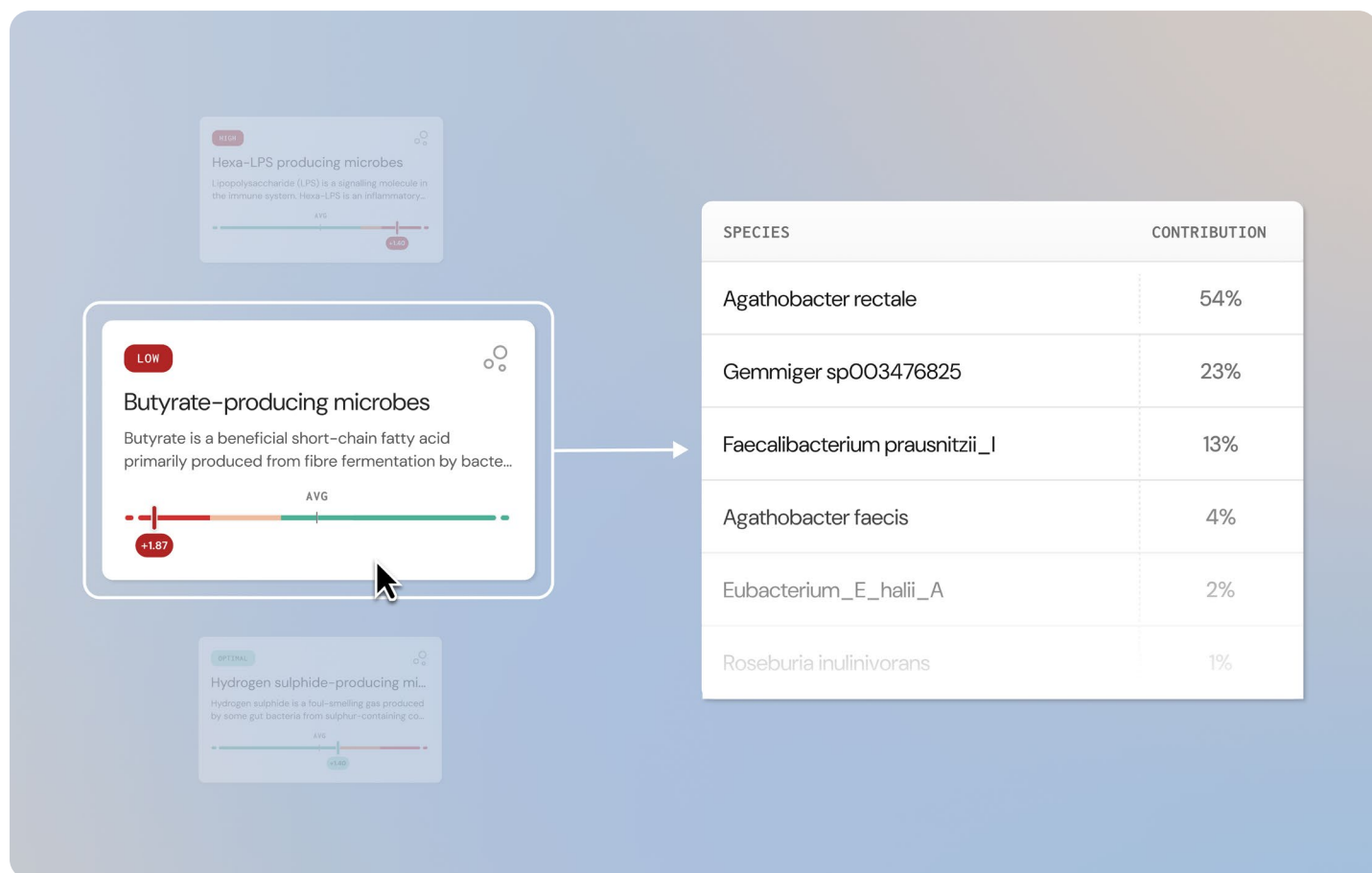


Species that inform this marker: a practitioner guide

How to read the contributing species list,
and what it does and does not tell you.



The species behind each marker are now visible in the report.

Every functional microbiome marker now shows the species contributing to it under Relationships, with each species' share of that marker given as a percentage.

