ZYMO RESEARCH
The Beauty of Science is to Make Things Simple®

Microbiome Sequencing Services

Your Trusted Next-Gen Sequencing Partner

A Journey to Discover the Microscopic World with **Zymo Research**

Welcome to the captivating realm of microbiome research, a field that has witnessed remarkable strides in recent decades. From decoding the intricacies of the human gut microbiome to exploring microbial communities in diverse environments, the journey of discovery has been nothing short of exhilarating.

At Zymo Research, we're proud to have been at the forefront of this scientific revolution, contributing innovative solutions that have propelled microbiome research forward. As the creator of the first and most cited Microbial Community Standard, Zymo Research's core value is to make microbiome research simple and comparable, empowering researchers worldwide to delve deeper into the mysteries of the microbial world.

With our microbiome sequencing service, we aim to further catalyze the advancement of microbiology by providing researchers with comprehensive and customizable solutions. Through our cutting-edge technologies and unwavering commitment to excellence, we're committed to driving innovation and shaping the future of microbiome research.

The Future of Microbiome Sequencing Service Is Here

Unrivalled End-to-End Solutions for Your Unique Microbiome Needs: From Scientific Discovery and Clinical Applications to Commercial Testing

- One-Stop-Shop
- Unmatched Data Quality
- Rapid Turnaround Time
- REGISTERED scientist.com SUPPLIER / Science EXCHANGE — 100% Satisfaction Guarantee

Broad Applications in Diverse Sectors

- Pathogen Surveillance
- Direct-to-Consumer Health
- Academic Research
- Food & Beverage
- Therapeutics & Pharmaceuticals
- Skin Care
- Agriculture & Animal Health
- Wastewater
- Bioremediation

illumina CSPro® CERTIFIED SERVICE PROVIDER

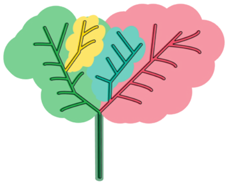
PacBio **PACBIO CERTIFIED** SERVICE PROVIDER

Microbiomics
Made Simple™

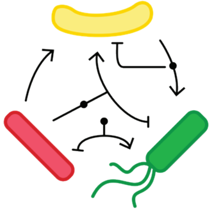
Microbiome Sequencing Services

The Complete Solution for Any Microbiome Applications

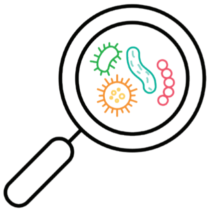
- ✓ Industry-Leading Turnaround Time
- ✓ Unmatched Data Quality
- ✓ Comprehensive Bioinformatics Analysis
- ✓ 100% Satisfaction Guaranteed



16S/ITS Amplicon Sequencing

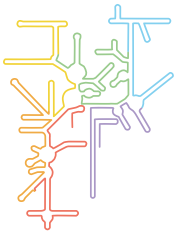


Metatranscriptomics Sequencing



Shotgun Metagenomics Sequencing

Custom Solutions for Industry Partners



Full-length 16S Sequencing

Long-read Metagenome Sequencing & Assembly

Long-read Microbial Whole Genome Assembly

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16S/ITS Amplicon Sequencing

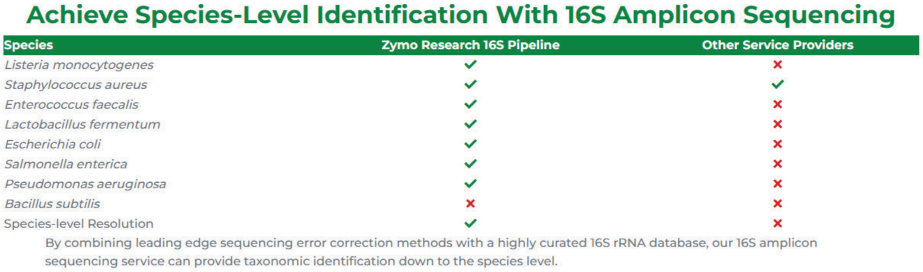
16S/ITS sequencing uses PCR to selectively amplify certain regions/genes from different bacteria or fungi and then sequences the amplicons. The taxonomy identification is achieved by comparing the amplicon sequences to reference 16S/ITS sequence databases. 16S/ITS sequencing is generally considered simpler and more cost-effective than metagenomic sequencing, and is the better choice for certain samples that contain microbes with unknown genomes (e.g. soil and water samples).

16S/ITS sequencing can achieve close to zero false positives in taxonomy identification and can differentiate even single-nucleotide variation in amplicon sequences.

