

The background of the cover is a dark teal color with a pattern of glowing, textured, rod-shaped bacteria. On the left side, there is a vertical decorative element consisting of a series of horizontal lines of varying lengths, each ending in a solid yellow circle of varying size. The text is centered and white, providing a high-contrast look against the dark background.

RANDOX
HEALTH

Microbiome

HEALTH RESULTS REPORT

UNDERSTANDING YOUR HEALTH STARTS WITH YOUR GUT

What is the Gut Microbiome?

The human gut is inhabited by a wide range of microorganisms including bacteria, viruses, fungi, and archaea. Together, these microorganisms make up a major component of the human gut microbiome.

There are many environmental, genetic and lifestyle factors that can influence the diversity of the gut microbiome. Studies have indicated that a diverse microbiome is usually a 'healthy' microbiome. A long-term imbalance or absence of particular microorganism could contribute to numerous chronic diseases such as:



Obesity



Cancer



Irritable Bowel Disorders



Autoimmune Conditions
such as Rheumatoid Arthritis

Optimising the microbial composition of your gut microbiome has a number of benefits to overall health including:



Reduced Inflammation



Reduced
gastrointestinal
complications



Reduced Cholesterol



Enhanced ability
to digest food and
dietary fibres



Improved Immunity



Improved integrity
of the gut barrier



Enhanced synthesis
of essential nutrients
e.g., Vitamin K

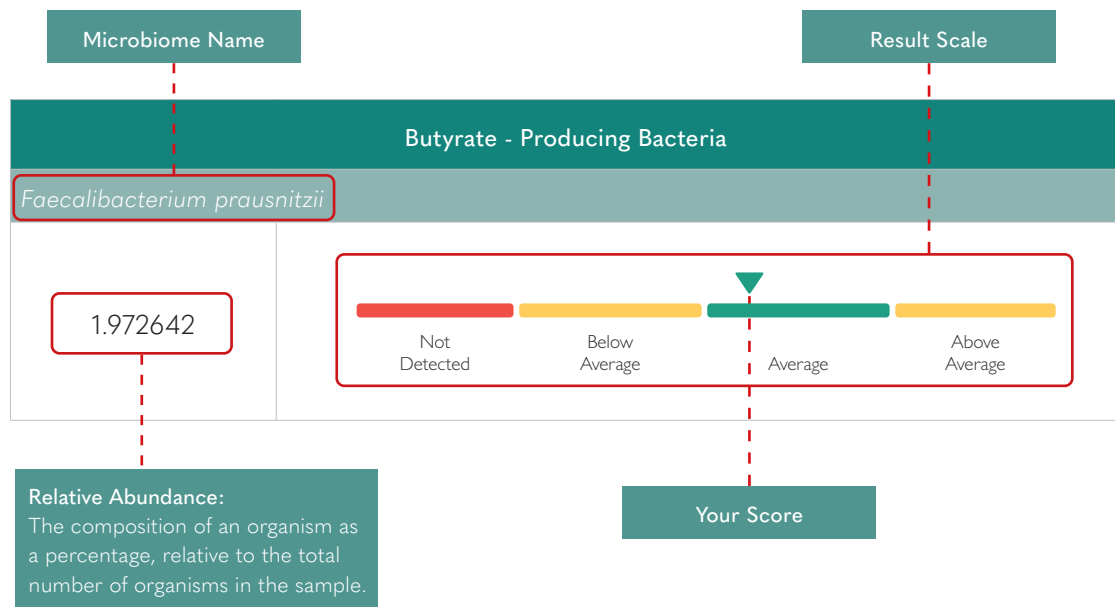
Interpreting Your Results

Within this report you will find personalised results regarding your gut microbiome composition. A comprehensive summarisation of the bacterial, viral, archaeal, fungal and parasitic species will be reported.

Remember that having a potentially pathogenic bacterium or parasite does not always mean that you will develop the associated disease or condition. Your score will be indicated using the dial on the results scale which is based off a reference range determined using healthy individuals.

The glossary at the back of the report contains more information on the scope of the test, microbial species and scientific terms used throughout the report.

Example Report



Disclaimer

This is not a diagnostic test, the results of this microbiome test and the recommendations provided are for educational purposes only. This should not be used in place of the advice provided by healthcare professionals. Any changes you wish to make to your diet or lifestyle based on these recommendations should be overseen by a registered dietitian or GP to ensure all nutritional needs are met.

The information provided in this test is not a complete overview of the entire gut microbiome and may be subject to change with the publication of new data from scientific studies. The composition of each sample will differ and therefore results will vary from person to person.

