ASX Announcement
13 April 2022

Microba CSO presents to US industry conference

Microba Life Sciences Limited (ASX: MAP) ("Microba" or the "Company") is pleased to announce Chief Scientific Officer A/Professor Lutz Krause will present to microbiome research and development professionals at the 7th Annual Translational Microbiome Conference running from 13 – 14 April in Washington, DC. The virtual presentation will be delivered on Day One at 4.30PM 13 April (US EDT) / 6:30AM 14 April (AUS EST).

A copy of the presentation is attached to this announcement.

This announcement has been authorised for release by the Chairman and Chief Executive Officer.

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About Microba Life Sciences Limited

Microba Life Sciences is a precision microbiome company driven to improve human health. With world-leading technology for measuring the human gut microbiome, Microba is driving the discovery and development of novel therapeutics for major chronic diseases and delivering gut microbiome testing services globally to researchers, clinicians, and consumers. Through partnerships with leading organisations, Microba is powering the discovery of new relationships between the microbiome, health and disease for the development of new health solutions.

For more information visit: www.microba.com

Microba encourages all current investors to go paperless by registering their details with the designated registry service provider, Automic Group.

MICROBA™

Empowering translational research outcomes with precision microbiome analysis & AI

Translational Microbiome Conference

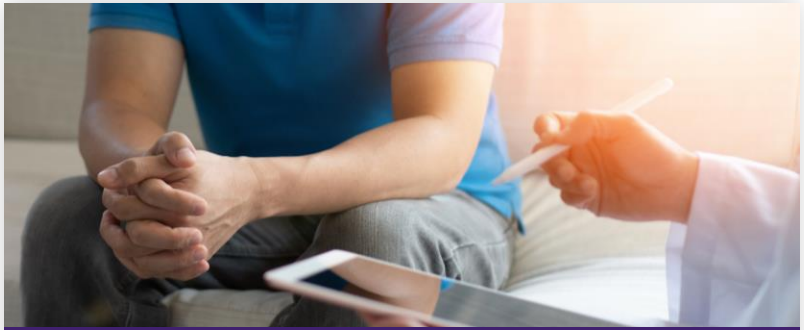
A/Professor Lutz Krause
Chief Scientific Officer, Microba Life Sciences

April 2022 | Authorised for release by the CEO and Chairman

Microbiome science is changing medicine and will **transform chronic disease management**

Microbiome therapy to treat chronic diseases

Microbiome modulating primary and adjuvant therapies are currently being developed to address autoimmune, inflammatory, metabolic, mental health disorders and cancer immunotherapy



Microbiome testing to match patients with the right treatment

Microbiome biomarkers and signatures are being developed for diagnosis, screening, drug response assessment and health risk monitoring.

Microba's Discovery Platform

Revealing new relationships between the microbiome, health and disease

MiCROBA

Microba analyses the entire microbiome using proprietary technology.

Precise and comprehensive measurement unlocks this rich source of opportunity to improve human health.

Other Technology

Microba technology

71% of the human gut microbiome remains uncultured

Almeida *et al* (2021) **Nature Biotechnology** DOI: 10.1038/s41587-020-0603-3

Illustrative visualisation of the gastrointestinal tract and the additional bacteria visible to Microba with its platform technology. This graphic is for illustrative purposes only

Microba's leading metagenomics analysis platform measures the microbiome with **unparalleled performance**

Microba Community Profiler

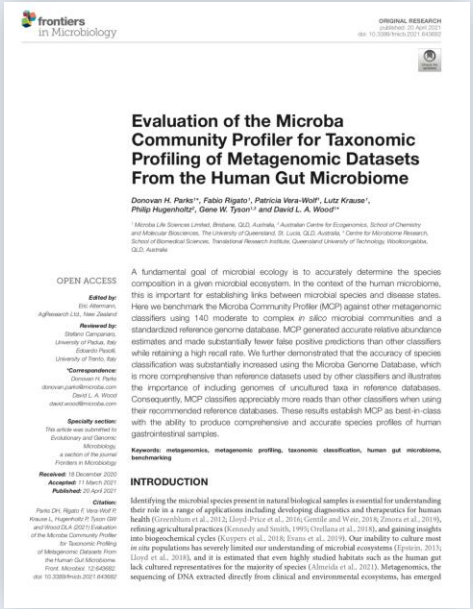
Metagenomic mapping technology delivering leading microbiome measurement when combined with Microba's Genome Database

+

Microba Genome Database

World leading, expertly curated microbial genome reference database of microbial genomes to deliver unmatched detection coverage of the human microbiome

Precision	Superior coverage
We have world leading specificity and sensitivity	*We classify up to **95%** per sample*[1]



frontiers in Microbiology

ORIGINAL RESEARCH

Evaluation of the Microba Community Profiler for Taxonomic Profiling of Metagenomic Datasets From the Human Gut Microbiome

Donovan H. Parks[1*], Fabio Rigato[1], Patricia Vera-Wolf[1], Lutz Krause[1], Philip Hugenholtz[2], Gene W. Tyson[1,3] and David L. A. Wood[1*]

OPEN ACCESS

A fundamental goal of microbial ecology is to accurately determine the species composition in a given microbial ecosystem. In the context of the human microbiome, this is important for establishing links between microbial species and disease states. Here we benchmark the Microba Community Profiler (MCP) against other metagenomic classifiers using 140 moderate to complex *in silico* microbial communities and a standardized reference genome database. MCP generated accurate relative abundance estimates and made substantially fewer false positive predictions than other classifiers while retaining a high recall rate. We further demonstrated that the accuracy of species classification was substantially increased using the Microba Genome Database, which is more comprehensive than reference datasets used by other classifiers and illustrates the importance of including genomes of uncultured taxa in reference databases. Consequently, MCP classifies appreciably more reads than other classifiers when using their recommended reference databases. These results establish MCP as best-in-class with the ability to produce comprehensive and accurate species profiles of human gastrointestinal samples.

Keywords: metagenomics, metagenomic profiling, taxonomic classification, human gut microbiome, benchmarking

INTRODUCTION

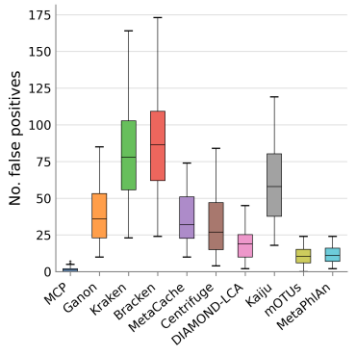
Identifying the microbial species present in natural biological samples is essential for understanding their role in a range of applications including developing diagnostics and therapeutics for human health (Greenblum et al., 2012; Lloyd-Price et al., 2016; Gentile and Weir, 2018; Zmora et al., 2019), refining agricultural practices (Kennedy and Smith, 1995; Orellana et al., 2018), and gaining insights into biogeochemical cycles (Kuypers et al., 2018; Evans et al., 2019). Our inability to culture most *in situ* populations has severely limited our understanding of microbial ecosystems (Epstein, 2013; Lloyd et al., 2018), and it is estimated that even highly studied habitats such as the human gut lack cultured representatives for the majority of species (Almeida et al., 2021). Metagenomics, the sequencing of DNA extracted directly from clinical and environmental ecosystems, has emerged

