tinyhealth

Gut Health Test Report

The attached results are from the Gut Health microbiome test. This test uses shotgun metagenomic sequencing to identify all microbes (i.e., bacteria, viruses, fungi, archaea) present during sampling.

This microbiome report is intended to be used exclusively for wellness purposes and to educate you about the microbes in your body. This test is not intended to diagnose or treat disease, nor is it a substitute for a physician's consultation. The microbes referenced in your report and their associations are based on emerging scientific research. These insights were determined by evaluating current research and may change over time to reflect the most up-to-date research available.

About Tiny Health

Tiny Health provides at-home gut microbiome testing for all ages and vaginal microbiome testing for ages 18 and older, with specific insights tailored for each phase of life: infants, toddlers, children, and adults. We also have specific insights for those who are pregnant or trying to conceive.

Tiny Health metrics are based on tens of thousands of samples reflecting both publicly available reference samples and proprietary Tiny Health customer data.

About our technology

This test uses shotgun metagenomic sequencing, the gold standard in microbiome research. Our report produces a comprehensive, high resolution picture of the microbiome compared to more traditional PCR tests, which are limited to a subset of microbes, or 16S methods, which have limited resolution.

All our tests are processed in a CLIA-certified lab using customized, proprietary technology. With strain-level precision, our test can detect over 120,000 microbes (i.e., bacteria, viruses, fungi, archaea, and many parasites) commonly found in gut and vaginal microbiomes.

For practitioners

We're building a community of practitioners who want to help patients understand the root cause of symptoms and conditions and be supported by the latest evidence-based microbiome research.

If you want to access our practitioner resources or have any questions for our scientific and clinical team, please contact us at practitioners@tinyhealth.com.

www.tinyhealth.com
www.poweredbytiny.com

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GUT HEALTH TEST
6104 Old Fredericksburg RD #91622
Austin, TX 78749

Patient name: Levi Heller
DOB: July 2, 2020
Sex: Male

Kit ID: VCJ143
System version: 4.8.1

Sample Collected: May 21, 2025
Sequence Sample Received: June 2, 2025
Sequence Results Ready: June 19, 2025
Report Generated: February 4, 2026

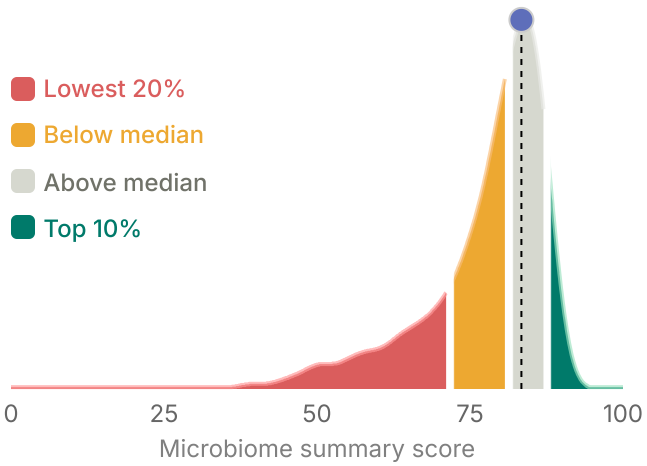
Microbiome Summary Score

Your Microbiome Summary Score (0-100) combines key microbiome metrics for your age range into a single number. Higher scores indicate better microbiome health.

We analyze factors like beneficial bacteria and opportunistic pathogens, then compare your results to samples from your age group (using public data and proprietary data from Tiny Health customers).

Your percentile shows where you rank. Example: 41st percentile means 41% of those tested scored lower than you, 59% scored higher.

Note: PRO stool chemistry and Beta metrics aren't included. Scores for pregnant women are calculated separately and should only be compared to other pregnant scores.



Tiny Health Lab Director: Carlos J Ruiz, MD • CLIA ID: 21D2062464

Sample at a glance

3 Needs support 1 Needs improvement

Metabolic Health
- Akkermansia 5.308%

Opportunistic Pathogens
- Staphylococcus 0.015%

Complex Sugar Digestion Capacity
- Xylooligosaccharides ..... 184 rpkm

Overabundant Species
- Akkermansia 5.308%

Results Summary

	Metrics	Clinical indication examples
Beneficial microbes	Beneficial Bifidobacterium Metabolic Health Anti-inflammatory Markers Common Probiotic Species	• Prebiotics / probiotics support • Review Akkemansia promoting supplements • Track and diversify fiber intake • Increase fermented foods • Move and stay physically active
Disruptive microbes	Antibiotic Resistance Signature Opportunistic Pathogens Potential Stomach Inflammation Parasites and Infection Potential Fungal Overgrowth Methane Production	• Potential anti-microbial support (e.g., herbs) • Prebiotics / probiotics support • Close monitoring post-antibiotics to track recovery • Nutritional support and therapeutic diet (e.g., AIP, candida diet, etc) • Review symptoms/conditions • Consider additional testing (e.g., SIBO, OAT, nutritional labs etc)
Gut barrier & inflammation	Mucus Degradation Index Hexa-LPS Index Hydrogen Sulfide Index Host DNA	
Short-chain fatty acids	Butyrate Capacity Propionate Capacity Acetate Capacity	• Track and diversify fiber intake • Prebiotics / probiotics / postbiotics support • Increase fermented foods • Supportive nutraceuticals (butyrate supplements, spore-based probiotics) • Detoxification supports (calcium d-glucarate, broccoli sprouts, DIM)
Digestive capacity	Fiber Digestion Capacity Complex Sugar Digestion Capacity Protein Breakdown Capacity Vitamin Production Capacity	
Diversity & resilience	Microbiome Diversity Overabundant Species Gut Resilience Score Oral Microbes in the Gut Major Bacterial Phyla Common Microbiome Members Gut Ratio	

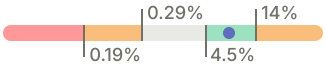
Microbial enzymes & metabolites	Histamine-producing Species Complex Compound Breakdown Microbial GABA Capacity Modified Bile Acid Production Capacity Mitochondrial Health Support

