Gut Microbiome Test Analysis

Name	Example User	**Age**	25
Country	United Kingdom	**Sample ID**	EXAMPLE43
Sampling Date	25 Feb 2025 17:02	**Test Date**	03 Mar 2025 17:02
Test Profile	Gut Microbiome	**Technology**	Shotgun metagenomics

Welcome to your gut microbiome report!

The gut microbiome represents the collection of microorganisms – mostly bacteria – that live in your gut. Its composition is known to be instrumental to determining overall good health. This report includes multiple analyses of your gut microbiome – looking at the types and amounts of beneficial (good) and pathogenic (disease-causing) bacteria; important functional capabilities of the microbiome, and distributions associated with specific health risks.

Results at a glance

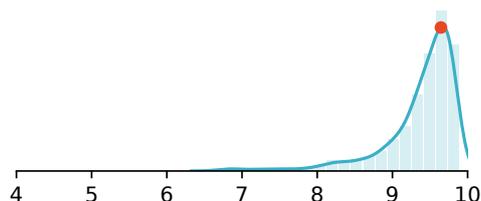|			
Microbiome diversity	9.6 / 10	**Pathogens**	None above normal levels
Beneficial bacteria	9 below normal levels	**Health risk scores**	1 high-risk scores

Contents

This report will guide you through the key aspects of the gut microbiome that influence your health and wellbeing. Background information and actionable advice is provided in each section. Please note that each section heading is clickable as a link to the relevant section.

Your gut diversity

9.6 / 10

very low	low	normal	high	very high

This chart shows how your sample compares to the distribution of healthy people – you can see that, in general, healthy microbiomes have higher diversity scores.

The diversity of your gut microbiome is a good overall indicator of health. A higher diversity score indicates more variety of species and more likely a healthier gut.

A diversity score of above 9 implies a diverse gut microbiome which is associated with good health.

A diversity score of below 9 indicates a medium level of diversity and a score below below 7 indicates a low level of microbiome diversity. Please see the "**Recommendations**" section of this report for suggestions about diet and lifestyle changes.

A more diverse gut microbiome containing many different species is known to be more healthy because the different species support each other to perform important metabolic functions, and the overall microbiome is more resilient to disruption.

An imbalance or reduction in diversity results in a decrease in the available functions of the gut microbiome, and can contribute to the development of chronic disease states such as diabetes, Crohn's disease, ulcerative colitis, and colorectal cancer. It is also recognised that poor gut biome diversity is likely to be associated with obesity, generalised inflammation, impaired digestion, allergic states, and weakened immune systems.

On the other hand, gut microbiome diversity varies between healthy individuals and reduced diversity is not necessarily an indicator of sub-optimal gut health. Therefore, it is important to seek advice from a clinician with expert knowledge of the gut biome when interpreting test results – symptoms and signs are of course all important to take into consideration at the same time.

Pathogens and Opportunistic Pathogens

This test also looks for the presence of >60 potential pathogenic (disease-causing) groups in your sample and only those detected in your sample are reported. Some of these bacteria may exist harmlessly within the normal gut microbiome, but could be problematic if their population grows too large – your results show what the normal range for each group is in a healthy population and how your sample compares.

We detected 5 potential pathogens in your sample, and **0 are above the levels expected in a healthy population**.

You should interpret your results in the context of any symptoms you may have. These results do not equate to a clinical diagnosis, and you should consult a medical professional before making any decisions about treatments. Please see the "**Recommendations**" section for more information.

Please note that descriptions of each of these species are provided in the **Key bacteria** section. You can also click on the name of any of the bacterial species below to jump to the relevant section.

Bacteroides fragilis: 1.7 %	Normal range: 0–10.68 %	Normal
Clostridioides difficile: 0.1 %	Normal range: 0–0.25 %	Normal
Collinsella: 3.4 %	Normal range: 0–4.05 %	Normal
Escherichia coli: 0.7 %	Normal range: 0–13.68 %	Normal
Sutterella: 0.9 %	Normal range: 0–1.35 %	Normal

Beneficial bacteria

These bacterial groups are associated with improved gastrointestinal health. Not all of the bacteria below need to be present to maintain a healthy gut microbiome, but identifying which are missing or present at low levels can help create a personalized diet and probiotic plan.

Please note that descriptions of each of these species are provided in the **Key bacteria** section. You can also click on the name of any of the bacterial species below to jump to the relevant section.