The results of the analysis are obtained using shotgun sequencing. This Next Generation Sequencing (NGS) technique enables the classification of microorganisms within a specific sample down to the species level. The classification at species level may not be as accurate as higher taxonomy levels.























PID	GMTEST031
Name	TEST TEST
DOB	01-Jan-2000
Date of Report	02-Sep-2024
Programme	Microbiome
Sample Collection Date	01-Aug-2024 12:00
Fasted for	Non-fasting Sample



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Main findings

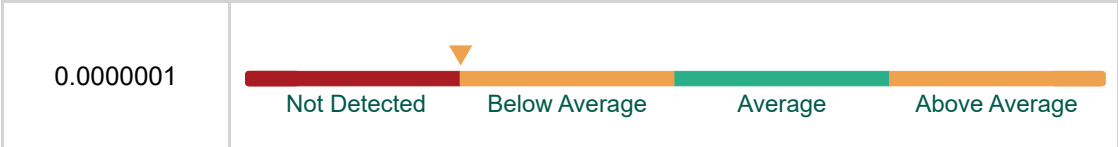
Test	Result
Bacteria	
Microbiome Diversity	 Below Average
F/B Ratio	 Average
Butyrate-Producing Bacteria	
<i>Faecalibacterium prausnitzii</i>	 Below Average
<i>Eubacterium rectale</i>	 Below Average
Roseburia	 Below Average
Ruminococcus	 Below Average
Coprococcus	 Below Average
Anaerostipes	 Below Average
<i>Butyrivibrio</i>	 Below Average
Bacteria with Probiotic Properties	
<i>Christensenella minuta</i>	 Below Average
Barnesiella	 Below Average
Lactobacillus	 Below Average
Bifidobacterium	 Below Average
<i>Akkermansia muciniphila</i>	 Below Average
<i>Prevotella copri</i>	 Below Average
Bacteroides uniformis	 Below Average
Hydrogen Sulphide Producing Bacteria	
<i>Desulfovibrio piger</i>	 Average
<i>Desulfovibrio desulfuricans</i>	 Average
Oxalate-Degrading Bacteria	
<i>Oxalobacter formigenes</i>	 Below Average
Potentially Pathogenic Bacteria	
<i>Clostridioides difficile</i>	 Above Average
Proteus	 Average
Klebsiella	 Average

Citrobacter	 Average
Pseudomonas	 Above Average
<i>Helicobacter pylori</i>	 Above Average
Enterobacteriaceae	 Average
Virus	
CrAss-like Viruses	 Not Detected
Fungi	
<i>Candida albicans</i>	 Detected
<i>Saccharomyces cerevisiae</i>	 Detected
Archaea	
<i>Methanobrevibacter smithii</i>	 Detected
Parasites	
<i>Cryptosporidium</i>	 Detected
<i>Dientamoeba fragilis</i>	 Not Detected
<i>Entamoeba histolytica</i>	 Not Detected
<i>Cyclospora cayetanensis</i>	 Not Detected
<i>Giardia lamblia</i>	 Not Detected
<i>Blastocystis</i>	 Not Detected

Bacteria	
Microbiome Diversity	
0	 <p>A horizontal bar chart showing a score of 0. The bar is divided into two sections: a red section on the left labeled 'Below Average' and a green section on the right labeled 'Average'. A red downward-pointing triangle is positioned at the start of the bar (score 0).</p>
Recommendations	
<p>The results show that your gut microbiome diversity score is below average. There are numerous ways to improve the diversity of your gut microbiome. This can include minimising the use of antibiotics and other microbial therapies, consuming plenty of fruit, vegetables and fermented foods. You should also limit or avoid artificial sweeteners and significantly reduce stress levels.</p>	
F/B Ratio	
0.202	 <p>A horizontal bar chart showing a score of 0.202. The bar is divided into two sections: a green section on the left labeled 'Average' and a red section on the right labeled 'Above Average'. A green downward-pointing triangle is positioned at the start of the bar (score 0.202).</p>
Recommendations	
<p>Your results shows that your gut microbiomes F/B ratio score is within the optimum range. In order to maintain an optimal ratio, eat a well-balanced diet high in fruit, vegetables, and wholegrains.</p>	

