



Your Microbiome Report

Comments

Your overall gut microbiome is variable compared to the American Gut Project reference dataset for 'healthy' individuals. Bacteroides and Alistipes were detected at higher abundance levels when compared to the average of Sun Genomics customers. Your Top 10 profile also detected an above average level of Alistipes. High levels of Alistipes are often associated with high fat diets (1). Faecalibacterium species were detected at low abundance levels in your profile. Lower levels of Faecalibacterium prausnitzii is known to be associated with Colitis (2). Harmful microbes Clostridioides, Streptococcus, Salmonella, Klebsiella, Serratia, and Pseudomonas were all detected at low levels. Sun Genomics will monitor these organisms on follow up testing.

Health and Nutrition Recommendations

Based off your comparison to healthy Americans and studies associating diet with abundance levels of specific gut microbes (1,2), your diet appears to contain high protein and high saturated fat with low fibrous vegetables. Provided there is no known allergy, we recommend increasing Faecalibacterium through the consumption of cruciferous vegetables such as broccoli, cauliflower and Brussels sprout. This will improve your healthy gut ratios.

References:

- 1) Singh et al., (2017). Influence of diet on the gut microbiome and implications for human health. *Journal of Translational Medicine*, 15. <https://doi.org/10.1186/s12967-017-1175-y>.
- 2) Wan et al., (2019). Effects of dietary fat on gut microbiota and faecal metabolites, and their relationship with cardiometabolic risk factors: a 6-month randomised controlled-feeding trial. *Gut*. doi:10.1136/gutjnl-2018-317609.

Probiotic Findings

We identified several probiotic strains in your profile. The level of abundance is the average (average-3) of Sun Genomics' customers. Key probiotic strain identified in your profile was Bifidobacterium. This Bifidobacterium organism possesses multiple catabolic pathways to metabolize complex oligosaccharides (starches) for carbon and energy. They also help to maintain a normal digestive tract, inhibits the growth of harmful bacteria, and also boost the immune system.

You were missing key probiotic strain of Streptococcus that is responsible for producing lactase, the enzyme required to break down lactose (the sugar in milk). They also collectively ferment carbohydrates in the gut, producing lactic acid which increases absorption of minerals such as calcium, copper, magnesium, and iron. You were also missing *A. muciniphila*, the most abundant mucolytic (mucus degrading) bacteria in a healthy individual. Also missing in your profile was key probiotic strains of *Lactobacillus* that are responsible for producing L-Lysine, an amino acid that supports protein absorption, hormone production, and boosts the immune system. Use Floré and let's boost your healthy microbiome!

Your Sun Genomics Score

The Sun Genomics Microbiome Score represents your overall gut balance from Dysbiosis (out of balance) to Symbiosis (in-balance). Upon retest, we will display your Microbiome Score trend and you will be able to track changes to your gut health.
Your Score: 49



