MetaBiome™ Score

98

0   100

The Metabiome™ score provides a snapshot of overall microbiome health, based on eleven key indicators. Their contribution to the MetaBiome™ score is weighted based on scientific evidence showing the level of influence each one has on health. When all indicators are within the healthy comparison range, the score will be 98-100.

Other markers in the Metabiome™ report provide additional information to be used in conjunction with the Metabiome™ score.

MetaBiome™ Score Contributors

Potential to promote health

Butyrate production

13.4 17.9 25.1

The typical range in healthy people is 13.4% to 25.13%

Butyrate is a 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, can reduce inflammation, and helps control appetite. 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]

Propionate production

2.6 7.2

The typical range in healthy people is 1.38% to 7.2%

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

Acetate production

64. 73.2

The typical range in healthy people is 64.09% to 78.06%

Acetate is the most abundant short chain fatty acid produced by our gut microbiome. It plays an important role in fat metabolism, glucose metabolism and the immune system. 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]

Fibre degradation

58.6 87.6

The typical range in healthy people is 52.4% to 87.58%

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

Potential to reduce health

Hexa-acylated lipopolysaccharide production

0 0.36

The typical range in healthy people is 0% to 0.36%

Hexa-lipopolysaccharide (hexa-LPS) is a pro-inflammatory compound produced by some species of bacteria within the Proteobacteria phylum. High levels of hexa-LPS in the blood have been observed in individuals with metabolic and inflammatory conditions. Diets high in fat, especially saturated fat, allow hexa LPS to cross the intestinal barrier and enter the bloodstream. Avoiding excessive intake of saturated fat can help reduce the ability of hexa-LPS to enter the bloodstream.Common dietary sources of saturated fats include butter, coconut products, palm oil, cheese, fatty meats, biscuit, cakes, chocolate and icecream.
[1] [2] [3] [4] [5] [6]

Trimethylamine production

1 .7 5.1

The typical range in healthy people is 1.65% to 5.15%

Trimethylamine is a compound produced by some gut microbes that is converted to another compound called trimethylamine-n-oxide (TMAO) in the liver. Increased TMAO levels have been observed in individuals with cardiometabolic and inflammatory disorders. However, the role of TMAO in these disorders is still not clear. Levels of TMAO are influenced by many factors including our gut microbiome, diet, integrity of the gut barrier, liver function and kidney function. The indoles diindolylmethane (DIM) and indole-3-carbinol (I3C) found in cruciferous vegetables (e.g. broccoli, cauliflower, cabbage, kale) may reduce the amount of trimethylamine that is converted to TMAO in the liver. In addition, excessive red meat consumption is associated with increased levels of TMAO in the blood. If your potential to produce trimethylamine is high, you may wish to increase your consumption of cruciferous vegetables and avoid eating excessive amounts of red meat.
[1] [2] [3] [4] [5] [6] [7]

Hydrogen sulphide production

6.2 14.6

The typical range in healthy people is 6.17% to 14.61%

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. Hydrogen sulphide plays an important role in gut health by acting as an energy source for gut cells and protecting the gut barrier function. However, some studies have suggested that high levels of hydrogen sulphide can also disrupt the gut mucus barrier. 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 Diversity

3.4   4.3   5

The typical range in healthy people is 3.37% to 4.56%

Microbial diversity is a measure of both the different types and the amount of bacterial species in your sample.
A varied diet rich in plant-based foods such as fruits, vegetables, whole grains and nuts is associated with increased microbial diversity. Low microbial diversity is often associated with poor health.

3-indolepropionic acid (IPA) production

0   0.36   1.8

The typical range in healthy people is 0.02% to 1.75%

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 glucose metabolism and research in animal models suggests that IPA may also play a role in maintaining the gut barrier. IPA is formed by breaking down the amino acid tryptophan. Studies have indicated that consuming foods high in dietary fibre, and in particular rye, can help increase IPA production.
[1] [2] [3] [4]

Protein degradation

88.2

The typical range in healthy people is 86.24% to 95.05%

A similar or low proportion of species that can break down protein compared to the healthy group is generally considered beneficial. Everyone's microbiome contains species that can break down protein. However, a high proportion of these species may reflect an insufficient amount of fibre in the diet or an excessive intake of protein.
Most protein is absorbed by your body, however excess protein will get passed to the large intestine where it is available to the gut microbiome. Microorganisms that break down protein produce a variety of compounds, including some compounds that promote inflammation.
If there are a high proportion of species that can break down protein in the microbiome, make sure there is sufficient fibre in the diet and consider avoiding excessive consumption of protein.

Human DNA

0.06   4

The typical range in healthy people is 0.03% to 4%

A high amount (greater than 4%) of human DNA may indicate gut inflammation. If there is greater than 4% human DNA, and there was no contamination (e.g. accidentally touched the swab during sampling), further clinical investigation is needed.

Going beyond which microbes are in the gut, what they are capable of doing is more important. Through comprehensive analysis of the genes in each and every microbe, we can understand the functional capacity of the microbiome to contribute to the health of different systems in the body.

General Gut Health   **100%**

These metabolites and microorganisms have been shown to influence your gut barrier function.

Metabolites

Potential to **promote** health

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The typical range in healthy people is 0.03% to 4%

A high amount (greater than 4%) of human DNA may indicate gut inflammation. If there is greater than 4% human DNA, and there was no contamination (e.g. accidentally touched the swab during sampling), further clinical investigation is needed.

Lactate production

61 | **69.8** | **79.7**

The typical range in healthy people is 61.01% to 79.68%

Lactate or lactic-acid producing bacteria have a long tradition of beng used to produce fermented foods such as yoghurt, kefir, sauerkraut and kimchi. Lactate can reduce inflammation and help keep the gut cell barrier intact. Some bacterial species can also convert lactate to the short chain fatty acids acetate, propionate and butyrate.

[1] [2]

3-indolepropionic acid (IPA) production

0 | **0.36** | **1.8**

The typical range in healthy people is 0.02% to 1.75%

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 glucose metabolism and research in animal models suggests that IPA may also play a role in maintaining the gut barrier. IPA is formed by breaking down the amino acid tryptophan. Studies have indicated that consuming foods high in dietary fibre, and in particular rye, can help increase IPA production.

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

Ammonia (urease) production

5.7 | **16.9**

The typical range in healthy people is 5.62% to 16.94%

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

[1] [2]

Histamine production

0.06 | **1.1** | **1.9**

The typical range in healthy people is 0.06% to 1.94%

Histamine is a chemical produced by the breakdown of the amino acid histidine. It is produced by both human cells and some bacterial species and plays an important role in immune regulation, gut function and the nervous system. Individuals with food allergies and irrritable bowel syndrome have been observed to have high levels of specific histamine receptors in the gut, making them more sensitive to histamine in the gut.

[1] [2] [3]

B. fragilis toxin production

0 | **0.01**

The typical range in healthy people is 0% to 0.01%

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]

Protein degradation

88.2

The typical range in healthy people is 86.24% to 95.05%

A similar or low proportion of species that can break down protein compared to the healthy group is generally considered beneficial. Everyone's microbiome contains species that can break down protein. However, a high proportion of these species may reflect an insufficient amount of fibre in the diet or an excessive intake of protein.
Most protein is absorbed by your body, however excess protein will get passed to the large intestine where it is available to the gut microbiome. Microorganisms that break down protein produce a variety of compounds, including some compounds that promote inflammation.
If there are a high proportion of species that can break down protein in the microbiome, make sure there is sufficient fibre in the diet and consider avoiding excessive consumption of protein.

Species

Potential to **promote** health

Potential to **reduce** health

Agathobacter faecis

0 | **0.15** | **4.2**

The typical range in healthy people is 0% to 4.17%

Previously named *Roseburia faecis*. This is a common and important member of the human gut microbiome.

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

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

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

Emerging research:
This species is commonly associated with healthy controls in research studies. Low levels of this bacterium have been observed in patients with liver cirrhosis.
[1] [2] [3]

Agathobacter rectale

0 | **4.2** | **2**

The typical range in healthy people is 0% to 7.22%

Previously named *Eubacterium rectale*, this is a common member of the human gut.

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

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

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

Emerging research:
This species is commonly associated with healthy controls in research studies. Low levels of this bacterium have been observed in inflammatory conditions.
[1] [2] [3]

Akkermansia muciniphila

0 | **1** | **1.2**

The typical range in healthy people is 0% to 1.19%

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 associated low levels of *A. muciniphila* with metabolic conditions. Research has also indicated this species can improve the efficacy of a common immunotherapy drug used in cancer patients 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 elevated levels are associated with neurodegenerative conditions.
[1] [2] [3] [4] [5] [6] [7] [8] [9]

Bilophila wadsworthia

0 | **0.05** | **0.2**

The typical range in healthy people is 0% to 0.2%

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

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

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

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

Emerging research:
High levels of this species can promote inflammation in the gut and is associated with a diet high in saturated fats.
[1] [2] [3] [4] [5] [6]

Clostridium_M bolteae

0

The typical range in healthy people is 0% to 0%

This is an inhabitant of the human gut.

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

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

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

Emerging research:
Elevated levels of this species has been associated with metabolic conditions.
[1] [2] [3] [4] [5] [6] [7] [8] [9] [10]

Eggerthella lenta

0 | **0.1**

The typical range in healthy people is 0% to 0.1%

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

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

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

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

Emerging research:
Elevated levels of this species have been associated with cardiovascular and metabolic conditions. This species can also inactivate the cardiac drug digoxin by breaking it down. Interestingly, this species prefers the amino acid arginine for growth. When arginine is present, this inhibits *E. lenta* from breaking down digoxin.
[1] [2] [3] [4] [5] [6] [7] [8] [9]

Bifidobacterium adolescentis

0	3

The typical range in healthy people is 0% to 2.98%

This is a common and beneficial inhabitant of the gut.

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

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

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

Emerging research:
Low levels of this species have been associated with inflammation.
[1] [2] [3] [4] [5].

Bifidobacterium animalis

0	0.36

The typical range in healthy people is 0% to 0.36%

This is a naturally occurring human gut bacterium and probiotic; it is sometimes also called *Bifidobacterium lactis*.

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

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

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

Emerging research:
B. animalis is associated with a low BMI and has been used to improve metabolic disorders such as obesity and diabetes. It can also produce antimicrobial substances effective against pathogenic bacteria and studies in mouse models suggest it can improve "leaky gut."
[1] [2] [3] [4] [5].

Bifidobacterium bifidum

0

The typical range in healthy people is 0% to 0%

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.

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

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

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.
[1] [2] [3] [4] [5].

Fusobacterium nucleatum

0

The typical range in healthy people is 0% to 0%

Although a common member of the human oral microbiome, this pro-inflammatory bacterium can also be found in the human gut.

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

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: 3-IPA, acetate, biotin (B7), butyrate, cobalamin (B12), lactate, propionate, riboflavin (B2).