Detailed Gut Health Test Results

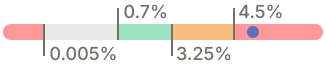
Legend: (p) Phylum (f) Family (g) Genus (sp) Species

Beneficial microbes

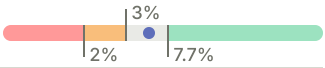
Beneficial Bifidobacterium

Bifidobacterium (g)	8.477%	
Bifidobacterium adolescentis (sp)	2.423%	
Bifidobacterium bifidum (sp)	2.066%	
Bifidobacterium breve (sp)	0.063%	
Bifidobacterium gallinarum (sp)	0.239%	
Bifidobacterium longum (sp)	2.975%	
Bifidobacterium pseudocatenulatum (sp)	0.583%	

Metabolic Health

Akkermansia (g)	5.308%	
Akkermansia muciniphila (sp)	5.301%	

Anti-inflammatory Markers

Faecalibacterium (g)	5.357%	
Faecalibacterium prausnitzii (sp)	0.193%	
Faecalibacterium prausnitzii_C (sp)	0.192%	
Faecalibacterium prausnitzii_D (sp)	4.356%	
Faecalibacterium prausnitzii_G (sp)	0.265%	
Faecalibacterium prausnitzii_I (sp)	0.077%	
Faecalibacterium prausnitzii_J (sp)	0.078%	
Faecalibacterium sp900539885 (sp)	0.067%	

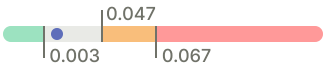
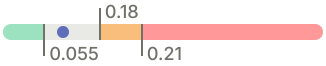
Faecalibacterium sp900758465 (sp)	0.060%

Common Probiotic Species

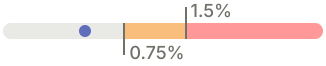
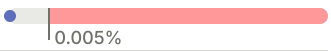
Bifidobacterium (g)	8.477%
Lactobacillaceae (f)	0.088%
Lacticaseibacillus rhamnosus (sp)	0.009%
Limosilactobacillus reuteri (sp)	0.030%
Lactiplantibacillus plantarum (sp)	0.006%
Bifidobacterium infantis (sp)	0.045%
Bifidobacterium bifidum (sp)	2.066%
Bifidobacterium longum (sp)	2.975%
Bifidobacterium breve (sp)	0.063%
Bifidobacterium animalis (sp)	0.030%
Bifidobacterium adolescentis (sp)	2.423%
Streptococcus thermophilus (sp)	0.078%

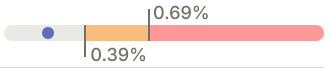
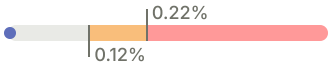
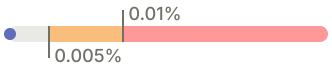
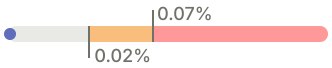
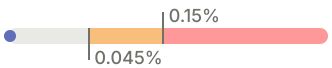
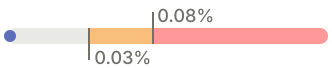
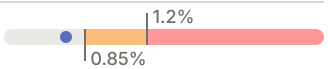
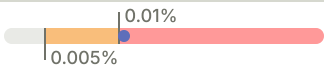
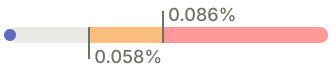
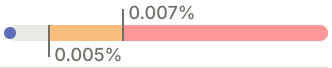
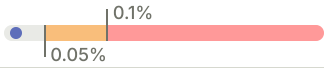
Disruptive microbes

Antibiotic Resistance Signature

Abundance index	0.01	
Richness index	0.09	

Opportunistic Pathogens

Enterobacteriaceae (f)	0.017%	
Klebsiella (g)	0.000%	
Klebsiella pneumoniae (sp)	0.000%	
Klebsiella oxytoca (sp)	0.000%	
Salmonella enterica (sp)	0.000%	

Escherichia coli (sp)	0.014%	
Escherichia flexneri (sp)	0.000%	
Escherichia dysenteriae (sp)	0.000%	
Citrobacter (g)	0.000%	
Enterobacter (g)	0.000%	
Morganella (g)	0.000%	
Raoultella (g)	0.000%	
Streptococcus (g)	0.410%	
Streptococcus salivarius (sp)	0.087%	
Streptococcus sp001556435 (sp)	0.253%	
Staphylococcus (g)	0.015%	
Pseudomonas aeruginosa (sp)	0.000%	
Haemophilus influenzae (sp)	0.000%	
Haemophilus parainfluenzae (sp)	0.000%	
Enterococcus faecium (sp)	0.000%	
Enterococcus faecalis (sp)	0.000%	
Clostridioides difficile (sp)	0.000%	
Clostridium perfringens (sp)	0.013%	
Acinetobacter baumannii (sp)	0.000%	
Campylobacter (g)	0.000%	
Potential Stomach Inflammation		
Helicobacter pylori (sp)	0.000%	
Parasites and Infection		
Blastocystis (g)	0.000%	

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Cryptosporidium (g)	0.000%	0.005%
Entamoeba histolytica (sp)	0.000%	0.005%
Entamoeba dispar (sp)	0.000%	0.005%
Giardia (g)	0.000%	0.005%
Yersinia enterocolitica (sp)	0.000%	0.005%
Vibrio (g)	0.000%	0.005%
Vibrio cholerae (sp)	0.000%	0.005%
Cyclospora cayetanensis (sp)	0.000%	

Potential Fungal Overgrowth

Aspergillus (g)	0.000%	0.005%
Cryptococcus (g)	0.000%	0.005%
Saccharomyces (g)	0.000%	0.5%
Rhodotorula (g)	0.000%	0.005%
Saprochaete (g)	0.000%	0.005%
Malassezia (g)	0.000%	0.005%
Microsporum (g)	0.000%	0.005%
Trichophyton (g)	0.000%	0.005%
Candida (g)	0.000%	0.005%

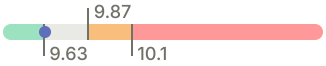
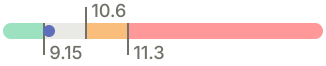
Methane Production

