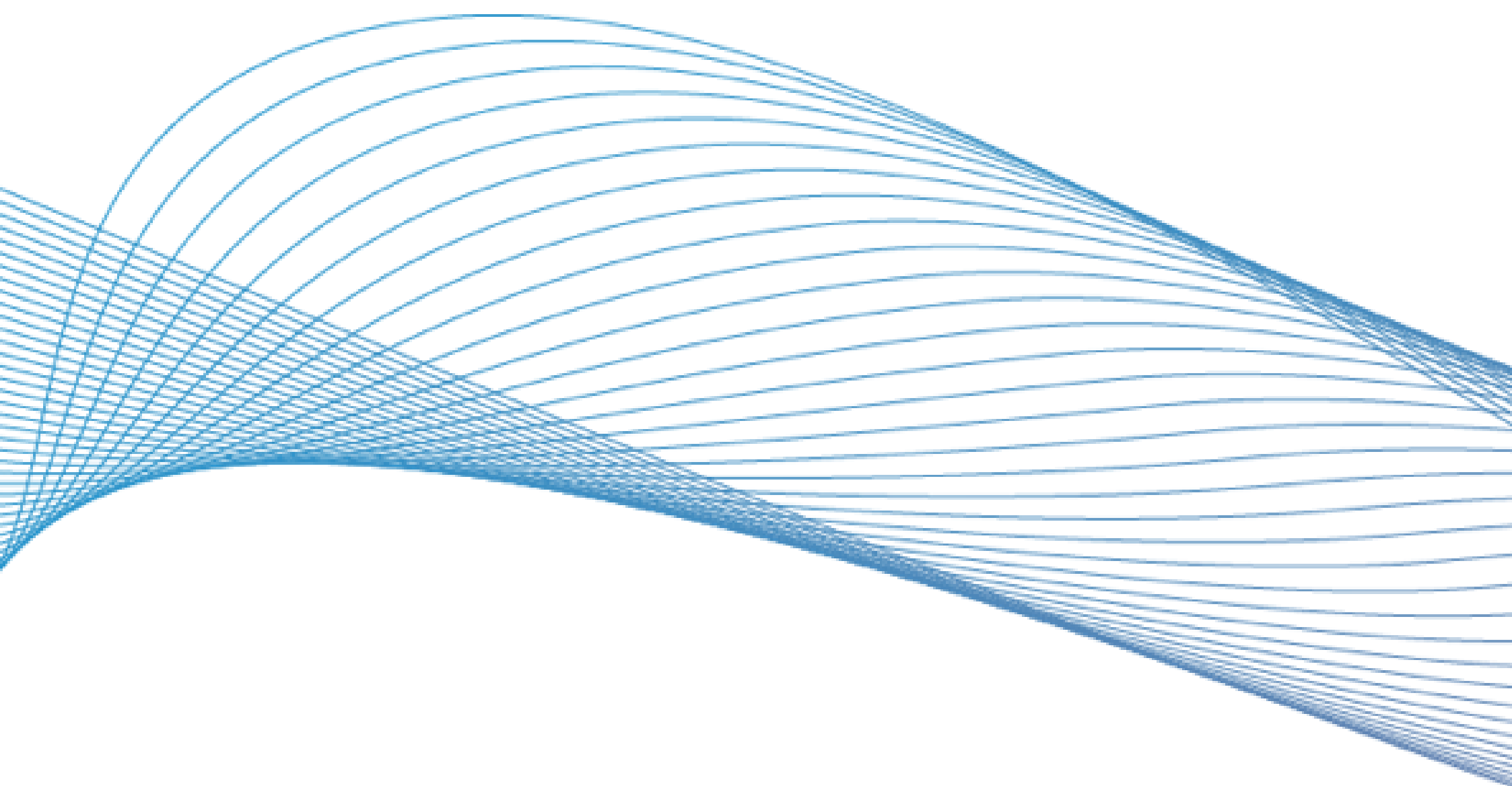




Microba *Insight*™

Gut microbiome report



Name: Freya Thebault

Sample ID: BBJ9987

Report generated on: 07-03-2022

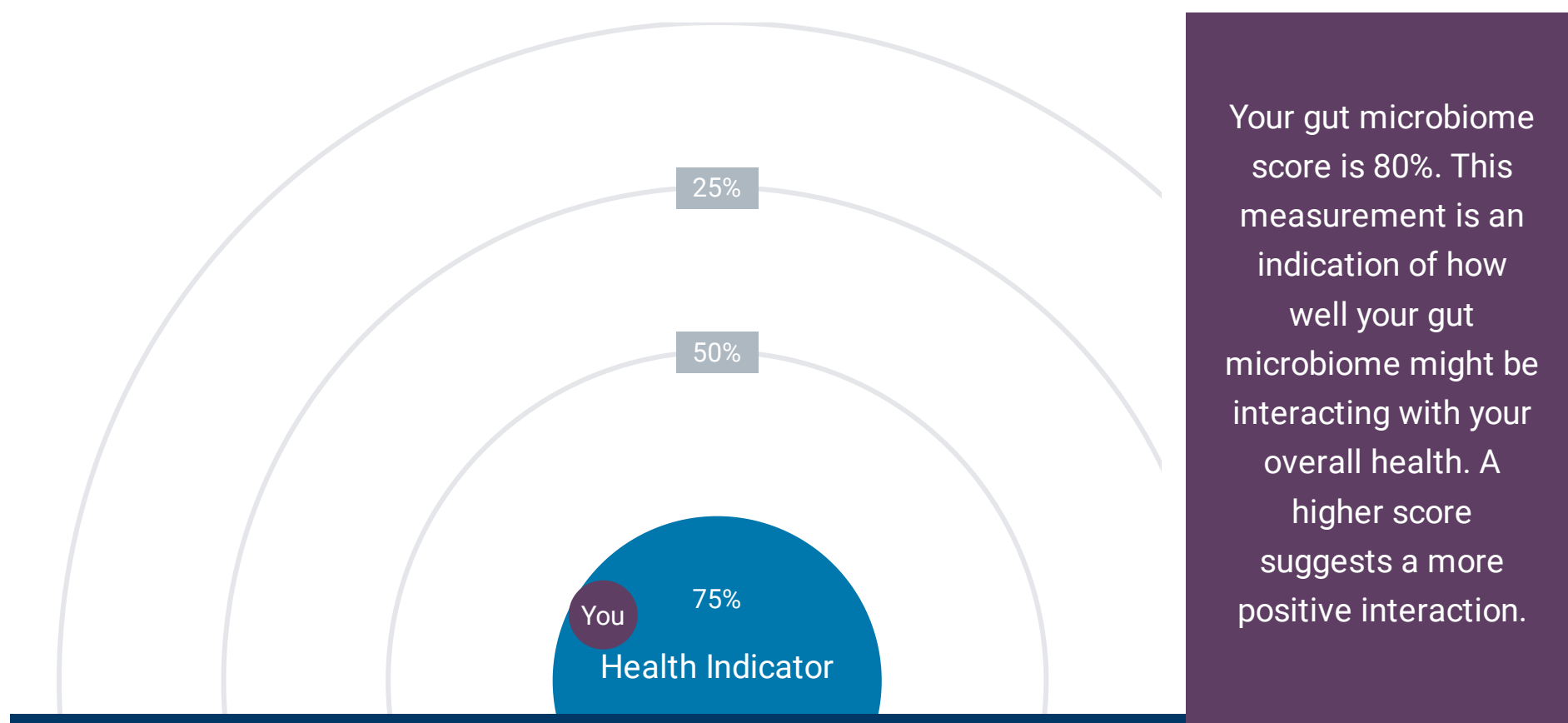
Introduction to *Microba Insight™* Report

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.

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

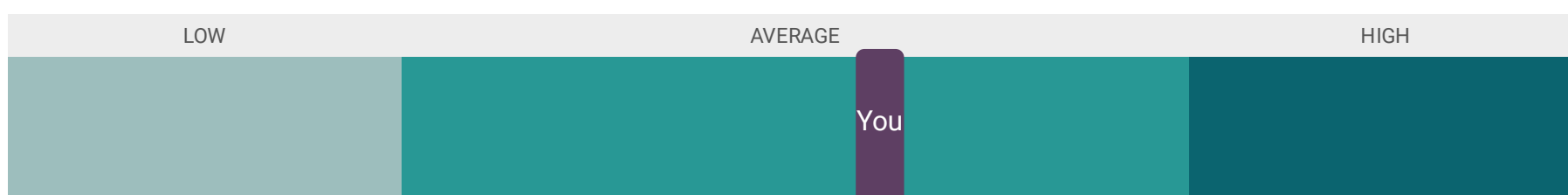
Welcome to the start of your journey to understanding how your microbiome affects your health. Throughout this report, the analysed sample is compared to a healthy comparison group. This group is a collection of gut microbiome samples from everyday healthy people, who have not reported any significant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



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

4.09

Your microbial community

YOUR TOP 5 MOST ABUNDANT SPECIES

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

Phylum	Species	Abundance	Range	Level
Firmicutes_A	<i>CAG-349 sp003539515</i>	15.2%	0.00 - 0.074%	High
Bacteroidota	<i>Alistipes obesi</i>	3.72%	0.00 - 0.430%	High
Firmicutes_A	<i>GCA-900066995 sp900291955</i>	3.60%	0.00 - 0.00%	High
Bacteroidota	<i>UBA7173 MIC9174</i>	3.20%	0.00 - 0.00%	High
● Bacteroidota	<i>Bacteroides_B vulgatus</i>	3.08%	0.00 - 6.38%	Average

Your key insights

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

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

A

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

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

EVIDENCE RATING ★★★★★

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

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

Everyone's microbiome contains species that can break down protein into a variety of compounds, including some compounds that promote inflammation. Having a high proportion of these species may reflect an insufficient amount of 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 low level. 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 **lower than 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 support glucose regulation. 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 **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 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 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

