SYNLAB

myBIOME

Gut microbiome report

Nome

ID campione Sample ID:

Report generato il 2024-12-30

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powered by MICROBA

Introduction to the myBIOME report

myBIOME™ is a comprehensive and detailed report with key information about your gut microbiome. With

As new information emerges about the links between the gut microbiome and health, we will continue to update the online report to include these new findings.

Report Summary

Nome Paziente YASMIN TIBERTI - **ID campione** D0MYB0010623 **Data del Report** 30/12/2024

Dichiarazione di esclusione di responsabilita (Disclaimer): This summary is intended to help interpret the myBiome report: it should only be used after the healthcare the aids health workers professional has conducted an assessment.

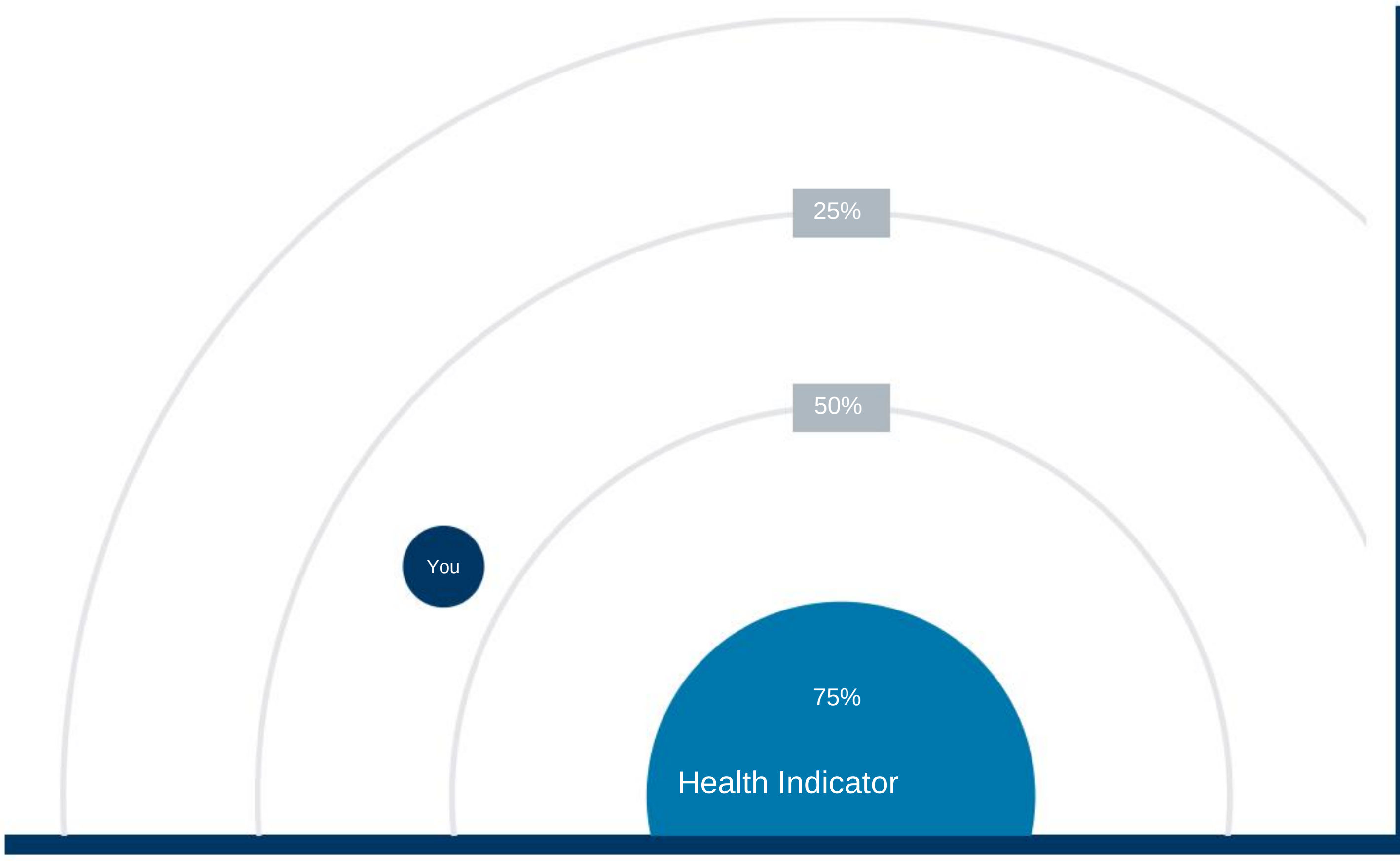
complete subject, including drug analysis, allergies, intolerances and the client's complete medical history.

Indicatore	**Suggerimento**
Pathobiontic Species	**Si raccomandano ulteriori indagini** The following species were detected in the sample and some strains may have an impact on health: [Escherichia coli (coli_D)]. Follow-up testing for intestinal pathogens is recommended.
Production of hydrogen sulfide (High)	**RS & FOS** Hydrogen sulfide is a gas that some intestinal bacteria produce by breaking down amino acids containing sulfur. High levels of hydrogen sulfide can inhibit energy production in intestinal cells and alter the mucus barrier of the gut, and this has been associated with inflammatory diseases intestinal. To prevent high production of hydrogen sulfide, make sure that the intake of amino acids methionine and cysteine is not excessive. Common sources of these amino acids include eggs, cheese, fish, red meat and poultry. Laboratory studies have suggested that eating foods high in resistant starch (e.g. lentils, peas, beans, rolled oats and potatoes cooked and cooled) or fructo-oligosaccharides (FOS) (e.g. onions, garlic, leeks, bananas, peaches, wheat, barley) can reduce the production of hydrogen sulfide by the microbiome. References [1] [2]
Consumption of oxalate (Poor)	**Dieta bassa di ossalato** If your microbiome has a low oxalate breakdown potential and you are prone to stones kidney, you may need to discuss a low-fat diet with a healthcare provider. oxalate. References [1] [2]
Production of cobalamin (B12) (Poor)	**Considera un supplemento di vitamina B** Consider this finding in the context of dietary intake of this vitamin and discuss with a healthcare professional whether a supplement might be suitable. References [1] [2] [3]
Production of biotin (B7) (Low)	**Considera un supplemento di vitamina B** Consider this finding in the context of dietary intake of this vitamin and discuss with a healthcare professional whether a supplement might be suitable. References [1] [2] [3] [4]

FINE DELLA SINTESI DEL REPORT

Overview

Welcome, on this journey we will show the effects of your microbiome on your health. In this report your sample is compared to a reference group of healthy individuals. The microbiome samples in this group are from individuals who have no significant health problems or symptoms, and are broadly representative of different ages, genders, and dietary habits.



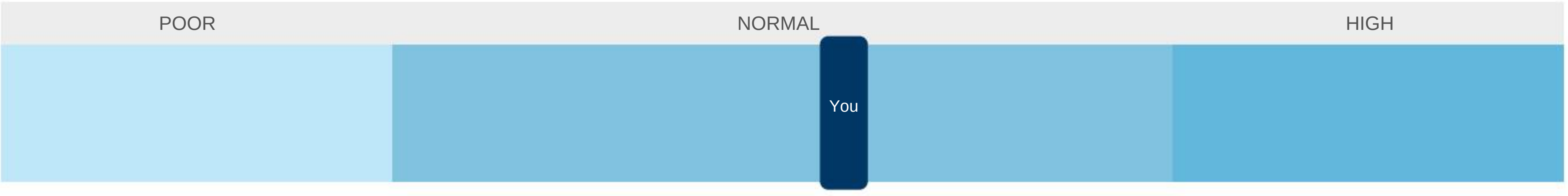
Your Microbiome Score

intestinal is Lower at 50%; this value is an indicator of the degree of interaction of the microbiome with general health. A higher score is an indicator of health improve.

Microbial diversity

MICROBIAL DIVERSITY

Microbial diversity is a measure of the number of different microorganisms and the amount of each in a sample. Moderate to high microbial diversity is associated with good health. A varied diet rich in plant-based foods (fruits, vegetables, whole grains, and nuts) can help increase microbiome diversity. The Shannon Index is a measure of diversity used by members of the scientific community to compare results over time.



Your level of diversity is

Normale

Shannon Index

4.11

Your key indicators

Potenziale del tuo microbioma intestinale di produrre butirrato, una fonte primaria di energia per le cellule intestinali

Buon livello! Your butyrate production potential is higher than healthy individuals. health. To continue to benefit from this important intestinal function, be sure to include in your diet foods rich in resistant starch.

A Questo campione ha un livello uguale a quello degli individui in buona salute

Butyrate production is a known function of the gut microbiome. This metabolite is a of the primary fuel sources for intestinal cells, capable of reducing inflammation throughout the body and help regulate appetite. Similar, or higher, levels of butyrate production are benefits your gut microbiome and helps maintain a healthy environment in your gut. Foods rich in resistant starch (e.g. lentils, peas, beans and oatmeal) stimulate microbes in your intestine to produce butyrate.

DATA EVALUATION ★★★★★

Potenziale del tuo microbioma di influire negativamente sull'infiammazione intestinale

Livello Normale. Your hexa-lipopolysaccharide (hexa-LPS) production potential is equal to that of healthy individuals, so it is unlikely that this substance is a major inflammation factor. A high-fiber diet may reduce levels of microbes that produce hexa-LPS.

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Hexa-lipopolysaccharides (hexa-LPS) are pro-inflammatory molecules, and one of the components of cell wall of some bacteria. When these bacteria die, hexa-LPS are released in the intestine. High-fat diets, especially saturated fats, allow hexa-LPS to cross the intestinal barrier and ultimately enter the bloodstream. High levels of hexa-LPS in the blood have been observed in individuals with heart disease, type 2 diabetes, obesity, and fatty liver disease non-alcoholic liver disease. If the production of hexa-LPS is high, it is best to avoid excessive consumption of saturated fats (e.g. butter, coconut oil, cheese, cured meats, chocolate, ice cream, cakes and biscuits).

DATA EVALUATION ★★★★★

Your key indicators

Capacità di tuo microbioma intestinale di scomporre le fibre

Buon livello! Your fiber breakdown potential is similar to that of the healthy group. Yes This is an important function of the intestinal microbiome to maintain, because it gives rise to production of beneficial substances that promote gut health. To ensure the production of these beneficial compounds, make sure your diet contains plenty of fiber.

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Fiber-degrading bacteria are responsible for the production of by-products such as acids short-chain fats, which play a vital role in keeping your gut healthy. prebiotic fibers, present in the recommended foods, promote the growth of beneficial bacteria, capable to degrade the fibers.

DATA EVALUATION ★★★★☆

Capacità del tuo microbioma intestinale di scomporre le proteine

Livello Normale. The percentage of bacteria in the sample capable of degrading proteins is equal to that of healthy individuals. The degradation of proteins by bacteria in the intestinal microbiome can lead to the production of substances that contribute to inflammation. To keep these levels normal, be sure to increase the flora of fiber-degrading bacteria, and not that of protein-degrading bacteria, through a diet rich in fibre.

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Each of our microbiomes contains species capable of degrading proteins in a variety of ways. compounds, including those that contribute to inflammation. Having a high percentage of these This may indicate an insufficient amount of fiber in the diet or an excessive intake of protein. A high percentage of protein-degrading bacteria suggests that the fiber needed to feed the bacteria fiber-degrading, which reaches the lower colon, is not sufficient.

DATA EVALUATION ★★★★☆

Your key indicators

Potenziale del tuo microbioma di produrre aminoacidi a catena ramificata

Buon Livello! Your branched chain amino acid (BCAA) production potential is at a good level equal to that of the healthy group. This is good, since it was observed that BCAAs, produced by bacteria, are associated with obesity and insulin resistance.

A **Questo campione ha un livello uguale a quello degli individui in buona salute**

BCAAs play an important role in building muscle and regulating metabolism. of fats and sugars. However, a high production potential of BCAAs, produced by your microbiome intestinal, may not be beneficial as high levels of BCAAs produced by the bacteria have been observed in subjects with obesity and insulin resistance. Have a BCAA production potential equal to or lower than that of healthy individuals is generally considered beneficial for the health. Maintaining muscle mass through regular physical activity helps regulate levels branched-chain amino acid blood samples.

DATA EVALUATION ★★★★☆

Potenziale del tuo microbioma di contribuire alle patologie cardiovascolari

Buon Livello! Your ability to produce trimethylamine (TMA) is at a level equal to that of healthy individuals. Trimethylamine is converted by the liver into methyl oxide trimethylamine (TMAO), which has been associated with cardiometabolic problems. It has been shown that Natural organic substances, such as indoles, reduce TMAO production.

A **Questo campione ha un livello più basso rispetto agli individui in buona salute**

A trimethylamine production capacity equal to or lower than that of healthy individuals is generally considered beneficial. Trimethylamine is converted by the liver to methyl oxide. trimethylamine (TMAO), which has been linked to cardio-metabolic problems. A high-protein diet animals and low in fiber has been associated with increased production of trimethylamine by gut microbes, while it has been shown that natural organic substances, such as indoles, reduce the production of TMAO.

DATA EVALUATION ★★★★☆

Your key indicators

Potenziale del tuo microbioma di proteggere il sistema nervoso

Buon Livello! The ability to produce indole propionic acid (IPA) is the same as that of healthy individuals. This is a good thing, because IPA is a powerful antioxidant capable of protect the body against insulin resistance and damage to nerve cells.

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IPA is a strong antioxidant produced by our gut bacteria that performs many functions important in our gut. It can protect nerve cells from damage, decrease inflammation, and protect against insulin resistance and type 2 diabetes. Consumption of foods high in fiber, particularly rye, has been associated with increased PAH production in the gut. A ability to produce indole propionic acid equal to or greater than that of individuals in good health is considered beneficial.

DATA EVALUATION ★★★☆☆

Potenziale del tuo microbioma di prevenire i calcoli renali

Questo non è un buon livello. Your oxalate degradation potential is low. Oxalate is a of the main components of calcium oxalate kidney stones. If you are prone to kidney stones, you may wish to discuss trying a low oxalate diet with a health care professional.

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The gut microbiome in individuals who suffer from frequent kidney stones often has a low ability to degrade oxalates. Oxalate is one of the main components of kidney stones. If I were prone to kidney stones, you may need to discuss a diet with a healthcare professional low in oxalate. If, on the other hand, you do not suffer from kidney stones then your ability to degrade Oxalates are not a cause for concern.

DATA EVALUATION ★★★☆☆

Your key indicators

Potenziale del tuo microbioma di produrre flatulenza

Questo non è un buon livello. The ability to produce hydrogen sulfide is high. Try adding foods high in prebiotic fiber, especially foods containing resistant starch (RS) and fructooligosaccharides (FOS) (e.g. potato salad, sweet potatoes, rye, lightly green bananas, nectarines, and pears) to reduce the production of hydrogen sulfide, which when produced by gut bacteria is associated with impaired intestinal barrier function.

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Following the digestion of various nutrients (fiber, protein, mucus, and bile acids) by gut microbes, various gases are produced as a byproduct. Flatulence is mainly composed of odorless gases such as nitrogen, hydrogen, carbon dioxide, and methane. However, a small percentage of flatulence may consist of hydrogen sulfide, which gives the characteristic rotten egg odor. Although a small amount of hydrogen sulfide has been shown to be protective for the gut, high production is associated with mitochondrial dysfunction and impaired intestinal barrier function. Production of hydrogen sulfide by gut bacteria can be inhibited by consuming foods high in resistant starch, prebiotic fiber (RS), and fructooligosaccharides (FOS).

DATA EVALUATION ★★★☆☆

Potenziale del tuo microbioma di contribuire alla replicazione e riparazione cellulari

Buon Livello! Your gut microbiome's ability to produce folate is higher than in healthy individuals. Folate is important for cell replication and repair. Your microbiome can contribute up to 37% of your daily folate needs.