Methanobrevibacter smithii (sp)	0.000%	0.005%
Methane production capacity	0.00 rpkm	0.1

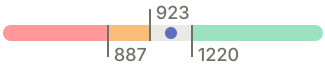
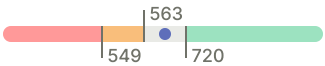
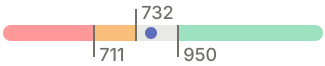
Gut barrier & inflammation

Mucus Degradation Index

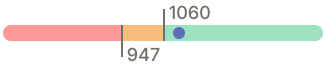
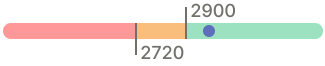
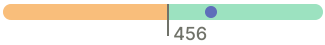
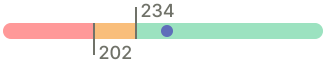
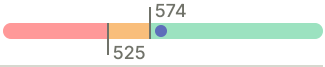
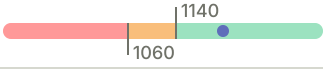
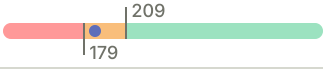
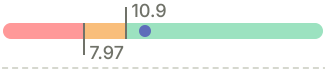
Mucus degradation index	9.31	8.57 11.5 12.2

Hexa-LPS Index		
Hexa-LPS index	9.63	
Hydrogen Sulfide Index		
Hydrogen sulfide index	9.18	
Host DNA		
Host DNA	0.063%	

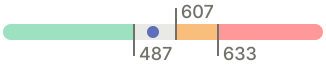
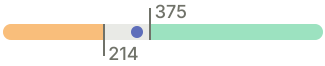
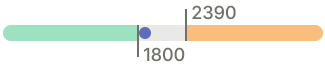
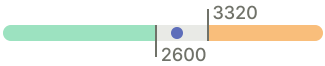
Short-chain fatty acids

Butyrate Capacity		
Butyrate	1051.28 rpkm	
Propionate Capacity		
Propionate	635.10 rpkm	
Acetate Capacity		
Acetate	792.18 rpkm	

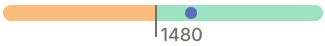
Digestive capacity

Fiber Digestion Capacity		
Cellulose	1211.55 rpkm	
Resistant starch	3509.95 rpkm	
Chitin	603.92 rpkm	
Pectin	348.52 rpkm	
Complex Sugar Digestion Capacity		
Fructooligosaccharides	646.73 rpkm	
Galactooligosaccharides	1703.68 rpkm	
Xylooligosaccharides	184.16 rpkm	
Isomaltooligosaccharides	26.31 rpkm	

Protein Breakdown Capacity

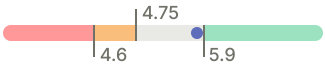
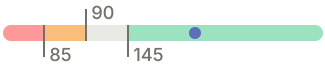
Protein breakdown	532.64 rpkm	
Indole-3-propionic acid	328.89 rpkm	
Trimethylamine	0.00 rpkm	
Ammonia	1844.80 rpkm	
Branched Chain Amino Acids	2853.96 rpkm	

Vitamin Production Capacity

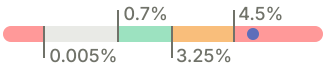
Vitamin B2	972.10 rpkm	
Vitamin B7	435.28 rpkm	
Vitamin B9	327.15 rpkm	
Vitamin B12	1907.90 rpkm	
Vitamin K	268.69 rpkm	

Diversity & resilience

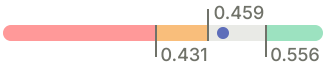
Microbiome Diversity

Shannon diversity	5.75	
Species richness	423.00 species	

Overabundant Species

Akkermansia (g)	5.308%	
Akkermansia muciniphila (sp)	5.301%	

Gut Resilience Score

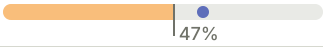
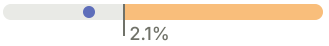
Gut resilience score	0.48	

Oral Microbes in the Gut

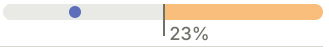
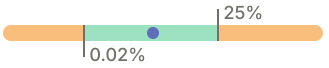
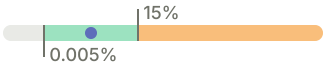
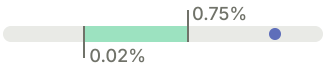
Oral microbes	0.023%	

Major Bacterial Phyla

Bacteroidota (p)	22.743%	

Firmicutes (p)	55.924%	
Actinobacteriota (p)	15.155%	
Proteobacteria (p)	0.824%	
Fusobacteriota (p)	0.000%	

Common Microbiome Members

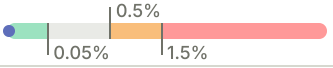
Bacteroides (g)	6.036%	
Bacteroides fragilis (sp)	0.006%	
Prevotella (g)	2.317%	
Ruminococcus (g)	7.041%	
Ruminococcus gnavus (sp)	0.151%	
Blautia (g)	9.696%	
Roseburia (g)	0.399%	
Phocaeicola dorei (sp)	0.065%	

Gut Ratio

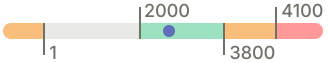
Firmicutes / Bacteroidota ratio	2.46	
Proteobacteria / Actinobacteriota ratio	0.05	
Prevotella / Bacteroides ratio	0.00	

Microbial enzymes & metabolites

Histamine-producing Species

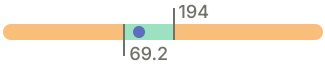
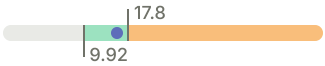
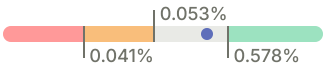
Histamine-producing species	0.000%	