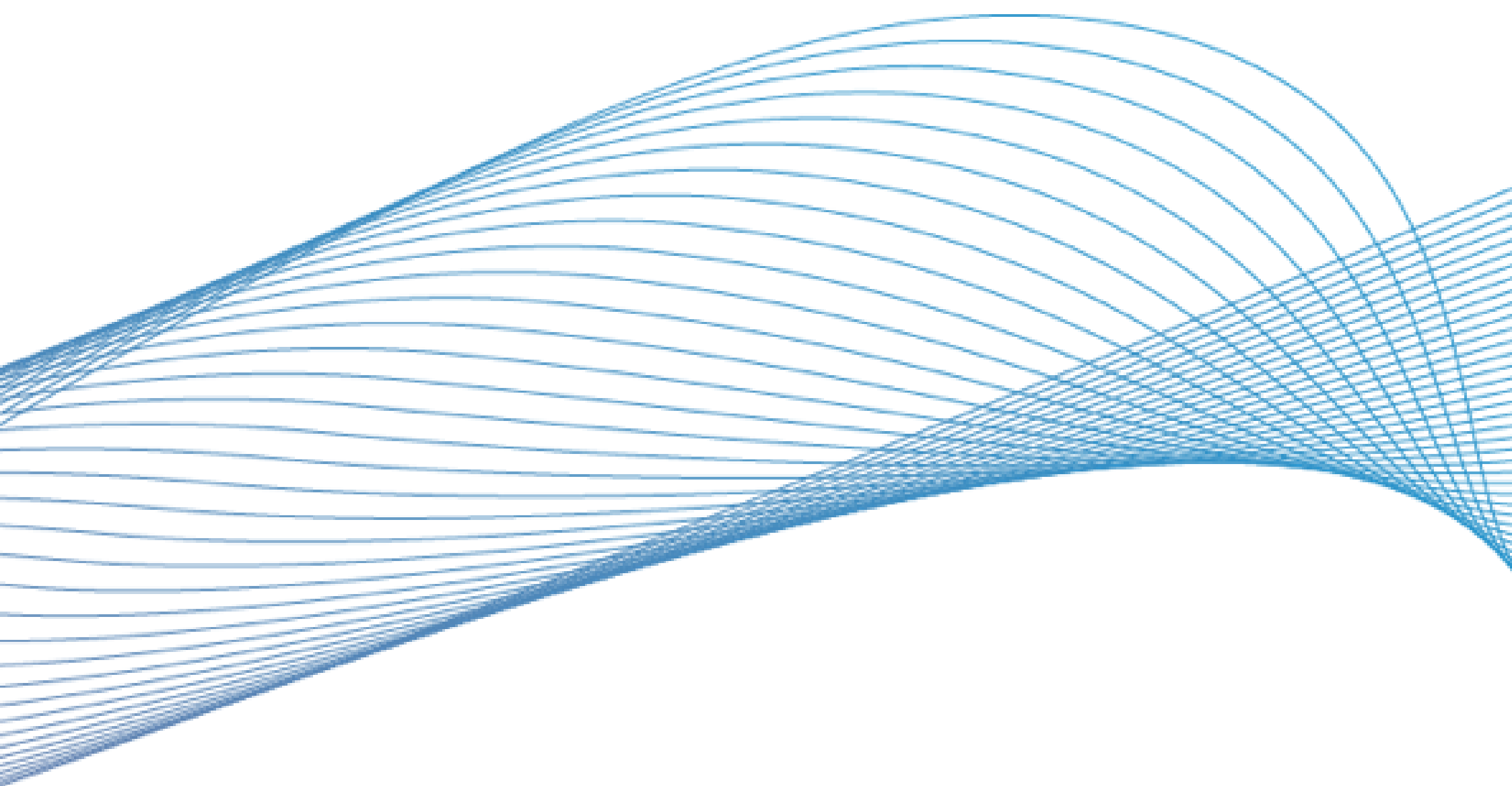
This sample reported a level **lower than the healthy group**

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.

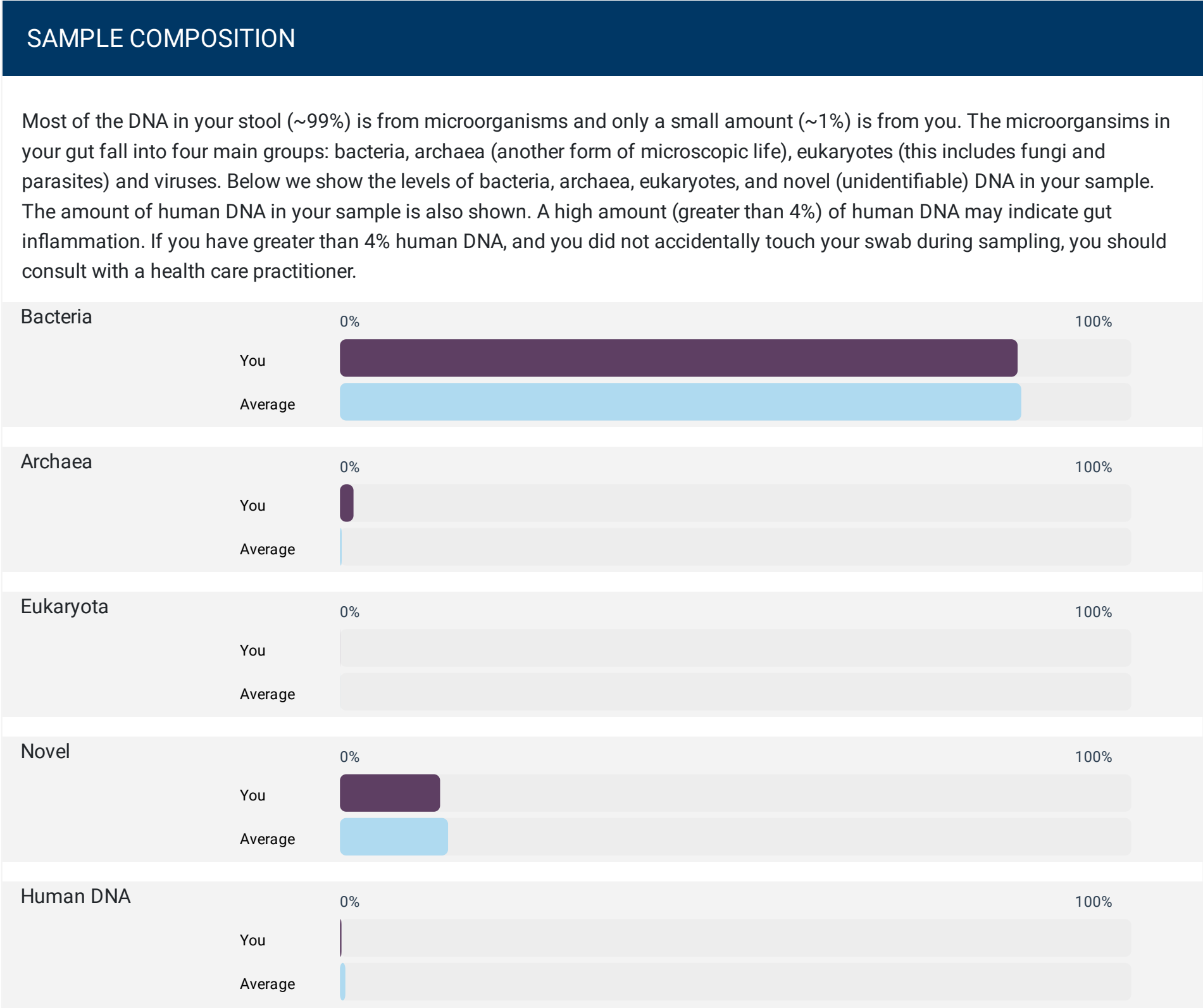
EVIDENCE RATING ★★☆☆☆

Digging deeper into the detail

Gut microbiome report



Sample Composition

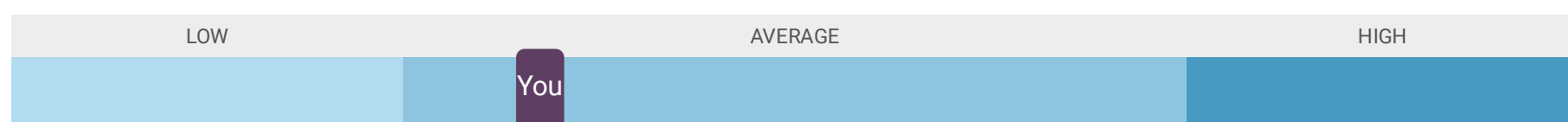


Microbiome Digestion Potential

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.

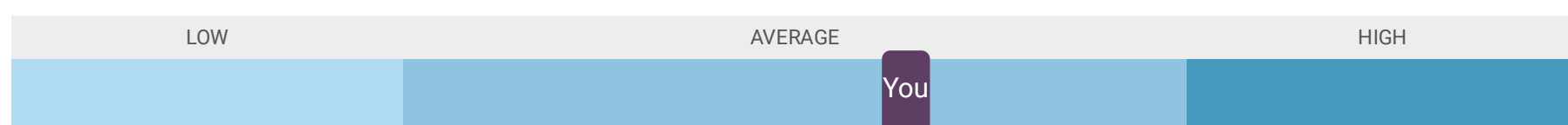
FIBRE

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.



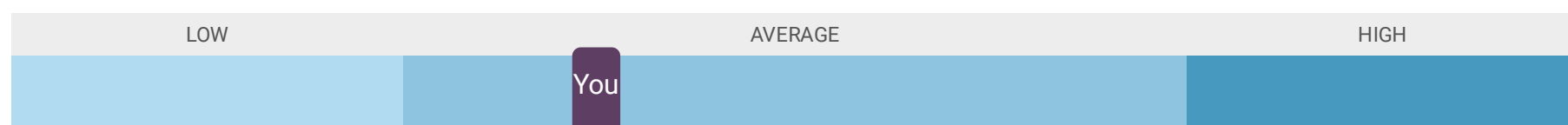
MUCIN

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

HEALTH INDICATORS

Produced

⊖

Ammonia (urease) production

4.52%

ND

LOW

AVERAGE

HIGH

You

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

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

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

⊖

B. fragilis toxin production

0.00%

ND

LOW

AVERAGE

HIGH

You

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

15.9%

ND

LOW

AVERAGE

HIGH

You

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

7.17%

ND

LOW

AVERAGE

HIGH

You

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 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

<i>Branched chain amino acids production</i>	39.1%	ND	LOW	AVERAGE	HIGH
			You		

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

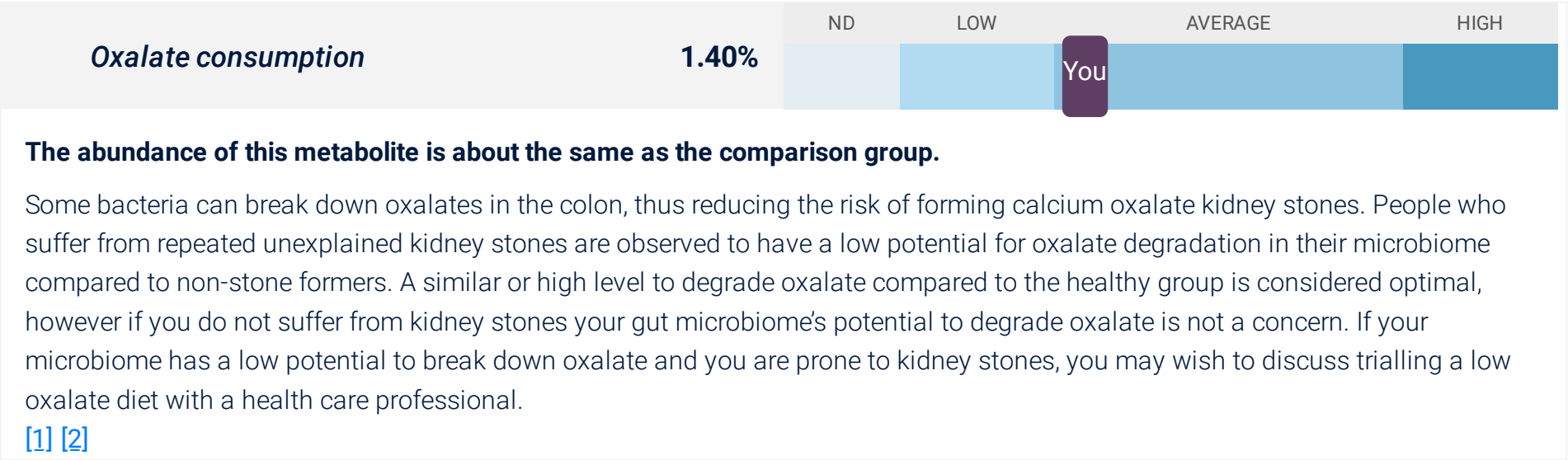
Branch chain amino acids (BCAAs) are involved in the regulation of glucose and fat metabolism and the immune system. High levels of BCAAs have been associated with metabolic diseases, such as obesity and poor glucose regulation. Muscle plays an important role in regulating BCAA levels. A high potential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



