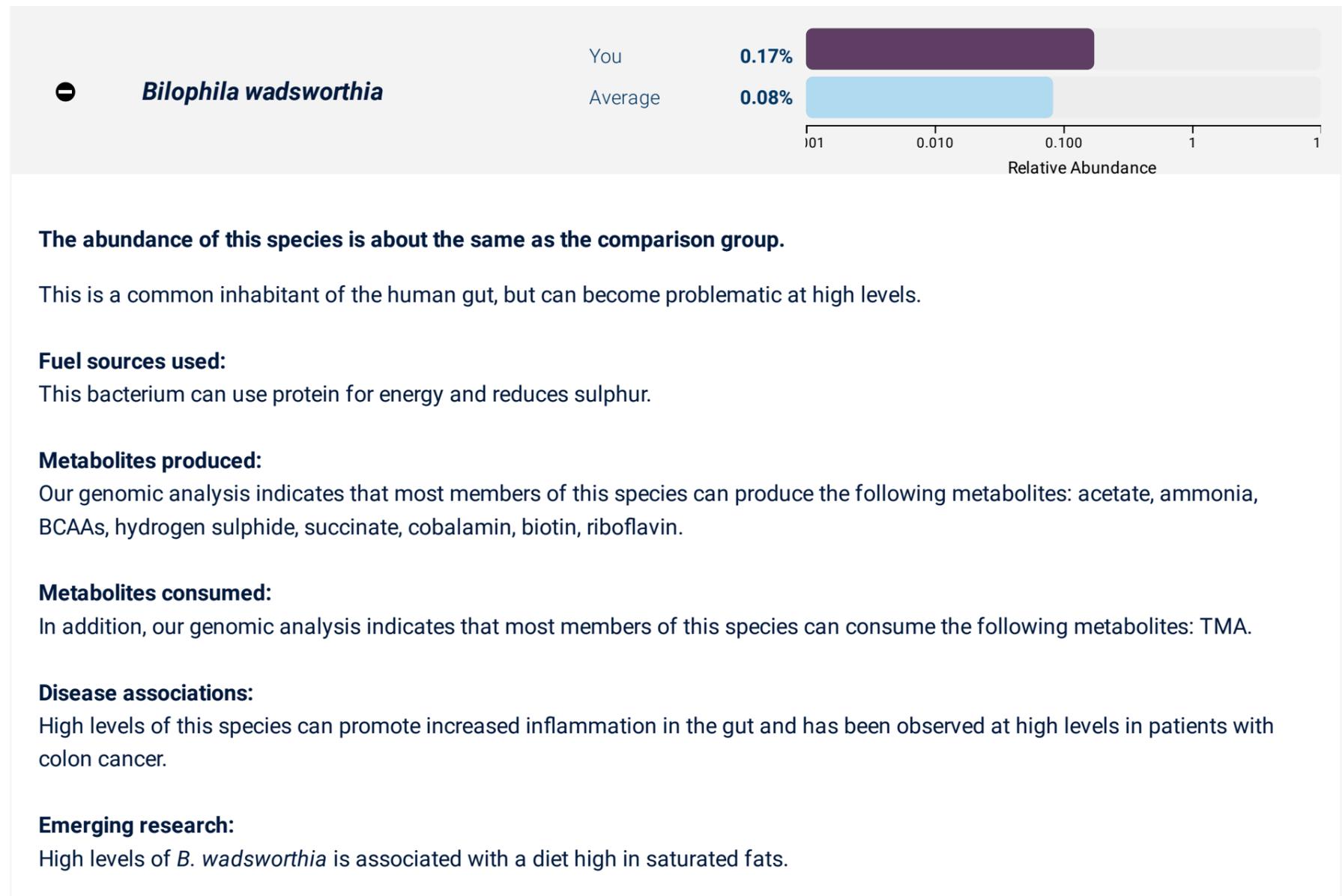
### Detected in you



# Species of Interest

## SPECIES OF INTEREST

### Detected in you



# Species of Interest

## SPECIES OF INTEREST

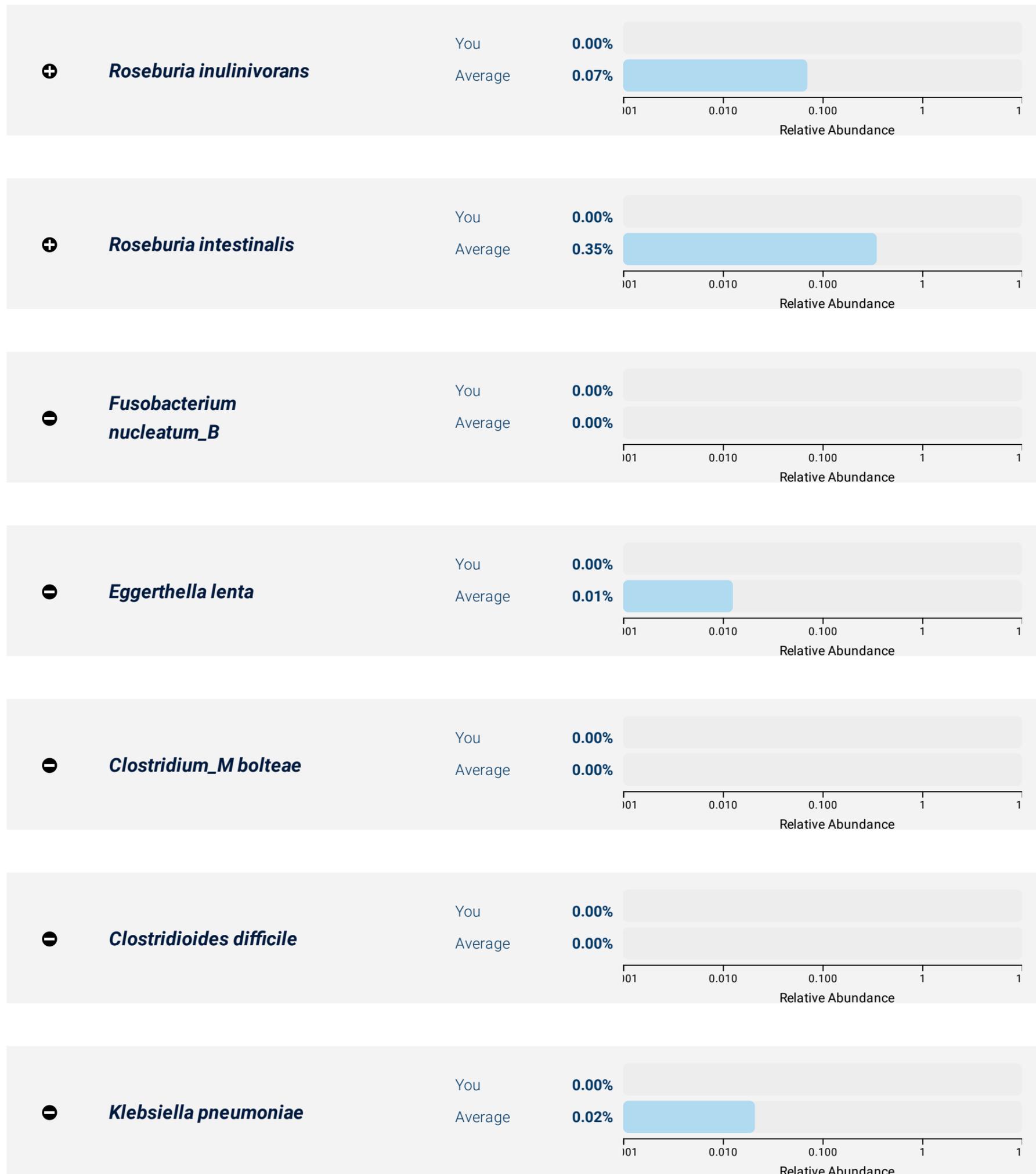
### Not detected in you



# Species of Interest

## SPECIES OF INTEREST

### Not detected in you



# Species of Interest

## SPECIES OF INTEREST

### Not detected in you



# Microbial Eukaryotes

A small percentage of the microorganisms in your gut are eukaryotes. These eukaryotes are primarily fungi (e.g. yeasts) and parasites (e.g. protists). Many eukaryotes are not evenly distributed throughout the bowel and require the collection of a whole stool sample for accurate detection.

We currently only report the Eukaryotic organisms listed, and do not detect other organisms that do not have genomic information available such as *Dientamoeba*.

Due to the nature and lifecycle of certain eukaryotes, and the small sample size required for your Insight™ test, some eukaryotes may avoid detection. If you have a positive result here or are concerned about any eukaryotes or parasites, please consult with a health care practitioner.

***New insights. New possibilities***

# Microbial Eukaryotes

## SPECIES



# 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

*New insights. New possibilities*

# Microbial Profile

## PHYLUM



Phylum	Abundance	Range	Level
Firmicutes_A	52.8%	21.8 - 50.5%	High
Bacteroidetes	14.1%	12.7 - 45.2%	Average
Verrucomicrobia	4.48%	0.00 - 2.95%	High
Actinobacteria	2.75%	0.08 - 2.19%	High
Proteobacteria	1.76%	0.49 - 4.42%	Average
Firmicutes_C	0.57%	0.00 - 1.26%	Average
Desulfobacterota	0.24%	0.00 - 0.43%	Average
Euryarchaeota	0.22%	0.00 - 0.19%	High
Thermoplasmatota	0.15%	0.00 - 0.00%	High