Butyrate-Producing Bacteria

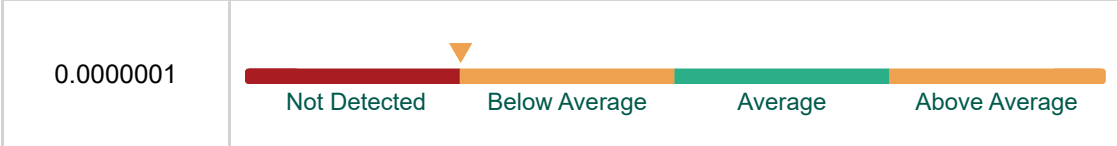
Faecalibacterium prausnitzii



Recommendations

The results show that the abundance of *Faecalibacterium prausnitzii* within your gut microbiome is below average. In order to improve the abundance of this bacterium, prebiotics such as inulin-type fructans and arabinoxylans should be consumed. Inulin naturally occurs in fruits and vegetables such as chicory roots, wheat, onion, banana, garlic, and leek. Meanwhile, arabinoxylans are in wheat, rye, rice, barley, oats, and sorghum. Significant reductions in *Faecalibacterium prausnitzii* has been detected in patients with diabetes and IBD (Crohn's, Ulcerative Colitis and IBS).

Eubacterium rectale



Recommendations

The results show that the abundance of *Eubacterium* within your gut microbiome is below average. In order to improve the abundance of this bacterium, a Mediterranean diet high in insoluble fibre is advised which maintains homeostasis of the gut microbiota. Foods high in insoluble fibre including wholewheat flour, wheat bran, beans, vegetables, potatoes, nuts, seeds, legumes, herbs, spices, fish, seafood, and extra virgin olive oil. Increasing age also contributes to a decrease of which is inevitable.

Roseburia



Recommendations

The results show that the abundance of *Roseburia* within your gut microbiome is below average. Studies have concluded that there is a link between reduced *Roseburia* abundance, type 2 diabetes, obesity and Inflammatory Bowel Diseases. In order to increase the abundance of this bacterium, certain dietary patterns should be avoided, including a high intake of animal protein in compliance with a gluten-free diet, which has been shown to reduce *Roseburia* abundance in the gut microbiome. A gluten-free diet should only be followed long-term if recommended by a healthcare professional.

Ruminococcus	
0.0000001	
Recommendations	
<p>The results show that the abundance of Ruminococcus within your gut microbiome is below average. Studies have determined that the reduced abundance of Ruminococcus could mediate the risk of Cardiovascular Diseases in the Obese. In order to improve the abundance of this bacterium, diets high in resistant starch, omega-3 fatty acids, and polyphenols should be consumed. Besides this, the relative abundance of genus Ruminococcus was positively correlated with the intake of protein, monounsaturated fats, vitamin A, and vitamin D. Foods such as legumes, lentils, nuts, seeds, starchy vegetables, dark chocolate, berries, and fatty fish will provide all these essential nutrients.</p>	
Coprococcus	
0.0000001	
Recommendations	
<p>The results show that the abundance of Coprococcus in your gut microbiome is below average. Studies have shown that a reduced abundance of Coprococcus is found in individuals with IBS and Parkinson's Disease. In order to improve the abundance of this bacterium, a diet rich in whole grains (brown rice, quinoa, barley, and oats), fruit (apples, pears, berries, and oranges), and vegetables (broccoli, cauliflower, brussels sprouts, and artichokes) is essential.</p>	
Anaerostipes	
0.0000001	
Recommendations	
<p>The results show that the abundance of Anaerostipes in your gut microbiome is below average. In order to increase the abundance of this bacterium, a diet rich in dairy (milk, cheese, and yoghurt) and simple carbohydrates (fresh, frozen, raw, or cooked vegetables e.g string beans and fresh, frozen, cooked, or dried fruits without added sugar) and eggs.</p>	
Butyrivibrio	
0.0000001	
Recommendations	
<p>The results show that the abundance of <i>Butyrivibrio</i> in your gut microbiome is below average. In order to improve the abundance of this bacterium, a diet rich in beef, lamb, dairy products (milk, cheese, butter, and yoghurt), and or dietary supplementation with Conjugated Linoleic Acid (CLA) is advised.</p>	

Bacteria with Probiotic Properties

Christensenella minuta

0.0000001



Recommendations

The results show that the abundance of *Christensenella minuta* in your gut microbiome is below average. In order to increase the abundance of this bacterium, foods such as cranberries, black tea, flaxseeds, and fish oil should be consumed. In addition, an omnivorous diet (a diet which is based on meat and plant sources) and a Mediterranean diet have been shown to optimise *Christensenella minuta* abundance.