Produced



[1] [2] [3]



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

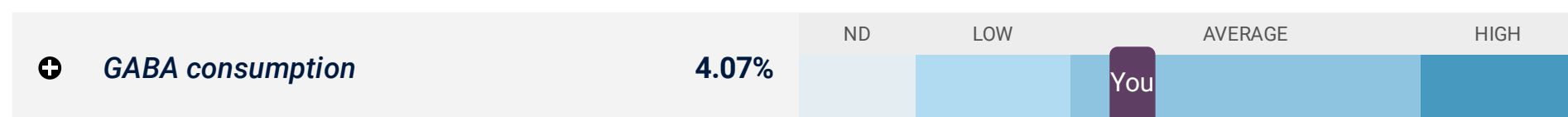


[1] [2] [3]

Microbial Metabolites

NEUROENDOCRINE

Consumed

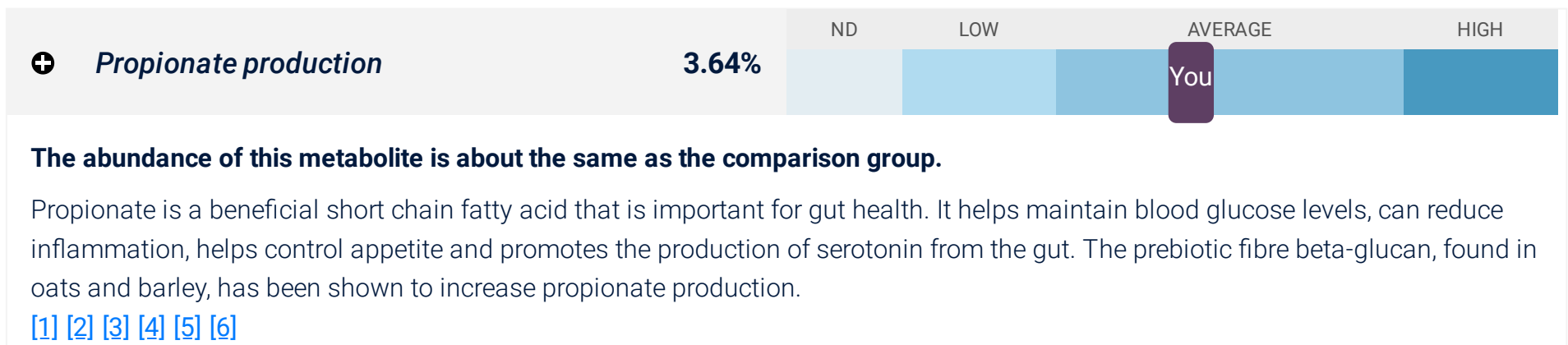


The abundance of this metabolite is about the same as the comparison group.

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

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

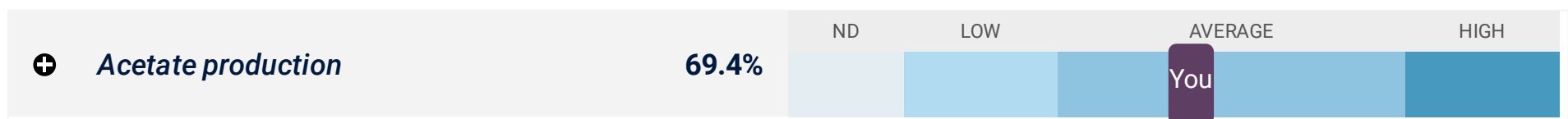
Produced



Microbial Metabolites

SHORT CHAIN FATTY ACIDS

Produced



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 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]

Produced



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 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]



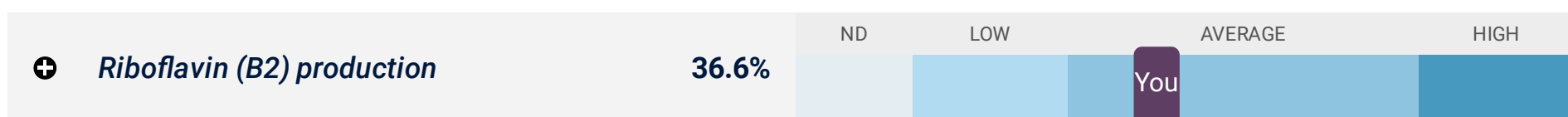
Biotin plays a critical role in metabolism and in the regulation of the immune system. Biotin cannot be produced by human cells and must be obtained through diet or the microbiome. The large intestine has the ability to absorb biotin but it is estimated that the gut microbiome can only provide up to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

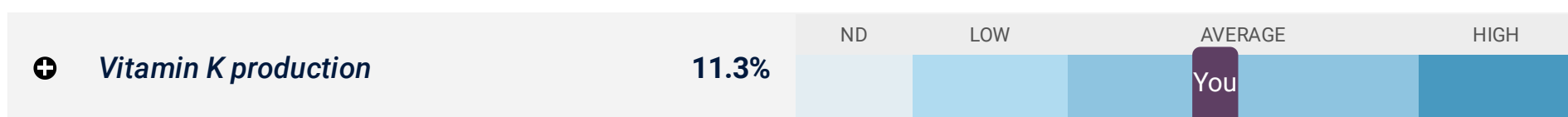
Produced



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

BACTERIA (PROKARYOTES)

