

# The Next Generation of Gut Health:

## GI SereniT™

complete microbiome mapping

### Microbiome Report

**PREPARED FOR**

[REDACTED]

**SPECIMEN ID #**

34009508

**RECEIVED DATE**

May 15, 2024

**KIT ID**

34009508

**TESTING DATE**

Jun 16, 2024

**REPORT DATE**

Jun 21, 2024

**ORDERING PHYSICIAN**

Floré Clinical

**ACCESSION #**

34009508

**Work Order IDs**

CM028239 & GI028239

**ORDERING FACILITY**

Customer Service Test

**COLLECTION DATE**

May 10, 2024

The GI SereniT™ is a convenient at-home stool collection providing a clinically relevant assessment of the gut microbiome in 5 key areas: Wellness Assessment and Health Scores, Microbiome Diversity, Disease Association, How You Compare, and the Identification of Organisms in one's microbiota.

**Floré**<sup>®</sup>  
**CLINICAL**  
by  sun genomics

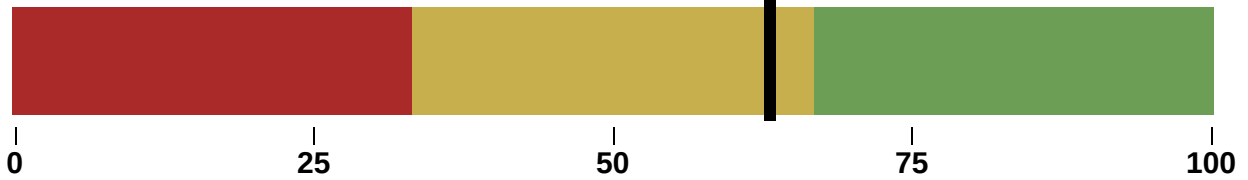
WELLNESS ASSESSMENT

# Overall Microbiome Score

Alterations in the composition of the gut microbiota are associated with various disease processes, otherwise known as dysbiosis (1). Gut microbiota dysregulation was studied in clinically ill patients that showed serious microbial imbalances such as the disappearance of bacterial genera known to contribute important functions in host metabolism (3,4)



Microbiome Score



WELLNESS ASSESSMENT

# Microbiome Diversity

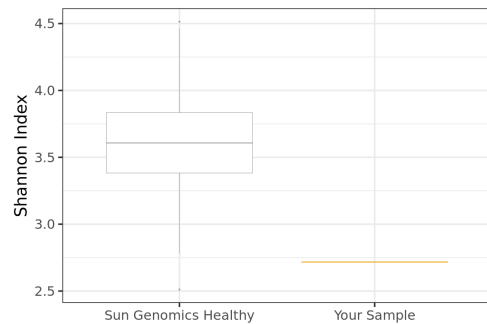
An imbalanced gut microbiome composition (dysbiosis) also correlates with inflammation and neurodegenerative disorders such as Alzheimer's disease and Parkinson's disease in the elderly. Decreased diversity, considered an indicator of an unhealthy microbiome, has been linked to different chronic conditions such as obesity and type 2 diabetes (17).



Diversity Score

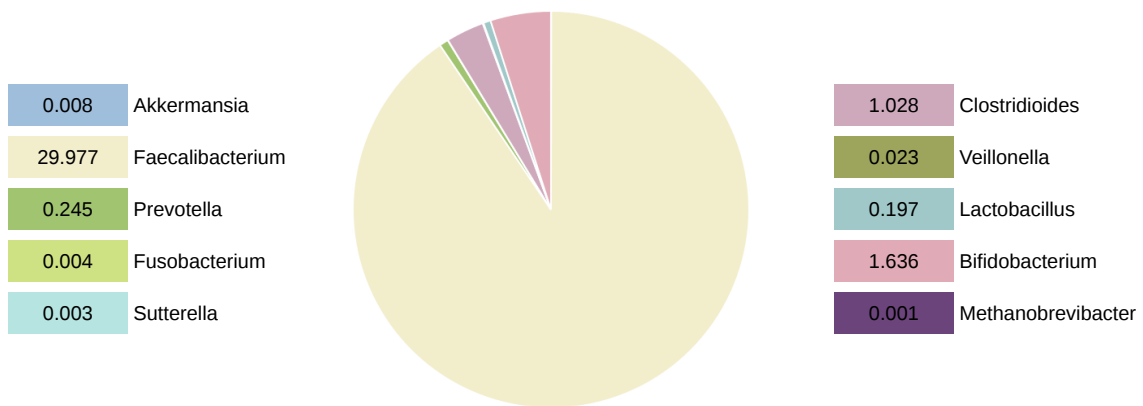
## Alpha Diversity Comparison

The Alpha Diversity test is used to compare your gut diversity with that of a healthy individual. This graph shows the total number of individual microbial species found within your gut compared to the gut of a healthy individual. It is a measure of microbiome diversity applicable to a single sample (18).



## Microbe Abundance by Genus

This chart shows the breakdown of your microbiome by genus and their percentages.



# Clinically Relevant Pathogens Tested

Bacteria and Bacterial toxins	Results
Campylobacter (C. jejuni, C. coli and C. lari only)	Not Detected
Clostridiodes difficile (C. difficile) toxin A/B	Not Detected
Escherichia coli (E. coli) O157:H7	Not Detected
Enterotoxigenic E. coli (ETEC) LT/ST	Not Detected
Shiga-like Toxin producing E. coli (STEC) stx1/stx2	Not Detected
Salmonella (S. enterica)	Not Detected
Shigella (S. boydii, S. sonnei, S. flexneri, and S. dysenteriae)	Not Detected
Vibrio cholerae, cholera toxin gene (ctx)	Not Detected

Parasites	Results
Cryptosporidium (C. parvum and C. hominis)	Not Detected
Entamoeba histolytica (E. histolytica)	Not Detected
Giardia (G. lamblia only - also known as G. intestinalis and G. duodenalis)	Not Detected

Viruses	Results
Norovirus GI/GII	Not Detected
Rotavirus A	Not Detected
Adenovirus 40/41	Not Detected

DISEASE ASSOCIATION

# Crohn's Disease

Crohn's Disease is an Inflammatory Bowel Disease that causes the lining of the digestive tract to become inflamed. Compared to healthy individuals, the microbiomes of those suffering from Crohn's Disease tend to be less diverse. The common microbiome profile of a Crohn's patient shows increased levels of species such as Escherichia coli (E. coli) and Ruminococcus gnavus, and decreased levels of Bacteroides, Roseburia, Bifidobacterium, and Faecalibacterium prausnitzii. The bacteria responsible for producing short chain fatty acids are also decreased or not present in individuals suffering from Crohn's Disease (19, 20).