Barnesiella

0.0000001



Recommendations

The results show that the abundance of Barnesiella in your gut microbiome is below average. In order to increase the abundance of this bacterium, fruits, vegetables, whole grains, all varieties of legumes/pulses, and other fibre-rich food sources should be consumed. Barnesiella is a probiotic species which is able to prevent Vancomycin-Resistant Enterococci (VRE) from colonising the gut and has even been used to treat infections caused by this pathogen. In addition, Barnesiella can even enhance the effectiveness of immunomodulatory therapy for certain types of cancer.

Lactobacillus

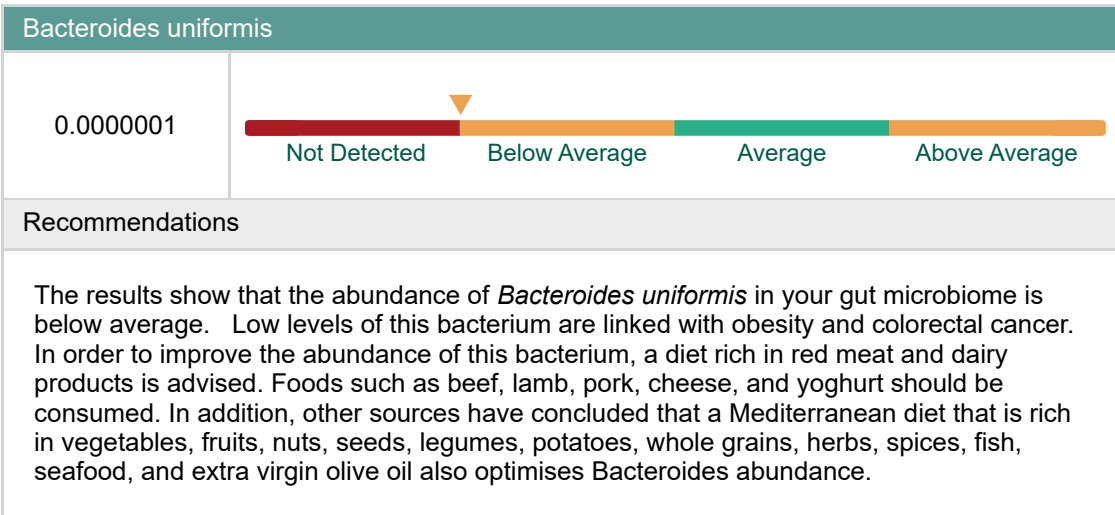
0.0000001



Recommendations

The results show that the abundance of Lactobacillus in your gut microbiome is below average. In order to increase the abundance of this bacterium, foods such as natural yoghurt, kimchi, kefir, sauerkraut, and tempeh should be consumed. In addition, foods or supplements rich in polyphenols (tea, red wine, dark chocolate) also has been shown to increase Lactobacillus abundance. Stress reduction is key in optimising Lactobacillus abundance, as heightened stress contributes to its depletion.

Bifidobacterium	
0.0000001	
<p>Recommendations</p> <p>The results show that the abundance of Bifidobacterium in your gut is below average. In order to increase the abundance of this bacterium eat more fermented foods such as kimchi, sauerkraut, and kefir as well as increase dietary fibre from a range of plant sources to contribute to higher levels of Bifidobacterium in the gut. Prebiotic fibre, found naturally in foods such as certain fruits, vegetables, or wholegrain oats also increases Bifidobacterium.</p>	
Akkermansia muciniphila	
0.0000001	
<p>Recommendations</p> <p>The results show that the abundance of <i>Akkermansia muciniphila</i> in your gut microbiome is below average. Reduced abundances of this bacterium have been observed in individuals with Inflammatory Bowel Diseases, diabetes and obesity. A thin mucus layer is observed resulting in a weakened gut lining. In order to increase the abundance of this bacterium, a diet rich in polyphenols is advised. Foods such as apples, cherries, beans, berries, grapes, flaxseed, green tea, nuts, olives, asparagus, onions, oats, and black tea are all rich in polyphenols so should be consumed. Polyphenols are very significant in the diet as they may offer protection against the development of certain cancers, cardiovascular diseases, diabetes, and neurodegenerative diseases.</p>	
Prevotella copri	
0.0000001	
<p>Recommendations</p> <p>The results show that the abundance of <i>Prevotella copri</i> in your gut microbiome is below average. In order to improve the abundance of this bacterium, coffee consumption as well as a diet rich in fibre from a vegetable-rich diet has been shown to promote an increased abundance of <i>Prevotella Copri</i>.</p>	




