



# Harnessing the Human Microbiome for Discovery

The composition and function of the human gut microbiome are linked to health and disease. Increasing evidence of microbes' involvement in disease development has driven efforts to better understand the molecular mechanisms of pathogenesis from microbiota perturbation, to identify novel targets for therapeutic development.

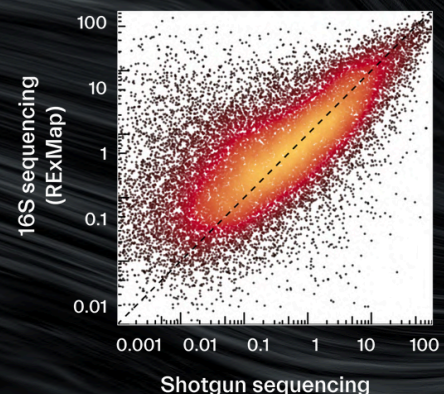
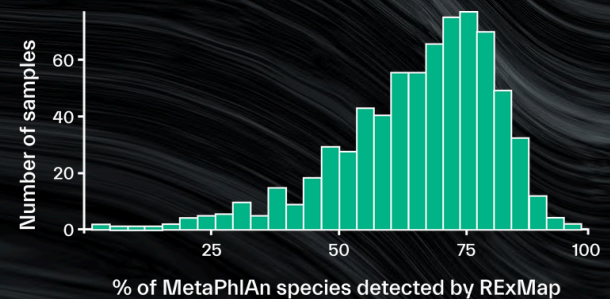
This requires comprehensive profiling of microbial communities across populations, typically done via 16S amplicon sequencing. While this method detects broad microbial targets, its resolution is limited to distinguishing microbes at the family/genus level. Computational assignments are missing or inconsistent at the species level, making mapping difficult to compare across studies.

This challenge led Sapient to develop Reference-based Exact Mapping (RExMap) of microbial amplicon variants that enables mapping of microbial species from standard 16S sequencing data.

## RExMap enables speciation from 16S amplicon data

RExMap analysis of 16S data captures ~75% of microbial species identified by whole-genome shotgun sequencing (WGS) despite hundreds-fold less sequencing depth. A key component of the method involves alignment of denoised sequences from the data directly to RExMapDB, a database of unique hypervariable regions of 16S genes from all isolate microbes, to avoid taxonomic assignment.

RExMap re-analysis of existing 16S data reveals a detailed landscape of gut microbial species across populations and geography.

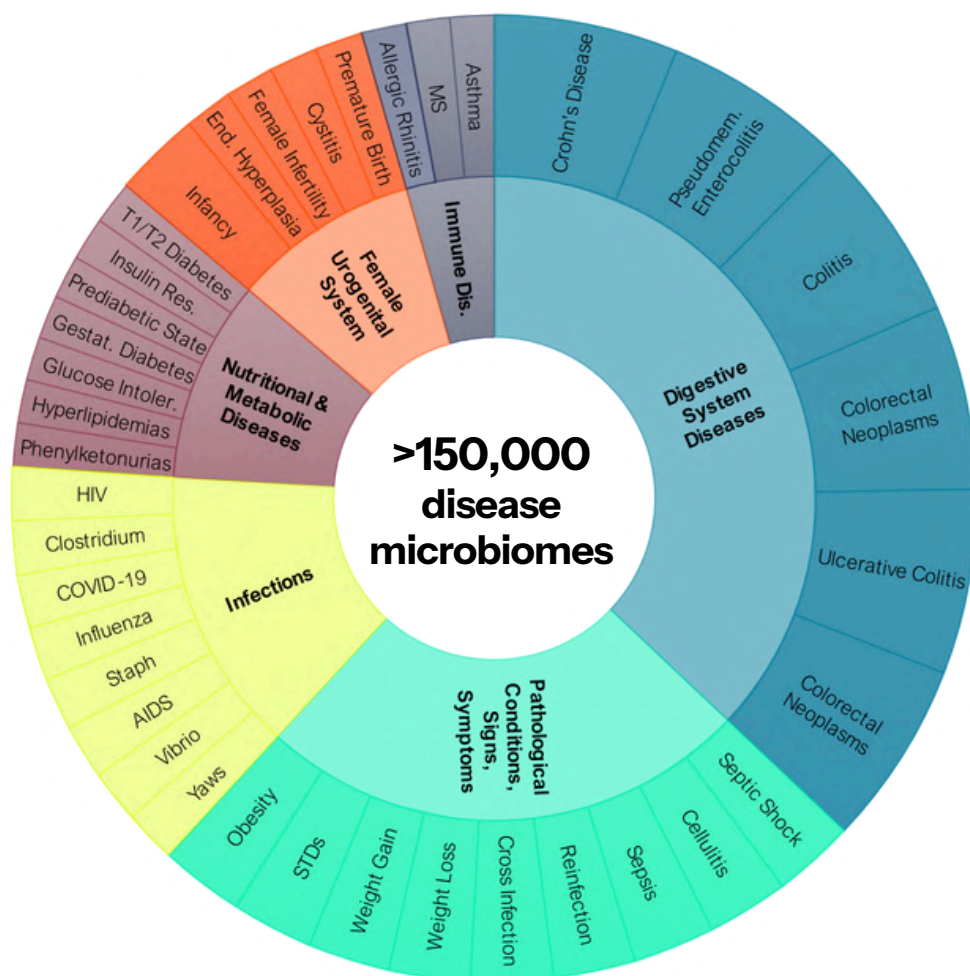


# Sapient's World Microbiome Data enables population-level discovery

Sapient has built a comprehensive repository of proprietary microbiome data, totaling over 1,000,000 samples consisting of over 150,000 microbiomes involved in spectrum of various diseases.

The samples come from more than 10,000 individuals in adult populations across the globe, from hunter-gatherer tribes to modern city dwellers, and include microbiomes for:

- Large intestine
- Mouth
- Skin
- Lung
- Vagina
- Nose
- Milk
- Urinary tract
- Small intestine
- Bile
- Brain
- Blood



## Advancing biomarker-based discovery of microbially derived metabolites

By combining RExMap methods and our expansive human microbiome data, we can effectively map thousands of microbial species across tens of thousands of diverse individuals, and measure and harness the thousands of secondary products that emerge from the microbiome in therapies to restore health or prevent disease.



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