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

Emerging research:
High levels of this species have been associated with inflammatory conditions and poor gut health. Laboratory-based studies suggest that black and green tea may reduce the growth of this species.
[1] [2] [3] [4] [5] [6] [7] [8]

Peptostreptococcus stomatis

0

The typical range in healthy people is 0% to 0%

This is an inhabitant of the oral microbiome that can also be found in the gut microbiome.

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

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

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

Emerging research:
Elevated levels of this species has been associated with poor gut health.
[1] [2] [3] [4] [5] [6] [7]

Bifidobacterium longum

| 0 | 0.88 | .5 |

The typical range in healthy people is 0% to 1.47%

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

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

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

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

Emerging research:
B.longum has been associated with reductions in harmful bacteria, anti-allergy effects, and anti-obesity effects in mouse models, but further research still needs to be done in humans.
[1] [2] [3] [4] [5] [6] [7]

Coprococcus eutactus

| 0 | 0.11 | 0.46 |

The typical range in healthy people is 0% to 0.46%

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

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

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

Emerging research:
This species has been observed at decreased levels in children with inflammatory conditions.

Eubacterium_E hallii

| 0 | 0.89 | 1.8 |

The typical range in healthy people is 0% to 1.75%

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 patients with intestinal disorders. Also, a study in mice suggested this species may be effective at improving insulin sensitivity.
[1] [2] [3] [4] [5]

Faecalibacterium prausnitzii_C

| 0 | 1.2 | 2 |

The typical range in healthy people is 0% to 2.02%

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

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

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

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

Emerging research:
Low levels of *F. prausnitzii* have been associated with inflammatory and metabolic conditions.
[1] [2] [3] [4] [5] [6] [7] [8] [9] [10]

Roseburia hominis

| 0 | 0.1 | 0.29 |

The typical range in healthy people is 0% to 0.29%

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

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

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

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

Emerging research:
This is a primary producer of the beneficial short chain fatty acid butyrate. Lower levels of this species have been observed in patients with inflammatory conditions. Another study observed higher levels in active women compared to sedentary women. Laboratory studies suggest this species can help regulate the immune system and reduce inflammation.
[1] [2] [3] [4] [5] [6] [7] [8] [9]

Roseburia intestinalis

| 0 | 1.1 |

The typical range in healthy people is 0% to 1.12%

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

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

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

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

Emerging research:
This species has been observed at reduced levels in individuals with metabolic and inflammatory conditions.
[1] [2] [3]

Roseburia inulinivorans

0	0.65

The typical range in healthy people is 0% to 0.65%

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

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

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

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

Emerging research:
This is a primary producer of the beneficial short chain fatty acid butyrate. This species has been observed at reduced levels in individuals with type 2 diabetes.
[1] [2] [3]

Ruminococcus_E bromii

0	

The typical range in healthy people is 0% to 0%

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

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

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

Emerging research:
Studies suggest the role of *R. bromii* as a primary starch degrader helps stimulate the growth of butyrate-producing bacterial species.
[1] [2] [3]

Gut Mucosal Health

100%

These metabolites and microorganisms have been shown to influence your gut barrier function.

Metabolites

Potential to **promote** health

Fibre degradation

| 58.6 | 87.6 |

The typical range in healthy people is 52.4% to 87.58%

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

Lactate production

| 61 | 69.8 | 79.7 |

The typical range in healthy people is 61.01% to 79.68%

Lactate or lactic-acid producing bacteria have a long tradition of beng used to produce fermented foods such as yoghurt, kefir, sauerkraut and kimchi. Lactate can reduce inflammation and help keep the gut cell barrier intact. Some bacterial species can also convert lactate to the short chain fatty acids acetate, propionate and butyrate.
[1] [2]

3-indolepropionic acid (IPA) production

| 0 | 0.36 | 1.8 |

The typical range in healthy people is 0.02% to 1.75%

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 glucose metabolism and research in animal models suggests that IPA may also play a role in maintaining the gut barrier. IPA is formed by breaking down the amino acid tryptophan. Studies have indicated that consuming foods high in dietary fibre, and in particular rye, can help increase IPA production.
[1] [2] [3] [4]

Butyrate production

| 13.4 | 17.9 | 25.1 |

The typical range in healthy people is 13.4% to 25.13%

Butyrate is a 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, can reduce inflammation, and helps control appetite. 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]

Potential to **reduce** health

Hydrogen sulphide production

| 6.2 | 14.6 |

The typical range in healthy people is 6.17% to 14.61%

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. Hydrogen sulphide plays an important role in gut health by acting as an energy source for gut cells and protecting the gut barrier function. However, some studies have suggested that high levels of hydrogen sulphide can also disrupt the gut mucus barrier. 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]

Ammonia (urease) production

| 5.7 | 16.9 |

The typical range in healthy people is 5.62% to 16.94%

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

Hexa-acylated lipopolysaccharide production

| 0 | 0.36 |

The typical range in healthy people is 0% to 0.36%

Hexa-lipopolysaccharide (hexa-LPS) is a pro-inflammatory compound produced by some species of bacteria within the Proteobacteria phylum. High levels of hexa-LPS in the blood have been observed in individuals with metabolic and inflammatory conditions. Diets high in fat, especially saturated fat, allow hexa LPS to cross the intestinal barrier and enter the bloodstream. Avoiding excessive intake of saturated fat can help reduce the ability of hexa-LPS to enter the bloodstream.Common dietary sources of saturated fats include butter, coconut products, palm oil, cheese, fatty meats, biscuit, cakes, chocolate and icecream.
[1] [2] [3] [4] [5] [6]

Protein degradation

| 88.2 |

The typical range in healthy people is 86.24% to 95.05%

A similar or low proportion of species that can break down protein compared to the healthy group is generally considered beneficial. Everyone's microbiome contains species that can break down protein. However, a high proportion of these species may reflect an insufficient amount of fibre in the diet or an excessive intake of protein.
Most protein is absorbed by your body, however excess protein will get passed to the large intestine where it is available to the gut microbiome. Microorganisms that break down protein produce a variety of compounds, including some compounds that promote inflammation.
If there are a high proportion of species that can break down protein in the microbiome, make sure there is sufficient fibre in the diet and consider avoiding excessive consumption of protein.

Human DNA

| 0.06 | 4 |

The typical range in healthy people is 0.03% to 4%

A high amount (greater than 4%) of human DNA may indicate gut inflammation. If there is greater than 4% human DNA, and there was no contamination (e.g. accidentally touched the swab during sampling), further clinical investigation is needed.

B. fragilis toxin production

`0` `0.01`

The typical range in healthy people is 0% to 0.01%

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]

Histamine production

`0.06` `1.1` `1.9`

The typical range in healthy people is 0.06% to 1.94%

Histamine is a chemical produced by the breakdown of the amino acid histidine. It is produced by both human cells and some bacterial species and plays an important role in immune regulation, gut function and the nervous system. Individuals with food allergies and irrritable bowel syndrome have been observed to have high levels of specific histamine receptors in the gut, making them more sensitive to histamine in the gut.

[1] [2] [3]

Species

Potential to promote health

Agathobacter faecis

`0` `0.15` `4.2`

The typical range in healthy people is 0% to 4.17%

Previously named *Roseburia faecis*. This is a common and important member of the human gut microbiome.

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

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

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

Emerging research:
This species is commonly associated with healthy controls in research studies. Low levels of this bacterium have been observed in patients with liver cirrhosis.
[1] [2] [3]

Agathobacter rectale

`0` `4.2` `2`

The typical range in healthy people is 0% to 7.22%

Previously named *Eubacterium rectale*, this is a common member of the human gut.

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

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

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

Emerging research:
This species is commonly associated with healthy controls in research studies. Low levels of this bacterium have been observed in inflammatory conditions.
[1] [2] [3]

Potential to reduce health

Bilophila wadsworthia

`0` `0.05` `0.2`

The typical range in healthy people is 0% to 0.2%

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

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

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

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

Emerging research:
High levels of this species can promote inflammation in the gut and is associated with a diet high in saturated fats.
[1] [2] [3] [4] [5] [6]

Akkermansia muciniphila

`0` ——————————————— `1` `1.2`

The typical range in healthy people is 0% to 1.19%

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 associated low levels of *A. muciniphila* with metabolic conditions. Research has also indicated this species can improve the efficacy of a common immunotherapy drug used in cancer patients 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 elevated levels are associated with neurodegenerative conditions.
[1] [2] [3] [4] [5] [6] [7] [8] [9]

Bifidobacterium animalis

`0` ——————————————— `0.36`

The typical range in healthy people is 0% to 0.36%

This is a naturally occurring human gut bacterium and probiotic; it is sometimes also called *Bifidobacterium lactis.*

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

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

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

Emerging research:
B. animalis is associated with a low BMI and has been used to improve metabolic disorders such as obesity and diabetes. It can also produce antimicrobial substances effective against pathogenic bacteria and studies in mouse models suggest it can improve "leaky gut."
[1] [2] [3] [4] [5].

Bifidobacterium bifidum

`0` ———————————————

The typical range in healthy people is 0% to 0%

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.

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

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

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.
[1] [2] [3] [4] [5].

Coprococcus eutactus

| 0 | 0.11 | 0.46 |

The typical range in healthy people is 0% to 0.46%

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

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

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

Emerging research:
This species has been observed at decreased levels in children with inflammatory conditions.

Eubacterium_E hallii

| 0 | 0.89 | 1.8 |

The typical range in healthy people is 0% to 1.75%

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 patients with intestinal disorders. Also, a study in mice suggested this species may be effective at improving insulin sensitivity.
[1] [2] [3] [4] [5].

Faecalibacterium prausnitzii_C

| 0 | 1.2 | 2 |

The typical range in healthy people is 0% to 2.02%

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

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

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

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

Emerging research:
Low levels of *F. prausnitzii* have been associated with inflammatory and metabolic conditions.
[1] [2] [3] [4] [5] [6] [7] [8] [9] [10]

Roseburia hominis

0	0.1	0.29	

The typical range in healthy people is 0% to 0.29%

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

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

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

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

Emerging research:
This is a primary producer of the beneficial short chain fatty acid butyrate. Lower levels of this species have been observed in patients with inflammatory conditions. Another study observed higher levels in active women compared to sedentary women. Laboratory studies suggest this species can help regulate the immune system and reduce inflammation.
[1] [2] [3] [4] [5] [6] [7] [8] [9]

Roseburia intestinalis

0	1.1	

The typical range in healthy people is 0% to 1.12%

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

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

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

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

Emerging research:
This species has been observed at reduced levels in individuals with metabolic and inflammatory conditions.
[1] [2] [3]

Roseburia inulinivorans

0	0.65	

The typical range in healthy people is 0% to 0.65%

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

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

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

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

Emerging research:
This is a primary producer of the beneficial short chain fatty acid butyrate. This species has been observed at reduced levels in individuals with type 2 diabetes.
[1] [2] [3]

Ruminococcus_E bromii

0

The typical range in healthy people is 0% to 0%

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

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

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

Emerging research:
Studies suggest the role of *R. bromii* as a primary starch degrader helps stimulate the growth of butyrate-producing bacterial species.
[1] [2] [3]

Ruminococcus_E bromii

0

The typical range in healthy people is 0% to 0%

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:
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

Gut Motility   **100%**

These metabolites and microorganisms have been shown to influence the rate at which food is moved through the digestive tract, which can impact bowel movement frequency.

