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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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PATIENT: XXXXXXXXXXXXXXXXXXX			TEST REF: TST-NL-XXXXX
TEST NUMBER: T-NL-XXXXXX	COLLECTED: 2025-XX-XX		PRACTITIONER: XXXXXXXXXXXXXXXXXXXX
GENDER: XXXXX			XXXXXXXXXXXXXXXXXX
AGE: XX			

TEST NAME: [Baby Gut Health] Tiny Health Sample Report

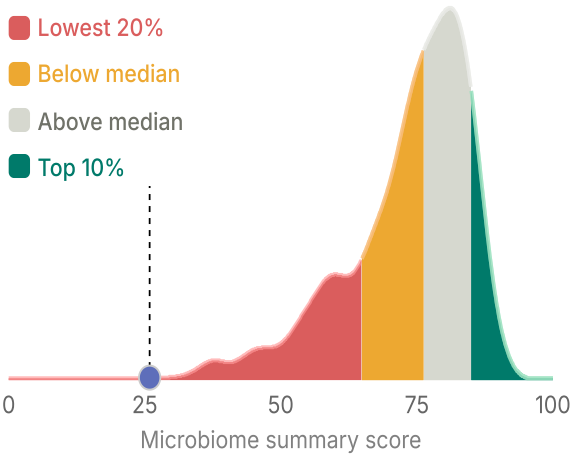
Microbiome Summary Score

Your gut microbiome score evaluates all the relevant metrics for your age range into a single number, giving you a clear picture of how your microbiome stacks up. The score ranges from 0 to 100. A score closer to 100 suggests your microbiome is in excellent shape compared to the reference population. Conversely, a score closer to 0 indicates more areas for improvement.

We calculate this score by looking at various factors in your gut/vaginal microbiome, such as the balance of beneficial bacteria versus opportunistic pathogens. We then compare these factors to a wide range of individuals. Our dataset includes publicly available reference samples and proprietary data from Tiny Health customers.

To determine your percentile, we compare your Microbiome Summary Score to others in the same age range to help you understand what is typical and where your sample falls. For example, if you are in the 41st percentile, 41% of comparable samples have a lower Microbiome Summary Score and 59% have a higher score.

25.9 Microbiome summary score



Sample at a glance

11 Needs support

6 Needs improvement

Immune Strength
- Bifidobacterium 0.315%
- HMO-digesting species 0.165%

Antibiotic Resistance Signature
- Abundance index 0.71

Opportunistic Pathogens
- Enterobacteriaceae 13.934%
- Klebsiella 12.338%
- Enterococcus faecium 3.273%
- Clostridium perfringens 0.262%

C-section Signature
- C-section Signature 0.74

Hydrogen sulfide index
- Hydrogen sulfide index 13

Acetate Capacity
- Acetate ..... 954 rpkm

HMO Digestion Capacity
- 2'-Fucosyllactose ..... 271 rpkm
- Sialyllactose ..... 131 rpkm
- Other HMOs ..... 611 rpkm

Microbiome Maturation
- Maturation index ..... 503 predicted days

Major Bacterial Phyla
- Actinobacteriota 0.913%

Common Microbiome Members
- Blautia 8.468%

Histamine-producing Species
- Histamine-producing species 0.532%

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TEST NAME: [Baby Gut Health] Tiny Health Sample Report

Results Summary

	Metrics	Clinical indication examples
Beneficial microbes	⚠ Immune Strength ✓ 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 ⚠ C-section Signature ○ 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 inflammation markers	○ Hexa-LPS index ✓ Mucus degradation index ⚠ Hydrogen sulfide index ○ Host DNA	• Modulate stress levels • Lifestyle changes (e.g., exercise, sleep) • Nutritional support and therapeutic diet (e.g., AIP, candida diet, etc) • Support GI motility (e.g., hydration, pysllium, acacia, pectin, HMOs etc) • GI barrier support (e.g., tumeric, quercetin, L-glutamine) • Soothe mucosal lining (i.e. SBI/ colostrum, marshmallow) • Consider additional testing (e.g., SIBO, OAT, nutritional labs etc)
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)
Digestion & absorption markers	! HMO Digestion Capacity	• Consider balanced, nutrient-dense whole foods diet • Track and diversify fiber intake • Gastric acid optimization (e.g., Betaine HCL, Apple Cider Vinegar) • Digestive enhancement (e.g., digestive bitters, digestive enzymes, bile salts) • Mindful eating habits (e.g., chew well, timing of meals, etc) • Support GI motility (e.g., hydration, pysllium, acacia, pectin, HMOs etc)

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TEST NAME: [Baby Gut Health] Tiny Health Sample Report

Balance and robustness	Microbiome Diversity Microbiome Maturation Major Bacterial Phyla Common Microbiome Members Gut Ratio	• Track and diversify fiber intake • Increase fermented foods • Use non-toxic cleaners / reduce antimicrobials
Microbial enzymes & metabolites	Histamine-producing Species	

