



○ **Easy to interpret summary of findings**

○ **Scientifically graded research insights¹**

- Targeted diet, supplemental and lifestyle research insights.
- All research insights are evidence-based and graded using a framework based on the National Health & Medical Research Council (NHMRC) guidelines.

○ **Diversity¹**

- Microbial diversity and richness (number of species) compared to a healthy cohort.

○ **28,000+ microbial species¹**

- Bacterial species identification included, but not limited to species within the following genus *Agathobacter*, *Akkermansia*, *Bifidobacterium*, *Bilophila*, *Citrobacter*, *Desulfovibrio*, *Eggerthella*, *Enterobacter*, *Escherichia*, *Faecalibacterium*, *Klebsiella*, *Lactobacillus*, *Oxalobacter*, *Porphyromonas*, *Prevotella*, *Rosburia*, *Ruminococcus*, *Streptococcus*.
- Fungi, parasite and archaea detection.

○ **Production of microbial markers (microbes with the genetic potential to produce metabolites)¹**

- Butyrate, acetate, propionate, 3-indolepropionic acid (IPA), hexa-acylated lipopolysaccharides (hexa-LPS), trimethylamine (TMA), hydrogen sulphide, branched-chain amino acids (BCAA), *B.fragilis* toxin, methane, beta-glucuronidase.

○ **Microbial consumption (microbes with the genetic potential to consume compounds)¹**

- Mucin, oxalate.

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1. The metagenomic assays used in MetaXplore™ are to determine the microbiome populations and associated functional pathways in a faecal sample. The application is for research use only and not for diagnosis.