Data generated by Microba Life Sciences

[1] Parks *et al* 2021 DOI: 10.3389/fmicb.2021.643682

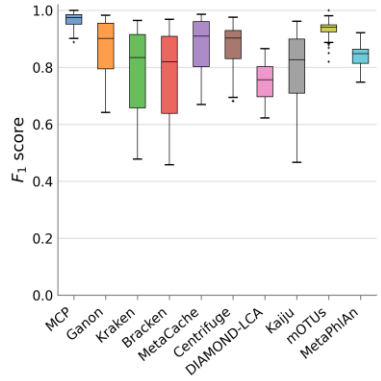
Microba's metagenomic analysis is **best in class,** as benchmarked in *Frontiers in Microbiology*

Precise



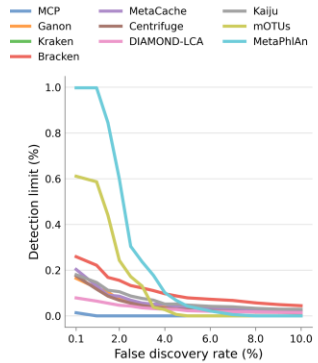
99% precision
Reports 8-65x less false positive species

Accurate



96% F_1 score
Outperforms other profilers by 3 – 22%

Sensitive

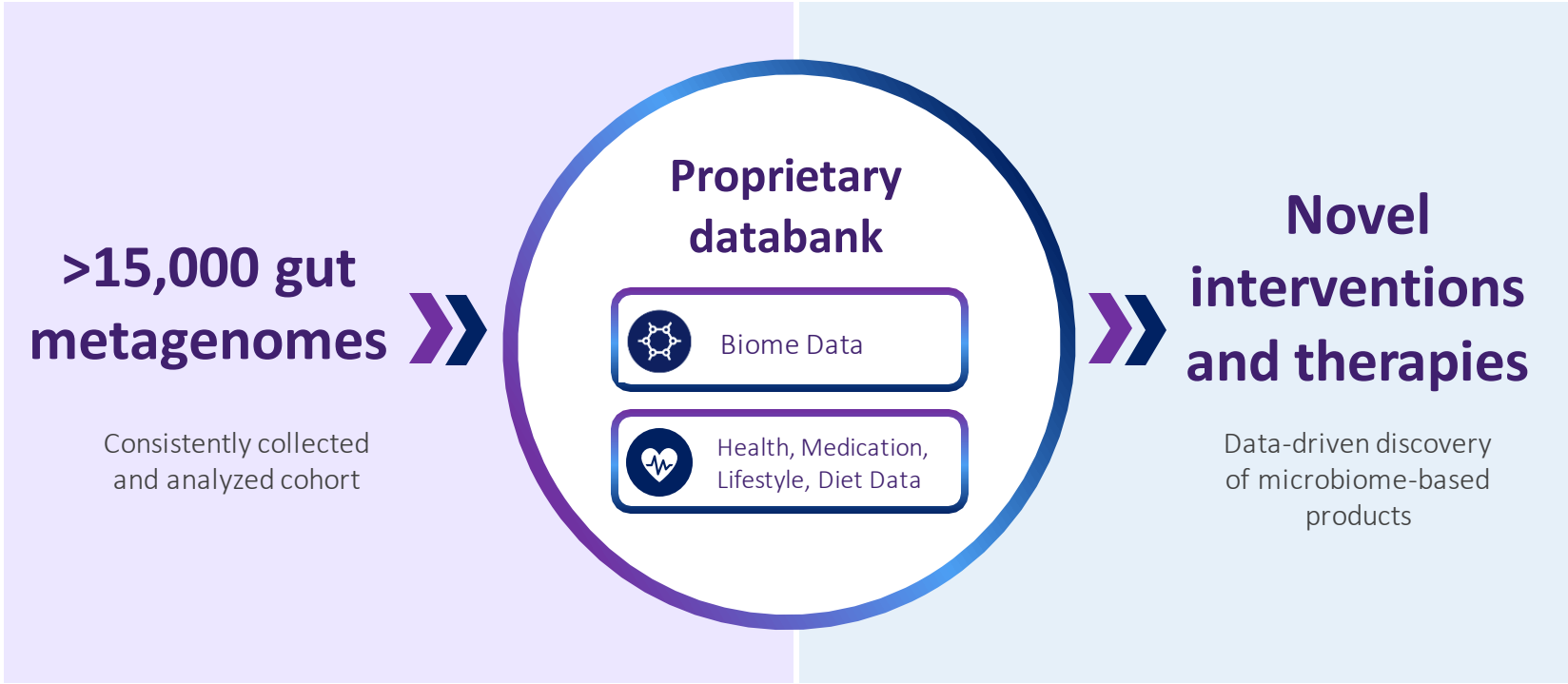


0.007% detection limit at FDR of 0.1%
4 – 86x improved detection limit

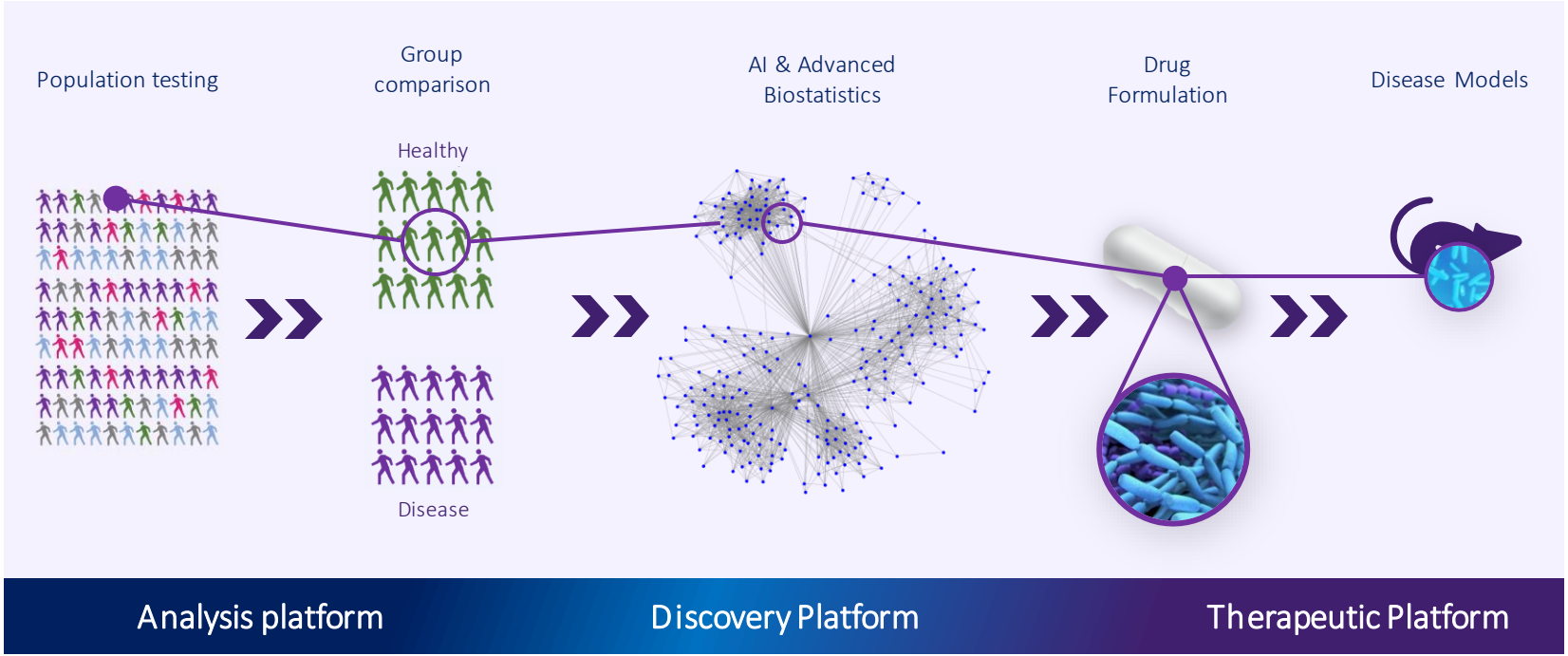
*MCP = Microba Community Profiler