Report Information

CUSTOMER NAME
Robert Stehlin

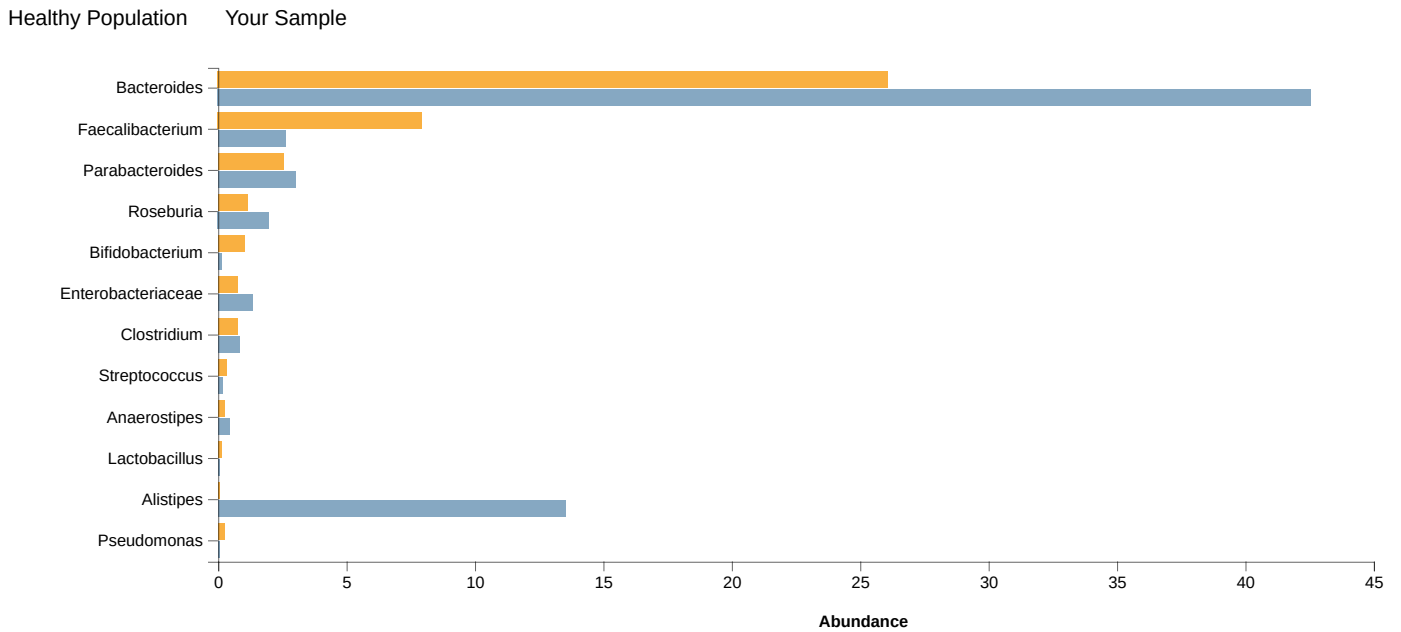
DATE RECEIVED
Aug 14, 2020

KIT ID
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SUN GENOMICS ID
SG003607

Your Gut Comparison

Your microbial relative abundance of key classes of organisms allows you to see how you stack up against an average of 10,000 participants in the American Gut Project that have been defined as 'healthy' from metrics such as Body Mass Index, cholesterol levels, and other biomarkers. These comparisons can help you understand what organisms may change with your diet, environment, geography, or other treatments you are taking.



Pseudomonas
 US Average Abundance: 0.234%
 Your Abundance: 0.06%

Anaerostipes
 US Average Abundance: 0.228%
 Your Abundance: 0.431%

Enterobacteriaceae
 US Average Abundance: 0.774%
 Your Abundance: 1.321%

Parabacteroides
 US Average Abundance: 2.556%
 Your Abundance: 3.019%

Alistipes
 US Average Abundance: 0.054%
 Your Abundance: 13.553%

Streptococcus
 US Average Abundance: 0.344%
 Your Abundance: 0.177%

Bifidobacterium
 US Average Abundance: 1.011%
 Your Abundance: 0.142%

Faecalibacterium
 US Average Abundance: 7.934%
 Your Abundance: 2.645%

Lactobacillus
 US Average Abundance: 0.154%
 Your Abundance: 0.096%

Clostridium
 US Average Abundance: 0.78%
 Your Abundance: 0.847%

Roseburia
 US Average Abundance: 1.149%
 Your Abundance: 2.006%

Bacteroides
 US Average Abundance: 26.116%
 Your Abundance: 42.558%



Your Top 10 Microbes

Bacteroides intestinalis

Microbe Type: beneficial
Abundance: 16.58%

Known to produce polyamines, which are organic molecules needed for animal cell growth and differentiation.

Average Abundance for Our Customers: 0.0% - 2.6%

Bacteroides stercoris

Microbe Type: neutral
Abundance: 5.26%

Isolated from human feces, *Bacteroides* species constitute the most abundant members of the intestinal microflora of mammals. Typically they are symbionts, but they can become opportunistic pathogens in the intra-abdominal cavity.

Average Abundance for Our Customers: 0.0% - 5.5%

Alistipes finegoldii

Microbe Type: variable
Abundance: 4.07%

Alistipes finegoldii has been isolated from cases of appendicitis and sepsis. This organism is usually isolated with in mixed culture with gastrointestinal bacteria and may be a member of the gastrointestinal tract microbial community.

Average Abundance for Our Customers: 0.0% - 3.9%

Alistipes shahii

Microbe Type: neutral
Abundance: 2.90%

This is a bile-resistant, pigment-producing bacterial species from human intestinal sources, from human specimens of intestinal origin. The habitat is probably the human gut.

