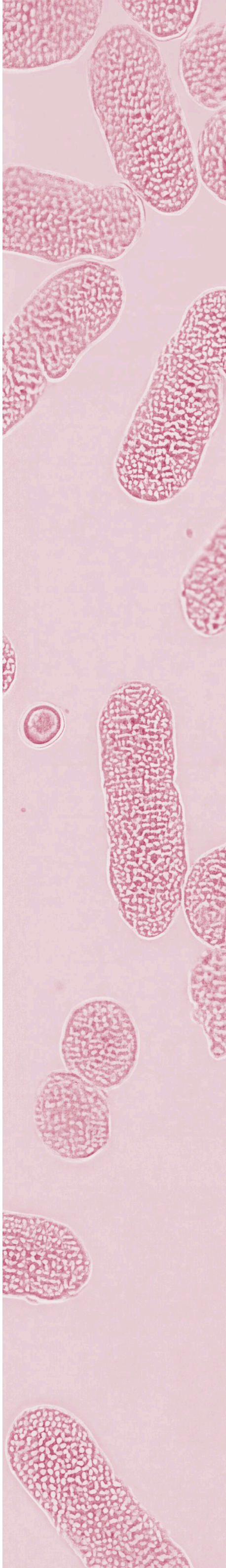
microba

Overview:

The science behind Microba's gut health testing

From validated sample preservation to peer-reviewed bioinformatics, here's how Microba Microbiome Explorer turns raw metagenomic data into clinically useful gut health insights.



The gut microbiome

The human gut harbours trillions of microorganisms whose collective genome — the microbiome — encodes metabolic capabilities far exceeding those of the human genome alone.[1] Over the past two decades, large-scale sequencing studies have demonstrated that the composition and function of this microbial community are associated with a wide range of health outcomes.[2,3] Disruption of a healthy gut microbiome, often called dysbiosis, has been linked to gastrointestinal disorders, autoimmune conditions, cardiometabolic diseases, and neurological conditions.[4]

Validated sample preservation protects the accuracy of every result

The moment a sample is collected, the clock starts. Microbial composition shifts fast if preservation isn't handled correctly — and most collection methods weren't designed with that in mind.

Microba's FLOQSwab-ADT was benchmarked head-to-head against the most widely used alternatives.[6] It came out on top. Practitioners can be confident the sample that leaves the patient's home is the sample that gets analysed. No degradation. No compromise.

Best reproducibility

Highest technical (between-replicate) reproducibility and compositional stability relative to flash-frozen controls in a peer-reviewed evaluation

Climate resilient

Stable across -20°C, room temperature, and 50°C for four weeks — suitable for postal collection Australia- wide

100,000 metagenomes processed in an accredited laboratory

Most providers are accredited for what happens in the lab. Microba is also accredited for what happens to the data after it leaves the bench.

Microba operates an ISO 15189 NATA-accredited laboratory with automated QC from sample receipt to data generation — anything outside predefined thresholds is flagged. 100,000+ metagenomes processed, every result a practitioner receives has been through the same rigorous process.

ISO 15189

Internationally recognised standard for medical laboratory processes — covering sample receipt, sequencing, and data generation

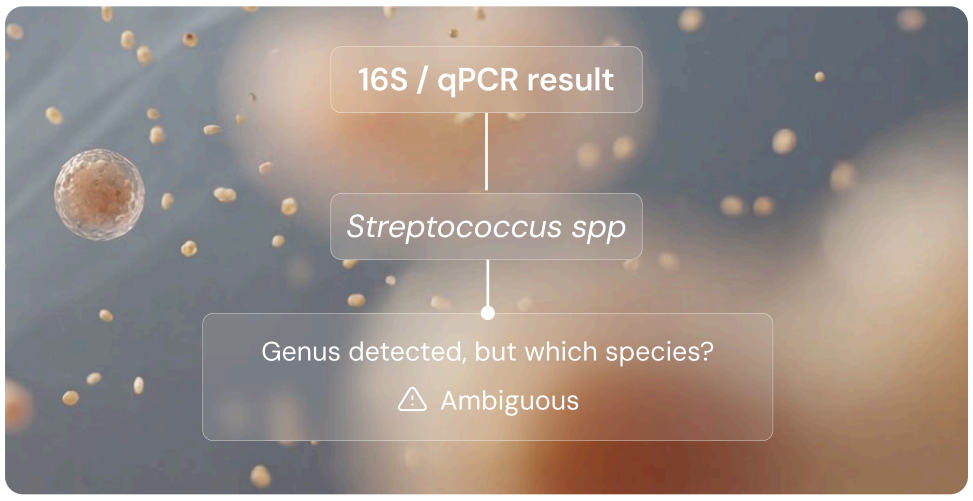
ISO 13485

Quality management system for software as a medical device — covering the bioinformatic analysis and interpretation pipeline

Shotgun metagenomics identifies species that other methods miss entirely

Shotgun metagenomics sequences all DNA from a faecal sample — not a single gene, not a predefined panel. The result is a comprehensive, unbiased view of the entire microbial community at species level (not genus level).[7] That distinction matters clinically. Different species within the same genus can have very different roles in health, and without species-level resolution you're working with an incomplete picture.

