

Summary

People develop an enterotype that will remain with them for most of their lives in the first three years of their life. These bacterial groups thrive on different food sources but fulfil a similar function. The enterotype mostly provides insight into a person's diet.

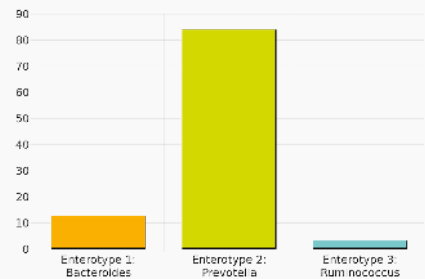
Enterotype 1: Bacteroides
This enterotype is characterized by a dominance of the genus Bacteroides. Bacteroides live off the carbohydrates of the mucus layer that your gut produces. The genus is often seen in people with a diet rich in meat. However, even people with a plant-based diet can have a Bacteroides enterotype, if they do not have Prevotella in their microbiome

Enterotype 2: Prevotella
Characterized by a dominance of the genus Prevotella. Prevotella lives off plant-based fibres and is therefore often found in people with plant-based diets. Unlike Bacteroides, Prevotella is not able to digest the carbohydrates that are provided by the mucus layer of the gut.

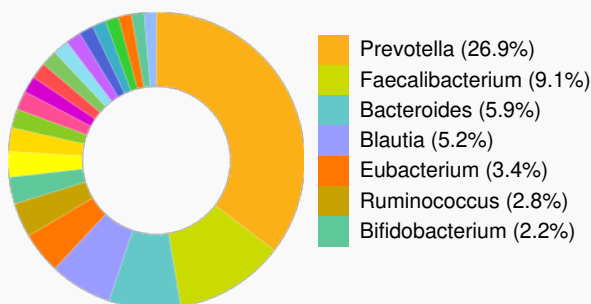
Enterotype 3: Ruminococcus
Characterized by a dominance of the genus Ruminococcus. They are often found in people with a higher intake of resistant starches. This enterotype is less clearly defined and given certain conditions (specific nutrition) this enterotype can transition to enterotype 1 or 2

Enterotype:

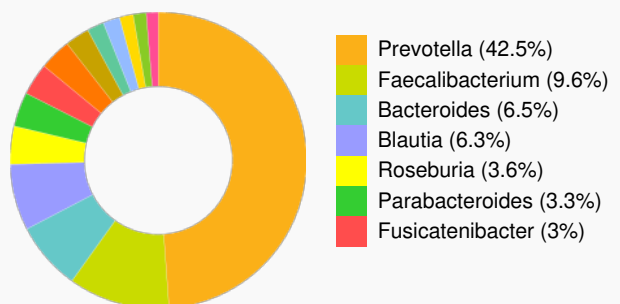
Your enterotype: 2: *Prevotella*



Genus level microbiome of people with your enterotype



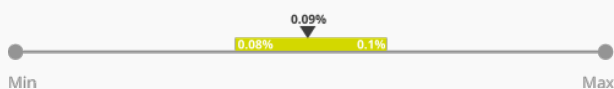
Your genus level microbiome



Different diversity scores with reference values

Species evenness

Balance of your microbiome



Species richness

The number of different bacteria



Diversity

Diversity of your microbiome



Species balance

The [species evenness \(Pielou index\)](#) provides an impression of evenness in the distribution of your microbiome. A high species evenness is a measure of a very uniform distribution of your microbiome. A low species evenness, on the other hand, is related to an uneven distribution of your microbiome.

The [species richness](#) is a measure for the number of different bacteria species present in your gut. The [diversity \(Shannon index\)](#) combines these two parameters and is a measure of how diverse your microbiome is.

For example, a [low diversity \(Shannon index\)](#) can be the result of a low number of different bacteria ([species richness](#)), but this can also be the result of several bacteria that dominate the gut microbiome, which is reflected by a low [species evenness](#).

Clinically Relevant Parameter

Chart example



x%: Result of this sample
Min: Lowest percentage identified in people in our database
Green bar: Percentage identified in healthy people in our database
Max: Highest percentage identified in people in our database

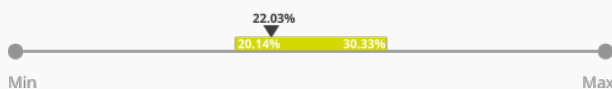
The microbiome in this report is compared with healthy individuals in the MyMicroZoo database. The upper and lower bounds of the reference bars of the respective bacteria are based on the bacterial abundance in 50% of the healthy individuals. The microbiome is compared with the microbiome of individuals with the same enterotype and who are over 18 years old, non-smokers, do not suffer from gut related complaints or other illness and have not used medication or antibiotics in the past 6 months.