Agathobacter

DETECTED



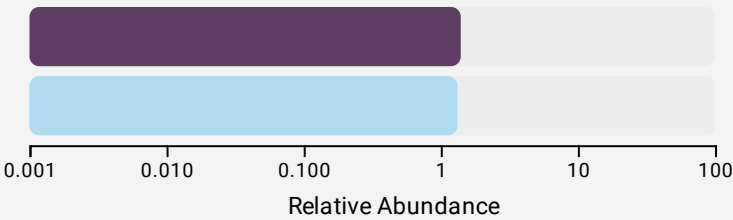
Agathobacter faecis

You

1.47%

Average

1.39%



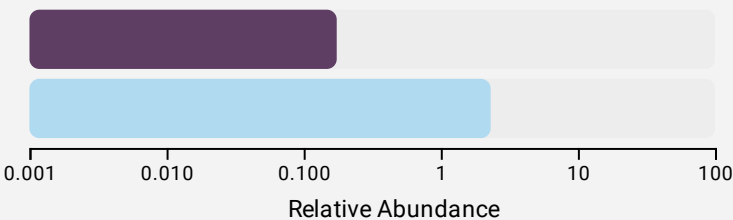
Agathobacter rectale

You

0.180%

Average

2.43%



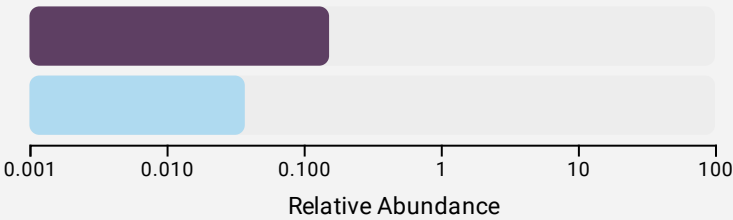
Agathobacter
sp000434275

You

0.158%

Average

0.038%



Akkermansia

DETECTED



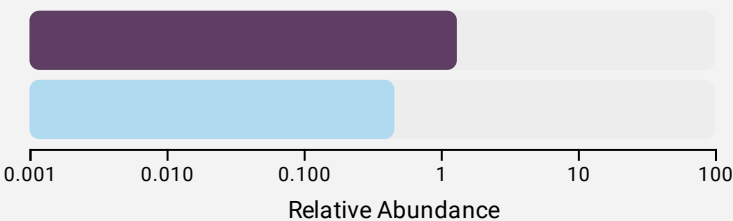
Akkermansia muciniphila

You

1.37%

Average

0.477%



Bifidobacterium

DETECTED



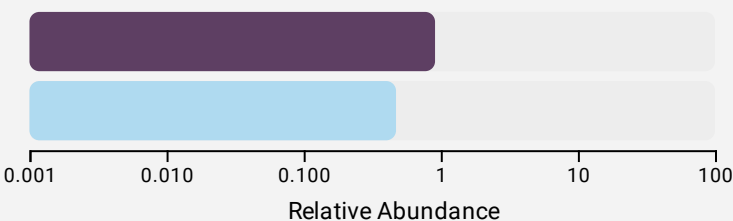
Bifidobacterium longum

You

0.950%

Average

0.491%



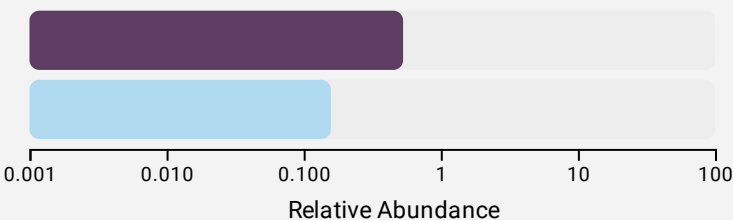
Bifidobacterium
pseudocatenulatum

You

0.553%

Average

0.163%





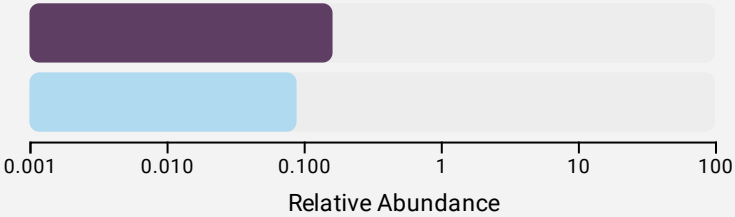
Bifidobacterium bifidum

You

0.168%

Average

0.091%



Bilophila

DETECTED



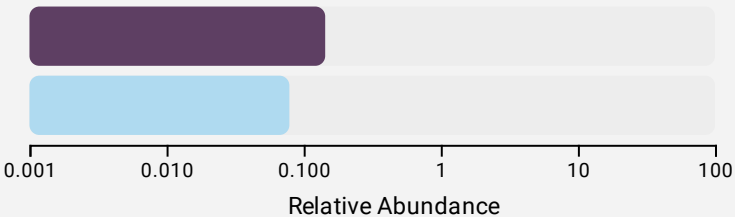
Bilophila wadsworthia

You

0.148%

Average

0.081%



Campylobacter

NOT DETECTED

Citrobacter

NOT DETECTED

Clostridioides

NOT DETECTED

Clostridium

DETECTED

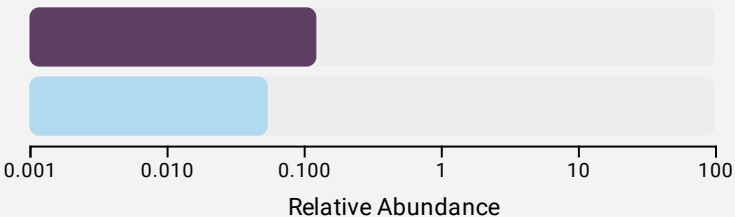
Clostridium
sp000435835

You

0.128%

Average

0.056%



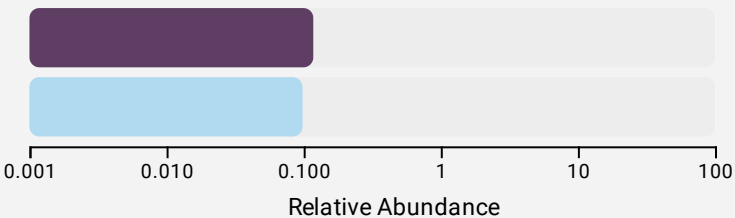
Clostridium MIC8163

You

0.121%

Average

0.101%



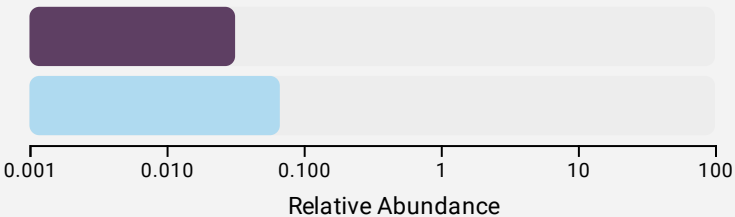
Clostridium saudiense

You

0.032%

Average

0.069%



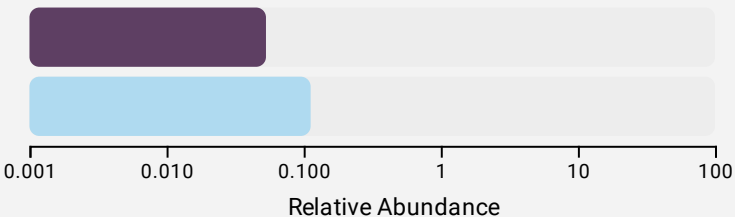
Clostridium_Q
sp003024715

You

0.054%

Average

0.116%



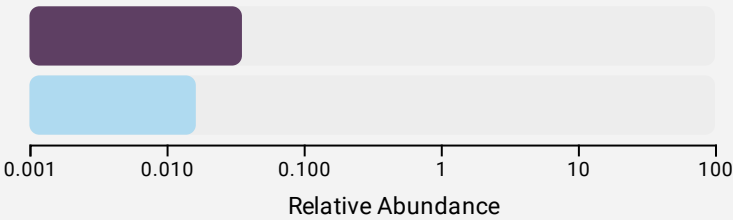
Corynebacterium

DETECTED

Corynebacterium
sp000755185

You
Average

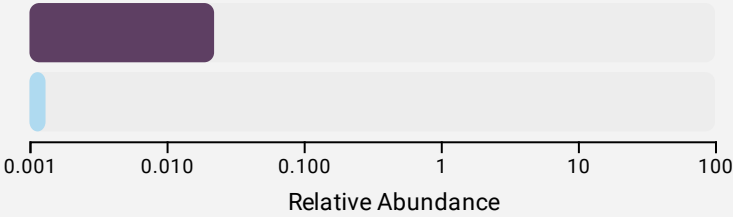
0.036%
0.017%



Corynebacterium
sp001767255

You
Average

0.023%
0.001%



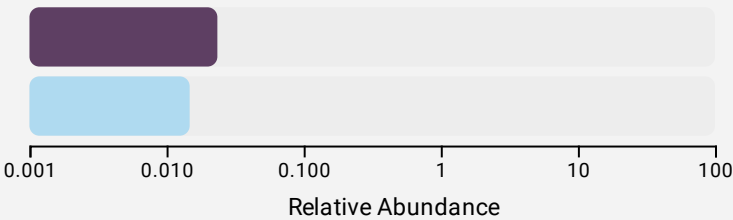
Desulfovibrio

DETECTED

Desulfovibrio
fairfieldensis

You
Average

0.024%
0.015%



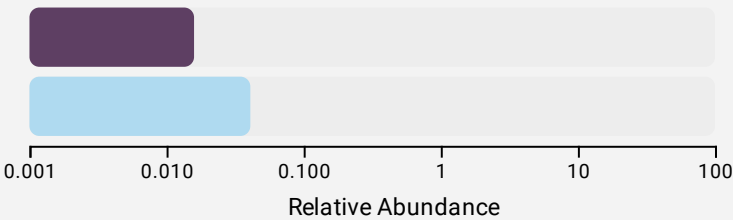
Eggerthella

DETECTED

● *Eggerthella lenta*

You
Average

0.016%
0.042%



Enterobacter

NOT DETECTED

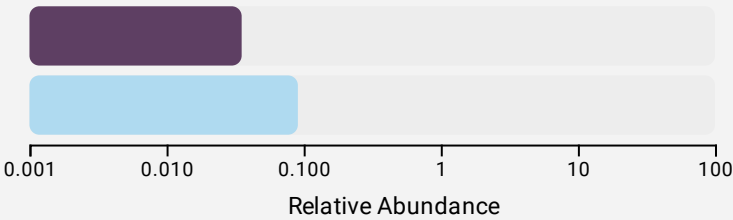
Escherichia

DETECTED

● *Escherichia coli*

You
Average

0.036%
0.093%



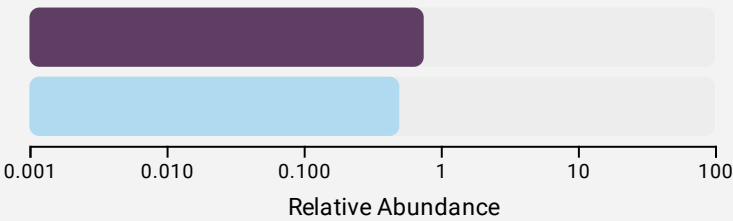
Faecalibacterium

DETECTED

Faecalibacterium
prausnitzii_J

You
Average

0.784%
0.519%



Faecalibacterium

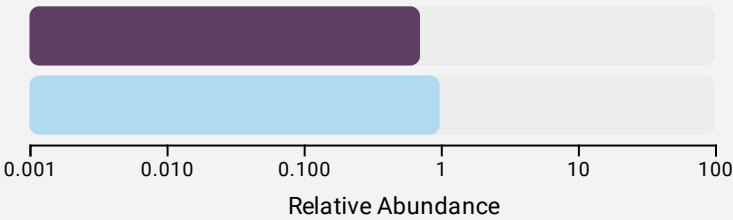
prausnitzii_G

You

Average

0.737%

1.03%



+

Faecalibacterium

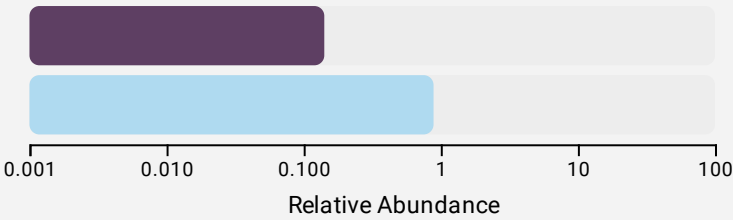
prausnitzii_C

You

Average

0.146%

0.926%



Faecalibacterium

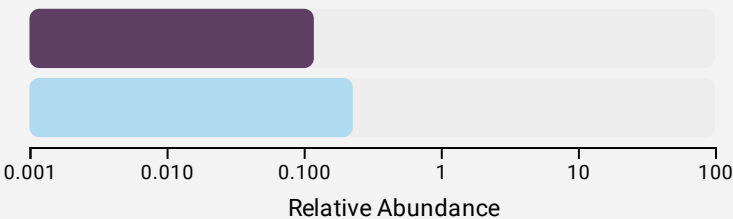
prausnitzii_I

You

Average

0.122%

0.236%



Faecalibacterium

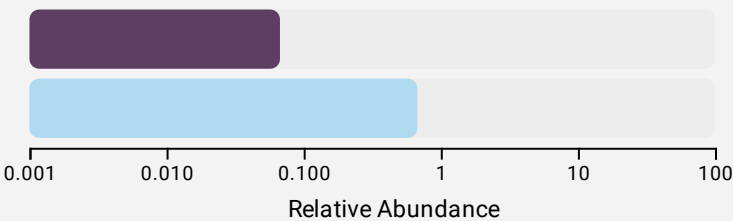
prausnitzii_D

You

Average

0.069%

0.705%



Faecalibacterium

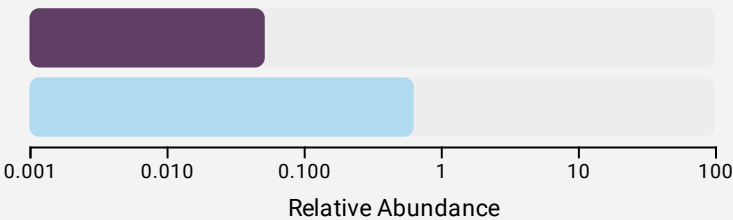
MIC7145

You

Average

0.053%

0.662%



Faecalibacterium

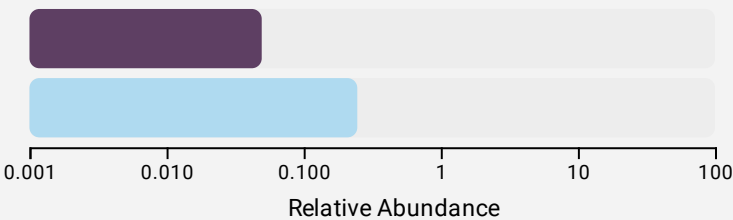
MIC9210

You

Average

0.051%

0.255%



Faecalibacterium

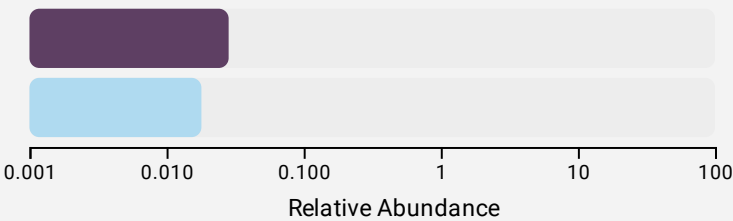
MIC8693

You

Average

0.029%

0.018%



Fusobacterium

NOT DETECTED

Helicobacter

NOT DETECTED

Klebsiella

NOT DETECTED

Lactobacillus

NOT DETECTED

Oxalobacter

NOT DETECTED

Porphyromonas

NOT DETECTED

Prevotella

NOT DETECTED

Roseburia

DETECTED



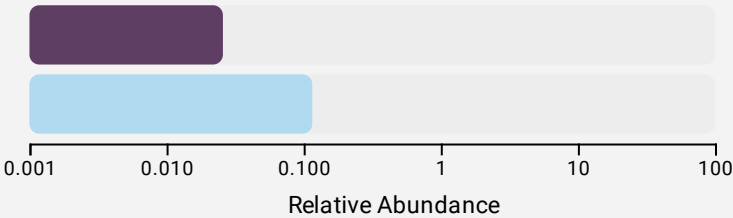
Roseburia hominis

You

0.026%

Average

0.119%



Ruminococcus

DETECTED

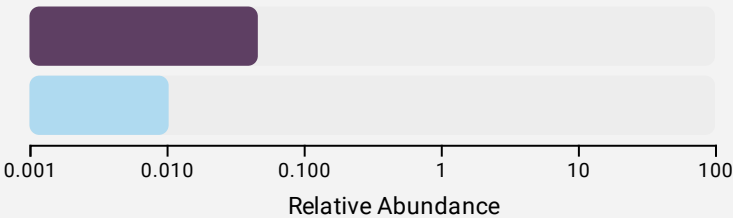
Ruminococcus_C
MIC7726

You

0.047%

Average

0.011%



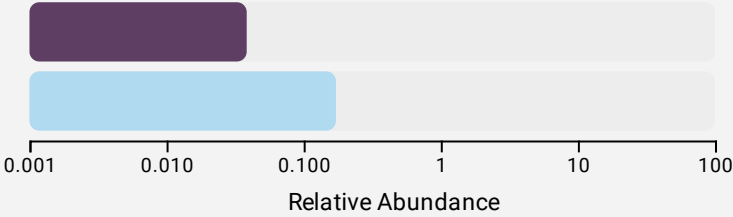
Ruminococcus_C
callidus

You

0.039%

Average

0.178%



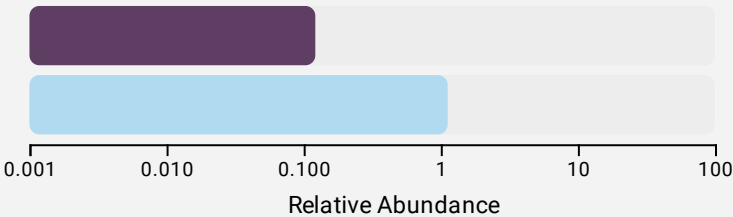
Ruminococcus_D
bicirculans

You

0.125%

Average

1.18%



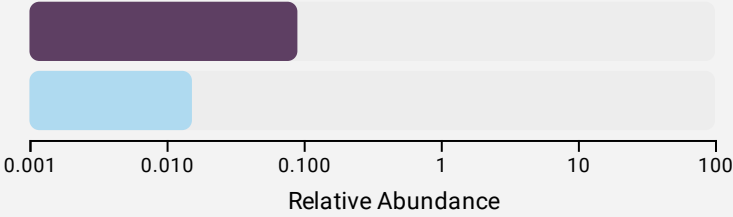
Ruminococcus_F
champanellensis

You

0.093%

Average

0.016%



Salmonella

NOT DETECTED

Streptococcus

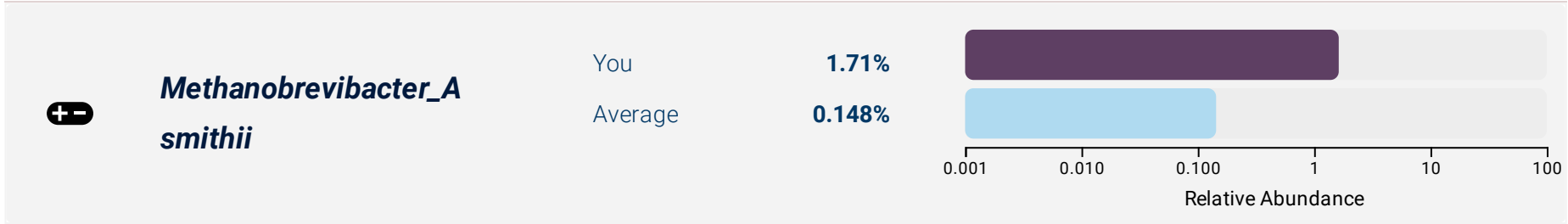
NOT DETECTED

Species of Interest

ARCHAEA (PROKARYOTES)

Methanogens

DETECTED



Other Archea

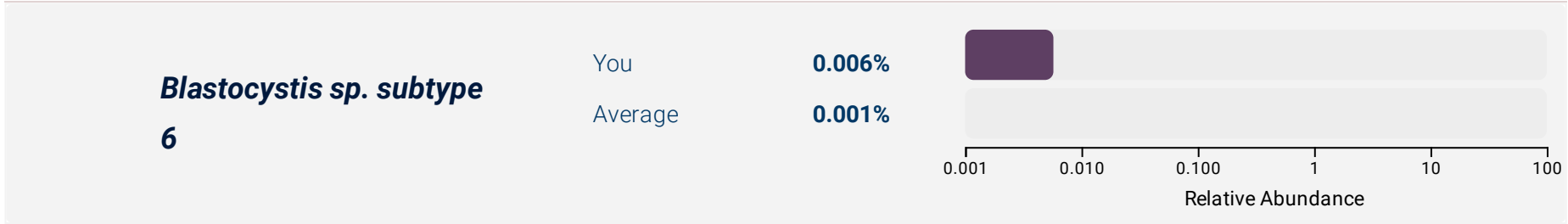
NOT DETECTED

Species of Interest

YEASTS/FUNGI & PROTISTS (EUKARYOTES)

Blastocystis

DETECTED



Candida

NOT DETECTED

Saccharomyces

NOT DETECTED

Other Eukaryotes

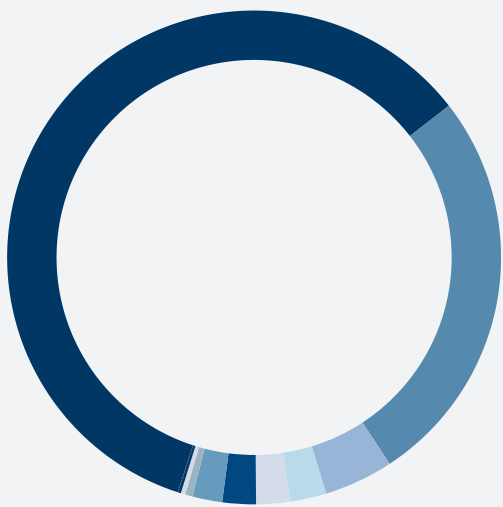
NOT DETECTED

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	51.9%	41.8 - 73.1%	Average
Bacteroidota	23.0%	10.4 - 26.4%	Average
Firmicutes	3.96%	0.741 - 9.75%	Average
Actinobacteriota	2.07%	1.03 - 7.36%	Average
Proteobacteria	1.94%	0.315 - 3.02%	Average
Verrucomicrobiota	1.92%	0.00 - 1.77%	High
Euryarchaeota	1.71%	0.00 - 0.717%	High
Firmicutes_C	0.419%	0.271 - 1.38%	Average
Cyanobacteria	0.257%	0.00 - 0.971%	Average
Desulfobacterota_A	0.172%	0.020 - 0.385%	Average
Eukaryote_unclassified	0.006%	0.00 - 0.00%	High

Species Profile

SPECIES

Phylum	Species	Abundance	Range	Level
Firmicutes_A	CAG-349 sp003539515	15.2%	0.00 - 0.074%	High
<p>Fuel Sources Used: This species is a poor degrader of fibre, a poor 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.</p> <p>Metabolites consumed: In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.</p> <p>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.</p>				
Bacteroidota	Alistipes obesi	3.72%	0.00 - 0.430%	High
<p>This is a recently discovered inhabitant of the human gut.</p> <p>Fuel Sources Used: This species is a moderate degrader of fibre, mucin, and protein.</p> <p>Metabolites produced: Our genomic analysis indicates that most members of this species can produce the following metabolites: branched chain amino acids, folate (B9), GABA, lactate, riboflavin (B2), vitamin K.</p> <p>Metabolites consumed: In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.</p> <p>Emerging Research: Reduced levels of this species were observed in individuals with poor intestinal health.</p>				