Data generated by Microba Life Sciences (Parks *et al* 2021 DOI: 10.3389/fmicb.2021.643682)

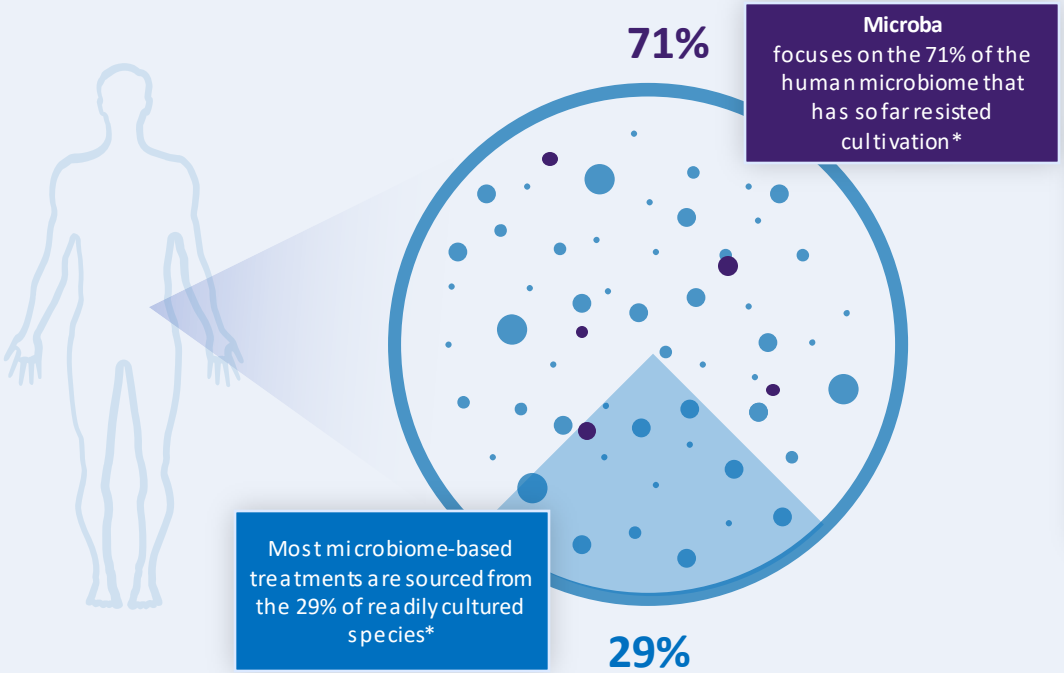
Using precision microbiome analysis to generate a **globally unique dataset** to power microbiome discovery



Human first, data-driven approach to microbiome discovery & development



Microba's **data-driven discovery** interrogates the novel microbiome



Precision techniques developed by Microba enable access to novel microbial biomarkers with precision and efficiency.

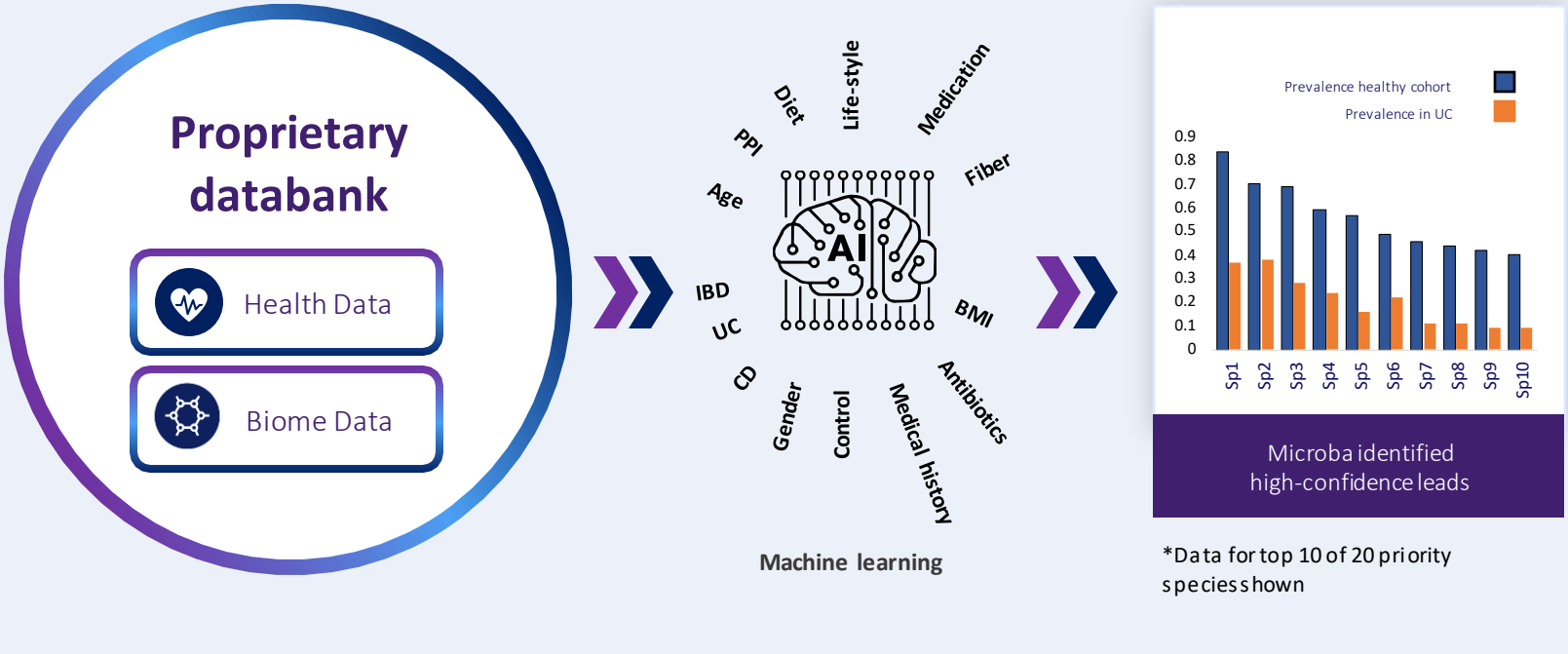
*Almeida *et al* (2020) DOI: 10.1038/s41587-020-0603-3