Complex Compound Breakdown

Beta-glucuronidase capacity	2601.94	

Microbial GABA Capacity

GABA production	42.47 rpkm	

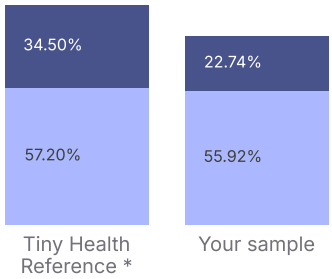
GABA breakdown	0.00 rpkm	
Modified Bile Acid Production Capacity		
Unconjugated bile acids	99.62 rpkm	
Secondary bile acids	15.50 rpkm	
Mitochondrial Health Support		
Urolithin-producing species (sp)	0.420%	

Major Microbial Members & Ratios

Common Bacterial Phyla

Firmicutes	55.92%	47%
Fusobacteriota	0.00%	
Bacteroidota	22.74%	
Proteobacteria	0.82%	2.1%
Actinobacteriota	15.15%	1.6%

Gut Ratio

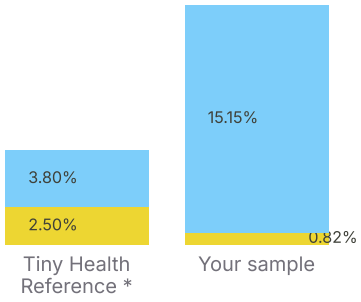


Firmicutes:Bacteroidota Ratio

2.46 (Ideally <30)

Firmicutes and Bacteroidota are the two largest phyla that make up the gut microbiome in humans. Historically and primarily in 16S studies, the ratio of Firmicutes/Bacteroidota has been associated with a number of conditions in adults, including obesity, Type 2 Diabetes, and inflammation. However, the use of these markers is now considered dated by current microbiome researchers, and the validity of these associations has been called into question.

Firmicutes Bacteroidota

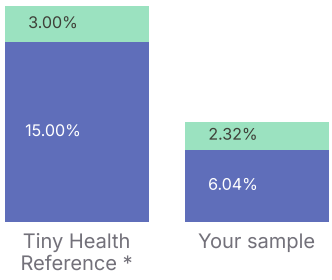


Proteobacteria:Actinobacteriota Ratio

0.05 (Ideally <14)

Aside from Firmicutes and Bacteroidota, Proteobacteria and Actinobacteriota are two common phyla in the gut microbiome in humans. Proteobacteria are widely associated with pathogens, while Actinobacteriota are associated with commensal species. Historically in primarily 16S studies, the ratio of Proteobacteria:Actionbacteriota has been associated with gut inflammation. However, the use of these markers is now considered dated by current microbiome researchers, and the validity of these associations has been called into question.

Proteobacteria Actinobacteriota



Prevotella:Bacteroides Ratio

0.00 (Ideally >4)

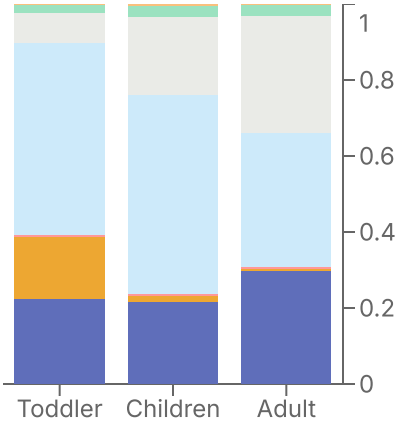
Prevotella and Bacteroides are two common genera in the gut microbiome in humans. One or the other often dominates the gut microbiome, and can define the Gut Type. Prevotella are widely associated with a high fiber diet, while Bacteroides are associated with a diet high in fat and protein. Historically in primarily 16S studies, the ratio of Prevotella:Bacteroides has been associated with body weight, fat loss, and diet success. However, the use of these markers is now considered dated by current microbiome researchers, and the validity of these associations has been called into question.

Bacteroides Prevotella

*Tiny Health Reference: This represents a cohort that is free of any acute or chronic conditions, so they may be considered a "healthy" cohort

Gut Type

Bacteroides	18.37%
Ruminococcaceae	13.22%
Prevotella	2.32%
Lachnospiraceae	24.04%
Enterobacteriaceae	0.02%
Bifidobacterium	8.48%
Other	33.54%



These bars represent the proportion of the different gut types in our database for different age ranges.

The gut type of a sample is determined by the dominant type of microbe in that sample.

Type Other

We classified this gut type as 'Other' because it doesn't fit well in the other types. Instead of being dominated by *Bacteroides*, *Prevotella*, *Ruminococcaceae*, *Lachnospiraceae*, or *Bifidobacterium*, the 'Other' gut type has higher levels of a variety of species.

Having this gut type is not a bad thing; in fact, its high diversity may be beneficial for gut health. As microbiome research continues, we may be able to give you more insights about this gut type.

Microbiome Breakdown

- **Beneficial:** These support microbiome health and overall health.
- **Unfriendly:** Low levels of these microbes are expected. Higher levels for extended periods of time can cause issues. This should make up a minority of the microbiome, kept in check by beneficial and variable microbes. Any unfriendly microbes out of range will be flagged in the "Detailed Gut Health Test Results" section above.
- **Variable:** These can be beneficial or unfriendly depending on their levels and what other microbes are around them. Lower levels are usually ok, and higher levels can cause issues.
- **Unknown:** These are lesser known microbes. Not enough is known to classify them as beneficial, unfriendly or variable at this time.

Your breakdown

Beneficial 61% Variable 26% Unfriendly 0% Unknown 12%

Top 20 species

Metric	Result	Description
Phocaeicola vulgatus	9.692%	*P. vulgatus* is one of the most abundant bacteria in the human gut, detected very early in babies. People with cardiovascular disease have low levels of *P. vulgatus* which could indicate it is a beneficial bacterium. But women with polycystic ovary syndrome have high levels of it. And *P. vulgatus* has been associated with Crohn's disease and ulcerative colitis, although the effects depend on the strain. Also, when in high numbers throughout the first two years of life, it may contribute to the development of Type 1 diabetes.
Akkermansia muciniphila	5.301%	*A. muciniphila* is a beneficial species that helps maintain the gut barrier and keeps your metabolism in check. Your gut lining includes a mucus layer. This is an organized network of proteins that acts as the first line of defense for your gastrointestinal system. *A. muciniphila* manages your mucus layer, both consuming old mucus and helping you make more. *A. muciniphila* also plays a role in regulating your metabolism. Interestingly, *A. muciniphila* is being investigated as a treatment for obesity and type 2 diabetes. However, too much *Akkermansia* could mean excess mucus production. In babies, very high levels have been associated with eczema.
Fusicatenibacter saccharivorans	5.190%	*F. saccharivorans* is a beneficial bacterium that produces short-chain fatty acids and promotes the production of anti-inflammatory molecules. People with active ulcerative colitis or rheumatoid arthritis have low levels of *F. saccharivorans*.