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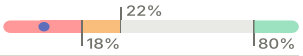
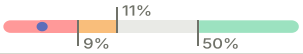
TEST NAME: [Baby Gut Health] Tiny Health Sample Report

Detailed Gut Health Test Results

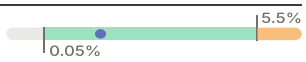
Legend: (p) Phylum (f) Family (g) Genus (sp) Species

Beneficial microbes

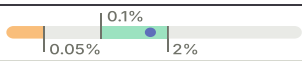
Immune Strength

⚠ Bifidobacterium (g)	0.315%	
Bifidobacterium breve (sp)	0.098%	
Bifidobacterium longum (sp)	0.067%	
Bifidobacterium pseudocatenulatum (sp)	0.097%	
⚠ HMO-digesting species	0.165%	

Metabolic Health

✓ Akkermansia (g)	0.097%	
Akkermansia muciniphila (sp)	0.087%	

Anti-inflammatory Markers

✓ Faecalibacterium (g)	1.468%	
Faecalibacterium prausnitzii (sp)	0.121%	
Faecalibacterium prausnitzii_C (sp)	0.325%	
Faecalibacterium prausnitzii_G (sp)	0.832%	

Common Probiotic Species

Bifidobacterium (g)	0.315%
Lactobacillaceae (f)	0.477%
Lacticaseibacillus rhamnosus (sp)	0.091%
Lacticaseibacillus paracasei (sp)	0.368%
Bifidobacterium longum (sp)	0.067%
Bifidobacterium breve (sp)	0.098%

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GENDER: XXXXX			XXXXXXXXXXXXXXXXXX
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TEST NAME: [Baby Gut Health] Tiny Health Sample Report

Disruptive microbes

Antibiotic Resistance Signature		
⚠ Abundance index	0.71	0.45 / 0.2 / 0.55
✓ Richness index	0.45	0.5 / 0.3 / 0.75

Opportunistic Pathogens		
! Enterobacteriaceae (f)	13.934%	0.5% / 0.05% / 17% / 13%
Citrobacter youngae (sp)	0.301%	
Enterobacter asburiae (sp)	0.102%	
Escherichia coli (sp)	0.327%	
Escherichia coli_C (sp)	0.056%	
Escherichia coli_D (sp)	0.073%	
Klebsiella pneumoniae (sp)	1.254%	
Klebsiella quasipneumoniae (sp)	0.494%	
Klebsiella quasivariicola (sp)	0.208%	
Klebsiella variicola (sp)	7.380%	
Klebsiella_A grimontii (sp)	0.341%	
Klebsiella_A michiganensis (sp)	2.197%	
Klebsiella_A oxytoca (sp)	0.474%	
Raoultella ornithinolytica (sp)	0.126%	
⚠ Klebsiella (g)	12.338%	6.5% / 5.5%
Klebsiella pneumoniae (sp)	1.254%	
Klebsiella quasipneumoniae (sp)	0.494%	
Klebsiella quasivariicola (sp)	0.208%	
Klebsiella variicola (sp)	7.380%	

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TEST NAME: [Baby Gut Health] Tiny Health Sample Report

Disruptive microbes

Klebsiella_A grimontii (sp)	0.341%	
Klebsiella_A michiganensis (sp)	2.197%	
Klebsiella_A oxytoca (sp)	0.474%	
Klebsiella pneumoniae (sp)	1.254%	2.5% – 3.5%
Klebsiella oxytoca (sp)	0.475%	0.5% – 1.5%
Salmonella enterica (sp)	0.000%	0.35% – 0.45%
Escherichia coli (sp)	0.456%	7.5% – 8.5%
Escherichia coli (sp)	0.327%	
Escherichia coli_C (sp)	0.056%	
Escherichia coli_D (sp)	0.073%	
Escherichia flexneri (sp)	0.000%	1.5% – 2.5%
Escherichia dysenteriae (sp)	0.000%	1% – 2%
Streptococcus (g)	0.301%	2.5% – 3.5%
Streptococcus anginosus_C (sp)	0.177%	
Streptococcus sp900543065 (sp)	0.061%	
Staphylococcus (g)	0.000%	0.05% – 0.1%
Pseudomonas aeruginosa (sp)	0.000%	0.05% – 0.1%
Haemophilus influenzae (sp)	0.000%	0.05% – 0.1%
Haemophilus parainfluenzae (sp)	0.000%	0.15% – 0.25%
Enterococcus faecium (sp)	3.273%	1.25% – 1.35%
Enterococcus faecalis (sp)	1.540%	2% – 3%
Clostridioides difficile (sp)	0.337%	0.55% – 0.65%
Clostridium perfringens (sp)	0.262%	0.15% – 0.25%
Acinetobacter baumannii (sp)	0.000%	