Please note: Results outside of the green reference values are not necessarily considered unhealthy if there are no complaints. We recommend speaking with a healthcare professional when complaints are present. A healthcare professional can help to provide personalized advice based on your gut microbiome.

Keystone species

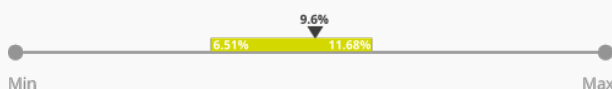
As the name suggests, keystone species fulfil a key role in the microbiota. Even though these species are often found in low abundance, they have a great effect on the gut microbiome. There is a great effect on other bacteria if keystone species are lost. This is because keystone species often play an essential role in the food chain or in communication between bacteria. Often, keystone species fulfil one or more roles that are not easily transferred to different species

Total keystone species



It is important to have a healthy balance between keystone species and other functional bacterial groups. A low score could indicate that a major function of the gut microbiome is not fulfilled by another species. Having too many keystone species is also not desirable because this group might suppress other bacteria who are also important for a healthy gut microbiome.

Total *Faecalibacterium prausnitzii*



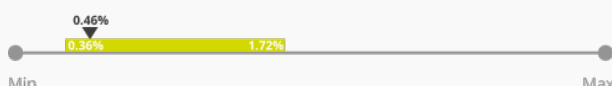
F. prausnitzii is a keystone species for its role as most common butyrate producing bacterium in humans. Butyrate contributes to a large extent to gut health (more on page 4). At lower abundance it is important that the total butyrate producing bacteria are at the right level (more on page 4). If there are no complaints, a high score is not considered unhealthy.

Total *Akkermansia muciniphila*



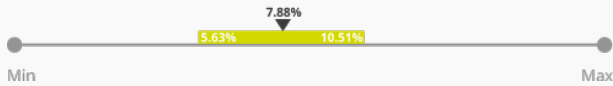
A. muciniphila is a well-known keystone species due to its ability to digest mucin (view page 5). Mucin covers the gut lining, and its digestion stimulates the regeneration of the gut lining. This regeneration enhances the gut lining integrity and hinders infection by other bacteria. Not everyone has a high presence of this bacterium, this is not considered unhealthy. These bacteria are a nice-to-have, but not a must-have.

Total *Eubacterium rectale*



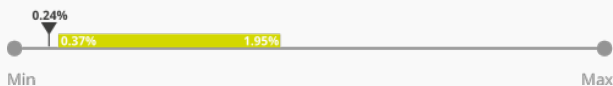
E. Eubacterium rectale is a keystone species because this species is present in almost everyone and is an important butyrate producer. *E. rectale* has an influence on the homeostasis of bile production and cholesterol transformations. When found in low abundance it is important, comparable to *F. prausnitzii*, to check whether total butyrate production is sufficient (view page 4). High abundance is not regarded as unhealthy since this is a frequently occurring bacterium.

Total *Blautia* and *Ruminococcus*



Blautia and *Ruminococcus* are closely related species who play a key role in the microbiome due to their ability to convert sugars and starch into lactate and acetate (view pages 4 and 6). A low abundance is not regarded as unhealthy if the total key stone species abundance is sufficient. These bacteria are often regarded as 'nice to have', but a high abundance of these bacteria could be the cause of irritable bowel syndrome symptoms.

Total other keystone species

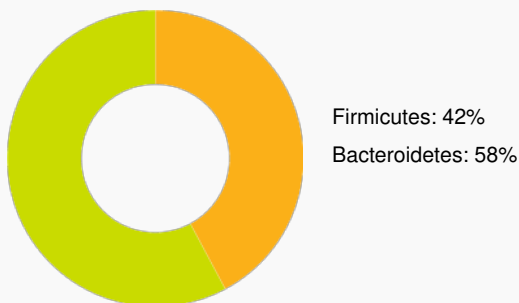


Other important keystone species are *Alistipes putredines*, *Bacteroides fragilis*, *Bacteroides stercoris*, *Bacteroides thetaiotaomicron*, *Bacteroides vulgatus*, *Bifidobacterium adolescentis*, *Bifidobacterium animalis*, *Bifidobacterium longum*, *Christensenella minuta*, *Oscillospira*, *Roseburia*. Members of these species are seldom found in larger quantities than a few percent.

The parameters above provide a general overview. When deviations are seen, more detailed information can be found by looking at the present of individual presence per genus (view page 9 'Genus level analysis' or view the scores per species in the online results)

F/B Ratio

Firmicutes/Bacteroidetes ratio (F/B ratio)

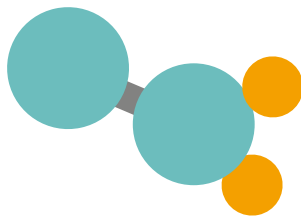


Firmicutes and *Bacteroides* are two phyla who together can account for 90% of the microbiome. The F/B ratio varies wildly between individuals and is very dependent on the diet. However, it is known that Firmicutes is more often seen in the developed world and is also correlated with obesity. Bacteroidetes is more often found in the developing countries with a more traditional diet and is correlated with irritable bowel symptoms.

