Gut Microbiome Test Analysis

Name	N/A	**Age**	N/A
Country	United Kingdom	**Sample ID**	145645717774_RandD
Sampling Date	26 Nov 2024 10:02	**Test Date**	30 Oct 2024 21:37
Test Profile	Gut Microbiome Plus	**Technology**	N/A

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

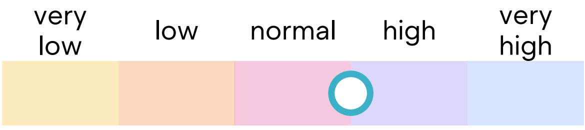
Microbiome diversity	9.7 / 10	**Pathogens**	None above normal levels
Beneficial bacteria	3 below normal levels	**Health risk scores**	1 high-risk scores

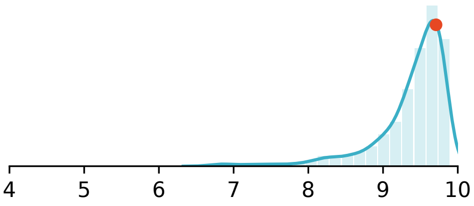
Contents

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

9.7 / 10





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.

Return to the Contents page

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 7 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.

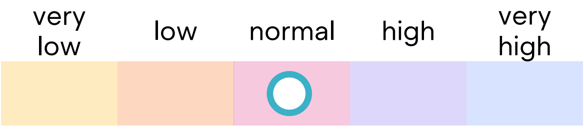
Please note that descriptions of each of these species are provided in the **Key bacteria** section. You can also click on the name of any of the bacterial species below to jump to the relevant section.

Bacteroides fragilis: 2.6 %	Normal range: 0.00–10.68 %	Normal
Campylobacter: 0.03 %	Normal range: 0.00–0.27 %	Normal
Campylobacter jejuni: 0.03 %	Normal range: 0.00–0.06 %	Normal
Clostridioides difficile: 0.2 %	Normal range: 0.00–0.25 %	Normal
Clostridium perfringens: 0.05 %	Normal range: 0.00–3.91 %	Normal
Collinsella: 0.07 %	Normal range: 0.00–4.05 %	Normal
Sutterella: 0.4 %	Normal range: 0.00–1.35 %	Normal

Return to the Contents page

Antimicrobial Resistance

5.2 / 10



Your sample was checked against a database of approximately 4000 known antimicrobial genes and compared to the average number of such genes found in the gut in a healthy population. The presence of these genes in your sample indicates that a small proportion of some microbes in your gut may be resistant to a specific antibiotic. This result does not indicate that antibiotic treatment will be ineffective when prescribed to treat an infection.

A low score indicates lower antimicrobial resistance, which is generally a good thing.

A high score, indicating more antibiotic resistance, could be due to the presence of a particular antibiotic resistant microbe, but sometimes also occurs as a general change to the microbiome after taking a course of antibiotics.

Top 5 AMR genes detected in your sample

These results may be of use to a clinician when making choices about antibiotics. This test cannot link a particular resistance gene to a particular microbe. Always make decisions about possible health interventions with the advice of a qualified practitioner.

- tet(W)
- tet(O)
- ErmF
- tet(X)
- tet(Q)

Return to the Contents page

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: 0.01 %	Normal range: 0.00–4.08 %	Normal
Bacteroides fragilis: 2.6 %	Normal range: 0.00–10.68 %	Normal
Bacteroides stercoris: 1.4 %	Normal range: 0.00–7.26 %	Normal
Bacteroides thetaiotaomicron: 2.1 %	Normal range: 0.00–3.03 %	Normal
Bacteroides uniformis: 10.3 %	Normal range: 0.00–10.17 %	High
Bifidobacterium adolescentis: 0.3 %	Normal range: 0.00–4.97 %	Normal
Bifidobacterium longum: 0.04 %	Normal range: 0.00–13.42 %	Normal
Bifidobacterium pseudolongum: Not detected	Normal range: 0.00–0.01 %	Low
Blautia wexlerae: 13.9 %	Normal range: 0.00–4.85 %	Very High
Christensenella minuta: 0.03 %	Normal range: 0.00–0.04 %	Normal
Faecalibacterium prausnitzii: 8.0 %	Normal range: 0.00–9.49 %	Normal
Lacticaseibacillus rhamnosus: Not detected	Normal range: 0.00–2.21 %	Low
Lactobacillus species: Not detected	Normal range: 0.00–0.67 %	Low
Limosilactobacillus reuteri: 0.01 %	Normal range: 0.00–0.59 %	Normal
Methanobrevibacter smithii: 0.1 %	Normal range: 0.00–4.73 %	Normal
Roseburia intestinalis: 0.8 %	Normal range: 0.00–3.39 %	Normal
Ruminococcus champanellensis: 0.05 %	Normal range: 0.00–0.26 %	Normal

You have 3 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 ***Lacticaseibacillus rhamnosus*** and ***Lactobacillus***. See the **Recommendations** section to find out more about probiotics.