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TEST NAME: [Baby Gut Health] Tiny Health Sample Report

Disruptive microbes	Campylobacter (g)	0.000%	0.1% / 0.05%
	Potential Stomach Inflammation		
	Helicobacter pylori (sp)	0.000%	0.05%
	Parasites and Infection		
	Blastocystis (g)	0.000%	0.12% / 0.08%
	Cryptosporidium (g)	0.000%	0.05%
	Entamoeba histolytica (sp)	0.000%	0.05%
	Entamoeba dispar (sp)	0.000%	0.05%
	Giardia (g)	0.000%	0.05%
	Yersinia enterocolitica (sp)	0.000%	0.05%
	Vibrio (g)	0.000%	0.05%
	Vibrio cholerae (sp)	0.000%	0.05%
	Cyclospora cayetanensis (sp)	0.000%	
	Potential Fungal Overgrowth		
	Candida (g)	0.000%	0.1% / 0.05%
	Aspergillus (g)	0.000%	0.05%
	Cryptococcus (g)	0.000%	0.05%
	Saccharomyces (g)	0.000%	0.5%
	Rhodotorula (g)	0.000%	0.05%
	Saprochaete (g)	0.000%	0.05%
	Malassezia (g)	0.000%	0.05%
	Microsporum (g)	0.000%	0.05%
	Trichophyton (g)	0.000%	0.05%
	C-section Signature		
	⚠ C-section Signature	0.74	0.18 / 0.15 / 0.22

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Disruptive microbes

Methane Production

Methanobrevibacter smithii (sp)	0.000%	0.05% – 0.5%

Gut inflammation markers

Hexa-LPS index

Hexa-LPS index	11.47	8 – 11.8 – 12.2

Mucus degradation index

Mucus degradation index	7.18	8.4 – 11.3 – 11.7

Hydrogen sulfide index

Hydrogen sulfide index	13.01	7.6 – 12.2 – 12.6

Host DNA

Host DNA	1.691%	10%

Short-chain fatty acids

Butyrate Capacity

Butyrate	780.72 rpkm	188

Propionate Capacity

Propionate	877.05 rpkm	879

Acetate Capacity

Acetate	954.81 rpkm	1000 – 1200

Digestion & absorption markers

HMO Digestion Capacity

2'-Fucosyllactose	271.52 rpkm	1332
Sialyllactose	131.21 rpkm	308
Other HMOs	611.94 rpkm	2281

Balance and robustness

Microbiome Diversity

Shannon diversity	5.14

Microbiome Maturation

Maturation index	503.69 predicted days

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Balance and robustness

Major Bacterial Phyla

Bacteroidota (p)	12.370%	0.1%
Firmicutes (p)	72.221%	
Actinobacteriota (p)	0.913%	12% / 8%
Proteobacteria (p)	14.196%	50%
Fusobacteriota (p)	0.000%	

Common Microbiome Members

Bacteroides (g)	5.996%	
Bacteroides fragilis (sp)	1.303%	
Prevotella (g)	0.742%	20% / 0.05%
Ruminococcus (g)	1.374%	
Ruminococcus gnavus (sp)	0.069%	
Blautia (g)	8.468%	5% / 0.05%
Roseburia (g)	0.286%	
Phocaeicola dorei (sp)	0.105%	

Gut Ratio

Firmicutes / Bacteroidota ratio	5.84	500
Proteobacteria / Actinobacteriota ratio	15.55	500
Prevotella / Bacteroides ratio	0.00	

Microbial enzymes & metabolites

Histamine-producing Species

Histamine-producing species	0.532%	0.5% / 0.05% / 1.5%

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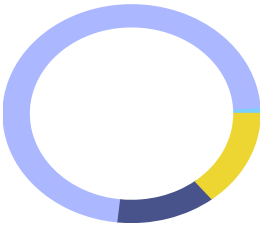
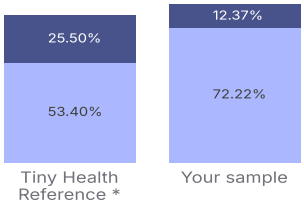
Major Microbial Members & Ratios

Common Bacterial Phyla



Actinobacteriota	0.91%	
Firmicutes	72.22%	
Bacteroidota	12.37%	
Proteobacteria	14.20%	
Fusobacteriota	0.00%	