Developing novel microbiome-based treatments

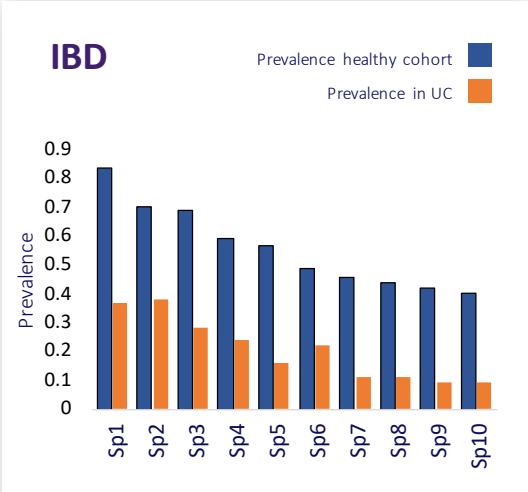
Flagship IBD program powered by
Microba's Therapeutics Platform

MICROBA

Microba uses **AI based approaches** to identify candidate microbial leads

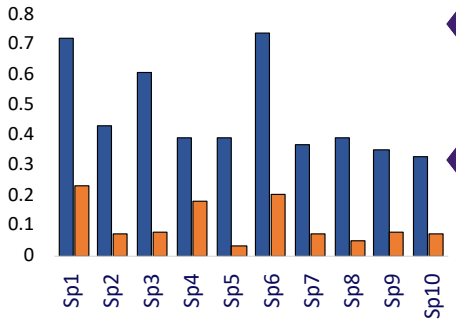


Key therapeutic leads missed without comprehensive measurement and analytic techniques



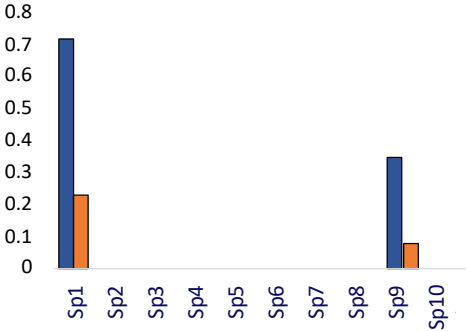
Leads discovered in Microba data

Microba results from analyzing independent data



Re-analysis of independent published clinical data using Microba's technology

Analysed using leading alternative profiler

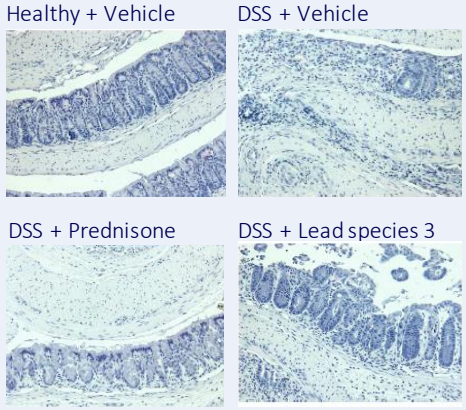


Independent published clinical study results

Data generated by Microba Life Sciences using raw data from Microba Life Sciences and Franzosa *et al.* 2018

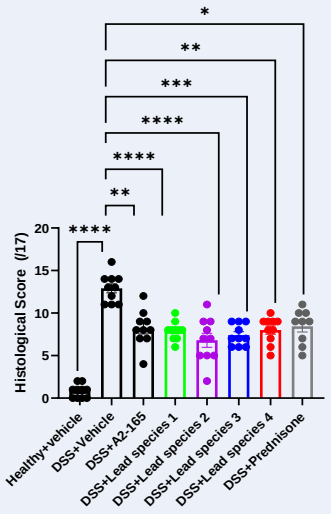
Lead candidates prevent colitis
in an acute model of DSS induced murine colitis

Leads promote mucosal healing

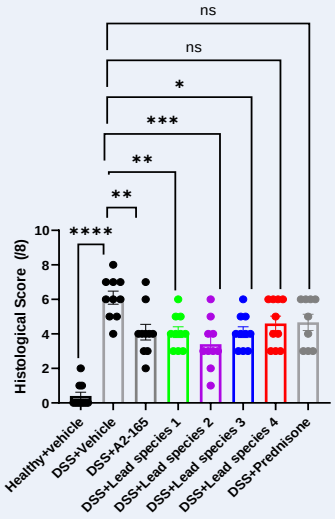


Acute DSS model in C57Bl/6, 200 µl of live bacterial solution (1 x 10^9 cells/ml) orally

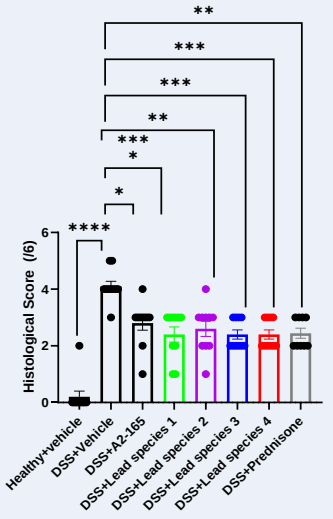
Histopathological score



Inflammation score

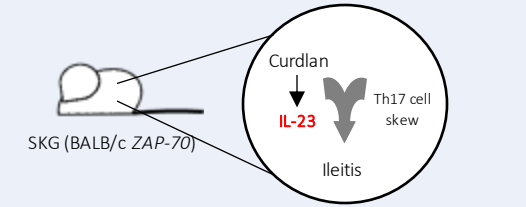


Epithelial injury

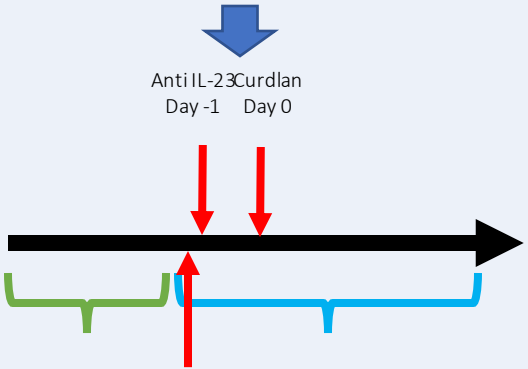


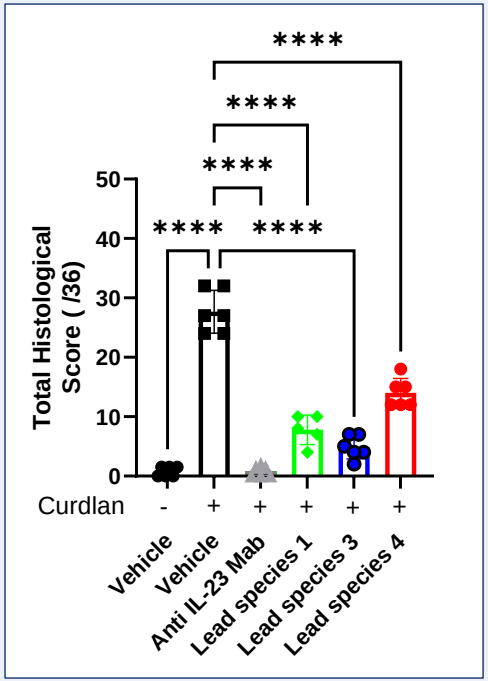
- No adverse effects observed in healthy animals