# Species Profile

## SPECIES

Phylum	Species	Abundance	Range	Level
Firmicutes_A	<i>UBA11524 sp1</i>	6.04%	0.00 - 3.45%	High
<p>This is a newly discovered species within a newly discovered genus (order Christensenellales) that has not been described by scientists yet. It is also a commonly encountered bacterial species in the gut.</p> <p><b>Fuel sources used:</b> By analysing the DNA of this new species, Microba has identified that it can use fibre, resistant starch and simple sugars for energy.</p> <p><b>Metabolites produced:</b> Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, B-glucuronidase, BCAAs.</p> <p><b>Metabolites consumed:</b> In addition, our genomic analysis indicates that most members of this species do not consume any reported metabolites.</p>				
Verrucomicrobia	<i>Akkermansia sp1</i>	4.34%	0.00 - 0.00%	High
<p>This is a newly discovered species within the genus <i>Akkermansia</i> that has not been described by scientists yet.</p> <p><b>Fuel sources used:</b> In general, species from the genus <i>Akkermansia</i> can use mucus as an energy source.</p> <p><b>Metabolites produced:</b> Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, BCAAs, GABA, lactate, propionate, succinate, folate, biotin, riboflavin.</p> <p><b>Metabolites consumed:</b> In addition, our genomic analysis indicates that most members of this species do not consume any reported metabolites.</p>				
Firmicutes_A	<i>CAG-83 sp2</i>	3.87%	0.00 - 0.44%	High
<p>This is a newly discovered species within a newly discovered genus in the family Oscillospiraceae that has not been described by scientists yet. Once information is available about this species, this description will be updated.</p> <p><b>Metabolites produced:</b> Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, butyrate, folate.</p> <p><b>Metabolites consumed:</b> In addition, our genomic analysis indicates that most members of this species do not consume any reported metabolites.</p>				
Firmicutes_A	<i>CAG-226 MIC3942</i>	3.34%	0.00 - 0.33%	High
<p><b>Metabolites produced:</b> Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, butyrate, hydrogen sulphide, propionate, biotin.</p>				

**Metabolites consumed:**

In addition, our genomic analysis indicates that most members of this species do not consume any reported metabolites.

Firmicutes_A	<b><i>CAG-349 sp1</i></b>	3.16%	0.00 - 0.00%	High
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This is a newly discovered species in a newly discovered genus from the class Clostridia that has not been described by scientists yet. As soon as information is available about this species we will update this description.

**Metabolites produced:**

Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, folate.

**Metabolites consumed:**

In addition, our genomic analysis indicates that most members of this species do not consume any reported metabolites.

+	Firmicutes_A	<b><i>Faecalibacterium prausnitzii_C</i></b>	2.84%	0.00 - 2.31%	High
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*Faecalibacterium prausnitzii\_C* (aka strain A2-165) is an important member of the human gut microbiome.

**Fuel sources used:**

It can use fibre, simple sugars and acetate produced by other bacteria for energy.

**Metabolites produced:**

Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, B-glucuronidase, BCAAs, butyrate, cobalamin.

**Metabolites consumed:**

In addition, our genomic analysis indicates that most members of this species can consume the following metabolites: oxalate.

**Emerging research:**

Low levels of *F. prausnitzii* have been linked to Crohn's disease, ulcerative colitis, colon cancer, type II diabetes and chronic fatigue syndrome.

+	Firmicutes_A	<b><i>Faecalibacterium prausnitzii_A</i></b>	2.73%	0.00 - 2.87%	Average
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*Faecalibacterium prausnitzii\_A* (aka strains SL3/3 and M21/2) is an inhabitant of the human gut microbiome.

**Fuel sources used:**

It can use fibre, resistant starch, simple sugars and acetate for energy.

**Metabolites produced:**

Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, B-glucuronidase, BCAAs, butyrate, cobalamin.

**Metabolites consumed:**

In addition, our genomic analysis indicates that most members of this species can consume the following metabolites: oxalate.

**Emerging research:**

Low levels of *F. prausnitzii* have been linked to Crohn's disease, ulcerative colitis, colon cancer, type II diabetes and chronic fatigue syndrome. This species produces lower levels of butyrate than *F. prausnitzii\_C*.

+	Firmicutes_A	<b><i>Ruminococcus_E bromii</i></b>	2.38%	0.00 - 2.50%	Average
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This is a common member of the human gut and is considered a keystone species of the gut microbiome for its ability to break down resistant starch.

**Fuel sources used:**

*Ruminococcus bromii* uses resistant starch for energy.

**Metabolites produced:**

Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, BCAAs, lactate, biotin.

**Metabolites consumed:**

In addition, our genomic analysis indicates that most members of this species do not consume any reported metabolites.

**Emerging research:**

Studies suggest the role of *R. bromii* as a primary starch degrader helps stimulate the growth of butyrate-producing bacterial species.

Firmicutes_A	<i>Faecalibacterium prausnitzii_B</i>	2.18%	0.00 - 2.48%	Average
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*Faecalibacterium prausnitzii\_B* (aka strain L2-6) is a common gut inhabitant.