Gut Ratio

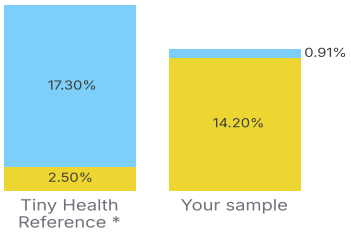


Firmicutes:Bacteroidota Ratio

5.84 (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

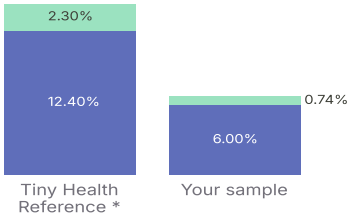


Proteobacteria:Actinobacteriota Ratio

15.55 (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

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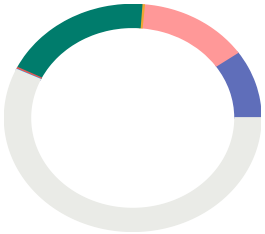
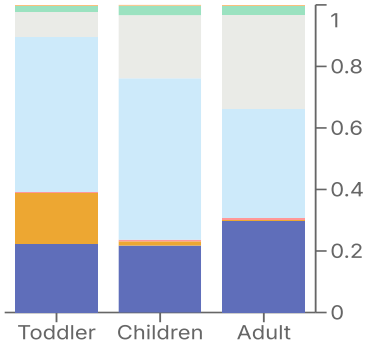
TEST NUMBER: T-NL-XXXXXX	COLLECTED: 2025-XX-XX		PRACTITIONER: XXXXXXXXXXXXXXXXXXX
GENDER: XXXXX			XXXXXXXXXXXXXXXXX
AGE: XX			

TEST NAME: [Baby Gut Health] Tiny Health Sample Report

Gut Type



Bacteroides	9.78%
Enterobacteriaceae	13.79%
Bifidobacterium	0.32%
Enterococcus	18.80%
Streptococcus	0.29%
Staphylococcus	0.00%
Other	56.93%



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 7b

Baby Gut Type 7b is dominated by some lesser known bacteria with beneficial *Bifidobacterium* at low levels. This gut type has significant imbalances and we recommend taking steps to improve it. How does your baby's results compare? See the Key Insights section for what metrics are out of range and what actions you can take.

Bifidobacterium are beneficial and protective, so when they are low, it leaves the door open for unfriendly and variable microbes to take hold.. In the first year of life, *Bifidobacterium* should dominate baby's gut. Click on the Immune Strength card in the Key Insights section for more info.

This gut type does not fit into any of the 6 gut types that we defined. Before 6 months, this is rare and is usually linked to a cesarian birth, vaginal birth with medical interventions, or formula-feeding.

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TEST NAME: [Baby Gut Health] Tiny Health Sample Report

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 21% Variable 56% Unfriendly 14% Unknown 9%

Top 20 species

Metric	Result	Description
Enterococcus_B lactis	13.097%	*E. lactis* usually grows in fermented milk and cheeses. In the gut, this bacterium may provide benefits, as some strains can inhibit the growth of unfriendly bacteria and cancer cells. *E. lactis* may dominate the gut of babies born by c-section, whose levels of bifidobacteria are low.
Enterocloster aldenensis	10.712%	*Enterocloster* are variable bacteria that contribute to gut health by producing short-chain fatty acids. On rare occasions, species such as *E. aldenensis* can cause infection outside of the gut. But this shouldn't be a concern for healthy people. A small study found that babies whose moms had a hypertensive pregnancy had lower levels of *E. aldenensis* than babies whose moms had a normotensive pregnancy. In adults, following a diet rich in dairy products for several weeks has been shown to reduce *E. aldenensis* levels. In contrast, eating more beans may increase the levels of these bacteria.
Clostridium neonatale	9.093%	*Clostridium neonatale* is present in 15-20% of healthy babies including preterm or C-section delivered babies. However, if given the opportunity, *C. neonatale* can cause infection. Increased numbers of this species have been associated with a disease called necrotizing enterocolitis, especially in preterm babies. It is better to watch out for the levels of this bug.
Klebsiella variicola	7.380%	*K. variicola* may live in the gut without causing any trouble, like other *Klebsiella* species. Outside of the gut though, it may cause infection if its numbers go up, especially in immunocompromised patients and babies. It can be resistant to several antibiotics.

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TEST NAME: [Baby Gut Health] Tiny Health Sample Report