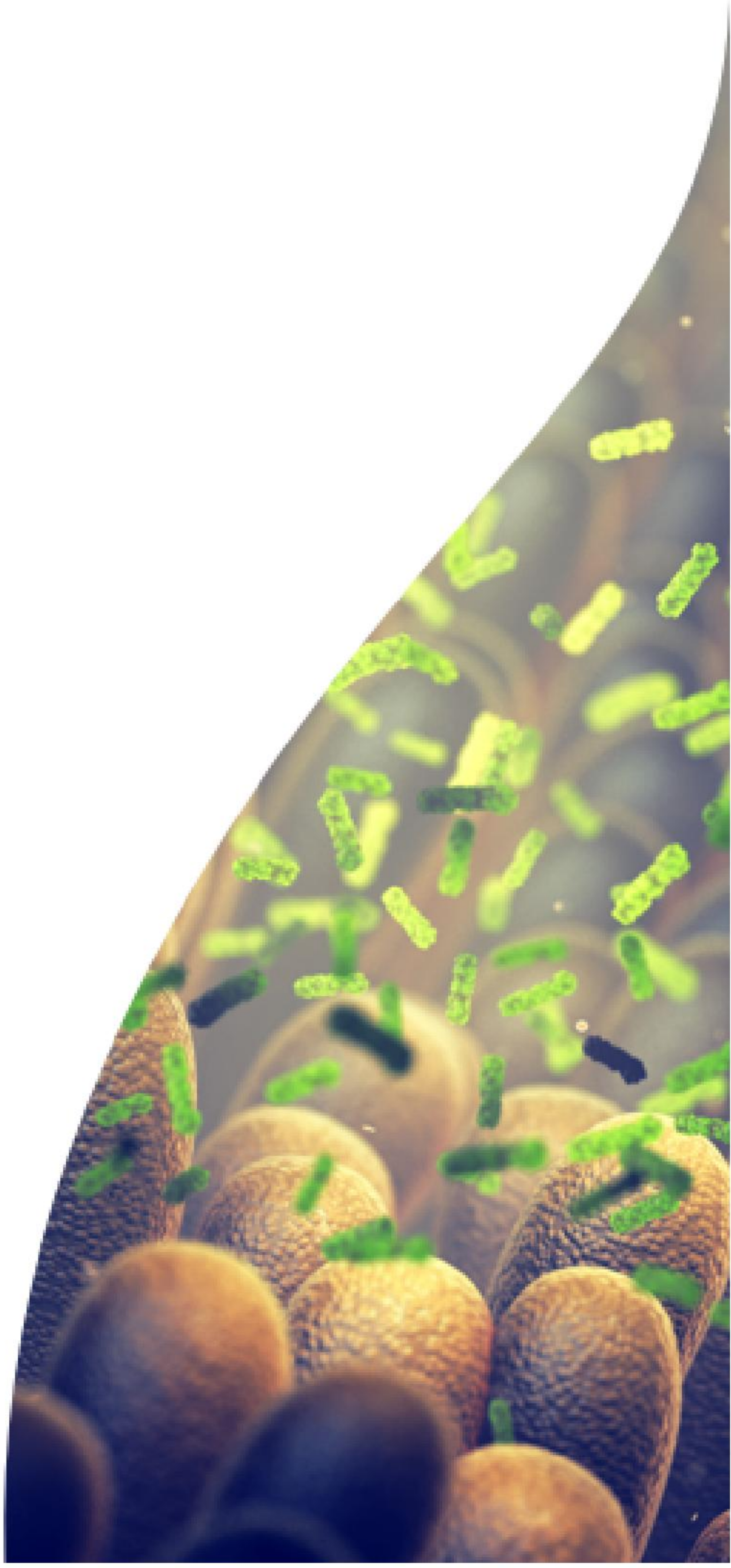
A Questo campione ha un livello più alto rispetto agli individui in buona salute

Folate plays an important role in cell replication and repair. Folate deficiencies can lead to an increased risk of heart disease, anemia, and stroke in adults. Our bodies cannot produce folic acid on their own, but we get it from plant foods (dark green leafy vegetables, fruits, and legumes) and from bacteria that live in our gut. Bacterial production can supplement your folate needs. A folic acid production potential equal to or greater than that of healthy individuals is generally considered beneficial to the body.

DATA EVALUATION ★★☆☆☆

In-depth analysis

Gut microbiome report



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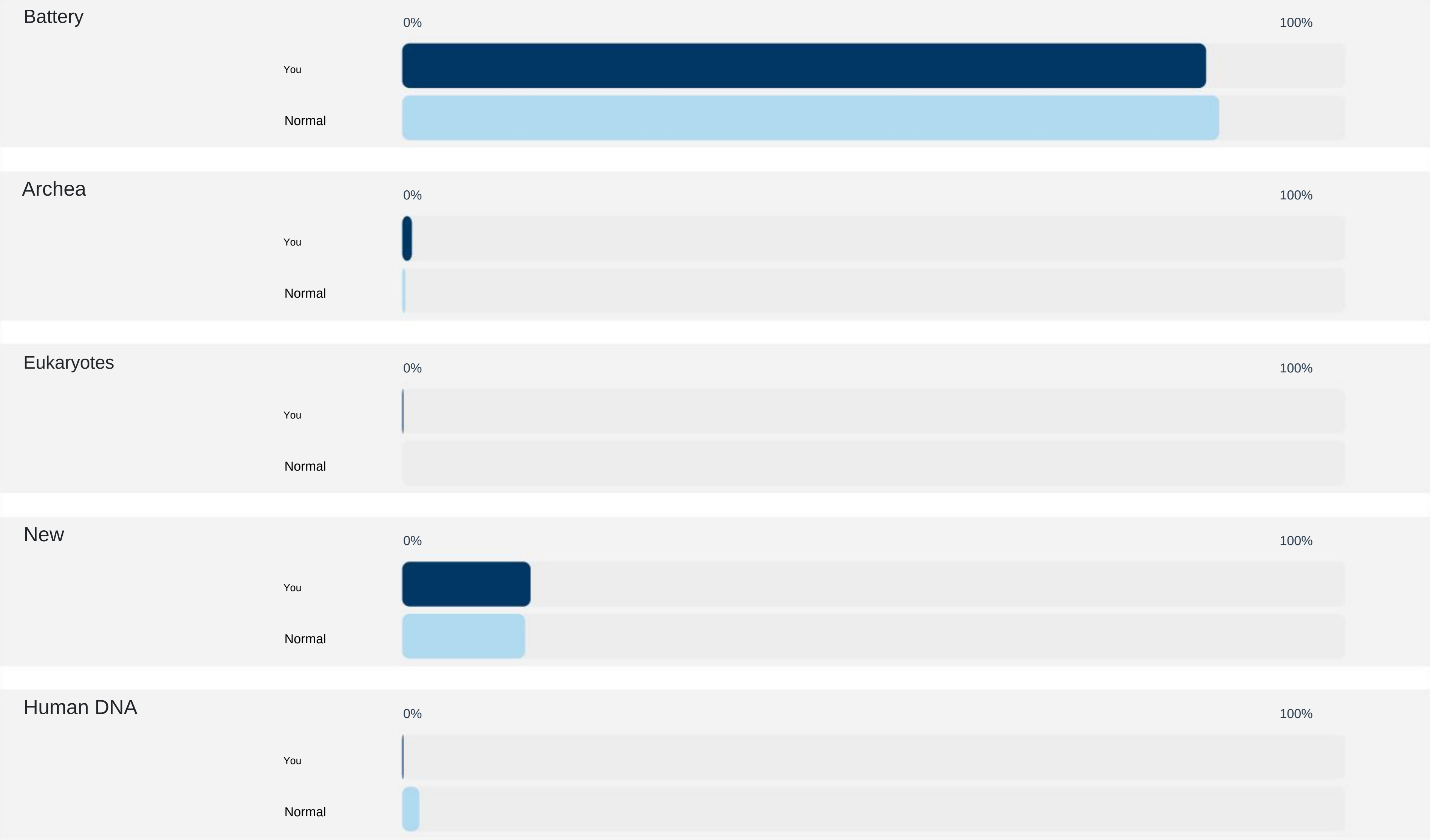
Sample composition

SAMPLE COMPOSITION

Most of the DNA in your stool (~99%) comes from microorganisms, and only a small amount (~1%) is your own DNA. Microorganisms in the gut are divided into four main groups: bacteria, archaea (another form of microscopic life), and eukaryotes. (this group includes fungi and parasites) and viruses. Shown below are the levels of bacteria, archaea, eukaryotes and new DNA (not identifiable) in the sample. The amount of human DNA present in the sample is also shown. A high amount of DNA human (greater than 4%) may indicate intestinal inflammation. If you have more than 4% human DNA, and you do not have accidentally touched the swab during sampling, you should consult a healthcare professional.

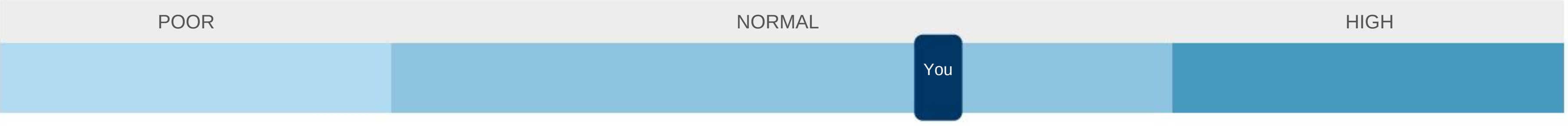


Digestive potential of the microbiome

The sources of food that bacteria can utilize vary according to the different species. The portion of species, present in the intestinal microbiome, which is able to break down energy sources: fiber, proteins and mucin. After the meal, the food is broken down in the stomach and then passes to the small intestine, where most of the nutrients are absorbed. Food components that cannot be absorbed in the small intestine, such as excess fiber and protein, pass into the small intestine large intestine, where the gut microbiota transforms these components into a variety of products called metabolites. Metabolites have an important role in health. In the tabs below you will find more information on energy sources and their correlations with health.

FIBRE

This scale indicates the species in your gut microbiome that can break down fiber. If your portion is low, you may Add more fiber to your diet to improve your gut health. Fiber is the source of energy main intestinal bacteria, which break them down into useful metabolites, such as short-chain fatty acids and B vitamins. Short-chain fatty acids like butyrate play an important role in keeping us healthy, and are one of the reasons which is why fiber is an important component of a healthy diet.

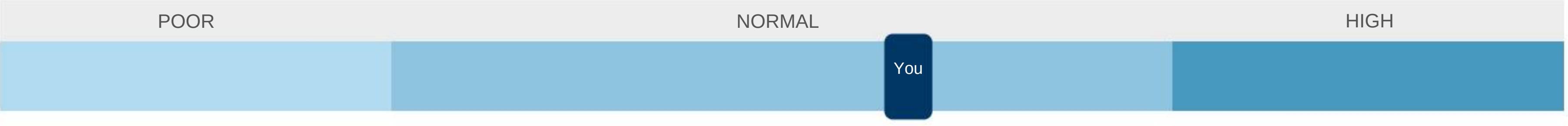


MUCINA

This scale indicates the species in your gut microbiome that are able to break down mucin, a component of the intestinal layer. protective mucosa of the intestine. Some bacteria can use mucin as an energy source. Mucus replacement is a normal intestinal function, but when the amount of bacteria feeding on mucus becomes excessive, it can result in a thinning of the mucous layer which causes the activation of the immune system. The mucous layer is important because it serves as a protective barrier between the cells lining the intestine and harmful bacteria. Mucus-breaking bacteria can increase when the amount of fiber reaching the lower large intestine is not sufficient. This allows bacteria to multiply intestinal that can use mucus as an energy source.

PROTEINS

This scale indicates the species in your gut microbiome that are able to break down proteins. If the portion is high, you may want to reduce the amount of protein in your diet to improve your gut health. Although most of protein is absorbed by the body, the excess that is not absorbed will be available to the gut microbiome. metabolites produced by the breakdown of proteins are various, some useful and others, which instead, promote inflammation. It has been observed that high-protein, low-fiber diets increase levels of pro-inflammatory intestinal metabolites.



Microbial metabolites

Gut bacteria can produce thousands of different substances, called metabolites, when using sources of different energy. These metabolites can interact with the system immune, metabolism and nervous system, influencing the health. Some of these metabolites have a beneficial effect on health, while others influence negatively on it.

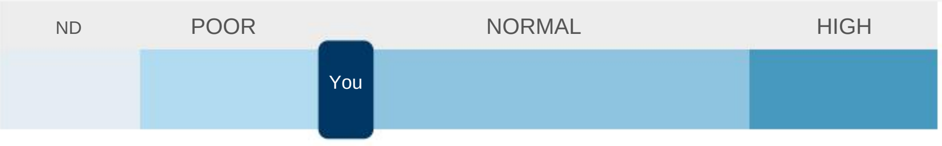
Microbial metabolites

Below we show the potential of the gut microbiome to produce or consume metabolites, associated with health or disease. Microorganisms in the gut can convert food components into thousands of products, called metabolites. Some metabolites are thought to be beneficial to health, while others have been associated with disease. Compare your potential microbiome to produce and consume metabolites with the selected comparison group. The "+" sign next to the compound name indicates that it is associated with health, while the "-" sign indicates that it is associated with disease. Click on the metabolite name to view its description.

HEALTH INDICATORS

Prodotti

⊖ Production of lipopolysaccharide ESA-acylate **0.088%**



L'abbondanza di il metabolita è circa la stessa del gruppo di confronto.

Hexa-acylated lipopolysaccharide (LPS) is a proinflammatory compound produced by certain species of bacteria within the phylum Proteobacteria. Elevated levels of hexa-acylated LPS in the blood have been observed in people with inflammatory conditions and metabolic diseases, such as obesity, heart disease, type II diabetes, and non-alcoholic fatty liver disease. Diets high in fat, especially saturated, allow hexa-acylated LPS to cross the intestinal barrier and enter the bloodstream. Avoid Excessive intake of saturated fat may help reduce the ability of hexa-acylated LPS to enter the bloodstream. Sources Common foods high in saturated fats include butter, coconut products, palm oil, cheese, fatty meats, biscuits, cakes, chocolate and ice cream.

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

⊖ Methane production **1.01%**

L'abbondanza di il metabolita è circa la stessa del gruppo di confronto.

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

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

Production of D-lactic acid **55.4%**

L'abbondanza di il metabolita è circa la stessa del gruppo di confronto.

Some species of lactobacilli can produce a special form of lactate called D-lactate. As a form of lactate, it has the beneficial properties of reducing inflammation, helping to maintain the intestinal cellular barrier and reducing colonization by part of pathogens by lowering the pH of the intestine. However, this form is not metabolized by the body as quickly rapidly and, in rare cases, in people with short bowel syndrome, D-lactate can accumulate and cause D-lactic acidosis.

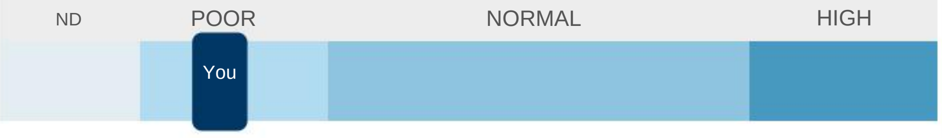
[1] [2] [3]

Microbial metabolites

HEALTH INDICATORS

Prodotti

⊖ Production of trimethylamine **1.13%**



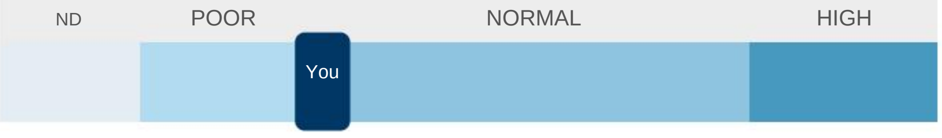
L'abbondanza di il metabolita è inferiore rispetto al gruppo di confronto.