Metabolites

Potential to **promote** health

Butyrate production

| 13.4 | **17.9** | 25.1 |

The typical range in healthy people is 13.4% to 25.13%

Butyrate is a 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, can reduce inflammation, and helps control appetite. 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]

Fibre degradation

| **58.6** | 87.6 |

The typical range in healthy people is 52.4% to 87.58%

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

Propionate production

| **2.6** | 7.2 |

The typical range in healthy people is 1.38% to 7.2%

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

Tyramine production

| **0.84** | .9 |

The typical range in healthy people is 0.06% to 1.89%

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]

Potential to **reduce** health

Methane production

| 0 | **1.4** |

The typical range in healthy people is 0% to 1.84%

The gas methane can be produced by some species of the gut microbiome, primarily through the reduction of carbon dioxide and hydrogen. Although methane production is often detected in healthy adult populations, elevated levels of methane production has been associated with slower intestinal transit times and constipation.
[1] [2] [3] [4]

Hydrogen sulphide production

| 6.2 2 | 14.6 |

The typical range in healthy people is 6.17% to 14.61%

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. Hydrogen sulphide plays an important role in gut health by acting as an energy source for gut cells and protecting the gut barrier function. However, some studies have suggested that high levels of hydrogen sulphide can also disrupt the gut mucus barrier. 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]

Protein degradation

| **88.2** |

The typical range in healthy people is 86.24% to 95.05%

A similar or low proportion of species that can break down protein compared to the healthy group is generally considered beneficial. Everyone's microbiome contains species that can break down protein. However, a high proportion of these species may reflect an insufficient amount of fibre in the diet or an excessive intake of protein.
Most protein is absorbed by your body, however excess protein will get passed to the large intestine where it is available to the gut microbiome. Microorganisms that break down protein produce a variety of compounds, including some compounds that promote inflammation.
If there are a high proportion of species that can break down protein in the microbiome, make sure there is sufficient fibre in the diet and consider avoiding excessive consumption of protein.

Species

Potential to **promote** health

Potential to **reduce** health

Methanobrevibacter_A smithii

| 0 | 0.58 | 1.4 |

The typical range in healthy people is 0% to 0.58%

This is a single celled organism belonging to the Archaea domain and is the most common archaeal species found in the human gut.

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

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

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

Emerging research:
M. smithii plays an important role in the gut because it is one of the few species that can remove excess hydrogen. However, large amounts of this species are not good either, as high levels of methane can promote constipation.
[1] [2] [3] [4] [5]

Bilophila wadsworthia

| 0 | 0.05 | 0.2 |

The typical range in healthy people is 0% to 0.2%

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

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

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

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

Emerging research:
High levels of this species can promote inflammation in the gut and is associated with a diet high in saturated fats.
[1] [2] [3] [4] [5] [6]

Metabolic Health   **90%**

These metabolites and microorganisms have been shown to influence how the body metabolises nutrients such as glucose and fats, as well as the health of the circulatory system.

Metabolites

Potential to **promote** health

Butyrate production

| 13.4 | **17.9** | 25.1 |

The typical range in healthy people is 13.4% to 25.13%

Butyrate is a 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, can reduce inflammation, and helps control appetite. 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]

Propionate production

| **2.6** | 7.2 |

The typical range in healthy people is 1.38% to 7.2%

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

Acetate production

| 64.1 | **73.2** |

The typical range in healthy people is 64.09% to 78.06%

Acetate is the most abundant short chain fatty acid produced by our gut microbiome. It plays an important role in fat metabolism, glucose metabolism and the immune system. 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]

Fibre degradation

| **58.6** | 87.6 |

The typical range in healthy people is 52.4% to 87.58%

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

3-indolepropionic acid (IPA) production

| 0 | **0.36** | 1.8 |

The typical range in healthy people is 0.02% to 1.75%

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 glucose metabolism and research in animal models suggests that IPA may also play a role in maintaining the gut barrier. IPA is formed by breaking down the amino acid tryptophan. Studies have indicated that consuming foods high in dietary fibre, and in particular rye, can help increase IPA production.
[1] [2] [3] [4]

Potential to **reduce** health

Branched chain amino acids production

| **45.2** 5.1 | 72 |

The typical range in healthy people is 46.09% to 71.96%

Branched chain amino acids (BCAAs) are building blocks for muscles, are involved in the regulation of glucose and fat metabolism, and are involved in the regulation of the immune system. They can be obtained from your diet as well as from your gut microbiome. However, the right amount of BCAAs is important. High levels of BCAAs have been associated with metabolic conditions. Maintaing muscle mass plays an important role in regulating BCAA levels. A study has shown that increased microbial gene abundance for BCAA production correlated with increased BCAA levels in the blood. 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]

Hexa-acylated lipopolysaccharide production

| 0 | 0.36 |

The typical range in healthy people is 0% to 0.36%

Hexa-lipopolysaccharide (hexa-LPS) is a pro-inflammatory compound produced by some species of bacteria within the Proteobacteria phylum. High levels of hexa-LPS in the blood have been observed in individuals with metabolic and inflammatory conditions. Diets high in fat, especially saturated fat, allow hexa LPS to cross the intestinal barrier and enter the bloodstream. Avoiding excessive intake of saturated fat can help reduce the ability of hexa-LPS to enter the bloodstream.Common dietary sources of saturated fats include butter, coconut products, palm oil, cheese, fatty meats, biscuit, cakes, chocolate and icecream.
[1] [2] [3] [4] [5] [6]

Trimethylamine production

| 1 | 1.7 | 5.1 |

The typical range in healthy people is 1.65% to 5.15%

Trimethylamine is a compound produced by some gut microbes that is converted to another compound called trimethylamine-n-oxide (TMAO) in the liver. Increased TMAO levels have been observed in individuals with cardiometabolic and inflammatory disorders. However, the role of TMAO in these disorders is still not clear. Levels of TMAO are influenced by many factors including our gut microbiome, diet, integrity of the gut barrier, liver function and kidney function. The indoles diindolylmethane (DIM) and indole-3-carbinol (I3C) found in cruciferous vegetables (e.g. broccoli, cauliflower, cabbage, kale) may reduce the amount of trimethylamine that is converted to TMAO in the liver. In addition, excessive red meat consumption is associated with increased levels of TMAO in the blood. If your potential to produce trimethylamine is high, you may wish to increase your consumption of cruciferous vegetables and avoid eating excessive amounts of red meat.
[1] [2] [3] [4] [5] [6] [7]

Succinate production

| 9.8 | **13.5** | 21.7 |

The typical range in healthy people is 9.83% to 21.68%

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]

Folate (B9) production

42.8 | 45.7 | 64.7

The typical range in healthy people is 45.74% to 64.69%

Folate or folic acid plays an important role in cell replication and repair and deficiencies can result in an increased risk of of heart disease, anemia, stroke, and neural tube defects in newborn infants. 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 folate while rich dietary sources include dark green leafy vegetables, fruit, legumes, and nuts.

[1] [2] [3]

Species

Potential to promote health

Akkermansia muciniphila

0 | 1 | 1.2

The typical range in healthy people is 0% to 1.19%

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 associated low levels of *A. muciniphila* with metabolic conditions. Research has also indicated this species can improve the efficacy of a common immunotherapy drug used in cancer patients 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 elevated levels are associated with neurodegenerative conditions.

[1] [2] [3] [4] [5] [6] [7] [8] [9]

Bifidobacterium adolescentis

0 | 3

The typical range in healthy people is 0% to 2.98%

This is a common and beneficial inhabitant of the gut.

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

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

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

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

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

Potential to reduce health

Bilophila wadsworthia

0 | 0.05 | 0.2

The typical range in healthy people is 0% to 0.2%

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

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

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

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

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

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

Eggerthella lenta

0 | 0.1

The typical range in healthy people is 0% to 0.1%

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

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

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

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

Emerging research:
Elevated levels of this species have been associated with cardiovascular and metabolic conditions. This species can also inactivate the cardiac drug digoxin by breaking it down. Interestingly, this species prefers the amino acid arginine for growth. When arginine is present, this inhibits *E. lenta* from breaking down digoxin.

[1] [2] [3] [4] [5] [6] [7] [8] [9]

Bifidobacterium animalis

0	0.36

The typical range in healthy people is 0% to 0.36%

This is a naturally occurring human gut bacterium and probiotic; it is sometimes also called *Bifidobacterium lactis.*

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

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

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

Emerging research:
B. animalis is associated with a low BMI and has been used to improve metabolic disorders such as obesity and diabetes. It can also produce antimicrobial substances effective against pathogenic bacteria and studies in mouse models suggest it can improve "leaky gut."
[1] [2] [3] [4] [5]

Bifidobacterium bifidum

0	

The typical range in healthy people is 0% to 0%

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.

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

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

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.
[1] [2] [3] [4] [5]

Bifidobacterium longum

0	0.88	.5

The typical range in healthy people is 0% to 1.47%

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

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

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

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

Emerging research:
B.longum has been associated with reductions in harmful bacteria, anti-allergy effects, and anti-obesity effects in mouse models, but further research still needs to be done in humans.
[1] [2] [3] [4] [5] [6] [7]

Prevotella copri

0	9.3

The typical range in healthy people is 0% to 9.26%

This is a common inhabitant of the human gut.

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

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, 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:
High levels of some strains within this species have been associated with metabolic and inflammatory conditions.
[1] [2] [3] [4] [5] [6]

Eubacterium_E hallii

`0` ——————————————— `0.89` `1.8` ————————

The typical range in healthy people is 0% to 1.75%

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 patients with intestinal disorders. Also, a study in mice suggested this species may be effective at improving insulin sensitivity.
[1] [2] [3] [4] [5].