● Faecalibacterium prausnitzii_D	4.356%	Common in many healthy microbiomes, *F. prausnitzii* is a beneficial species. These bugs are known for curbing inflammation, keeping your gut healthy, and protecting you from disease. These bacteria produce a special molecule called butyrate. It plays a role in supporting immune system function and the structural integrity of your gut. Low *F. prausnitzii* counts are linked to type 2 diabetes, obesity and a handful of gut-related conditions. All the more reason to show these friendly partners some love.
● Blautia_A massiliensis	3.770%	*B. massiliensis* was first isolated from human feces in 2017. Although most *Blautia* species are known to contribute to a healthy gut this one may have a different role. One study showed that a plant-based diet increased the levels of *Blautia obeum* and *Blautia faecis*. Instead, the levels of *B. massiliensis* decreased. Therefore, it may be that *B. massiliensis* is not as fond of fiber as other *Blautia* species.
● Bacteroides uniformis	3.627%	Lots of healthy people have *B. uniformis* in their gut. This bacterium is very good at digesting a wide range of plant-based foods. It has anti-inflammatory properties that keep your gut healthy. It may also have a role in reducing binge eating and anxiety. Breastfeeding is a good way to boost *B. uniformis* levels in babies.
● Ruminococcus_D bicirculans	3.539%	*R. bicirculans* are common members of the gut microbiome. They contribute to gut health by breaking down fiber and producing acetate, a beneficial short-chain fatty acid. One of their favorite fibers to digest is that of barley.
● Bifidobacterium longum	2.975%	*B. longum* can be passed from mom to baby through vaginal birth or breastfeeding. It can live in the baby's gut up to 6 months of age; but it can stay for longer if acquired early in life. While it can use breast milk sugars (HMOs) as its only energy source; *B. bifidum* also likes to eat carbohydrates typical of an adult diet. This is why it is often found in the adult gut. Studies have shown that *B. longum* can improve physical performance, bowel movements, and body weight. In children, high numbers of this species may contribute to constipation. In turn, low numbers of this bug have been associated with celiac disease and childhood obesity.
● Collinsella sp902362275	2.946%	This is a newly detected species of *Collinsella* so we don't know much about it. *Collinsella* are variable bacteria in your gut. One of the great benefits they provide to gut health is the production of butyrate. And one study found that for some people, high levels of *Collinsella* may contribute to recovery from COVID. However, some studies suggest that *Collinsella* may also have a role in metabolic disorders. For some babies, having high levels of *Collinsella* before 6 months of age may predict higher adiposity later in toddlerhood. Compared to healthy adults, some adults with type 2 diabetes or with high cholesterol have higher levels of *Collinsella*. And for some overweight pregnant women, *Collinsella* levels positively correlate with insulin levels.

● Bifidobacterium adolescentis	2.423%	*B. adolescentis* can be passed from mom to baby through vaginal birth or breastfeeding. While it can be found in the baby's gut, it is more common in adults. Why? *B. adolescentis* prefers to eat carbohydrates typical of an adult diet. In fact, it can help you digest foods high in resistant starch, like oats and beans. Low levels of this bug have been associated with Type 1 diabetes. Another advantage is its production of GABA, a compound that helps us sleep well, have a good mood, and better cognition. Having *B. adolescentis* could also promote a longer life, as it has been detected in people over 100 years old.
● Ruminococcus_E bromii_B	2.393%	*Ruminococcus bromii* are beneficial bacteria that can be present in high levels in healthy humans. They are more prevalent in the adult gut [3] but can also be present in children and babies. Helpful in small numbers, these bugs break down starches and fiber from your food that you can't digest on your own. This gives you and other bacteria in your gut the energy you need. Also, this species may be protective against allergies. Luckily, it's easy to keep your *R. bromii* happy. Focus on eating plenty of fiber from plant-based foods.
● Blautia_A wexlerae	2.141%	*B. wexlerae* is one of the most abundant *Blautia* species in humans. Along with a healthy diet high in fiber, it may contribute to healthy metabolism. High levels of *B. wexlerae* may protect against obesity, insulin resistance, eczema and inflammation.
● Prevotella copri	2.085%	*P. copri* is one the most common species in the gut. Its role in health is not quite clear. Some studies have associated *P. copri* with better blood sugar metabolism and protection from food allergy.However, high numbers of this bug in babies may contribute to development of respiratory allergies later in life. Other research indicates that high amounts of *P. copri* are linked to rheumatoid arthritis, insulin resistance, and diabetes.
● Bifidobacterium bifidum	2.066%	*B. bifidum* can be passed from mom to baby through vaginal birth or breastfeeding. It can also be acquired from the environment. It is very common in breastfed babies. Adults can also have it, but at lower abundance. Most strains of *B. bifidum* can digest breastmilk sugars (HMOs) and like to share the leftovers with other microbes. This species is often used as a probiotic to help with eczema and allergies. But its benefits might be more, as laboratory studies have shown it can fight bad bacteria regulate the immune response and protect the gut during severe diarrhea.
● Gemmiger qucibialis	1.907%	*Gemmiger* bacteria are generally friendly members of the gut microbiome. Scientists don't know enough about *G. qucibialis* to tell you anything about it. But other members of this genus are beneficial, and no association between high levels of *Gemmiger* and bad health has been reported. So, we classified *G. qucibialis* as beneficial. We'll keep track of new research and let you know if there is anything to worry about *G. qucibialis*.

