ZYMO RESEARCH

The Beauty of Science is to Make Things Simple®

Microbiomics Services

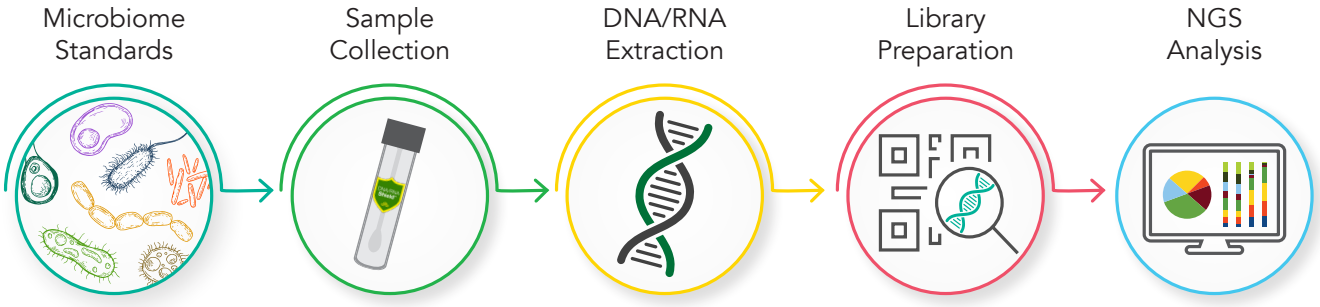
Celebrate your discoveries

ZymoBIOMICS® 16S rRNA Gene Sequencing in ≤ 2 weeks

ZymoBIOMICS® Shotgun Metagenomic Sequencing in ≤ 6 weeks

ZymoBIOMICS® Services

Simple. Accurate. Reproducible.



A Complete Solution for Unbiased Microbiome Profiling

- Simply submit samples and receive a comprehensive, customizable, and user-friendly report
- Unbiased & contamination-free sample processing validated using microbial standards

Quick Turnaround

- Results in ≤ 2 weeks for 16S rRNA gene sequencing
- Results in ≤ 6 weeks for shotgun metagenomic sequencing

Superior Taxonomic Resolution

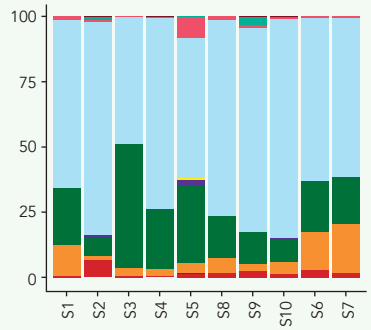
- Species-level resolution with 16S rRNA gene sequencing
- Strain-level resolution with shotgun metagenomic sequencing

Comprehensive and User-Friendly Report

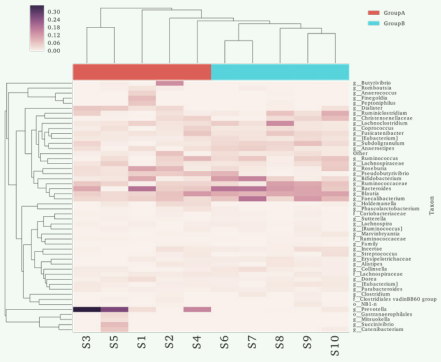
All ZymoBIOMICS® Services include comprehensive bioinformatics and statistical analyses for each microbiomics project. The report can be customized according to each unique project or application. Let Zymo Research do the bioinformatics so that you don't have to!

Typical Analyses Include:

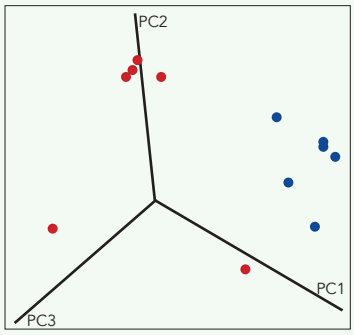
- Composition Barplots
- Taxonomy Heatmap
- Alpha-Diversity
- Beta-Diversity
- LEfSe Biomarker Discovery
- Taxa2SV Decomposer