Faecalibacterium prausnitzii_C

`0` ——————————————— `1.2` `2` ————————

The typical range in healthy people is 0% to 2.02%

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

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

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

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

Emerging research:
Low levels of *F. prausnitzii* have been associated with inflammatory and metabolic conditions.
[1] [2] [3] [4] [5] [6] [7] [8] [9] [10]

Roseburia hominis

`0` —————— `0.1` ———— `0.29` ——————————

The typical range in healthy people is 0% to 0.29%

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

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

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

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

Emerging research:
This is a primary producer of the beneficial short chain fatty acid butyrate. Lower levels of this species have been observed in patients with inflammatory conditions. Another study observed higher levels in active women compared to sedentary women. Laboratory studies suggest this species can help regulate the immune system and reduce inflammation.
[1] [2] [3] [4] [5] [6] [7] [8] [9]

Roseburia intestinalis

0 ———— **1.1** ————

The typical range in healthy people is 0% to 1.12%

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

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

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

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

Emerging research:
This species has been observed at reduced levels in individuals with metabolic and inflammatory conditions.
[1] [2] [3]

Roseburia inulinivorans

0 ———— **0.65** ————

The typical range in healthy people is 0% to 0.65%

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

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

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

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

Emerging research:
This is a primary producer of the beneficial short chain fatty acid butyrate. This species has been observed at reduced levels in individuals with type 2 diabetes.
[1] [2] [3]

Ruminococcus_E bromii

0

The typical range in healthy people is 0% to 0%

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

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

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

Emerging research:
Studies suggest the role of *R. bromii* as a primary starch degrader helps stimulate the growth of butyrate-producing bacterial species.
[1] [2] [3]

Nervous System Health   **91%**

These metabolites and microorganisms have been shown to have a role in regulating the function of the brain and nervous system.

Metabolites

Potential to promote health

3-indolepropionic acid (IPA) production

`0` `0.36` `1.8`

The typical range in healthy people is 0.02% to 1.75%

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 glucose metabolism and research in animal models suggests that IPA may also play a role in maintaining the gut barrier. IPA is formed by breaking down the amino acid tryptophan. Studies have indicated that consuming foods high in dietary fibre, and in particular rye, can help increase IPA production.

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

Butyrate production

`13.4` `17.9` `25.1`

The typical range in healthy people is 13.4% to 25.13%

Butyrate is a 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, can reduce inflammation, and helps control appetite. 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]

Fibre degradation

`58.6` `87.6`

The typical range in healthy people is 52.4% to 87.58%

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

GABA production

`5.2` `9.6` `21.4`

The typical range in healthy people is 5.24% to 21.39%

GABA is short for gamma-butyric acid and is an important signaling molecule for the brain (called a neurotransmitter). GABA's role is to reduce the activity of nerve cells and it is thought to reduce anxiety. GABA is primarily produced by your body, but some bacterial species can also produce (and consume) GABA. It is unknown if bacterially produced GABA can influence nerve cells in humans and this is currently an active area of research. If you are concerned about your mental health, it is important to seek professional help.

[1] [2] [3]

Propionate production

`2.6` `7.2`

The typical range in healthy people is 1.38% to 7.2%

Propionate is a beneficial short chain fatty acid that is important for gut health. It helps maintain blood glucose levels, can reduce inflammation, and helps control appetite. The prebiotic fibre beta-glucan, found in oats and barley, has been shown to increase propionate production.

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

Potential to reduce health

Histamine production

`0.06` `1.1` `1.9`

The typical range in healthy people is 0.06% to 1.94%

Histamine is a chemical produced by the breakdown of the amino acid histidine. It is produced by both human cells and some bacterial species and plays an important role in immune regulation, gut function and the nervous system. Individuals with food allergies and irrritable bowel syndrome have been observed to have high levels of specific histamine receptors in the gut, making them more sensitive to histamine in the gut.

[1] [2] [3]

GABA consumption

`3.7` `10.4`

The typical range in healthy people is 2.71% to 10.42%

GABA is short for gamma-butyric acid and is an important signaling molecule for the brain (called a neurotransmitter). GABA's role is to reduce the activity of nerve cells and it is thought to reduce anxiety. GABA is primarily produced by your body, but some bacterial species can also produce (and consume) GABA. It is unknown if bacterially produced GABA can influence nerve cells in humans and this is currently an active area of research. If you are concerned about your mental health, it is important to seek professional help.

[1] [2] [3]

Hexa-acylated lipopolysaccharide production

`0` `0.36`

The typical range in healthy people is 0% to 0.36%

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

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

Trimethylamine production

`1` `1.7` `5.1`

The typical range in healthy people is 1.65% to 5.15%

Trimethylamine is a compound produced by some gut microbes that is converted to another compound called trimethylamine-n-oxide (TMAO) in the liver. Increased TMAO levels have been observed in individuals with cardiometabolic and inflammatory disorders. However, the role of TMAO in these disorders is still not clear. Levels of TMAO are influenced by many factors including our gut microbiome, diet, integrity of the gut barrier, liver function and kidney function. The indoles diindolylmethane (DIM) and indole-3-carbinol (I3C) found in cruciferous vegetables (e.g. broccoli, cauliflower, cabbage, kale) may reduce the amount of trimethylamine that is converted to TMAO in the liver. In addition, excessive red meat consumption is associated with increased levels of TMAO in the blood. If your potential to produce trimethylamine is high, you may wish to increase your consumption of cruciferous vegetables and avoid eating excessive amounts of red meat.

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

Tyramine production

| 0.84 | .9 |

The typical range in healthy people is 0.06% to 1.89%

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]

Folate (B9) production

| 42.8 | 45.7 | 64.7 |

The typical range in healthy people is 45.74% to 64.69%

Folate or folic acid plays an important role in cell replication and repair and deficiencies can result in an increased risk of of heart disease, anemia, stroke, and neural tube defects in newborn infants. 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 folate while rich dietary sources include dark green leafy vegetables, fruit, legumes, and nuts.

[1] [2] [3]

Immune Health   89%

These metabolites and microorganisms have been shown to be involved in regulating the immune system.

Metabolites

Potential to **promote** health

Butyrate production

13.4 17.9 25.1

The typical range in healthy people is 13.4% to 25.13%

Butyrate is a 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, can reduce inflammation, and helps control appetite. 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]

Propionate production

2.6 7.2

The typical range in healthy people is 1.38% to 7.2%

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

Acetate production

64.1 73.2

The typical range in healthy people is 64.09% to 78.06%

Acetate is the most abundant short chain fatty acid produced by our gut microbiome. It plays an important role in fat metabolism, glucose metabolism and the immune system. 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]

Fibre degradation

58.6 87.6

The typical range in healthy people is 52.4% to 87.58%

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

Folate (B9) production

42.8 45.7 64.7

The typical range in healthy people is 45.74% to 64.69%

Folate or folic acid plays an important role in cell replication and repair and deficiencies can result in an increased risk of of heart disease, anemia, stroke, and neural tube defects in newborn infants. 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 folate while rich dietary sources include dark green leafy vegetables, fruit, legumes, and nuts.
[1] [2] [3]

Potential to **reduce** health

Hexa-acylated lipopolysaccharide production

0 0.36

The typical range in healthy people is 0% to 0.36%

Hexa-lipopolysaccharide (hexa-LPS) is a pro-inflammatory compound produced by some species of bacteria within the Proteobacteria phylum. High levels of hexa-LPS in the blood have been observed in individuals with metabolic and inflammatory conditions. Diets high in fat, especially saturated fat, allow hexa LPS to cross the intestinal barrier and enter the bloodstream. Avoiding excessive intake of saturated fat can help reduce the ability of hexa-LPS to enter the bloodstream.Common dietary sources of saturated fats include butter, coconut products, palm oil, cheese, fatty meats, biscuit, cakes, chocolate and icecream.
[1] [2] [3] [4] [5] [6]

B. fragilis toxin production

0 0.01

The typical range in healthy people is 0% to 0.01%

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]

Histamine production

0.06 1.1 1.9

The typical range in healthy people is 0.06% to 1.94%

Histamine is a chemical produced by the breakdown of the amino acid histidine. It is produced by both human cells and some bacterial species and plays an important role in immune regulation, gut function and the nervous system. Individuals with food allergies and irrritable bowel syndrome have been observed to have high levels of specific histamine receptors in the gut, making them more sensitive to histamine in the gut.
[1] [2] [3]

Protein degradation

88.2

The typical range in healthy people is 86.24% to 95.05%

A similar or low proportion of species that can break down protein compared to the healthy group is generally considered beneficial. Everyone's microbiome contains species that can break down protein. However, a high proportion of these species may reflect an insufficient amount of fibre in the diet or an excessive intake of protein.
Most protein is absorbed by your body, however excess protein will get passed to the large intestine where it is available to the gut microbiome. Microorganisms that break down protein produce a variety of compounds, including some compounds that promote inflammation.
If there are a high proportion of species that can break down protein in the microbiome, make sure there is sufficient fibre in the diet and consider avoiding excessive consumption of protein.

Species

Potential to **promote** health

Potential to **reduce** health

Bifidobacterium adolescentis

0	3

The typical range in healthy people is 0% to 2.98%

This is a common and beneficial inhabitant of the gut.

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

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

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

Emerging research:
Low levels of this species have been associated with inflammation.
[1] [2] [3] [4] [5]

Bifidobacterium animalis

0	0.36

The typical range in healthy people is 0% to 0.36%

This is a naturally occurring human gut bacterium and probiotic; it is sometimes also called *Bifidobacterium lactis*.

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

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

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

Emerging research:
B. animalis is associated with a low BMI and has been used to improve metabolic disorders such as obesity and diabetes. It can also produce antimicrobial substances effective against pathogenic bacteria and studies in mouse models suggest it can improve "leaky gut."
[1] [2] [3] [4] [5]

Bifidobacterium bifidum

0

The typical range in healthy people is 0% to 0%

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.

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

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

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.
[1] [2] [3] [4] [5]

Eggerthella lenta

0	0.1

The typical range in healthy people is 0% to 0.1%

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

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

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

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

Emerging research:
Elevated levels of this species have been associated with cardiovascular and metabolic conditions. This species can also inactivate the cardiac drug digoxin by breaking it down. Interestingly, this species prefers the amino acid arginine for growth. When arginine is present, this inhibits *E. lenta* from breaking down digoxin.
[1] [2] [3] [4] [5] [6] [7] [8] [9]

Fusobacterium nucleatum

0

The typical range in healthy people is 0% to 0%

Although a common member of the human oral microbiome, this pro-inflammatory bacterium can also be found in the human gut.

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

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: 3-IPA, acetate, biotin (B7), butyrate, cobalamin (B12), lactate, propionate, riboflavin (B2).

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

Emerging research:
High levels of this species have been associated with inflammatory conditions and poor gut health. Laboratory-based studies suggest that black and green tea may reduce the growth of this species.
[1] [2] [3] [4] [5] [6] [7] [8]

Bifidobacterium longum

```
0          0.88 .5
```

The typical range in healthy people is 0% to 1.47%

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

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

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

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

Emerging research:
B.longum has been associated with reductions in harmful bacteria, anti-allergy effects, and anti-obesity effects in mouse models, but further research still needs to be done in humans.
[1] [2] [3] [4] [5] [6] [7]

Coprococcus eutactus

```
0        0.11        0.46
```

The typical range in healthy people is 0% to 0.46%

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

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

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

Emerging research:
This species has been observed at decreased levels in children with inflammatory conditions.