Blautia_A sp900120195	4.538%	This is a newly detected species of *Blautia* so we don't know much about it. Like most *Blautia*, it probably thrives on plant-based foods and provides benefits to your gut.
Clostridium paraputrificum	3.975%	*Clostridium paraputrificum* are variable bacteria found in the gut. This means that they can either disrupt your health or support it. This bug can also be present in preterm babies in neonatal care units. When given the opportunity, *C. paraputrificum* can cause infection. *C. paraputrificum* have been associated with infections in children and adults, such as: • Bacteremia • Necrotizing enterocolitis • Septic arthritis • Cysts However this is extremely rare. This bug only accounts for 1% of human infections caused by *Clostridium* species. This mostly occurs in immunocompromised, elderly, and diabetic patients.
Enterococcus_B faecium	3.273%	*E. faecium* is a variable member of the gut microbiome, present in many people. It may not cause any harm and even be beneficial but it can cause different infections outside of the gut. It is considered an important bacterial species to monitor by the World Health Organization due to its widespread antibiotics resistance. Because of this resistance, *E. faecium* may temporarily predominate in the gut of babies after antibiotic treatment.
Phocaeicola vulgatus	3.199%	*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.
Veillonella parvula_A	2.968%	*V. parvula* is a common member of the mouth and gut microbiome. While in the gut it contributes to health by producing beneficial short-chain fatty acids too much *V. parvula* may not be optimal for babies. Babies born by c-section have higher levels of *Veillonella* than babies born vaginally. On occasions, *V. parvula* can become unfriendly and cause abscesses.
Klebsiella_A michiganensis	2.197%	*K. michiganensis* may live in the gut without causing any trouble, like other *Klebsiella* species. Outside of the gut though, it may cause infection if its numbers go up, especially in immunocompromised patients and babies. It can be resistant to several antibiotics which may be a problem for preterm babies, who have been shown to have this species in their gut.
Bacteroides xylanisolvens	1.909%	*B. xylanisolvens* is very good at digesting soluble fiber from fruits and insoluble fiber from cereals. It contributes to gut health by transforming fiber into beneficial short-chain fatty acids. We don't know for sure, but it may be protective against certain diseases. People with atherosclerosis and children with type 1 diabetes have low levels of *B. xylanisolvens* in their gut.

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TEST NAME: [Baby Gut Health] Tiny Health Sample Report

Blautia_A wexlerae	1.668%	*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.
Bacteroides uniformis	1.594%	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.
Enterococcus faecalis	1.539%	*E. faecalis* is a variable member of the gut microbiome, present in many people. It provides benefits to our immune system and helps us get nutrients from food. If the gut barrier is disrupted, *E. faecalis* may cross it and cause infection outside of the gut. But this is very unlikely to occur in healthy, young people.
Bacteroides fragilis	1.261%	*B. fragilis* is a variable bacteria species in your gut microbiome. In low counts, it can benefit your health and well-being. However, if your *B. fragilis* levels are too high, you can get into trouble. Not only can they contribute to inflammation by damaging your gut's structure, but the species can cause serious infections. In children, high levels of *B. fragilis* may contribute to constipation. One study suggests that high levels of B. fragilis can also increase the risk of asthma and eczema development. It's important to keep levels of "friend or foe" in the sweet spot. *B. fragilis*' competitors in your gut community love a high-fiber diet. Stick to fruits, veggies, and complex carbohydrates.
Klebsiella pneumoniae	1.254%	Lots of healthy people have *K. pneumoniae* bacteria in their gut microbiomes. However, these unfriendly microbes can cause infection if their numbers get too high outside of the gut. This can be a problem for immunocompromised people and babies, especially in healthcare settings and nursing homes. Having a catheter or undergoing antibiotic treatment can also put you at risk. In babies, high levels of this bug may also contribute to development of allergies. *K. pneumoniae* infections can be dangerous since they're often resistant to antibiotic treatment. Luckily, these bacteria don't typically cause any issue for healthy people.
Flavonifractor plautii	1.120%	*F. plautii* is a variable species of bacteria that lives in your gut. It can digest flavonoids, compounds found in fruits and veggies. In low numbers, it's not a cause for concern in healthy people. In fact, some studies suggest it may protect you against allergies and the flu. But if its numbers go up and your gut barrier is compromised, it may use that opportunity to cause infection.
Enterocloster clostridioformis	1.038%	*E. clostridioformis* is a variable species of bacteria that lives in your gut. In low numbers, it's not a cause for concern in healthy people. But if its numbers go up and your gut barrier is compromised, it may cause intra-abdominal infections and abscesses. *E. clostridioformis* levels may temporarily increase after antibiotic treatment because some strains are antibiotic-resistant. A good way to keep it at bay is to boost beneficial bacteria with a healthy diet and probiotics.

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TEST NAME: [Baby Gut Health] Tiny Health Sample Report

Robinsoniella sp900540475	0.995%	The role of *Robinsoniella sp900540475* in gut health is not clear. We know that *R. peoriensis*, a related species, can cause infections outside of the gut, usually following trauma and/or surgery. In some cases this seems to be related to a disrupted gut barrier.
Faecalibacterium prausnitzii_G	0.832%	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.