- ✓ **Quick Turnaround:** From sample collection to report in as little as **1 weeks.**
- ✓ **Species-Level Resolution:** We provide species level resolution in 16S sequencing while others normally restrict to genus.
- ✓ **Unbiased Microbial Lysis:** Our DNA extraction methods are validated unbiased for microbiome profiling.
- ✓ **Absolute Quantification:** 16S/ITS copy number measurement for each species along with standard percentage measurement.

Species-Level Resolution

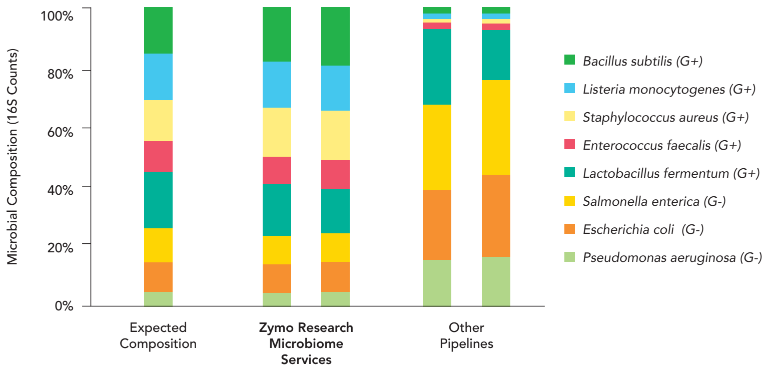
By combining sequence-analysis algorithm, DADA2, and a well-curated 16S reference database, we can provide species-level resolution with regular Illumina® sequencing of different 16S regions, e.g. V3-V4, V1-V2 and V1-V3.



Achieve Species-Level Identification With 16S Amplicon Sequencing

Species	Zymo Research 16S Pipeline	Other Service Providers
Listeria monocytogenes	✓	✗
Staphylococcus aureus	✓	✓
Enterococcus faecalis	✓	✗
Lactobacillus fermentum	✓	✗
Escherichia coli	✓	✗
Salmonella enterica	✓	✗
Pseudomonas aeruginosa	✓	✗
Bacillus subtilis	✗	✗
Species-level Resolution	✓	✗

By combining leading edge sequencing error correction methods with a highly curated 16S rRNA database, our 16S amplicon sequencing service can provide taxonomic identification down to the species level.



Unbiased Microbial Lysis

Many service providers use DNA extraction kits that are not validated for microbiome profiling, which can result in massive skew in the final profile. Our DNA extraction step is validated unbiased using the ZymoBIOMICS™ Microbial Community Standard. The standard is used as a positive control in every run.

Shotgun Metagenomic Sequencing

Shotgun Metagenomic Sequencing, in comparison to amplicon sequencing (e.g. 16S sequencing), is a more comprehensive way to characterize a microbiome sample. Shotgun sequencing provides across-kingdom identification and in theory, can detect all microbes except RNA viruses.

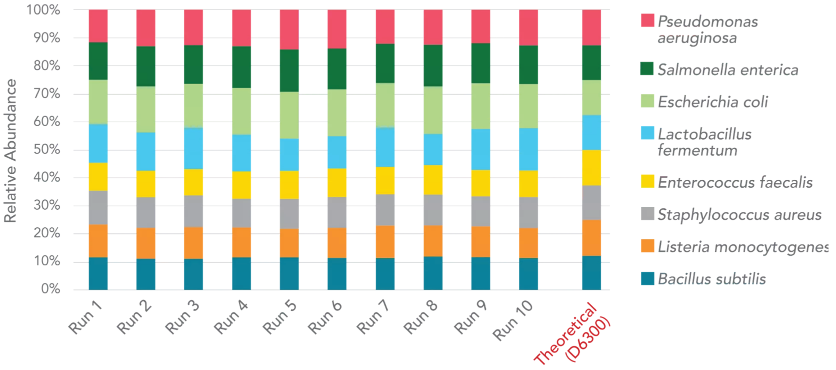
Metagenomic approaches provide strain-level taxonomy resolution with sufficient sequencing depth. Unlike amplicon sequencing, identification of functional genes and pathways is also possible.

Shotgun Metagenomic Sequencing is now more affordable with advanced sequencing technology.

- ✓ **Quick Turnaround:** Results from sample to report in as little as 3 weeks
- ✓ **Strain-Level Resolution:** High confidence strain identification through our curated reference database
- ✓ **Comprehensive Bioinformatic Analysis:** Includes bar plots, heatmaps, diversity analysis, gene family & metabolic pathway profiling, identification of virulence genes & antibiotic resistance genes, and statistical group analysis.
- ✓ **Minimize False Positives:** innovative algorithms that minimize the number of false positives

High-Confidence Data You Can Trust

Our validated workflow is optimized at every step to reduce noise and improve accuracy. Proprietary analysis algorithms minimize false positives in taxonomic assignment, while ultra-clean reagents reduce background contamination.