Akkermansia muciniphila: Not detected	Normal range: 0–4.08 %	Not detected
Bacteroides fragilis: 1.7 %	Normal range: 0–10.68 %	Normal
Bacteroides stercoris: Not detected	Normal range: 0–7.26 %	Not detected
Bacteroides thetaiotaomicron: 3.9 %	Normal range: 0–3.03 %	High
Bacteroides uniformis: 17.2 %	Normal range: 0–10.17 %	High
Bifidobacterium adolescentis: 3.0 %	Normal range: 0–4.97 %	Normal
Bifidobacterium longum: 3.2 %	Normal range: 0–13.42 %	Normal
Bifidobacterium pseudolongum: Not detected	Normal range: 0–0.01 %	Not detected
Blautia wexlerae: 4.0 %	Normal range: 0–4.85 %	Normal
Christensenella minuta: Not detected	Normal range: 0–0.04 %	Not detected
Faecalibacterium prausnitzii: 9.2 %	Normal range: 0–9.49 %	Normal
Lacticaseibacillus rhamnosus: Not detected	Normal range: 0–2.21 %	Not detected
Lactobacillus species: Not detected	Normal range: 0–0.67 %	Not detected
Limosilactobacillus reuteri: Not detected	Normal range: 0–0.59 %	Not detected
Methanobrevibacter smithii: Not detected	Normal range: 0–4.73 %	Not detected
Roseburia intestinalis: 1.4 %	Normal range: 0–3.39 %	Normal
Ruminococcus champanellensis: Not detected	Normal range: 0–0.26 %	Not detected

You have 9 beneficial microbes below normal levels.

Probiotic supplements can also be useful if the microbe is absent, though they are not available for every microbe. Of the beneficial microbes you are lacking, probiotic supplements are widely available for *Akkermansia muciniphila*, *Lacticaseibacillus rhamnosus*, *Lactobacillus*, and *Limosilactobacillus reuteri*. See the **Recommendations** section to find out more about probiotics.

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Health risks

The gut microbiome and health

Scientists are finding an increasing number of links between microbiomes and a wide variety of health conditions, with particular patterns of microbes associated with particular diseases. Sometimes these patterns of microbial growth could be the cause of the particular health condition, but they can also be caused by the disease changing the gut environment. Either way, identifying a disease-associated pattern of growth in the microbiome can indicate that an individual has or is at risk of that disease.

Health risk scores

The following health risk scores are based on the similarity of your microbiome to the average microbiome of healthy people and people with certain diseases. Microbiome similarity is assessed in one of two ways: either by looking for patterns of microbial growth that have been described in peer-reviewed research, or by using a machine-learning tool called SIGNAL. SIGNAL has been trained with thousands of microbiome samples, and can categorise a sample microbiome as healthy or diseased with high accuracy.

What does your result mean?

These scores only assess your risk for a disease based on the similarity of your microbiome to others. The results are not a clinical diagnosis but are intended to signpost you towards further investigations. Any decisions about further tests or possible treatments should be taken in consultation with a medical professional.

Taking Crohn's Disease as an example:

- If you have a high risk score it means your microbiome is very similar to the average Crohn's Disease patient. This does not definitely mean you have Crohn's, as there could be other factors influencing your microbiome.

- If you have a low risk score it means your microbiome is not similar to people with Crohn's. This means it is less likely that you have Crohn's, however you may still have it but your microbiome is being affected in a different way to the average sufferer.

It is important to interpret your results in the context of any symptoms and additional test results you may have. Each health risk score page also summarises relevant information to help provide a holistic view of your disease risk.

Crohn's disease – Low risk

Crohn's disease is a chronic form of inflammatory bowel disease (IBD) which is thought to occur in genetically predisposed individuals after being exposed to bacterial, immune, or environmental triggers. The main symptoms are diarrhoea, stomach pain and cramps, tiredness, weight loss, and blood in your poo, and the severity of symptoms can increase and decrease. There is no cure for Crohn's disease but treatment options are available to help manage symptoms and prevent further severe inflammation.

This risk score was calculated by SIGNAL – microbiome health analysis powered by Machine Learning. This is a risk score based on microbiome similarity, not a diagnosis. If you have a high risk score it means your microbiome is very similar to that of a person with this disease. Our model is 94 % accurate at classifying microbiomes of people with Crohn's disease.

Your risk score for Crohn's disease is **low** and you do not have many of the symptoms normally associated with this disease, which indicates a good, healthy result. Having a low risk score is not a formal diagnosis however, and if you have any concerns about your health you should discuss them with a qualified healthcare practitioner.

Symptoms summary

Relevant symptoms from the information registered with this sample are summarised here:

Symptom	Sample information
Diarrhoea	None in past week
Stomach pain	Yes
Blood in stool	No
Tiredness	No
Weight loss	No problems gaining/losing weight
Urgent bowel movement	One time in the past week
Loss of appetite	Never

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Ulcerative colitis – **High risk**

Ulcerative colitis is another type of inflammatory bowel disease (IBD). Similar to Crohn's, it is a long-term condition with symptoms that can come and go, including diarrhea, stomach pain, tiredness and weight loss, and stool may contain blood, pus or mucus. Unlike Crohn's which can affect the entire digestive system, it affects only the lower intestine and rectum. Symptoms can often be managed with medicines, with surgery an option for severe cases.