Species Profile

SPECIES

Phylum	Species	Abundance	Range	Level
Firmicutes_A	<i>GCA-900066995 sp900291955</i>	3.60%	0.00 - 0.00%	High
<p>Fuel Sources Used: This species is a poor degrader of fibre, a poor 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, branched chain amino acids, lactate, riboflavin (B2).</p> <p>Metabolites consumed: In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.</p> <p>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.</p>				
Bacteroidota	<i>UBA7173 MIC9174</i>	3.20%	0.00 - 0.00%	High
<p>Fuel Sources Used: This species is a moderate degrader of fibre, a poor 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), folate (B9), lactate, riboflavin (B2).</p> <p>Metabolites consumed: In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.</p> <p>Emerging Research: This is a newly defined species in the Microba database.</p>				

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
⊖	Bacteroidota	<i>Bacteroides_B vulgatus</i>	3.08%	0.00 - 6.38%	Average
<p>This is one of the most common inhabitants of the human gut.</p> <p>Fuel Sources Used: This species is a good 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 bacteria have been associated with a wide range of poor health conditions. This species has been associated with a diet high in red meat.</p>					
⊕	Bacteroidota	<i>Alistipes shahii</i>	2.96%	0.00 - 0.523%	High
<p>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: beta-glucuronidase, branched chain amino acids, folate (B9), GABA, lactate, riboflavin (B2).</p> <p>Metabolites consumed: In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.</p> <p>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.</p>					


Species Profile

SPECIES

Phylum	Species	Abundance	Range	Level
Firmicutes_A	<i>CAG-103 sp000432375</i>	2.32%	0.00 - 0.635%	High
<p>Fuel Sources Used: This species is a poor degrader of fibre, a poor 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, folate (B9).</p> <p>Metabolites consumed: In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.</p> <p>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.</p>				
⊕ Firmicutes_A	<i>Fusicatenibacter saccharivorans</i>	1.95%	0.518 - 7.34%	Average
<p>This is a recently discovered species and an inhabitant of the human gut.</p> <p>Fuel Sources Used: This species is a moderate degrader of fibre, mucin, and protein.</p> <p>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.</p> <p>Metabolites consumed: In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.</p> <p>Emerging Research: Lower levels of this species were observed in people with poor intestinal health.</p>				


Species Profile

SPECIES

Phylum	Species	Abundance	Range	Level
Firmicutes_A	<i>UBA11524 sp000437595</i>	1.83%	0.00 - 2.87%	Average
<p>Fuel Sources Used: This species is a moderate degrader of fibre, a poor 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, beta-glucuronidase, branched chain amino acids.</p> <p>Metabolites consumed: In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.</p> <p>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.</p>				
 Bacteroidota	<i>Bacteroides cellulosilyticus</i>	1.72%	0.00 - 0.987%	High
<p>This is a common gut inhabitant.</p> <p>Fuel Sources Used: This species is a good 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, beta-glucuronidase, biotin (B7), branched chain amino acids, folate (B9), GABA, lactate, riboflavin (B2).</p> <p>Metabolites consumed: In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.</p> <p>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.</p>				

Species Profile

SPECIES

Phylum	Species	Abundance	Range	Level
 Euryarchaeota	<i>Methanobrevibacter_A smithii</i>	1.71%	0.00 - 0.583%	High
<p>This is a single celled organism belonging to the Archaea domain and is the most common archaeal species found in the human gut.</p> <p>Fuel Sources Used: This species is a poor degrader of fibre, a poor 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, branched chain amino acids, histamine, methane.</p> <p>Metabolites consumed: In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.</p> <p>Emerging Research: Higher levels of <i>M. smithii</i> have been observed with constipation, diverticulosis, and other conditions. However, lower levels have been observed in patients with poor intestinal health. <i>M. smithii</i> plays an important role in the gut because it is one of the few species that can remove excess hydrogen.</p>				
Firmicutes_A	<i>Phil1 sp001940855</i>	1.60%	0.00 - 0.369%	High

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
+	Firmicutes_A	<i>Agathobacter faecis</i>	1.47%	0.00 - 4.17%	Average
<p>Previously named <i>Roseburia faecis</i>. This is a common and important member of the human gut microbiome.</p> <p>Fuel Sources Used: This species is a moderate degrader of fibre, mucin, and protein.</p> <p>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).</p> <p>Metabolites consumed: In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.</p> <p>Emerging Research: This species is commonly associated with healthy people in research studies. Low levels of this bacterium have been observed in patients with poor liver health.</p>					
	Firmicutes_A	<i>UBA10281 MIC9325</i>	1.39%	0.00 - 0.00%	High

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
+ -	Verrucomicrobiot	<i>Akkermansia muciniphila</i>	1.37%	0.00 - 1.19%	High
	a				

This species is associated with a healthy metabolic status and it is being investigated as a probiotic to treat obesity, diabetes and other related metabolic disorders.