Return to the Contents page

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.

Return to the Contents page

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	2 days in past week
Stomach pain	Not collected
Blood in stool	Not collected
Tiredness	Not collected
Weight loss	Not collected
Urgent bowel movement	2-6 times in the past week
Loss of appetite	Never

Return to the Contents page

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	2 days in past week
Stomach pain	Not collected
Blood in stool	Not collected
Tiredness	Not collected
Weight loss	Not collected
Urgent bowel movement	2-6 times in the past week
Loss of appetite	Never

Return to the Contents page

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 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
Tiredness	Not collected
BMI	<25 kg/m^2
Weight loss	Not collected

Return to the Contents page

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	2 days in past week
Stomach pain	Not collected
Tiredness	Not collected
Constipation	A little
Bloating	Often
Swelling	Yes
Excessive wind	Not collected
Urgent bowel movement	2-6 times in the past week
Loss of appetite	Never

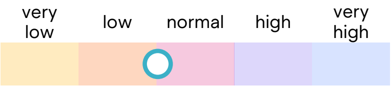
Return to the Contents page

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.

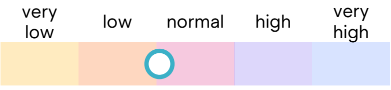
One of the most important functions of the gut microbiome is to produce **short-chain fatty acids (SCFAs)**. These are produced by bacteria from the breakdown of **dietary fibre**. SCFAs in the gut are known to suppress inflammation, maintain the gut barrier and to prevent a 'leaky gut', reduce appetite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

Butyrate Score: 4.8 Normal range: 4.78–6.74



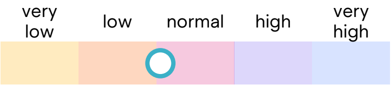
Butyrate is a SCFA mainly produced by bacteria in the phylum Bacillota (Firmicutes). It is a major energy source for the cells lining the gut and helps to maintain the integrity of the gut lining and mucous layer. It is anti-inflammatory and helps protect against cancer.

Propionate Score: 4.9 Normal range: 4.73–8.12



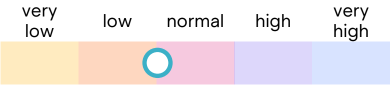
Microbial production of the SCFA propionate has a range of benefits to metabolic health, including regulating appetite, reducing internal fat deposition, and controlling glucose levels, and so helps reduce the risk of type II diabetes. It also has a protective effect on the gut lining and reduces gut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

Acetate Score: 4.9 Normal range: 4.85–6.22



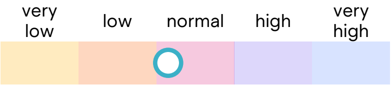
Acetate is the most abundant SCFA. Acetate production has been correlated with decreased fat around the internal organs and other beneficial effects on host metabolism that combat obesity. Acetate may also have a protective role over cognitive functions.

Lactate Score: 5.0 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 SCFA-producing bacteria. They can also help convert lactose (the main sugar found in dairy products) to lactic acid. A higher score may be due to microbiome adaptation to either a high dairy diet or to lactose intolerance.

H_2S Score: 4.9 Normal range: 4.71–6.04



Hydrogen sulphide (H_2S) is a gas that can have important positive and negative effects on gut health. At low levels, H_2S 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 H_2S can be toxic, causing increased gut inflammation, disrupting the gut mucous lining, and negatively affecting populations of 'good' gut bacteria. Excessive H_2S production can often be reduced by increasing the consumption of fibre and decreasing protein intake.

Return to the Contents page

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 **7 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: ***Lacticaseibacillus rhamnosus*** and ***Lactobacillus***.

Return to the Contents page

Key bacteria

Pathogens

Ancylostoma Normal range: Not Detected

Also known as Old World hookwork, these roundworms infect the intestine, with symptoms ranging from abdominal pain and loss of appetite to anaemia, swelling, and dry skin resulting from iron and protein deficiency.

