

# 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.<sup>1</sup> 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.<sup>2,3</sup> Disruption of a healthy gut microbiome, often called dysbiosis, has been linked to gastrointestinal disorders, autoimmune conditions, cardiometabolic diseases, and neurological conditions.<sup>4</sup>

## 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.<sup>6</sup> 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. One accredited laboratory. Zero compromises

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 with no shortcuts at any stage.

### ISO 15189

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

### ISO 13485

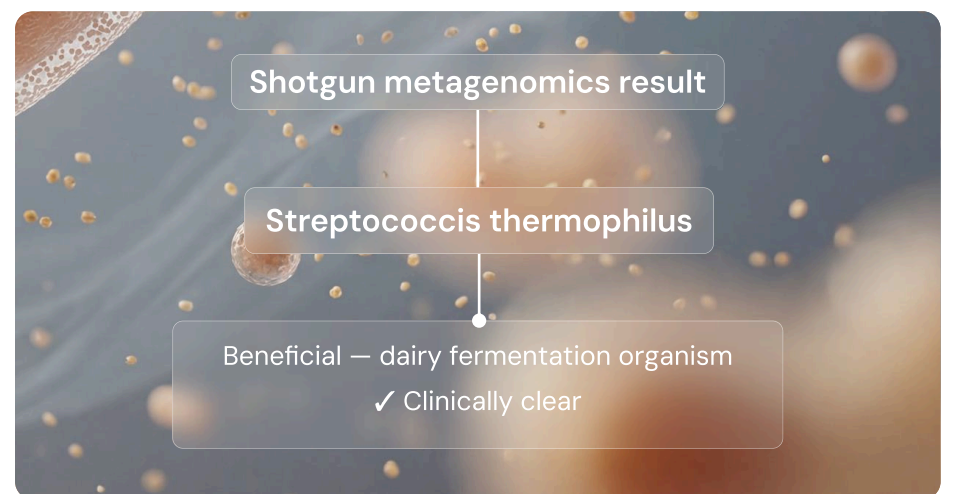
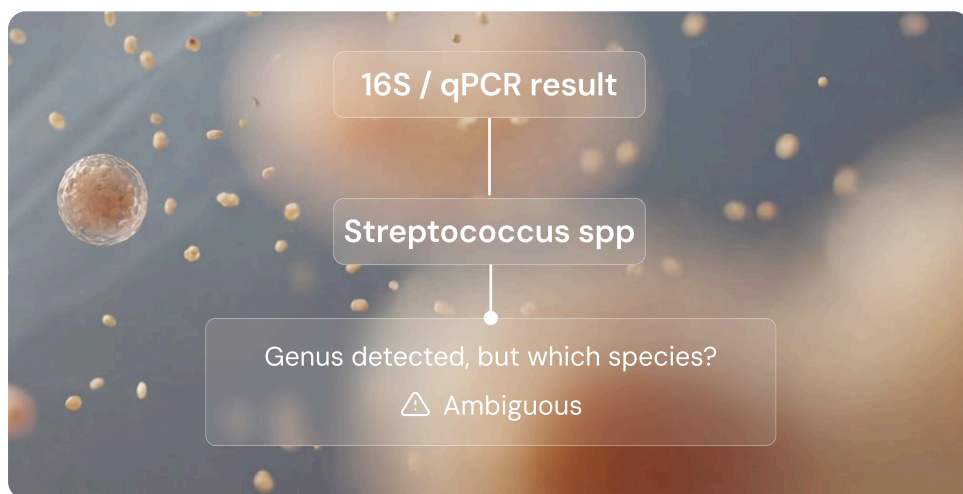
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Quality management system for software as a medical device — covering the bioinformatic analysis and interpretation pipeline

# Shotgun metagenomics identifies species that other methods miss entirely

Shotgun metagenomics sequences all DNA from a faecal sample — no single gene, no predefined panel. The result is a comprehensive, unbiased view of the entire microbial community at species level, not just at the genus level.<sup>7</sup> That distinction matters clinically. Without species-level resolution, you can't differentiate between species and that difference can be clinically significant.