Parabacteroides merdae	1.870%	*Parabacteroides merdae*, previously known as *Bacteroides merdae* are a variable species found in the human gut. This means this species can either disrupt your health or benefit it. Some studies have associated high numbers of *P. merdae* to a variety of health conditions, such as: • Ulcerative colitis • Cardiovascular disease • Parkinson's disease On the good side, *P. merdae* has been associated with longevity. Luckily, having *P. merdae* in your gut isn't much of a concern unless its populations grow out of balance.
Anaerobutyricum hallii	1.675%	*Anaerobutyricum hallii* (previously known as *Eubacterium hallii*) are beneficial bacteria that produce the short-chain fatty acids known as butyrate and propionate. These friendly bugs have been detected in little ones and grown ups. Their levels increase in the first years of life and remain stable from childhood and into adulthood. About 74% of healthy adults have *A. hallii* in their gut. Animal experiments have shown that *A. hallii* can improve insulin sensitivity which is why these bacteria are being tested as a supplement for blood sugar control in a clinical trial. Compared to healthy women, those with a history of recurrent urinary tract infections have lower levels of *A. hallii* in their gut.
Dialister invisus	1.611%	*D. invisus* are common members of the mouth microbiome. While normally present at low levels, their numbers in the mouth are elevated in those with tooth infections or periodontitis. They are also more often detected in people who smoke. From the mouth, *D. invisus* can reach the gut and quietly live there. Unlike beneficial gut bacteria, *D. invisus* cannot digest carbohydrates from the diet and are not major producers of short-chain fatty acids. In babies and toddlers with a genetic predisposition to developing type 1 diabetes, complete absence of this species in the gut has been associated with development of the disease.
Mediterraneibacter faecis	1.484%	*M. faecis* are beneficial gut bacteria that produce short-chain fatty acids. Animal and human studies suggest they may protect against liver damage.
Blautia_A faecis	1.351%	*B. faecis* was first isolated from human feces in 2013. We don't know much about it, but like other *Blautia* species, it probably contributes to a healthy gut by digesting dietary fiber and producing beneficial and anti-inflammatory molecules. A plant-based diet increases gut levels of *B. faecis*. People with Crohn's disease have low levels of *B. faecis*.

All species

Alistipes onderdonkii	1.190%	Mediterraneibacter torques	1.062%
Ruthenibacterium lactatiformans	1.058%	Gemmiger sp900539695	1.053%
Acutalibacter sp900548545	0.939%	Bacteroides thetaiotaomicron	0.927%
Holdemanella sp002299315	0.906%	Blautia_A wexlerae_A	0.882%
Bacteroides stercoris	0.872%	Eubacterium_R sp000433975	0.856%
Lachnoclostridium_B sp900543315	0.758%	Alistipes putredinis	0.740%
Ruminococcus_C callidus	0.703%	Anaerostipes hadrus	0.695%
KLE1615 sp900066985	0.683%	Romboutsia timonensis	0.661%
Bifidobacterium pseudocatenulatum	0.583%	Dysosmobacter welbionis	0.572%
Sellimonas intestinalis	0.557%	Collinsella stercoris	0.504%
Bacteroides xylanisolvens	0.498%	Intestinibacter bartlettii	0.462%
Collinsella phocaeensis	0.456%	Dorea formicigenerans	0.429%
Flavonifractor sp000508885	0.401%	CAG-521 sp000437635	0.394%
Phocaeicola massiliensis	0.390%	Lawsonibacter sp900066825	0.386%
Agathobacter rectalis	0.383%	Sutterella wadsworthensis_A	0.371%
CAG-317 sp900543415	0.370%	Blautia_A obeum	0.327%
Clostridium_A leptum	0.309%	Collinsella tanakaei	0.309%
Evtepia gabavorous	0.306%	Blautia_A hydrogenotrophica	0.298%
Agathobacter faecis	0.296%	Anaeromassilibacillus sp002159845	0.288%
Eubacterium_I ramulus	0.274%	Collinsella sp003479805	0.269%
Blautia_A caecimuris	0.268%	Flavonifractor plautii	0.268%
Faecalibacterium prausnitzii_G	0.265%	Enterocloster bolteae	0.263%
Streptococcus sp001556435	0.253%	Bifidobacterium gallinarum	0.239%
UBA11774 sp003507655	0.235%	Catenibacillus sp900557175	0.221%
Parabacteroides distasonis	0.219%	CAG-81 sp000435795	0.203%
Anaerostipes hadrus_B	0.200%	Faecalibacterium prausnitzii	0.193%
Faecalibacterium prausnitzii_C	0.192%	Negativibacillus sp900547455	0.182%
Lachnoclostridium_B sp000765215	0.178%	Dialister sp900555245	0.172%
GCA-900066135 sp900543575	0.171%	UMGS1975 sp900546685	0.163%

Roseburia inulinivorans	0.151%	Ruminococcus_B gnavus	0.151%
Collinsella sp900541285	0.144%	Clostridium saudiense	0.142%
Blautia_A sp003480185	0.137%	Prevotella sp900557255	0.128%
Agathobaculum butyriciproducens	0.125%	BX12 sp014333425	0.125%
Ruminococcus_A sp000432335	0.122%	Hungatella effluvii	0.120%
Turicibacter sp001543345	0.116%	CAG-317 sp000433535	0.115%
Roseburia hominis	0.105%	Lawsonibacter sp000177015	0.102%
Slackia_A piriformis	0.102%	Eggerthella lenta	0.101%
UBA1191 sp900549125	0.100%	Blautia_A sp900542045	0.093%
Collinsella sp003459245	0.088%	Gordonibacter pamelaeae	0.087%
Streptococcus salivarius	0.087%	Collinsella sp002232035	0.085%
Roseburia sp900552665	0.084%	Eubacterium_G sp000435815	0.083%
Erysipelatoclostridium ramosum	0.082%	Enterocloster sp900547035	0.078%
Faecalibacterium prausnitzii_J	0.078%	Streptococcus thermophilus	0.078%
Faecalibacterium prausnitzii_I	0.077%	Clostridium sp900540255	0.074%
Collinsella sp900554655	0.074%	UMGS1472 sp900552095	0.073%
Faecalibacillus intestinalis	0.071%	Clostridium_Q symbiosum	0.068%
Collinsella sp900541145	0.067%	Faecalibacterium sp900539885	0.067%
Longibaculum muris	0.067%	Clostridium_Q saccharolyticum_A	0.065%
Phocaeicola dorei	0.065%	Bifidobacterium breve	0.063%
Intestinibacter sp900553485	0.063%	CAG-41 sp900066215	0.062%
Lawsonibacter sp900545895	0.062%	Phocaeicola sp900554435	0.062%
Hydrogeniiclostridium mannosilyticum	0.061%	Faecalibacterium sp900758465	0.060%
Collinsella sp003439125	0.058%	Enterocloster citroniae	0.058%
Blautia sp900541955	0.056%	Collinsella sp900554455	0.056%
Collinsella sp003487125	0.055%	Hungatella sp005845265	0.055%
UMGS1670 sp900548595	0.054%	Gemmiger formicilis	0.051%
Blautia_A sp900547615	0.049%	Eisenbergiella sp003478085	0.049%
Intestinibacter sp900540355	0.049%	Blautia sp003287895	0.048%
Faecalimonas phoceensis	0.048%	Eisenbergiella sp900066775	0.047%
Bifidobacterium infantis	0.045%	Merdimonas faecis	0.045%