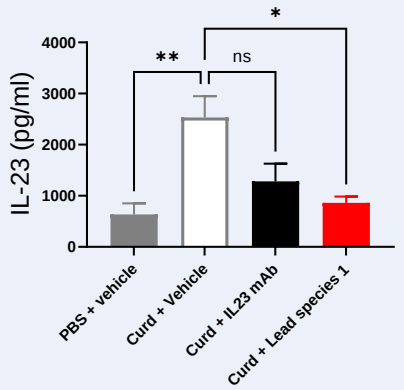
Lead candidates **prevent Crohn's like ileitis** and **suppress pro-inflammatory serum cytokines** in SKG mice



SKG mice develop IL-23 dependent ileitis



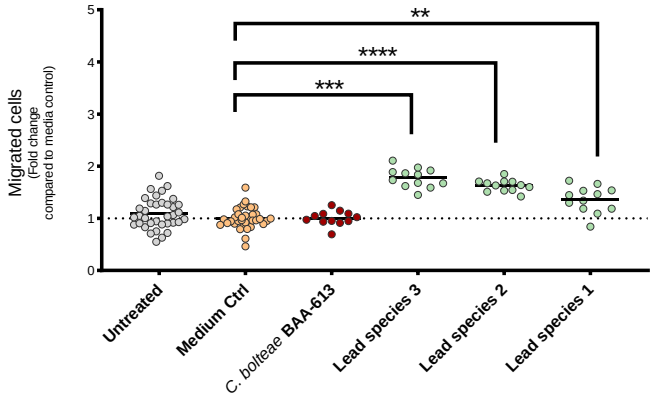




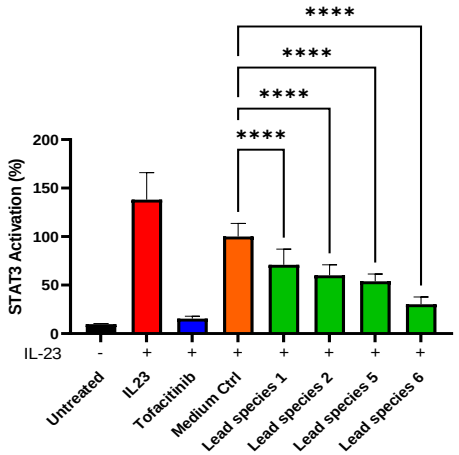
Lead species 1 treatment results in reduced serum concentrations of IL-23, IL-12p70, IL-6 and GM-CSF.

Leads show strong *in vitro* therapeutic activity of cell migration and immune suppression - further elucidating mechanism of action

Leads promotes epithelial cell migration – a key process underpinning effective wound repair and mucosal healing

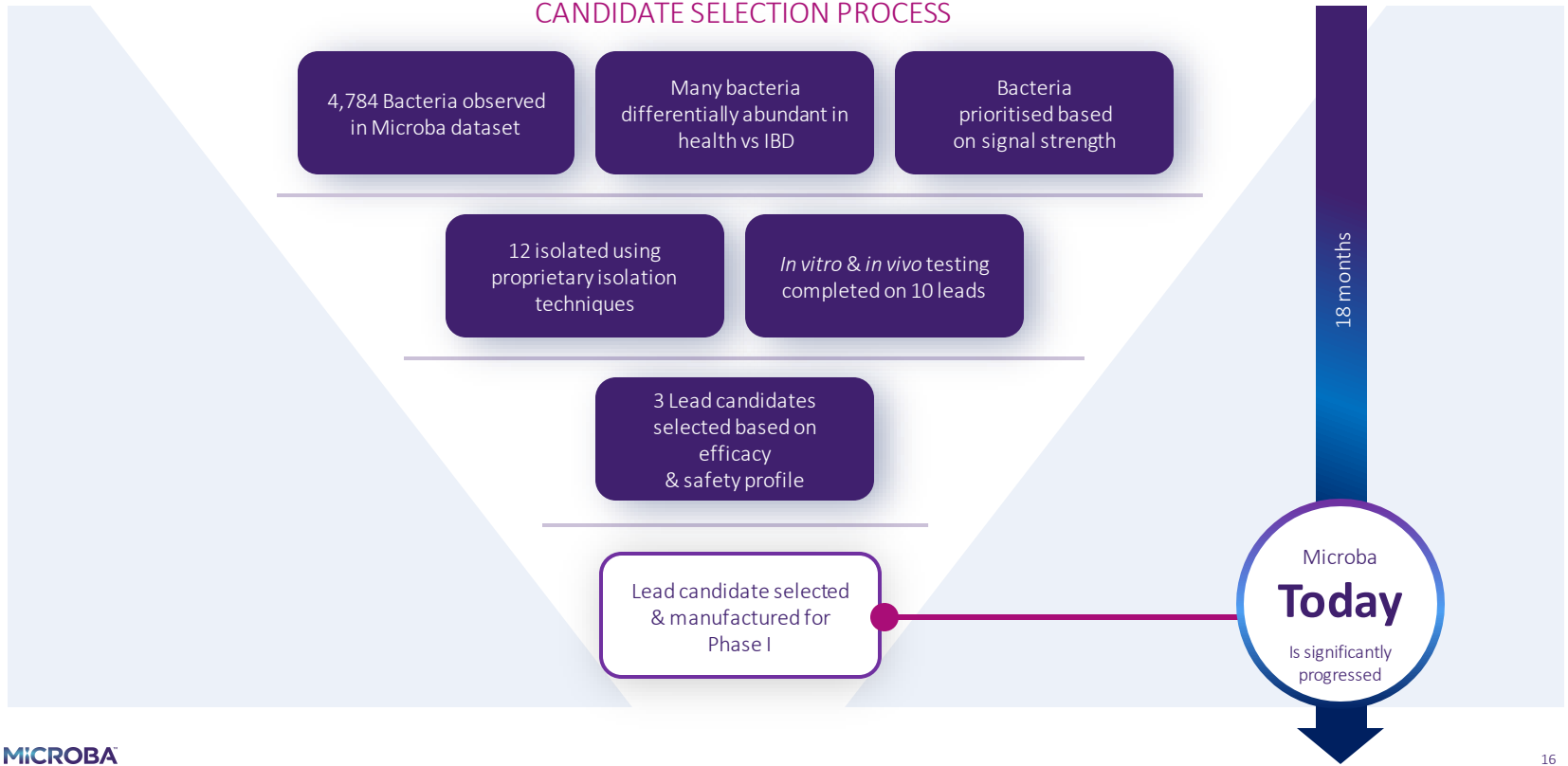


Leads suppresses IL-23 mediated STAT3 activation – a crucial pathway in the uncontrolled intestinal inflammatory process of IBD