The *Streptococcus* example



632 species vs 57

In a direct comparison, shotgun metagenomics identified 632 species in a sample where 16S rRNA gene sequencing detected only 57[8] — an order-of-magnitude difference in resolution that directly affects clinical utility.

A comparison of technologies

	16S rRNA	qPCR / culture	Shotgun metagenomics
Taxonomic resolution	Genus level	Predefined targets only	Species and strain level
Coverage	Bacteria and Archaea only	Limited panel	Bacteria, Archaea, eukaryotes
Functional profiling	Not possible	Limited panel	Gene and pathway level
Novel species detection	No	No	Yes
PCR bias	Yes	Yes	Minimal

Species tell you who's present. Function tells you what they're doing.

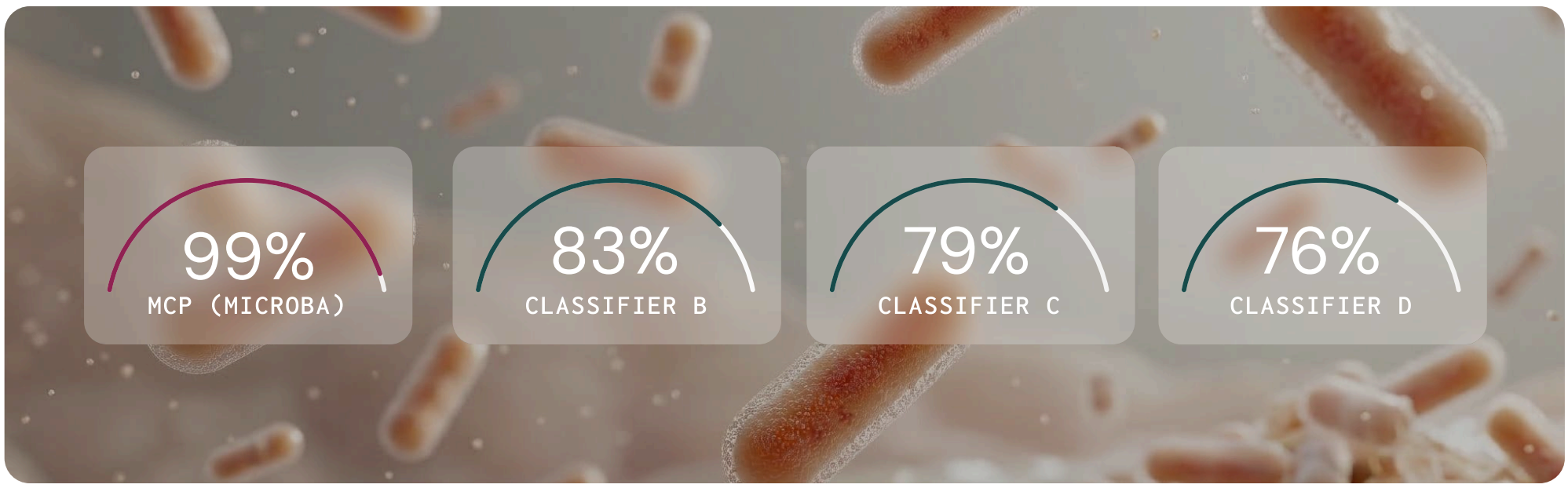
Identifying what's in the microbiome is the starting point, not the finish line. Shotgun metagenomics goes further, identifying not only the species, but also the presence of key health-associated metabolic genes and pathways across the entire microbial community. Can this community produce butyrate? Is there a high relative abundance of species that can consume mucin?

That means assessing functional capacity, not just composition or metabolite levels.These are the questions that move a result from interesting to actionable. Measuring outputs alone tells you what's happening right now. Functional capacity tells you what the community is capable of and that's a different clinical conversation entirely. One that genus-level and output-only methods can't have.

Against nine widely used classifiers, MCP had the strongest overall performance

Generating sequence data is only the first step. The bioinformatic classifier determines what gets identified, what gets missed, and what gets falsely reported. Microba's Community Profiler (MCP) was benchmarked against nine other classifiers across 140 simulated microbial communities in a peer-reviewed study.[5] The benchmarking results highlight the difference.

Precision (% — Higher better)



Fewest false positives

4–16x fewer species reported that aren't actually there, compared to other classifiers.[5]

Lowest detection limit

MCP can detect species present at levels 20 to 60 times lower than other tools would miss entirely.[5]

Highest accuracy

MCP achieved the highest combined precision and recall across all tested conditions – outperforming every other evaluated classifier by five to 20 percentage points.