Controlling False Positives

Many other service providers suffer from false positive species identification due to the presence of host DNA in samples and the use of reference microbial genomes contaminated by human genome sequences. The pipeline of service provider D (built on Kraken) reported 202 total taxa from a vaginal swab sample and 197 of these taxa were determined to be false positives. Zymo Research's bioinformatic pipeline is able to accurately identify 5 taxa in the sample.

Species	Zymo Research (%)	Service Provider D (%)
Lactobacillus iners	48.9	20.3
Klebsiella michiganensis	46.7	0.5
Candida albicans	1.9	0.1
Enterococcus faecalis	1.7	0.2
Klebsiella oxytoca	0.7	4.1
Coprobacillus sp.	-	48.2
Klebsiella sp.	-	6.7
Beggiatoa sp.	-	7.5
Candidatus Pelagibacter	-	4.5
(k) Bacteria sp.	-	2.6
(f) Enterobacteriaceae	-	1.1
(o) Enterobacterales	-	0.3
Vibrio campbellii	-	0.3
Psychrobacillus sp. FJAT-21963	-	0.3
Vibrio agarivorans	-	0.2
Mycobacterium kansasii	-	0.1
Paeniglutamicibacter antarcticus	-	0.1
Salmonella enterica	-	0.1
181 more taxa	-	**2.7**

🟩 Accurate Species Identification

🟥 False Positives

Results of two bioinformatics pipelines analyzing the same raw sequence data derived from a vaginal swab sample.

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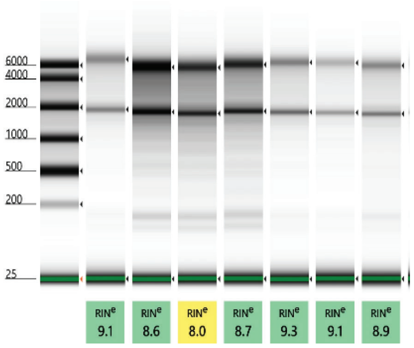
Metatranscriptomics Sequencing

By analyzing the RNA transcripts present in a sample, metatranscriptomics provides researchers with a comprehensive understanding of the functional dynamics and metabolic activities within complex microbial ecosystems. Compared to metagenomics, which focuses on the DNA content of microbial communities, metatranscriptomics offers a dynamic and real-time view of microbial activity, providing a deeper understanding of ecosystem dynamics, microbial response to environmental changes, and the functional roles of individual species within a community. This advantages make metatranscriptomics a more powerful approach for studying complex microbial systems.

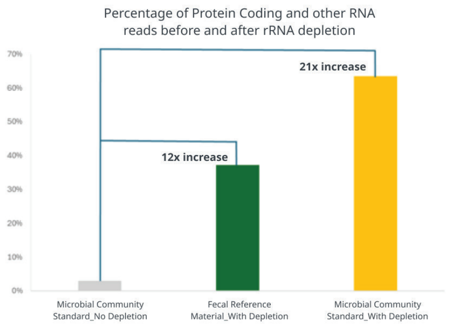
- ✓ **Unbiased high quality RNA extraction:** Ensure true profile representation for reliable analysis.
- ✓ **Efficient rRNA depletion:** Enhance assay sensitivity and resolution by depleting noncoding host and bacterial ribosomal RNA (rRNA) from complex microbial samples.
- ✓ **Species-level Metabolic Pathway Detection:** Our robust bioinformatic pipeline confidently identify abundant functional pathways to species-level resolution.
- ✓ **Complete Multi-Kingdom Profiling:** Detect RNA from any kingdom (Bacteria, Archaea, Eukaryote, and RNA Viruses).

High-Quality RNA from Any Sample Type

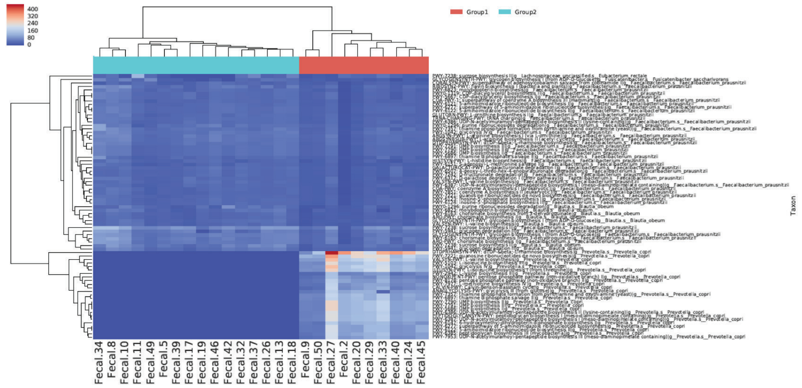


Achieve consistent, unbiased extraction using mechanical lysis. Shown: Fragment size distribution and RIN scores from RNA isolated with the ZymoBIOMICS MagBead RNA Kit (R2137) and RNA Miniprep Kit (R2001).