Ancylostoma duodenale Normal range: Not Detected

A common species of Ancylostoma.

Ascaris Normal range: Not Detected

Infections of these intestinal parasitic worms are often asymptomatic but can cause abdominal pain, intestinal blockage, impaired growth in children, and cough due to migrating worms.

Ascaris lumbricoides Normal range: Not Detected

The most common Ascaris species and most common parasitic worm in humans.

Bacteroides fragilis Normal range: 0.00–10.68 %

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.

Bilophila wadsworthia Normal range: Not Detected

Can make up part of a healthy gut microbiome, but often associated with infections including appendicitis. In combination with a high fat diet, this bacterium can cause increased gut inflammation and metabolic disorders.

Blastocystis Normal range: Not Detected

These microscopic parasites are usually asymptomatic. Their link to gut disease is not well understood but infections can correlate with symptoms such as diarrhoea, nausea, fatigue, bloating, and loss of appetite.

Blastocystis hominis Normal range: Not Detected

The most commonly identified species of Blastocystis.

Caliciviridae Normal range: Not Detected

Symptoms can include gastrointestinal inflammation, vomiting and diarrhoea.

Campylobacter Normal range: 0.00–0.27 %

Campylobacter is a leading cause of gastric illness in developed countries, often caused by improperly cooked poultry. Symptoms include cramps, fever and diarrhoea, sometimes bloody.

Campylobacter coli Normal range: 0.00–0.25 %

The second most common species causing Campylobacter gut infections.

Continued on next page...

Return to the Contents page

Campylobacter jejuni Normal range: 0.00–0.06 %

The most common species causing Campylobacter gut infections.

Campylobacter upsaliensis Normal range: Not Detected

One of the more common species causing Campylobacter gut infections.

Candida Normal range: 0.00–0.73 %

Candida are yeast that cause thrush infections They are a normal part of your gut microbiome but overgrowth can cause diarrhoea (sometimes bloody), vomiting, and fever.

Clostridioides difficile Normal range: 0.00–0.25 %

This bacterium can infect the large intestine and cause diarrhoea.

Clostridium perfringens Normal range: 0.00–3.91 %

A common cause of food poisoning, and an opportunistic invasive pathogen which can infect wounds.

Collinsella Normal range: 0.00–4.05 %

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

Cryptosporidium Normal range: Not Detected

This parasite causes lethargy and watery diarrhoea, possibly accompanied with a persistent cough. Infection is normally self-limiting but can be severe in immunocompromised individuals.

Cyclospora cayetanensis Normal range: Not Detected

Infections of this parasite cause (possibly explosive) diarrhoea, loss of appetite, fatigue and nausea. Infections may persist for over a month with symptoms abating and relapsing.

Cytomegalovirus Normal range: Not Detected

A common virus that normally is asymptomatic, it may be a cause of gut symptoms in immunocompromised individuals.

Dientamoeba fragilis Normal range: Not Detected

Infections of this parasite of the large intestine are usually asymptomatic, but can cause loos of appetite, weight loss, fatigue and nausea.

Encephalitozoon cuniculi Normal range: Not Detected

An opportunistic fungal pathogen that can affect immunocompromised individuals.

Entamoeba histolytica Normal range: Not Detected

The cause of amoebic dysentery. 90% of infections are asymptomatic, but symptoms include lethargy, abdominal pain, and diarrhoea, sometimes bloody, and infections can sometimes progress to cause severe gut inflammation and infection of the liver.

Continued on next page...

Return to the Contents page

Enterobius vermicularis
Normal range: Not Detected

Also known as human pinworm, infections are often asymptomatic, but the most common symptom is an itchy anus, especially at night time.

Enterococcus gallinarum
Normal range: 0.00–3.67 %

This normal gut bacterium has the potential to be an opportunistic invasive pathogen in conditions where the barrier of the gut lining is weakened.

Enterocytozoon bieneusi
Normal range: Not Detected

The most common cause of Microsporidia infections.

Escherichia coli ETEC 1392/75
Normal range: Not Detected

Transmitted by contaminated food or water, this is the major cause of diarrhoea whilst travelling.

Escherichia coli ETEC H10407
Normal range: Not Detected

Transmitted by contaminated food or water, this is the major cause of diarrhoea whilst travelling.

Escherichia coli ETEC TW03439
Normal range: Not Detected

Transmitted by contaminated food or water, this is the major cause of diarrhoea whilst travelling.

Escherichia coli ETEC TW03452
Normal range: Not Detected

Transmitted by contaminated food or water, this is the major cause of diarrhoea whilst travelling.