A high potential for trimethylamine production has been linked to heart disease and type II diabetes. Once it has been produced by intestinal microbes, trimethylamine is transported to the liver and converted to trimethylamine-N-oxide (TMAO). It is TMAO has been shown to be involved in blood sugar control, blood clotting, and in inflammation.

The indoles diindolylmethane (DIM) and indole-3-carbinol (I3C) found in cruciferous vegetables (e.g. broccoli, cauliflower, cabbage, Savoy cabbage) can reduce the amount of trimethylamine that is converted to TMAO in the liver. Additionally, excessive consumption of red meat is associated with higher levels of TMAO in the blood. If the potential for trimethylamine production is high, it would be good increase consumption of cruciferous vegetables and avoid excessive amounts of red meat. The Heart Foundation recommends limiting red meat consumption to less than 350 g per week.

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

⊖ Production of ammonia (urease) **5.37%**



L'abbondanza di il metabolita è inferiore rispetto al gruppo di confronto.

Ammonia production is the normal way bacteria in the gut recycle proteins. However, high levels of ammonia production have been observed in people with compromised intestinal barrier function and inflammation of the intestine.

[1] [2]

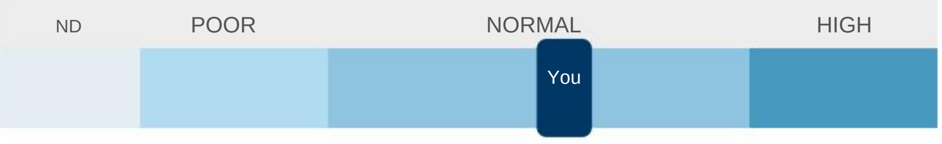
⊖ Production of B. toxin fragilis **0.00%**

il metabolita non viene rilevata in questo microbioma.

The gut microbiome of most people contains a species of bacteria called reduced strains of diarrhea, while in others Bacteroides fragilis . A share it can remain B. fragilis has the ability to secrete a toxin. In some people this toxin can cause symptoms such as asymptomatic. This toxin is suspected to cause intestinal inflammation. In If diarrhea occurs along with this toxin, it would be best to seek medical attention.

[1] [2]

Production of beta-glucuronidase **17.6%**



L'abbondanza di il metabolita è circa la stessa del gruppo di confronto.

Beta-glucuronidase is a bacterial enzyme that can limit the secretion of compounds from the body, such as drugs, hormones, and environmental toxins. One human study suggested that glucomannan consumption may reduce fecal beta-glucuronidase activity. Glucomannan is a type of prebiotic fiber found in konjac root and is commonly used to make low-calorie pasta and noodles.

[1] [2]

Microbial metabolites

HEALTH INDICATORS

Prodotti

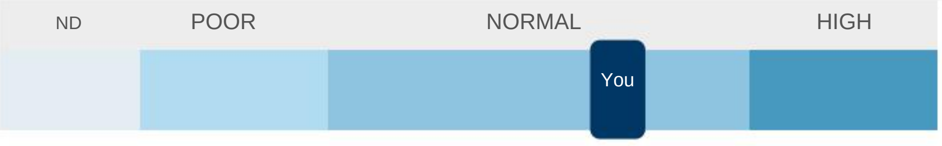
⊖ Hydrogen sulfide production **10.0%**

L'abbondanza di il metabolita è superiore rispetto al gruppo di confronto.

Hydrogen sulfide gas is produced by bacteria when they break down sulfur-containing amino acids found in foods. such as eggs, meat and fish. This gas is responsible for the rotten egg smell in flatulence. At low to medium levels, sulfide hydrogen may have a beneficial role by acting as an energy source for cells in the intestine. However, at high levels, hydrogen sulfide hydrogen can inhibit energy production in intestinal cells and compromise the intestinal mucosal barrier. High levels of hydrogen sulfide have been associated with inflammatory bowel disease. Laboratory studies have suggested that the intake of foods rich in resistant starch (e.g. lentils, peas, beans, oat flakes and cooked and cooled potatoes) or fructooligosaccharides (FOS) (e.g. onions, garlic, leeks, bananas, peaches, wheat and barley) may reduce the production of hydrogen sulfide by the microbiome.

[1] [2]

Production of amino acid chain a branched **65.7%**



L'abbondanza di il metabolita è circa la stessa del gruppo di confronto.

Branched-chain amino acids (BCAAs) are involved in the regulation of glucose and fat metabolism and the immune system. immune. High levels of BCAAs have been associated with metabolic disorders, such as obesity and type II diabetes. muscles have an important role in regulating BCAA levels. A high potential for BCAA production has been also associated with people with a low-fiber diet. Maximizing muscle mass through an activity Regular exercise can help maintain metabolic balance.

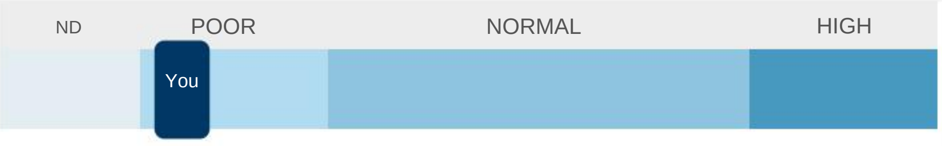
[1] [2]

Microbial metabolites

HEALTH INDICATORS

Consumati

Consumption of oxalate **0.206%**



L'abbondanza di il metabolita è inferiore rispetto al gruppo di confronto.

Some bacteria can break down oxalates in the colon, thus reducing the risk of oxalate kidney stones forming. calcium. It has been observed that people who suffer inexplicably and repeatedly from kidney stones have a low potential for oxalate degradation in the microbiome compared to those who do not suffer from it. A similar or elevated level for the oxalate degradation compared to the healthy subjects group is considered optimal, but if you do not suffer from kidney stones the potential of the intestinal microbiome for oxalate degradation is not a concern. If the microbiome has a low potential for oxalate breakdown and are predisposed to kidney stones, it would be good to talk about the possibility of trying a low-oxalate diet with a healthcare professional.

[1] [2]

Microbial metabolites

NEUROENDOCRINO

Prodotti

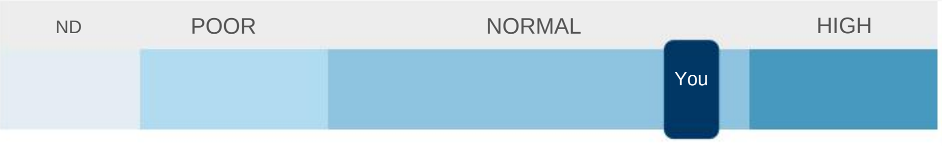
⊕ Production of FRONT **4.77%**

L'abbondanza di il metabolita è circa la stessa del gruppo di confronto.

Gamma-aminobutyric acid (GABA) plays an important role in regulating mental state by calming the nervous system. Low levels of GABA have been associated with depression and anxiety. GABA is mostly produced in the brain, but the gut microbiome can affect GABA levels because some bacteria can produce or consume it. The role of bacteria intestinal cells that produce GABA in anxiety and depression is not yet understood. If you have any concerns about this to your mental health, it is important to seek professional help.

[1] [2] [3]

Production of 3-acid indolepropionic (VIOLENCE) **0.983%**

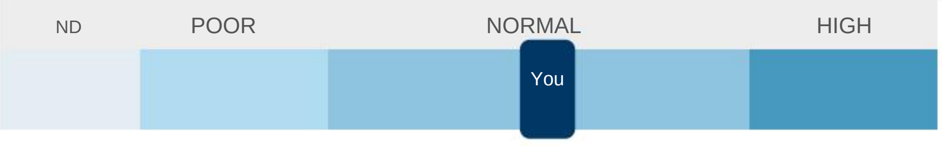


L'abbondanza di il metabolita è circa la stessa del gruppo di confronto.

3-Indolepropionic acid (IPA) is a beneficial substance produced by some intestinal bacteria when they break down the amino acid tryptophan. This is a strong antioxidant that can help protect the nervous system from damage. Research has also demonstrated that IPA may play a role in the prevention of type II diabetes and research in animal models suggests how IPA may suppress inflammation and help maintain the intestinal barrier. Studies have indicated that consumption of Foods rich in dietary fiber, especially rye, may help increase PAH production.

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

Histamine production **1.07%**



L'abbondanza di il metabolita è circa la stessa del gruppo di confronto.

Histamine is a chemical produced by the breakdown of the amino acid histidine. It is produced by human cells and also by some species of bacteria in the intestine. It plays an important role in regulating the immune system, the function intestinal and nervous system. Increased levels of intestinal bacteria that can produce histamine have been observed in patients with asthma. Additionally, people with food allergies and irritable bowel syndrome may be more sensitive to histamine in the intestine.

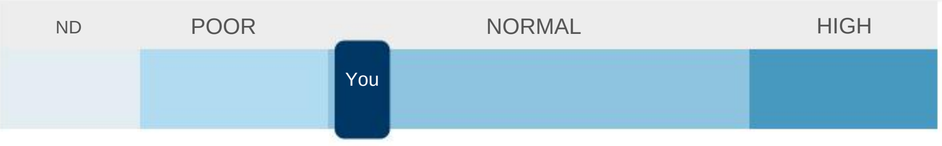
[1] [2] [3]

Microbial metabolites

NEUROENDOCRINO

Consumati

⊕ Consumption Of FRONT **3.23%**



L'abbondanza di il metabolita è circa la stessa del gruppo di confronto.

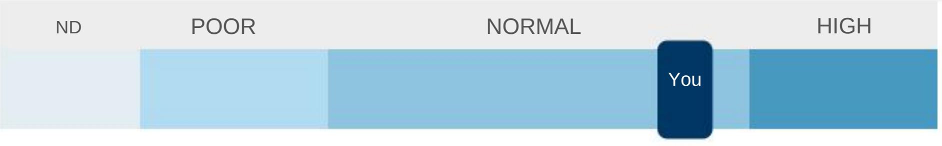
Gamma-aminobutyric acid (GABA) plays an important role in regulating mental state by calming the nervous system. Low levels of GABA have been associated with depression and anxiety. GABA is mostly produced in the brain, but the gut microbiome can affect GABA levels because some bacteria can produce or consume it. The role of bacteria intestinal cells that produce GABA in anxiety and depression is not yet understood. If you have any concerns about this to your mental health, it is important to seek professional help.
[1] [2] [3]

Microbial metabolites

SHORT CHAIN FATTY ACIDS

Prodotti

⊕ **Butyrate production** **24.5%**

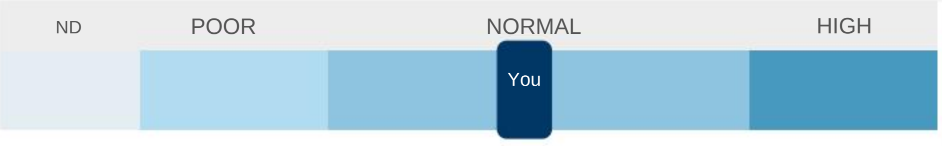


L'abbondanza di il metabolita è circa la stessa del gruppo di confronto.

Butyrate is a beneficial short-chain fatty acid that is very important for gut health. It is the source of energy main for the cells of the intestine, helps to keep the intestinal cell barrier intact, suppresses inflammation, helps to control appetite and promotes serotonin production in the gut. Low levels of butyrate production have been observed in people with inflammatory bowel disease. It has been shown that the consumption of starchy foods resistant (e.g. lentils, peas, beans, cooked and cooled potatoes, oat flakes) or pectin (e.g. avocado, kiwi, berries, citrus fruits, pumpkin, zucchini) increase butyrate levels.

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

Lactate production **70.2%**

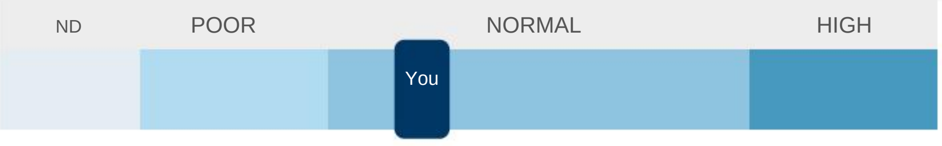


L'abbondanza di il metabolita è circa la stessa del gruppo di confronto.

Lactate, or lactic acid, is a beneficial substance produced by intestinal bacteria. It can reduce inflammation, helps maintain the intestinal cell barrier and protects against intestinal infections by lowering the pH in the intestine. Lactate can also be converted by some species of bacteria into beneficial short-chain fatty acids. Bacteria that produce lactate or lactic acid have a long tradition of use in the production of fermented foods, such as yogurt, kefir, sauerkraut and kimchi.

[1] [2]

⊕ **Propionate production** **2.48%**



L'abbondanza di il metabolita è circa la stessa del gruppo di confronto.

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

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

Microbial metabolites

SHORT CHAIN FATTY ACIDS

Prodotti

⊕ Acetate production **72.1%**

L'abbondanza di il metabolita è circa la stessa del gruppo di confronto.

Acetate is the most abundant short-chain fatty acid produced by the gut microbiome. It has a beneficial role due to the suppression of inflammation and regulation of appetite and fat metabolism. Several species of bacteria can also convert acetate into the beneficial short-chain fatty acid butyrate. Consuming whole grains, fruits, vegetables, legumes, nuts and seeds are associated with increased short-chain fatty acids, including acetate.

[1] [2] [3]

Microbial metabolites

ESSENTIAL VITAMINS

Prodotti

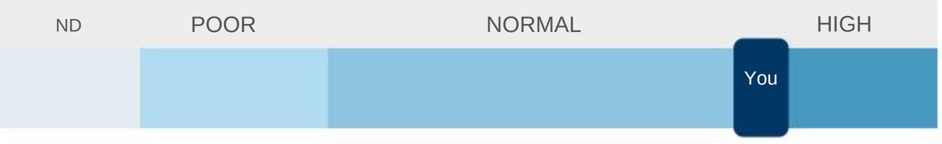
⊕ Cobalamin production (B12) **12.6%**

L'abbondanza di il metabolita è inferiore rispetto al gruppo di confronto.

Vitamin B12 is important for the normal functioning of the nervous system and for the development of red blood cells. Although intestinal bacteria can produce this vitamin, humans can only absorb it in the small intestine, so the vitamin B12 produced in the large intestine will not be used by our body. Even bacteria need vitamin B12 to function, so while it is unlikely that our gut bacteria provide us with usable vitamin B12, a medium to high B12 production potential means your bacteria won't compete with you for vitamin B12 available. Reduced production of vitamin B12 is often found in the gut microbiome of older people and A study conducted on elderly individuals observed that a multi-stage probiotic increased plasma B12 levels. Sources The most important sources of vitamin B12 are meat, milk and dairy products.

[1] [2] [3]

⊕ Folate production (B9) **64.1%**

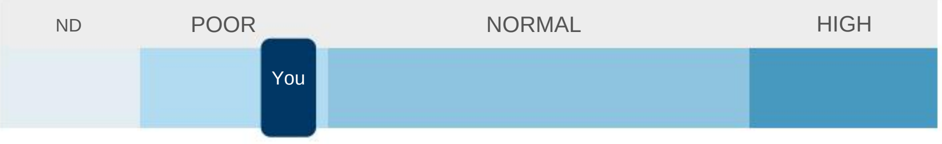


L'abbondanza di il metabolita è superiore rispetto al gruppo di confronto.

Folate or folic acid plays an important role in cell replication and repair. Low folate levels can lead to anemia and have been associated with an increased risk of heart disease and stroke. Folate cannot be produced by human cells and must be obtained from food 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 requirement. In Australia all non-organic bread must be fortified with folic acid, while among the food sources rich in this substance we find dark green leafy vegetables, fruit, legumes and nuts.

[1] [2] [3]

⊕ Biotin production (B7) **5.57%**



L'abbondanza di il metabolita è inferiore rispetto al gruppo di confronto.