Eubacterium_E hallii

```
0            0.89 1.8
```

The typical range in healthy people is 0% to 1.75%

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 patients with intestinal disorders. Also, a study in mice suggested this species may be effective at improving insulin sensitivity.
[1] [2] [3] [4] [5]

Faecalibacterium prausnitzii_H

0

The typical range in healthy people is 0% to 0%

This is an important member of the gut microbiome.

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

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

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

Emerging research:
This species can also use branched chain amino acids and the short chain fatty acid acetate for energy.

This species has recently been split into several different species, and low levels of some of these species have been observed in individuals with inflammatory conditions.

[1] [2] [3] [4] [5] [6] [7] [8] [9]

Roseburia hominis

0   **0.1**   **0.29**

The typical range in healthy people is 0% to 0.29%

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

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

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

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

Emerging research:
This is a primary producer of the beneficial short chain fatty acid butyrate. Lower levels of this species have been observed in patients with inflammatory conditions. Another study observed higher levels in active women compared to sedentary women. Laboratory studies suggest this species can help regulate the immune system and reduce inflammation.

[1] [2] [3] [4] [5] [6] [7] [8] [9]

Roseburia intestinalis

0   **1.1**

The typical range in healthy people is 0% to 1.12%

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

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

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

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

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

[1] [2] [3]

Roseburia inulinivorans

0	0.65

The typical range in healthy people is 0% to 0.65%

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

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

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

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

Emerging research:
This is a primary producer of the beneficial short chain fatty acid butyrate. This species has been observed at reduced levels in individuals with type 2 diabetes.
[1] [2] [3]

Inflammatory Balance   **100%**

These metabolites and microorganisms have been associated with the levels of inflammation in the body.

Metabolites

Potential to **promote** health

Butyrate production

17.9 | **25.1**

The typical range in healthy people is 13.4% to 25.13%

Butyrate is a 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, can reduce inflammation, and helps control appetite. 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]

Propionate production

2.6 | **7.2**

The typical range in healthy people is 1.38% to 7.2%

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

Acetate production

73.2 | **4.1** | **78.1**

The typical range in healthy people is 64.09% to 78.06%

Acetate is the most abundant short chain fatty acid produced by our gut microbiome. It plays an important role in fat metabolism, glucose metabolism and the immune system. 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]

Fibre degradation

58.6 | **52.4** | **87.6**

The typical range in healthy people is 52.4% to 87.58%

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

Lactate production

69.8 | **1** | **79.7**

The typical range in healthy people is 61.01% to 79.68%

Lactate or lactic-acid producing bacteria have a long tradition of beng used to produce fermented foods such as yoghurt, kefir, sauerkraut and kimchi. Lactate can reduce inflammation and help keep the gut cell barrier intact. Some bacterial species can also convert lactate to the short chain fatty acids acetate, propionate and butyrate.
[1] [2]

3-indolepropionic acid (IPA) production

0 | **0.36** | **1.8**

The typical range in healthy people is 0.02% to 1.75%

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 glucose metabolism and research in animal models suggests that IPA may also play a role in maintaining the gut barrier. IPA is formed by breaking down the amino acid tryptophan. Studies have indicated that consuming foods high in dietary fibre, and in particular rye, can help increase IPA production.
[1] [2] [3] [4]

Potential to **reduce** health

Hexa-acylated lipopolysaccharide production

0 | **0.36**

The typical range in healthy people is 0% to 0.36%

Hexa-lipopolysaccharide (hexa-LPS) is a pro-inflammatory compound produced by some species of bacteria within the Proteobacteria phylum. High levels of hexa-LPS in the blood have been observed in individuals with metabolic and inflammatory conditions. Diets high in fat, especially saturated fat, allow hexa LPS to cross the intestinal barrier and enter the bloodstream. Avoiding excessive intake of saturated fat can help reduce the ability of hexa-LPS to enter the bloodstream.Common dietary sources of saturated fats include butter, coconut products, palm oil, cheese, fatty meats, biscuit, cakes, chocolate and icecream.
[1] [2] [3] [4] [5] [6]

Histamine production

0.06 | **1.1** | **1.9**

The typical range in healthy people is 0.06% to 1.94%

Histamine is a chemical produced by the breakdown of the amino acid histidine. It is produced by both human cells and some bacterial species and plays an important role in immune regulation, gut function and the nervous system. Individuals with food allergies and irrritable bowel syndrome have been observed to have high levels of specific histamine receptors in the gut, making them more sensitive to histamine in the gut.
[1] [2] [3]

Ammonia (urease) production

5.7 | **6** | **16.9**

The typical range in healthy people is 5.62% to 16.94%

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

Trimethylamine production

1 | **1.7** | **5.1**

The typical range in healthy people is 1.65% to 5.15%

Trimethylamine is a compound produced by some gut microbes that is converted to another compound called trimethylamine-n-oxide (TMAO) in the liver. Increased TMAO levels have been observed in individuals with cardiometabolic and inflammatory disorders. However, the role of TMAO in these disorders is still not clear. Levels of TMAO are influenced by many factors including our gut microbiome, diet, integrity of the gut barrier, liver function and kidney function. The indoles diindolylmethane (DIM) and indole-3-carbinol (I3C) found in cruciferous vegetables (e.g. broccoli, cauliflower, cabbage, kale) may reduce the amount of trimethylamine that is converted to TMAO in the liver. In addition, excessive red meat consumption is associated with increased levels of TMAO in the blood. If your potential to produce trimethylamine is high, you may wish to increase your consumption of cruciferous vegetables and avoid eating excessive amounts of red meat.
[1] [2] [3] [4] [5] [6] [7]

Human DNA

0.06 | **4**

The typical range in healthy people is 0.03% to 4%

A high amount (greater than 4%) of human DNA may indicate gut inflammation. If there is greater than 4% human DNA, and there was no contamination (e.g. accidentally touched the swab during sampling), further clinical investigation is needed.

Protein degradation

88.2

The typical range in healthy people is 86.24% to 95.05%

A similar or low proportion of species that can break down protein compared to the healthy group is generally considered beneficial. Everyone's microbiome contains species that can break down protein. However, a high proportion of these species may reflect an insufficient amount of fibre in the diet or an excessive intake of protein.

Most protein is absorbed by your body, however excess protein will get passed to the large intestine where it is available to the gut microbiome. Microorganisms that break down protein produce a variety of compounds, including some compounds that promote inflammation.

If there are a high proportion of species that can break down protein in the microbiome, make sure there is sufficient fibre in the diet and consider avoiding excessive consumption of protein.

Hydrogen sulphide production

6.2   6.2   **14.6**

The typical range in healthy people is 6.17% to 14.61%

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. Hydrogen sulphide plays an important role in gut health by acting as an energy source for gut cells and protecting the gut barrier function. However, some studies have suggested that high levels of hydrogen sulphide can also disrupt the gut mucus barrier. 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. fragilis toxin production

0   **0.01**

The typical range in healthy people is 0% to 0.01%

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]

Species

Potential to promote health

Agathobacter faecis

0   **0.15**   **4.2**

The typical range in healthy people is 0% to 4.17%

Previously named *Roseburia faecis*. This is a common and important member of the human gut microbiome.

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

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

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

Emerging research:
This species is commonly associated with healthy controls in research studies. Low levels of this bacterium have been observed in patients with liver cirrhosis.
[1] [2] [3]

Potential to reduce health

Bilophila wadsworthia

0   **0.05**   **0.2**

The typical range in healthy people is 0% to 0.2%

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

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

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

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

Emerging research:
High levels of this species can promote inflammation in the gut and is associated with a diet high in saturated fats.
[1] [2] [3] [4] [5] [6]

Agathobacter rectale

0 — **4.2** — **7.2**

The typical range in healthy people is 0% to 7.22%

Previously named *Eubacterium rectale*, this is a common member of the human gut.

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

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

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

Emerging research:
This species is commonly associated with healthy controls in research studies. Low levels of this bacterium have been observed in inflammatory conditions.
[1] [2] [3]

Akkermansia muciniphila

0 — **1.2** — **1.2**

The typical range in healthy people is 0% to 1.19%

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.
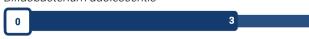
Emerging research:
By living in the mucus layer, *A. muciniphila* prevents potentially harmful bacteria from colonising this space through competition. Studies have associated low levels of *A. muciniphila* with metabolic conditions. Research has also indicated this species can improve the efficacy of a common immunotherapy drug used in cancer patients 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 elevated levels are associated with neurodegenerative conditions.
[1] [2] [3] [4] [5] [6] [7] [8] [9]

Bifidobacterium adolescentis

0 — **3**

The typical range in healthy people is 0% to 2.98%

This is a common and beneficial inhabitant of the gut.

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

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

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

Emerging research:
Low levels of this species have been associated with inflammation.
[1] [2] [3] [4] [5]

Clostridium_M bolteae

0

The typical range in healthy people is 0% to 0%

This is an inhabitant of the human gut.

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

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

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

Emerging research:
Elevated levels of this species has been associated with metabolic conditions.
[1] [2] [3] [4] [5] [6] [7] [8] [9] [10]

Eggerthella lenta

0 — **0.1**

The typical range in healthy people is 0% to 0.1%

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

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

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

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

Emerging research:
Elevated levels of this species have been associated with cardiovascular and metabolic conditions. This species can also inactivate the cardiac drug digoxin by breaking it down. Interestingly, this species prefers the amino acid arginine for growth. When arginine is present, this inhibits *E. lenta* from breaking down digoxin.
[1] [2] [3] [4] [5] [6] [7] [8] [9]

Fusobacterium nucleatum

0

The typical range in healthy people is 0% to 0%

Although a common member of the human oral microbiome, this pro-inflammatory bacterium can also be found in the human gut.

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

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: 3-IPA, acetate, biotin (B7), butyrate, cobalamin (B12), lactate, propionate, riboflavin (B2).

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

Emerging research:
High levels of this species have been associated with inflammatory conditions and poor gut health. Laboratory-based studies suggest that black and green tea may reduce the growth of this species.
[1] [2] [3] [4] [5] [6] [7] [8]

Bifidobacterium longum

0	0.88	1.5

The typical range in healthy people is 0% to 1.47%

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

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

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

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

Emerging research:
B.longum has been associated with reductions in harmful bacteria, anti-allergy effects, and anti-obesity effects in mouse models, but further research still needs to be done in humans.
[1] [2] [3] [4] [5] [6] [7]

Coprococcus eutactus

0	0.11	0.46

The typical range in healthy people is 0% to 0.46%

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

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

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

Emerging research:
This species has been observed at decreased levels in children with inflammatory conditions.