Open a marker and scroll to Relationships, then "Species that inform this marker". The table lists the contributing species and their percentage contribution, sorted highest to lowest. Because the list is generated from the individual microbiome profile, it will differ between patients and between retests.

Previously, identifying the species contributing to a marker meant looking them up individually in Species Explorer. Now, the species list sits alongside the functional marker it informs, making it easier to see how the marker was derived.

Contribution is a share of the marker, not an amount.

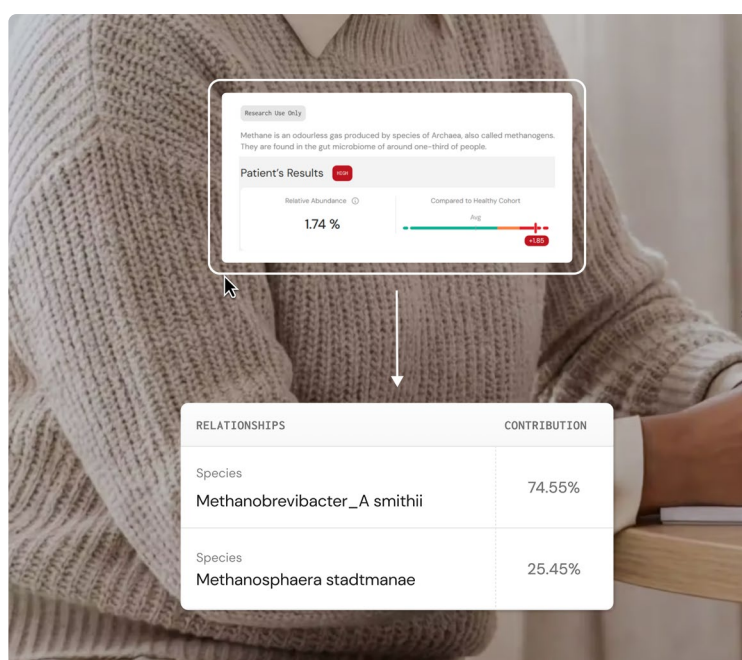
Contributions sum to 100% within each marker. A species at 75% accounts for most of this patient's capacity for that function. It does not indicate whether functional capacity is high or low.

The order of operations matters. First, read the marker value and its comparison to the healthy cohort to understand whether functional capacity is high, low or within range. Then open the contributing species list to see how that capacity is distributed across the microbial community.

The species list does not answer "how much?" It answers "which organisms contribute, and in what proportion?" For example, a species contributing 74.55% in a patient whose marker sits high and a species contributing 74.55% in a patient whose marker sits within range represent the same relative contribution, but across very different marker results. The contribution percentage, therefore, needs to be interpreted in the context of the marker value.

METHANE PRODUCING ARCHAEA

Methane-producing Archaea, flagged high at 1.74% relative abundance. The two contributors account for 74.55% and 25.45% of the marker, summing to 100%. The "Species that inform this marker" describes how the functional capacity is divided, not how much of it there is.

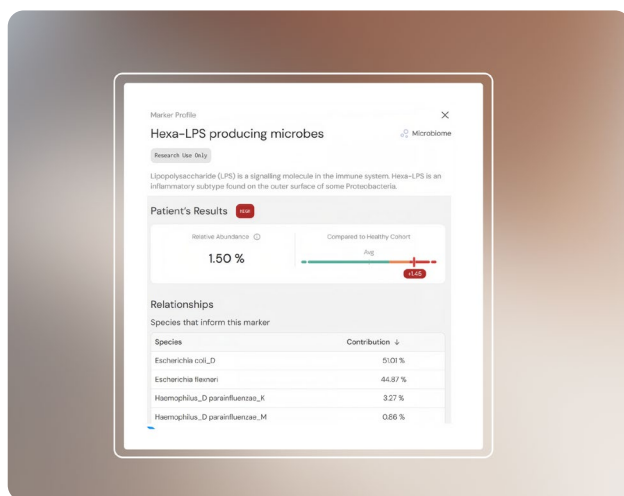


Example: Two patients, the same result, almost no species in common.

Worked example: hexa-LPS producing microbes.