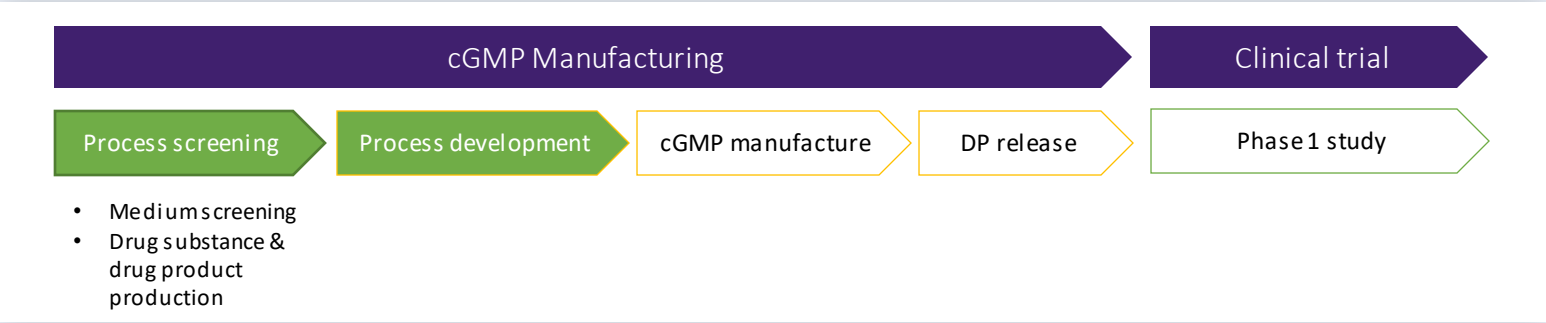
Inflammatory Bowel Disease Program

Demonstrating rapid translation from data to first in human



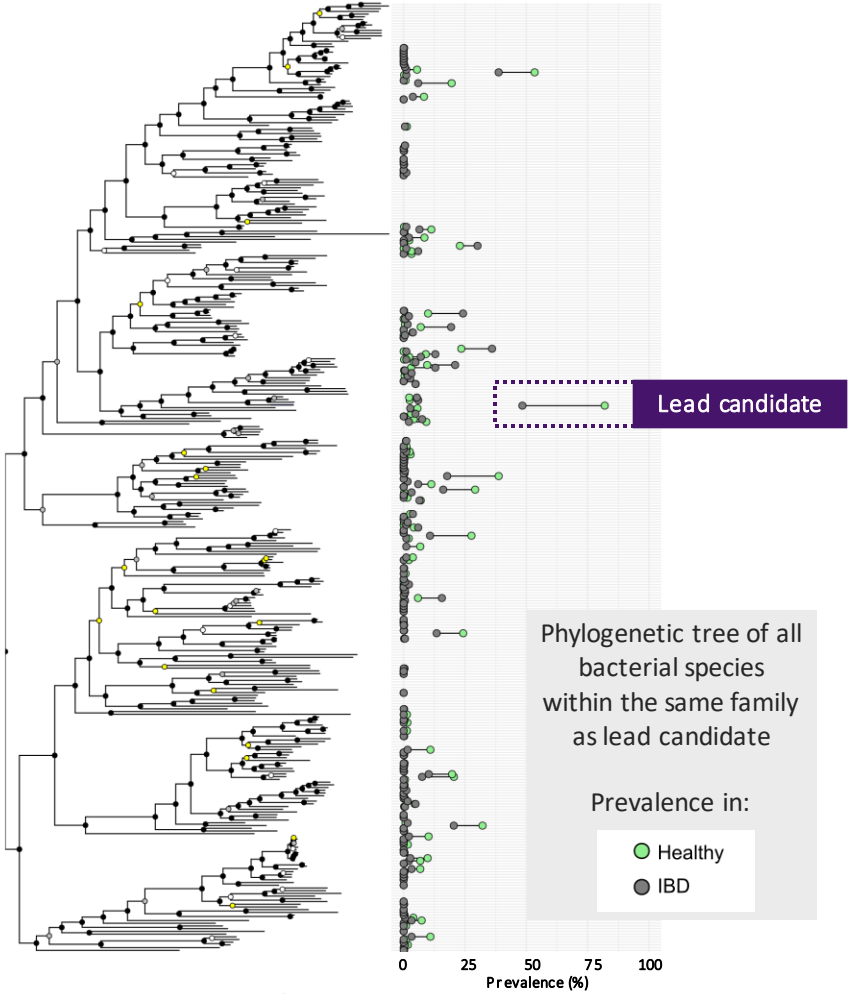
Clinical cGMP Manufacturing of lead candidate

- Single strain bacterial cell therapy developed from a previously uncultivated species
- Commonly found in healthy population, rarely detected in IBD
- Strictly anaerobic and has been cultivated from healthy human donor
- Safe and strong efficacy in multiple mouse models.
- **Small scale manufacturing of drug substance successfully completed**
- **Now progressing into cGMP manufacture.**



Data-driven discovery of IBD lead candidate

- Identification enabled by Microba's precision microbiome analysis
- A previously uncultivated, uncharacterized species
- Rationally discovered from human samples
- Clearly stands out from other species



Data generated by Microba Life Sciences

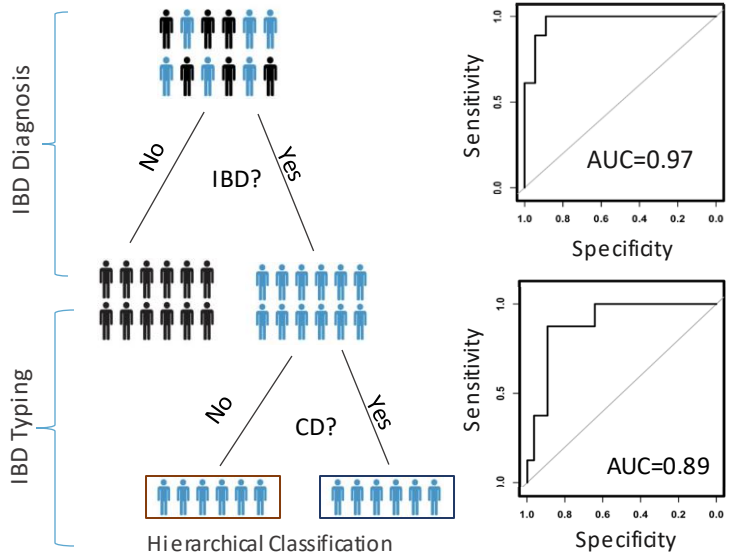
Biomarker discovery

Diagnostic predictors
and response to treatment

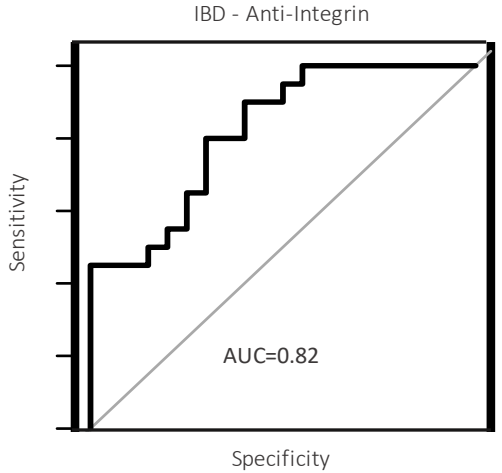
MiCROBA

Advanced machine learning tools needed to achieve high powered predictive models for disease diagnosis or treatment response