Eubacterium_E hallii

0	0.89	1.8

The typical range in healthy people is 0% to 1.75%

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 patients with intestinal disorders. Also, a study in mice suggested this species may be effective at improving insulin sensitivity.
[1] [2] [3] [4] [5]

Faecalibacterium prausnitzii_C

```
0          1.2    2
```

The typical range in healthy people is 0% to 2.02%

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

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

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

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

Emerging research:
Low levels of *F. prausnitzii* have been associated with inflammatory and metabolic conditions.
[1] [2] [3] [4] [5] [6] [7] [8] [9] [10]

Roseburia hominis

```
0      0.1    0.29
```

The typical range in healthy people is 0% to 0.29%

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

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

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

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

Emerging research:
This is a primary producer of the beneficial short chain fatty acid butyrate. Lower levels of this species have been observed in patients with inflammatory conditions. Another study observed higher levels in active women compared to sedentary women. Laboratory studies suggest this species can help regulate the immune system and reduce inflammation.
[1] [2] [3] [4] [5] [6] [7] [8] [9]

Roseburia intestinalis

```
0                  1.1
```

The typical range in healthy people is 0% to 1.12%

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

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

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

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

Emerging research:
This species has been observed at reduced levels in individuals with metabolic and inflammatory conditions.
[1] [2] [3]

Roseburia inulinivorans

`| 0 |──────────────── 0.65 ────────────────|`

The typical range in healthy people is 0% to 0.65%

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

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

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

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

Emerging research:
This is a primary producer of the beneficial short chain fatty acid butyrate. This species has been observed at reduced levels in individuals with type 2 diabetes.
[1] [2] [3]

Ruminococcus_E bromii

`| 0 |────────────────────────────────|`

The typical range in healthy people is 0% to 0%

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

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

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

Emerging research:
Studies suggest the role of *R. bromii* as a primary starch degrader helps stimulate the growth of butyrate-producing bacterial species.
[1] [2] [3]

Detoxification

100%

These markers and microorganism have been shown to influence the rates of inactivation and elimination of drugs and toxins from the body.

Metabolites

Potential to promote health

Oxalate consumption

1.7	7.6

The typical range in healthy people is 0.8% to 7.63%

Calcium oxalate is a common component of kidney stones. People who suffer from repeated unexplained kidney stones have been observed to have a reduced level of genes for oxalate degradation in their microbiome compared to healthy people. **[1] [2]**

Fibre degradation

58.6	52.4	87.6

The typical range in healthy people is 52.4% to 87.58%

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

Potential to reduce health

Beta-glucuronidase production

15.6	8.2	25.2

The typical range in healthy people is 8.17% to 25.17%

The human body will process and inactivate drugs and other compounds (hormones, neurotransmitters and environmental toxins) by adding a type of sugar to them called glucuronic acid. However, some bacteria can use this sugar as a fuel source, and they remove the sugar using beta-glucuronidase, thus re-activating the compound. These re-activated compounds can then be re-absorbed into the blood stream, increasing their potency. How increased levels of beta-glucuronidase in the gut influences drug metabolism is an active area of research. 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]**

Species

Potential to promote health

Oxalobacter formigenes_B

0

The typical range in healthy people is 0% to 0%

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

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

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

Potential to reduce health

Eggerthella lenta

0	0.1

The typical range in healthy people is 0% to 0.1%

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

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

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

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

Emerging research:
Elevated levels of this species have been associated with cardiovascular and metabolic conditions. This species can also inactivate the cardiac drug digoxin by breaking it down. Interestingly, this species prefers the amino acid arginine for growth. When arginine is present, this inhibits *E. lenta* from breaking down digoxin. **[1] [2] [3] [4] [5] [6] [7] [8] [9]**

Microbiome Diversity

Microbial diversity is a measure of the number of different microorganisms and the amount of each of these microorganisms in the 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.

3.4   4.3   4.6

Shannon Diversity Index

Microbiome Composition

Complete Microbiome Profile

Below is a list of each species detected in your microbiome, listed in order of abundance. Click on any species name to learn more about that species. Some microbes have been associated with health outcomes in scientific studies, while for others, little is known about them.

Everybody's microbiome composition is different, and science is telling us that the functional capacity of the microbiome is more important than which species inhabit it.

➕ *Species with this symbol beside the table have been implicated in influencing health.*

Search microbiome composition | Clear

	Phylum	Species	Abundance	Range	Level	
	Firmicutes_A	GCA-900066995 MIC7355	8.27%	0.00% - 0.00%	High	▼
	Bacteroidota	UBA7173 MIC9174	4.39%	0.00% - 0.00%	High	▼
➕	Firmicutes_A	Agathobacter rectale	4.19%	0.00% - 7.22%	Average	▼
➕	Firmicutes_A	Fusicatenibacter saccharivorans	3.15%	0.52% - 7.34%	Average	▼
	Firmicutes_A	CAG-110 sp000434635	2.90%	0.00% - 0.56%	High	▼
	Proteobacteria	CAG-495 sp000432275	2.65%	0.00% - 0.22%	High	▼
➕	Bacteroidota	Bacteroides uniformis	2.56%	0.14% - 4.89%	Average	▼
	Firmicutes_A	Ruminococcus_E bromii_B	1.90%	0.00% - 6.16%	Average	▼
	Firmicutes_A	Gemmiger sp003476825	1.70%	0.00% - 2.86%	Average	▼
➕	Firmicutes_A	Anaerostipes hadrus	1.58%	0.29% - 5.33%	Average	▼
➕	Actinobacteriota	Bifidobacterium catenulatum	1.54%	0.00% - 0.00%	High	▼
	Firmicutes_A	CAG-269 sp000431335	1.51%	0.00% - 0.10%	High	▼
➕	Euryarchaeota	Methanobrevibacter_A smithii	1.45%	0.00% - 0.58%	High	▼
	Firmicutes_A	CAG-475 MIC8449	1.37%	0.00% - 0.00%	High	▼
	Firmicutes_A	Gemmiger formicilis	1.32%	0.00% - 2.51%	Average	▼
	Firmicutes_A	Lachnospira eligens_B	1.32%	0.00% - 1.74%	Average	▼
	Firmicutes_A	Gemmiger MIC8010	1.30%	0.00% - 0.23%	High	▼
➕	Verrucomicrobiota	Akkermansia muciniphila	1.23%	0.00% - 1.19%	High	▼
➕	Firmicutes_A	Faecalibacterium prausnitzii_C	1.16%	0.00% - 2.02%	Average	▼
➕	Bacteroidota	Bacteroides_B vulgatus	1.13%	0.00% - 6.38%	Average	▼
	Firmicutes_A	Blautia_A sp900066335	1.09%	0.00% - 0.97%	High	▼
➕	Firmicutes_A	Ruminiclostridium_E siraeum	1.08%	0.00% - 1.58%	Average	▼
	Firmicutes	CAG-345 sp000433315	1.08%	0.00% - 0.06%	High	▼
	Firmicutes_A	Ruminococcus_C MIC7726	1.06%	0.00% - 0.00%	High	▼
	Firmicutes_A	CAG-127 sp900319515	1.03%	0.00% - 0.89%	High	▼
	Firmicutes_A	Faecalibacterium MIC9210	0.92%	0.00% - 0.74%	High	▼

	Phylum	Species	Abundance	Range	Level	
	Firmicutes_A	UBA11524 sp000437595	0.92%	0.00% - 2.87%	Average	▼
➕	Firmicutes_A	Eubacterium_E hallii	0.89%	0.00% - 1.75%	Average	▼
➕	Actinobacteriota	Bifidobacterium longum	0.88%	0.00% - 1.47%	Average	▼
	Firmicutes_A	CAG-272 MIC7612	0.87%	0.00% - 0.00%	High	▼
	Firmicutes_A	KLE1615 sp900066985	0.79%	0.17% - 2.22%	Average	▼
	Firmicutes_A	Acetatifactor sp900066365	0.75%	0.00% - 0.82%	Average	▼
	Firmicutes_A	CAG-273 sp000435755	0.68%	0.00% - 0.04%	High	▼
	Firmicutes_A	CAG-56 sp900066615	0.64%	0.00% - 0.97%	Average	▼
	Firmicutes_A	Lachnospira rogosae	0.61%	0.00% - 1.05%	Average	▼
	Firmicutes	CAG-594 sp000434835	0.60%	0.00% - 0.00%	High	▼
	Bacteroidota	Alistipes onderdonkii	0.59%	0.00% - 0.68%	Average	▼
➕	Bacteroidota	Alistipes shahii	0.58%	0.00% - 0.52%	High	▼
	Firmicutes_A	CAG-170 sp000432135	0.57%	0.00% - 0.64%	Average	▼
➕	Bacteroidota	Alistipes putredinis	0.56%	0.00% - 2.61%	Average	▼
	Firmicutes_A	CAG-115 sp003531585	0.53%	0.00% - 0.36%	High	▼
	Firmicutes_A	Blautia_A sp900066165	0.49%	0.19% - 2.41%	Average	▼
	Firmicutes_A	CAG-41 sp900066215	0.49%	0.00% - 0.82%	Average	▼
➕	Firmicutes	Streptococcus salivarius	0.47%	0.00% - 0.31%	High	▼
	Firmicutes_A	Blautia_A wexlerae	0.46%	0.34% - 6.60%	Average	▼
	Firmicutes_A	Faecalibacterium prausnitzii_J	0.45%	0.00% - 1.65%	Average	▼
	Firmicutes_A	Faecalibacterium prausnitzii_I	0.45%	0.00% - 0.53%	Average	▼
	Firmicutes_A	Acetatifactor sp003447295	0.43%	0.00% - 0.04%	High	▼
	Bacteroidota	Bacteroides MIC7573	0.39%	0.00% - 0.00%	High	▼
	Bacteroidota	Bacteroides stercoris	0.38%	0.00% - 2.66%	Average	▼
	Bacteroidota	Bacteroides faecis	0.37%	0.00% - 0.25%	High	▼
	Firmicutes_A	CAG-83 sp000435555	0.35%	0.00% - 1.33%	Average	▼
	Firmicutes_A	F23-B02 sp001916715	0.34%	0.00% - 0.51%	Average	▼
	Firmicutes_A	Eubacterium_F sp003491505	0.33%	0.00% - 0.48%	Average	▼
	Firmicutes_A	Blautia_A MIC8050	0.32%	0.00% - 0.33%	Average	▼
	Firmicutes_A	Angelakisella MIC6791	0.31%	0.00% - 0.31%	High	▼
	Firmicutes_A	CAG-882 sp003486385	0.31%	0.00% - 0.38%	Average	▼
	Firmicutes_A	Blautia_A sp000436615	0.30%	0.00% - 1.55%	Average	▼
	Firmicutes_A	Faecalibacterium prausnitzii_G	0.29%	0.00% - 2.39%	Average	▼
	Firmicutes_A	Ruminococcus_A sp003011855	0.29%	0.00% - 0.89%	Average	▼
	Firmicutes	CAG-433 sp000433675	0.29%	0.00% - 0.14%	High	▼
➕	Firmicutes_A	Dorea longicatena	0.25%	0.00% - 1.76%	Average	▼