This risk score was calculated by SIGNAL – microbiome health analysis powered by Machine Learning. This is a risk score based on microbiome similarity, not a diagnosis. If you have a high risk score it means your microbiome is very similar to that of a person with this disease. Our model is 95 % accurate at classifying microbiomes of people with Ulcerative colitis.

Your risk score for Ulcerative colitis is **high** but you don't have many of the symptoms normally associated with this disease. Symptoms come and go, so this may be because the disease is in remission or is a mild form. You might also have a microbiome that is similar to diseased individuals, without having the disease yourself. Monitor your symptoms and seek further advice from a healthcare practitioner if you are concerned.

Symptoms summary

Relevant symptoms from the information registered with this sample are summarised here:

Symptom	Sample information
Diarrhoea	None in past week
Stomach pain	Yes
Blood in stool	No
Tiredness	No
Weight loss	No problems gaining/losing weight
Urgent bowel movement	One time in the past week
Loss of appetite	Never

Obesity – **Low risk**

Obesity is characterised by excess body fat, and overweight or obese individuals have a higher risk of secondary diseases such as diabetes or heart disease. There are strong links between the gut microbiome and obesity. Unhealthy diets that could cause obesity will alter the microbiome, but the microbiome can also influence body weight due to the effects it has on factors such as metabolism, appetite and hormonal systems.

This risk score was calculated by SIGNAL – microbiome health analysis powered by Machine Learning. This is a risk score based on microbiome similarity, not a diagnosis. If you have a high risk score it means your microbiome is very similar to that of a person with this disease. Our model is 95 % accurate at classifying microbiomes of people with Obesity.

Your risk score for Obesity is **low** and you don't have a high BMI – though note that BMI categories sometimes need to be adjusted for ethnicity which this test does not do. This indicates a good, healthy result. Having a low risk score is not a formal diagnosis however, it is important to maintain a healthy diet and lifestyle. Talk to your healthcare practitioner and see the "**Recommendations**" section for more information.

Symptoms summary

Relevant symptoms from the information registered with this sample are summarised here:

Symptom	Sample information
Tiredness	No
BMI	$<25\,\mathrm{kg\,m^{-2}}$
Weight loss	No problems gaining/losing weight

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Irritable Bowel Syndrome – Low risk

Irritable bowel syndrome (IBS) is a common condition with intermittent symptoms including stomach pain and cramps, diarrhea or constipation, and bloating. IBS is sometimes subtyped by the effect it has on your bowel movements, for example IBS-C for constipation. Unlike IBD there is usually no inflammation of the bowel. The cause has been linked to factors including stress, genetic predisposition, and food transiting the gut at the wrong speed. There is no cure but symptoms can often be controlled using medicines and dietary changes.

This risk score was calculated based on patterns of microbial growth identified by peer-reviewed research. This is a risk score based on microbiome similarity, not a diagnosis. If you have a high risk score it means your microbiome is similar to published signatures defined by scientists.

Your risk score for Irritable Bowel Syndrome is **low** but you have many of the symptoms that are usually associated with this disease. Many symptoms overlap with other diseases, so seek advice from a healthcare practitioner about alternative causes. Bear in mind that your risk score is based on microbiome similarity and is not a diagnosis.

Symptoms summary

Relevant symptoms from the information registered with this sample are summarised here:

| Symptom	Sample information
Diarrhoea	None in past week
Stomach pain	Yes
Tiredness	No
Constipation	A little
Bloating	Rarely
Swelling	No
Excessive wind	Not unusually high
Urgent bowel movement	One time in the past week
Loss of appetite	Never

Gut function

Gut bacteria are involved in a wide range of metabolic processes in the human body, which include the ability to break down different components of your diet and to produce chemicals which interact with the cells lining your gut. Our analysis directly detects which functional genes are present in your sample. The higher the score, the more potential your microbiome has to perform that function. Your score is compared to the average score of a healthy population.