Disease Diagnosis[1]



Treatment Response[2]



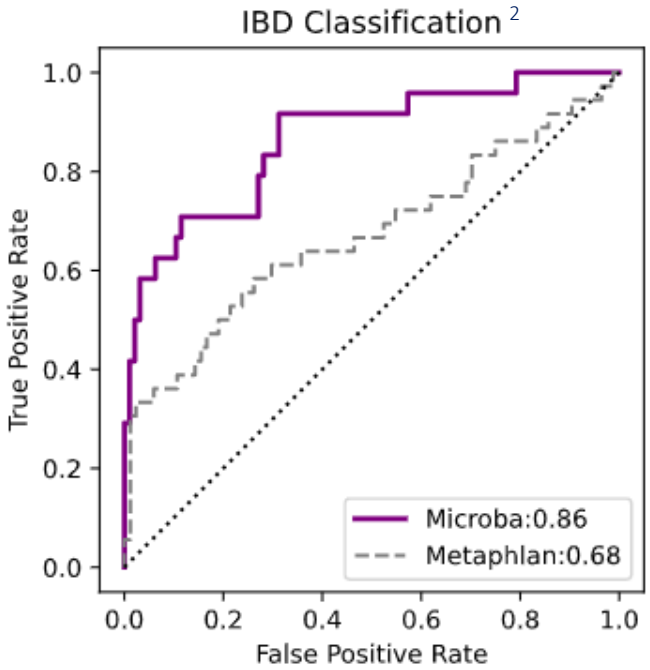
[1] Data generated by Microba Life Sciences
[2] Data generated by Microba Life Sciences using raw data from Ananthakrishnan *et al*. 2017

Precise measurement is critical for development of microbiome-based diagnostics

Dataset: Faecal metagenomes from 128 IBD cases and 30 controls from Franzosa *et al.* 2018 was re-analysed using Microba's MCP technology.

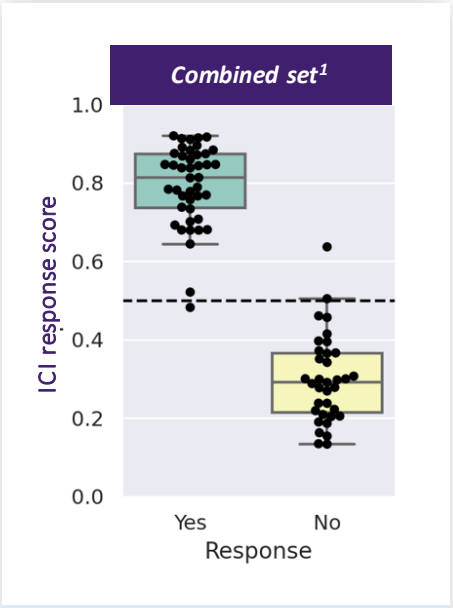
Species profiles were generated from faecal metagenomic data using both MetaPhlAn[1] and Microba's technology.

Machine learning approaches were then applied to the species profile data to assess the ability to diagnose IBD.

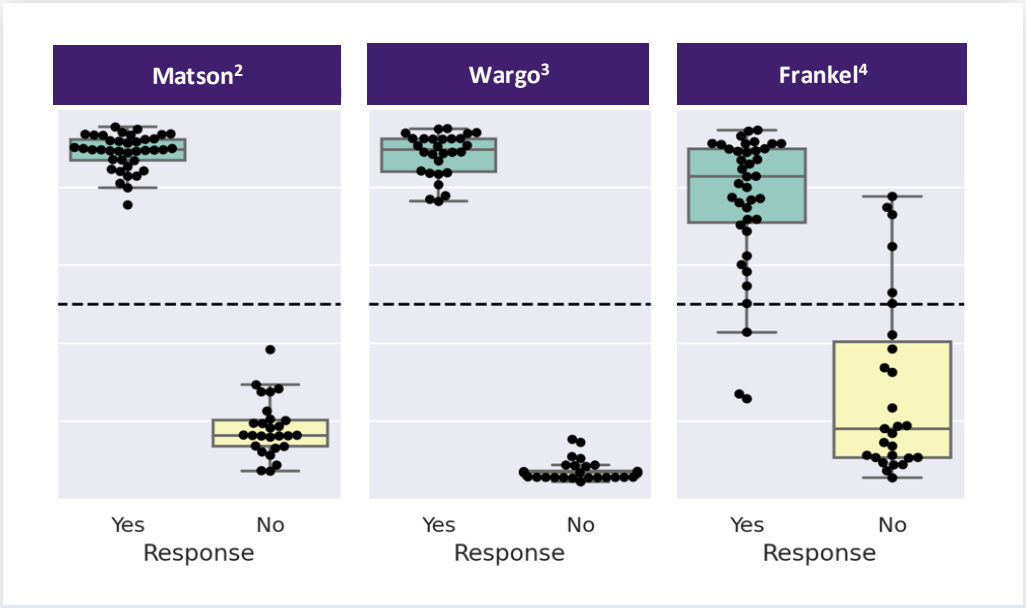


[1] Nicola Segata, Levi Waldron, Annalisa Ballarini, Vagheesh Narasimhan, Olivier Jousson, Curtis Huttenhower. ***Nature Methods,*** 8, 811–814, 2012
[2] Data generated by Microba Life Sciences using raw data from Franzosa *et al*. 2018

Microba's re-analysis of published data confirms **strong microbial signal associated with immune checkpoint inhibitors response**



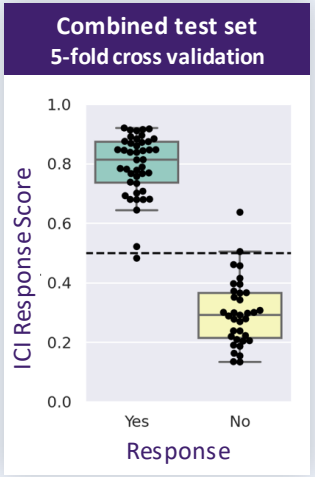
5-fold cross validation

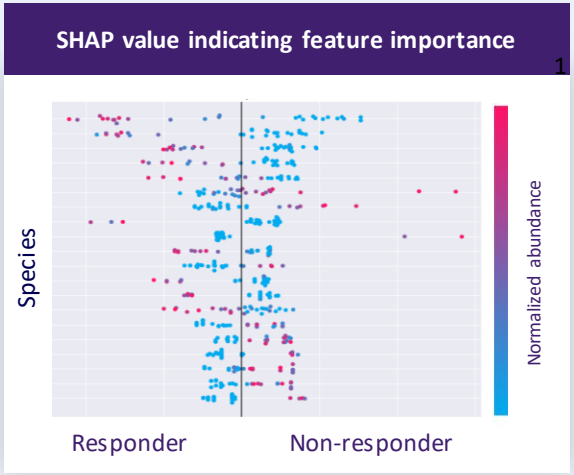


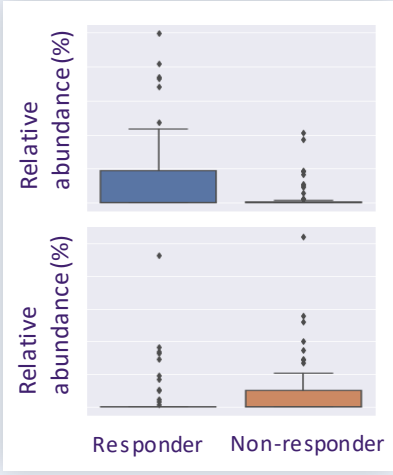
Tested on individual dataset after trained on remaining 2 datasets