Biotin plays a crucial role in metabolism and regulation of the immune system. Biotin cannot be produced from human cells and must be obtained through food or the microbiome. The large intestine has the ability to absorb biotin, but it is estimated that the human gut microbiome can only provide up to 4.5% of the daily biotin requirement humans. Food sources of biotin include liver, meat, fish, eggs, and nuts.

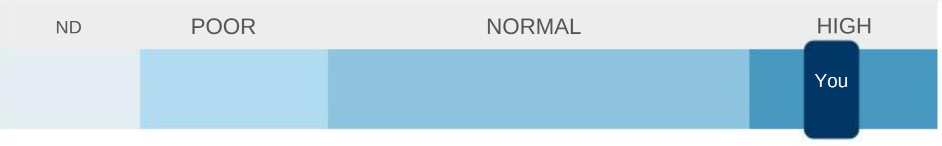
[1] [2] [3] [4]

Microbial metabolites

ESSENTIAL VITAMINS

Prodotti

⊕ Riboflavin production (B2) **54.1%**

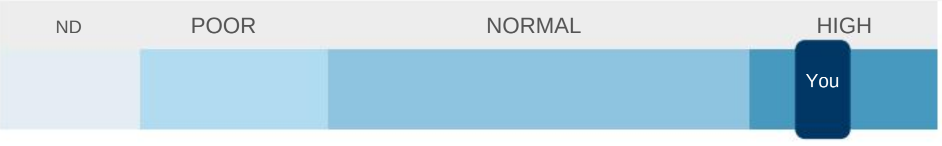


L'abbondanza di il metabolita è superiore rispetto al gruppo di confronto.

Riboflavin plays a crucial role in the metabolism of fats, vitamin B6, folate, tryptophan and homocysteine. Riboflavin cannot be produced by human cells and must be obtained from food or the microbiome. The large intestine has the ability to absorb riboflavin, but it is estimated that the human gut microbiome can only supply up to 2.8% of the daily requirement of riboflavin in humans. Food sources of riboflavin include milk and milk products, eggs, green vegetables, mushrooms, and fortified breads and cereals.

[1] [2] [3]

⊕ Vitamin production K **23.6%**



L'abbondanza di il metabolita è superiore rispetto al gruppo di confronto.

Vitamin K is a family of fat-soluble vitamins that play an important role in blood clotting. Vitamin K cannot be produced by human cells and must be obtained from food or the microbiome. Vitamin K1 (phylloquinone) is found in plants, such as dark green leafy vegetables and canola oil, and is the main form of dietary vitamin K used by the body. Bacterial vitamin K (menaquinone) is produced by intestinal bacteria and is found in fermented foods, dairy products and meat. The amount of bacterial vitamin K (menaquinone) that can be absorbed from the large intestine is still unknown.

[1] [2]

Species of interest

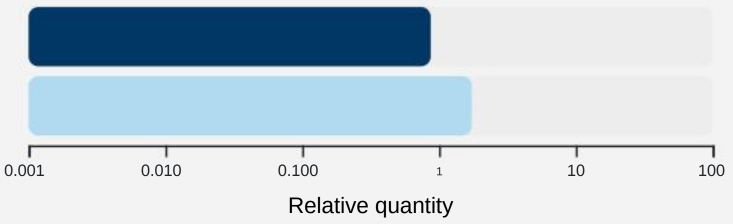
BACTERIA (PROKARYOTES)

Agathobacter — RILEVATI

⊕ ***Agathobacter faecis***

You 0.870%

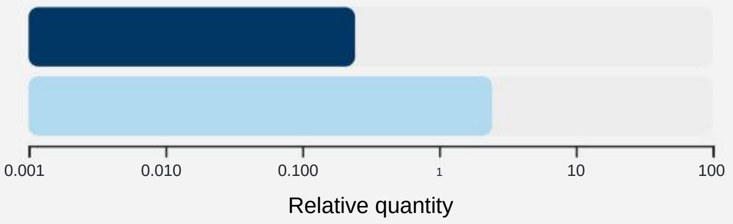
Normal 1.73%



⊕ ***Agathobacter rectale***

You 0.244%

Normal 2.44%

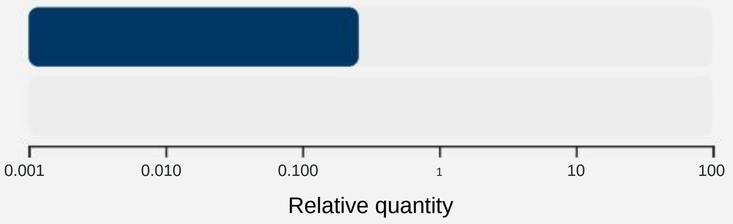


Akkermansia — RILEVATI

Akkermansia sp001580195

You 0.259%

Normal 0.00%



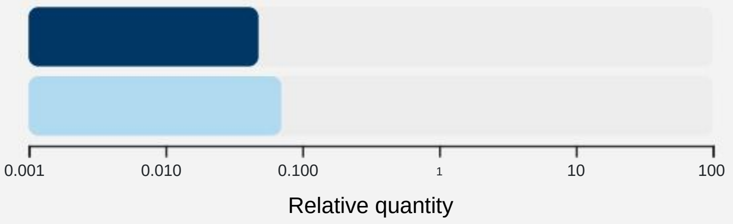
Bifidobacterium — NON RILEVATI

Bilophila — RILEVATI

⊖ ***Bilophila wadsworthia***

You 0.048%

Normal 0.070%



Campylobacter — NON RILEVATI

Citrobacter — NON RILEVATI

Clostridioides — NON RILEVATI

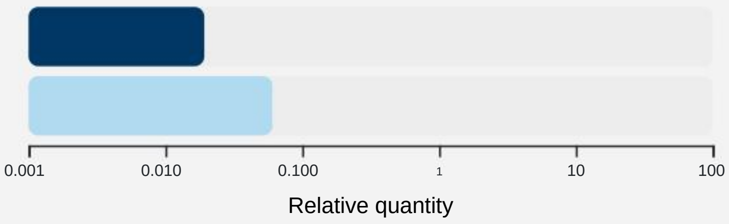
Clostridium

RILEVATI

Clostridium_M sp000431375

You **0.019%**

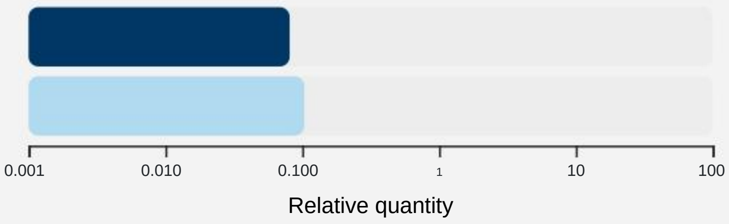
Normal **0.061%**



Clostridium_Q sp003024715

You **0.081%**

Normal **0.104%**



Corynebacterium

NON RILEVATI

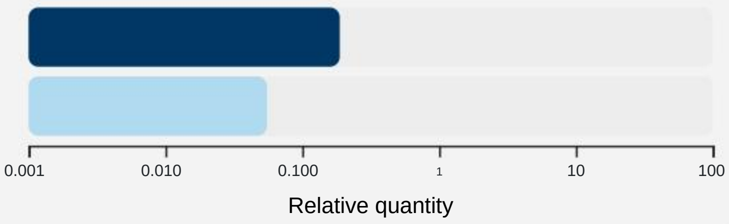
Desulfovibrio

RILEVATI

⊖ ***Desulfovibrio piger***

You **0.188%**

Normal **0.055%**



Eggerthella

NON RILEVATI

Enterobacter

NON RILEVATI

Enterococcus

NON RILEVATI

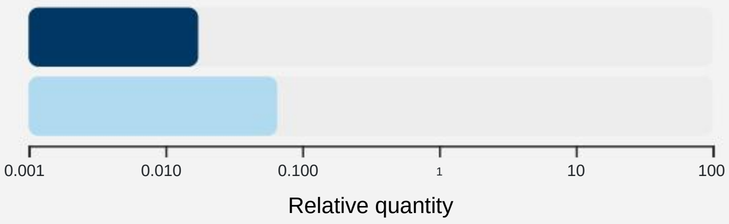
Escherichia

RILEVATI

⊖ ***Escherichia coli (coli_D)***

You **0.017%**

Normal **0.066%**

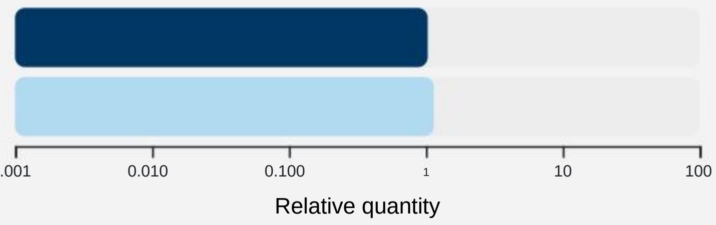


Faecalibacterium

RILEVATI

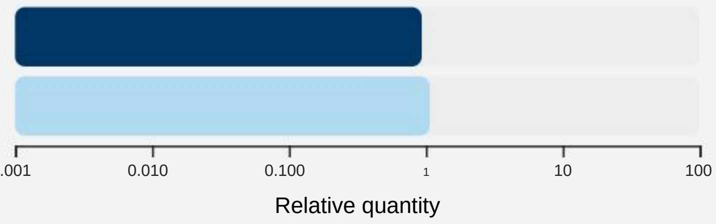
Faecalibacterium prausnitzii_D

You	1.03%
Normal	1.14%



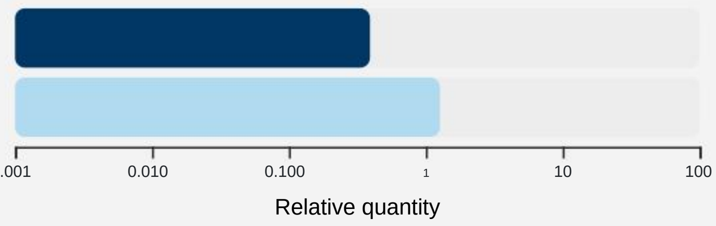
⊕ ***Faecalibacterium prausnitzii_C***

You	0.934%
Normal	1.07%



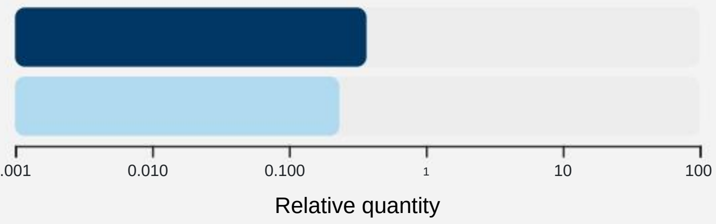
Faecalibacterium prausnitzii_G

You	0.391%
Normal	1.27%



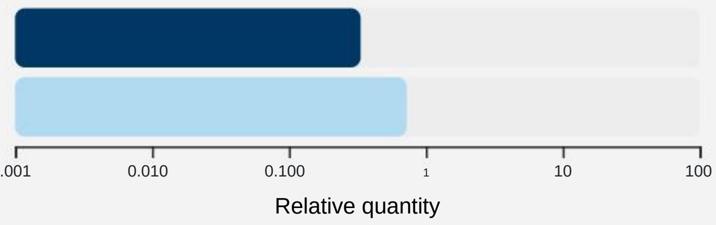
Faecalibacterium MIC8666

You	0.369%
Normal	0.234%



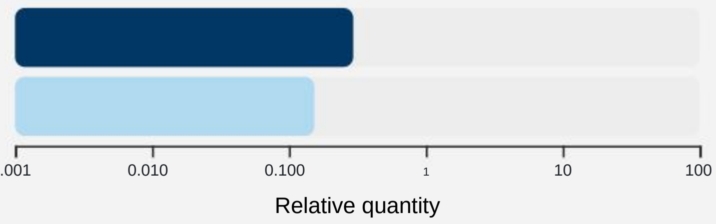
Faecalibacterium MIC7145

You	0.334%
Normal	0.726%



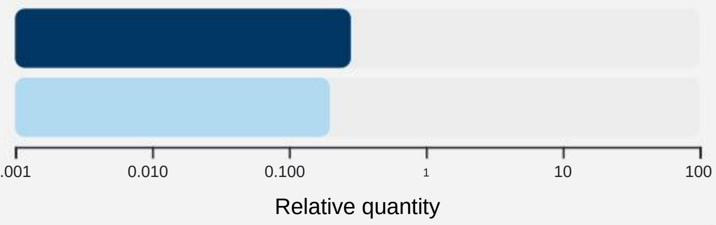
Faecalibacterium MIC9210

You	0.295%
Normal	0.154%



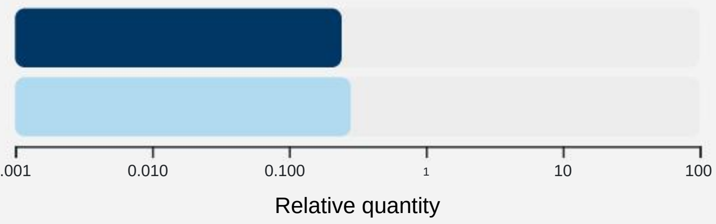
Faecalibacterium prausnitzii_A

You	0.283%
Normal	0.199%



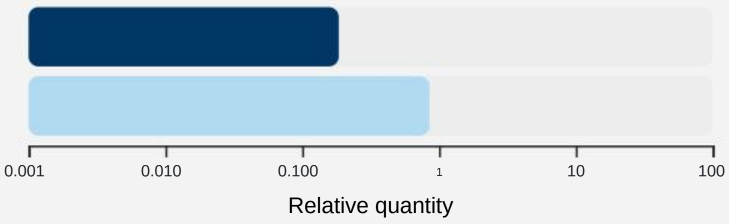
Faecalibacterium prausnitzii_I

You	0.243%
Normal	0.282%



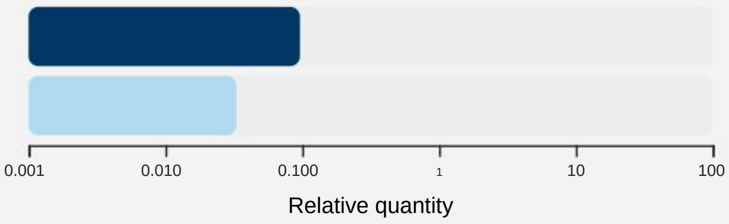
⊕ ***Faecalibacterium prausnitzii_K***

You	**0.185%**
Normal	**0.851%**



Faecalibacterium MIC8693

You	**0.096%**
Normal	**0.033%**



Fusobacterium	**NON RILEVATI**
Helicobacter	**NON RILEVATI**
Klebsiella	**NON RILEVATI**
Lactobacillus	**NON RILEVATI**
Porphyromonas	**NON RILEVATI**