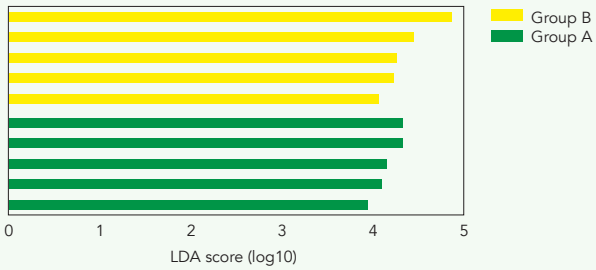
Composition Barplots



Composition Heatmap



Beta-Diversity 3D Plots



LEfSe Analysis

View an Example Report at **http://www.zymobiomics.com/report2.html**

Microbiomics-Grade Technologies

Process Any Sample Type

Human samples, water, soil, food testing, pathogen surveillance

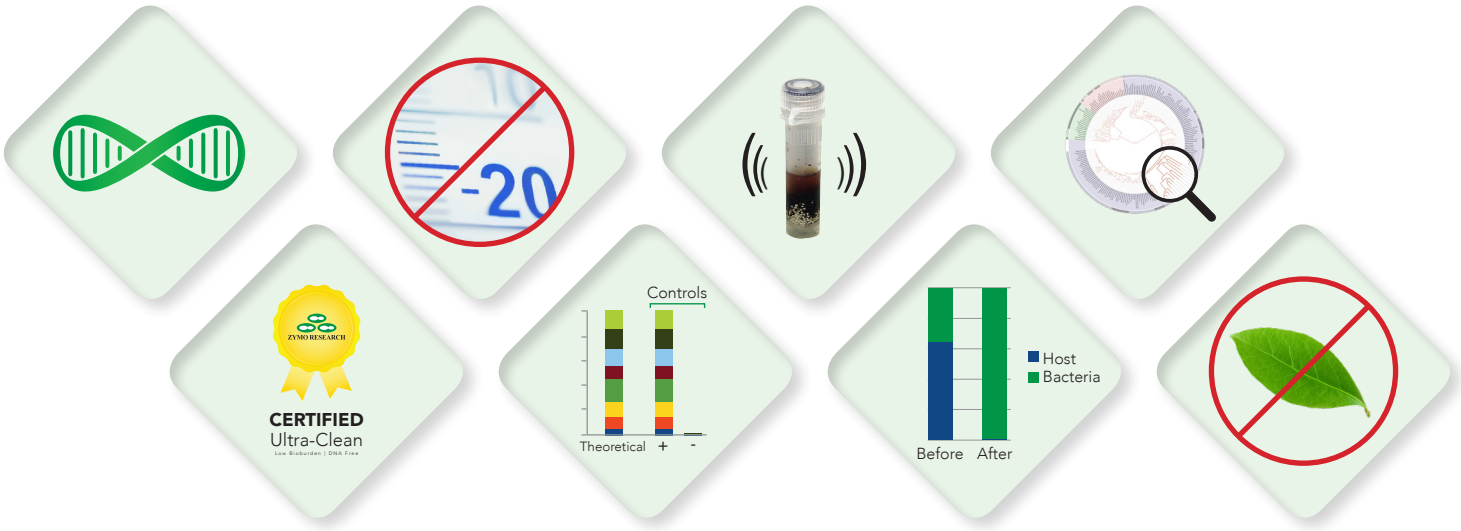
Cold-Free & Safe Sample Transportation

DNA/RNA Shield™

Unbiased Lysis

Bias-free microbial lysis with ZR BashingBead™ lysis tubes

Superior Taxonomic Resolution



Low Bioburden & DNA Free Reagents

Rigorous Quality Controls

ZymoBIOMICS® standards as positive controls

Host DNA Depletion

Plant Plastid 16S rRNA Suppression

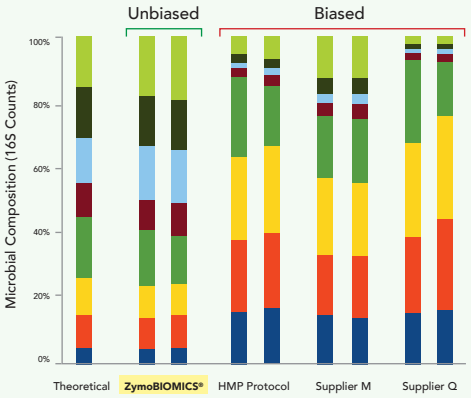
Zymo Research was the first company to develop microbiomics solutions, from collection to conclusion, based on new rigorous standards for microbiome measurements. Zymo Research is leading the initiative to improve reproducibility and accuracy in the field by developing the first commercially available microbiome standards. The ZymoBIOMICS® Microbial Community Standards were utilized to develop and optimize every step of the microbiomics workflow, ensuring high-quality, unbiased results.