Crohn's Disease Association Score


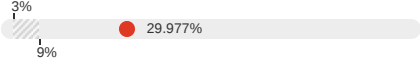




## Bacteria Associated with Crohn's Disease

The following microbes are associated with Crohn's disease. Those noted with an alert symbol **⚠** have an over-abundance and should be reduced.

Microbes	Abundance in Your Microbiome	Ideal Range Comparison
Dialister invisus	0.000%	
<b>⚠</b> Faecalibacterium prausnitzii	29.763%	
Bifidobacterium adolescentis	1.291%	
[Ruminococcus] gnavus	0.160%	
Harmful Clostridium	0.02%	

## Microbes Providing Increased Protection from Crohn's Disease

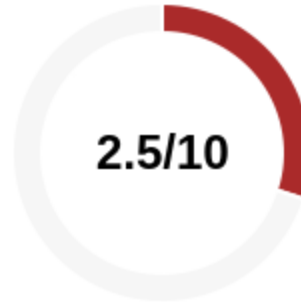
The following microbes may help mitigate Crohn's disease. Those noted with an alert symbol **⚠** have a low microbial abundance and should be increased (23). When the below listed microbes are at an ideal range a good gut health is favored.

Microbes	Abundance in Your Microbiome	Ideal Range Comparison
Bacteroides	6.766%	
Faecalibacterium	29.977%	
Roseburia	5.478%	
Blautia	2.931%	
Ruminococcus	0.657%	
Coprococcus	0.474%	

DISEASE ASSOCIATION


# Short Chain Fatty Acid Production


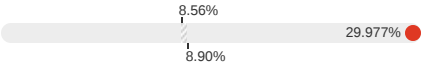








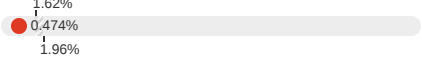
Short Chain Fatty Acids (SCFAs) are produced as a result of bacterial fermentation in the gut. During this process, bacteria ferment complex carbohydrates that our bodies are unable to digest for carbon and energy, as a result SCFAs are produced. The three main SCFAs produced by this process are acetate, propionate, and butyrate. SCFAs are important for maintaining the integrity of the intestinal barrier, reducing inflammation associated with colorectal cancer, and mucus production. The main SCFA producing bacteria in the gut are *Faecalibacterium prausnitzii* and *Roseburia intestinalis* (21). A high score indicates a potentially favorable gut environment for SCFA production.



SCFA Production

## SCFA Production

The following microbes are associated with SCFA Production. Those noted with an alert symbol  have an over-abundance and should be reduced (22).

Microbes	Abundance in Your Microbiome	Ideal Range Comparison
 Faecalibacterium	29.977%	
 Roseburia	5.478%	
Ruminococcus	0.657%	
 Anaerostipes	1.835%	
Butyricoccus	0.136%	
Butyrivibrio	0.087%	
Butyricimonas	0.193%	
Coprococcus	0.474%	

Microbes	Abundance in Your Microbiome	Ideal Range Comparison
[Eubacterium] hallii	0.186%	<p>0.13% ● 0.186% 0.47%</p>
Flavonifractor	0.459%	<p>0.34% ● 0.459% 0.67%</p>
Odoribacter	0.308%	<p>0.30% ● 0.308% 0.64%</p>
Bifidobacterium adolescentis	1.291%	<p>0.22% ● 1.291% 0.56%</p>
Dialister invisus	0.000%	<p>0.06% ● 0.000% 0.40%</p>
Lactobacillus	0.197%	<p>0.27% ● 0.197% 0.61%</p>
[Eubacterium] eligens	1.060%	<p>2.12% ● 1.060% 2.45%</p>

**Sun Genomics**  
 Phone: 661-888-4799  
 Email: customerservice@sungenomics.com

**Mailing & Laboratory Address**  
 5151 Shoreham Place  
 Suite 180, San Diego, CA 92122

**Laboratory Information**  
 CLIA ID: 05D2194956  
 Lab director: Saurabh Gombar, M.D., Ph.D.



WELLNESS ASSESSMENT

# Disease Association (Part 1)

Disease association score reflects your overall microbial balance/imbalance in the gut and aids in early identification and possible prevention of gastrointestinal dysbiosis. Individualized intervention of probiotics may minimize the burden of microbial associated risk factors causing dysbiosis.