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TEST NAME: [Baby Gut Health] Tiny Health Sample Report

All species

Prevotella copri	0.680%	Enterococcus_B durans	0.674%
Enterocloster bolteae	0.633%	Agathobacter rectalis	0.607%
KLE1615 sp900066985	0.587%	Fusicatenibacter saccharivorans	0.553%
Blautia_A sp900066355	0.504%	Klebsiella quasipneumoniae	0.494%
Klebsiella_A oxytoca	0.474%	Ruminococcus_C callidus	0.440%
Alistipes finegoldii	0.439%	Mediterraneibacter faecis	0.423%
Barnesiella intestinihominis	0.422%	Veillonella_A seminalis	0.388%
Lachnospira eligens_A	0.373%	Lacticaseibacillus paracasei	0.368%
Anaerostipes hadrus	0.365%	Ruminococcus_E bromii_B	0.351%
Klebsiella_A grimontii	0.341%	Ruminococcus_D bicirculans	0.335%
Blautia_A obeum_B	0.334%	Odoribacter splanchnicus	0.330%
Escherichia coli	0.327%	Faecalibacterium prausnitzii_C	0.325%
Clostridioides difficile	0.322%	Alistipes shahii	0.307%
Citrobacter youngae	0.301%	Clostridium beijerinckii	0.286%
Bacteroides ovatus	0.274%	Blautia_A wexlerae_A	0.267%
Mediterraneibacter lactaris	0.266%	Clostridium_P perfringens	0.262%
Blautia_A massiliensis	0.255%	Blautia_A obeum	0.244%
Bacteroides caccae	0.239%	Blautia_A sp900066145	0.209%
Coprococcus eutactus	0.209%	Klebsiella quasivariicola	0.208%
Anaerobutyricum hallii	0.197%	Bacteroides thetaiotaomicron	0.189%
Flavonifractor sp000508885	0.189%	Agathobacter faecis	0.181%
Lachnospira sp000436535	0.180%	Streptococcus anginosus_C	0.177%
Blautia_A sp003480185	0.175%	Robinsoniella sp900539655	0.175%
Robinsoniella peoriensis	0.169%	Eggerthella lenta	0.160%
CAG-217 sp000436335	0.152%	Parabacteroides merdae	0.150%
Lachnospira sp000437735	0.143%	CAG-269 sp000437215	0.140%
Roseburia inulinivorans	0.138%	Enterocloster sp000431375	0.135%
Parabacteroides distasonis	0.131%	Raoultella ornithinolytica	0.126%
Faecalibacterium prausnitzii	0.121%	Faecalibacillus intestinalis	0.116%

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TEST NAME: [Baby Gut Health] Tiny Health Sample Report

Ruminococcus_A faecicola	0.113%	Collinsella aerofaciens_H	0.107%
Agathobaculum butyriciproducens	0.106%	Phocaeicola dorei	0.105%
CAG-41 sp900066215	0.103%	Dorea formicigenerans	0.102%
Enterobacter asburiae	0.102%	CAG-269 sp003525075	0.101%
Parasutterella excrementihominis	0.099%	Bifidobacterium breve	0.098%
Bifidobacterium pseudocatenulatum	0.097%	Clostridium_AP scindens	0.096%
Anaerostipes hadrus_B	0.095%	Bacteroides stercoris	0.093%
COE1 sp001916965	0.092%	Enterococcus_B hirae	0.091%
Lacticaseibacillus rhamnosus	0.091%	Paenibacillus lactis	0.090%
Alistipes putredinis	0.089%	Bacteroides sp900556215	0.089%
Veillonella dispar	0.088%	Akkermansia muciniphila	0.087%
Alistipes onderdonkii	0.085%	Veillonella dispar_A	0.080%
Veillonella sp900757715	0.078%	Bacteroides finegoldii	0.077%
Bacteroides faecis	0.075%	Acetatifactor sp900066565	0.074%
Escherichia coli_D	0.073%	CAG-81 sp900066785	0.070%
Blautia_A sp003471165	0.069%	Ruminococcus_B gnavus	0.069%
Bifidobacterium longum	0.067%	Clostridium_Q symbiosum	0.066%
TF01-11 sp001414325	0.066%	TF01-11 sp003529475	0.066%
Phocaeicola sp900553715	0.064%	Roseburia intestinalis	0.062%
Streptococcus sp900543065	0.061%	UBA3402 sp003478355	0.060%
UMGS743 sp900545085	0.058%	Enterocloster citroniae	0.057%
Escherichia coli_C	0.056%	Serratia_A fonticola	0.054%
Clostridium sp900540255	0.053%	Roseburia sp900552665	0.053%
Agathobacter sp900317585	0.052%	Bacteroides eggerthii	0.051%
Clostridium butyricum	0.051%	CAG-274 sp000432155	0.049%
Erysipelatoclostridium ramosum	0.049%	UBA11774 sp003507655	0.049%
Faecalibacterium prausnitzii_D	0.048%	Eisenbergiella sp900066775	0.047%
CAG-81 sp900066535	0.046%	Enterobacter roggenkampii	0.045%
Raoultella planticola	0.045%	Alistipes sp900541585	0.044%
Phocaeicola sp900554435	0.044%	Klebsiella aerogenes	0.043%
Bacteroides fragilis_A	0.042%	Blautia_A sp000436615	0.041%