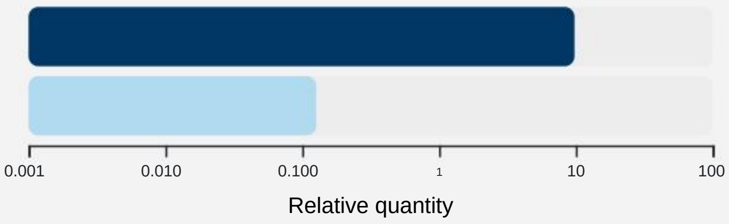
Prevotella

RILEVATI

Prevotella MIC6921

You **9.78%**

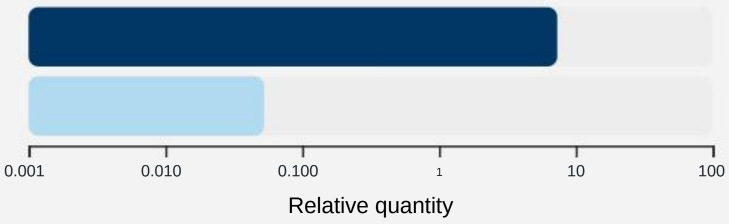
Normal **0.126%**



Prevotella sp000434515

You **7.32%**

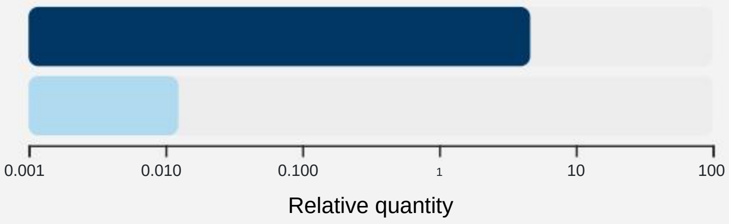
Normal **0.053%**



Prevotella sp000436035

You **4.64%**

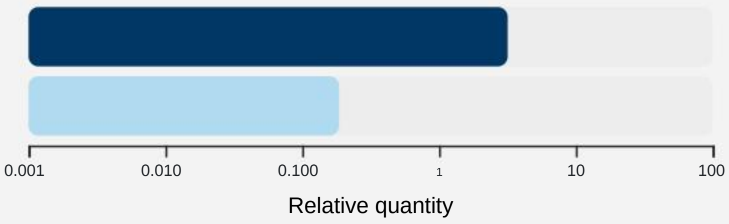
Normal **0.012%**



Prevotella sp900313215

You **3.18%**

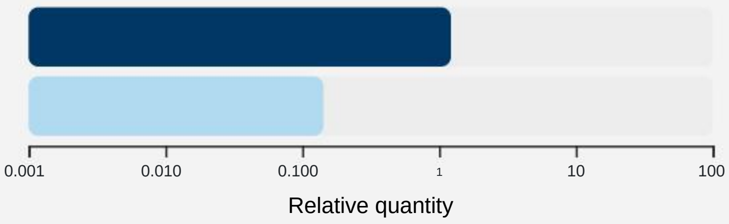
Normal **0.186%**



Prevotella sp003447235

You **1.22%**

Normal **0.143%**



Pseudomonas

NON RILEVATI

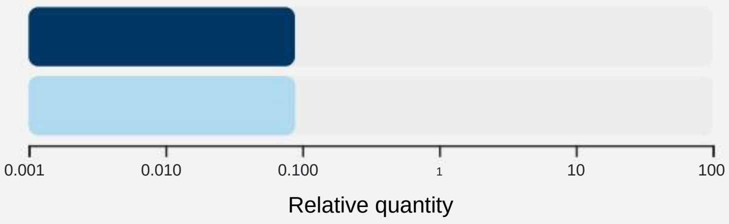
Roseburia

RILEVATI

⊕ **Roseburia hominis**

You **0.088%**

Normal **0.089%**



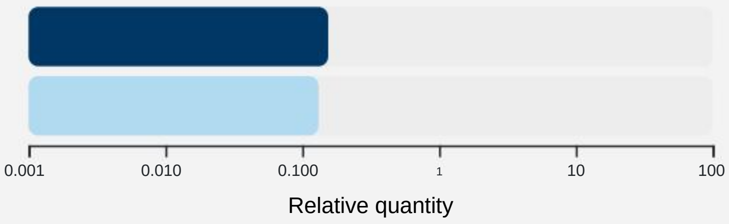
Ruminococcus

RILEVATI

Ruminococcus_A sp000437095

You **0.155%**

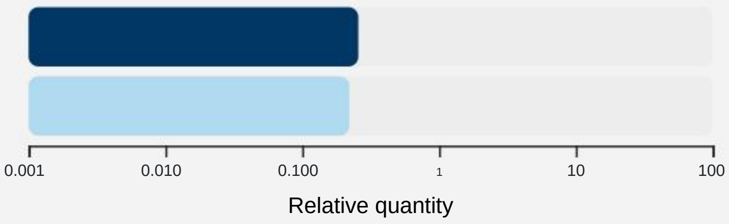
Normal **0.132%**



Ruminococcus_C sp000433635

You **0.257%**

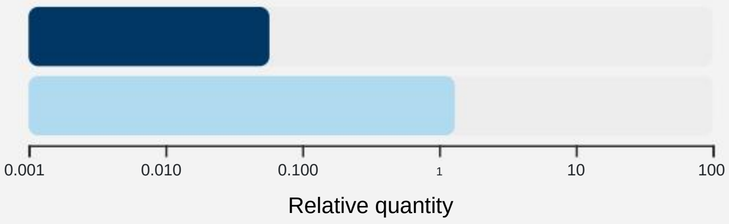
Normal **0.221%**



Ruminococcus_D bicirculans

You **0.058%**

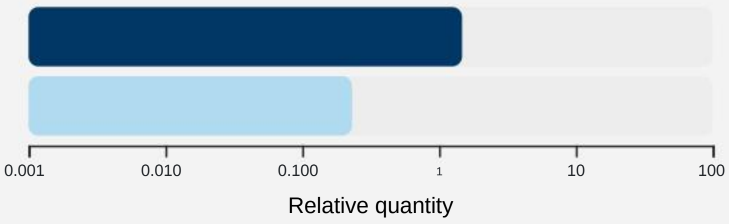
Normal **1.30%**



Ruminococcus_E sp900314705

You **1.47%**

Normal **0.231%**

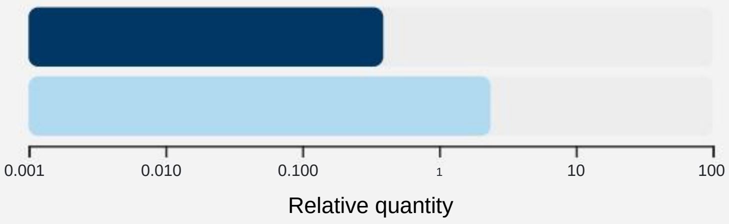


⊕

Ruminococcus_E bromii_B

You **0.391%**

Normal **2.38%**



Salmonella

NON RILEVATI

Streptococcus

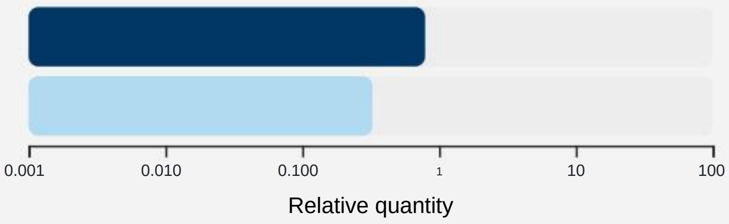
RILEVATI

⊖

Streptococcus salivarius

You **0.792%**

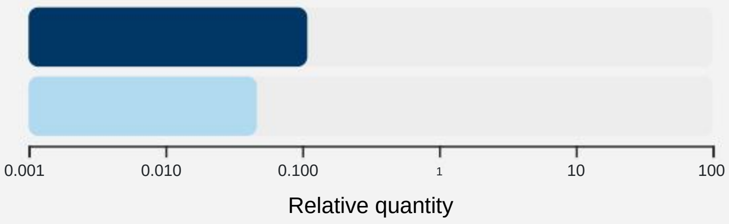
Normal **0.326%**



Streptococcus parasanguinis_B

You **0.109%**

Normal **0.047%**



Species of interest

ARCHAE (PROKARYOTES)

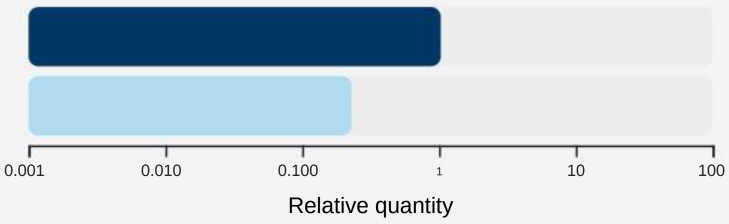
Metanogeni — RILEVATI

+−

Methanobrevibacter_A smithii

You **1.03%**

Normal **0.229%**



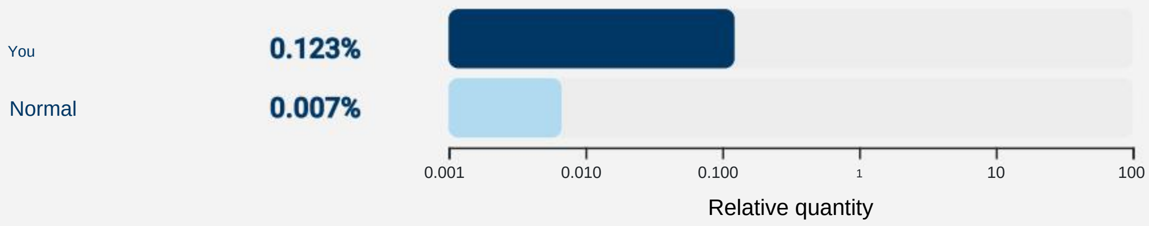
Altri Archea — NON RILEVATI

Species of interest

YEASTS / FUNGI AND PARASITES (EUKARYOTES)

Blastocystis **RILEVATI**

Blastocystis sp. subtype 4



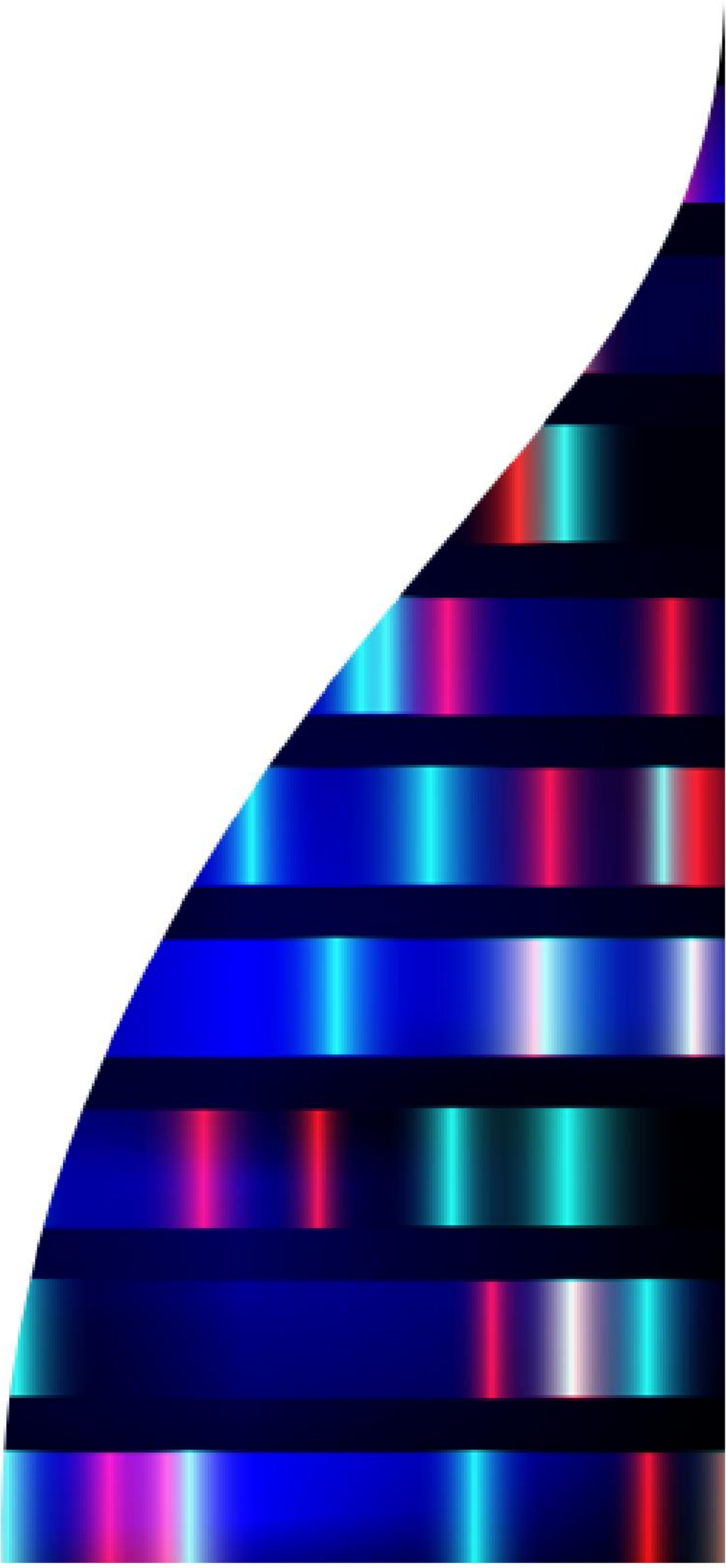
Candida **NON RILEVATI**

Saccharomyces **NON RILEVATI**

Altri Eucarioti **NON RILEVATI**

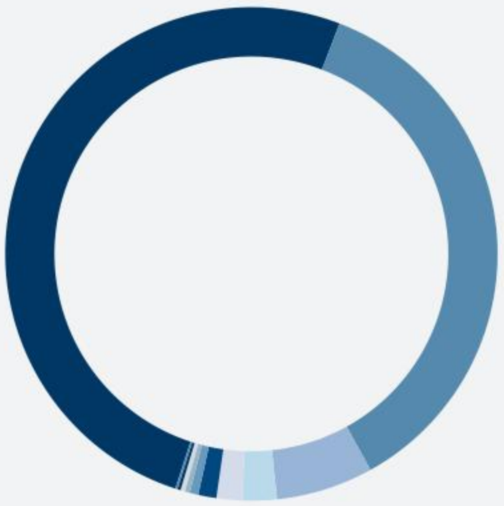
Microbial profile

Bacteria, Archaea, Eukaryotes



Your microbiome profile

PHYLUM



Sample composition

Phylum	Quantità	Intervallo	Livello
■ Firmicutes_A	43.9%	41.6 - 74.7%	Normal
■ Bacteroidota	31.2%	9.86 - 20.9%	High
■ Firmicutes	5.50%	0.926 - 12.2%	Normal
■ Proteobacteria	1.93%	0.389 - 5.10%	Normal
■ Actinobacteriota	1.47%	2.15 - 19.6%	Poor
■ Euryarchaeota	1.03%	0.00 - 0.932%	High
■ Firmicutes_C	0.493%	0.301 - 1.89%	Normal
■ Verrucomicrobiota	0.279%	0.00 - 0.731%	Normal
■ Desulfobacterota_A	0.249%	0.052 - 0.351%	Normal
■ Cyanobacteria	0.179%	0.00 - 0.810%	Normal
■ Eukaryotes_without classification	0.123%	0.00 - 0.00%	High

Species profile

SPECIES

	Phylum	Specie	Quantità	Intervallo	Livello
	Bacteroidota	***Prevotella MIC6921***	9.78%	0.00 - 0.00%	High

Fonti di energia utilizzate:

This species is an excellent degrader of fibres, a moderate degrader of mucin and a moderate degrader of proteins.

Metaboliti prodotti:

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.

Metaboliti consumati:

Genomic analysis indicates that most members of this species do not consume any reported metabolites.

Ricerca emergente:

This is a kind of new definition in the Microba database.

⊕	Firmicutes_A	***Butyrivibrio_A crossotus***	7.73%	0.00 - 0.850%	High

This species is found in the human intestine.

Fonti di energia utilizzate:

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

Metaboliti prodotti:

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), hydrogen sulfide.

Metaboliti consumati:

Genomic analysis indicates that most members of this species do not consume any reported metabolites.

Ricerca emergente:

This species plays an important role in reducing the availability of branched-chain amino acids (BCAAs). High levels of BCAAs have been linked to insulin resistance. In one study, reduced levels of this species were observed in people with inflammatory bowel disease.

Species profile

SPECIES

Phylum	Specie	Quantità	Intervallo	Livello
Bacteroidota	***Prevotella sp000434515***	7.32%	0.00 - 0.00%	High

Fonti di energia utilizzate:

This species is an excellent degrader of fibres, a moderate degrader of mucin and a moderate degrader of proteins.

Metaboliti prodotti:

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.