Enterocloster sp001517625	0.044%	Marseille-P3106 sp900169975	0.044%
NSJ-32 sp014384895	0.043%	Finegoldia magna	0.042%
OF09-33XD sp003481995	0.041%	Bacteroides ovatus	0.040%
Collinsella sp900541645	0.040%	Dysosmobacter sp014297375	0.040%
Enterocloster lavalensis	0.040%	GCA-900066905 sp900066905	0.040%
Clostridium_AQ innocuum	0.039%	Enterocloster aldenensis	0.039%
Collinsella aerofaciens_F	0.038%	Blautia_A sp900066205	0.037%
CAG-81 sp900066535	0.037%	Lactobacillus paragasseri	0.037%
CAG-196 sp002102975	0.036%	Collinsella sp900550815	0.036%
Eubacterium callanderi	0.036%	Eubacterium_G sp000432355	0.036%
Enterocloster sp900541315	0.035%	Lachnospira eligens_A	0.035%
UMGS856 sp900546265	0.035%	Coprobacillus cateniformis	0.034%
CAG-83 sp000431575	0.033%	Collinsella sp003466125	0.033%
Collinsella sp003469205	0.033%	Collinsella sp900544425	0.033%
Massilioclostridium coli	0.033%	Roseburia sp003470905	0.033%
UMGS1071 sp900542375	0.033%	Bifidobacterium animalis	0.030%
Lawsonibacter asaccharolyticus	0.030%	Limosilactobacillus reuteri	0.030%
UBA1191 sp900545775	0.030%	UBA1820 sp003150615	0.030%
Blautia coccoides	0.029%	Collinsella sp900551195	0.029%
Collinsella sp900759335	0.029%	Holdemanella biformis	0.029%
Lawsonibacter sp900754605	0.029%	Collinsella sp900541235	0.028%
Megamonas funiformis	0.028%	Ruminococcus_C sp000980705	0.028%
Agathobaculum sp900291975	0.027%	GCA-900066135 sp900066135	0.027%
Blautia sp001304935	0.026%	Collinsella aerofaciens_J	0.026%
Alistipes finegoldii	0.025%	Blautia_A sp900066355	0.025%
Collinsella aerofaciens_H	0.025%	Erysipelatoclostridium spiroforme	0.025%
Blautia_A sp000436615	0.024%	Lachnospira sp000437735	0.024%
UBA1417 sp900552925	0.024%	An92 sp900199495	0.023%
Collinsella sp900541695	0.023%	Collinsella sp900549025	0.023%
Mediterraneibacter sp900541505	0.023%	Anaerococcus hydrogenalis	0.022%
Collinsella sp900543515	0.022%	Emergencia sp900551775	0.022%

Longicatena caecimuris	0.022%	Robinsoniella sp900539655	0.022%
Blautia_A sp003471165	0.021%	Collinsella sp900541055	0.021%
Lactonifactor sp009677585	0.021%	Lawsonibacter sp002160305	0.021%
Muricomes contortus_B	0.021%	NK3B98 sp900758315	0.021%
Anaerotruncus colihominis	0.020%	Clostridium sp900543325	0.020%
Collinsella intestinalis	0.020%	Ruminococcus_E bromii	0.020%
Bacteroides cellulosilyticus	0.019%	Bifidobacterium catenulatum	0.019%
Collinsella sp900541035	0.019%	Collinsella sp900542305	0.019%
Roseburia intestinalis	0.019%	Schaedlerella glycyrrhizinilytica	0.019%
Anaerobutyricum sp900554965	0.018%	Anaerococcus prevotii_A	0.018%
Collinsella sp003471585	0.018%	Collinsella sp900544875	0.018%
Collinsella sp900547345	0.018%	Holdemanella sp003436425	0.018%
Lawsonibacter sp900066645	0.018%	Streptococcus parasanguinis_B	0.018%
Acetatifactor sp900066365	0.017%	Bariatricus comes	0.017%
Blautia_A sp900066335	0.017%	Collinsella sp900540945	0.017%
Dorea_A longicatena	0.017%	Eisenbergiella sp900555195	0.017%
Faecalibacterium prausnitzii_A	0.017%	Prevotella copri_A	0.017%
UBA5416 sp900539175	0.017%	Collinsella sp900544995	0.016%
Collinsella sp900549275	0.016%	Collinsella sp902388345	0.016%
NSJ-63 sp014384805	0.016%	Parasutterella excrementihominis	0.016%
Prevotella sp900551275	0.016%	Anaerostipes sp900756035	0.015%
Collinsella sp900550205	0.015%	Faecalibacterium prausnitzii_E	0.015%
Frisingicoccus caecimuris	0.015%	Lawsonibacter sp902363045	0.015%
Muricomes sp000509105	0.015%	Phocaeicola sp900553715	0.015%
Acetatifactor sp900066565	0.014%	Acutalibacter sp000432995	0.014%
Collinsella sp900754525	0.014%	Collinsella sp900758375	0.014%
Holdemanella sp900551285	0.014%	Massilimaliae timonensis	0.014%
Mediterraneibacter_A butyricigenes	0.014%	Anaerostipes sp900066705	0.013%
Bifidobacterium kashiwanohense	0.013%	Blautia_A sp900066505	0.013%
Butyrivibrio_A sp900543865	0.013%	Clostridium_P perfringens	0.013%
Dorea_B phocaeensis	0.013%	Faecalibacterium sp900772565	0.013%