One of the most important functions of the gut microbiome is to produce **short-chain fatty acids (SCFAs)**. These are produced by bacteria from the breakdown of **dietary fibre**. SCFAs in the gut are known to suppress inflammation, maintain the gut barrier and to prevent a 'leaky gut', reduce appetite and maintain blood sugar levels, modulate the immune system, and assist with cancer prevention.

| Butyrate Score: 4.7	Normal range: 4.78–6.74
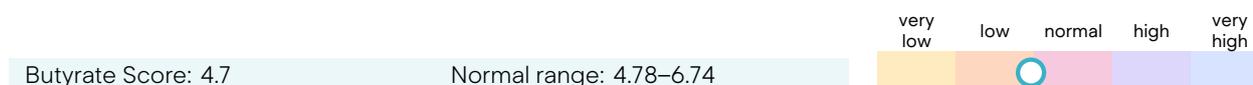
Butyrate is mainly produced by bacteria in the phylum Bacillota (Firmicutes). The short-chain fatty acid is a major energy source for the cells lining the gut and helps to maintain the integrity of the gut lining and mucous layer. It is anti-inflammatory and helps protect against cancer.

| Propionate Score: 4.7	Normal range: 4.73–8.12
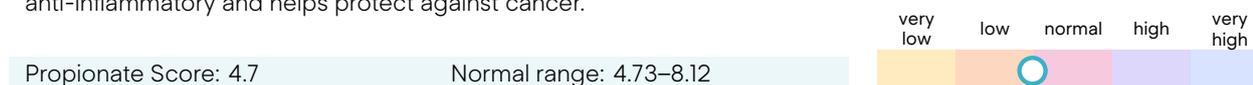
Microbial production of propionate has a range of benefits to metabolic health, including regulating appetite, reducing internal fat deposition, and controlling glucose levels, and so helps reduce the risk of type II diabetes. It also has a protective effect on the gut lining and reduces gut inflammation.

Acetate Score: 5.0	Normal range: 4.85–6.22
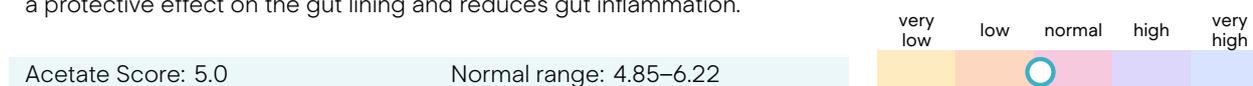
Acetate is the most abundant short-chain fatty acid. Acetate production has been correlated with decreased fat around the internal organs and other beneficial effects on host metabolism that combat obesity. Acetate may have a protective role over cognitive functions.

Lactate Score: 5.1	Normal range: 4.97–7.29
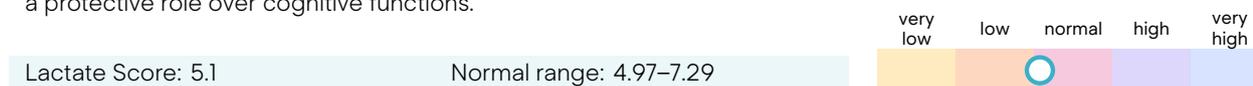
Some gut bacteria, mostly Lactobacillales and Bifidobacteria, ferment dietary fibre to lactic acid (lactate), which is then used as a food source by short-chain fatty acid-producing bacteria. They can also help convert lactose (the main sugar found in dairy products) to lactic acid, which helps to limit the symptoms of lactose-intolerant individuals.

H_2S Score: 4.9	Normal range: 4.71–6.04
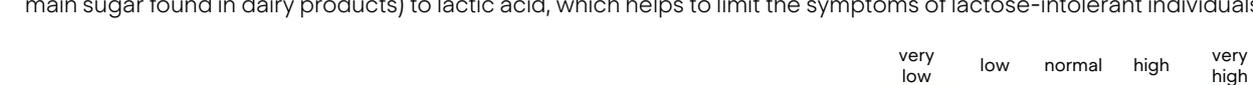
Hydrogen sulphide (H2S) is a gas that can have important positive and negative effects on gut health. At low levels, H2S helps to maintain the mucous layer of the gut, and improves the interaction between bacterial and human cells lining the gut, and can act to improve healing and reduce inflammation. At high levels H2S can be toxic, causing increased gut inflammation, disrupting the gut mucous lining, and negative affecting populations of 'good' gut bacteria. Excessive H2S production can often be reduced by increasing the consumption of fibre and decreasing protein intake.

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Recommendations

Here is a summary of your test results and actions you can take to improve your gut health. For fully personalized advice, please consult with a qualified healthcare practitioner.

Health

Pathogens

We detected **5 potential pathogens** in your sample, and **0** are above the levels expected in a healthy population. This means you **probably do not have** a gut infection, but you should interpret your results in the context of any symptoms you may have. Maintaining a healthy gut microbiome is a good general defence against gut pathogens, as is ensuring safe food hygiene and cooking practices.