Unbiased Microbiome Profiling

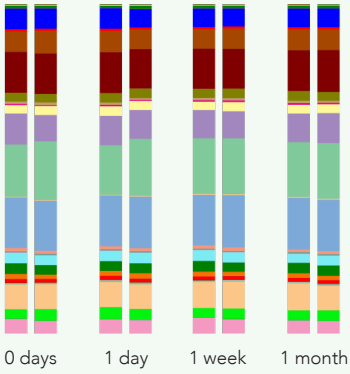
Unbiased DNA Extraction

Only the ZymoBIOMICS® DNA Miniprep Kit was unbiased when compared to three other DNA extraction kits using the ZymoBIOMICS® Microbial Community Standard. All other kits, including the Human Microbiome Project (HMP) fecal DNA extraction protocol, overrepresented the abundance of easy-to-lyse microbes.

- *Bacillus subtilis* (G+)
- *Lactobacillus fermentum* (G+)
- *Listeria monocytogenes* (G+)
- *Salmonella enterica* (G-)
- *Staphylococcus aureus* (G+)
- *Escherichia coli* (G-)
- *Enterococcus faecalis* (G+)
- *Pseudomonas aeruginosa* (G-)

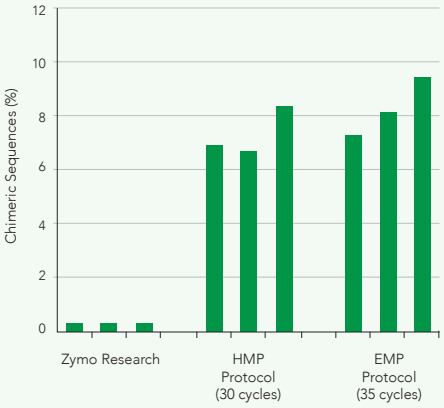


Stabilize Microbiome Profiles at Ambient Temperature for > 1 Month



A fecal sample preserved in DNA/RNA Shield® was profiled at various time points over 1 month using 16S rRNA gene sequencing. The microbial profile of the sample remained the same over time when stored at room temperature in DNA/RNA Shield®.

Minimize PCR Chimera Formation During 16S Library Prep



The Zymo Research *Quick*-16S™ NGS Library Prep Kit minimizes PCR chimera formation. PCR chimera formation during library preparation of 16S sequencing corrupts microbiome profiling.

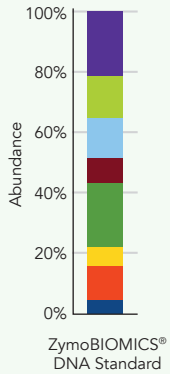
Background:

The field of microbiomics is full of biased and inaccurate data, making it difficult to compare results across labs. Prominent leaders in the field have notably reported contradictory data. This led Zymo Research to develop the first commercially available microbiome standards, which were also used to systematically address and eliminate major sources of bias. The figures above illustrate three examples of eliminating substantial bias during sample collection, DNA extraction, and library preparation, respectively. The ZymoBIOMICS® Services, powered by these products from Zymo Research, are guaranteed to produce the most accurate microbiome profiling.

Redefining 16S Microbiome Profiling

Species-Level Resolution

Zymo Research 16S Pipeline



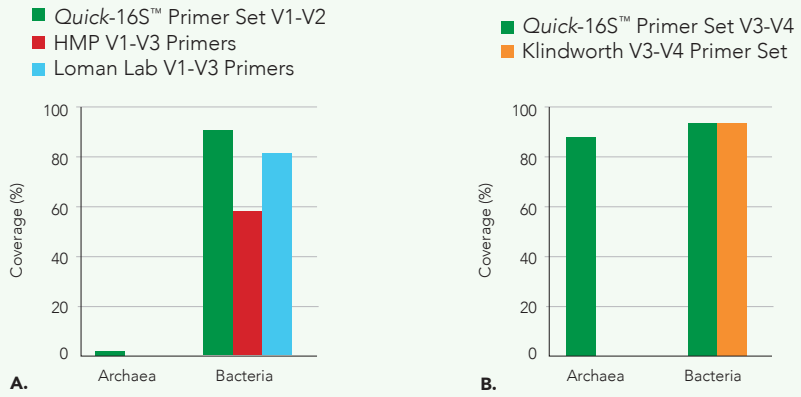
Species-Level Identification

Species	16S Pipeline (Zymo Research)	QIIME + Greengenes
Bacillus subtilis	×	×
Listeria monocytogenes	✓	×
Staphylococcus aureus	✓	✓
Enterococcus faecalis	✓	×
Lactobacillus fermentum	✓	×
Escherichia coli	✓	×
Salmonella enterica	✓	×
Pseudomonas aeruginosa	✓	×

Species-level resolution was achieved using the Zymo Research 16S pipeline. The ZymoBIOMICS® Microbial Community DNA Standard was analyzed using 16S sequencing with primers targeting the 16S V1-V2 region. The sequencing data from an Illumina® MiSeq® was analyzed using the two bioinformatics pipelines shown above. The example report of real fecal samples can be found at: http://www.zymobiomics.com/report2.html.