Average Abundance for Our Customers: 0.0% - 1.5%

Alistipes putredinis

Microbe Type: variable
Abundance: 2.61%

Alistipes putredinis is a gram negative bacteria, formerly known as *Bacteroides putredinis*, and is commonly isolated from human feces and farm soil. This organism has also been isolated from cases of appendicitis, abdominal and rectal abscesses, and cases of foot rot in

Average Abundance for Our Customers: 0.0% - 3.5%

Bacteroides vulgatus

Microbe Type: variable
Abundance: 5.28%

Bacteroides vulgatus is among the most commonly isolated microbes from the human gastrointestinal tract, and it has been found to constitute part of the core gut microbiota in healthy humans.

Average Abundance for Our Customers: 0.0% - 12.8%

Bacteroides caccae

Microbe Type: variable
Abundance: 5.24%

This is a normal resident of the healthy human gut microbiome. However, this organism is also a pathogenic factor in inflammatory bowel disease (IBD)

Average Abundance for Our Customers: 0.0% - 3.4%

Blautia obeum

Microbe Type: beneficial
Abundance: 2.95%

Found in the gut, anaerobe. Plays an important role in the recovery process from *V. cholerae* infection and microbiota maturation in children.

Average Abundance for Our Customers: 0.0% - 1.5%

Bacteroides fragilis

Microbe Type: variable
Abundance: 2.80%

Bacteroides fragilis is a non-spore-forming obligate anaerobe that is part of the normal enteric flora. Some enterotoxin-secreting strains have been associated with diarrhea in piglets, calves, lambs, foals, and humans.

Average Abundance for Our Customers: 0.0% - 6.7%

Faecalibacterium prausnitzii

Microbe Type: beneficial
Abundance: 2.55%

Bacteria of the human gut microbiota.

Average Abundance for Our Customers: 1.4% - 12.8%



Your Probiotics

Bifidobacterium longum

Microbe Type: probiotic

Abundance: 0.11%

It's one of the most important inhabitants in the human body. This bacterium is very helpful because it maintains a normal digestive tract, inhibits the growth of harmful bacteria, and also boosts the immune system

Average Abundance for Our Customers: 0.0% - 5.1%

Lactococcus lactis

Microbe Type: probiotic

Abundance: 0.01%

Lactococcus lactis is used widely for industrial production of fermented dairy products such as milk, cheese, and yogurt. It helps digestion and encourages a normal gut environment, especially helping to defend against leaky gut.

Average Abundance for Our Customers: 0.0% - 0.2%

Oxalobacter formigenes

Microbe Type: probiotic

Abundance: 0.07%

Oxalobacter formigenes is an obligate anaerobe that depends exclusively on oxalate metabolism for energy, and it colonizes the GI tracts of most vertebrate animals, including humans, helping to prevent hyperoxaluria and disorders such as the development of kidney stones.

Average Abundance for Our Customers: 0.0% - 0.1%



Beneficial Microbes

Bacteroides intestinalis

Microbe Type: beneficial

Abundance: 16.58%

Known to produce polyamines, which are organic molecules needed for animal cell growth and differentiation.

Average Abundance for Our Customers: 0.0% - 2.6%

Faecalibacterium prausnitzii

Microbe Type: beneficial

Abundance: 2.55%

Bacteria of the human gut microbiota.

Average Abundance for Our Customers: 1.4% - 12.8%

Roseburia hominis

Microbe Type: beneficial

Abundance: 0.66%

Roseburia hominis is one of the most numerous Firmicutes in the human gut. A significant decrease of *R. hominis* colonization in the gut of ulcerative colitis patients has been demonstrated.

Average Abundance for Our Customers: 0.0% - 0.8%

Coprococcus eutactus

Microbe Type: beneficial

Abundance: 0.34%

Anaerobic bacterium isolated from human feces.

Average Abundance for Our Customers: 0.0% - 1.2%

Clostridium citroniae

Microbe Type: beneficial

Abundance: 0.23%

Clostridium citroniae is a species in the *C. clostridioforme* group. It has been isolated from clinical specimens. Part of the human intestinal flora

Average Abundance for Our Customers: 0.0% - 0.2%

Blautia obeum

Microbe Type: beneficial

Abundance: 2.95%

Found in the gut, anaerobe. Plays an important role in the recovery process from *V. cholerae* infection and microbiota maturation in children.