Accurate abundance estimates

MCP reports how much of each species is present with a level of accuracy that matches or exceeds every other leading classifier tested.[5]

Three integrated layers translate microbial presence into clinical meaning

Separately, each layer is informative. Together they deliver something no single method can. Microba's Microbiome Explorer combines three layers of information to connect what's present in the microbiome with measurable clinical markers of gut function and inflammation.

Pathogen detection
A panel of 13 common bacterial pathogens and five parasites detected via CE-certified multiplex PCR assays.

Human stool markers
Six GI health markers including calprotectin, lactoferrin, faecal occult blood, secretory IgA, pancreatic elastase, and zonulin — assessed using CE certified immunohistochemistry assays. Faecal pH is also measured as an investigative marker for research use only.

Microbiome profiling
Species-level profiling of 28,000+ species including microbial diversity score, microbial richness, and 16 health-associated functional markers —
such as butyrate production, trimethylamine, hexa-acylated lipopolysaccharides, mucin degradation, and oxalate consumption.

Reported markers are clinically relevant and evidence-backed

Not every microbial signal is clinically meaningful. Microba applies a rigorous three-tier scientific curation framework – only markers that are both evidence-backed and clinically relevant are included in the report.* Practitioners can be confident that everything reported has a reason to be there. Here's the standard every marker is held to:

TIER 1

PLAUSIBLE MECHANISM OF ACTION
In-vitro or in-vivo data must demonstrate why the microbial marker is biologically connected to the relevant health category.

TIER 2

REPRODUCIBLE HUMAN ASSOCIATIONS
At least two peer-reviewed human studies must show a direct or indirect link between the marker and the health outcome.

TIER 3

SIGNIFICANT ASSOCIATIONS IN MICROBA'S DATASET
The marker must show a statistically significant association in Microba's own database of 19,000+ consented patient profiles, controlled for age, sex, BMI, and bowel habits.

**A small number of markers are included with clearly disclosed exceptions — acetate and intestinal inflammation, beta-glucuronidase and impaired detoxification (both mechanism only), and Emerging Markers. Where exceptions exist, they are explicitly flagged in the report.*

A rigorously defined reference group of 450+ individuals removes technical bias from every result

Results are only meaningful when compared against the right baseline. Many commercially available tests either provide no details about their reference cohort, use publicly available microbiome data, or compare samples against their entire database regardless of health status. Microba's cohort of more than 450 individuals meet strict health inclusion criteria – and all reference samples were collected and processed using the same workflow as patient samples, eliminating a significant source of technical bias

The Microba's healthy reference group

- More than 450 individuals.
- Strict inclusion criteria.
- Processed through the same workflow as patient samples

Selected inclusion criteria

Selected participants met key lifestyle criteria consistent with general health, including:

- BMI above 30
- Regular daily intake of fruits and vegetables
- Low to moderate alcohol consumption.
- Individuals also reported no or minimal gastrointestinal symptoms.
- No major medical conditions
- Mild or lower stress, anxiety, and depression

The report tells you what's there. Evidence-graded actions tell you what to do about it.

Microbial markers and gastrointestinal markers are organised into six health categories that map to recognisable clinical concepts. Where a marker falls outside the healthy reference range, the report provides evidence-graded possible actions – reviewed against the available scientific evidence and graded using the NHMRC evidence grading framework. The result is a report that doesn't just tell you what's there; it also helps identify which dietary, supplement, or lifestyle interventions are most strongly supported by the evidence.

- Intestinal inflammation
- Systemic inflammation
- Metabolic health
- Gut barrier function
- Gut motility
- Pathogen presence

Worked example: Mucin degradation and intestinal inflammation

Mechanism: When dietary fibre is insufficient, mucin-degrading microbes can consume the protective mucus layer lining the gut, increasing microbial contact with the intestinal epithelium and triggering immune activation.

Human associations: A cross-sectional study of more than 1,000 individuals found a significant positive association between mucin-degrading pathway abundance and faecal calprotectin.[8] Elevated mucin degrading pathways have also been observed in colorectal cancer cohorts.[9,10]
Internal validation: In Microba's dataset, mucin-degrading species are significantly increased in conditions related to intestinal inflammation.

What sets Microba's approach apart

High-resolution metagenomics

632 vs 57 species identified in the same sample — shotgun vs 16S

Peer-reviewed, benchmarked bioinformatics

9 classifiers tested against MCP in a formal peer-reviewed study

Whole-microbiome functional assessment

Entire community assessed for metabolic function, not just a handful of known species

Rigorous three-tier evidence curation

3 tiers mechanistic, human association, and internal validation —all required*

Like-for-like healthy reference group

450+ individuals meeting strict health criteria, same workflow as patient samples

Dual accreditation

ISO 15189 + ISO 13485 medical laboratory + software as a medical device

The microbiome component of Microba Microbiome Explorer is for research use only and is not a diagnostic tool. Microbiome results should be interpreted by qualified healthcare practitioners in the context of a patient's clinical history, symptoms, and other diagnostic findings.

Better science.
Better Insights.
Better Health.

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