↑ = high risk association  
↓ = low risk association

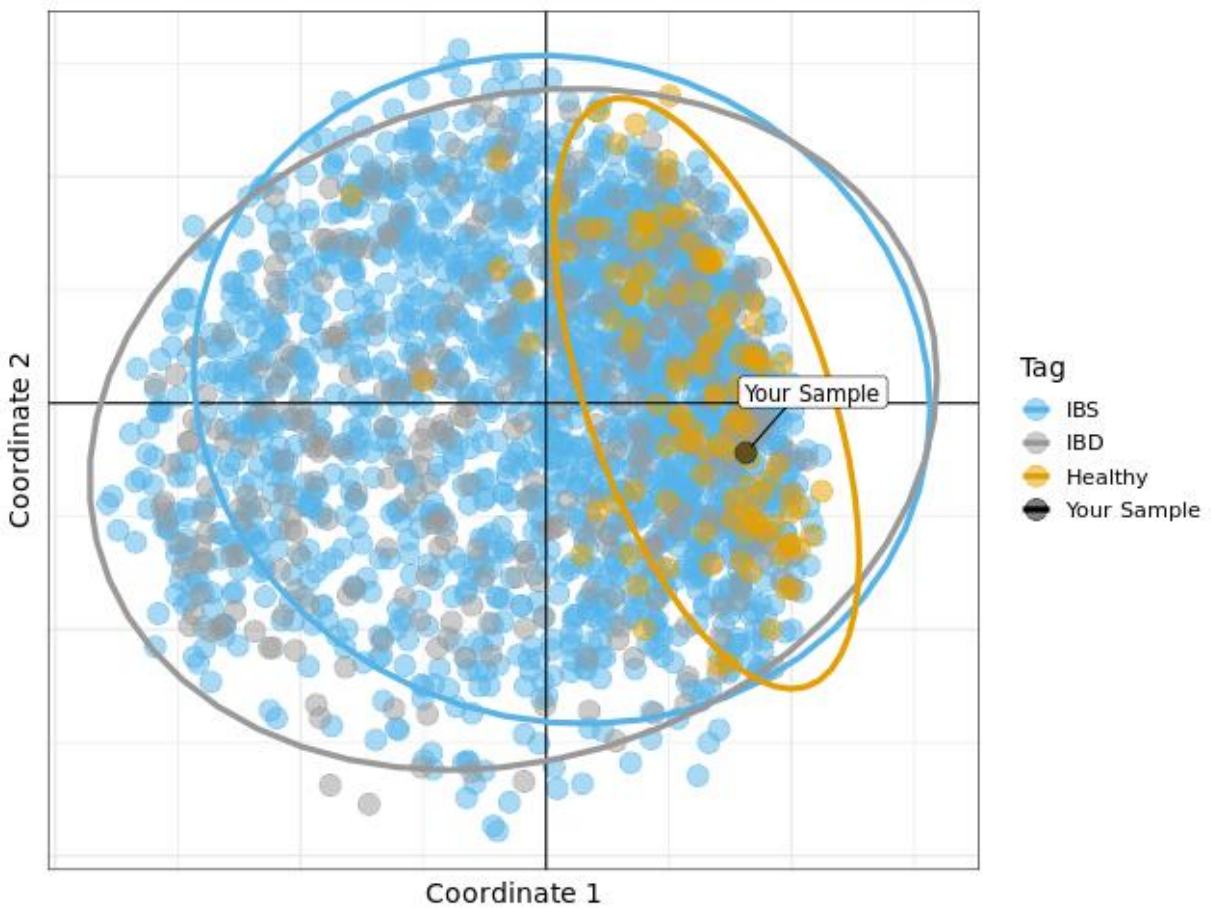
Disease	Risk Association Score
↓ Crohn's Disease	10/10
↓ Inflammatory Bowel Disease (IBD)	10/10
↓ Irritable Bowel Syndrome with Diarrhea (IBS-D)	8/10
↓ Irritable Bowel Syndrome with Constipation (IBS-C)	7/10
↓ Irritable Bowel Syndrome (IBS)	9/10
↓ Small Intestinal Bacterial Overgrowth (SIBO)	10/10

Present = symptom present  
Absent = symptom absent  
Not Available = unanswered survey

Symptoms	Status
Diarrhea	Absent
Bloating	Present
Constipation	Absent
Fatigue	Absent
Gas	Present

# Disease Association (Part 2)

Microbial species abundances of the gut are calculated using Bray-Curtis dissimilarity. The figure illustrates the dissimilarity of the patient sample compared to healthy, IBS, and IBD cohorts in the Sun Genomics database. The variance between all samples is displayed across the X and Y axes. The black dot represents the patient sample, the yellow represents normal healthy population and blue and grey clusters represents IBS and IBD, respectively. This representation shows how close your microbial profile is to the other cohorts- healthy or diseased, but do not indicate the health condition.



---

# Health Scores

Here at Sun Genomics we understand how important gut health is to the overall health. Microbiome signatures can define the susceptibility to certain ailments. Our whole genome sequencing technology allows us to detect these microbiome signatures for Immunity, Microbe Diversity, Joint Health, Longevity, and Dysbiosis. Gut is the key to diagnosing and alleviating many of these issues.

---

## Immunity

The gut microbiota plays an integral role in educating your innate immune system for recognition of pathogenic vs. commensal microbes. Alterations of the enteric microenvironment promote opportunistic pathogen growth and reduce the abundance of commensal bacteria, (2,3,4). A high score indicates presence of balanced microbial diversity and immunity.



### BioMarkers

- Bifidobacterium
- Enterobacteriaceae
- Eukaryota

### Remarks

- Diet has a profound influence on microbial composition and metabolic capacity of gut microbes. Defined metabolites are known to have an influence on the immune system.
  - Dietary-derived AHR ligands from cruciferous vegetables are important signals for intestinal immune development and immune responses.
  - Micronutrients including iron, folate, zinc, selenium, and Vitamin C, D and E may control certain aspects of the immune system.
- 

## Joint Health

Gut microbiota plays a role in Rheumatoid arthritis pathogenesis, an immune-mediated chronic disease through mechanisms including mainly production of proinflammatory metabolites. One of the microbial signatures in patients with early RA was increased abundance of *Prevotella copri* while *Bacteroidetes* was decreased. Presence of *P. copri* was correlated with a reduction in the abundance of other bacterial groups, including many beneficial microbes(6,7,8). A high score indicates a potential joint health associated issue.



### BioMarkers

- *Prevotella copri*
- *Escherichia coli* (E. coli)
- *Bacteroides fragilis*

### Remarks

- *Lactobacillus casei* or *Lactobacillus acidophilus* supplementation ameliorates gut dysbiosis and consequential RA pathogenesis, in the long term(8).
-

---

## Longevity

Studies on longevity indicated an age-related decline of the beneficial functions of gut microbiota, as well as an increase of inflammation and diseases, especially for elderly people (9,10). Aging affects physiological, metabolic and immunological functions of the organism and is accompanied by inflammation and metabolic dysfunctions. A high score indicates high potential longevity.