Short chain fatty acids (SCFAs)

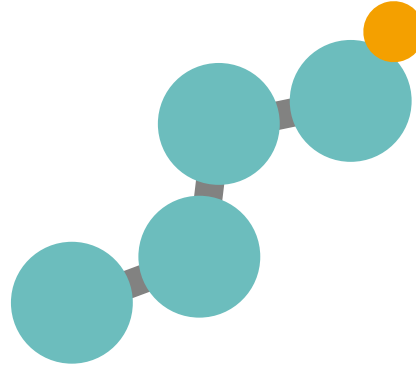
The short chain fatty acids: acetate, propionate and butyrate are the most important substances produced by the microbiome. Acetate is a food source for many other bacteria of the microbiome and is often provided to the bloodstream to be used as an energy source for our organs and muscles. Propionate plays a major part in the feeling of satiety and in the sugar metabolism. A large portion of propionate is processed in the liver. Butyrate is a direct food source for the cell that make up our gut lining; the colonocytes. Healthy colonocytes provide the gut lining of structural integrity which inhibits 'leaky gut'. This is done by reinforcing the tight junctions. Tight junctions are the strong connections between colonocytes. When colonocytes do not have the necessary food sources (short chain fatty acids) the tight junctions will weaken creating 'leaks'. This causes 'leaky gut' and is often associated with inflammation. The unhealthy colonocytes also contribute to an increased risk in (colon)cancer due to the worsened cell division.

Acetate



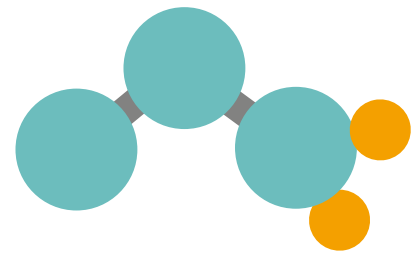
Energy for bacteria, muscles and organs

Butyrate



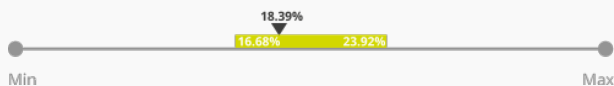
Food source for colonocytes (maintaining tight junctions) and anti-inflammatory

Propionate



Plays an important role in feel of satiety and sugar metabolism.

Butyrate producing bacteria

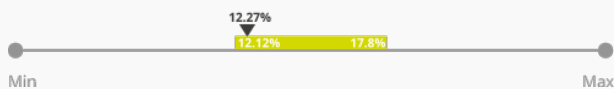


A healthy gut requires sufficient production of butyrate. There are an estimated 60 species who are capable of butyrate production from various substrates. Fibers are the main and most important source for these substrates.

Low levels of butyrate lead to a weak gut lining with irritable bowel or leaky gut as a result.

A high butyrate production is not regarded as unhealthy since a surplus of butyrate exits the body with the feces.

Propionate producing bacteria



Propionate is essential for proper sugar metabolism. Much of the propionate that is produced in the gut is broken down in the liver, where it influences the sugar homeostasis. Propionate is also important for the feeling of satiety after a meal. Fibres are also an important substrate for bacteria to produce propionate.

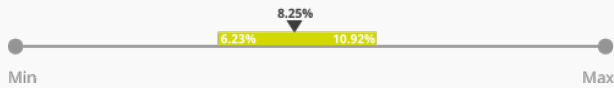
A low production of propionate can, comparable to butyrate, cause irritable bowel symptoms. A high propionate production is not regarded as unhealthy since a surplus of butyrate exits the body with the feces.

Footnote

Many bacteria can produce different short chain fatty acids. Whether a bacteria produces acetate, propionate or butyrate is dependent on the substrates available to the bacteria. Butyrate and propionate production can be estimated based on the butyrate and propionate producing bacteria that are found in the gut microbiome. It can be said for both metabolites that a high production is favourable. However, it is not possible to estimate acetate production based on the amount of acetate producing bacteria found in the gut microbiome. Which bacteria actually produce acetate is much more dependent on the substrate intake (diet) than for butyrate or propionate.