Hydrogen Sulphide Producing Bacteria	
<i>Desulfovibrio piger</i>	
0.000005	
Recommendations	
<p>Results show that the abundance of <i>Desulfovibrio piger</i> in your gut microbiome is within the average range. In order to maintain the abundance of this bacterium, a diet low in simple sugars and fat is advised. Therefore, minimise the intake of biscuits, cakes, confectionery, fatty cuts of meat, processed meats e.g., sausages and pies, and cheese.</p>	
<i>Desulfovibrio desulfuricans</i>	
0.0000053	
Recommendations	
<p>The results show that the abundance of <i>Desulfovibrio desulfuricans</i> in your gut microbiome is within the average range. In order to maintain the abundance of this bacterium, a diet low in fat and protein is advised. Therefore, prioritise organic extra virgin olive oils and essential fatty acids (EFAs) from wild-caught, and cold-water fish. Then reduce intake of grass-fed butter, ghee, and organic coconut oil- with plenty of fibre, which may help to reduce the chances of a <i>Desulfovibrio desulfuricans</i> overgrowth.</p>	

Oxalate-Degrading Bacteria	
<i>Oxalobacter formigenes</i>	
0.0000001	<p>Not Detected Below Average Average Above Average</p>
Recommendations	
<p>The results shows that the abundance of <i>Oxalobacter formigenes</i> in your gut microbiome is below the average. In order to increase the abundance of this bacterium, dietary oxalate consumption must be reduced to 80 - 100 mg/day in order to be effective. Foods rich in oxalate include spinach, nuts/nut butters, beets, potatoes, and rhubarb. Calcium is also required in order to bind the oxalates within the digestive tract. Sources of calcium should not be obtained in supplement form as this can contribute to kidney stones but through the diet. Foods rich in calcium include dairy products (milk, cheese, yoghurt), green leafy vegetables, soya drink and bread in which the flour is fortified with calcium.</p>	

Potentially Pathogenic Bacteria	
<i>Clostridioides difficile</i>	
0.0002509	
Recommendations	
<p>Results show that the abundance of <i>Clostridioides difficile</i> in your gut microbiome is above the average range. An increase in the abundance of <i>C. difficile</i> can contribute to a diarrhoea induced bowel infection. Symptoms range from diarrhoea to life threatening damage to the colon, dehydration and an increase in body temperature. Most individuals are treated successfully using antibiotic therapy. During the infection and treatment period probiotic food sources such as kefir, kombucha, sauerkraut should be prioritised in the diet.</p>	
Proteus	
0.0000007	
Recommendations	
<p>The results show that the abundance of Proteus in your gut microbiome is within the average range.</p>	
Klebsiella	
0.0000109	
Recommendations	
<p>The results show that the abundance of Klebsiella in your gut microbiome is within the average range.</p>	
Citrobacter	
0.0000077	
Recommendations	
<p>The results show that the abundance of Citrobacterin in your gut microbiome is within the average range.</p>	

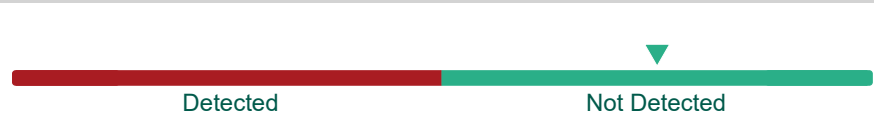
Pseudomonas	
0.0000956	
<p>Recommendations</p> <p>Results show that the abundance of <i>Pseudomonas</i> in your gut microbiome is above the average range. This is a commensal bacterium that is present in relatively low abundances in the majority of individuals. This bacterium is what is referred to as "opportunistic" and so only is harmful in certain conditions. In immunocompromised individuals for example patients with cancer or transplant recipients this can be detrimental. A higher abundance of this bacterium has been associated with antibiotic-induced diarrhoea and gut-derived sepsis in immunocompromised individuals. Other than anti-microbial therapy, little is known nutritionally regarding foods that prevent or eradicate <i>Pseudomonas</i>. If undergoing antibiotic therapy probiotic rich foods such as kimchi, kombucha, kefir and sauerkraut should be consumed to prevent dysbiosis of the gut microbiome.</p>	
<i>Helicobacter pylori</i>	
0.0000041	
<p>Recommendations</p> <p>Results show that the abundance of <i>Helicobacter pylori</i> in your gut microbiome is above the average range. This is a commensal bacterium that is present in relatively low abundances in the majority of individuals. This bacterium is what is referred to as "opportunistic" and so only is harmful in certain conditions. Certain dietary factors can disrupt the gastrointestinal microbiota, therefore increasing the likelihood of <i>H.pylori</i> overgrowth. A diet rich in fried food, meat, milk and drinking untreated water should be avoided. In addition, the reduction or the avoidance of tobacco usage is also advised. Foods that should be incorporated into the diet to inhibit <i>H.pylori</i> overgrowth include cauliflower, swede, cabbage, radishes, other Brassica vegetables and berries, (blueberries, blackberries, raspberries, and strawberries). Finally, foods which reduce <i>H.Pylori</i> overgrowth once infected and improve antibiotic efficacy include probiotic rich foods such as yoghurt, tempeh, miso, kimchi and sauerkraut.</p>	
Enterobacteriaceae	
0.005877	
<p>Recommendations</p> <p>The results show that the abundance of Enterobacteriaceae in your gut microbiome is within the average range.</p>	