### BioMarkers

- Bacteroides fragilis
- Enterobacteriaceae
- Faecalibacterium

### Remarks

- Some important characteristics of age-onset dysbiosis is reduced microbiota diversity, and increased Enterobacteriaceae.
- Supplementation with Bifidobacteria resulted in reduced accumulation of lipofuscin, a marker of aging, improved locomotor function and increased longevity (11).

---

## Firmicutes/Bacteroidetes Ratio

The Ratio between Firmicutes and Bacteroidetes can be indicative of risk for a number of conditions, including but not limited to diabetes (Type 2), cardiovascular disease, and metabolic disease (12). People with a normal weight tend to have a higher ratio of Firmicutes to Bacteroidetes as Firmicutes tend to produce butyrate, a special compound that can increase insulin sensitivity, regulate metabolism, and has anti-inflammatory properties. This score is defined by calculating the ratio and its association to disease. A lower score indicates closer association to disease conditions.



### Remarks

- It was shown that GDM (Gestational diabetes mellitus ) patients had increased Firmicutes to Bacteroidetes ratio, an important factor that facilitates obesity and aggravates inflammation(12).
- Resistance starch, beta-glucans, inulin, pectin and cellulose containing supplements can improve F/B ratios.

---

## Harmful Microbes

The pathogenic microbes secrete toxic chemicals that damage intestinal epithelial cells and cause a chronic inflammatory response leading to dysbiosis (13, 14, 15). A high score indicates presence of high number of harmful microbes.



### BioMarkers

- Clostridioides difficile (C. diff)
- Enterobacteriaceae
- Streptococcus
- Eukaryotes

### Remarks

- Probiotic metabolites can act on the microbiota by cross-feeding interactions, changes in the gastrointestinal microenvironment (e.g., pH lowering), competition for nutrients and binding sites, and inhibition of growth via the production of strain-specific antibacterial compounds including bacteriocins.

---

# Dysbiosis Index

Crohn's disease had increased markers of inflammation and dysbiosis while ulcerative colitis had even higher inflammation and dysbiosis compared to those with Crohn's disease. The gut microbial dysbiosis index is associated significantly with clinical and biological measures of disease severity (16). A high dysbiosis Index indicates the presence of major pathogens in the gut.



### BioMarkers

- Enterobacteriaceae
- Fusobacteriaceae
- Archaea/Eukaryota

### Remarks

- Personalized nutrition and precision medicine are beginning to influence the application of probiotics and prebiotics, with growing interest in modulation of microbial signatures of health and disease.

# How You Compare

A diverse gut is a healthy gut. The following graphs show how the levels of certain microbes found in your gut compare with those of the general population, Crohn's Disease patients, IBS patients, and IBD patients.

## Pseudomonas

The genus *Pseudomonas* is made up of over 140 species of bacteria; of these, around 25 are associated with human health. The *Pseudomonas* species that are known to cause disease, like *P. aeruginosa*, are known as opportunistic pathogens. An opportunistic pathogen is one that will not cause an infection in a healthy host, however, can cause an infection in an unhealthy one.

Your Sample	0.034%
Healthy Population	0.047%
Crohn's Disease	0.095%
IBS	0.128%
IBD	0.314%

## Alistipes

*Alistipes* is a relatively new genus of bacteria typically isolated from the gut microbiome. Studies have shown that an *Alistipes* dysbiosis within the gut can have both positive and negative consequences. Decreased levels of some *Alistipes* species such as *A. shahii* and *A. putredinis* have been associated with liver fibrosis, whereas increased levels of some species, such as *A. finegoldii*, are believed to be protective against intestinal inflammatory diseases like Colitis.

Your Sample	10.454%
Healthy Population	3.959%
Crohn's Disease	3.045%
IBS	4.470%
IBD	3.972%

## Lactobacillus

*Lactobacillus* is a genus of lactic acid producing bacteria that play many important roles. *Lactobacillus* species are most commonly used for lacto-fermentation to produce yogurt, sauerkraut, kimchi, and other fermented food products. They are labeled as a probiotic genus and are regularly found in the gut. Their presence is known to aid in balancing the gut microbiome and fighting off pathogenic species growth.

Your Sample	0.197%
Healthy Population	0.441%
Crohn's Disease	0.265%
IBS	0.284%
IBD	0.379%

## Anaerostipes

*Anaerostipes* is a genus of bacteria that produce butyrate. It is commonly found in the gut and its presence is believed to have positive effects on our gut health. Butyrate, a product of *Anaerostipes*, has anti-inflammatory properties, helps maintain homeostasis in the gut, and promotes new intestinal epithelial cell growth.

Your Sample	1.835%
Healthy Population	0.760%
Crohn's Disease	0.756%
IBS	0.803%
IBD	0.907%

## Streptococcus

The Streptococcus genus of bacteria are known lactic acid producers, producing d-lactic acid. The genus can be broken down into two groups: Group A Streptococcus and group B Streptococcus. Group A is made up of species that are not normally apart of our flora composition. Within this group are the pathogenic species that cause strep throat and skin infections. Unlike Group A, Group B Streptococcus can be found as a part of our normal flora makeup and is not usually harmful, however it can cause infection in infants and individuals with weakened immune systems.

Your Sample	0.202%
Healthy Population	0.266%
Crohn's Disease	0.926%
IBS	0.552%
IBD	0.661%

## Clostridium

Clostridium is a common genus found in our gut microbiome and has been shown to be one of the earlier colonizers of our guts. They are one of the few groups of bacteria in our gut that can ferment carbohydrates to produce short-chain fatty acids (SCFAs) which are important for intestinal health. However, there are also species within the Clostridium genus of bacteria that are toxin producing. *C. difficile* is a common opportunistic pathogen which tends to cause infection following the use of antibiotics; symptoms usually include diarrhea and abdominal discomfort. *C. perfringens*, another Clostridium species, is the cause of food poisoning in humans.