Metaboliti consumati:

Genomic analysis indicates that most members of this species do not consume any reported metabolites.

Ricerca emergente:

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

Bacteroidota	***Prevotella sp000436035***	4.64%	0.00 - 0.00%	High

Fonti di energia utilizzate:

This species is an excellent degrader of fibres, a moderate degrader of mucin and a moderate degrader of proteins.

Metaboliti prodotti:

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

Metaboliti consumati:

Genomic analysis indicates that most members of this species do not consume any reported metabolites.

Ricerca emergente:

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

Species profile

SPECIES

Phylum	Specie	Quantità	Intervallo	Livello
Bacteroidota	***Prevotella sp900313215***	3.18%	0.00 - 0.00%	High

Fonti di energia utilizzate:

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

Metaboliti prodotti:

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

Metaboliti consumati:

Genomic analysis indicates that most members of this species do not consume any reported metabolites.

Ricerca emergente:

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

Firmicutes_A	***Acetatifactor sp003447295***	3.11%	0.00 - 0.086%	High

Fonti di energia utilizzate:

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

Metaboliti prodotti:

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

Metaboliti consumati:

Genomic analysis indicates that most members of this species do not consume any reported metabolites.

Ricerca emergente:

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

Species profile

SPECIES

	Phylum	Specie	Quantità	Intervallo	Livello
	Firmicutes_A	***CAG-411 sp000437275***	2.26%	0.00 - 0.00%	High

Fonti di energia utilizzate:

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

Metaboliti prodotti:

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

Metaboliti consumati:

Genomic analysis indicates that most members of this species do not consume any reported metabolites.

Ricerca emergente:

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

⊕	Firmicutes_A	***Coprococcus eutactus_A***	1.72%	0.00 - 2.23%	Normal

It is a common inhabitant of the human intestine.

Fonti di energia utilizzate:

This species is a moderate degrader of fiber, mucin and proteins.

Metaboliti prodotti:

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).

Metaboliti consumati:

Genomic analysis indicates that most members of this species do not consume any reported metabolites.

Ricerca emergente:

This species has been observed at lower levels in people with asthma, children with type 1 diabetes, and people with Crohn's disease, indicating that it most likely has a beneficial role in health.

Species profile

SPECIES

	Phylum	Specie	Quantità	Intervallo	Livello
	Firmicutes	***Holdemanella sp002299315***	1.61%	0.00 - 0.724%	High

Fonti di energia utilizzate:

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

Metaboliti prodotti:

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

Metaboliti consumati:

Genomic analysis indicates that most members of this species do not consume any reported metabolites.

Ricerca emergente:

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

	Firmicutes_A	***CAG-127 sp900319515***	1.53%	0.00 - 1.28%	High

Fonti di energia utilizzate:

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

Metaboliti prodotti:

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).

Metaboliti consumati:

Genomic analysis indicates that most members of this species do not consume any reported metabolites.

Ricerca emergente:

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

Species profile

SPECIES

	Phylum	Specie	Quantità	Intervallo	Livello
	Firmicutes_A	***Ruminococcus_E sp900314705***	1.47%	0.00 - 0.00%	High
⊖	Bacteroidota	***Bacteroides_B dorei***	1.22%	0.00 - 2.68%	Normal
	Bacteroidota	***Prevotella sp003447235***	1.22%	0.00 - 0.00%	High
	Firmicutes_A	***F23-B02 sp001916715***	1.22%	0.00 - 0.429%	High
	Firmicutes_A	***Blautia_A obeum***	1.16%	0.134 - 2.01%	Normal
	Firmicutes_A	***Faecalibacterium prausnitzii_D***	1.03%	0.119 - 2.51%	Normal

It is a common inhabitant of the intestine and is closely related to the bacterium Bacteroides vulgaris

Fonti di energia utilizzate:

This species is an excellent degrader of fibres, an excellent degrader of mucin and a moderate degrader of proteins.

Metaboliti prodotti:

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

Metaboliti consumati:

Genomic analysis shows that most members of this species can consume: GABA.

Ricerca emergente:

Higher levels of this species have been observed in patients with colon cancer and during the development of type II diabetes in children. This species has also been associated with a diet high in red meat.

Species profile

SPECIES

	Phylum	Specie	Quantità	Intervallo	Livello
⊖	Euryarchaeota	***Methanobrevibacter_A smithii***	1.03%	0.00 - 0.769%	High

It is a unicellular organism belonging to the domain Archaea and is the most common archaeal species found in the gut. supposedly.

Fonti di energia utilizzate:

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

Metaboliti prodotti:

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

Metaboliti consumati:

Genomic analysis indicates that most members of this species do not consume any reported metabolites.

Ricerca emergente:

Higher levels of M. smithii have been observed with irritable bowel syndrome characterized by the presence of constipation, the diverticulosis and multiple sclerosis. However, lower levels were observed in patients with Crohn's disease and ulcerative colitis. hydrogen M. smithii It plays an important role in the intestine because it is one of the few species capable of removing excess bacterium. However, even large quantities of this species are not beneficial, as high levels of methane can cause constipation.

	Firmicutes_A	***CAG-83 sp000435555***	0.999%	0.00 - 0.913%	High
	Firmicutes	***CAG-313 sp000433035***	0.979%	0.00 - 0.005%	High
	Firmicutes_A	***Blautia_A sp900120195***	0.956%	0.00 - 0.123%	High

Species profile

SPECIES

	Phylum	Specie	Quantità	Intervallo	Livello
⊕	Firmicutes_A	***Faecalibacterium prausnitzii_C***	0.934%	0.176 - 2.34%	Normal

™ Faecalibacterium prausnitzii_C (i.e., strain A2-165) is an important component of the human gut microbiome.

Fonti di energia utilizzate:

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

Metaboliti prodotti:

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

Metaboliti consumati:

Genomic analysis indicates that most members of this species do not consume any reported metabolites.

Ricerca emergente:

Low levels of F. prausnitzii have been associated with Crohn's disease, ulcerative colitis, colon cancer, type 2 diabetes, and chronic fatigue.

	Phylum	Specie	Quantità	Intervallo	Livello
⊕	Firmicutes_A	***Fusicatenibacter saccharivorans***	0.924%	0.831 - 8.06%	Normal

This is a recently discovered species and an inhabitant of the human intestine.

Fonti di energia utilizzate:

This species is a moderate degrader of fiber, mucin and proteins.

Metaboliti prodotti:

Our genomic analysis indicates that most members of this species can produce the following metabolites:
acetate, branched chain amino acids, ammonia (urease), beta-glucuronidase, cobalamin (B12), folate (B9), lactate, sodium sulfide hydrogen.

Metaboliti consumati:

Genomic analysis indicates that most members of this species do not consume any reported metabolites.

Ricerca emergente:

Lower levels of this species have been observed in patients with colon cancer.

Species profile

SPECIES

	Phylum	Specie	Quantità	Intervallo	Livello
⊕	Firmicutes_A	***Agathobacter faecis***	0.870%	0.00 - 4.36%	Normal

Bacterium previously called Roseburia faeces . It is a common and important inhabitant of the human gut microbiome.

Fonti di energia utilizzate:

This species is a moderate degrader of fiber, mucin and proteins.

Metaboliti prodotti:

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).

Metaboliti consumati:

Genomic analysis indicates that most members of this species do not consume any reported metabolites.

Ricerca emergente:

This species is commonly associated with healthy control subjects in research studies. Low levels of this bacterium are have been observed in patients with liver cirrhosis.

	Phylum	Specie	Quantità	Intervallo	Livello
⊖	Firmicutes	***Streptococcus salivarius***	0.792%	0.00 - 0.327%	High

It is a common inhabitant of the human oral microbiota and is also found in the human gut.

Fonti di energia utilizzate:

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

Metaboliti prodotti:

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

Metaboliti consumati:

Genomic analysis indicates that most members of this species do not consume any reported metabolites.

Ricerca emergente:

This species has been observed at higher levels in patients with hypertension, Crohn's disease and atherosclerosis, although one study observed lower levels in patients with colon cancer.

Species profile

SPECIES

	Phylum	Specie	Quantità	Intervallo	Livello
	Firmicutes_A	***Lachnospira sp000436535***	0.700%	0.00 - 0.096%	High
	Firmicutes_A	***UBA5884 MIC7917***	0.684%	0.00 - 0.00%	High
	Firmicutes_A	***Eubacterium_R sp000436835***	0.656%	0.00 - 1.06%	Normal
	Proteobacteria	***CAG-495 sp000436375***	0.606%	0.00 - 0.099%	High
⊖	Firmicutes_A	***Faecalicatena lactaris***	0.578%	0.00 - 1.20%	Normal

Bacterium previously called Ruminococcus lactaris, It is a common inhabitant of the human intestine.

Fonti di energia utilizzate:

This species is a poor degrader of fibres, a moderate degrader of mucin and a moderate degrader of proteins.

Metaboliti prodotti:

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.

Metaboliti consumati:

Genomic analysis indicates that most members of this species do not consume any reported metabolites.

Ricerca emergente:

For this species, lower levels have been observed in people with insulin resistance, inflammatory bowel disease and irritable bowel syndrome. However, despite the probable beneficial role of this species, in one study it was higher levels observed in patients with rheumatoid arthritis.

	Phylum	Specie	Quantità	Intervallo	Livello
	Firmicutes	***CAG-611 MIC7816***	0.533%	0.00 - 0.00%	High

Species profile

SPECIES

	Phylum	Specie	Quantità	Intervallo	Livello
−	Bacteroidota	***Bacteroides cellulosilyticus***	0.502%	0.00 - 0.200%	High

It is a common inhabitant of the intestine.

Fonti di energia utilizzate:

This species is an excellent degrader of fibres, an excellent degrader of mucin and a moderate degrader of proteins.

Metaboliti prodotti:

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

Metaboliti consumati:

Genomic analysis indicates that most members of this species do not consume any reported metabolites.

Ricerca emergente:

Higher levels of this species have been observed in patients with hypertension. In another study, however, levels were observed lower in people with irritable bowel syndrome.

	Firmicutes_A	***Blautia_A wexlerae***	0.502%	0.525 - 6.58%	Poor
	Firmicutes_C	***Phascolarctobacterium_A succinatutens***	0.493%	0.00 - 0.396%	High
	Proteobacteria	***Duodenibacillus massiliensis***	0.492%	0.00 - 0.269%	High

Species profile

SPECIES

	Phylum	Specie	Quantità	Intervallo	Livello
⊕	Firmicutes_A	***Eubacterium_E hallii***	0.488%	0.312 - 2.37%	Normal

It is an important component of the gut microbiome.

Fonti di energia utilizzate:
This species is a poor degrader of fiber, a poor degrader of mucin, and a moderate degrader of protein.

Metaboliti prodotti:
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).

Metaboliti consumati:
Genomic analysis indicates that most members of this species do not consume any reported metabolites.

Ricerca emergente:
This species can also use the acetate of short-chain fatty acids, as well as the lactate produced by bacterial species, for example the Bifidobacterium spp., for energy.

In one study, lower levels of this species were observed in patients with colon cancer. In addition, a study in mice has suggested that this species may be effective in improving insulin sensitivity.

	Phylum	Specie	Quantità	Intervallo	Livello
±	Firmicutes_A	***Dorea longicatena***	0.480%	0.347 - 3.10%	Normal

It is a common inhabitant of the human intestine.

Fonti di energia utilizzate:
This species is a moderate degrader of fibre, a poor degrader of mucin and a moderate degrader of proteins.

Metaboliti prodotti:
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.

Metaboliti consumati:
Genomic analysis indicates that most members of this species do not consume any reported metabolites.

Ricerca emergente:
In several studies, higher levels of this species have been observed in obese people compared to lean control subjects. In obese postmenopausal women, this species has however been associated with improved insulin sensitivity. For this species, Lower levels were also observed in people with chronic fatigue syndrome and inflammatory bowel disease.

Species profile

SPECIES

	Phylum	Specie	Quantità	Intervallo	Livello
	Firmicutes_A	***Blautia_A sp900066165***	0.461%	0.258 - 2.72%	Normal
	Firmicutes_A	***Agathobaculum butyriciproducens***	0.434%	0.00 - 0.635%	Normal
	Firmicutes	***Catenibacterium sp000437715***	0.407%	0.00 - 0.538%	Normal
	Proteobacteria	***CAG-267 sp001917135***	0.401%	0.00 - 1.06%	Normal
⊕	Firmicutes_A	***Ruminococcus_E bromii_B***	0.391%	0.00 - 8.49%	Normal

Fonti di energia utilizzate:

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

Metaboliti prodotti:

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

Metaboliti consumati:

Genomic analysis indicates that most members of this species do not consume any reported metabolites.

	Firmicutes_A	***Faecalibacterium prausnitzii_G***	0.391%	0.120 - 3.47%	Normal
	Firmicutes_A	***ER4 sp900317525***	0.383%	0.00 - 0.330%	High

Species profile

SPECIES

	Phylum	Specie	Quantità	Intervallo	Livello
	Firmicutes_A	***Faecalibacterium MIC8666***	0.369%	0.00 - 0.569%	Normal
	Bacteroidota	***UBA11471 sp000434215***	0.363%	0.00 - 0.253%	High
	Firmicutes	***Solobacterium MIC7977***	0.338%	0.00 - 0.00%	High
	Firmicutes_A	***Faecalibacterium MIC7145***	0.334%	0.00 - 1.74%	Normal
⊕	Bacteroidota	***Alistipes senegalensis***	0.331%	0.00 - 0.079%	High

This is a newly discovered inhabitant of the human intestine.

Fonti di energia utilizzate:

This species is a moderate degrader of fibres, an excellent degrader of mucin and a moderate degrader of proteins.

Metaboliti prodotti:

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

Metaboliti consumati:

Genomic analysis indicates that most members of this species do not consume any reported metabolites.

Ricerca emergente:

A high body mass index has been associated with a low amount of this species. Lower levels of this species are They have also been observed in people with irritable bowel syndrome, suggesting that it may have a beneficial role in health.

	Firmicutes_A	***CAG-56 sp900066615***	0.329%	0.00 - 1.18%	Normal
	Firmicutes_A	***Blautia_A massiliensis***	0.320%	0.113 - 2.43%	Normal

Species profile

SPECIES

	Phylum	Specie	Quantità	Intervallo	Livello
	Firmicutes_A	***Gemmiger MIC9530***	0.309%	0.00 - 0.423%	Normal
	Bacteroidota	***Alistipes onderdonkii***	0.301%	0.00 - 0.279%	High
⊖	Bacteroidota	***Paraprevotella clara***	0.298%	0.00 - 0.329%	Normal

This is a recently discovered bacterial species and a common inhabitant of the human gut microbiome.

Fonti di energia utilizzate:

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

Metaboliti prodotti:

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

Metaboliti consumati:

Genomic analysis indicates that most members of this species do not consume any reported metabolites.

Ricerca emergente:

Higher levels of this species have been observed in patients with colon cancer.

	Actinobacteriota	***Eggerthellaceae MIC8667***	0.297%	0.00 - 0.235%	High
	Firmicutes_A	***KLE1615 sp900066985***	0.295%	0.00 - 1.44%	Normal
	Firmicutes_A	***Faecalibacterium MIC9210***	0.295%	0.00 - 0.291%	High
	Firmicutes_A	***Faecalibacterium prausnitzii_A***	0.283%	0.00 - 0.423%	Normal

Species profile

SPECIES

	Phylum	Specie	Quantità	Intervallo	Livello
	Firmicutes_A	***Gemmiger formicilis***	0.279%	0.299 - 2.96%	Poor
	Firmicutes_A	***TF01-11 sp001414325***	0.269%	0.00 - 0.341%	Normal
+−	Bacteroidota	***Bacteroides uniformis***	0.261%	0.173 - 2.19%	Normal

It is one of the most common inhabitants of the human intestine.