**Fuel sources used:**

**Fuels sources used:** It can use fibre, simple sugars, acetate and mucus for energy. It can produce ethanol, lactate and the short chain fatty acids acetate and butyrate.

**Metabolites produced:**

Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, BCAAs, butyrate, cobalamin.

**Metabolites consumed:**

In addition, our genomic analysis indicates that most members of this species can consume the following metabolites: oxalate.

**Disease associations:**

This species has been observed at high levels in individuals with atopic dermatitis.

Bacteroidetes	<i>Bacteroides_A plebeius_A</i>	2.08%	0.00 - 0.00%	High
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**Fuel sources used:**

This species can use fibre, resistant starch, simple sugars (including lactose), protein and mucus for energy. This species has also acquired an enzyme that allows it to use a carbohydrate found in red seaweeds called porphyran.

**Metabolites produced:**

Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, BCAAs, butyrate, LPS, propionate, succinate, cobalamin, folate, biotin, riboflavin.

**Metabolites consumed:**

In addition, our genomic analysis indicates that most members of this species do not consume any reported metabolites.

**Emerging research:**

Studies have found this bacterium is most common in the gut of Japanese.

Bacteroidetes	<i>Alistipes inops</i>	2.03%	0.00 - 0.34%	High
Firmicutes_A	<i>CAG-170 MIC6238</i>	2.03%	0.00 - 0.20%	High
Firmicutes_A	<i>CAG-83 sp3</i>	1.91%	0.00 - 2.11%	Average
⊕ Bacteroidetes	<i>Bacteroides uniformis</i>	1.44%	0.00 - 4.39%	Average

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

**Fuel sources used:**

It can use fibre, resistant starch, simple sugars (including lactose), protein and mucus for energy.

**Metabolites produced:**

Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, B-glucuronidase, BCAAs, butyrate, GABA, lactate, LPS, propionate, succinate, cobalamin, folate, biotin, riboflavin.

**Metabolites consumed:**

In addition, our genomic analysis indicates that most members of this species do not consume any reported metabolites.

**Emerging research:**

Certain strains have been observed to promote the production of anti-inflammatory compounds, improve immune function, and provide protection against diet induced obesity in mouse models. Further research needs to be conducted to determine if these benefits translate to humans.

	Firmicutes_A	<i>ER4 sp1</i>	1.35%	0.00 - 1.00%	High
⊖	Bacteroidetes	<i>Bacteroides caccae</i>	1.31%	0.00 - 0.51%	High

This is a common member of the human gut.

**Fuel sources used:**

It uses mostly simple sugars, limited fibre types, protein, and mucus for energy.

**Metabolites produced:**

Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, BCAAs, butyrate, GABA, lactate, LPS, propionate, succinate, folate, biotin, riboflavin.

**Metabolites consumed:**

In addition, our genomic analysis indicates that most members of this species do not consume any reported metabolites.

**Disease associations:**

A protein produced by this species has been linked to inflammatory bowel disease and elevated levels of this species have been associated with gout.

⊕	Firmicutes_A	<i>Agathobacter rectalis</i>	1.13%	0.00 - 4.77%	Average
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Previously named *Eubacterium rectale*, this is a common member of the human gut.

**Fuel sources used:**

It can use resistant plant resistant starches after initial degradation by *Ruminococcus bromii*.

**Metabolites produced:**

Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, BCAAs, butyrate, lactate, cobalamin, folate, biotin, riboflavin.

**Metabolites consumed:**

In addition, our genomic analysis indicates that most members of this species do not consume any reported metabolites.

**Emerging research:**

Low levels of this bacterium have been observed in Crohn's disease and ulcerative colitis.

	Actinobacteria	<i>Bifidobacterium stercoris</i>	1.04%	0.00 - 0.55%	High
⊕	Firmicutes_A	<i>Coprococcus eutactus_A</i>	1.04%	0.00 - 1.52%	Average

This is a common inhabitant of the human gut.

**Fuel sources used:**

It can use fibre, simple sugars (including lactose) and limited types of protein for energy.

**Metabolites produced:**

Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, BCAAs, butyrate, lactate, propionate, folate, biotin, riboflavin.

**Metabolites consumed:**

In addition, our 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 children with type 1 diabetes and children with Crohn's disease.

⊖	Bacteroidetes	<i>Bacteroides_B massiliensis</i>	0.98%	0.00 - 1.32%	Average
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This is a normal inhabitant of the human gut microbiome.

**Fuel sources used:**

This species can use resistant starch, simple sugars (including lactose), protein and mucus for energy.

**Metabolites produced:**

Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, BCAAs, butyrate, GABA, lactate, LPS, propionate, cobalamin, folate, biotin, riboflavin.

**Metabolites consumed:**

In addition, our genomic analysis indicates that most members of this species do not consume any reported metabolites.

**Disease associations:**

High levels of this species have been observed in individuals with colon cancer.

**Emerging research:**

This species has been associated with a diet high in red meat.