## 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 — 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.

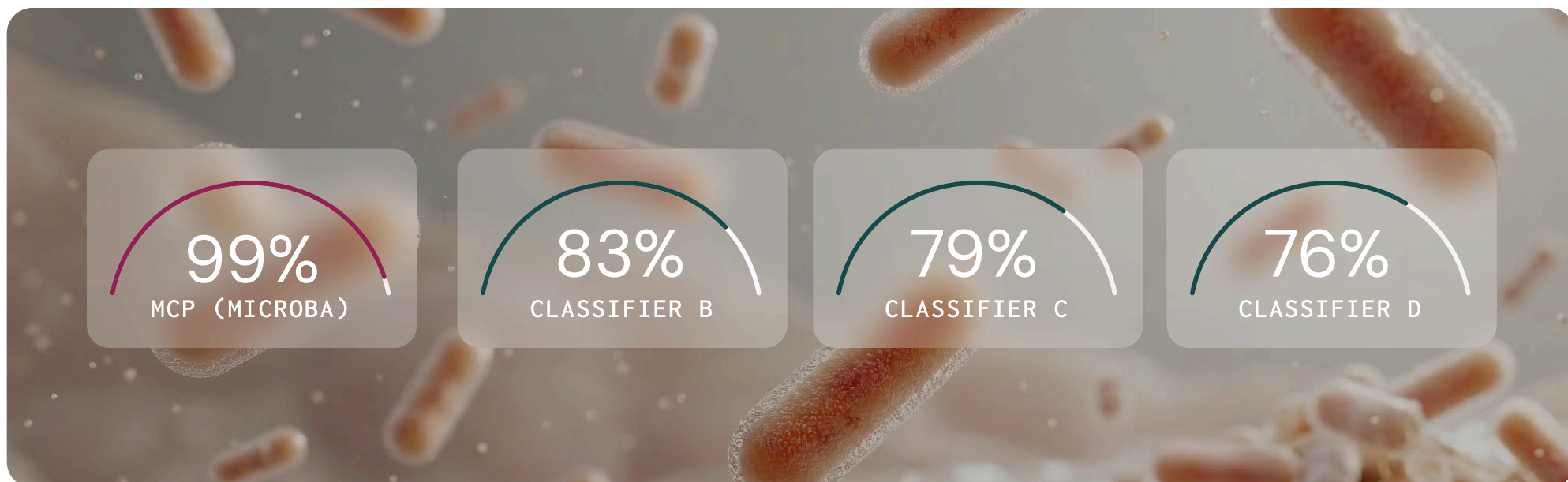
Identifying what's in the microbiome is the starting point, not the finish line. Shotgun metagenomics goes further, identifying the metabolic genes and pathways present across the entire microbial community — assessing functional capacity, not just composition. Can it produce butyrate? Is it degrading the protective mucus layer?

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 classifiers. MCP outperformed every one.

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.<sup>5</sup> The numbers tell the rest of the story.

Precision (% — Higher better)



### Fewest false positives

4–16x fewer species reported that aren't actually there, compared to other classifiers.<sup>5</sup>

### Highest accuracy

99% of species MCP reports are genuinely present in the sample, outperforming every other classifier by five to 20 percentage points across every condition tested.

### Lowest detection limit

MCP can detect species present at levels 20 to 60 times lower than other tools would miss entirely.<sup>5</sup>

### 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.<sup>5</sup>

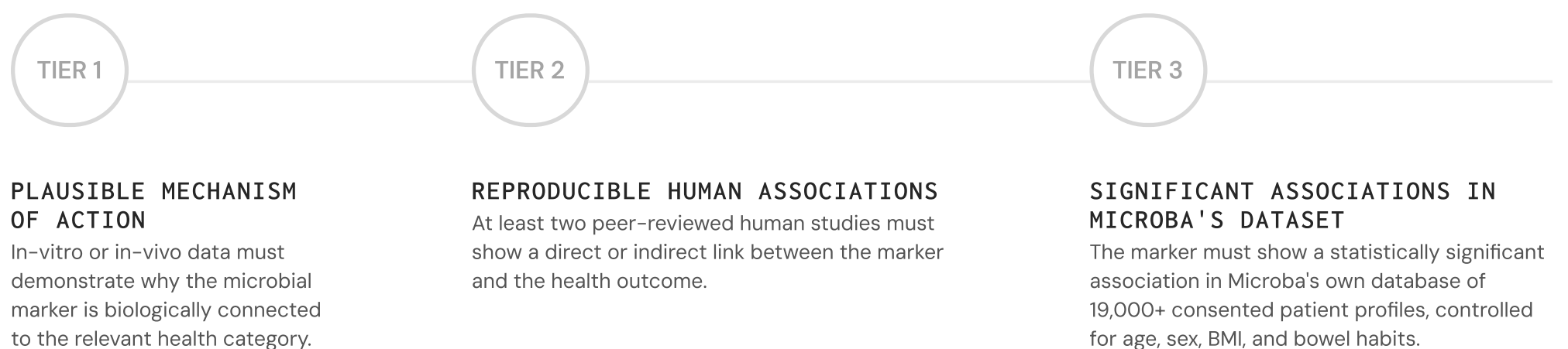
# Three integrated layers translate microbial presence into clinical meaning