Your Sample	0.982%
Healthy Population	1.168%
Crohn's Disease	1.635%
IBS	1.321%
IBD	1.720%

## Enterobacteriaceae

There are over 120 species of bacteria that fall within the Enterobacteriaceae family. Of these, there are less than 25 species that are considered clinically significant to human health. Enterobacteriaceae species are common inhabitants of the gastrointestinal tract, however some species are pathogenic and can be detrimental to human health. The most common species within the family are *Escherichia coli* (*E. coli*), *Klebsiella pneumoniae*, and *Shigella flexneri*.

Your Sample	0.15%
Healthy Population	0.625%
Crohn's Disease	5.774%
IBS	2.852%
IBD	7.593%

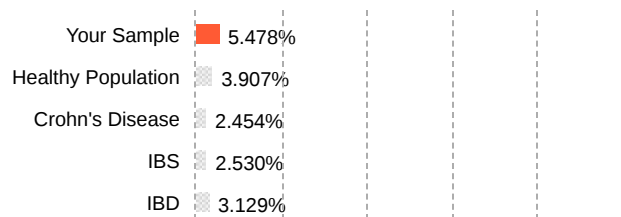
## Bifidobacterium

Species within the Bifidobacterium genus are some of the first to colonize the human gut following birth. Members of this genus are considered probiotic species and play an important role in promoting immune health, reducing inflammation, and inhibiting the growth of harmful microbes.

Your Sample	1.636%
Healthy Population	1.130%
Crohn's Disease	1.100%
IBS	1.334%
IBD	1.601%

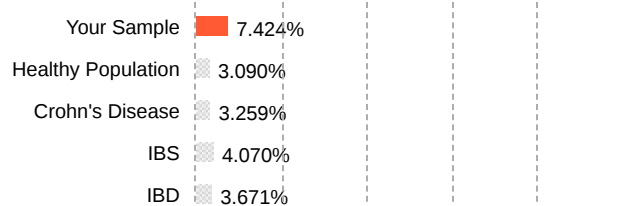
## Roseburia

The species within the Roseburia genus colonize the human colon. Increased levels of Roseburia in the gut is associated with weight loss and a reduction in glucose intolerance.



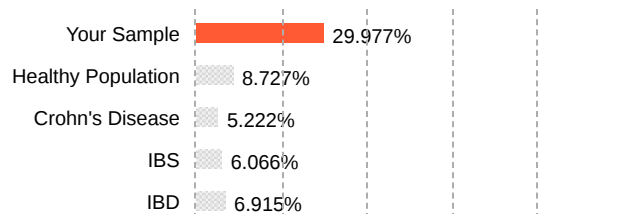
## Parabacteroides

The genus Parabacteroides is made up of 15 species. Species in this genus were once classified under the Bacteroides genus, however they were reclassified into their own genus due to phylogenetic differences. Their presence in the gut has been associated with both positive and negative effects.



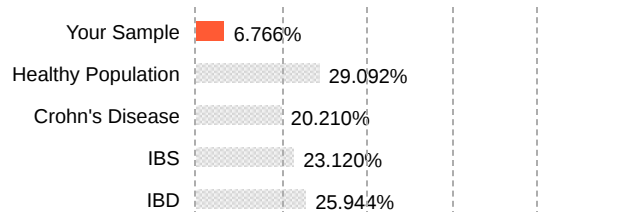
## Faecalibacterium

The genus Faecalibacterium is solely made up of the species Faecalibacterium prausnitzii. It is a common gut bacterium whose presence is believed to be indicative of good gut health. Individuals suffering from inflammatory bowel diseases tend to have low levels of Faecalibacterium in their guts.



## Bacteroides

The genus Bacteroides is made up of a group gram-negative, anaerobic bacteria belonging to the family Bacteroidaceae. They are the most common gut bacteria and can be found in the lower gastrointestinal tract of humans. When in the gut, they are generally harmless, however when spread to other parts of the body they are known to be the cause of numerous anaerobic infections.





MICROBE DETAILS

# Top 10 Microbes


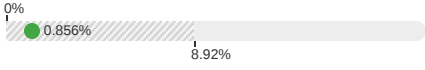



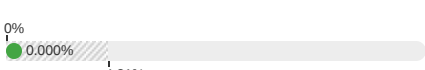


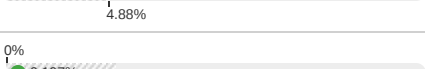



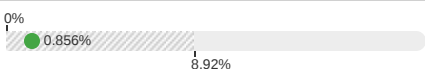


This list is made up of the 10 most abundant microbial species inhabiting your gut biome.









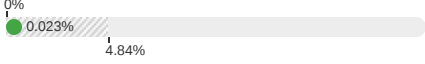

Microbes	Category	Abundance in Your Microbiome	Ideal Range Comparison
Faecalibacterium prausnitzii	beneficial	29.763%	<p>2.58%   29.763%   14.58%</p>
Alistipes putredinis	variable	5.155%	<p>0%   5.155%   7.50%</p>
Roseburia faecis	beneficial	4.512%	<p>0%   4.512%   7.62%</p>
Parabacteroides merdae	neutral	4.024%	<p>0%   4.024%   6.82%</p>
Alistipes finegoldii	variable	3.002%	<p>0%   3.002%   6.84%</p>
Gemmiger formicilis	neutral	2.793%	<p>0%   2.793%   7.16%</p>
[Eubacterium] rectale	neutral	2.644%	<p>0%   2.644%   11.98%</p>
Barnesiella intestinihominis	neutral	2.424%	<p>0%   2.424%   6.57%</p>
Collinsella aerofaciens	neutral	2.156%	<p>0%   2.156%   6.51%</p>
Parabacteroides distasonis	neutral	2.063%	<p>0%   2.063%   7.13%</p>

MICROBE DETAILS

# Probiotics & Beneficial Microbes

Probiotic species and beneficial microbes are an integral part of our guts and health. Their presence is important for digestion and immunity, as well as easing inflammation and controlling the overgrowth of harmful species. Probiotics include species in the Lactobacillus, Bifidobacterium, and Saccharomyces genres, among others (24).