	Firmicutes_A	<i>Ruthenibacterium lactatiformans</i>	0.96%	0.00 - 0.00%	High
	Proteobacteria	<i>51-20 MIC6194</i>	0.95%	0.00 - 1.05%	Average
	Bacteroidetes	<i>Alistipes obesi</i>	0.92%	0.00 - 0.61%	High
	Firmicutes_A	<i>Subdoligranulum formicile</i>	0.92%	0.00 - 1.53%	Average
⊕	Actinobacteria	<i>Bifidobacterium adolescentis</i>	0.84%	0.00 - 0.40%	High

This is a common and beneficial inhabitant of the gut.

**Fuel sources used:**

It can use fibre, resistant starch, and simple sugars (including lactose) for energy.

**Metabolites produced:**

Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, BCAAs, GABA, lactate, propionate, succinate, folate.

**Metabolites consumed:**

In addition, our genomic analysis indicates that most members of this species do not consume any reported metabolites.

**Emerging research:**

Low levels of this species have been observed in Crohn's disease, obesity and celiac disease.

	Firmicutes_A	<b>CAG-103 MIC465</b>	0.82%	0.00 - 0.38%	High
⊖	Bacteroidetes	<b>Bacteroides_B dorei</b>	0.77%	0.00 - 2.32%	Average

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

**Fuel sources used:**

It can use fibre, resistant starch, simple sugars (including lactose), a wide range of proteins and mucus as energy sources.

**Metabolites produced:**

Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, BCAAs, butyrate, GABA, lactate, LPS, propionate, succinate, cobalamin, folate, biotin, riboflavin.

**Metabolites consumed:**

In addition, our genomic analysis indicates that most members of this species do not consume any reported metabolites.

**Disease associations:**

High levels of this species have been associated with colon cancer and the development of type 1 diabetes in children.

**Emerging research:**

This species has been associated with diets high in red meat.

	Firmicutes_A	<b>Faecalibacterium MIC76</b>	0.71%	0.12 - 1.14%	Average
	Firmicutes_A	<b>Oscillibacter MIC1893</b>	0.66%	0.00 - 0.43%	High
⊖	Bacteroidetes	<b>Bacteroides_B vulgatus</b>	0.65%	0.00 - 3.86%	Average

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

**Fuel sources used:**

It can use dietary fibre, simple sugars, protein and mucus for energy.

**Metabolites produced:**

Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, BCAAs, butyrate, GABA, lactate, LPS, propionate, succinate, cobalamin, folate, biotin, riboflavin.

**Metabolites consumed:**

In addition, our genomic analysis indicates that most members of this species do not consume any reported metabolites.

**Disease associations:**

High levels of this bacterium have been associated with insulin resistance and the progression of Crohn's disease.

**Emerging research:**

This species has been associated with a diet high in red meat.

	Firmicutes_A	<b>CAG-314 MIC230</b>	0.62%	0.00 - 0.23%	High
	Firmicutes_A	<b>CAG-138 MIC1553</b>	0.60%	0.00 - 0.00%	High
	Firmicutes_A	<b>Ruminiclostridium_E siraeum</b>	0.59%	0.00 - 0.80%	Average
	Firmicutes_A	<b>CAG-177 sp1</b>	0.58%	0.00 - 0.43%	High
	Bacteroidetes	<b>Barnesiella intestinhominis</b>	0.57%	0.00 - 1.01%	Average
	Firmicutes_A	<b>Lachnospira eligens</b>	0.57%	0.00 - 1.32%	Average

	Firmicutes_A	<b>CAG-103 MIC2697</b>	0.52%	0.00 - 1.26%	Average
	Firmicutes_A	<b>Fusicatenibacter saccharivorans</b>	0.48%	0.00 - 2.34%	Average
	Firmicutes_A	<b>CAG-110 MIC5879</b>	0.47%	0.00 - 0.29%	High
	Firmicutes_A	<b>Ruminococcus_D bicirculans</b>	0.42%	0.00 - 2.22%	Average
	Firmicutes_C	<b>Dialister MIC5173</b>	0.41%	0.00 - 0.45%	Average
⊖	Bacteroidetes	<b>Alistipes finegoldii</b>	0.40%	0.00 - 0.58%	Average

This is a common inhabitant of the gut microbiome.

**Fuel sources used:**

It can use simple sugars and protein for energy.

**Metabolites produced:**

Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, BCAAs, butyrate, GABA, lactate, LPS, propionate, succinate, folate, riboflavin, vitamin K.

**Metabolites consumed:**

In addition, our genomic analysis indicates that most members of this species do not consume any reported metabolites.

**Disease associations:**

High levels of this species have been associated with colon cancer.

**Emerging research:**

This species has been associated with diets high in red meat and/or low in fruits and vegetables.