Gas producing bacteria

Total gas producing bacteria



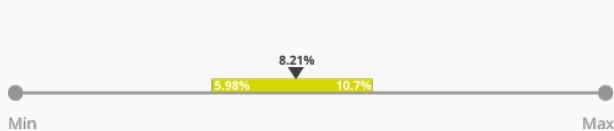
Desulfovibrio (Hydrogen sulfide producing bacteria)



Methanobrevibacter (methane producing bacteria)



Ruminococcus + Eubacterium + Roseburia (Hydrogen producing bacteria)



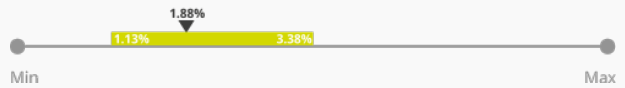
Certain bacteria in the gut will produce different types of gas when they are fermenting food sources. Food sources like certain sugars or non-digestible polysaccharides (like starch and cellulose) are not digested in the small intestine but are fermented in the large intestine by gas producing bacteria. The gasses that these bacteria produce are mainly carbon dioxide (CO₂), hydrogen (H₂), methane (CH₄) and hydrogen sulfide (H₂S). Gas production in the gut is a natural process which provides the gut and body with energy. Most of the produced gas is used by bacteria in other processes. A smaller part of the produced gas exits the body as flatulence or is exhaled after it is transferred in the blood to the lungs.

A high abundance of gas producing bacteria can cause different intestinal complaints, such as bloating or excess flatulence. This can be reduced by decreasing the intake of the food sources of the gas producing bacteria. A low-FODMAP diet (fermentable oligosaccharides, disaccharides, monosaccharides and polyols) can help to decrease the abundance of gas producing bacteria. Important food groups that are eliminated are beans, but also sugar from milk products (lactate) or sugars from fruit (fructose) are excluded in a low-FODMAP diet.

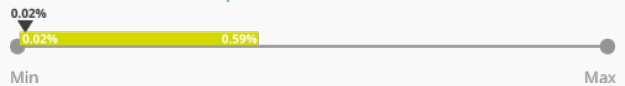
A low abundance of gas producing bacteria does is not regarded as unhealthy for the (gut) health.

Mucin converting bacteria

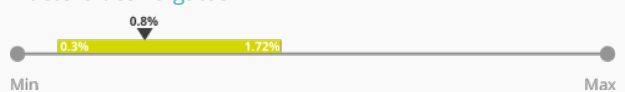
Total mucin converting bacteria



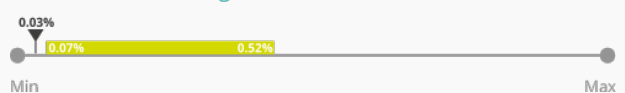
Akkermansia muciniphila



Bacteroides vulgatus



Bifidobacterium longum



Mucus is a slimy layer that is produced by the lining of our gut. The building blocks of this mucus layer are mucins. Mucins are important for our gut health because they function as lubrication, hydration for the gut lining, protection against pathogenic microbes and as a food source for mucin converting bacteria. Mucin converting bacteria are important because when they digest the mucins, they also stimulate the renewal of the gut lining and stimulate the production of new mucins.

Akkermansia muciniphila is an example of a mucin converting bacteria that converts mucins into products which are used by other bacteria, such as *Bacteroides*, as a food source while also stimulating the renewal of the gut lining and the production of mucins.

A low abundance of mucin converting bacteria is often seen with a reduced gut lining renewal and reduced mucin production. This is regarded as unfavourable due to the many functions of mucins.

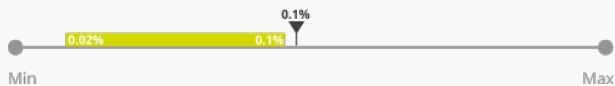
A high abundance of mucin converting bacteria is not regarded as unhealthy for the (gut) health.

Sulphate reducing bacteria

Total Sulfate Reducing Bacteria



Bilophila wadsworthia



Desulfobacter



Desulfovibrio

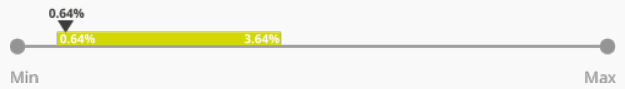


Sulphate naturally occurs in our digestion and is, among other things, needed to produce mucins and bile. Sulphate reducing bacteria have specialized in using sulphate for their metabolic processes during which they produce hydrogen sulfide (H₂S). A low or average abundance (a few percent) is commonly seen in the microbiome and is not regarded as unhealthy.

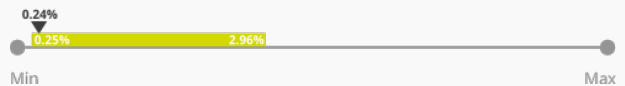
A high abundance of sulphate reducing bacteria is regarded as unhealthy. Hydrogen sulfide disrupts the cell lining of the intestines (colonocytes) and therefore damages the gut lining. This damage could be the start of an inflammation of the gut and is typically associated with diseases of the gut, such as ulcerative colitis (UC).