Virus	
CrAss-like Viruses	
Not Detected	
Recommendations	
The results show that CrAss-like Viruses were not detected in your gut microbiome.	

Fungi	
<i>Candida albicans</i>	
Detected	
Recommendations	
<p>The result shows that <i>Candida albicans</i> was detected within your gut microbiome. <i>C. albicans</i> is referred to as an "opportunistic" pathogen and under optimal conditions can be harmful to health. <i>C. albicans</i> is primarily a concern for immunocompromised individuals. An overgrowth of this fungus has been shown to worsen Irritable Bowel Disorders such as Ulcerative Colitis and Crohn's Disease. A western diet rich in cornstarch, soyabean oil and sucrose all contribute to an overgrowth in <i>C. albicans</i>. The inclusion of fatty fish such (salmon, mackerel, and herring) and coconut oil which is shown to reduce <i>C. albicans</i> colonisation.</p>	
<i>Saccharomyces cerevisiae</i>	
Detected	
Recommendations	
<p>The result shows that the <i>Saccharomyces cerevisiae</i> was detected within your gut microbiome. This fungus is a commensal organism which occurs in the gut and can act as a probiotic under the correct conditions. It can significantly protect the normal microbiota while preventing the growth of potentially harmful bacteria. <i>S. cerevisiae</i> has been found to be a biotherapeutic agent due to its antibacterial, antiviral, anti-carcinogenic, antioxidant, anti-inflammatory and immune-modulatory properties.</p>	

Archaea	
<i>Methanobrevibacter smithii</i>	
Detected	
Recommendations	
<p>The result shows that <i>Methanobrevibacter smithii</i> was detected within your gut microbiome. This archaeon has been linked with improving energy extraction and producing of beneficial molecules such as butyrate.</p>	

Parasites	
<i>Cryptosporidium</i>	
Detected	
Recommendations	
<p>The results show that the parasite <i>Cryptosporidium spp.</i> was detected within your sample. It has been shown that <i>cryptosporidiosis infection</i> causes long-term effects such as weight loss, abdominal, eye, and joint pain, and, in some cases, irritable bowel syndrome (IBS).</p>	
<i>Dientamoeba fragilis</i>	
Not Detected	
Recommendations	
<p>The results show that the parasite <i>Dientamoeba fragilis</i> was not detected within your sample.</p>	
<i>Entamoeba histolytica</i>	
Not Detected	
Recommendations	
<p>The results show that the parasite <i>E. histolytica</i> was not detected within your sample.</p>	
<i>Cyclospora cayetanensis</i>	
Not Detected	
Recommendations	
<p>The results show that the parasite <i>Cyclospora cayetanensis</i> was not detected within your sample.</p>	
<i>Giardia lamblia</i>	
Not Detected	
Recommendations	
<p>The results show that the parasite <i>G.lamblia</i> was not detected within your sample.</p>	

<i>Blastocystis</i>	
Not Detected	
Recommendations	
The results show that the parasite <i>Blastocystis</i> was not detected within your sample.	

Glossary

Microbiome Diversity



Microbiome diversity is a description of the number of different microbial species that reside in your gut. Generally, a more diverse microbiome correlates with a 'healthier' gut and has been linked with many health benefits. A reduction in microbiome diversity is referred to as a dysbiosis and would be classified as an 'unhealthy' gut.

A microbiome diversity score of less than 3.0 would be considered low, and is usually associated with a poor diet, gastrointestinal disorders, or the use of antibiotics. A microbiome diversity score of greater than or equal to 3.0 would be considered a good diversity score, and this can usually be maintained by continuing to eat a healthy well-balanced diet.