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: 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:

By living in the mucus layer, *A. muciniphila* prevents potentially harmful bacteria from colonising this space through competition. Studies have observed low levels of *A. muciniphila* in patients with poor intestinal health, poor glucose regulation, and poor weight management, indicating it plays a beneficial role in metabolism. Research has also indicated this species can improve the efficacy of an immunotherapy medicine called PD-1 inhibitors. Levels of this bacterium tend to decrease with age. Although this bacterium appears to have mostly beneficial effects, studies have shown it is elevated in patients with some neurodegenerative health conditions.

	Firmicutes_A	<i>Blautia_A wexlerae</i>	1.35%	0.344 - 6.60%	Average
	Firmicutes_A	<i>CAG-552 MIC9340</i>	1.12%	0.00 - 0.00%	High
	Proteobacteria	<i>CAG-495 sp000432275</i>	1.11%	0.00 - 0.216%	High
	Bacteroidota	<i>Bacteroides MIC7573</i>	1.02%	0.00 - 0.00%	High
	Firmicutes_A	<i>CAG-138 MIC9630</i>	1.00%	0.00 - 0.479%	High

Species Profile

SPECIES

Phylum	Species	Abundance	Range	Level
 Bacteroidota	<i>Alistipes putredinis</i>	0.983%	0.00 - 2.61%	Average
<p>This is a common inhabitant of the gut microbiome.</p> <p>Fuel Sources Used: This species is a poor degrader of fibre, a poor 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: butyrate, folate (B9), GABA, lactate, riboflavin (B2), vitamin K.</p> <p>Metabolites consumed: In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.</p> <p>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.</p>				
Firmicutes	<i>CAG-288 sp000437395</i>	0.963%	0.00 - 0.203%	High
Firmicutes	<i>CAG-307 sp001916215</i>	0.956%	0.00 - 0.454%	High


Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
+	Actinobacteriota	<i>Bifidobacterium longum</i>	0.950%	0.00 - 1.47%	Average
<p>This is a beneficial inhabitant of the gut in adults and a popular probiotic.</p> <p>Fuel Sources Used: This species is a moderate degrader of fibre, a poor 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, branched chain amino acids, folate (B9), lactate.</p> <p>Metabolites consumed: In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.</p> <p>Emerging Research: <i>B.longum</i> has been associated with reductions in harmful bacteria, anti-allergy effects, and anti-obesity effects in mouse models, but further research still needs to be done in humans.</p>					
	Bacteroidota	<i>Bacteroides stercoris</i>	0.829%	0.00 - 2.66%	Average

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
	Bacteroidota	<i>Bacteroides uniformis</i>	0.820%	0.136 - 4.89%	Average
<p>This is one of the most common inhabitants of the human gut.</p> <p>Fuel Sources Used: This species is a good 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, beta-glucuronidase, biotin (B7), branched chain amino acids, folate (B9), GABA, lactate, riboflavin (B2).</p> <p>Metabolites consumed: In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.</p> <p>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.</p>					
	Firmicutes_A	<i>Faecalibacterium prausnitzii_J</i>	0.784%	0.00 - 1.65%	Average
	Firmicutes_A	<i>CAG-170 sp002404795</i>	0.777%	0.00 - 0.301%	High
	Firmicutes_A	<i>Gemmiger sp003476825</i>	0.771%	0.00 - 2.86%	Average


Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
+	Firmicutes_A	<i>Anaerostipes hadrus</i>	0.743%	0.294 - 5.33%	Average
<p>Formerly known as <i>Eubacterium hadrum</i>. This is a common inhabitant of the human gut.</p> <p>Fuel Sources Used: This species is a moderate degrader of fibre, a poor 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, branched chain amino acids, butyrate, folate (B9), hydrogen sulphide, lactate, riboflavin (B2).</p> <p>Metabolites consumed: In addition, the genomic analysis shows that most members of this species can consume: oxalate.</p>					
	Firmicutes_A	<i>Faecalibacterium prausnitzii_G</i>	0.737%	0.00 - 2.39%	Average
	Firmicutes_A	<i>CAG-110 sp000434635</i>	0.735%	0.00 - 0.560%	High
	Firmicutes_A	<i>CAG-83 sp000435555</i>	0.734%	0.00 - 1.33%	Average
	Firmicutes_A	<i>Blautia_A sp900066165</i>	0.671%	0.193 - 2.41%	Average

Species Profile

SPECIES

Phylum	Species	Abundance	Range	Level
 Bacteroidota	<i>Bacteroides_B massiliensis</i>	0.671%	0.00 - 1.39%	Average
<p>This is a normal inhabitant of the human gut microbiome.</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 indicates that most members of this species do not consume any reported metabolites.</p> <p>Emerging Research: Higher levels of this species have been observed in individuals with poor intestinal health. This species has also been associated with a diet high in red meat.</p>				
Firmicutes_A	<i>CAG-273 sp003534295</i>	0.666%	0.00 - 0.272%	High
Bacteroidota	<i>Alistipes_A sp900240235</i>	0.628%	0.00 - 0.069%	High
Firmicutes_A	<i>CAG-83 MIC8701</i>	0.619%	0.00 - 0.089%	High

Species Profile

SPECIES

Phylum	Species	Abundance	Range	Level	
+	Actinobacteriota	<i>Bifidobacterium pseudocatenulatum</i>	0.553%	0.00 - 0.250%	High
<p>This is a beneficial bacterial species found in the human gut.</p> <p>Fuel Sources Used: This species is a moderate degrader of fibre, mucin, and protein.</p> <p>Metabolites produced: Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, folate (B9), lactate.</p> <p>Metabolites consumed: In addition, the genomic analysis shows that most members of this species can consume: oxalate.</p> <p>Emerging Research: This species has been observed at lower levels in people with poor glucose regulation and gout. It has also has been associated with a protective effect on the liver and anti-obesity effects in mouse models, but further research still needs to be done in humans.</p>					
	Firmicutes_A	<i>CAG-103 MIC7540</i>	0.548%	0.00 - 0.418%	High
	Firmicutes_A	<i>Gemmiger formicilis</i>	0.496%	0.00 - 2.51%	Average
	Firmicutes_A	<i>Romboutsia timonensis</i>	0.461%	0.00 - 0.642%	Average
	Firmicutes	<i>CAG-313 sp003539625</i>	0.442%	0.00 - 0.410%	High
	Firmicutes_A	<i>CAG-353 sp900066885</i>	0.422%	0.00 - 0.128%	High
	Firmicutes_A	<i>F23-B02 sp001916715</i>	0.422%	0.00 - 0.510%	Average

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
	Firmicutes_C	<i>Phascolarctobacterium faecium</i>	0.419%	0.00 - 0.443%	Average
	Firmicutes	<i>CAG-302 sp001916775</i>	0.416%	0.00 - 0.282%	High
	Firmicutes_A	<i>Eubacterium_R sp000434995</i>	0.408%	0.00 - 0.700%	Average
	Bacteroidota	<i>Barnesiella intestinihominis</i>	0.392%	0.00 - 0.743%	Average
	Firmicutes_A	<i>UBA738 sp003522945</i>	0.386%	0.00 - 0.163%	High
⊖	Bacteroidota	<i>Paraprevotella clara</i>	0.386%	0.00 - 0.326%	High

This is a recently discovered bacterial species and a common inhabitant 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, biotin (B7), branched chain amino acids, folate (B9), 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:

Higher levels of this species have been observed in people with poor intestinal health.

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
⊖	Bacteroidota	<i>Parabacteroides merdae</i>	0.385%	0.00 - 0.482%	Average
<p>Formerly known as <i>Bacteroides merdae</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, beta-glucuronidase, 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 individuals with elevated blood pressure, and poor intestinal health. This species has been associated with a diet low in fruits and vegetables.</p>					
	Verrucomicrobiota	<i>UBA1829 MIC8218</i>	0.382%	0.00 - 0.00%	High
	Proteobacteria	<i>Sutterella wadsworthensis_B</i>	0.381%	0.00 - 0.720%	Average
	Firmicutes_A	<i>Oscillibacter sp001916835</i>	0.360%	0.00 - 0.377%	Average
	Firmicutes_A	<i>Acutalibacteraceae MIC9692</i>	0.334%	0.00 - 0.00%	High
	Bacteroidota	<i>Alistipes_A ihumii</i>	0.316%	0.00 - 0.088%	High
	Bacteroidota	<i>Alistipes onderdonkii</i>	0.309%	0.00 - 0.680%	Average

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
	Firmicutes	<i>CAG-345 sp000433315</i>	0.301%	0.00 - 0.064%	High
	Proteobacteria	<i>CAG-495 sp001917125</i>	0.294%	0.00 - 0.158%	High
	Firmicutes_A	<i>ER4 sp900317525</i>	0.266%	0.00 - 0.375%	Average
●	Bacteroidota	<i>Parabacteroides distasonis</i>	0.264%	0.00 - 0.516%	Average

Formerly known as *Bacteroides distasonis*, 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, 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 with poor glucose regulation during pregnancy.

	Firmicutes	<i>CAG-460 sp000437355</i>	0.247%	0.00 - 0.00%	High
	Firmicutes_A	<i>QALS01 sp003150575</i>	0.236%	0.00 - 0.077%	High
	Firmicutes_A	<i>PeH17 sp000435055</i>	0.232%	0.00 - 0.834%	Average

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
	Firmicutes_A	<i>KLE1615 sp900066985</i>	0.226%	0.172 - 2.22%	Average
	Firmicutes	<i>CAG-533 sp000434495</i>	0.210%	0.00 - 0.133%	High
	Cyanobacteria	<i>Zag111 sp002102825</i>	0.209%	0.00 - 0.00%	High
	Firmicutes_A	<i>CAG-170 sp000432135</i>	0.200%	0.00 - 0.637%	Average
	Firmicutes_A	<i>CAG-83 MIC7830</i>	0.193%	0.00 - 0.082%	High
⊖	Bacteroidota	<i>Bacteroides ovatus</i>	0.185%	0.00 - 0.791%	Average

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

Fuel Sources Used:

This species is a good degrader of fibre, a good degrader of mucin, and a moderate degrader of protein.