Escherichia coli ETEC TW03574
Normal range: Not Detected

Transmitted by contaminated food or water, this is the major cause of diarrhoea whilst travelling.

Escherichia coli ETEC TW03576
Normal range: Not Detected

Transmitted by contaminated food or water, this is the major cause of diarrhoea whilst travelling.

Escherichia coli ETEC TW03585
Normal range: Not Detected

Transmitted by contaminated food or water, this is the major cause of diarrhoea whilst travelling.

Escherichia coli ETEC TW03741
Normal range: Not Detected

Transmitted by contaminated food or water, this is the major cause of diarrhoea whilst travelling.

Escherichia coli ETEC TW14691
Normal range: Not Detected

Transmitted by contaminated food or water, this is the major cause of diarrhoea whilst travelling.

Escherichia coli ETEC WS1896A
Normal range: Not Detected

Transmitted by contaminated food or water, this is the major cause of diarrhoea whilst travelling.

Continued on next page...

Return to the Contents page

Escherichia coli ETEC WS2068A Normal range: Not Detected

Transmitted by contaminated food or water, this is the major cause of diarrhoea whilst travelling.

Escherichia coli ETEC WS3080A Normal range: Not Detected

Transmitted by contaminated food or water, this is the major cause of diarrhoea whilst travelling.

Escherichia coli O157:H7 Normal range: Not Detected

Most E. coli strains are beneficial for the gut, but this strain is a cause of severe gastrointestinal illness due to the toxins it produces.

Fasciolopsis buski Normal range: Not Detected

Also known as giant intestinal flukes, these parasites attach to the intestinal wall. Most infections are light, but severe infections can cause symptoms including diarrhoea, anaemia, swelling, and allergic reactions.

Geotrichum Normal range: Not Detected

Geotrichium fungi are normal members of the human microbiome, but can be opportunistic pathogens. Gut inflammation can be caused by Geotrichium species, as can oral and vaginal infections similar to thrush, and airway infections.

Giardia intestinalis Normal range: Not Detected

More common in areas with poor water sanitation, this parasite causes smelly diarrhoea, stomach pain and bloating.

Helicobacter pylori Normal range: 0.00–0.01 %

This bacterium causes peptic ulcers but most people are asymptomatic; symptoms include stomach pain, nausea, bloating, and weight loss.

Human gammaherpesvirus 4 Normal range: Not Detected

The cause of infectious mononucleosis (glandular fever), spread through spit, with symptoms including lethargy and swollen neck glands.

Hymenolepis Normal range: Not Detected

These tapeworms are often asymptomatic but can cause symptoms such as stomach cramps, diarrhoea and weight loss.

Hymenolepis diminuta Normal range: Not Detected

One of two species of Hymenolepsis that parasitize humans.

Klebsiella pneumoniae Normal range: 0.00–3.25 %

This opportunistic pathogen can be found in healthy gut microbiomes, but can infect the respiratory and urinary tracts and wounds, and may contribute to inflammatory bowel disease.

Continued on next page...

Return to the Contents page

Listeria monocytogenes Normal range: 0.00–0.01 %

This pathogen is especially serious for pregnant women. Intestinal Listeria infections can cause diarrhoea and vomiting, whilst invasive infections cause fever and flu-like symptoms.

Microsporidia Normal range: Not Detected

Infection by Microsporidia parasites is more common in immunocompromised individuals, with diarrhoea the most common symptom; invasive infection can be very serious.

Necator americanus Normal range: Not Detected

Also known as New World hookworm, these parasites infect the intestine, with symptoms ranging from abdominal pain and loss of appetite to anaemia, swelling, and dry skin resulting from iron and protein deficiency.

Norovirus Normal range: Not Detected

A highly contagious virus causing vomiting and diarrhoea.

Porphyromonas gingivalis Normal range: 0.00–0.02 %

This bacterium causes the oral infection gingivitis and is associated with rheumatoid arthritis, and proteins secreted by this organism have been linked to Alzheimer's disease.

Proteus Normal range: 0.00–6.15 %

Proteus bacteria can be found in a healthy gut microbiome at low abundance, and are normally thought of as a urinary tract pathogen. However there is also some association of these bacteria with gastrointestinal disorders such as Crohn's disease.

Proteus mirabilis Normal range: 0.00–6.47 %

A common species of Proteus.