Background:
While it is generally assumed that 16S sequencing is limited to genus-level resolution, this technique actually has the potential to go beyond. With innovations in bioinformatics analysis and a well-curated 16S database, Zymo Research has brought 16S sequencing to species-level resolution.

Best Phylogenetic Coverage



A. The Zymo Research *Quick*-16S™ Primer Set V1-V2 includes coverage of common human-associated microbes, including *Bifidobacterium*, *Propionibacterium*, and *Chlamydia*, which are missed in common V1-V2 or V1-V3 primers.

B. The Zymo Research *Quick*-16S™ Primer Set V3-V4 provides up to 87% coverage for archaea, organisms commonly found in the human gut. However, the common V3-V4 primers provide 0% coverage for archaea.

Background:
The phylogenetic coverage of 16S sequencing is determined by the selection of general bacterial 16S primers used. As more and more microbes are newly discovered, there is an urgent need to redesign the common 16S primer sets. The 16S primers designed by Zymo Research significantly improve coverage for more sensitive identification of microbes.

ZymoBIOMICS® Shotgun Service

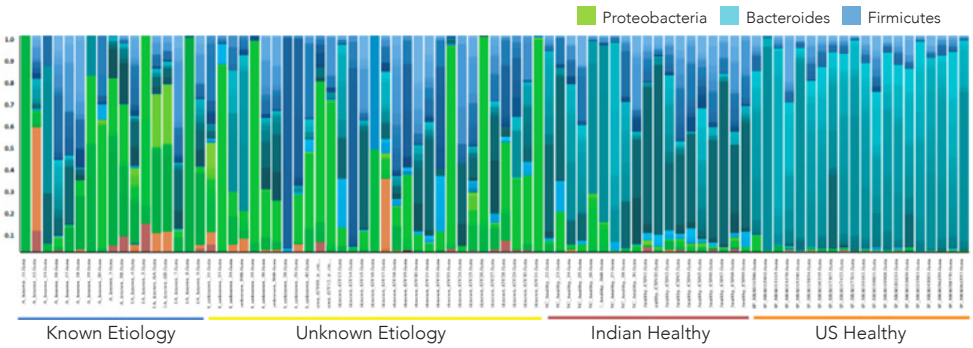
Partnership with COSMOSID® Unlocking The Microbiome

Shotgun metagenomic sequencing offers strain-level resolution, multiple-kingdom identification, and functional profiling.

In partnership with CosmosID, Zymo Research provides the most complete and sophisticated solution for shotgun metagenomics. The bioinformatics analysis for the ZymoBIOMICS® Shotgun Service features:

Performance

- Identification with industry leading sensitivity and precision.
- Strain-level resolution of all microbial kingdoms (bacteria, archaea, viruses, protists, fungi).

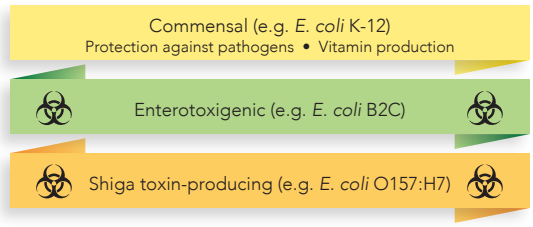


World's largest curated and customizable databases

- 150,000+ genomes and gene sequences.
- 100s of millions of biomarkers.
- Data structure follows the phylogenetic hierarchy of genomes, enabling accurate classification, even of unknown strains, based on this virtual tree of life.

Why does strain level identification matter?

Consider the species *E. coli*: Some stains keep us healthy, while others are life threating.



Multi-Kingdom Identification

Bacteria

Viruses

Fungi

Protists

Specialty Databases (MDR Pathogens & HAI, Biothreat Agents, Food Safety)

Functional Gene Profiling

Plasmids

Bacteriophages

Antibiotic Resistance

Virulence Factors

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