Metabolites produced:

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

Metabolites consumed:

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

Emerging Research:

Higher levels of this species have been associated with poor glucose regulation in children and poor intestinal health in adults.

	Actinobacteriota	<i>Collinsella sp002232035</i>	0.185%	0.00 - 0.229%	Average
--	------------------	--------------------------------	--------	---------------	---------

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
	Firmicutes_A	<i>CAG-110 sp003525905</i>	0.185%	0.00 - 0.331%	Average
+	Firmicutes_A	<i>Agathobacter rectale</i>	0.180%	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.

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
⊖	Bacteroidota	<i>Alistipes finegoldii</i>	0.172%	0.00 - 0.450%	Average
<p>This is a common inhabitant of the gut microbiome.</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: ammonia (urease), branched chain amino acids, folate (B9), GABA, lactate, riboflavin (B2), vitamin K.</p> <p>Metabolites consumed: In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.</p> <p>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.</p>					
⊕	Actinobacteriota	<i>Bifidobacterium bifidum</i>	0.168%	0.00 - 0.00%	High
<p>This is a naturally occurring human gut bacterium and a probiotic. This is one of the first colonisers of the human gut, and is important in the development of the infant immune system.</p> <p>Fuel Sources Used: This species is a moderate degrader of fibre, mucin, and protein.</p> <p>Metabolites produced: Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, folate (B9), lactate.</p> <p>Metabolites consumed: In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.</p>					

Species Profile

SPECIES

Phylum	Species	Abundance	Range	Level
Firmicutes_A	<i>Terrisporobacter MIC9205</i>	0.162%	0.00 - 0.288%	Average
Firmicutes_A	<i>4C28d-15 MIC7065</i>	0.162%	0.00 - 0.010%	High
Firmicutes_A	<i>CAG-83 sp001916855</i>	0.161%	0.00 - 0.574%	Average
Firmicutes_A	<i>Agathobacter sp000434275</i>	0.158%	0.00 - 0.043%	High
Firmicutes	<i>RUG131 MIC9218</i>	0.157%	0.00 - 0.00%	High
Firmicutes_A	<i>GCA-900066135 MIC6659</i>	0.156%	0.00 - 0.247%	Average
Firmicutes	<i>CAG-313 sp000433035</i>	0.156%	0.00 - 0.229%	Average
Firmicutes_A	<i>UBA7597 MIC7484</i>	0.152%	0.00 - 0.060%	High

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
⊖	Desulfobacterota_	<i>Bilophila wadsworthia</i>	0.148%	0.00 - 0.200%	Average
	A				
<p>This is a common inhabitant of the human gut, but can become problematic at high levels.</p> <p>Fuel Sources Used: This species is a poor degrader of fibre, a poor 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, ammonia (urease), branched chain amino acids, hydrogen sulphide, lactate, riboflavin (B2), trimethylamine.</p> <p>Metabolites consumed: In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.</p> <p>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.</p>					
⊕	Bacteroidota	<i>Odoribacter splanchnicus</i>	0.146%	0.023 - 0.253%	Average
<p>Formerly known as <i>Bacteroides splanchnicus</i>. This 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, ammonia (urease), biotin (B7), branched chain amino acids, butyrate, 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: 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.</p>					

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
+	Firmicutes_A	<i>Faecalibacterium prausnitzii_C</i>	0.146%	0.00 - 2.02%	Average
<p><i>Faecalibacterium prausnitzii_C</i> (aka strain A2-165) is an important member of the human gut microbiome.</p> <p>Fuel Sources Used: This species is a moderate degrader of fibre, a poor 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, beta-glucuronidase, branched chain amino acids.</p> <p>Metabolites consumed: In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.</p> <p>Emerging Research: Low levels of <i>F. prausnitzii</i> have been linked to a range of poor health conditions, including intestinal, metabolic, and mental health.</p>					
	Bacteroidota	<i>Bacteroides thetaiotaomicron</i>	0.143%	0.00 - 0.465%	Average
	Firmicutes_A	<i>CAG-110 MIC8481</i>	0.143%	0.00 - 0.00%	High
	Firmicutes_A	<i>Acetatifactor sp900066565</i>	0.140%	0.00 - 1.29%	Average
	Firmicutes_A	<i>Intestinibacter bartlettii</i>	0.136%	0.00 - 0.254%	Average
	Verrucomicrobiota	<i>UBA11452 sp003526375</i>	0.132%	0.00 - 0.057%	High
	Firmicutes_A	<i>UBA644 MIC9235</i>	0.128%	0.00 - 0.015%	High

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
	Firmicutes_A	<i>Clostridium sp000435835</i>	0.128%	0.00 - 0.186%	Average
+	Firmicutes_A	<i>Coprococcus_B comes</i>	0.127%	0.086 - 0.813%	Average
<p>This is a common inhabitant of the human gut.</p> <p>Fuel Sources Used: This species is a moderate degrader of fibre, a poor 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, branched chain amino acids, butyrate, cobalamin (B12), folate (B9), lactate, riboflavin (B2), trimethylamine.</p> <p>Metabolites consumed: In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.</p> <p>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.</p>					
	Firmicutes_A	<i>Ruminococcus_D bicirculans</i>	0.125%	0.00 - 3.46%	Average

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
⊖	Bacteroidota	<i>Bacteroides caccae</i>	0.125%	0.00 - 0.482%	Average
<p>This is a common member 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, propionate, riboflavin (B2), vitamin K.</p> <p>Metabolites consumed: In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.</p> <p>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.</p>					
	Firmicutes_A	<i>Faecalibacterium prausnitzii_I</i>	0.122%	0.00 - 0.535%	Average
	Actinobacteriota	<i>QAMH01 MIC6543</i>	0.122%	0.00 - 0.147%	Average
	Firmicutes_A	<i>Faecalicatena faecis</i>	0.121%	0.00 - 1.35%	Average
	Firmicutes_A	<i>Clostridium MIC8163</i>	0.121%	0.00 - 0.305%	Average
	Firmicutes_A	<i>Ruminiclostridium_C MIC7261</i>	0.115%	0.00 - 0.198%	Average
	Firmicutes_A	<i>ER4 sp000765235</i>	0.108%	0.00 - 0.635%	Average

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
	Bacteroidota	<i>Bacteroides nordii</i>	0.106%	0.00 - 0.056%	High
	Firmicutes_A	<i>CAG-882 sp003486385</i>	0.104%	0.00 - 0.376%	Average
	Bacteroidota	<i>Odoribacter laneus</i>	0.102%	0.00 - 0.00%	High
	Firmicutes_A	<i>Oscillibacter MIC9361</i>	0.100%	0.00 - 0.016%	High
+	Firmicutes_A	<i>Eubacterium_E hallii</i>	0.095%	0.00 - 1.75%	Average

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.

	Bacteroidota	<i>Bacteroides finegoldii</i>	0.094%	0.00 - 0.271%	Average
	Firmicutes_A	<i>Eisenbergiella sp900066775</i>	0.094%	0.00 - 0.437%	Average

Species Profile

SPECIES

Phylum	Species	Abundance	Range	Level
Firmicutes_A	<i>Ruminococcus_F champanellensis</i>	0.093%	0.00 - 0.00%	High
Firmicutes_A	<i>Blautia_A massiliensis</i>	0.092%	0.00 - 1.83%	Average
Firmicutes_A	<i>Agathobaculum butyriciproducens</i>	0.091%	0.00 - 0.621%	Average
Firmicutes_A	<i>Lachnospira sp003451515</i>	0.085%	0.00 - 0.400%	Average
Firmicutes_A	<i>CAG-170 MIC8868</i>	0.081%	0.00 - 0.068%	High
Firmicutes_A	<i>CAG-272 MIC8971</i>	0.080%	0.00 - 0.036%	High
Firmicutes_A	<i>CAG-115 sp003531585</i>	0.079%	0.00 - 0.362%	Average
Firmicutes_A	<i>Monoglobaceae MIC9391</i>	0.076%	0.00 - 0.00%	High
Proteobacteria	<i>Parasutterella excrementihominis</i>	0.073%	0.00 - 0.389%	Average
Firmicutes_A	<i>CAG-452 sp000434035</i>	0.073%	0.00 - 0.00%	High
Firmicutes_A	<i>UBA11774 sp003507655</i>	0.073%	0.00 - 0.802%	Average
Firmicutes_A	<i>CAG-74 MIC7044</i>	0.073%	0.00 - 0.260%	Average
Firmicutes_A	<i>Faecalibacterium prausnitzii_D</i>	0.069%	0.00 - 1.72%	Average

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
	Firmicutes_A	<i>Intestinibacter MIC8174</i>	0.069%	0.00 - 0.051%	High
	Firmicutes_A	<i>Eubacterium_E hallii_A</i>	0.069%	0.00 - 0.687%	Average
	Firmicutes_A	<i>UBA1417 sp003531055</i>	0.068%	0.00 - 0.982%	Average
	Firmicutes_A	<i>CAG-177 sp003514385</i>	0.066%	0.00 - 0.619%	Average
	Firmicutes_A	<i>CAG-74 MIC9650</i>	0.065%	0.00 - 0.022%	High
	Firmicutes_A	<i>CAG-74 MIC6989</i>	0.062%	0.00 - 0.065%	Average
+	Firmicutes_A	<i>Dorea formicigenerans</i>	0.061%	0.107 - 0.418%	Low

Formerly known as *Eubacterium formicigenerans*. 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.