Health risks

This test is intended as a tool for assessing disease risk and cannot be used to provide a formal diagnosis. Based on the similarity of your gut microbiome to diseased populations, and on the symptoms you reported, you have:

- **some indications** of Ulcerative colitis and Irritable Bowel Syndrome – continue to monitor your symptoms and follow up with a healthcare professional if you are concerned.
- **a low risk** of Crohn's disease and Obesity but trust your instincts about your own health and seek further advice if you are still concerned about these or other diseases.

Diet

Unless you have a specific allergy or intolerance, most people will benefit from a diet which is mostly plant-based and contains **high levels of fibre**. Vegetables, fruit, beans and other legumes, and wholegrains all contain fibre which feeds beneficial bacteria, and is transformed into short-chain fatty acids (SCFAs) which have numerous health benefits. It will also help with effective movement of food through the gut, preventing constipation.
Fermented foods such as yoghurt, kimchi, or tempeh contain probiotic bacteria and help to increase the diversity of the gut microbiome. On the other hand, diets that are high in **animal protein** or **saturated fats** can decrease microbiome diversity and encourage growth of harmful bacteria.

Probiotics

Following a healthy diet is the best way to build and maintain a healthy gut microbiome. However, if some beneficial microbes are missing, particularly after illness or antibiotic treatment, it may be worthwhile to use probiotic supplements to reintroduce them. Discuss possible probiotic supplements with a qualified healthcare practitioner, and be aware of any unwanted side effects such as bloating or altered bowel movements.
Your sample contained **low levels** of these widely available probiotic strains: *Akkermansia muciniphila*, *Lacticaseibacillus rhamnosus*, *Lactobacillus*, and *Limosilactobacillus reuteri*.

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Key bacteria

Pathogens

Bacteroides fragilis	Normal range: 0–10.68 %

This bacterium is a normal component of a healthy gut, but may cause opportunistic infections elsewhere; particularly relevant after gut surgery or in immunocompromised individuals.

Clostridioides difficile	Normal range: 0–0.25 %

This bacterium can infect the large intestine and cause diarrhoea.

Collinsella	Normal range: 0–4.05 %

Overgrowth of this species is correlated with several health disorders, including non-alcoholic fatty liver disease, obesity, and high insulin levels.

Escherichia coli	Normal range: 0–13.68 %

E. coli is a common gut bacterium and usually contributes to a healthy gut, however it can cause problems if the population grows too large, such as increased risk of IBS/IBD. Certain strains of E. coli are pathogenic and are associated with acute gut symptoms such as severe stomach pain and (sometimes bloody) diarrhea.

Sutterella	Normal range: 0–1.35 %

These species of bacteria are often present at low abundance in a healthy gut microbiome, but have been shown to be pro-inflammatory, and increased abundance has been correlated with diseases such as irritable bowel disease, Crohn's disease, and autistic spectrum disorder.

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Beneficial microbes

Bacteroides fragilis	Normal range: 0–10.68 %

Bacteriodes fragilis has been shown to be a key modulator of immune response. This speces could protect against disease by stimulating an immune response.

Bacteroides thetaiotaomicron	Normal range: 0–3.03 %

While reseach into this species is in its early stages, Bacteroides thetaiotaomicron seems to play an important role in the digestion of fibre and nutrient scavenging, producing compounds that are useful to other microbes in the gut.

Bacteroides uniformis	Normal range: 0–10.17 %

This SCFA-producing bacterium helps regulate the gut microbiome and may be protective against colitis.

Bifidobacterium adolescentis	Normal range: 0–4.97 %

This bacterium has been shown to restore the homeostasis of the gut microbiota, increase the abundance of short-chain fatty acid-producing flora, and alleviate inflammation. In addition, a below-average abundance of this species has been associated with Crohns disease.

Bifidobacterium longum	Normal range: 0–13.42 %

This species reduces constipation and helps inhibit inflammation by regulating the balance of the immune system, improving the intestinal barrier function, and increasing acetate production.

Blautia wexlerae	Normal range: 0–4.85 %

Studies have shown that this bacterium may help reduce obesity and gut inflammation. It produces SCFAs and the neurotransmitter acetylcholine which may give it a role in regulating gut function.

Faecalibacterium prausnitzii	Normal range: 0–9.49 %

This species has been shown to be one of the main butyrate producers in the intestine and to have possible anti-inflammatory properties. Note there is some evidence that this is strain specific.

Roseburia intestinalis	Normal range: 0–3.39 %

A key butyrate producing bacterium, Roseburia intestinalis is an integral part of a healthy gut. A low abundance of this species has been correlated with inflammatory diseases and increased risk of colorectal cancer.