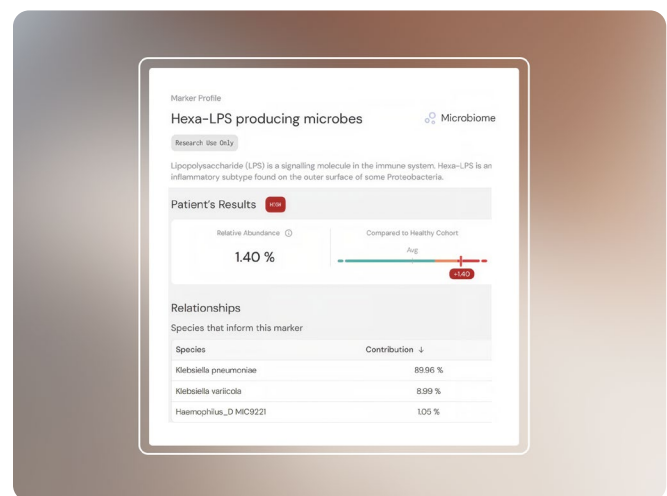
Two patients both have high hexa-LPS-producing microbe results at similar values. One is driven almost entirely by *Escherichia* species, the other by *Klebsiella*, with no *Escherichia* species detected.

Patient A sits at 1.50% relative abundance, flagged high, with *Escherichia coli_D* contributing 51.01% and *Escherichia flexneri* 44.87%. Patient B sits at 1.40%, flagged high, with *Klebsiella pneumoniae* contributing 89.96% and *Klebsiella variicola* 8.99%. Despite the similar marker results, the species contributing to them are almost entirely different.



PATIENT A.

Hexa-LPS flagged high at 1.50%, held almost entirely by *Escherichia*.



PATIENT B.

Hexa-LPS flagged high at 1.40%, held almost entirely by *Klebsiella*, with no *E. coli* present.

The list explains how a result was derived. It is not a decision aid.

Its value is in transparency: showing how a marker's functional capacity is distributed across the microbial community and identifying the species contributing to that result.

Seeing that a marker draws on many different organisms, in proportions that vary between patients, helps clarify what the marker is actually measuring: a community-level function rather than a single species. This new feature supports understanding of the result, rather than directing a decision.

It can also be useful in the consultation. Patients often arrive having read about a particular organism and want to know whether they have it. The list lets you see whether that species contributes to the marker, and importantly how its contribution sits alongside other species performing the same function. That helps address the common misunderstanding that a community-level function can be attributed to a single organism.

A large contribution share is not a reason to target a species.

A high contribution to a marker does not, by itself, make a species-targeted intervention appropriate. Many microbial functions are shared across multiple species, so reducing one organism may not meaningfully reduce the community's overall capacity to perform that function.

Two common pitfalls to avoid. Both read a community-level finding at species level, and both misuse the contribution share, in opposite directions.

- **Acting on a large share.** A species contribution of 90% does not mean that a species should be targeted, just as a contribution of 9% does not mean it is unimportant. The percentage describes how functional capacity is distributed across the contributing species; it does not predict the effect of removing any one of them.
- **Acting on the absence of a familiar species.** Scanning the list for a familiar organism and treating its absence from the contributor list as the key finding makes the same mistake in reverse. The functional capacity represented by the marker may be contributed by entirely different species you were not looking for.

The contribution list is intended to explain how the marker result was derived, not to identify species for treatment.

Capacity is not the same as measurement.

A marker describes what the community has the potential to do, not the amount of the metabolite itself. Whether that potential is realised depends partly on substrate availability, which is why diet is a central lever.

A metagenomic result is built from genes, so it describes the community's genetic capacity to perform a function rather than a direct measurement of the product. Potential becomes reality only when the right substrates are present. That is why diet is both context for interpretation and a possible point of intervention, and why results are read alongside symptoms, clinical history and medications rather than on their own. The contributing species list sits within this: it shows how the capacity is distributed, not how much of anything is being produced.

At Microba, expect better. Because we do.

We develop world-leading microbiome research and technology.
We deliver tests that go deeper and broader. We craft insights that improve
people's lives.

Why?

Because better is possible. Because better means more freedom and
confidence. And, most importantly, because more freedom and confidence means
better, happier lives. We are an ecosystem of people organised around one simple
principle – making you better. Because better care doesn't just transform individual
lives, it builds healthier, happier communities.



MICROBA LIFE SCIENCES LIMITED
ABN 78 604 991 173

1300 974 621
HELLO@MICROBA.COM