	Firmicutes_A	<b>Ruminiclostridium_C MIC856</b>	0.39%	0.00 - 0.23%	High
	Firmicutes_A	<b>Ruminococcus_B faecis</b>	0.38%	0.00 - 0.49%	Average
	Firmicutes_A	<b>CAG-170 MIC2758</b>	0.37%	0.00 - 0.48%	Average
	Firmicutes_A	<b>UBA5394 MIC3590</b>	0.37%	0.00 - 0.51%	Average
	Firmicutes_A	<b>CAG-353 MIC4793</b>	0.37%	0.00 - 1.55%	Average
	Bacteroidetes	<b>Alistipes onderdonkii</b>	0.36%	0.00 - 1.72%	Average
	Firmicutes_A	<b>ER4 MIC360</b>	0.35%	0.00 - 0.54%	Average
	Firmicutes_A	<b>Blautia_A MIC5792</b>	0.35%	0.00 - 0.38%	Average
	Firmicutes_A	<b>Subdoligranulum MIC5128</b>	0.35%	0.00 - 1.47%	Average
	Bacteroidetes	<b>CAG-144 MIC575</b>	0.33%	0.00 - 0.65%	Average
	Firmicutes_A	<b>CAG-56 MIC5514</b>	0.33%	0.00 - 0.65%	Average
	Firmicutes_A	<b>UBA1394 MIC353</b>	0.33%	0.00 - 0.09%	High
	Firmicutes_A	<b>TF01-11 sp1</b>	0.32%	0.00 - 0.44%	Average
	Firmicutes_A	<b>Oscillibacter MIC5816</b>	0.30%	0.00 - 0.41%	Average
	Bacteroidetes	<b>Alistipes MIC6359</b>	0.30%	0.00 - 0.00%	High

	Bacteroidetes	<i>Odoribacter laneus</i>	0.29%	0.00 - 0.00%	High
	Proteobacteria	<i>Parasutterella excrementihominis</i>	0.28%	0.00 - 0.39%	Average
⊖	Bacteroidetes	<i>Parabacteroides merdae</i>	0.28%	0.00 - 0.66%	Average

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

**Fuel sources used:**

It can use simple sugars (including lactose), protein and mucus as energy sources.

**Metabolites produced:**

Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, BCAAs, GABA, lactate, LPS, propionate, succinate, cobalamin, folate, biotin, riboflavin.

**Metabolites consumed:**

In addition, our genomic analysis indicates that most members of this species do not consume any reported metabolites.

**Disease associations:**

High levels of this species have been observed in individuals with hypertension and colon cancer.

**Emerging research:**

This species has been associated with a diet low in fruits and vegetables.

	Firmicutes_A	<i>Oscillibacter MIC2940</i>	0.28%	0.00 - 0.24%	High
	Firmicutes_A	<i>Eubacterium_F sp1</i>	0.28%	0.00 - 0.44%	Average
	Proteobacteria	<i>Dakarella MIC2437</i>	0.28%	0.00 - 0.00%	High
	Bacteroidetes	<i>Bacteroides salyersiae</i>	0.27%	0.00 - 0.08%	High
	Firmicutes_A	<i>Butyricoccus MIC5408</i>	0.27%	0.00 - 0.64%	Average
	Actinobacteria	<i>CAG-1427 MIC6313</i>	0.27%	0.00 - 0.00%	High
⊖	Bacteroidetes	<i>Bacteroides cellulosilyticus</i>	0.27%	0.00 - 1.36%	Average

This is a common gut inhabitant.

**Fuel sources used:**

It can use numerous types of fibre, as well as resistant starch, simple sugars, protein and mucus for energy.

**Metabolites produced:**

Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, B-glucuronidase, BCAAs, butyrate, GABA, lactate, LPS, propionate, succinate, cobalamin, folate, biotin, riboflavin.

**Metabolites consumed:**

In addition, our genomic analysis indicates that most members of this species do not consume any reported metabolites.

**Disease associations:**

Elevated levels have been observed in patients with hypertension.

	Firmicutes_A	<i>Neglecta sp1</i>	0.25%	0.00 - 0.67%	Average
⊕	Firmicutes_A	<i>Eubacterium_E hallii</i>	0.24%	0.00 - 0.63%	Average

This is an important member of the gut microbiome.

**Fuel sources used:**

It uses the acetate and lactate produced by bacterial species such as *Bifidobacterium spp.* and *Akkermansia muciniphila* for energy.

**Metabolites produced:**

Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, BCAAs, butyrate, lactate, propionate, cobalamin, folate, biotin, riboflavin.

**Metabolites consumed:**

In addition, our genomic analysis indicates that most members of this species do not consume any reported metabolites.