Lactate producing bacteria

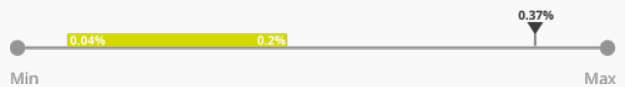
Total number of lactate-forming bacteria



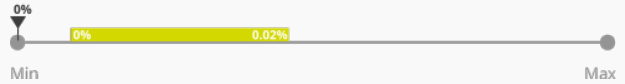
Bifidobacterium



Lactobacillus



Enterococcus



Streptococcus



Lactate producing bacteria (also called lactic acid bacteria) are known for their production of lactate. Lactate is an important food source for lactate converting bacteria who cannot live on the sugars from food sources. These bacteria convert lactate into propionate and butyrate (view page 4).

Lactate producing bacteria also produce other metabolites which are known to have a beneficial impact on gut health. These bacteria are often used, due to their ability to produce lactate and other beneficial metabolites, as probiotics.

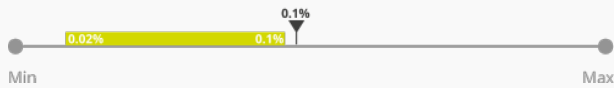
The most well-known groups of lactate producing bacteria are *Bifidobacterium* and the *Lactobacillus*. However, also *Enterococcus* and *Streptococcus* are known to produce lactate.

A low abundance of lactate producing bacteria can inhibit the production of propionate and butyrate and is therefore regarded as unhealthy (view page 4).

A high abundance of lactate producing bacteria can, when combined with not many butyrate and propionate producing bacteria, result in an excess of lactate in the gut. This can cause several complaints and is mainly seen in people with Crohn's disease or colitis.

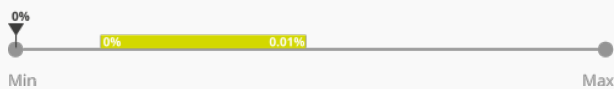
Unwanted species and genera

Bilophila wadsworthia



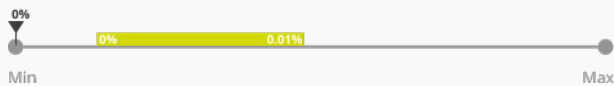
B. Bilophila wadsworthia belongs to the sulphate reducing bacteria. Higher abundance (more than 1%) can cause irritation and inflammation of the gut lining (view page 6 for other sulphate reducing bacteria)

Clostridioides difficile



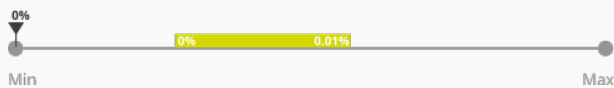
Clostridioides difficile (previously named *Clostridium difficile*) belongs to the family Clostridiaceae. This species can produce toxins that damage the gut lining. They are commonly found in low abundance (<0.1%) but can increase rapidly after treatment with antibiotics. A high abundance of *C. difficile* can lead to diarrhoea and a damaged gut.

Clostridium perfringens



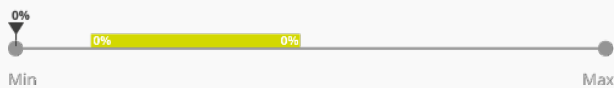
Clostridium perfringens belongs to the same family as *C. difficile* (Clostridiaceae). An abundance of up to 1% is commonly seen without any complaints. If the abundance of *C. perfringens* increases due to a high contamination of spores in food sources, then they can produce toxins in the small intestines which is detrimental for the health.

Enterobacter



Enterobacter (not to be confused with Enterobacteriaceae) is a genus that belongs to the family proteobacteria. Enterobacter can ferment sugars with acids and gasses as by-products. It is an opportunistic pathogen and is often the cause of hospital infections. High abundance of *Enterobacter* is often seen with inflammation in the guts.

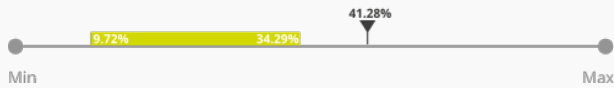
Fusobacterium



Fusobacterium is a genus which is related to Bacteroides. How exactly fusobacterium influences the gut is unknown, but it is known that it is through the lipopolysaccharides (LPS) they produce. This substance causes chronic infections by overstimulating the immune system. A very high abundance is correlated with inflammation of the gut and ulcerative colitis (UC) and is regarded as very unhealthy.

