DAYHOFF
TECHNOLOGIES

Microbiome Analysis Report

Sarah Johnson - 43 years old

Kit #: AJM2Q6N7P8K9 Report Date: 9/16/2025 Sample Type: Stool

Executive Summary

Your gut bacteria profile looks well-balanced. Key groups that help break down carbs and fiber, like Bacteroides, Prevotella, Akkermansia, and Ruminococcus, are at healthy levels, showing good digestion and gut barrier support. Helpful "peacekeeper" bacteria like Faecalibacterium and Roseburia are present in high amounts, which means strong production of gut-healing compounds and reduced inflammation. One group, Eubacterium, is lower than expected, which may mean less variety in certain beneficial functions, but this is made up for by other supportive bacteria. Overall, the microbiome appears strong, healthy, and resilient, with just small areas where diversity could improve.

Overall Score

728.45

Your potential to produce propionate is optimal.
Great job maintaining gut health!

Average Score

Individual Sample Scores

715.2	**732.8**	**737.3**
Sample 1	Sample 2	Sample 3
Aug 12, 2025	Aug 14, 2025	Aug 15, 2025

Health Associations

● Fiber Breakers & Digesters

● Gut Soothers & Healers

● Mucus Layer Maintainers

● Everyday Balancers

Related Bacteria Species

Analysis includes 3 samples per test kit. Relative abundance values shown are averages across all samples. Individual sample variations are displayed in the trend charts below.

Bacterial Species	Avg. Abundance	Sample Trend	Status
● *Bacteroides thetaiotaomicron* S1: 7.8% S2: 8.9% S3: 8.7%	8.45%		Normal
● *Prevotella spp.* S1: 5.9% S2: 6.2% S3: 6.3%	6.12%		Normal
● *Faecalibacterium prausnitzii* S1: 11.8% S2: 13.2% S3: 13.0%	12.67%		High
● *Akkermansia muciniphila* S1: 3.9% S2: 4.4% S3: 4.4%	4.23%		Normal
● *Eubacterium* S1: 1.9% S2: 2.3% S3: 2.3%	2.18%		Low
● *Ruminococcus* S1: 5.4% S2: 6.1% S3: 6.2%	5.89%		Normal
● *Roseburia* S1: 6.8% S2: 7.6% S3: 7.7%	7.34%		High

Descriptions

Detailed scientific descriptions of each bacterial species found in your sample, including key research studies and clinical significance.

Bacteroides thetaiotaomicron

Description:

A Gram-negative anaerobe specialized in degrading dietary and host glycans, supporting nutrient absorption and mucus regulation. Plays a key role in shaping gut carbohydrate availability and immune modulation.

Key Studies:

- Expanded polysaccharide utilization loci (PULs)
- OMVs promoting barrier function
- Nitrogen metabolism dependence on ammonium

Normal typical and balanced in healthy gut microbiota.

Prevotella spp.

Description:

Gram-negative anaerobes specializing in fermentation of plant polysaccharides; linked to fiber-rich diets and distinct from Bacteroides-dominated enterotypes. Often diet-associated rather than universally beneficial or harmful.

Key Studies:

- Diet and global microbiome differences
- Prevotella copri and glycemic control
- Biomarker role of Prevotella vs Bacteroides

Normal commonly present depending on dietary fiber intake.

Faecalibacterium prausnitzii

Description:

One of the most abundant Firmicutes in healthy individuals; a major butyrate producer with strong anti-inflammatory activity. Frequently considered a "sentinel species" for intestinal health.

Key Studies:

- Review on intestinal health
- Reduced abundance in ulcerative colitis/Crohn's
- Carbohydrate metabolism regulation

High enrichment typically indicates healthy, anti-inflammatory gut environment.

Akkermansia muciniphila

Description:

Mucin-degrading Verrucomicrobia that colonizes the mucus layer; improves barrier function and is linked to favorable metabolic outcomes. Widely studied for its potential as a next-generation probiotic.