Fonti di energia utilizzate:

This species is an excellent degrader of fibres, an excellent degrader of mucin and a moderate degrader of proteins.

Metaboliti prodotti:

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

Metaboliti consumati:

Genomic analysis indicates that most members of this species do not consume any reported metabolites.

Ricerca emergente:

Some strains have been observed to promote the production of anti-inflammatory compounds, improve immune function and provide protection against diet-induced obesity in mouse models, however this has not yet been validated in humans. In one study, higher levels of this species were observed in patients with ulcerative colitis.

	Verrucomicrobiota	***Akkermansia sp001580195***	0.259%	0.00 - 0.00%	High
	Firmicutes_A	***Ruminococcus_C sp000433635***	0.257%	0.00 - 0.766%	Normal

Species profile

SPECIES

	Phylum	Specie	Quantità	Intervallo	Livello
⊕	Firmicutes_A	***Agathobacter rectale***	0.244%	0.00 - 6.22%	Normal

Bacterium previously called Eubacterium rectale . It is a common component of the human intestine.

Fonti di energia utilizzate:
This species is a moderate degrader of fibre, a poor degrader of mucin and a moderate degrader of proteins.

Metaboliti prodotti:
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).

Metaboliti consumati:
Genomic analysis indicates that most members of this species do not consume any reported metabolites.

Ricerca emergente:
This species is commonly associated with healthy control subjects in research studies. Low levels of this bacterium in Crohn's disease and ulcerative colitis.

	Phylum	Specie	Quantità	Intervallo	Livello
	Firmicutes_A	***Faecalibacterium prausnitzii_I***	0.243%	0.00 - 0.582%	Normal
	Firmicutes_A	***UBA11774 sp003507655***	0.226%	0.00 - 0.334%	Normal

Species profile

SPECIES

	Phylum	Specie	Quantità	Intervallo	Livello
⊖	Bacteroidota	***Bacteroides ovatus***	0.226%	0.00 - 0.392%	Normal

It is one of the most common inhabitants of the intestine.

Fonti di energia utilizzate:

This species is an excellent degrader of fibres, an excellent degrader of mucin and a moderate degrader of proteins.

Metaboliti prodotti:

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

acetate, branched chain amino acids, beta-glucuronidase, biotin (B7), folate (B9), GABA, lactate, propionate, riboflavin (B2), vitamin K.

Metaboliti consumati:

Genomic analysis indicates that most members of this species do not consume any reported metabolites.

Ricerca emergente:

Higher levels of this species have been associated with type 1 diabetes in children and progression of Crohn's disease in adults.

⊕	Actinobacteriota	***Senegalimassilia anaerobia***	0.220%	0.00 - 0.294%	Normal

This is a newly discovered inhabitant of the human intestine.

Fonti di energia utilizzate:

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

Metaboliti prodotti:

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

acetate, branched chain amino acids, lactate, riboflavin (B2), vitamin K.

Metaboliti consumati:

Genomic analysis indicates that most members of this species do not consume any reported metabolites.

Ricerca emergente:

Lower levels of this species have been observed in people with Crohn's disease and ulcerative colitis, suggesting that it may have a beneficial role for health.

Species profile

SPECIES

	Phylum	Specie	Quantità	Intervallo	Livello
	Firmicutes_A	***Oscillibacter sp001916835***	0.219%	0.00 - 0.261%	Normal
	Firmicutes_A	***UBA7160 MIC6745***	0.218%	0.00 - 0.131%	High
	Firmicutes_A	***Angelakisella MIC6791***	0.214%	0.00 - 0.176%	High
⊕	Firmicutes_A	***Dorea formicigenerans***	0.214%	0.138 - 0.597%	Normal

Bacterium previously called Eubacterium formicgenerans . It is a common inhabitant of the human intestine.

Fonti di energia utilizzate:

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

Metaboliti prodotti:

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).

Metaboliti consumati:

Genomic analysis indicates that most members of this species do not consume any reported metabolites.

Ricerca emergente:

This species has been observed at lower levels in people with colon cancer, inflammatory bowel disease, and chronic fatigue, indicating that it most likely has a beneficial role in health.

	Firmicutes_A	***TF01-11 sp003524945***	0.214%	0.00 - 0.166%	High
	Firmicutes	***CAG-536 sp000434355***	0.203%	0.00 - 0.00%	High
	Firmicutes_A	***QALR01 MIC9250***	0.202%	0.00 - 0.00%	High

Species profile

SPECIES

	Phylum	Specie	Quantità	Intervallo	Livello
	Firmicutes_A	***Blautia_A sp000436615***	0.202%	0.00 - 0.525%	Normal
	Proteobacteria	***Duodenibacillus MIC7456***	0.195%	0.00 - 0.00%	High
	Actinobacteriota	***CAG-1427 sp000436075***	0.190%	0.00 - 0.301%	Normal
	Firmicutes_A	***UBA11524 sp000437595***	0.190%	0.00 - 2.86%	Normal
⊖	Desulfobacterota_A	***Desulfovibrio piger***	0.188%	0.00 - 0.195%	Normal

This species can be found in the gut microbiome.

Fonti di energia utilizzate:

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

Metaboliti prodotti:

Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, lactate, riboflavin (B2), hydrogen sulfide, vitamin K.

Metaboliti consumati:

Genomic analysis indicates that most members of this species do not consume any reported metabolites.

Ricerca emergente:

This species can also use lactate for energy.

One study observed elevated levels of this species in patients with inflammatory bowel disease.

	Phylum	Specie	Quantità	Intervallo	Livello
	Firmicutes_A	***UBA1242 MIC9537***	0.186%	0.00 - 0.00%	High

Species profile

SPECIES

	Phylum	Specie	Quantità	Intervallo	Livello
⊕	Firmicutes_A	***Faecalibacterium prausnitzii_K***	0.185%	0.00 - 2.59%	Normal

Bacteria previously called the human Faecalibacterium prausnitzii_A (i.e. strains SL3/3 and M21/2), it is a common inhabitant of the gut microbiome.

Fonti di energia utilizzate:

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

Metaboliti prodotti:

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

Metaboliti consumati:

Genomic analysis indicates that most members of this species do not consume any reported metabolites.

Ricerca emergente:

Low levels of F. prausnitzii have been associated with Crohn's disease, ulcerative colitis, colon cancer, type 2 diabetes, and chronic fatigue. This species produces lower levels of butyrate than the bacterium F. prausnitzii_C

	Firmicutes_A	***CAG-74 MIC7649***	0.185%	0.00 - 0.254%	Normal
	Actinobacteriota	***Senegalimassilia MIC8876***	0.183%	0.00 - 0.00%	High

Species profile

SPECIES

	Phylum	Specie	Quantità	Intervallo	Livello
⊖	Bacteroidota	***Bacteroides_B vulgatus***	0.183%	0.114 - 4.15%	Normal

It is one of the most common inhabitants of the human intestine.

Fonti di energia utilizzate:
This species is an excellent degrader of fibres, an excellent degrader of mucin and a moderate degrader of proteins.

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

Metaboliti consumati:
Genomic analysis shows that most members of this species can consume: GABA.

Ricerca emergente:
Higher levels of this bacterium have been associated with polycystic ovary syndrome, insulin resistance, advanced liver fibrosis and progression of Crohn's disease. This species has been associated with a diet high in red meat.

	Firmicutes_A	***CAG-488 sp000434055***	0.172%	0.00 - 0.00%	High
	Firmicutes_A	***CAG-492 sp000434335***	0.171%	0.00 - 0.269%	Normal
	Firmicutes_A	***CAG-170 sp002404795***	0.168%	0.00 - 0.260%	Normal

Species profile

SPECIES

	Phylum	Specie	Quantità	Intervallo	Livello
⊕	Firmicutes_A	***Coprococcus_A catus***	0.163%	0.00 - 0.536%	Normal
	Firmicutes_A	***Blautia_A sp900066355***	0.163%	0.00 - 0.392%	Normal
	Firmicutes_A	***Ruminococcus_A sp000437095***	0.155%	0.00 - 0.353%	Normal
	Firmicutes_A	***Ruminiclostridium_C MIC7261***	0.154%	0.00 - 0.285%	Normal
	Firmicutes_A	***Eubacterium_F sp003491505***	0.151%	0.00 - 0.294%	Normal
	Firmicutes_A	***Coprococcus MIC8538***	0.139%	0.00 - 0.00%	High
	Firmicutes_A	***GCA-900066995 sp900291955***	0.136%	0.00 - 0.580%	Normal

It is an inhabitant of the human intestine.

Fonti di energia utilizzate:

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

Metaboliti prodotti:

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

Metaboliti consumati:

Genomic analysis indicates that most members of this species do not consume any reported metabolites.

Ricerca emergente:

Lower levels of this species have been observed in people with irritable bowel syndrome and depression, indicating that in most likely it has a beneficial role in health.

Species profile

SPECIES

	Phylum	Specie	Quantità	Intervallo	Livello
⊕	Bacteroidota	***Alistipes shahii***	0.135%	0.00 - 0.260%	Normal
	Firmicutes	***CAG-417 sp000432835***	0.134%	0.00 - 0.085%	High
	Firmicutes_A	***COE1 sp001916965***	0.132%	0.00 - 0.115%	High
	Bacteroidota	***Barnesiella intestinihominis***	0.131%	0.00 - 0.345%	Normal
	Eukaryotes_without classification	***Blastocystis sp. subtype 4***	0.123%	0.00 - 0.00%	High
	Firmicutes_A	***Oscillibacter sp900066435***	0.122%	0.00 - 0.102%	High
	Firmicutes_A	***Eisenbergiella sp900066775***	0.121%	0.00 - 0.371%	Normal

It is a common inhabitant of the human intestine.

Fonti di energia utilizzate:
This species is a moderate degrader of fibres, an excellent degrader of mucin and a moderate degrader of proteins.

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

Metaboliti consumati:
Genomic analysis indicates that most members of this species do not consume any reported metabolites.

Ricerca emergente:
This species appears to have mainly beneficial effects. It has been associated with positive markers of cardiac health (triglycerides low, high levels of good HDL cholesterol), and depleted levels have been observed in patients with atherosclerotic heart disease and Crohn's disease. In addition, a study on mice has shown that this species can improve the effectiveness of immunotherapy against tumors. However, this species has also been observed at high levels in patients with Parkinson's disease.

Species profile

SPECIES

	Phylum	Specie	Quantità	Intervallo	Livello
	Firmicutes_A	***CAG-41 sp900066215***	0.120%	0.00 - 0.732%	Normal
⊖	Bacteroidota	***Parabacteroides merdae***	0.117%	0.00 - 0.341%	Normal

Bacterium previously called Bacteroides merdae . It is a common inhabitant of the human intestine.

Fonti di energia utilizzate:

This species is a moderate degrader of fibres, an excellent degrader of mucin and a moderate degrader of proteins.

Metaboliti prodotti:

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

Metaboliti consumati:

Genomic analysis shows that most members of this species can consume: GABA.

Ricerca emergente:

Higher levels of this species have been observed in people with hypertension and colon cancer. This species has been associated with a diet low in fruit and vegetables.

Species profile

SPECIES

	Phylum	Specie	Quantità	Intervallo	Livello
⊖	Bacteroidota	***Bacteroides caccae***	0.110%	0.00 - 0.496%	Normal
	Firmicutes	***Streptococcus parasanguinis_B***	0.109%	0.00 - 0.00%	High
	Firmicutes_A	***CAG-45 sp000438375***	0.107%	0.00 - 0.030%	High
	Firmicutes_A	***UBA1394 MIC7365***	0.103%	0.00 - 0.00%	High
	Firmicutes	***CAG-594 sp000434835***	0.103%	0.00 - 0.049%	High
	Bacteroidota	***Bacteroides faecis***	0.102%	0.00 - 0.080%	High
	Actinobacteriota	***Slackia_A MIC8451***	0.102%	0.00 - 0.218%	Normal

It is a common component of the human intestine.

Fonti di energia utilizzate:

This species is a moderate degrader of fibres, an excellent degrader of mucin and a moderate degrader of proteins.

Metaboliti prodotti:

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

Metaboliti consumati:

Genomic analysis indicates that most members of this species do not consume any reported metabolites.

Ricerca emergente:

A protein produced by this species has been associated with inflammatory bowel disease, and elevated levels of this species have been observed in people with gout.

Species profile

SPECIES

	Phylum	Specie	Quantità	Intervallo	Livello
	Firmicutes_A	***CAG-74 MIC8062***	0.101%	0.00 - 0.054%	High
	Actinobacteriota	***Eggerthellaceae MIC7588***	0.098%	0.00 - 0.00%	High
	Firmicutes_A	***Faecalibacterium MIC8693***	0.096%	0.00 - 0.107%	Normal
	Firmicutes_A	***Faecalicatena faecis***	0.096%	0.151 - 1.73%	Poor
	Firmicutes_A	***CAG-74 MIC9837***	0.095%	0.00 - 0.076%	High
	Firmicutes_A	***Lachnospira sp000437735***	0.093%	0.00 - 0.229%	Normal
	Cyanobacteria	***CAG-484 sp000431315***	0.093%	0.00 - 0.00%	High
	Actinobacteriota	***Collinsella MIC8519***	0.093%	0.00 - 0.084%	High
	Firmicutes_A	***Eubacterium_E hallii_A***	0.093%	0.00 - 0.354%	Normal
	Bacteroidota	***UBA6398 sp003150315***	0.093%	0.00 - 0.00%	High

Species profile

SPECIES

	Phylum	Specie	Quantità	Intervallo	Livello
⊖	Bacteroidota	***Bacteroides_B massiliensis***	0.090%	0.00 - 0.782%	Normal

It is a normal inhabitant of the human gut microbiome.

Fonti di energia utilizzate:

This species is a moderate degrader of fibres, an excellent degrader of mucin and a moderate degrader of proteins.

Metaboliti prodotti:

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

Metaboliti consumati:

Genomic analysis indicates that most members of this species do not consume any reported metabolites.

Ricerca emergente:

Higher levels of this species have been observed in people with colon cancer. This species has also been associated with a diet rich in red meat.

	Phylum	Specie	Quantità	Intervallo	Livello
⊖	Firmicutes_A	***Faecalicatena torques***	0.089%	0.00 - 0.274%	Normal

Bacterium previously called Ruminococcus torques. It is a common inhabitant of the human intestine.

Fonti di energia utilizzate:

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

Metaboliti prodotti:

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).

Metaboliti consumati:

Genomic analysis indicates that most members of this species do not consume any reported metabolites.

Ricerca emergente:

For this species, higher levels have been observed in people with obesity, colon cancer, insulin resistance and high levels of triglycerides.

Species profile

SPECIES

	Phylum	Specie	Quantità	Intervallo	Livello
⊕	Firmicutes_A	***Roseburia hominis***	0.088%	0.00 - 0.260%	Normal
	Firmicutes_A	***Eubacterium_F sp000433735***	0.087%	0.00 - 0.070%	High
	Firmicutes_A	***Acetatifactor sp900066565***	0.087%	0.00 - 0.689%	Normal
	Proteobacteria	***Duodenibacillus MIC7471***	0.086%	0.00 - 0.00%	High
	Firmicutes_A	***CAG-138 MIC9630***	0.085%	0.00 - 0.439%	Normal
	Firmicutes_A	***CAG-273 sp003534295***	0.083%	0.00 - 0.148%	Normal
	Firmicutes_A	***Clostridium_Q sp003024715***	0.081%	0.00 - 0.226%	Normal

It is a common and important inhabitant of the human gut microbiome.

Fonti di energia utilizzate:

This species is a moderate degrader of fiber, mucin and proteins.

Metaboliti prodotti:

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

Metaboliti consumati:

Genomic analysis indicates that most members of this species do not consume any reported metabolites.

Ricerca emergente:

It is a primary producer of the beneficial short-chain fatty acid butyrate. Lower levels of this species have been observed in patients with inflammatory bowel disease and hypertension. In another study, higher levels were observed in active women compared to sedentary women. Laboratory studies suggest that this species may help regulate the immune system and reduce inflammation.