Microbes	Category	Abundance in Your Microbiome	Ideal Range Comparison
Akkermansia muciniphila	probiotic	0.008%	
Bacteroides uniformis	beneficial	0.856%	
Blautia wexlerae	beneficial	0.413%	
Coprococcus eutactus	beneficial	0.091%	
Roseburia faecis	beneficial	4.512%	
Saccharomyces cerevisiae	probiotic	0.000%	
Bifidobacterium		1.636%	
Bacillus		0.032%	
Lactobacillus		0.197%	
Faecalibacterium prausnitzii	beneficial	29.763%	
Roseburia faecis	beneficial	4.512%	
Bacteroides uniformis	beneficial	0.856%	
Acidaminococcus sp. BV3L6	beneficial	0.852%	
Blautia obeum	beneficial	0.711%	
Blautia wexlerae	beneficial	0.413%	

Microbes	Category	Abundance in Your Microbiome	Ideal Range Comparison
[Eubacterium] hallii	beneficial	0.186%	
Ruminococcus bromii	beneficial	0.185%	
Roseburia hominis	beneficial	0.129%	
Bacteroides xylanisolvens	beneficial	0.117%	
Coprococcus eutactus	beneficial	0.091%	
[Clostridium] leptum	beneficial	0.079%	
Tyzzrella nexilis	beneficial	0.036%	
Bacteroides intestinalis	beneficial	0.029%	
Streptococcus salivarius	beneficial	0.023%	
Bacteroides finegoldii	beneficial	0.021%	

MICROBE DETAILS

# Pathogens

Pathogens are microbes that can cause disease in humans. They can enter our bodies through the air, contact with a contaminated surface, animal vectors, or by consuming contaminated food or water. While pathogens are usually absent or found in low quantities in the gut, their presence can have negative effects on our health. Pathogens in our gut are associated with a wide range of possible symptoms such as pain, irregular bowel movements, and inflammation. Their presence can also have more serious consequences such as damage to the intestinal walls. Having a more diverse microbiome provides protection against pathogenic growth in the gut (13, 14, 15).

Microbes	Category	Abundance in Your Microbiome	Ideal Range Comparison
Citrobacter		0.000%	0% ● 0.000%   0.20%
Enterobacter		0.006%	0% ● 0.006%   0.19%
Klebsiella pneumoniae	harmful	0.019%	0% ● 0.019%   0.19%
Helicobacter pylori	harmful	0.001%	0% ● 0.001%   0.17%
Serratia marcescens	harmful	0.010%	0% ● 0.010%   0.18%
Streptococcus agalactiae	harmful	0.026%	0% ● 0.026%   0.19%
Pseudomonas		0.034%	0% ● 0.034%   0.22%
Yersinia enterocolitica	harmful	0.001%	0% ● 0.001%   0.17%
Porphyromonas somerae	harmful	0.008%	0% ● 0.008%   0.17%

---

MICROBE DETAILS

# Parasitology/Eukaryotes

Eukaryotes are a group of nucleated organisms found in our gut that include fungi, protozoans, and parasites. Eukaryotes play many roles in our gut ranging from pathogenic, to commensal, to beneficial. For example, *Saccharomyces boulardii*, a species of yeast, is a beneficial eukaryote that is used to treat diarrhea and promote digestive health. However, parasitic eukaryotes are associated with a range of gastrointestinal issues, some of which are more serious than others. Parasites usually enter our guts through the consumption of contaminated food and water. Some examples of parasitic eukaryotes are tapeworms, flatworms, roundworms, and protozoans such as the species that causes Giardia.

## Nematodes - Roundworms

Species	Result
<i>Ancylostoma caninum</i>	Not Detected
<i>Ancylostoma ceylanicum</i>	Not Detected
<i>Ancylostoma duodenale</i>	Not Detected
<i>Necator americanus</i>	Not Detected
<i>Enterobius vermicularis</i>	Not Detected
<i>Trichuris trichiura</i>	Not Detected

## Cestodes - Tapeworms

Species	Result
<i>Hymenolepis diminuta</i>	Not Detected
<i>Dibothriocephalus latus</i>	Not Detected
<i>Rodentolepis nana</i>	Not Detected

---

## Trematodes - Flukes

Species	Result
Taenia asiatica	Not Detected
Taenia multiceps	Not Detected
Taenia saginata	Not Detected
Taenia solium	Not Detected
Clonorchis sinensis	Not Detected
Opisthorchis felineus	Not Detected
Opisthorchis viverrini	Not Detected
Fasciola gigantica	Not Detected
Fasciolopsis buski	Not Detected
Paragonimus westermani	Not Detected
Schistosoma japonicum	Not Detected
Schistosoma bovis	Not Detected
Schistosoma haematobium	Not Detected
Schistosoma curassoni	Not Detected
Schistosoma mattheei	Not Detected
Schistosoma margrebowiei	Not Detected
Schistosoma mansoni	Not Detected