Key Studies:

- Cross-talk with epithelium and metabolic health
- Reduction in ulcerative colitis
- Association with obesity and T2D

Normal steady populations are favorable for mucus and metabolic balance.

Eubacterium (genus)

Description:

A diverse genus of Firmicutes with many butyrate-producers; contribute significantly to SCFA pools and modulation of inflammation. Important in maintaining colonic epithelial health.

Key Studies:

- Butyrate production and immunomodulation
- Reduced levels in inflammatory diseases and cancer

Low may reflect reduced butyrate production and impaired gut barrier support.

Ruminococcus

Description:

Anaerobic Firmicutes known for degrading resistant starch, cellulose, and complex polysaccharides. Contribute to fermentation and SCFA production but also produce hydrogen as a by-product.

Key Studies:

- Hydrogen and gas production roles
- Abundance shifts with diet and disease

Normal core member of fiber-fermenting gut community.

Roseburia

Description:

Butyrate-producing Firmicutes, strongly anti-inflammatory and associated with improved barrier integrity. Often depleted in metabolic or inflammatory disorders.

Key Studies:

- Reduced abundance in IBD and colorectal cancer
- Butyrate-producers review

High enrichment suggests strong SCFA production and good barrier/immune health.

Action Plan

Support Eubacterium 🥦🍇

Since this group is low, focus on increasing microbial diversity with a wide variety of plant fibers (beans, leafy greens, nuts, seeds) and polyphenol-rich foods (berries, green tea, dark chocolate).

Maintain strong "peacekeepers" (Faecalibacterium & Roseburia) 🥔🍌🥣

These are high (a good sign), so keep feeding them with resistant starch (cooked/cooled potatoes, rice, oats) and prebiotic fibers (onions, garlic, asparagus).

Stabilize the core community (Bacteroides, Prevotella, Ruminococcus, Akkermansia) 🥕🍎🌾

All are at normal levels, so maintain balance with a steady intake of fruits, vegetables, and whole grains, plus some fermented foods for gut barrier support.

Protect mucus layer (Akkermansia) 🥬🥒

Keep supporting this mucus-maintaining bacteria with polyphenol-rich foods (cranberries, pomegranate) and avoiding excessive processed sugar that can thin the mucus barrier.

Lifestyle synergy 🏃🛌🧘

Exercise, restorative sleep, and stress control reinforce the positive effects of these bacteria and help keep the microbiome resilient.

Book a Consultation

Our Expert Team

Microbiome Specialists

Schedule time with our experts to discuss your needs and get tailored recommendations. Our gut microbiome specialists are available to walk you through your lab report, explain what your results mean, and provide personalized recommendations based on your data. They can also answer questions, highlight key insights, and help you understand how your microbiome may impact your health.

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Method Limitation

Dayhoff Technologies' results and insights are based on shotgun metagenomics sequencing, which allows us to identify and quantify thousands of microbial taxa in the gut microbiome. However, not all microorganisms have been fully captured in current genomic reference databases, meaning it is not yet possible to assess the microbiome comprehensively. Some organisms present in the gut may not have sequenced genomes; in such cases, our pipeline can identify their closest relatives based on sequence homology. Certain taxa also cannot be distinguished at very fine resolution (e.g., strain level) due to high sequence similarity. In addition, some sequences may not align to a known organism if they are poorly characterized or lack a reliable consensus reference.

Dayhoff Technologies continuously monitors updates in public genomic databases and incorporates new reference data when sufficient high-quality information becomes available. Detection of a microorganism in this test does not indicate the presence of disease, and absence of detection does not exclude it. Other organisms may also be present but not identified by this method. This test is not a substitute for clinical diagnostics or antimicrobial susceptibility testing. Results are qualitative and indicate the presence or absence of annotated organisms detected through sequencing.

This report was generated on 9/16/2025 by Dayhoff Technologies

For questions about this report, please contact our support team at support@dayhoff.ai