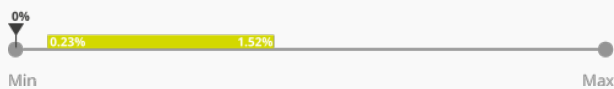
A selection of commonly found species

Prevotella copri



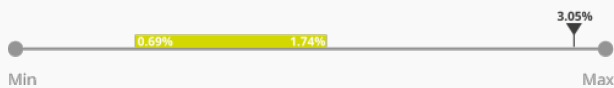
Prevotella copri is a well-known species that belongs to the phylum Bacteroidetes. Not all people carry *P. copri* in their gut microbiome and the role it plays can be fulfilled by other bacterial species. Not all people carry *P. copri* in their gut microbiome and the role it plays can be fulfilled by other bacterial species. Combining a healthy and fibre rich diet with regular exercise and a healthy lifestyle can cause this bacteria, if present, to occupy 50% of the microbiota. This is not regarded as unhealthy but does lower the diversity score (view page 1).

Ruminococcus bromii



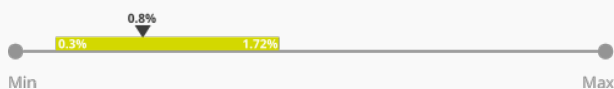
Ruminococcus bromii is also a keystone species (view page 2) due to its presence in nearly all human gut microbiomes. This species is especially well equipped to convert starch in many different products which other bacteria can use as a food source. A low or high abundance is not regarded as either healthy or unhealthy for the (gut) health.

Fusicatenibacter saccharivorans



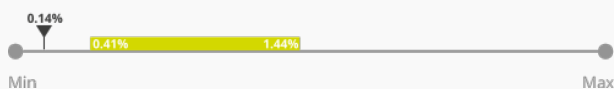
Fusicatenibacter saccharivorans is a species that is commonly found in most people and can occupy a sizeably part of the microbiome. Surprisingly, there is no clue as to what the function of the specific bacteria is.

Bacteroides vulgatus



Bacteroides vulgatus is also a keystone species and a bacteria that is found in almost all humans. This bacteria produces propionate and butyrate and is generally regarded as safe. However, when combined with 'leaky gut' (view page 4), they are well known instigators of inflammation outside the gut.

Roseburia intestinalis



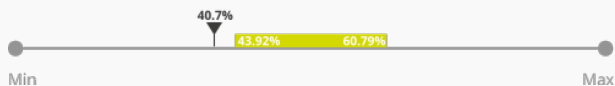
Roseburia intestinalis is one of the most important bacteria that is involved in the degradation of polysaccharides from the cell wall of plant cells (beta mannans). This makes it a good indicator for a healthy plant-based diet. It is also an important butyrate producing species. A low or high abundance is not regarded as either healthy or unhealthy for the (gut) health).

Genus level ordered by phylum

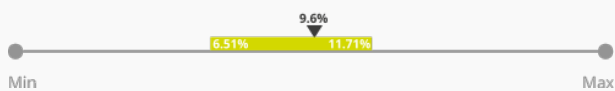
Note: A selection has been made of relevant genera. Please view the online results to investigate the different taxonomic levels, such as families, genera or species, in more detail.