Separately, each layer is informative. Together they deliver something no single method can. Microba Microbiome Explorer combines three layers of information — integrating microbiome profiling with direct markers of gut function and inflammation to give a complete clinical picture.

- 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.

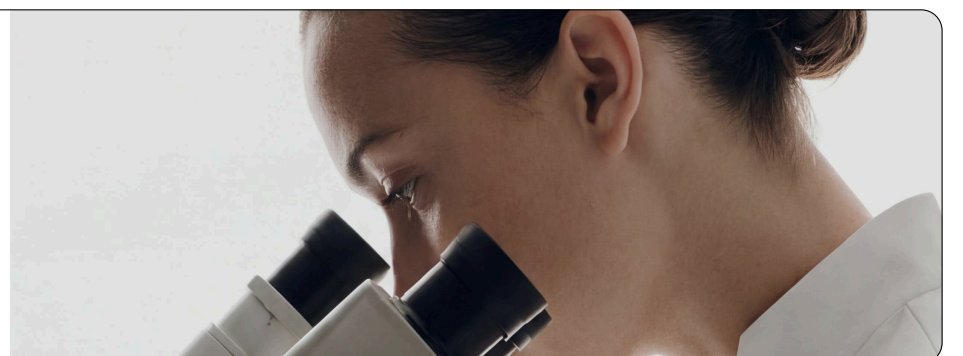
## Every marker reported is clinically relevant and evidence-backed

Not every microbial signal is clinically meaningful. Microba applies a rigorous three-tier evidence 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:



Looking for the deep dive?

[Read the full article](#)



\*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. Microba's cohort of more than 450 individuals meets strict health inclusion criteria – and all reference samples were collected and processed using exactly 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 gives you a clinically defensible starting point for what to do next.

 Intestinal inflammation

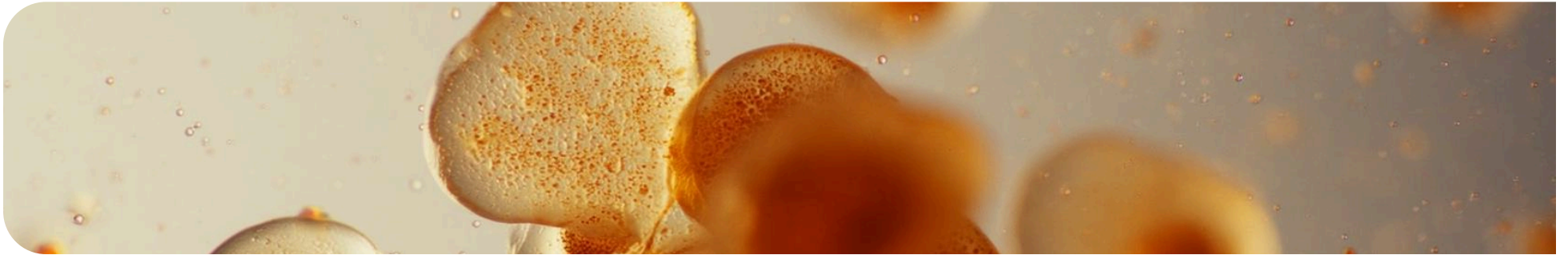
 Systemic inflammation

 Metabolic health

 Gut barrier function

 Gut motility

 Pathogen presence



## Worked example: Mucin degradation and intestinal inflammation

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. A cross-sectional study of more than 1,000 individuals found a significant positive association between mucin-degrading pathway abundance and faecal calprotectin.<sup>8</sup> Elevated mucin degrading pathways have also been observed in colorectal cancer cohorts.<sup>9,10</sup> 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

# Better science. Better Insights. Better Health.

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