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Agathobacter sp900546625	0.040%	Ruminococcus_A sp003011855	0.039%
Coprococcus sp900066115	0.038%	Ruthenibacterium lactatiformans	0.038%
Enterococcus_B mundtii_B	0.037%	UBA7057 sp900542735	0.037%
Bifidobacterium infantis	0.035%	UBA11524 sp000437595	0.035%
Citrobacter gillenii	0.033%	Phocaeicola coprocola	0.033%
Dialister succinatiphilus	0.032%	Eubacterium_F sp003491505	0.032%
Veillonella atypica	0.032%	CAG-115 sp000432175	0.031%
Clostridium botulinum_A	0.031%	Porphyromonas_A bennonis	0.031%
Veillonella rogosae	0.031%	CAG-180 sp000432435	0.030%
Corynebacterium vitaeruminis_A	0.030%	Enterobacter asburiae_B	0.030%
F23-B02 sp001916715	0.030%	Faecalibacterium prausnitzii_A	0.029%
Faecalibacterium prausnitzii_E	0.029%	Faecalibacterium prausnitzii_I	0.029%
Lachnospira rogosae_A	0.029%	CAG-269 sp900553125	0.028%
Enterococcus_D sp002850555	0.028%	Blautia sp900543715	0.027%
Escherichia sp005843885	0.027%	Lachnoclostridium_B sp900066765	0.027%
Veillonella sp900545205	0.027%	CAG-170 sp002404795	0.026%
Clostridium_Q sp003024715	0.026%	Dysosmobacter welbionis	0.025%
Intestinimonas butyriciproducens	0.025%	Anaerobutyricum sp900554965	0.024%
Parasutterella sp900552195	0.024%	Raoultella sp003752615	0.024%
Roseburia hominis	0.024%	Veillonella_A sp000431435	0.024%
Alistipes communis	0.023%	Faecalibacterium prausnitzii_J	0.023%
Pauljensenia odontolytica_B	0.023%	Prevotella sp900557255	0.023%
Blautia_A sp900066205	0.022%	Butyrivibrio_A crossotus	0.022%
CAG-269 sp000438255	0.022%	Collinsella sp900554255	0.022%
Enterobacter kobei	0.022%	Acinetobacter radioresistens	0.021%
Bacteroides cellulosilyticus	0.021%	Blautia_A sp003477525	0.021%
Sphingobacterium multivorum	0.021%	Veillonella sp003463825	0.021%
Anaerobutyricum soehngenii	0.020%	Bariatricus comes	0.020%
Coprococcus sp000154245	0.020%	Escherichia fergusonii	0.020%
uncultured crAssphage	0.020%	Eisenbergiella massiliensis	0.019%
Eubacterium_G ventriosum	0.019%	Lachnospira sp900316325	0.019%

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PATIENT: XXXXXXXXXXXXXXXXXXX
TEST NUMBER: T-NL-XXXXXX
GENDER: XXXXX
AGE: XX
COLLECTED: 2025-XX-XX
TEST REF: TST-NL-XXXXX
PRACTITIONER:
XXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXX

TEST NAME: [Baby Gut Health] Tiny Health Sample Report

Sutterella wadsworthensis_A	0.019%	Blautia_A faecis	0.018%
Clostridium cuniculi	0.018%	Coprococcus eutactus_A	0.018%
Dysosmobacter sp001916835	0.018%	Evtepia gabavorous	0.018%
Lawsonibacter asaccharolyticus	0.018%	Blautia_A sp900066335	0.017%
Collinsella sp002232035	0.017%	Faecalimonas phoceensis	0.017%
Salmonella enterica	0.017%	UMGS1071 sp900548305	0.017%
Agathobacter sp900550845	0.016%	CAG-127 sp900319515	0.016%
CAG-1427 sp000436075	0.016%	CAG-81 sp900066055	0.016%
Campylobacter_A concisus_F	0.016%	Citrobacter sp005281345	0.016%
Enterobacter cloacae_M	0.016%	Enterococcus phage phiFL4A	0.016%
Mediterraneibacter torques	0.016%	UMGS1375 sp900066615	0.016%
Dialister sp900555245	0.015%	Dorea_A longicatena_B	0.015%
Enterocloster lavalensis	0.015%	Intestinibacter bartlettii	0.015%
Pantoea sp008632075	0.015%	Blautia_A sp000285855	0.014%
CAG-45 sp000438375	0.014%	Clostridium saudiense	0.014%
Collinsella sp900754745	0.014%	Desulfovibrio sp900556755	0.014%
Dorea_A longicatena	0.014%	Escherichia flexneri	0.014%
Bifidobacterium bifidum	0.013%	CAG-196 sp002102975	0.013%
Prevotella copri_A	0.013%	TF01-11 sp003524945	0.013%
Varibaculum cambriense_B	0.013%	Bacteroides acidifaciens	0.012%
Clostridium tertium	0.012%	Coprobacillus cateniformis	0.012%
Eisenbergiella tayi	0.012%	Finegoldia magna	0.012%
Hungatella effluvii	0.012%	Pantoea ananatis	0.012%
Peptoniphilus_A harei	0.012%	Phocaeicola massiliensis	0.012%
UBA3789 sp900543055	0.012%	Veillonella sp900552715	0.012%
Blautia_A caecimuris	0.011%	Campylobacter_A concisus_T	0.011%
Clostridioides difficile_A	0.011%	Clostridium_AQ innocuum	0.011%
Enterobacter hormaechei_A	0.011%	GCA-900066135 sp900543575	0.011%
Lachnospira sp003451515	0.011%	Ruminiclostridium_E sp900539195	0.011%
Veillonella sp900538355	0.011%	Bacteroides nordii	0.010%
CAG-317 sp900543415	0.010%	CAG-495 sp001917125	0.010%