---

## Protists

Species	Result
Blastocystis hominis	Not Detected
Blastocystis sp. subtype 2	Not Detected
Blastocystis sp. subtype 3	Not Detected
Blastocystis sp. subtype 4	Not Detected
Blastocystis sp. subtype 6	Not Detected
Blastocystis sp. subtype 8	Not Detected
Blastocystis sp. subtype 9	Not Detected
Blastocystis sp. ATCC 50177-Nand II	Not Detected
Chilomastix caulleryi	Not Detected
Chilomastix cuspidata	Not Detected
Cryptosporidium hominis	Not Detected
Cryptosporidium parvum Iowa II	Not Detected
Cryptosporidium muris	Not Detected
Cryptosporidium andersoni	Not Detected
Cryptosporidium tyzzeri	Not Detected
Cryptosporidium baileyi	Not Detected
Cryptosporidium meleagridis	Not Detected
Cryptosporidium viatorum	Not Detected
Cryptosporidium ubiquitum	Not Detected
Cryptosporidium cuniculus	Not Detected
Cryptosporidium sp. 37763	Not Detected
Cryptosporidium sp. chipmunk LX-2015	Not Detected

Species	Result
Cyclospora cayetanensis	Not Detected
Entamoeba invadens	Not Detected
Entamoeba dispar	Not Detected
Entamoeba nuttalli	Not Detected
Entamoeba histolytica	Not Detected
Entamoeba moshkovskii	Not Detected
Giardia muris	Not Detected
Giardia lamblia	Not Detected
Plasmodium falciparum	Not Detected
Plasmodium vivax	Not Detected
Toxoplasma gondii	Not Detected
Trypanosoma cruzi	Not Detected

## Fungi

Species	Result
Candida albicans	Not Detected
Candida boidinii	Not Detected
Candida glabrata	Not Detected
Saccharomyces cerevisiae	Not Detected



---

# Clinical Report Comment

Your overall gut microbiome is variable compared to the Sun Genomics' healthy cohort. Bacteroides were detected at average abundance levels in your profile when compared to the average of Sun Genomics customers. Faecalibacterium species were detected at above average abundance levels in your profile. High levels of Faecalibacterium prausnitzii is known to be associated with atopic dermatitis (eczema) (1). Alistipes were detected at higher abundance levels when compared to the average of Sun Genomics customers. High levels of Alistipes are often associated with high fat diets (2). Harmful microbes Streptococcus, Salmonella and Clostridioides were all detected at low levels. Sun Genomics will monitor these organisms on follow up testing.

*Saurabh Gombhar*

Disclaimer: The Floré Clinical Microbiome Test is a laboratory developed test, validated, verified and its performance characteristics determined by Flore Laboratories under the CLIA ID: 05D2194956. It has not been cleared or approved by the US Food and Drug Administration for diagnosis and is used for investigational purposes. The methodology is based on whole genome sequencing (WGS), a comprehensive method for analyzing entire genomes of the gut microbiome and identifies potential causative variants for further follow-up studies. All positive results are presumptive and must be confirmed by FDA cleared tests or other acceptable reference methods and do not rule out co-infection with other organisms, including multicellular organisms that may not be detected in this test. The results of this test should not be used as the sole basis for diagnosis, medical treatment, or other patient management decisions. The clinically relevant pathogens were detected using the Floré Gastrointestinal Pathogen Test (Floré GPT) validation and verified at Flore Laboratories. The GPT assay is based on the xTAG technology by Luminex. All positive results are presumptive and must be confirmed by FDA cleared tests or other acceptable reference methods and do not rule out co-infection with other organisms that are not detected in this test panel. The results of this test should not be used as the sole basis for diagnosis, treatment, or other patient management decisions. Negative results in the setting of clinical illness compatible with gastroenteritis may be due to infection by pathogens that are not detected by this test or non-infectious causes such as ulcerative colitis, irritable bowel syndrome, or Crohn's disease. This Floré Gastrointestinal Pathogen Test is not intended to monitor or guide treatment for C. difficile infections.