Pseudomonas aeruginosa Normal range: 0.00–0.24 %

This bacterium can become established in the gut after antibiotic treatment or in immunocompromised individuals. It is associated with increased risk of lung infections and sepsis, and contributes to long-term disruption of the gut microbiome.

Raoultella ornithinolytica Normal range: 0.00–0.37 %

A rare opportunistic pathogen that may cause gut infections, especially in individuals with other health problems, with symptoms including fever and bloody stool.

Rhodotorula Normal range: Not Detected

These fungi may be found in low abundance in a normal gut microbiome, but high abundance indicates disruption to the healthy balance of the microbiome, and may lead to infections in vulnerable individuals.

Rodentolepis nana Normal range: Not Detected

One of two species of Hymenolepis that parasitize humans.

Continued on next page...

Return to the Contents page

Rotavirus Normal range: Not Detected

Usually infecting young children, this virus is highly infectious and causes diarrhoea, vomiting and elevated temperature.

Salmonella Normal range: 0.00–0.31 %

Salmonella gut infections can cause fever, diarrhoea, vomiting and intestinal damage, and may increase the risk of inflammatory bowel disease.

Salmonella enterica Normal range: 0.00–0.31 %

A common species causing Salmonella gut infections.

Shigella Normal range: 0.00–0.50 %

Shigella infections can cause fever and bloody diarrhoea, and in rare cases may stimulate reactive arthritis.

Staphylococcus aureus Normal range: 0.00–0.19 %

Can cause acute vomiting and diarrhoea, and infections may destabilise the gut microbiome and promote inflammation.

Strongyloides Normal range: Not Detected

Parasitic roundworms that cause long-term infections of the intestine. Generally asymptomatic, but can cause a variety of symptoms throughout the body and may interact with other diseases to cause more severe complications.

Strongyloides stercoralis Normal range: Not Detected

The major species causing Strongolides infections.

Sutterella Normal range: 0.00–1.35 %

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.

Taenia Normal range: Not Detected

These tapeworm species usually cause asymptomatic infections, but symptoms include abdominal pain and weight loss, and more serious infections are possible.

Taenia asiatica Normal range: Not Detected

A species of Taenia tapeworm.

Taenia saginata Normal range: Not Detected

A species of Taenia tapeworm, usually transmitted via infected beef. Infections with this species are more likely to be symptomatic.

Taenia solium Normal range: Not Detected

A species of Taenia tapeworm, usually transmitted via infected pork.

Continued on next page...

Return to the Contents page

Trichuris trichiura	Normal range: Not Detected

This parasite of the large intestine, also known as whipworm, can cause chronic (bloody) diarrhoea and anaemia, leading to poor growth of children.

Vibrio cholerae	Normal range: Not Detected

Rare in industrialised nations due to its spread via contaminated water, this bacterium can cause severe diarrhoea and vomiting.

Vibrio parahaemolyticus	Normal range: Not Detected

Often transmitted via contaminated seafood, symptoms of infection can include watery or bloody diarreha, cramps, fever and vomiting.

Yersinia	Normal range: 0.00–0.03 %

Often transmitted by undercooked pork, infections cause fever and often bloody diarrhoea, with right-sided abdominal pain in older children and adults.

Yersinia enterocolitica	Normal range: 0.00–0.05 %

The most common species causing Yersinia gut infections.

Yersinia pseudotuberculosis	Normal range: Not Detected

A less common species causing Yersinia gut infections.

Return to the Contents page

Beneficial microbes

Akkermansia muciniphila Normal range: 0.00–4.08 %

This is a mucin-degrading (a component of the mucus which lines the gut) species which is shown to be more abundant in healthy individuals. It has potential in prevention and treatment of diabetes, obesity and their associated metabolic disorders.

Bacteroides fragilis Normal range: 0.00–10.68 %

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 stercoris Normal range: 0.00–7.26 %

A microbiome modulator, this species can affect the overall composition of a microbiome. It is also a linking species involved in reactions beneficial to the human host.

Bacteroides thetaiotaomicron Normal range: 0.00–3.03 %

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: 0.00–10.17 %

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

Bifidobacterium adolescentis Normal range: 0.00–4.97 %

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: 0.00–13.42 %

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.

Bifidobacterium pseudolongum Normal range: 0.00–0.01 %

Promising research carried out on this species shows that it is able to break up compounds that other species are unable to. Additionally this species reduces intestinal inflammation helping with IBD

Blautia wexlerae Normal range: 0.00–4.85 %

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.

Christensenella minuta Normal range: 0.00–0.04 %

Research has shown that this species helps mitigate diet induced obesity and other metabolic diseases, with a high abundance of this species shown to be associated with lower BMI.