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TEST NAME: [Baby Gut Health] Tiny Health Sample Report

CAG-83 sp003487665	0.010%	Citrobacter werkmanii	0.010%
Corynebacterium sp001807205	0.010%	Enterocloster asparagiformis	0.010%
Klebsiella_A huaxiensis	0.010%	Phocaeicola sartorii	0.010%
UBA7182 sp003481535	0.010%	Veillonella parvula	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.

Bacteroides intestinalis	0.009%	Bacteroides sp003463205	0.009%
Blautia_A sp900548245	0.009%	Butyrivibrio_A sp900543865	0.009%
crAssphage cr4_1	0.009%	Intestinibacter sp900553485	0.009%
Phascolarctobacterium faecium	0.009%	Porphyromonas_A somerae	0.009%
Ruminococcus_C sp000980705	0.009%	Streptococcus sp001556435	0.009%
UBA1777 sp900547315	0.009%	Veillonella infantium	0.009%
Veillonella sp900549845	0.009%	Bacteroides sp902362375	0.008%
Blautia stercoris	0.008%	CAG-83 sp000435555	0.008%
Collinsella sp003487125	0.008%	Collinsella sp900760905	0.008%
Enterobacter bugandensis	0.008%	Enterocloster sp005845215	0.008%
Enterococcus_B sp011038845	0.008%	Erysipelatoclostridium spiroforme	0.008%
Ezakiella massiliensis	0.008%	Lachnospira sp003537285	0.008%
MWCK01 sp002070005	0.008%	Adlercreutzia celatus_A	0.007%
Clostridium baratii	0.007%	Collinsella sp900544725	0.007%
Collinsella sp900547765	0.007%	Collinsella sp900549455	0.007%
Collinsella sp900554135	0.007%	Collinsella sp900556205	0.007%
Corynebacterium sp001767255	0.007%	Corynebacterium sp001831515	0.007%
Dorea_B phocaeensis	0.007%	Enterococcus_A avium	0.007%
F23-B02 sp002472405	0.007%	Faecalibacterium prausnitzii_H	0.007%
Gemmiger qucibialis	0.007%	Hafnia proteus	0.007%
NK3B98 sp900758315	0.007%	Romboutsia timonensis	0.007%
RUG115 sp900066395	0.007%	Sellimonas intestinalis	0.007%
Sutterella wadsworthensis	0.007%	Acetatifactor sp900066365	0.006%
Bacteroides sp007097645	0.006%	Bacteroides sp012113595	0.006%

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PATIENT: XXXXXXXXXXXXXXXXXXXX
TEST REF: TST-NL-XXXXX
TEST NUMBER: T-NL-XXXXXX
GENDER: XXXXX
AGE: XX
COLLECTED: 2025-XX-XX
PRACTITIONER:
XXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXX

TEST NAME: [Baby Gut Health] Tiny Health Sample Report

CAG-110 sp000435995	0.006%	CAG-83 sp000431575	0.006%
CAG-83 sp900552475	0.006%	Collinsella sp900540945	0.006%
Collinsella sp900541745	0.006%	Cronobacter malonaticus	0.006%
D5 sp900113995	0.006%	Dialister invisus	0.006%
Dysosmobacter sp014297375	0.006%	Enterocloster sp001517625	0.006%
Enterococcus_B pernyi	0.006%	Erwinia coffeiphila	0.006%
Erwinia sp003751505	0.006%	Faecalibacterium sp900539945	0.006%
Haemophilus_D parainfluenzae_M	0.006%	Kosakonia radicincitans	0.006%
Kosakonia sacchari_B	0.006%	Peptoniphilus_A grossensis	0.006%
Pseudoruminococcus massiliensis	0.006%	Roseburia sp003470905	0.006%
Streptococcus sp900766505	0.006%	Yersinia frederiksenii_A	0.006%

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