Species profile

SPECIES

	Phylum	Specie	Quantità	Intervallo	Livello
	Firmicutes_A	***Blautia_A sp900066145***	0.078%	0.00 - 0.262%	Normal
	Bacteroidota	***Butyricimonas sp900258545***	0.076%	0.00 - 0.048%	High
	Proteobacteria	***Haemophilus_D sp001815355***	0.075%	0.00 - 0.029%	High
	Firmicutes_A	***UBA7096 MIC8091***	0.074%	0.00 - 0.00%	High
⊖	Bacteroidota	***Parabacteroides distasonis***	0.072%	0.034 - 0.340%	Normal
	Actinobacteriota	***Collinsella sp003487125***	0.072%	0.00 - 0.711%	Normal
	Firmicutes_A	***CAG-349 sp003539515***	0.070%	0.00 - 0.703%	Normal

Bacterium previously called Bacteroides distasonis . It is a common inhabitant of the human intestine.

Fonti di energia utilizzate:

This species is a moderate degrader of fibres, an excellent degrader of mucin and a moderate degrader of proteins.

Metaboliti prodotti:

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

Metaboliti consumati:

Genomic analysis shows that most members of this species can consume: GABA.

Ricerca emergente:

Higher levels of this species have been observed in people with colon cancer and pregnant women with diabetes. gestational.

Species profile

SPECIES

	Phylum	Specie	Quantità	Intervallo	Livello
	Cyanobacteria	***QAMI01 MIC7050***	0.070%	0.00 - 0.00%	High
	Firmicutes_A	***CAG-81 sp000435795***	0.069%	0.00 - 0.081%	Normal
	Firmicutes_A	***TF01-11 sp003529475***	0.069%	0.00 - 0.289%	Normal
	Bacteroidota	***Bacteroides thetaiotaomicron***	0.068%	0.00 - 0.283%	Normal
	Actinobacteriota	***Libanicoccus MIC9408***	0.067%	0.00 - 0.00%	High
	Bacteroidota	***Alistipes obesi***	0.064%	0.00 - 0.234%	Normal
	Firmicutes_A	***Dorea sp900066555***	0.063%	0.00 - 0.140%	Normal

Species profile

SPECIES

	Phylum	Specie	Quantità	Intervallo	Livello
⊖	Firmicutes_A	***Eubacterium_I ramulus***	0.062%	0.00 - 0.475%	Normal

It is a common inhabitant of the gut microbiome.

Fonti di energia utilizzate:

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

Metaboliti prodotti:

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).

Metaboliti consumati:

Genomic analysis indicates that most members of this species do not consume any reported metabolites.

Ricerca emergente:

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

This species has been observed at higher levels in obese postmenopausal women with insulin resistance. Another study has However, lower levels were found in patients with Crohn's disease.

	Firmicutes	***CAG-302 sp000431795***	0.062%	0.00 - 0.236%	Normal
	Bacteroidota	***Butyricimonas virosa***	0.062%	0.00 - 0.039%	High
	Firmicutes	***Holdemanella MIC8202***	0.060%	0.00 - 0.00%	High
	Actinobacteriota	***Olsenella_E MIC6865***	0.059%	0.00 - 0.148%	Normal
	Firmicutes_A	***GCA-900066135 MIC6659***	0.058%	0.00 - 0.278%	Normal
	Firmicutes_A	***CAG-170 MIC9129***	0.058%	0.00 - 0.089%	Normal

Species profile

SPECIES

	Phylum	Specie	Quantità	Intervallo	Livello
	Firmicutes_A	***Ruminococcus_D bicirculans***	0.058%	0.00 - 4.36%	Normal
	Bacteroidota	***Parabacteroides sp900155425***	0.057%	0.00 - 0.00%	High
	Firmicutes_A	***Negativibacillus MIC7916***	0.056%	0.00 - 0.00%	High
	Firmicutes_A	***Lachnospiraceae MIC8879***	0.056%	0.00 - 0.155%	Normal
	Bacteroidota	***Bacteroides salyersiae***	0.052%	0.00 - 0.138%	Normal
	Firmicutes_A	***Blautia_A MIC7077***	0.052%	0.00 - 0.145%	Normal
	Firmicutes_A	***Anaerovoracaceae MIC7478***	0.051%	0.00 - 0.068%	Normal
	Firmicutes_A	***CAG-170 MIC6856***	0.050%	0.00 - 0.057%	Normal
	Firmicutes_A	***Anaerostipes hadrus***	0.050%	0.229 - 4.73%	Poor
	Firmicutes_A	***CAG-81 sp900066535***	0.050%	0.00 - 0.155%	Normal
	Firmicutes_A	***Hungatella_A MIC8772***	0.050%	0.00 - 0.064%	Normal

Species profile

SPECIES

	Phylum	Specie	Quantità	Intervallo	Livello
⊖	Desulfobacterota_A	***Bilophila wadsworthia***	0.048%	0.00 - 0.154%	Normal

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

Fonti di energia utilizzate:

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

Metaboliti prodotti:

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

Metaboliti consumati:

Genomic analysis indicates that most members of this species do not consume any reported metabolites.

Ricerca emergente:

Higher levels of this species have been observed in patients with colon cancer and in people with a diet rich in saturated fats. Studies in mice have also suggested that this species may promote increased inflammation of the intestine and increased barrier dysfunction, although further human research is needed to confirm these results.

	Phylum	Specie	Quantità	Intervallo	Livello
	Firmicutes_A	***Romboutsia timonensis***	0.046%	0.063 - 0.854%	Poor

Species profile

SPECIES

	Phylum	Specie	Quantità	Intervallo	Livello
⊕	Bacteroidota	***Odoribacter splanchnicus***	0.044%	0.053 - 0.296%	Poor

Bacterium previously called Bacteroides splanchnicus . It is a common inhabitant of the human intestine.

Fonti di energia utilizzate:

This species is a moderate degrader of fibres, an excellent degrader of mucin and a moderate degrader of proteins.

Metaboliti prodotti:

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

Metaboliti consumati:

Genomic analysis shows that most members of this species can consume: GABA.

Ricerca emergente:

Lower levels of this species have been observed in obese postmenopausal women with insulin resistance, patients with irritable bowel syndrome and women with painful bladder syndrome, indicating that it most likely plays a role beneficial for health.

	Phylum	Specie	Quantità	Intervallo	Livello
⊕	Firmicutes_A	***Coprococcus_B comes***	0.043%	0.077 - 1.08%	Poor

It is a common inhabitant of the human intestine.

Fonti di energia utilizzate:

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

Metaboliti prodotti:

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

Metaboliti consumati:

Genomic analysis indicates that most members of this species do not consume any reported metabolites.

Ricerca emergente:

It is likely that this species has a beneficial role in health since lower levels have been observed in people with Crohn's disease, liver cirrhosis, and chronic fatigue syndrome.

Species profile

SPECIES

	Phylum	Specie	Quantità	Intervallo	Livello
⊕	Firmicutes	***Erysipelatoclostridium saccharogumia***	0.042%	0.00 - 0.00%	High

Bacterium previously called Clostridium saccharogumia . It is an inhabitant of the human intestine.

Fonti di energia utilizzate:

This species is a moderate degrader of fiber, mucin and proteins.

Metaboliti prodotti:

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

Metaboliti consumati:

Genomic analysis indicates that most members of this species do not consume any reported metabolites.

Ricerca emergente:

This species can break down a type of tough plant fiber called lignan. It has been shown that metabolites produced by The breakdown of lignan has therapeutic potential against numerous human pathologies.

	Phylum	Specie	Quantità	Intervallo	Livello
	Firmicutes_A	***UBA7160 MIC9207***	0.041%	0.00 - 0.152%	Normal
	Firmicutes_A	***Oscillibacter MIC8609***	0.040%	0.00 - 0.00%	High
	Firmicutes_A	***NK3B98 MIC8311***	0.039%	0.00 - 0.034%	High
	Firmicutes	***Erysipelatoclostridium sp000752095***	0.039%	0.00 - 0.847%	Normal
	Firmicutes	***CAG-302 MIC8491***	0.037%	0.00 - 0.072%	Normal
	Firmicutes_A	***UBA9502 MIC6887***	0.035%	0.00 - 0.070%	Normal

Species profile

SPECIES

<table>
<tr><th></th><th>Phylum</th><th>Specie</th><th>Quantità</th><th>Intervallo</th><th>Livello</th></tr>
<tr><td>⊕</td><td>Firmicutes_A</td><td><i>Eubacterium_G ventriosum</i></td><td>0.035%</td><td>0.00 - 0.303%</td><td>Normal</td></tr>
<tr><td colspan="6">
It is a common inhabitant of the human intestine.
Fonti di energia utilizzate:
This species is a poor degrader of fiber, a poor degrader of mucin, and a moderate degrader of protein.
Metaboliti prodotti:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, butyrate, folate (B9), lactate.
Metaboliti consumati:
Genomic analysis indicates that most members of this species do not consume any reported metabolites.
Ricerca emergente:
This species has been observed at lower levels in people with chronic fatigue syndrome, Crohn's disease, and breast cancer. colon, indicating that it most likely has a beneficial role in health.
</td></tr>
<tr><td></td><td>Firmicutes_A</td><td><i>Oscillibacter MIC7603</i></td><td>0.035%</td><td>0.00 - 0.00%</td><td>High</td></tr>
</table>

Species profile

SPECIES

	Phylum	Specie	Quantità	Intervallo	Livello
⊕	Firmicutes_A	***Ruminiclostridium_E siraeum***	0.035%	0.00 - 0.762%	Normal

Bacterium previously called Eubacterium siraeum . It is a common inhabitant of the human intestine.

Fonti di energia utilizzate:

This species is a moderate degrader of fibres, an excellent degrader of mucin and a moderate degrader of proteins.

Metaboliti prodotti:

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

Metaboliti consumati:

Genomic analysis indicates that most members of this species do not consume any reported metabolites.

Ricerca emergente:

This species has been observed at lower levels in people with type II diabetes, insulin resistance, and Crohn's disease, suggesting which most likely has a beneficial role in health.

	Actinobacteriota	***Collinsella MIC6963***	0.034%	0.00 - 0.00%	High
	Firmicutes	***Turicibacter sp001543345***	0.034%	0.00 - 0.059%	Normal
	Firmicutes_A	***CAG-110 MIC9052***	0.033%	0.00 - 0.099%	Normal
	Actinobacteriota	***Coriobacteriales MIC6482***	0.033%	0.00 - 0.00%	High
	Firmicutes_A	***CAG-964 sp000435335***	0.033%	0.00 - 0.00%	High
	Firmicutes_A	***Blautia_A MIC7810***	0.032%	0.00 - 0.050%	Normal

Species profile

SPECIES

Phylum	Specie	Quantità	Intervallo	Livello
Firmicutes_A	***Dorea sp000433215***	0.032%	0.00 - 0.079%	Normal
Firmicutes_A	***Lawsonibacter asaccharolyticus***	0.031%	0.00 - 0.083%	Normal
Firmicutes_A	***Oscillibacter MIC7608***	0.030%	0.00 - 0.053%	Normal
Firmicutes_A	***Blautia_A MIC9663***	0.030%	0.00 - 0.037%	Normal
Firmicutes_A	***CAG-83 sp000431575***	0.029%	0.00 - 0.199%	Normal
Firmicutes_A	***Coprococcus_B MIC8649***	0.029%	0.00 - 0.00%	High
Firmicutes_A	***CAG-170 sp003516765***	0.029%	0.00 - 0.080%	Normal
Bacteroidota	***Coprobacter fastidiosus***	0.028%	0.00 - 0.065%	Normal
Firmicutes_A	***Terrisporobacter MIC9205***	0.027%	0.00 - 0.169%	Normal
Firmicutes_A	***CAG-727 MIC8506***	0.027%	0.00 - 0.007%	High
Firmicutes	***CAG-776 MIC7263***	0.027%	0.00 - 0.00%	High
Firmicutes_A	***UBA7182 MIC8422***	0.027%	0.00 - 0.064%	Normal
Firmicutes_A	***UBA1685 MIC6819***	0.026%	0.00 - 0.00%	High

Species profile

SPECIES

	Phylum	Specie	Quantità	Intervallo	Livello
	Bacteroidota	**Bacteroides sp900066265**	0.025%	0.00 - 0.002%	High
	Firmicutes_A	**UBA10677 sp003533505**	0.024%	0.00 - 0.00%	High
	Firmicutes_A	**UBA866 MIC8205**	0.024%	0.00 - 0.022%	High
	Proteobacteria	**RF32 MIC6842**	0.024%	0.00 - 0.00%	High
	Actinobacteriota	**Collinsella MIC9387**	0.023%	0.00 - 0.00%	High
	Firmicutes_A	**UBA4285 MIC9245**	0.023%	0.00 - 0.095%	Normal
	Firmicutes_A	**CAG-74 MIC7629**	0.023%	0.00 - 0.048%	Normal
	Verrucomicrobiot a	**Victivallaceae MIC9489**	0.021%	0.00 - 0.021%	Normal
	Proteobacteria	**Sutterella wadsworthensis_B**	0.019%	0.00 - 0.471%	Normal
	Firmicutes_A	**Clostridium_M sp000431375**	0.019%	0.00 - 0.099%	Normal
	Firmicutes_A	**UBA1390 MIC7760**	0.019%	0.00 - 0.00%	High
	Firmicutes_A	**Blautia_A MIC8343**	0.018%	0.00 - 0.128%	Normal
	Firmicutes_A	**UBA9475 MIC7490**	0.018%	0.00 - 0.021%	Normal

Species profile

SPECIES

	Phylum	Specie	Quantità	Intervallo	Livello
	Bacteroidota	***Alistipes_A ihumii***	0.018%	0.00 - 0.073%	Normal
	Proteobacteria	***Oxalobacter MIC6654***	0.018%	0.00 - 0.029%	Normal
⊖	Proteobacteria	***Escherichia coli (coli_D)***	0.017%	0.00 - 0.031%	Normal

Fonti di energia utilizzate:

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

Metaboliti prodotti:

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

Metaboliti consumati:

Genomic analysis shows that most members of this species can consume: GABA, oxalate.

Ricerca emergente:

This species is considered a pathogen and is a common cause of diarrhea. If this species has been detected and is present diarrhea, it is a good idea to consider consulting a doctor for a diagnostic test.

	Firmicutes_A	***UBA7182 MIC8257***	0.017%	0.00 - 0.040%	Normal
	Firmicutes_A	***QALS01 MIC6548***	0.017%	0.00 - 0.036%	Normal
	Cyanobacteria	***CAG-306 MIC9186***	0.016%	0.00 - 0.00%	High
	Bacteroidota	***Coprobacter secundus***	0.016%	0.00 - 0.052%	Normal

Species profile

SPECIES

Phylum	Specie	Quantità	Intervallo	Livello
Desulfobacterota_ A	*Mailhella sp003150275*	0.013%	0.00 - 0.013%	High
Firmicutes_A	*CAG-552 MIC9697*	0.013%	0.00 - 0.00%	High
Bacteroidota	*UBA1820 sp002314265*	0.013%	0.00 - 0.040%	Normal
Bacteroidota	*Alistipes_A sp900240235*	0.013%	0.00 - 0.045%	Normal
Firmicutes_A	*Marvinbryantia MIC7005*	0.013%	0.00 - 0.00%	High
Firmicutes_A	*Oscillibacter MIC7169*	0.013%	0.00 - 0.013%	Normal
Firmicutes_A	*Oscillibacter MIC6596*	0.012%	0.00 - 0.028%	Normal
Firmicutes_A	*Oscillibacter MIC7379*	0.012%	0.00 - 0.00%	High
Firmicutes_A	*Oscillospirales MIC6586*	0.011%	0.00 - 0.00%	High

Gut microbiome report