Average Abundance for Our Customers: 0.0% - 1.5%

Bacteroides uniformis

Microbe Type: beneficial

Abundance: 2.28%

Bacteroides uniformis is part of the normal human gut flora. They assist in breaking down food and producing valuable nutrients and energy that the body needs.

Average Abundance for Our Customers: 0.0% - 8.0%

Eubacterium hallii

Microbe Type: beneficial

Abundance: 0.39%

This species was isolated from feces from a healthy adult human. The abundance of *Eubacterium hallii* in the colonic ecosystem suggests that these bacteria play important roles in preventing lactate accumulation.

Average Abundance for Our Customers: 0.0% - 0.6%

Blautia wexlerae

Microbe Type: beneficial

Abundance: 0.26%

Present in human feces with high frequency as the dominant bacteria. May assist in the digestion of complex carbohydrates.

Average Abundance for Our Customers: 0.0% - 1.6%

Bacteroides finegoldii

Microbe Type: beneficial

Abundance: 0.16%

Rod bacteria that occurs in human feces, contains species that maintain a beneficial relationship with the host when retained in the gut. helps maintain healthy stool and gut microbiome. Possibly plays a role in maintaining a healthy colon and potentially act as a possible probiotic to

Average Abundance for Our Customers: 0.0% - 1.0%



Unfavorable Microbes

Clostridioides difficile

Microbe Type: harmful

Abundance: 0.68%

Causes symptoms ranging from diarrhea to life threatening inflammation of the colon. Illness typically occurs after antibiotic use. Small number of people carry the bacteria in their large intestine but don't have ill effects from it.

Average Abundance for Our Customers: 0.0% - 1.9%

Salmonella enterica

Microbe Type: harmful

Abundance: 0.06%

Salmonella enterica is the causative agent of a spectrum of diseases, including enteric fever (typhoid) and self-limiting gastroenteritis, and remains a significant food-borne pathogen throughout both developed and developing countries.

Average Abundance for Our Customers: 0.0% - 2.7%

Serratia marcescens

Microbe Type: harmful

Abundance: 0.03%

Serratia marcescens is an opportunistic human pathogen that can be associated with hospital-acquired infections. It is an environmental organism that has a broad host range, and is capable of infecting vertebrates and invertebrates, as well as plants. In humans, *Serratia*

Average Abundance for Our Customers: 0.0% - 0.5%

Streptococcus agalactiae

Microbe Type: harmful

Abundance: 0.06%

This organism is the leading cause of meningitis and sepsis in newborns. Additionally this organism is the cause of serious infections in immunocompromised adults. Clinical manifestations of infection include urinary tract and soft tissue infections as well as life-threatening sepsis

Average Abundance for Our Customers: 0.0% - 0.1%

Klebsiella pneumoniae

Microbe Type: harmful

Abundance: 0.04%

Has the ability to colonize many sites of the body and cause a wide range of infections including pneumonias and urinary tract infections.

Average Abundance for Our Customers: 0.0% - 4.3%

Pseudomonas aeruginosa

Microbe Type: harmful

Abundance: 0.02%

Pseudomonas aeruginosa is an opportunistic human pathogen that rarely infects healthy individuals. On the contrary, immunocompromised patients, like burn victims, AIDS-, cancer- or cystic fibrosis-patients have a higher risk of infection.

Average Abundance for Our Customers: 0.0% - 9.1%



Neutral Microbes

Bacteroides stercoris

Microbe Type: neutral
Abundance: 5.26%

Isolated from human feces. *Bacteroides* species constitute the most abundant members of the intestinal microflora of mammals. Typically they are symbionts, but they can become opportunistic pathogens in the intra-abdominal cavity.

Average Abundance for Our Customers: 0.0% - 5.5%

Oscillibacter sp. ER4

Microbe Type: neutral
Abundance: 2.12%

Group of uncharacterized isolates of *Oscillibacter*

Average Abundance for Our Customers: 0.0% - 1.5%

Clostridiales bacterium KLE1615

Microbe Type: neutral
Abundance: 1.41%

Group of uncharacterized isolates of Clostridiales

Average Abundance for Our Customers: 0.0% - 1.4%

Butyrivibrio crossotus

Microbe Type: neutral
Abundance: 0.96%

bacteria commonly isolated from the gastrointestinal tract of mammals.