---

**Sun Genomics**  
Phone: 661-888-4799  
Email: customerservice@sungenomics.com

**Mailing & Laboratory Address**  
5151 Shoreham Place  
Suite 180, San Diego, CA 92122

**Laboratory Information**  
CLIA ID: 05D2194956  
Lab director: Saurabh Gombhar, M.D., Ph.D.

---

## References

1. DeGruttola AK, Low D, Mizoguchi A, Mizoguchi E. Current Understanding of Dysbiosis in Disease in Human and Animal Models. *Inflamm Bowel Dis*. 2016 May;22(5):1137-50. doi: 10.1097/MIB.0000000000000750. PMID: 27070911; PMCID: PMC4838534.
2. Fakharian F, Thirugnanam S, Welsh DA, Kim W-K, Rappaport J, Bittinger K, Rout N. The Role of Gut Dysbiosis in the Loss of Intestinal Immune Cell Functions and Viral Pathogenesis. *Microorganisms*. 2023; 11(7):1849. <https://doi.org/10.3390/microorganisms11071849>
3. Campbell C, Kandalgaonkar MR, Golonka RM, Yeoh BS, Vijay-Kumar M, Saha P. Crosstalk between Gut Microbiota and Host Immunity: Impact on Inflammation and Immunotherapy. *Biomedicines*. 2023; 11(2):294. <https://doi.org/10.3390/biomedicines11020294>.
4. Lankelma, J.M.; van Vught, L.A.; Belzer, C.; Schultz, M.J.; van der Poll, T.; de Vos, W.M.; Wiersinga, W.J. Critically ill patients demonstrate large interpersonal variation in intestinal microbiota dysregulation: A pilot study. *Intensive Care Med*. 2017, 43, 59–68.
5. Sandberg ME, Bengtsson C, Klareskog L, Alfredsson L, Saevarsdottir S. Recent infections are associated with decreased risk of rheumatoid arthritis: a population-based case-control study. *Annals of the rheumatic diseases*. 2015
6. Scher JU, Sczesnak A, Longman RS, et al. Expansion of intestinal *Prevotella copri* correlates with enhanced susceptibility to arthritis. *eLife*. 2013;2:e01202.
7. Zhao T, Wei Y, Zhu Y, Xie Z, Hai Q, Li Z, Qin D. Gut microbiota and rheumatoid arthritis: From pathogenesis to novel therapeutic opportunities. *Front Immunol*. 2022 Sep 8;13:1007165. doi: 10.3389/fimmu.2022.1007165. PMID: 36159786; PMCID: PMC9499173.
8. Paul AK, Paul A, Jahan R, Jannat K, Bondhon TA, Hasan A, Nissapatorn V, Pereira ML, Wilairatana P, Rahmatullah M. Probiotics and Amelioration of Rheumatoid Arthritis: Significant Roles of *Lactobacillus casei* and *Lactobacillus acidophilus*. *Microorganisms*. 2021 May 16;9(5):1070. doi: 10.3390/microorganisms9051070. PMID: 34065638; PMCID: PMC8157104.
9. Kim M, Benayoun BA. The microbiome: an emerging key player in aging and longevity. *Transl Med Aging*. 2020;4:103-116. Epub 2020 Jul 21. PMID: 32832742; PMCID: PMC7437988.
10. Xu C, Zhu H, and Qiu P, Aging progression of human gut microbiota. *BMC Microbiol*, 2019. 19 (1) 236.
11. Ilie OD, Ciobica A, Riga S, Dhunna N, McKenna J, Mavroudis I, Doroftei B, Ciobanu AM, Riga D. Mini-Review on Lipofuscin and Aging: Focusing on The Molecular Interface, The Biological Recycling Mechanism, Oxidative Stress, and The Gut-Brain Axis Functionality. *Medicina (Kaunas)*. 2020 Nov 19;56(11):626. doi: 10.3390/medicina56110626. PMID: 33228124; PMCID: PMC7699382.
12. Houtman, T.A., Eckermann, H.A., Smidt, H. et al. Gut microbiota and BMI throughout childhood: the role of firmicutes, bacteroidetes, and short-chain fatty acid producers. *Sci Rep* 12, 3140 (2022). <https://doi.org/10.1038/s41598-022-07176-6>.
13. Zhang YJ, Li S, Gan RY, Zhou T, Xu DP, Li HB. Impacts of gut bacteria on human health and diseases. *Int J Mol Sci*. 2015 Apr 2;16(4):7493-519. doi: 10.3390/ijms16047493. PMID: 25849657; PMCID: PMC4425030.
14. Fakharian F, Thirugnanam S, Welsh DA, Kim W-K, Rappaport J, Bittinger K, Rout N. The Role of Gut Dysbiosis in the Loss of Intestinal Immune Cell Functions and Viral Pathogenesis. *Microorganisms*. 2023; 11(7):1849. <https://doi.org/10.3390/microorganisms11071849>.
15. Chen Y, Zhou J, Wang L. Role and Mechanism of Gut Microbiota in Human Disease. *Front Cell Infect Microbiol*. 2021 Mar 17;11:625913. doi: 10.3389/fcimb.2021.625913. PMID: 33816335; PMCID: PMC8010197.

- 
16. Shaw, K.A., Bertha, M., Hofmekler, T. et al. Dysbiosis, inflammation, and response to treatment: a longitudinal study of pediatric subjects with newly diagnosed inflammatory bowel disease. *Genome Med* 8, 75 (2016). <https://doi.org/10.1186/s13073-016-0331-y>.
17. Deng F, Li Y, Zhao J. The gut microbiome of healthy long-living people. *Aging (Albany NY)*. 2019 Jan 15;11(2):289-290. doi: 10.18632/aging.101771. PMID: 30648974; PMCID: PMC6366966.
18. Hagerty SL, Hutchison KE, Lowry CA, Bryan AD. An empirically derived method for measuring human gut microbiome alpha diversity: Demonstrated utility in predicting health-related outcomes among a human clinical sample. *PLoS One*. 2020 Mar 2;15(3):e0229204. doi: 10.1371/journal.pone.0229204. PMID: 32119675; PMCID: PMC7051054.
19. Khanna S, Raffals LE. The Microbiome in Crohn's Disease: Role in Pathogenesis and Role of Microbiome Replacement Therapies. *Gastroenterol Clin North Am*. 2017 Sep;46(3):481-492. doi: 10.1016/j.gtc.2017.05.004. Epub 2017 Jul 19. PMID: 28838410.
20. Rashed R, Valcheva R, Dieleman LA. Manipulation of Gut Microbiota as a Key Target for Crohn's Disease. *Front Med (Lausanne)*. 2022 Jun 16;9:887044. doi: 10.3389/fmed.2022.887044. PMID: 35783604; PMCID: PMC9244564.
21. Parada Venegas D, De la Fuente MK, Landskron G, González MJ, Quera R, Dijkstra G, Harmsen HJM, Faber KN, Hermoso MA. Short Chain Fatty Acids (SCFAs)-Mediated Gut Epithelial and Immune Regulation and Its Relevance for Inflammatory Bowel Diseases. *Front Immunol*. 2019 Mar 11;10:277. doi: 10.3389/fimmu.2019.00277. Erratum in: *Front Immunol*. 2019 Jun 28;10:1486. PMID: 30915065; PMCID: PMC6421268.
22. Loh G, Blaut M. Role of commensal gut bacteria in inflammatory bowel diseases. *Gut Microbes*. 2012 Nov-Dec;3(6):544-55. doi: 10.4161/gmic.22156. Epub 2012 Oct 11. PMID: 23060017; PMCID: PMC3495792.
23. Pascal V, Pozuelo M, Borrueal N, Casellas F, Campos D, Santiago A, Martinez X, Varela E, Sarraibayrouse G, Machiels K, Vermeire S, Sokol H, Guarner F, Manichanh C. A microbial signature for Crohn's disease. *Gut*. 2017 May;66(5):813-822. doi: 10.1136/gutjnl-2016-313235. Epub 2017 Feb 7. PMID: 28179361; PMCID: PMC5531220.
24. Hitch, T.C.A., Hall, L.J., Walsh, S.K. et al. Microbiome-based interventions to modulate gut ecology and the immune system. *Mucosal Immunol* 15, 1095–1113 (2022). <https://doi.org/10.1038/s41385-022-00564-1>. <https://doi.org/10.1038/s41385-022-00564-1>.