	Firmicutes_A	<i>Eubacterium_R sp2</i>	0.24%	0.00 - 0.47%	Average
	Firmicutes_A	<i>UBA4263 MIC5332</i>	0.23%	0.00 - 0.25%	Average
	Firmicutes_A	<i>Anaerostipes hadrus_A</i>	0.22%	0.00 - 0.24%	Average
	Firmicutes_A	<i>CAG-382 MIC3624</i>	0.22%	0.00 - 0.00%	High
	Firmicutes_A	<i>Butyricoccus sp1</i>	0.22%	0.00 - 0.78%	Average
	Euryarchaeota	<i>Methanobrevibacter_A MIC1132</i>	0.22%	0.00 - 0.00%	High
+	Actinobacteria	<i>Bifidobacterium longum</i>	0.21%	0.00 - 0.70%	Average

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

**Fuel sources used:**

It can use fibre, resistant starch, simple sugars (including lactose), and mucus as energy sources.

**Metabolites produced:**

Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, B-glucuronidase, BCAAs, lactate, propionate, succinate, folate.

**Metabolites consumed:**

In addition, our genomic analysis indicates that most members of this species can consume the following metabolites: oxalate.

**Emerging research:**

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

	Firmicutes_A	<i>Blautia_A MIC5125</i>	0.21%	0.00 - 0.41%	Average
+	Proteobacteria	<i>Oxalobacter formigenes_A</i>	0.20%	0.00 - 0.00%	High

**Fuel sources used:**

This bacterial species use a compound called oxalate for energy, which is one of the main components of calcium oxalate kidney stones.

**Metabolites produced:**

Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, BCAAs, GABA, LPS, folate, biotin, riboflavin.

**Metabolites consumed:**

In addition, our genomic analysis indicates that most members of this species can consume the following metabolites: oxalate.

### Emerging research:

People that suffer from kidney stones often do not have this species. It is very sensitive to antibiotics, and is less abundant in people that have been treated by antibiotics at some point in their lives.

	Firmicutes_A	<b>CAG-170 MIC2776</b>	0.20%	0.00 - 0.19%	High
	Firmicutes_A	<b>CAG-110 MIC508</b>	0.20%	0.00 - 0.72%	Average
	Firmicutes_A	<b>CAG-41 sp1</b>	0.18%	0.00 - 0.33%	Average
	Firmicutes_A	<b>Flavonifractor MIC4117</b>	0.18%	0.00 - 0.00%	High
	Firmicutes_A	<b>Blautia_A obeum_A</b>	0.18%	0.00 - 0.17%	High
●	Desulfobacterota	<b>Bilophila wadsworthia</b>	0.17%	0.00 - 0.20%	Average

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

### Fuel sources used:

This bacterium can use protein for energy and reduces sulphur.

### Metabolites produced:

Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, ammonia, BCAAs, hydrogen sulphide, succinate, cobalamin, biotin, riboflavin.

### Metabolites consumed:

In addition, our genomic analysis indicates that most members of this species can consume the following metabolites: TMA.

### Disease associations:

High levels of this species can promote increased inflammation in the gut and has been observed at high levels in patients with colon cancer.

### Emerging research:

High levels of *B. wadsworthia* is associated with a diet high in saturated fats.

	Bacteroidetes	<b>UBA7173 MIC834</b>	0.16%	0.00 - 0.00%	High
	Firmicutes_A	<b>D16 phoceensis</b>	0.16%	0.00 - 0.10%	High
	Firmicutes_A	<b>UBA11512 MIC4563</b>	0.16%	0.00 - 0.08%	High
⊕	Bacteroidetes	<b>Alistipes shahii</b>	0.16%	0.00 - 1.47%	Average

This is a common inhabitant of the human gut.

### Fuel sources used:

It can use fibre, simple sugars (including lactose) and protein for energy.

### Metabolites produced:

Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, B-glucuronidase, BCAAs, butyrate, GABA, lactate, LPS, propionate, succinate, folate, riboflavin.

### Metabolites consumed:

In addition, our genomic analysis indicates that most members of this species do not consume any reported metabolites.

### Emerging research:

This species appears to have mostly beneficial effects. It has been associated with beneficial markers of cardiac health (low triglycerides, high beneficial cholesterol HDL levels), and was observed as depleted in patients with atherosclerotic heart disease.

Additionally, a study in mice showed this species may improve the efficacy of cancer immunotherapy. However, this species was also observed at elevated levels in patients with Parkinson's Disease.

	Bacteroidetes	<i>Odoribacter massiliensis</i>	0.15%	0.00 - 0.00%	High
	Thermoplasmata	<i>Methanomassiliicoccus_A intestinalis</i>	0.15%	0.00 - 0.00%	High
	Firmicutes_C	<i>CAG-207 MIC1796</i>	0.15%	0.00 - 0.38%	Average
	Firmicutes_A	<i>Eubacterium_F MIC2171</i>	0.14%	0.00 - 0.00%	High
	Firmicutes_A	<i>Blautia_A MIC807</i>	0.13%	0.00 - 1.29%	Average
	Firmicutes_A	<i>Subdoligranulum MIC5784</i>	0.13%	0.00 - 0.35%	Average
	Firmicutes_A	<i>Anaerotruncus MIC1532</i>	0.12%	0.00 - 0.00%	High
	Actinobacteria	<i>Collinsella MIC5138</i>	0.12%	0.00 - 0.00%	High
+	Firmicutes_A	<i>Ruminococcus_B lactaris</i>	0.12%	0.00 - 0.34%	Average

This is a common inhabitant of the human gut.