F/B Ratio



Firmicutes (F) and Bacteroidetes (B) are the two most important phyla found in the gastrointestinal tract. An F/B ratio of 1 is deemed optimal and results greater than 1 are related to increased caloric extraction, fat deposition, and increased inflammation.

Butyrate Producing Bacteria



Butyrate producing bacteria as their name suggests degrades dietary fibre to produce a Short Chain Fatty Acid (SCFA) known as butyrate. It is the main energy source for the colonocytes, and it has protective properties against colorectal cancer (CRC) and Inflammatory Bowel Diseases (IBD).



Probiotic bacterial species are referred to as the 'Good Bacteria' as they maintain homeostasis i.e. the natural balance of bacteria in the gut microbiome when disrupted by illness or anti-microbial therapies. There is evidence that probiotics are useful in alleviating the severity of Irritable Bowel Disorders (IBD) and Irritable Bowel Syndrome (IBS). The two genera which provide most benefit to the consumer include *Lactobacillus* and *Bifidobacterium*.

Christensenella minuta

Christensenella minuta is strongly associated with therapeutic anti-obesity potential. It does this through balancing the ratio between Firmicutes and Bacteroidetes, producing SCFAs that up regulate the hunger-suppressing hormone leptin and regulating gut epithelial integrity.

Barnesiella

Barnesiella is a small group of bacteria that reside in the gut at relatively low abundances. These species have been linked with preventing Vancomycin-Resistant Enterococci (VRE) from colonising the gut and has even been used to cure infections caused by it. It has also been associated of having a negative influence on the growth of *Clostridioides difficile*.

Lactobacillus

Lactobacillus has a mutualistic relationship with humans, offering the host aid in digestion and protection from invading pathogens such as *C. difficile*, *C. perfringens*, and *C. Jejuni* to name a few. *Lactobacillus* is probiotic in nature, as it is thought to modulate the intestinal microbiota, enhance the intestinal barrier via mucus secretions and strengthen the intestinal barrier to invading pathogens.

Bifidobacteria

Bifidobacteria are helpful in maintaining appropriate balances between the various bacteria in different sections of the human intestine. Some *Bifidobacterium* strains of human origin are capable of synthesising vitamins such as thiamine, folic acid, biotin, nicotinic acid, riboflavin, pyridoxine, cobalamin, and ascorbic acid. Some of the many benefits of Bifidobacteria include enhanced lactose digestion, influence in development of the immune system and prevent or treat diarrhoea caused by foodborne infection.

Akkermansia muciniphila

Akkermansia muciniphila colonises the mucosal layer of the human intestine where it triggers both host metabolic and immune responses. It is particularly effective in increasing mucus thickness and increasing gut barrier function. The metabolic activity of *A. muciniphila* leads to the production of SCFAs that are beneficial to the host and other microbes and contributes to the production of anti-microbial compounds that kill pathogens.

Bacteroides uniformis

Bacteroides uniformis is a fibre-degrading bacteria. It colonises the gut in early infancy and is promoted by breast feeding. It has been linked with enhancing the gut barrier through the production of butyrate and GABA. This bacterium also produces beta glucuronidase, degrades mucin, and folate. Some studies have identified *B. uniformis* as a potential probiotic for use in inflammatory and metabolic disorders.

Prevotella copri

Prevotella copri in the human gut is associated with high fibre non-Western diets as they possess an extensive supply of enzymes that allow this species to metabolise complex carbohydrates. This bacterium has been associated with improved glucose control which in turn can improve chronic disease such as type 2 diabetes.

Hydrogen Sulphide Producing Bacteria

H₂S

Hydrogen sulphide (H₂S) producing bacteria acquire energy by reducing sulphur to the by-product H₂S. Optimal levels of H₂S directly stabilise mucus layers and help resolve inflammation and tissue injury in the gastrointestinal tract.

Oxalate - Degrading Bacteria

GIT

Humans lack the enzymes needed to metabolise dietary oxalate, a toxic compound causing kidney stones. Oxalate in humans can be eliminated through excretion in urine, forming insoluble calcium oxalate and elimination in faeces, or oxalate degradation by gastrointestinal (GIT) microorganisms. *Oxalobacter formigenes* is the best studied species known to degrade Oxalate. Species in the *Lactobacillus* and *Bifidobacterium* genera are known to share similar functions. A low abundance of these bacteria could result in being a higher risk of calcium oxalate urolithiasis due to oxalate build-up.