Continued on next page...

Return to the Contents page

Faecalibacterium prausnitzii Normal range: 0.00–9.49 %

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.

Lacticaseibacillus rhamnosus Normal range: 0.00–2.21 %

A widely used probiotic strain, this species of bacteria can protect against stomach bugs and diarrhoea. Furthermore, Lactobacillus rhamnosus is an important part of a healthy gut.

Lactobacillus Normal range: 0.00–0.67 %

The Lactobacillus genus is an important probiotic group in the gut microbiome, though usually present at low abundance. Research shows these species play a key role in regulating the host immune repsonse as well as protecting the gut epithelial lining.

Limosilactobacillus reuteri Normal range: 0.00–0.59 %

Often referred to as Lactobacillus reuteri, this species is implicated in a range of beneficial gut outcomes including protecting against pathogenic bacteria, improving host immune response and potecting and strengthening the intestinal barrier.

Methanobrevibacter smithii Normal range: 0.00–4.73 %

A known gut microbiome modulator, this species affects how other bacteria break down food in the gut, therefore impacting calorie absorption and harvest. As such, this species plays a role in obesity and metabolic disorders more broadly.

Roseburia intestinalis Normal range: 0.00–3.39 %

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.

Ruminococcus champanellensis Normal range: 0.00–0.26 %

This species breaks down dietary cellulose producing key SCFAs that are vital for bodily function. The SCFAs not only have positive effects on host health but also improve overall gut health by increasing bacterial diversity.

Return to the Contents page

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.

Return to the Contents page

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

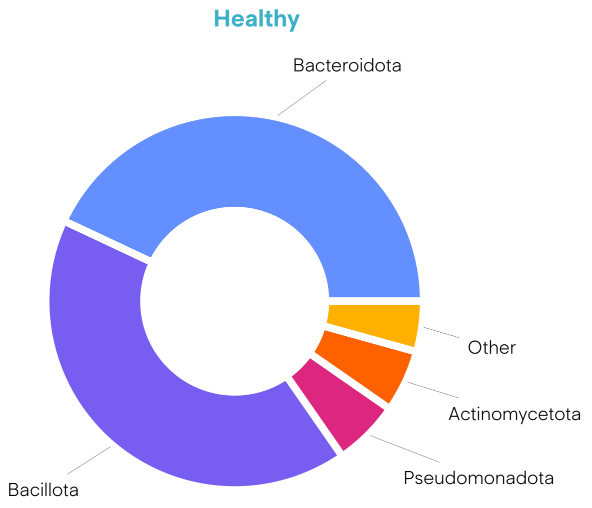
We use this information to produce your gut health report which tells you about the balance of important microbes in your gut – both those that help keep you healthy and those that could cause disease. We use insights from peer-reviewed scientific studies and compare your information to a database of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

Return to the Contents page

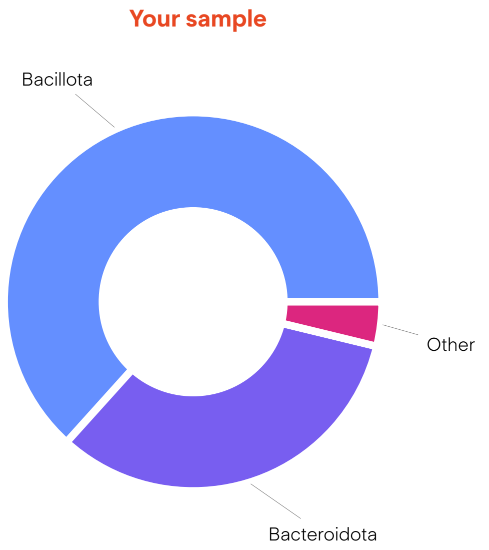
Full taxonomy report

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.



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



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

Top species

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

Taxonomic name	Relative abundance
Blautia wexlerae	13.9 %
Bacteroides uniformis	10.3 %
Faecalibacterium prausnitzii	8.0 %
Phocaeicola vulgatus	6.1 %
[Ruminococcus] torques	3.6 %
Coprococcus eutactus	3.3 %
Parabacteroides distasonis	2.9 %
Anaerobutyricum hallii	2.7 %
Bacteroides fragilis	2.6 %
Blautia obeum	2.6 %
Faecalibacterium sp. I3-3-89	2.4 %
Butyrivibrio crossotus	2.4 %
Bacteroides thetaiotaomicron	2.1 %
Bacteroides stercoris	1.4 %

Continued on next page...