**Fuel sources used:**

It can use simple sugars (including lactose) and protein for energy.

**Metabolites produced:**

Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, BCAAs, lactate, propionate, cobalamin, folate, biotin.

**Metabolites consumed:**

In addition, our genomic analysis indicates that most members of this species do not consume any reported metabolites.

**Disease associations:**

This species has been observed at elevated levels in individuals with rheumatoid arthritis, but at reduced levels in individuals with insulin resistance.

	Firmicutes_A	<i>Lachnospira MIC895</i>	0.11%	0.00 - 0.33%	Average
	Firmicutes_A	<i>CAG-83 MIC6219</i>	0.11%	0.00 - 0.12%	Average
	Actinobacteria	<i>Adlercreutzia MIC5417</i>	0.11%	0.00 - 0.14%	Average
	Firmicutes_A	<i>CAG-110 MIC5846</i>	0.10%	0.00 - 0.28%	Average
	Firmicutes_A	<i>CAG-170 MIC1808</i>	0.10%	0.00 - 0.15%	Average
	Actinobacteria	<i>Collinsella MIC4055</i>	0.10%	0.00 - 0.00%	High
	Firmicutes_A	<i>Oscillospiraceae MIC4348</i>	0.10%	0.00 - 0.00%	High
	Firmicutes_A	<i>Lachnospira MIC140</i>	0.09%	0.00 - 0.09%	High
	Firmicutes_A	<i>Blautia_A MIC594</i>	0.09%	0.00 - 0.23%	Average
	Bacteroidetes	<i>Butyricimonas virosa</i>	0.08%	0.00 - 0.00%	High
	Bacteroidetes	<i>CAG-485 MIC2186</i>	0.08%	0.00 - 0.00%	High

	Verrucomicrobia	<b>UBA11452 MIC5926</b>	0.08%	0.00 - 0.17%	Average
	Firmicutes_A	<b>UBA2862 MIC5863</b>	0.08%	0.00 - 0.00%	High
	Bacteroidetes	<b>Butyricimonas MIC1139</b>	0.08%	0.00 - 0.08%	Average
	Bacteroidetes	<b>Alistipes MIC2680</b>	0.08%	0.00 - 0.00%	High
	Firmicutes_A	<b>D5 MIC4780</b>	0.07%	0.00 - 0.00%	High
	Firmicutes_A	<b>CAG-81 MIC6089</b>	0.07%	0.00 - 0.11%	Average
	Actinobacteria	<b>Cryptobacterium MIC2685</b>	0.07%	0.00 - 0.00%	High
	Desulfobacterota	<b>Desulfovibrio fairfieldensis</b>	0.06%	0.00 - 0.00%	High
⊖	Bacteroidetes	<b>Alistipes_A indistinctus</b>	0.06%	0.00 - 0.15%	Average

This is a recently discovered inhabitant of the human gut.

**Fuel sources used:**

It can use simple sugars (including lactose) and protein for energy.

**Metabolites produced:**

Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, BCAAs, butyrate, GABA, propionate, succinate, folate, biotin, riboflavin, vitamin K.

**Metabolites consumed:**

In addition, our genomic analysis indicates that most members of this species do not consume any reported metabolites.

**Disease associations:**

High levels of this species have been observed in individuals with type II diabetes.

	Verrucomicrobia	<b>CAG-312 MIC2164</b>	0.06%	0.00 - 0.00%	High
	Firmicutes_A	<b>UBA5446 MIC4816</b>	0.06%	0.00 - 0.00%	High
	Firmicutes_A	<b>Coprococcus_A catus</b>	0.05%	0.00 - 0.22%	Average
	Firmicutes_A	<b>CAG-74 MIC3751</b>	0.05%	0.00 - 0.00%	High
	Bacteroidetes	<b>UBA1820 MIC2188</b>	0.05%	0.00 - 0.00%	High
⊖	Proteobacteria	<b>Escherichia coli</b>	0.04%	0.00 - 0.33%	Average

This species is a common inhabitant of the gut, although it is usually present at a low abundance compared to other normal gut species. This species encompasses a large number of strains with diverse properties; the most well-known are the pathogenic strains that are a common cause of gastrointestinal disease. However, most strains are not harmful.

**Fuel sources used:**

This species can use fibre, simple sugars (including lactose), protein and fats.

**Metabolites produced:**

Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, B-glucuronidase, BCAAs, butyrate, GABA, hydrogen sulphide, lactate, LPS, succinate, folate, biotin, riboflavin, vitamin K.

**Metabolites consumed:**

In addition, our genomic analysis indicates that most members of this species can consume the following metabolites: GABA,

oxalate.

**Disease associations:**

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



# Gut microbiome report