Average Abundance for Our Customers: 0.0% - 1.9%

Parabacteroides sp. 20_3

Microbe Type: neutral
Abundance: 0.85%

Group of uncharacterized isolates of *Parabacteroides*

Average Abundance for Our Customers: 0.0% - 1.0%

Alistipes shahii

Microbe Type: neutral
Abundance: 2.90%

This is a bile-resistant, pigment-producing bacterial species from human intestinal sources, from human specimens of intestinal origin. The habitat is probably the human gut.

Average Abundance for Our Customers: 0.0% - 1.5%

Alistipes onderdonkii

Microbe Type: neutral
Abundance: 1.55%

Isolated from human specimens (intestine and urine). The habitat is probably the human gut.

Average Abundance for Our Customers: 0.0% - 1.1%

Fusicatenibacter saccharivorans

Microbe Type: neutral
Abundance: 1.05%

Fusicatenibacter saccharivorans is part of the human gut microbiota.

Average Abundance for Our Customers: 0.0% - 3.0%

Bacteroides pectinophilus

Microbe Type: neutral
Abundance: 0.85%

Bacteroides pectinophilus was isolated from human feces. Bacteria from the human intestinal tract

Average Abundance for Our Customers: 0.0% - 0.3%

Roseburia inulinivorans

Microbe Type: neutral
Abundance: 0.83%

Roseburia inulinivorans contributes to butyrate formation from a variety of dietary polysaccharide substrates in the human large intestine.

Average Abundance for Our Customers: 0.0% - 2.1%



Variable Microbes

Bacteroides vulgatus

Microbe Type: variable
Abundance: 5.28%

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Average Abundance for Our Customers: 0.0% - 3.5%

Enterococcus faecium

Microbe Type: variable
Abundance: 1.25%

Enterococcus faecium is a gut commensal of many mammals but is also recognized as a major nosocomial human pathogen.

Average Abundance for Our Customers: 0.0% - 1.1%

Eisenbergiella tayi

Microbe Type: variable
Abundance: 0.89%

Seems to be associated with bacteremia. The presence of *E. tayi* in the human gastrointestinal tract suggests that bacteremia might be caused by bacterial translocation, a phenomenon in which live bacteria cross the intestinal barrier.

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Average Abundance for Our Customers: 0.0% - 3.4%

Bacteroides fragilis

Microbe Type: variable
Abundance: 2.80%

Bacteroides fragilis is a non-spore-forming obligate anaerobe that is part of the normal enteric flora. Some enterotoxin-secreting strains have been associated with diarrhea in piglets, calves, lambs, foals, and humans.

Average Abundance for Our Customers: 0.0% - 6.7%

Eubacterium eligens

Microbe Type: variable
Abundance: 1.98%

Eubacterium eligens is a member of the normal human gut microflora. *Eubacterium* spp. are thought to play a beneficial role in maintaining the normal ecology of the large intestine, in part by producing chemicals like butyric acid which act to inhibit the growth of other bacteria. These

Average Abundance for Our Customers: 0.0% - 3.9%

Escherichia coli

Microbe Type: variable
Abundance: 1.15%

Most *E. coli* strains are harmless but some can cause food poisoning. Harmless strains are part of the normal flora of the gut and can benefit the host by producing vitamin k2 and by preventing the establishment of pathogenic bacteria.

Average Abundance for Our Customers: 0.0% - 16.2%

Bacteroides dorei

Microbe Type: variable
Abundance: 0.87%

Bacteroides dorei was isolated from human feces. *Bacteroides dorei* plays an important role in the normal function of the intestinal system of both human and animal species. Along with many beneficial functions, it come with a few pathogenic functions that could take place as well.

Average Abundance for Our Customers: 0.0% - 5.1%

This test is performed under GLP processing standards. The performance of the probes, reagents, and instruments has been determined by Sun Genomics and its partners. Testing is limited to verification of the microbes contained within our database and identifications outside of database assignments is outside the scope of this test. This test has not been reviewed by the US Food & Drug Administration. However the FDA has determined that such clearance or approval is not necessary for research use only.

This report is generated for: Robert Stehlin