Firmicutes

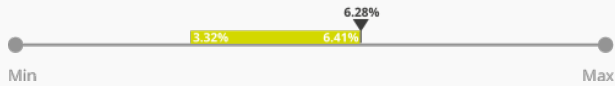
Total Firmicutes



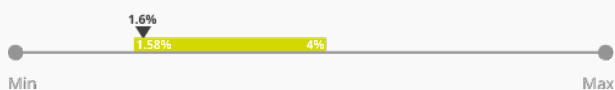
Faecalibacterium



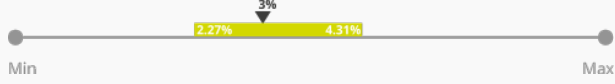
Blautia



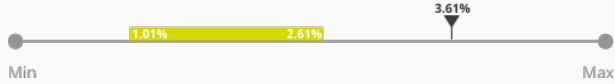
Ruminococcus



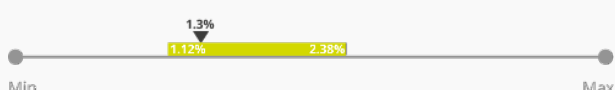
Eubacterium



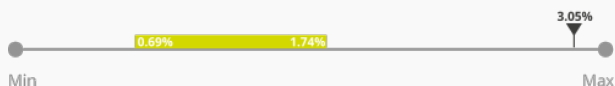
Roseburia



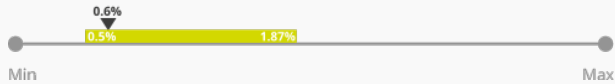
Lachnoclostridium



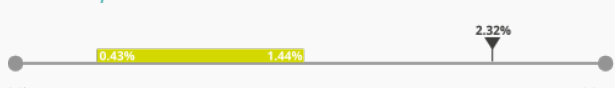
Fusicatenibacter



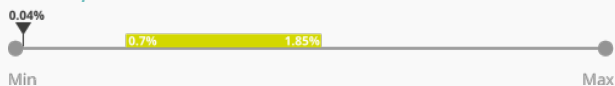
Lachnospiracus



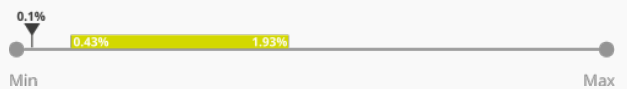
Anaerostipes



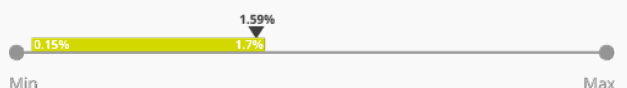
Oscillospira



Clostridium



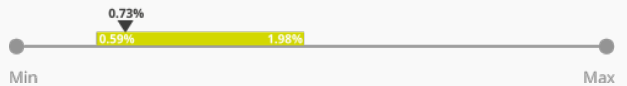
Phascolarctobacterium



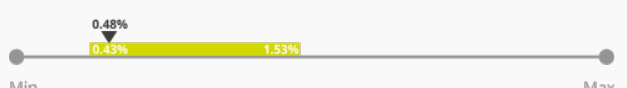
Megamonas



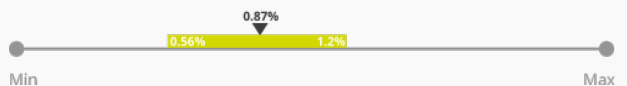
Coprococcus



Oscillibacter



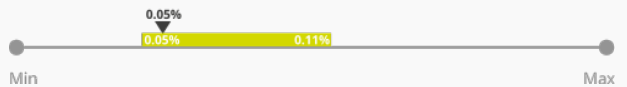
Dorea



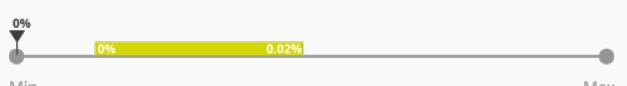
Dialister



Clostridiales



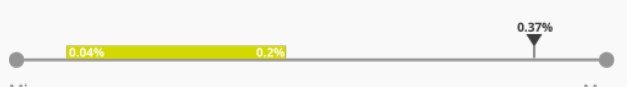
Christensenella



Acidaminococcus



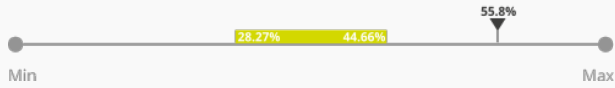
Lactobacillus



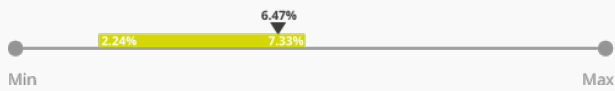
Firmicutes forms the biggest group of bacteria. Most butyrate producing bacteria belong to this phylum.

Bacteroidetes

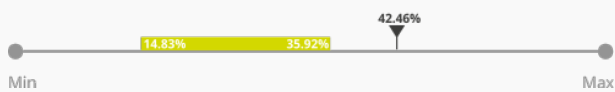
Total Bacteroidetes



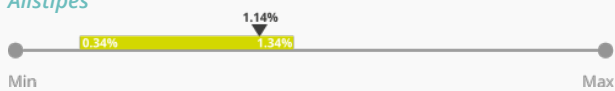
Bacteroides



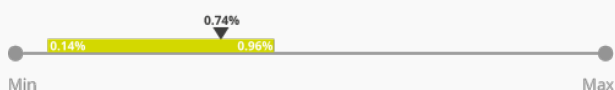
Prevotella



Alistipes



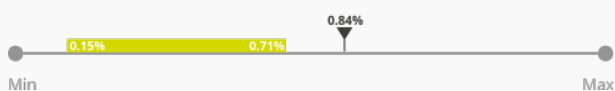
Barnesiella



Parabacteroides



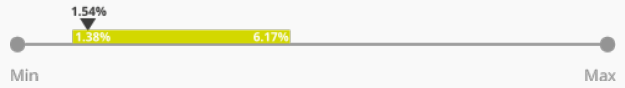
Paraprevotella



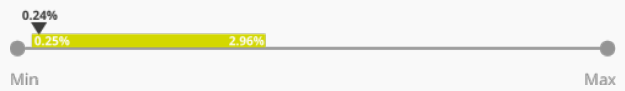
Bacteroidetes are often the second biggest group of bacteria found in the guts. This group contains many keystone species, which are important for a healthy balance of the gut microbiome.