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Key terms

Microbe / Microorganism – A general term for microscopic organisms, very small living things that can only be seen using a microscope, and include bacteria, fungi, viruses and other single-celled organisms. Microbes can exist in a huge range of environments, including soil, water, air, and they also exist on and within larger organisms (such as humans). Whilst some microbes can cause infections, many are beneficial or even essential for human health. All organisms are classified by how closely related (or genetically similar) they are to each other, which also usually determines how similarly they behave. This is their *taxonomic* classification. We normally talk about organisms at the level of *species*, which in sexual organisms describes those that are similar enough to produce fertile offspring. Species are grouped together into a *genus*. An example here would be the genus *Lactobacillus* which contains many different species that all produce lactic acid, but are adapted to exist in different environments, e.g. *Lactobacillus crispatus* in the vagina and *Lactobacillus acidophilus* in the gut. Sometimes it is useful to talk about *strains*, which are organisms from the same species that have a handful of genetic differences: these might not be important, or may result in key differences such as antibiotic resistance. At a much higher level organisms can be grouped into *phyla*.

Microbiome – This is the term for a group of microbes that live in a particular habitat, either in the environment or in association with a host organism. There are microbiomes associated with almost all parts of the body, including the mouth, skin, and gut. When we talk about a microbiome we are often interested in the overall behaviours of the microbial community, for example a microbiome's ability to break down certain foods. We can predict the behaviour of a microbiome by measuring which microbes are present and how many there are of each type.

Dysbiosis – This refers to an imbalance in a microbiome, away from a 'healthy' community of microbes, and is often associated with disease. In general this can be a useful description, but it is important to remember that the collection of microbes in a microbiome is always changing, that those changes may not always be harmful, that they are often temporary, and there is rarely only one definition of a 'healthy' microbiome.

Diversity (of the microbiome) – This refers to the number of different microbial species present in a microbiome. In the gut microbiome we usually aim for high diversity, because only a few species make up most of the population. If the diversity is lower this might indicate that undesirable species have taken over.

Commensal – If a microorganism is commensal it is able to exist in the microbiome without harming the host or other microorganisms.

Opportunistic pathogen – A microorganism that is able to cause infections if the host's resistance to disease is reduced, for example after injury or another infection, or in immunocompromised people. Opportunistic infections often involve the microorganism invading parts of the body where they are not normally found, for example a commensal gut bacterium might become an opportunistic pathogen if it enters the bloodstream.

About this test

What is the gut microbiome?

This is the collection of microorganisms that live in your gut – the numbers of these individual organisms are in the trillions, and exceed the total body cell count. They include bacteria, fungi and viruses. Until recently very little was understood about the relation between these organisms and the gut. These microorganisms create a complex network of interactions with each other and with their host, which can alter over time and in response to changes in the gut environment. When we talk about a microbiome we are mostly interested in the overall behaviours of the microbial community. For example, the gut microbiome helps the body break down food, and we would describe this as a healthy behaviour. An unhealthy behaviour might be to cause inflammation of the cells that line the gut. We can predict the behaviour of a microbiome by using a technology called DNA sequencing to detect which microbes are present, and how many there are of each type.

Why is the gut microbiome important?

The gut microbiome is closely linked to human health, and in an 'unhealthy' state harmful effects may be triggered – ranging from digestive disruption and gut disease, to mental health issues and other diseases affecting parts of the body far away from the gut, such as arthritis and dementia.

A 'healthy' microbiome might be different between two people, but in general a healthy gut microbiome works in harmony with the body to digest food and reduce inflammation, helping to suppress pathogenic microorganisms associated with disease. An 'unhealthy' microbiome might contain pathogens which directly cause acute illness, or it could contain a distribution of microorganisms that increases the risk of a disease occurring, or indeed it could reflect changes in the human host that are caused by a disease.

What we do with your sample

When your sample arrives at our testing laboratory, the DNA from the microorganisms within is extracted and processed by our scientists. We have rigorously developed our methods to make sure we extract as much DNA as possible without bias toward one type of microorganism or another, which is essential to accurately assess the microbiome. The DNA is then prepared for sequencing by turning it into short lengths that the sequencing machine can read. The millions of DNA sequences are then matched to a database of microbiome genomes to allow us to work out which microorganisms are present and the amounts of each group.

Creating your report

We use this information to produce your gut health report which tells you about the balance of important microbes in your gut – both those that help keep you healthy and those that could cause disease. We use insights from peer-reviewed scientific studies and compare your information to a database of many healthy and unhealthy gut samples to help you spot possible health risks.

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Full taxonomy report

Phyla overview

The doughnut charts show the proportion of different microbial phyla in your sample, alongside an average healthy sample for comparison. Everybody's gut microbiome is unique – if your sample is not an exact match it is not necessarily an indicator of poor gut health.