Phylum	Species	Abundance	Range	Level	
Cyanobacteria	QAMI01 sp003150395	0.25%	0.00% - 0.00%	High	▼
Firmicutes_A	CAG-74 MIC7649	0.25%	0.00% - 0.33%	Average	▼
Bacteroidota	Bacteroides intestinalis_A	0.24%	0.00% - 0.01%	High	▼
Firmicutes_A	CAG-170 sp002404795	0.24%	0.00% - 0.30%	Average	▼
Actinobacteriota	Bifidobacterium pseudocatenulatum	0.24%	0.00% - 0.25%	Average	▼
Bacteroidota	Alistipes obesi	0.23%	0.00% - 0.43%	Average	▼
Firmicutes_A	ER4 sp900317525	0.23%	0.00% - 0.38%	Average	▼
Firmicutes_A	Eubacterium_F sp000433735	0.22%	0.00% - 0.08%	High	▼
Actinobacteriota	CAG-1427 sp000435475	0.22%	0.00% - 0.06%	High	▼
Firmicutes_A	Eubacterium_G ventriosum	0.22%	0.00% - 0.27%	Average	▼
Firmicutes_A	Faecalibacterium prausnitzii_D	0.22%	0.00% - 1.72%	Average	▼
Firmicutes_A	TF01-11 sp003529475	0.22%	0.00% - 0.40%	Average	▼
Firmicutes_A	CAG-138 MIC9630	0.21%	0.00% - 0.48%	Average	▼
Firmicutes_A	PeH17 sp000435055	0.21%	0.00% - 0.83%	Average	▼
Firmicutes	Erysipelatoclostridium sp000752095	0.20%	0.00% - 1.02%	Average	▼
Firmicutes_A	Lachnospira sp003451515	0.20%	0.00% - 0.40%	Average	▼
Firmicutes_A	Faecalibacterium MIC7145	0.19%	0.00% - 1.48%	Average	▼
Proteobacteria	Sutterella wadsworthensis_B	0.19%	0.00% - 0.72%	Average	▼
Bacteroidota	Bacteroides_B dorei	0.19%	0.00% - 2.99%	Average	▼
Firmicutes_C	Phascolarctobacterium faecium	0.19%	0.00% - 0.44%	Average	▼
Firmicutes_A	Eisenbergiella sp900066775	0.19%	0.00% - 0.44%	Average	▼
Firmicutes_A	CAG-245 sp000435175	0.18%	0.00% - 0.22%	Average	▼
Firmicutes	CAG-417 sp000432835	0.18%	0.00% - 0.06%	High	▼
Firmicutes_A	Coprococcus_B comes	0.17%	0.09% - 0.81%	Average	▼
Firmicutes_A	Faecalicatena faecis	0.16%	0.00% - 1.35%	Average	▼
Bacteroidota	Barnesiella intestinihominis	0.16%	0.00% - 0.74%	Average	▼
Bacteroidota	Parabacteroides distasonis	0.16%	0.00% - 0.52%	Average	▼
Verrucomicrobiota	CAG-312 MIC7045	0.16%	0.00% - 0.00%	High	▼
Firmicutes_A	Romboutsia timonensis	0.16%	0.00% - 0.64%	Average	▼
Bacteroidota	Parabacteroides merdae	0.15%	0.00% - 0.48%	Average	▼
Firmicutes_A	Acetatifactor sp900066565	0.15%	0.00% - 1.29%	Average	▼
Firmicutes_A	Agathobacter faecis	0.15%	0.00% - 4.17%	Average	▼
Proteobacteria	CAG-495 sp001917125	0.14%	0.00% - 0.16%	Average	▼
Actinobacteriota	Collinsella aerofaciens_F	0.14%	0.00% - 0.51%	Average	▼
Firmicutes_A	CAG-217 sp000436335	0.14%	0.00% - 1.30%	Average	▼
Firmicutes_A	CAG-83 sp001916855	0.14%	0.00% - 0.57%	Average	▼

	Phylum	Species	Abundance	Range	Level	
	Firmicutes_A	*Coprococcus_A MIC9199*	0.14%	0.00% - 0.27%	Average	▼
	Firmicutes	*Merdibacter MIC6626*	0.14%	0.00% - 0.07%	High	▼
	Firmicutes_A	*Blautia_A sp000285855*	0.13%	0.00% - 0.13%	High	▼
➕	Bacteroidota	*Odoribacter splanchnicus*	0.12%	0.02% - 0.25%	Average	▼
	Actinobacteriota	*QAMH01 MIC6543*	0.12%	0.00% - 0.15%	Average	▼
	Firmicutes_A	*CAG-269 sp003525075*	0.12%	0.00% - 0.23%	Average	▼
	Firmicutes_A	*Gemmiger MIC9530*	0.12%	0.00% - 0.44%	Average	▼
	Firmicutes_A	*Agathobaculum butyriciproducens*	0.12%	0.00% - 0.62%	Average	▼
	Bacteroidota	*UBA11471 sp000434215*	0.11%	0.00% - 0.28%	Average	▼
	Actinobacteriota	*Adlercreutzia MIC8014*	0.11%	0.00% - 0.27%	Average	▼
	Firmicutes_A	*Ruminiclostridium_C sp000435295*	0.11%	0.00% - 0.30%	Average	▼
	Firmicutes_A	*UBA11774 sp003507655*	0.11%	0.00% - 0.80%	Average	▼
	Firmicutes_A	*Agathobaculum MIC7900*	0.11%	0.00% - 0.63%	Average	▼
	Firmicutes_A	*Coprococcus eutactus*	0.11%	0.00% - 0.46%	Average	▼
	Firmicutes_A	*TF01-11 sp001414325*	0.11%	0.00% - 0.48%	Average	▼
	Firmicutes_A	*ER4 sp000765235*	0.11%	0.00% - 0.64%	Average	▼
	Firmicutes_A	*Lachnospira sp900316325*	0.10%	0.00% - 0.59%	Average	▼
➕	Bacteroidota	*Bacteroides fragilis*	0.10%	0.00% - 0.37%	Average	▼
➕	Firmicutes_A	*Roseburia hominis*	0.10%	0.00% - 0.29%	Average	▼
	Bacteroidota	*UBA1820 sp002314265*	0.10%	0.00% - 0.02%	High	▼
	Firmicutes	*CAG-313 sp003539625*	0.10%	0.00% - 0.41%	Average	▼
	Actinobacteriota	*Collinsella MIC7079*	0.10%	0.00% - 0.00%	High	▼
	Firmicutes_A	*Faecalibacterium MIC8666*	0.09%	0.00% - 0.75%	Average	▼
	Firmicutes_A	*Blautia_A massiliensis*	0.09%	0.00% - 1.83%	Average	▼
	Firmicutes_A	*Monoglobus pectinilyticus*	0.09%	0.00% - 0.12%	Average	▼
➕	Firmicutes_A	*Eubacterium_I ramulus*	0.09%	0.00% - 0.43%	Average	▼
	Firmicutes_A	*Blautia_A sp900066205*	0.09%	0.00% - 0.66%	Average	▼
➕	Bacteroidota	*Bacteroides caccae*	0.09%	0.00% - 0.48%	Average	▼
	Firmicutes_A	*NK3B98 MIC8354*	0.09%	0.00% - 0.07%	High	▼
➕	Firmicutes_A	*Dorea formicigenerans*	0.08%	0.11% - 0.42%	Low	▼
	Desulfobacterota_A	*Desulfovibrio fairfieldensis*	0.08%	0.00% - 0.03%	High	▼
	Firmicutes_A	*CAG-110 sp003525905*	0.08%	0.00% - 0.33%	Average	▼
	Firmicutes_A	*CAG-81 sp900066785*	0.08%	0.00% - 0.15%	Average	▼
	Firmicutes_A	*Ruminococcus_D bicirculans*	0.08%	0.00% - 3.46%	Average	▼
➕	Bacteroidota	*Bacteroides ovatus*	0.07%	0.00% - 0.79%	Average	▼
	Firmicutes_A	*Blautia_A obeum*	0.07%	0.00% - 1.41%	Average	▼

	Phylum	Species	Abundance	Range	Level	
	Firmicutes_A	UBA738 sp003522945	0.07%	0.00% - 0.16%	Average	▼
➕	Firmicutes_A	Coprococcus_A catus	0.07%	0.00% - 0.43%	Average	▼
	Firmicutes_A	UBA1417 sp003531055	0.07%	0.00% - 0.98%	Average	▼
	Firmicutes_A	UBA10281 MIC9325	0.07%	0.00% - 0.00%	High	▼
➕	Firmicutes_A	Dorea longicatena_B	0.07%	0.00% - 0.75%	Average	▼
	Firmicutes_A	Oscillibacter sp001916835	0.07%	0.00% - 0.38%	Average	▼
	Firmicutes_A	Blautia_A sp900066505	0.06%	0.00% - 0.09%	Average	▼
	Firmicutes_A	Lawsonibacter asaccharolyticus	0.06%	0.00% - 0.13%	Average	▼
	Bacteroidota	Butyricimonas synergistica_A	0.06%	0.00% - 0.06%	Average	▼
➕	Firmicutes	Streptococcus thermophilus	0.06%	0.00% - 0.22%	Average	▼
	Firmicutes_A	Butyricicoccus_A sp002395695	0.06%	0.00% - 0.20%	Average	▼
	Firmicutes_A	Blautia_A sp900066355	0.05%	0.00% - 0.25%	Average	▼
➕	Desulfobacterota_A	Bilophila wadsworthia	0.05%	0.00% - 0.20%	Average	▼
	Firmicutes_A	Dorea sp900066555	0.05%	0.00% - 0.13%	Average	▼
	Firmicutes_A	Eubacterium_G sp000432355	0.05%	0.00% - 0.06%	Average	▼
	Firmicutes_A	CAG-349 sp003539515	0.05%	0.00% - 0.07%	Average	▼
	Firmicutes_A	Clostridium_Q sp003024715	0.05%	0.00% - 0.26%	Average	▼
	Firmicutes_A	Eubacterium_F MIC7104	0.05%	0.00% - 0.16%	Average	▼
	Actinobacteriota	Collinsella sp002232035	0.05%	0.00% - 0.23%	Average	▼
	Firmicutes_A	Oscillibacter sp900066435	0.05%	0.00% - 0.13%	Average	▼
	Firmicutes_A	Acutalibacteraceae MIC6974	0.05%	0.00% - 0.04%	High	▼
	Cyanobacteria	Gastranaerophilales MIC8890	0.05%	0.00% - 0.00%	High	▼
	Firmicutes_A	Lachnospira sp000437735	0.05%	0.00% - 0.26%	Average	▼
	Firmicutes_A	CAG-45 sp000438375	0.05%	0.00% - 0.11%	Average	▼
	Firmicutes_A	Lachnospiraceae MIC8879	0.05%	0.00% - 0.13%	Average	▼
	Firmicutes	CAG-288 sp000437395	0.04%	0.00% - 0.20%	Average	▼
	Firmicutes_A	UBA5446 MIC7134	0.04%	0.00% - 0.00%	High	▼
	Verrucomicrobiota	UBA11452 sp003526375	0.04%	0.00% - 0.06%	Average	▼
	Firmicutes_A	Lachnospiraceae MIC7886	0.04%	0.00% - 0.05%	Average	▼
	Firmicutes_A	CAG-269 sp000438255	0.04%	0.00% - 0.01%	High	▼
	Firmicutes	CAG-826 sp000437235	0.04%	0.00% - 0.00%	High	▼
	Firmicutes_A	CAG-74 MIC8932	0.04%	0.00% - 0.10%	Average	▼
	Bacteroidota	Bacteroides finegoldii	0.04%	0.00% - 0.27%	Average	▼
	Cyanobacteria	Zag111 sp002102825	0.04%	0.00% - 0.00%	High	▼
	Bacteroidota	Bacteroides xylanisolvens	0.04%	0.00% - 0.43%	Average	▼
	Firmicutes_A	Anaerovoracaceae MIC7478	0.04%	0.00% - 0.05%	Average	▼