Actinobacteria

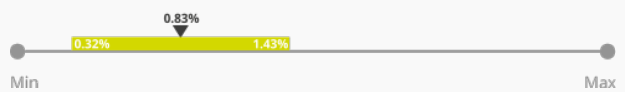
Total Actinobacteria



Bifidobacterium

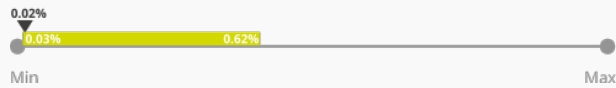


Colinsella



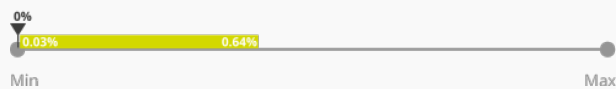
Actinobacteria are mostly represented by the *Bifidobacteria*. This genus is a well-known probiotic and one of the most common genus found during in babies and young children. These bacteria thrive on the so-called 'human milk oligosaccharides' (HMO) which are found in breast milk and are important for the development of the immune system. This bacteria can also be found in a later stage of life, but it will then function as a lactate producing bacteria (view page 6).

Verrucomicrobia



The only representative of this phyla is the species *Akkermansia muciniphila* (view page 2). This is one of the keystone species and contributes to a healthy gut and gut microbiome.

Cyanobacteria



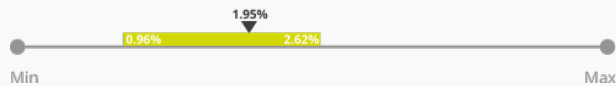
Cyanobacteria only account for a small percentage of the gut microbiome. The representatives of this phyla must play a role in the gut microbiome, but we do not know what role yet. It is a possibility that these bacteria live off products produced by other bacteria in small amount or that they thrive on food sources that are scarcely represented in the diet.

Euryarchaeota



Euryarchaeota form an important and special group since these are not bacteria but archaea. Archaea is a kingdom that exists parallel to bacteria. Methanobacteria, who produce methane, are the most well-known representatives of this group.

Proteobacteria

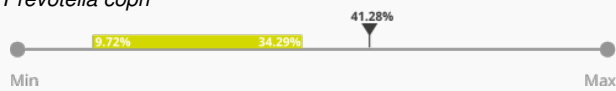


The most important representative of this group is *Escherichia coli*. This group is also known as an opportunistic pathogen, which are bacteria who only cause illness when new strains are encountered. This is often the cause of food poisoning since new strains are often encountered while visiting new places. A high abundance of proteobacteria is often not a good sign and is also often found in people with obesity.

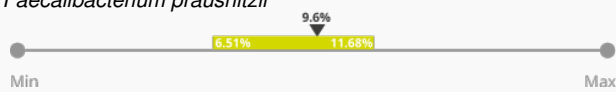
Top 10 species

Personal top 10

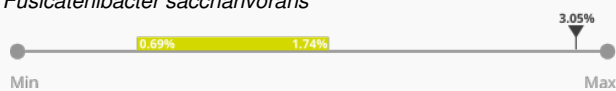
Prevotella copri



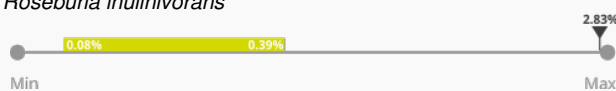
Faecalibacterium prausnitzii



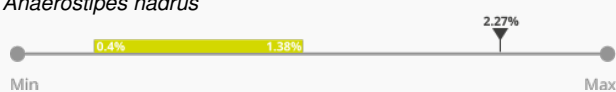
Fusicatenibacter saccharivorans



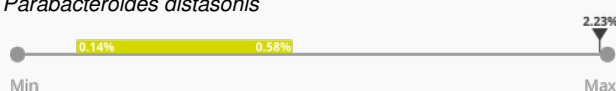
Roseburia inulinivorans



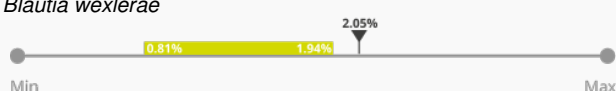
Anaerostipes hadrus



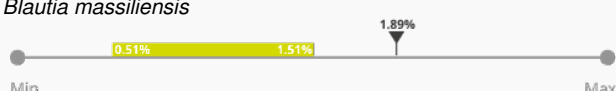
Parabacteroides distasonis



Blautia wexlerae



Blautia massiliensis



Phascolarctobacterium succinatutens



Eubacterium eligens