Healthy
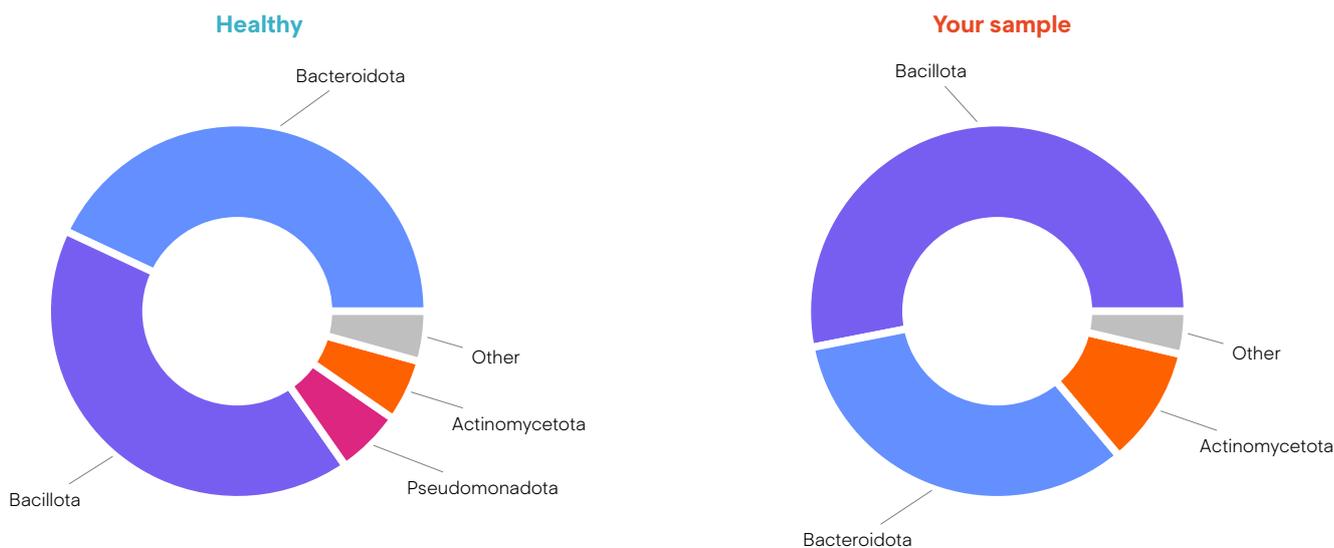
Your sample

This chart shows the proportions of the different bacterial phyla in a representative healthy sample.

This chart shows the proportions of the different bacterial A phyla in your sample.

healthy microbiome is typically dominated by the bacterial phyla Bacteroidota and Bacillota (formerly Firmicutes), together making up roughly 90 % of the total microbiome. Microbiomes that do not match this pattern may have an increased potential for an unstable microbiome and/or pro-inflammatory states.

Full species list

Here are all the species present in your sample, ordered by relative abundance.

Taxonomic name	Relative abundance	Normal range
Bacteroides uniformis	17.2 %	0–10.2 %
Faecalibacterium prausnitzii	9.2 %	0–9.5 %
Phocaeicola dorei	7.8 %	0–9.7 %
Blautia obeum	4.0 %	0–1.9 %
Blautia wexlerae	4.0 %	0–4.8 %
Bacteroides thetaiotaomicron	3.9 %	0–3.0 %
Collinsella aerofaciens	3.4 %	0–4.0 %
Lachnospira eligens	3.2 %	0–3.8 %
Bifidobacterium longum	3.2 %	0–13.4 %
Bifidobacterium adolescentis	3.0 %	0–5.0 %
Anaerostipes hadrus	2.4 %	0–3.0 %
Carjivirus communis	2.1 %	0–29.8 %