Return to the Contents page

Taxonomic name	Relative abundance
Bacteroides cellulosilyticus	1.4 %
Faecalibacterium sp. HTF-F	1.3 %
Dorea formicigenerans	1.1 %
Coprococcus catus	1.1 %
Faecalibacterium duncaniae	1.1 %
Parabacteroides merdae	1.1 %
Anaerostipes hadrus	1 %
Faecalibacterium sp. I2-3-92	1 %
Simiaoa sunii	0.9 %
Vescimonas fastidiosa	0.9 %
Blautia sp. SC05B48	0.9 %
Vescimonas coprocola	0.9 %
Faecalibacterium sp. IP-3-29	0.8 %
Roseburia intestinalis	0.8 %
Alistipes shahii	0.7 %
Lachnospira eligens	0.7 %
Lawsonibacter asaccharolyticus	0.7 %
Dysosmobacter welbionis	0.7 %
Adlercreutzia hattorii	0.6 %
Methanobrevibacter sp. TLL-48-HuF1	0.6 %
Phascolarctobacterium succinatutens	0.6 %
Phascolarctobacterium sp. Marseille-Q4147	0.5 %
Flavonifractor plautii	0.5 %
Bilophila wadsworthia	0.5 %
Dorea longicatena	0.4 %
Intestinimonas butyriciproducens	0.4 %
Bacteroides sp. A1C1	0.4 %
[Ruminococcus] gnavus	0.4 %
Faecalitalea cylindroides	0.4 %
Roseburia hominis	0.4 %
Bacteroides salyersiae	0.4 %
Faecalibacterium sp. I4-3-84	0.4 %
Sutterella wadsworthensis	0.4 %
Duodenibacillus massiliensis	0.4 %
Thomasclavelia ramosa	0.3 %
Bacteroides sp. CACC 737	0.3 %
Leyella stercorea	0.3 %
Bifidobacterium adolescentis	0.3 %
Bacteroides xylanisolvens	0.3 %
Bacteroides ovatus	0.3 %
Coprococcus comes	0.3 %
Faecalibacterium sp. IP-1-18	0.3 %
Longicatena caecimuris	0.3 %
Coprococcus sp. ART55/1	0.2 %
Bacteroides humanifaecis	0.2 %
Clostridioides difficile	0.2 %

Continued on next page...

Return to the Contents page

Taxonomic name	**Relative abundance**
[Clostridium] scindens	0.2 %
Phocaeicola dorei	0.2 %
Pusillibacter faecalis	0.2 %
Odoribacter splanchnicus	0.2 %
Lacticaseibacillus paracasei	0.2 %
Ruthenibacterium lactatiformans	0.2 %
[Ruminococcus] lactaris	0.2 %
Enterococcus faecium	0.2 %
[Clostridium] innocuum	0.2 %
Subdoligranulum variabile	0.2 %
Faecalibacterium sp. I4-1-79	0.2 %
Alistipes communis	0.2 %
Oscillibacter hominis	0.2 %
Lactococcus cremoris	0.2 %
Blautia sp. NBRC 113351	0.2 %
Sellimonas intestinalis	0.2 %
Alistipes ihumii	0.2 %
Streptococcus thermophilus	0.2 %
Enterocloster bolteae	0.1 %
Eggerthella lenta	0.1 %
Alistipes senegalensis	0.1 %
Hungatella hathewayi	0.1 %
Parabacteroides chongii	0.1 %
Wansuia hejianensis	0.1 %
Oxalobacter aliiformigenes	0.1 %
Schaalia odontolytica	0.1 %
Butyricimonas virosa	0.1 %
Bacteroides sp. HF-162	0.1 %
Methanobrevibacter smithii	0.1 %
Anaerotruncus colihominis	0.1 %
Clostridium sp. M62/1	0.1 %
Faecalibacterium sp. I3-3-33	0.1 %
Eubacterium ventriosum	0.1 %
Enterocloster asparagiformis	0.09 %
Segatella copri	0.09 %
Bacteroides caccae	0.08 %
Adlercreutzia equolifaciens	0.08 %
Anaerostipes caccae	0.08 %
Prevotella bivia	0.08 %
Ligilactobacillus murinus	0.08 %
Berryella intestinalis	0.08 %
Roseburia rectibacter	0.07 %
Blautia argi	0.07 %
Alistipes onderdonkii	0.07 %
Gallibacterium salpingitidis	0.07 %
Collinsella aerofaciens	0.07 %

Continued on next page...