Many of the potentially pathogenic bacteria naturally reside in the gut as commensal bacteria. These are bacteria that can be found in the microbiome at relatively low abundances without causing harm to health. However, under dysbiosis an overgrowth of these bacteria can occur causing vomiting, diarrhoea and elevating the symptoms of gastrointestinal disorders such as Inflammatory Bowel Disease (IBD). Each potentially pathogenic bacterium has an individualistic response and so will not result in the same symptoms.

Clostridium difficile

Clostridium difficile is a bacterium that causes an infection of the colon which is the longest part of the large intestine. Symptoms can range from diarrhoea to life-threatening damage to the colon. The illness from *C. difficile* often occurs after using antibiotic therapies and mostly affects older adults in hospitals or in long-term care settings.

Proteus spp.

Proteus species are typically considered commensals in the gastrointestinal (GI) tract, their abundance as a proportion of the microbial community is very low (<0.05%). *Proteus* species, especially *P. mirabilis*, are often antibiotic resistant, giving them a survival advantage when colonising the gastrointestinal tract. There is increasing evidence that *Proteus* species may play a role in inflammatory bowel diseases.

Klebsiella spp.

Klebsiella pneumoniae (KLP), is a common cause of antimicrobial-resistant opportunistic infections in hospitalised patients. KLP can colonise in the human gastrointestinal tract, especially in patients with inflammatory bowel diseases. *Klebsiella* also has the innate ability to form biofilms which protects itself from the hosts immune system and antibiotic treatments.

Citrobacter spp.

Citrobacter spp. are also known to be commensal bacteria found in a healthy human gut. It only becomes problematic when given the space and nutrients to grow. Acute symptoms can include watery diarrhoea without abdominal pain and passing blood in stools.

Pseudomonas spp.

Gut colonisation by *Pseudomonas aeruginosa* underpins the development of invasive infections such as gut-derived sepsis and is associated with higher ICU mortality rates. *P. aeruginosa* has been widely reported as a cause of antibiotic-associated diarrhoea in adult immunocompromised hosts.

Helicobacter pylori

Helicobacter pylori (*H. pylori*) is generally regarded as a human pathogen, but it can act as a commensal bacterium also. *H. pylori* colonisation may have beneficial effects on the host by regulating gastrointestinal microbiota and protecting against some autoimmune disorders and inflammatory bowel diseases. Infection with *H. pylori* causes chronic inflammation and significantly increases the risk of developing gastric ulcer disease and gastric cancer.

Enterobacteriaceae

Enterobacteriaceae is a commensal family found within the gastrointestinal tract which under optimal conditions can be pathogenic. It has been widely reported that there is an increase in relative abundance of bacterial species in the *Enterobacteriaceae* family in IBD patients. Hosts inflammatory response could be triggered by the increased abundances of *Enterobacteriaceae* species, causing dysbiosis which may lead to the persistence of IBD's inflammatory state.

Glossary of Microbial Terms

Shotgun Sequencing	This is a genetic laboratory technique used to read the DNA sequence of an organism.
Colonocyte	The cells that make up the lining of the colon, the longest part of the large intestine.
Prebiotics	Foods, typically plant fibres that promote the growth of beneficial bacteria that reside in the gut.
Probiotics	Foods or supplements that contain live microorganisms that have been linked with health benefits when consumed.
Inulin-Type Fructans	Plant carbohydrates that cannot be digested in the upper gastrointestinal tract but can be in the colon.
Arabinoxylans	A dietary fibre naturally found in cereal grains.
Homoeostasis of Gut Microbiota	The self-regulation of the balance of microorganisms in the gut.
Opportunistic Infections	Infections that occur more frequently and more severely in individuals with weakened immune systems.
Opportunistic Microorganisms	Typically are non-pathogenic when found at lower abundances and suppressed by the immune systems. However, when dysbiosis occurs, these microorganisms can quickly take over and become pathogenic.
Dysbiosis	An imbalance in gut microbiota, usually associated with disease.
Commensal Organism	An organism that resides in the gut and has no negative or positive effects.

Pathogenic	Used to describe an organism that is capable of causing disease.
Mediterranean Diet	This diet mainly consists of plant foods such as fruit, vegetables, nuts, beans, and whole grains. Along with moderate amounts of dairy, poultry, and fish.
Western Diet	This diet mainly consists of processed meats, food/drink with a high sugar content, red meat, fried foods, and high fat dairy products.
Vegan Diet	This is a plant- based diet that does not consist of animal products.
Antibiotic Resistance	Bacteria that cannot be treated with antibiotics.
Essential Fatty Acids	Compounds that are essential to human health that cannot be synthesised in the body.