Species Profile

SPECIES

Phylum	Species	Abundance	Range	Level
Bacteroidota	<i>Bacteroides xylanisolvens</i>	0.060%	0.00 - 0.429%	Average
Firmicutes_A	<i>Ezakiella MIC8494</i>	0.060%	0.00 - 0.00%	High
Firmicutes_A	<i>CAG-272 MIC7215</i>	0.059%	0.00 - 0.075%	Average
Firmicutes	<i>CAG-460 MIC6729</i>	0.059%	0.00 - 0.00%	High
Firmicutes_A	<i>CAG-41 sp900066215</i>	0.056%	0.00 - 0.815%	Average
Firmicutes_A	<i>UBA1777 sp003150355</i>	0.056%	0.00 - 0.154%	Average
Firmicutes_A	<i>NK3B98 MIC8354</i>	0.056%	0.00 - 0.072%	Average
Firmicutes_A	<i>Clostridium_Q sp003024715</i>	0.054%	0.00 - 0.265%	Average
Firmicutes_A	<i>Faecalibacterium MIC7145</i>	0.053%	0.00 - 1.48%	Average
Firmicutes_A	<i>Blautia_A obeum</i>	0.052%	0.00 - 1.41%	Average
Firmicutes_A	<i>Faecalibacterium MIC9210</i>	0.051%	0.00 - 0.736%	Average
Firmicutes_A	<i>UBA7160 MIC9207</i>	0.050%	0.00 - 0.188%	Average
Firmicutes	<i>Erysipelatoclostridium sp000752095</i>	0.049%	0.00 - 1.02%	Average

Species Profile

SPECIES

Phylum	Species	Abundance	Range	Level
Proteobacteria	<i>51-20 sp001917175</i>	0.049%	0.00 - 0.466%	Average
Bacteroidota	<i>Parabacteroides goldsteinii</i>	0.049%	0.00 - 0.056%	Average
Cyanobacteria	<i>QAMI01 MIC7050</i>	0.048%	0.00 - 0.00%	High
Firmicutes_A	<i>Ruminococcus_C MIC7726</i>	0.047%	0.00 - 0.00%	High
Firmicutes_A	<i>UBA1191 sp900066305</i>	0.047%	0.00 - 0.022%	High
Firmicutes_A	<i>Lachnospira sp000436535</i>	0.047%	0.00 - 0.234%	Average
Bacteroidota	<i>Bacteroides bouchesdurhonensis</i>	0.044%	0.00 - 0.00%	High
Firmicutes_A	<i>UBA1191 MIC6696</i>	0.043%	0.00 - 0.133%	Average
Firmicutes_A	<i>Acutalibacteraceae MIC9774</i>	0.041%	0.00 - 0.00%	High

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
+	Firmicutes_A	<i>Dorea longicatena</i>	0.041%	0.00 - 1.76%	Average
<p>This is a common inhabitant of the human gut.</p> <p>Fuel Sources Used: This species is a moderate degrader of fibre, a poor 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, branched chain amino acids, cobalamin (B12), folate (B9), lactate, riboflavin (B2), trimethylamine.</p> <p>Metabolites consumed: In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.</p> <p>Emerging Research: Multiple studies have observed this species at higher levels in individuals with obesity compared 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.</p>					
	Firmicutes_A	<i>Acutalibacteraceae MIC6974</i>	0.040%	0.00 - 0.037%	High
	Firmicutes_A	<i>Ruminococcaceae MIC8405</i>	0.040%	0.00 - 0.00%	High
	Firmicutes_A	<i>CAG-170 sp003516765</i>	0.040%	0.00 - 0.087%	Average
	Firmicutes_A	<i>Blautia_A sp900066355</i>	0.040%	0.00 - 0.247%	Average

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
+	Firmicutes_A	<i>Ruminococcus_C callidus</i>	0.039%	0.00 - 0.696%	Average
<p>This is a common inhabitant of the human gut.</p> <p>Fuel Sources Used: This species is a moderate degrader of fibre, a poor 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, branched chain amino acids, cobalamin (B12), folate (B9), lactate, riboflavin (B2).</p> <p>Metabolites consumed: In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.</p> <p>Emerging Research: Lower levels of this species have been observed in individuals with poor intestinal health.</p>					
	Firmicutes_A	<i>Blautia_A sp900066505</i>	0.037%	0.00 - 0.092%	Average
	Actinobacteriota	<i>Corynebacterium sp000755185</i>	0.036%	0.00 - 0.00%	High
	Firmicutes_A	<i>Fenollaria timonensis</i>	0.036%	0.00 - 0.00%	High

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
⊖	Proteobacteria	<i>Escherichia coli</i>	0.036%	0.00 - 0.027%	High
<p>This species is a common inhabitant of the gut, although it is usually present at a low abundance compared to other gut microbiome species.</p> <p>Fuel Sources Used: This species is a moderate degrader of fibre, a poor 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, beta-glucuronidase, biotin (B7), branched chain amino acids, folate (B9), GABA, hexa-LPS, hydrogen sulphide, lactate, propionate, riboflavin (B2), vitamin K.</p> <p>Metabolites consumed: In addition, the genomic analysis shows that most members of this species can consume: GABA, oxalate.</p> <p>Emerging Research: This species encompasses a large number of strains with diverse properties; a few well-known strains are a common cause of poor intestinal health. However, most strains will not cause health problems. Studies have observed this species at higher levels in individuals with poor intestinal and liver health. Additionally, a recent study identified several strains from this species can produce a toxin called colibactin which can lead to inflammation and damage DNA in human cells.</p>					
	Firmicutes_A	<i>Anaerococcus prevotii_A</i>	0.034%	0.00 - 0.00%	High
	Firmicutes_A	<i>Intestinimonas massiliensis</i>	0.034%	0.00 - 0.032%	High
	Bacteroidota	<i>Butyricimonas MIC9201</i>	0.034%	0.00 - 0.00%	High
	Firmicutes_A	<i>CAG-74 MIC7629</i>	0.033%	0.00 - 0.065%	Average
	Firmicutes_A	<i>Oscillospiraceae MIC9740</i>	0.032%	0.00 - 0.00%	High
	Firmicutes_A	<i>Clostridium saudiense</i>	0.032%	0.00 - 0.170%	Average

Species Profile

SPECIES

Phylum	Species	Abundance	Range	Level
Firmicutes_A	<i>CAG-382 MIC9861</i>	0.031%	0.00 - 0.015%	High
Firmicutes_A	<i>Blautia_A sp000436615</i>	0.031%	0.00 - 1.55%	Average
Firmicutes_A	<i>Anaerovoracaceae MIC8502</i>	0.031%	0.00 - 0.061%	Average
Firmicutes_A	<i>Faecalibacterium MIC8693</i>	0.029%	0.00 - 0.064%	Average
Verrucomicrobiota	<i>Victivallaceae MIC9727</i>	0.029%	0.00 - 0.00%	High
Firmicutes_A	<i>CAG-81 sp900066785</i>	0.029%	0.00 - 0.146%	Average
Bacteroidota	<i>Alistipes MIC9770</i>	0.028%	0.00 - 0.059%	Average
Firmicutes_A	<i>UBA7182 MIC8257</i>	0.027%	0.00 - 0.036%	Average
Firmicutes_A	<i>Fusicatenibacter MIC7088</i>	0.027%	0.00 - 0.00%	High

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
+	Firmicutes_A	<i>Roseburia hominis</i>	0.026%	0.00 - 0.290%	Average
<p>This is a common and important member of the human gut microbiome.</p> <p>Fuel Sources Used: This species is a moderate degrader of fibre, mucin, and protein.</p> <p>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.</p> <p>Metabolites consumed: In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.</p> <p>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.</p>					
	Firmicutes_A	<i>UBA7182 MIC8422</i>	0.026%	0.00 - 0.090%	Average
	Firmicutes_A	<i>Oscillibacter MIC7430</i>	0.024%	0.00 - 0.027%	Average

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
+	Firmicutes_A	<i>Coprococcus_A catus</i>	0.024%	0.00 - 0.431%	Average
<p>This is an inhabitant of the human gut.</p> <p>Fuel Sources Used: This species is a poor degrader of fibre, a poor 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, branched chain amino acids, cobalamin (B12), folate (B9), lactate, propionate, riboflavin (B2).</p> <p>Metabolites consumed: In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.</p> <p>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.</p>					
	Firmicutes_A	<i>CAG-269 sp003525075</i>	0.024%	0.00 - 0.233%	Average
	Firmicutes_A	<i>CAG-145 MIC8493</i>	0.024%	0.00 - 0.029%	Average
	Desulfobacterota_A	<i>Desulfovibrio fairfieldensis</i>	0.024%	0.00 - 0.030%	Average
	Firmicutes_A	<i>Dorea sp900066555</i>	0.024%	0.00 - 0.130%	Average
	Firmicutes_A	<i>QANA01 MIC6812</i>	0.023%	0.00 - 0.025%	Average
	Actinobacteriota	<i>Corynebacterium sp001767255</i>	0.023%	0.00 - 0.00%	High

Species Profile

SPECIES

Phylum	Species	Abundance	Range	Level
Firmicutes_A	<i>Anaerostipes hadrus_A</i>	0.022%	0.00 - 0.655%	Average
Firmicutes_A	<i>CAG-727 MIC8506</i>	0.022%	0.00 - 0.030%	Average
Firmicutes_A	<i>CAG-110 sp000435995</i>	0.021%	0.00 - 0.245%	Average
Firmicutes_A	<i>Anaerovoracaceae MIC7478</i>	0.021%	0.00 - 0.046%	Average
Firmicutes_A	<i>Monoglobaceae MIC7227</i>	0.019%	0.00 - 0.00%	High
Firmicutes_A	<i>Christensenellales MIC6424</i>	0.018%	0.00 - 0.00%	High
Firmicutes_A	<i>Dorea sp000433215</i>	0.017%	0.00 - 0.077%	Average
Firmicutes_A	<i>QAND01 MIC9470</i>	0.017%	0.00 - 0.00%	High

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
⊖	Actinobacteriota	<i>Eggerthella lenta</i>	0.016%	0.00 - 0.105%	Average
<p>This is an inhabitant of the gut microbiota, but has also been associated with gastrointestinal infections.</p> <p>Fuel Sources Used: This species is a poor degrader of fibre, a poor 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, branched chain amino acids, GABA, histamine, lactate, vitamin K.</p> <p>Metabolites consumed: In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.</p> <p>Emerging Research: This species can also use some steroids such as the stress hormone cortisol, and the neurotransmitter dopamine, for energy.</p> <p>Elevated levels of <i>E. lenta</i> have been associated with frailty, poor health health, poor glucose regulation and poor intestinal health. This species can also inactivate the cardiac drug digoxin by breaking it down. Interestingly, this species prefers the amino acid arginine for growth. When arginine is present, this inhibits <i>E. lenta</i> from breaking down digoxin.</p>					
⊖	Firmicutes_A	<i>Faecalicatena torques</i>	0.015%	0.00 - 0.464%	Average
<p>Previously called <i>Ruminococcus torques</i>. This is a common inhabitant of the human gut.</p> <p>Fuel Sources Used: This species is a moderate degrader of fibre, a poor 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, branched chain amino acids, cobalamin (B12), folate (B9), lactate, riboflavin (B2).</p> <p>Metabolites consumed: In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.</p> <p>Emerging Research: This species has been observed at higher levels in individuals with poor metabolic and intestinal health.</p>					

Species Profile

SPECIES

	Phylum	Species	Abundance	Range	Level
	Firmicutes_A	<i>Coprococcus eutactus</i>	0.014%	0.00 - 0.457%	Average
	Firmicutes_A	<i>Murdochiella MIC8251</i>	0.013%	0.00 - 0.00%	High
	Actinobacteriota	<i>Urmitella timonensis</i>	0.012%	0.00 - 0.00%	High
	Firmicutes_A	<i>Acutalibacteraceae MIC8097</i>	0.012%	0.00 - 0.00%	High
	Firmicutes_A	<i>UBA7160 MIC6745</i>	0.011%	0.00 - 0.308%	Average
	Firmicutes_A	<i>Lachnospiraceae MIC9747</i>	0.009%	0.00 - 0.00%	High
	Eukaryote_unclassified	<i>Blastocystis sp. subtype 6</i>	0.006%	0.00 - 0.00%	High



Gut microbiome report