Return to the Contents page

Taxonomic name	Relative abundance
Bacteroides faecis	0.06 %
Alistipes megaguti	0.06 %
Alistipes finegoldii	0.06 %
Lachnoclostridium phocaeense	0.06 %
Solibaculum mannosilyticum	0.06 %
Catenibacterium mitsuokai	0.06 %
Flintibacter sp. KGMB00164	0.05 %
Clostridium perfringens	0.05 %
Ruminococcus champanellensis	0.05 %
Monoglobus pectinilyticus	0.05 %
Lactococcus lactis	0.05 %
Streptococcus suis	0.05 %
Parabacteroides johnsonii	0.04 %
Bacteroides eggerthii	0.04 %
Romboutsia ilealis	0.04 %
Blautia hansenii	0.04 %
Massilistercora timonensis	0.04 %
Bifidobacterium longum	0.04 %
Catenibacterium sp. co_0103	0.04 %
Blautia producta	0.03 %
Bacteroides intestinalis	0.03 %
Enterocloster clostridioformis	0.03 %
Eubacterium hominis	0.03 %
Christensenella minuta	0.03 %
Eubacterium sp. MSJ-33	0.03 %
Mogibacterium diversum	0.03 %
Actinomyces oris	0.03 %
Novisyntrophococcus fermenticellae	0.03 %
Parolsenella massiliensis	0.03 %
Streptococcus salivarius	0.03 %
Campylobacter jejuni	0.03 %
Bacteroides sp. DH3716P	0.02 %
Bacteroides caecimuris	0.02 %
Eubacterium sp. c-25	0.02 %
Actinomyces naeslundii	0.02 %
Ruminococcus bicirculans (ex Wegman et al. 2014)	0.02 %
Wujia chipingensis	0.02 %
Marvinbryantia formatexigens	0.02 %
[Clostridium] hylemonae	0.02 %
Alistipes dispar	0.02 %
Paraprevotella clara	0.02 %
Blautia liquoris	0.02 %
Rothia mucilaginosa	0.02 %
Barnesiella viscericola	0.02 %
Coprobacter fastidiosus	0.02 %
Parolsenella catena	0.02 %

Continued on next page...

Return to the Contents page

Taxonomic name	**Relative abundance**
Gordonibacter pamelaeae	0.02 %
Murdochiella vaginalis	0.02 %
Amedibacterium intestinale	0.02 %
Eubacterium callanderi	0.01 %
Emergencia timonensis	0.01 %
Bacteroides sp. ZJ-18	0.01 %
Lacrimispora saccharolytica	0.01 %
Butyricimonas faecalis	0.01 %
Blautia pseudococcoides	0.01 %
Acutalibacter muris	0.01 %
Lachnoanaerobaculum gingivalis	0.01 %
Chordicoccus furentiruminis	0.01 %
Arachnia propionica	0.01 %
Qiania dongpingensis	0.01 %
Actinomyces sp. oral taxon 169	0.01 %
Actinomyces sp. oral taxon 414	0.01 %
Bifidobacterium breve	0.01 %
Gordonibacter urolithinfaciens	0.01 %
Bacteroides zhangwenhongii	0.01 %
Sodaliphilus pleomorphus	0.01 %
Eubacterium maltosivorans	0.01 %
Phocaeicola salanitronis	0.01 %
Clostridium cadaveris	0.01 %
Faecalibacillus intestinalis	0.01 %
Parvimonas micra	0.01 %
Parabacteroides goldsteinii	0.01 %
Parabacteroides faecis	0.01 %
Enterococcus cecorum	0.01 %
Anaerostipes rhamnosivorans	0.01 %
Clostridium sp. C1	0.01 %
Limosilactobacillus reuteri	0.01 %
Ligilactobacillus agilis	0.01 %
Clostridium sp. SY8519	0.01 %
Leyella lascolaii	0.01 %
Streptococcus acidominimus	0.01 %
Maliibacterium massiliense	0.01 %
Streptococcus sanguinis	0.01 %
Ligilactobacillus ruminis	0.01 %
Akkermansia muciniphila	0.01 %
Ruminococcus gauvreauii	0.0 %
Pseudobutyrivibrio xylanivorans	0.0 %
Bacteroides helcogenes	0.0 %
Arabiibacter massiliensis	0.0 %
Bacteroides faecium	0.0 %
Anaerotignum propionicum	0.0 %

Return to the Contents page

Return to the Contents page