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Taxonomic name	Relative abundance	Normal range
Dorea longicatena	2.1 %	0–2.0 %
Simiaoa sunii	2.1 %	0–3.1 %
Anaerobutyricum hallii	1.9 %	0–1.7 %
Bacteroides fragilis	1.7 %	0–10.7 %
Faecalibacterium duncaniae	1.6 %	0–1.2 %
Roseburia intestinalis	1.4 %	0–3.4 %
Dorea formicigenerans	1.4 %	0–0.7 %
Blautia sp. SC05B48	1.4 %	0–1.1 %
[Ruminococcus] lactaris	1.3 %	0–0.8 %
Coprococcus catus	1.2 %	0–0.4 %
Faecalibacterium sp. I3-3-33	1.2 %	0–0.6 %
Faecalibacterium sp. I4-1-79	1.1 %	0–0.8 %
Roseburia rectibacter	1.0 %	0–0.4 %
Faecalibacterium sp. IP-1-18	1 %	0–1 %
Sutterella wadsworthensis	0.9 %	0–1.3 %
Roseburia hominis	0.8 %	0–1.2 %
Coprococcus comes	0.8 %	0–1.4 %
Faecalibacterium sp. IP-3-29	0.8 %	0–0.6 %
[Ruminococcus] torques	0.8 %	0–2.0 %
Faecalibacterium sp. I2-3-92	0.8 %	0–0.5 %
Escherichia coli	0.7 %	0–13.7 %
Parabacteroides distasonis	0.7 %	0–5.1 %
Faecalibacillus intestinalis	0.7 %	0–0.9 %
Bacteroides sp. A1C1	0.7 %	0–0.7 %
Faecalibacterium sp. I4-3-84	0.6 %	0–1.2 %
Faecalibacterium sp. HTF-F	0.5 %	0–0.8 %
Eggerthella lenta	0.5 %	0–0.4 %
Streptococcus thermophilus	0.5 %	0–1.5 %
[Clostridium] scindens	0.4 %	0–0.4 %
Streptococcus salivarius	0.3 %	0–1.9 %
[Ruminococcus] gnavus	0.3 %	0–5.5 %
Bacteroides humanifaecis	0.3 %	0–0.9 %
Flavonifractor plautii	0.3 %	0–1.4 %
Intestinimonas butyriciproducens	0.3 %	0–0.4 %
Faecalibacterium sp. I3-3-89	0.3 %	0–0.9 %
Bacteroides sp. HF-162	0.2 %	0–0.9 %
Vescimonas coprocola	0.2 %	0–1.4 %
Ruminococcus bicirculans (ex Wegman et al. 2014)	0.2 %	0–3.0 %
Dysosmobacter welbionis	0.2 %	0–0.7 %
Eubacterium ventriosum	0.2 %	0–0.6 %
Bacteroides sp. CACC 737	0.2 %	0–0.4 %
Butyrivibrio crossotus	0.2 %	0–4.4 %
Anaerotruncus colihominis	0.2 %	0–0.2 %
Pusillibacter faecalis	0.2 %	0–0.3 %
Subdoligranulum variabile	0.2 %	0–0.3 %
Vescimonas fastidiosa	0.2 %	0–0.7 %

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Taxonomic name	Relative abundance	Normal range
Phocaeicola vulgatus	0.2 %	0–17.4 %
Ruminococcus bovis	0.1 %	0–0.6 %
Clostridium sp. M62/1	0.1 %	0–0.2 %
Ruthenibacterium lactatiformans	0.1 %	0–0.8 %
Clostridioides difficile	0.1 %	0–0.2 %
Wujia chipingensis	0.1 %	0–2.2 %
Faecalitalea cylindroides	0.09 %	0–0.3 %
Lawsonibacter asaccharolyticus	0.08 %	0–0.3 %
Oscillibacter hominis	0.08 %	0–0.2 %
Bifidobacterium catenulatum	0.08 %	0–1.7 %
Enterocloster bolteae	0.07 %	0–0.7 %
Hungatella hathewayi	0.07 %	0–0.3 %
Blautia hansenii	0.07 %	0–0.2 %
Enterococcus faecium	0.07 %	0–0.5 %
Eubacterium hominis	0.06 %	0–0.06 %
Wansuia hejianensis	0.06 %	0–0.04 %
Coprococcus sp. ART55/1	0.06 %	0–2.2 %
Rothia mucilaginosa	0.06 %	0–0.2 %
[Clostridium] innocuum	0.05 %	0–1.9 %
Marvinbryantia formatexigens	0.05 %	0–0.04 %
Blautia argi	0.05 %	0–0.2 %
Coprococcus eutactus	0.05 %	0–1 %
Bacteroides ovatus	0.04 %	0–4.9 %
Enterocloster clostridioformis	0.04 %	0–0.4 %
Bacteroides salyersiae	0.04 %	0–0.7 %
Novisyntrophococcus fermenticellae	0.04 %	0–0.02 %
Longicatena caecimuris	0.04 %	0–0.6 %
Sellimonas intestinalis	0.04 %	0–0.4 %
Qiania dongpingensis	0.04 %	0–0.02 %
Enterocloster asparagiformis	0.03 %	0–0.2 %
Blautia pseudococcoides	0.03 %	0–0.03 %
Pseudobutyrivibrio xylanivorans	0.03 %	0–0.03 %
Eubacterium sp. MSJ-33	0.03 %	0–0.2 %
Blautia liquoris	0.03 %	0–0.02 %
Monoglobus pectinilyticus	0.03 %	0–0.3 %
Blautia producta	0.02 %	0–0.09 %
Parabacteroides faecis	0.02 %	0–0.07 %
Bacteroides eggerthii	0.02 %	0–3.1 %