Phylum	Species	Abundance	Range	Level	
Firmicutes	Erysipelatoclostridium sp003024675	0.03%	0.00% - 0.22%	Average	▼
Bacteroidota	Alistipes MIC9770	0.03%	0.00% - 0.06%	Average	▼
Eukaryote_unclassified	Blastocystis sp. subtype 1	0.03%	0.00% - 0.00%	High	▼
Proteobacteria	Parasutterella excrementihominis	0.03%	0.00% - 0.39%	Average	▼
Firmicutes_A	CAG-74 MIC7629	0.03%	0.00% - 0.07%	Average	▼
Firmicutes_A	CAG-110 MIC9052	0.03%	0.00% - 0.09%	Average	▼
Firmicutes_A	Anaerovoracaceae MIC8502	0.03%	0.00% - 0.06%	Average	▼
Firmicutes_A	CAG-269 sp001915995	0.03%	0.00% - 0.00%	High	▼
Firmicutes_A	CAG-170 MIC6856	0.03%	0.00% - 0.08%	Average	▼
Firmicutes_A	GCA-900066135 MIC6659	0.03%	0.00% - 0.25%	Average	▼
Firmicutes_A	UBA11475 sp003538975	0.03%	0.00% - 0.00%	High	▼
Firmicutes_A	CAG-170 sp003516765	0.03%	0.00% - 0.09%	Average	▼
Bacteroidota	Alistipes_A ihumii	0.03%	0.00% - 0.09%	Average	▼
Bacteroidota	Alistipes MIC8513	0.03%	0.00% - 0.09%	Average	▼
Bacteroidota	Coprobacter fastidiosus	0.02%	0.00% - 0.10%	Average	▼
Firmicutes_A	CAG-727 MIC7825	0.02%	0.00% - 0.05%	Average	▼
Bacteroidota	Alistipes finegoldii	0.02%	0.00% - 0.45%	Average	▼
Firmicutes_A	CAG-74 MIC9156	0.02%	0.00% - 0.00%	High	▼
Bacteroidota	Alistipes_A sp900240235	0.02%	0.00% - 0.07%	Average	▼
Firmicutes_A	Blautia_A sp900066145	0.02%	0.00% - 0.37%	Average	▼
Verrucomicrobiota	Victivallis MIC7293	0.02%	0.00% - 0.00%	High	▼
Firmicutes_A	CAG-272 MIC6999	0.02%	0.00% - 0.04%	Average	▼
Firmicutes_A	Blautia_A MIC7810	0.02%	0.00% - 0.08%	Average	▼
Proteobacteria	Sutterella MIC7554	0.02%	0.00% - 0.00%	High	▼
Firmicutes_A	UCG-010 MIC9407	0.02%	0.00% - 0.00%	High	▼
Firmicutes	Erysipelatoclostridium spiroforme	0.02%	0.00% - 0.07%	Average	▼
Firmicutes_A	UBA7160 MIC9207	0.02%	0.00% - 0.19%	Average	▼
Firmicutes_A	UBA7160 MIC6745	0.02%	0.00% - 0.31%	Average	▼
Firmicutes_A	UBA9502 MIC7149	0.02%	0.00% - 0.06%	Average	▼
Firmicutes_A	CAG-74 MIC8717	0.02%	0.00% - 0.04%	Average	▼
Firmicutes_A	GCA-900066135 sp900066135	0.02%	0.00% - 0.09%	Average	▼
Firmicutes_A	UBA7102 MIC9705	0.02%	0.00% - 0.02%	Average	▼
Firmicutes_A	CAG-74 MIC6989	0.02%	0.00% - 0.07%	Average	▼
Firmicutes_A	Clostridium_M sp000431375	0.02%	0.00% - 0.22%	Average	▼
Firmicutes_A	UBA866 MIC8205	0.02%	0.00% - 0.03%	Average	▼
Firmicutes_A	Faecalicatena MIC9341	0.02%	0.00% - 0.00%	High	▼

	Phylum	Species	Abundance	Range	Level	
	Firmicutes_A	*CAG-103 MIC6381*	0.02%	0.00% - 0.43%	Average	▼
	Firmicutes_A	*UBA3818 MIC8425*	0.02%	0.00% - 0.04%	Average	▼
	Firmicutes_A	*CAG-145 MIC8493*	0.01%	0.00% - 0.03%	Average	▼
	Firmicutes_A	*QALS01 sp003150575*	0.01%	0.00% - 0.08%	Average	▼
	Firmicutes_A	*Lachnospiraceae MIC6593*	0.01%	0.00% - 0.04%	Average	▼
	Firmicutes_A	*CAG-382 MIC9861*	0.01%	0.00% - 0.01%	Average	▼
	Firmicutes_A	*Butyricicoccaceae MIC8222*	0.01%	0.00% - 0.02%	Average	▼
	Firmicutes_A	*Clostridium saudiense*	0.01%	0.00% - 0.17%	Average	▼
	Firmicutes_A	*QAND01 MIC9470*	0.01%	0.00% - 0.00%	High	▼
	Firmicutes_A	*Oscillibacter MIC9243*	0.01%	0.00% - 0.01%	Average	▼
	Actinobacteriota	*Gordonibacter pamelaeae*	0.01%	0.00% - 0.04%	Average	▼
	Firmicutes_A	*CAG-74 MIC9650*	0.01%	0.00% - 0.02%	Average	▼
	Firmicutes_A	*Anaerovoracaceae MIC7161*	0.01%	0.00% - 0.01%	Average	▼

Health Associated Species

Below is a list of all species detected in the sample that have been implicated in influencing health.

Search microbiome composition   Clear

	Phylum	Species	Abundance	Range	Level	
➕	Firmicutes_A	*Agathobacter rectale*	4.19%	0.00% - 7.22%	Average	▼
➕	Firmicutes_A	*Fusicatenibacter saccharivorans*	3.15%	0.52% - 7.34%	Average	▼
➕	Bacteroidota	*Bacteroides uniformis*	2.56%	0.14% - 4.89%	Average	▼
➕	Firmicutes_A	*Anaerostipes hadrus*	1.58%	0.29% - 5.33%	Average	▼
➕	Actinobacteriota	*Bifidobacterium catenulatum*	1.54%	0.00% - 0.00%	High	▼
➕	Euryarchaeota	*Methanobrevibacter_A smithii*	1.45%	0.00% - 0.58%	High	▼
➕	Verrucomicrobiota	*Akkermansia muciniphila*	1.23%	0.00% - 1.19%	High	▼
➕	Firmicutes_A	*Faecalibacterium prausnitzii_C*	1.16%	0.00% - 2.02%	Average	▼
➕	Bacteroidota	*Bacteroides_B vulgatus*	1.13%	0.00% - 6.38%	Average	▼
➕	Firmicutes_A	*Ruminiclostridium_E siraeum*	1.08%	0.00% - 1.58%	Average	▼
➕	Firmicutes_A	*Eubacterium_E hallii*	0.89%	0.00% - 1.75%	Average	▼
➕	Actinobacteriota	*Bifidobacterium longum*	0.88%	0.00% - 1.47%	Average	▼
➕	Bacteroidota	*Alistipes shahii*	0.58%	0.00% - 0.52%	High	▼
➕	Bacteroidota	*Alistipes putredinis*	0.56%	0.00% - 2.61%	Average	▼
➕	Firmicutes	*Streptococcus salivarius*	0.47%	0.00% - 0.31%	High	▼
➕	Firmicutes_A	*Dorea longicatena*	0.25%	0.00% - 1.76%	Average	▼
➕	Actinobacteriota	*Bifidobacterium pseudocatenulatum*	0.24%	0.00% - 0.25%	Average	▼

	Phylum	Species	Abundance	Range	Level	
➕	Firmicutes_A	*Eubacterium_G ventriosum*	0.22%	0.00% - 0.27%	Average	▼
➕	Bacteroidota	*Bacteroides_B dorei*	0.19%	0.00% - 2.99%	Average	▼
➕	Firmicutes_A	*Coprococcus_B comes*	0.17%	0.09% - 0.81%	Average	▼
➕	Bacteroidota	*Parabacteroides distasonis*	0.16%	0.00% - 0.52%	Average	▼
➕	Bacteroidota	*Parabacteroides merdae*	0.15%	0.00% - 0.48%	Average	▼
➕	Firmicutes_A	*Agathobacter faecis*	0.15%	0.00% - 4.17%	Average	▼
➕	Bacteroidota	*Odoribacter splanchnicus*	0.12%	0.02% - 0.25%	Average	▼
➕	Bacteroidota	*Bacteroides fragilis*	0.10%	0.00% - 0.37%	Average	▼
➕	Firmicutes_A	*Roseburia hominis*	0.10%	0.00% - 0.29%	Average	▼
➕	Firmicutes_A	*Eubacterium_I ramulus*	0.09%	0.00% - 0.43%	Average	▼
➕	Bacteroidota	*Bacteroides caccae*	0.09%	0.00% - 0.48%	Average	▼
➕	Firmicutes_A	*Dorea formicigenerans*	0.08%	0.11% - 0.42%	Low	▼
➕	Bacteroidota	*Bacteroides ovatus*	0.07%	0.00% - 0.79%	Average	▼
➕	Firmicutes_A	*Coprococcus_A catus*	0.07%	0.00% - 0.43%	Average	▼
➕	Firmicutes_A	*Dorea longicatena_B*	0.07%	0.00% - 0.75%	Average	▼
➕	Firmicutes	*Streptococcus thermophilus*	0.06%	0.00% - 0.22%	Average	▼
➕	Desulfobacterota_A	*Bilophila wadsworthia*	0.05%	0.00% - 0.20%	Average	▼
➕	Bacteroidota	*Alistipes finegoldii*	0.02%	0.00% - 0.45%	Average	▼