[1] Data generated by Microba Life Sciences using raw data from Matson *et al*. 2018, Gopalakrishnan et al, 2018 (Wargo) and Frankel et al, 2017
[2] Data generated by Microba Life Sciences using raw data from Matson *et al*. 2018
[3] Data generated by Microba Life Sciences using raw data from Gopalakrishnan *et al*. 2018 (Wargo)
[4] Data generated by Microba Life Sciences using raw data from Frankel *et al.* 2017

Inspection of model identifies **potential biomarker** and **therapeutic candidates**







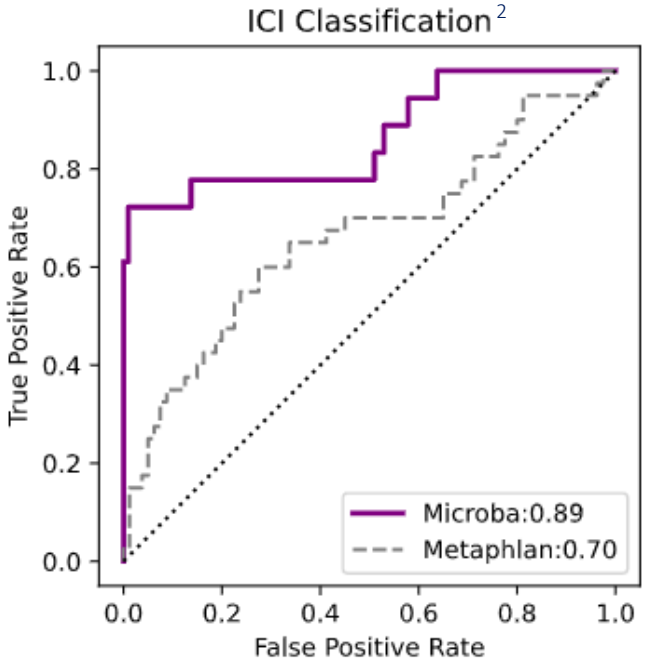
Gut microbiome predicts response to **immune checkpoint inhibitors**

Precise measurement is critical for development of microbiome-based diagnostics

Dataset: Metastatic melanoma data from Frankel *et al*. 2017 & Matson *et al*. 2018, were re-analysed using Microba's MCP technology (n = 77, responders = 39, non-responders = 38)

Species profiles were generated from faecal sample metagenomic data using both MetaPhlAn[1] and Microba's technology.

Machine learning approaches were then applied to the species profile data and patient metadata to assess the ability to classify patients.

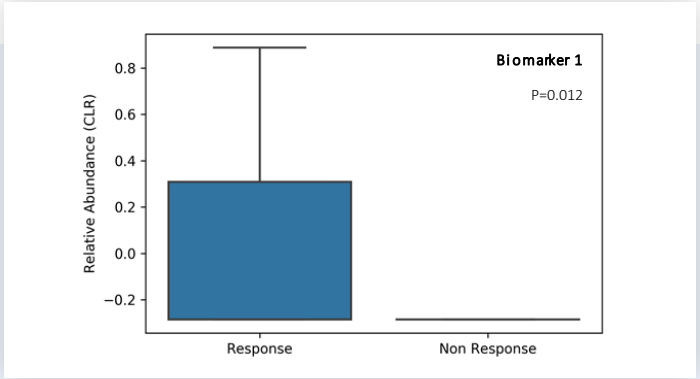


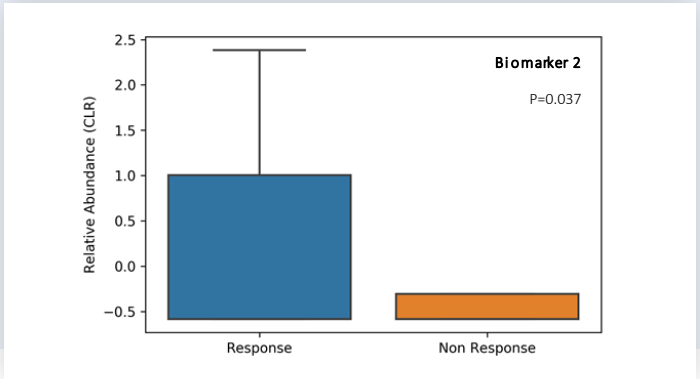
[1] Segata *et al*. (2012). ***Nature Methods***. DOI: 10.1038/nmeth.2066
[2] Data generated by Microba Life Sciences using raw data from Frankel *et al.* 2017 & Matson *et al.* 2018,

Microbial species biomarkers predict response to **immune checkpoint inhibitors**

Microba tools identify
19 response biomarkers

MetaPhlAn identifies
0 biomarkers





MiCROBA

Data generated by Microba Life Sciences using raw data from Frankel *et al.* 2017 & Matson *et al.* 2018,

Microbiome research services

Providing partners with access to
Microba's world-leading technology

MiCROBA

Opportunities for partnership
to drive new discovery

Analysis Platform

End-to-end solution for **precise and comprehensive** microbiome analysis

- Clinical trial support
- End-to-end research services, including sample collection, bioinformatics and statistical analysis, and results interpretation

Discovery Platform

A **globally unique data resource** and advanced capabilities in **data mining and AI**

- Identify microbial biomarkers associated with health, disease, environment and lifestyle
- Discover microbiome directed interventions and probiotic leads

Therapeutic Platform

Human first, data-driven **lead identification** and proprietary **isolation** methods

- Develop novel microbiome derived drugs, including live microbial drugs and bioactive molecules

Access **world-leading technology and expertise** in microbiome analysis at any stage of your research.

Acknowledgements

Prof Gene Tyson
Co-Founder,
Non-Executive Director

Prof Phil Hugenholtz
Co-Founder, Chair of
Scientific Advisory Board

Dr Páraic Ó Cuív
VP Drug Discovery

Dr Nicola Angel
Laboratory Director

Blake Wills
Advisor, Strategic Alliances

Dr Luke Holtham
Chief Executive Officer

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Dr Andrea Rabellino
Senior Scientist
Cell Biology

Dr Joyce Chou
Scientist Microbiology

Dr Annika Krueger
Scientist Cell Biology

Dr Donovan Parks
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Precision microbiome science