GCA-900066495 hominis_A	0.013%	Holdemanella sp003458715	0.013%
Prevotella buccalis	0.013%	Slackia_A sp900553655	0.013%
Staphylococcus epidermidis	0.013%	Alistipes shahii	0.012%
Blautia sp900539145	0.012%	CAG-245 sp000435175	0.012%
Collinsella sp002391315	0.012%	Collinsella sp900542165	0.012%
Eisenbergiella tayi	0.012%	Gemmiger variabilis_B	0.012%
Gemmiger variabilis_C	0.012%	Gordonibacter urolithinfaciens	0.012%
Anaerococcus obesiensis	0.011%	Clostridium sp900547475	0.011%
Enterocloster clostridioformis	0.011%	Gemmiger sp900545545	0.011%
Massiliomicrobiota sp002160815	0.011%	Peptacetobacter hiranonis	0.011%
Phocea massiliensis	0.011%	Ruminococcus_A sp003011855	0.011%
Terrisporobacter othiniensis	0.011%	Agathobacter sp900546625	0.010%
Bacteroides faecis	0.010%	Butyricimonas virosa	0.010%
Collinsella sp900541245	0.010%	Collinsella sp900547855	0.010%
Collinsella sp900556285	0.010%	Collinsella sp900760325	0.010%
Collinsella sp900761035	0.010%	Escherichia coli	0.010%
Eubacterium_R sp900539775	0.010%	Peptoniphilus_A harei	0.010%
Prevotella sp900313215	0.010%	Ruminococcus_C sp000437175	0.010%

Our high confidence detection limit is 0.01% abundance. Very low abundance organisms can be important members of the microbiome but also very difficult to accurately detect. Detections below 0.01% abundance have an increased risk of being false positives. However, in our testing, we have observed that most false positive identifications are closely related to a detected species.

CAG-269 sp900551615	0.009%	Clostridium cuniculi	0.009%
Clostridium paraputrificum	0.009%	Collinsella aerofaciens_L	0.009%
Collinsella sp003436275	0.009%	Collinsella sp003465825	0.009%
Collinsella sp900540855	0.009%	Collinsella sp900541875	0.009%
Collinsella sp900542635	0.009%	Collinsella sp900554325	0.009%
Collinsella sp900556365	0.009%	Gemmiger variabilis	0.009%
Holdemania filiformis	0.009%	Lacticaseibacillus rhamnosus	0.009%
Porphyromonas_A bennonis	0.009%	Prevotella sp900546535	0.009%
Streptococcus mutans	0.009%	TF01-11 sp001414325	0.009%
Agathobacter sp900317585	0.008%	Amedibacterium intestinale	0.008%

Bifidobacterium ruminantium	0.008%	CAG-611 sp000434175	0.008%
Clostridium_AP sp000509125	0.008%	Collinsella sp900544205	0.008%
Collinsella sp900549215	0.008%	Collinsella sp900551975	0.008%
Collinsella sp900755005	0.008%	Eisenbergiella sp900550285	0.008%
Eubacterium_G ventriosum	0.008%	Holdemanella sp900754615	0.008%
Mediterraneibacter massiliensis	0.008%	Peptococcus niger	0.008%
Peptoniphilus_A sp900538655	0.008%	Romboutsia ilealis	0.008%
UBA7182 sp003481535	0.008%	Agathobacter sp900550545	0.007%
Anaerococcus vaginalis	0.007%	Anaerostipes caccae	0.007%
Bacteroides finegoldii	0.007%	Bacteroides sp007097645	0.007%
Bifidobacterium sp002742445	0.007%	Bittarella massiliensis	0.007%
Blautia_A obeum_B	0.007%	Blautia_A sp900549015	0.007%
CAG-81 sp900066785	0.007%	Collinsella aerofaciens_I	0.007%
Collinsella sp003437035	0.007%	Collinsella sp900540995	0.007%
Collinsella sp900545605	0.007%	Collinsella sp900761995	0.007%
Corynebacterium propinquum	0.007%	Eubacterium_R sp000434995	0.007%
Eubacterium_R sp003526845	0.007%	Ezakiella sp900540185	0.007%
Faecalibacterium sp900539945	0.007%	Finegoldia magna_H	0.007%
Gemmiger sp900540775	0.007%	Holdemanella sp900547815	0.007%
RUG115 sp900066395	0.007%	Ruminococcus_E sp003526955	0.007%
Sellimonas sp002161525	0.007%	Acutalibacter sp000435395	0.006%
Akkermansia muciniphila_B	0.006%	Blautia_A sp900548245	0.006%
Blautia_A wexlerae_B	0.006%	CAG-460 sp900546715	0.006%
Christensenella hongkongensis	0.006%	Collinsella aerofaciens_G	0.006%
Collinsella sp000763055	0.006%	Collinsella sp900544115	0.006%
Collinsella sp900545745	0.006%	Collinsella sp900546115	0.006%
Collinsella sp900550415	0.006%	Collinsella sp900550835	0.006%
Collinsella sp900552425	0.006%	Collinsella sp900762355	0.006%
Coprobacter sp900555475	0.006%	Faecalibacterium prausnitzii_F	0.006%
Faecalibacterium prausnitzii_H	0.006%	Faecalimonas sp900550975	0.006%
Faecalimonas umbilicata	0.006%	HGM13006 sp900757695	0.006%

Lachnoclostridium_B sp002160985	0.006%	Lactiplantibacillus plantarum	0.006%
Roseburia sp900542495	0.006%	Ruminococcus_C sp000433635	0.006%
Turicibacter sanguinis	0.006%	UBA3402 sp003478355	0.006%
UBA7748 sp900314535	0.006%		

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