Maximize Data Relevance with Universal rRNA Depletion

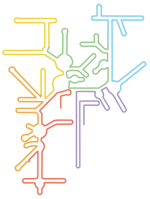


Achieve more informative metatranscriptomic profiles with efficient rRNA removal. Shown: rRNA depletion and RNA library prep results using the Zymo-Seq RiboFree Total RNA Library Kit (R3000) on the ZymoBIOMICS Community Standard (D6300) and Fecal Reference Material (D6323).



Metabolic Pathway and Gene Expression Analysis

The metabolic pathway profiling heatmap reveals abundance patterns of key pathways, while hierarchical clustering highlights functional relationships and potential sample groupings.



Full-Length 16S Sequencing

With the introduction of full-length gene sequencing, researchers can now leverage the complete taxonomic resolution power of the full 16S rRNA gene. Full-length 16S sequencing finds applications in various fields like microbiology, environmental science, medicine, and agriculture. It's used in studying gut microbiomes, identifying pathogens, assessing soil or water microbial diversity, and more. As a Certified PacBio Service Provider, Zymo Research ensures the meticulous handling of your samples.

- ✓ **Unrivaled Species Resolution:** Resolve the full 16S rRNA gene with PacBio HiFi Sequencing and Zymo Research's expert-level bioinformatic analyses.
- ✓ **Unbiased Sample Preparation:** Standardized, unbiased workflows with rigorous QC and Microbial Standards provide accurate and reliable data.
- ✓ **Quick Turnaround Time:** Receive full-length 16S sequencing results in as little as 3 weeks.

A Better Way to Resolve Closely Related Species

Bacteria species	Full-length 16S	V1-V3 (short read)	V3-V4 (short read)	V4 (short read)
Bacillus subtilis	🟩	*Bacillus mojavensis-subtilis*	*Bacillus sp.*	*Bacillus sp.*
Listeria monocytogenes	🟩	🟩	*Listeria sp.*	*Listeria sp.*
Enterococcus faecalis	🟩	🟩	🟩	*Enterococcus sp.*
Lactobacillus fermentum	🟩	🟩	🟩	🟩
Escherichia coli	🟩	🟩	🟩	*Escherichia coli-fergusonii-vulneris*
Salmonella enterica	🟩	🟩	🟩	*Enterobacteriaceae sp.*
Pseudomonas aeruginosa	🟩	🟩	🟩	*Pseudomonadales sp.*
Staphylococcus aureus	*Staphylococcus argenteus-aureus*	*Staphylococcus argenteus-aureus*	*Staphylococcus argenteus-aureus-simiae*	*Staphylococcus sp.*

🟩 **Fully Resolved to Species Level** 🟨 **Partially Resolved**

Full-length 16S sequencing was able to distinguish closely related species by looking at the whole 16S rRNA gene, as compared to traditional snapshots of smaller regions with short read (V4, V3-V4, V1-V3, V1-V2 and V4-V5).

Versatile Expertise for Diverse Samples

Fecal **Soil** **Women's Health** **Oral** **Environmental**

Zymo Research scientists have worked with 1,000's of diverse samples.

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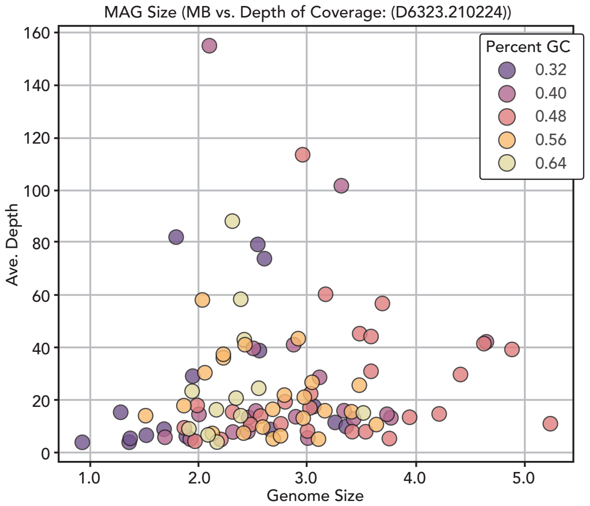
Long-Read Metagenomic Sequencing & Assembly

Zymo Research offers high-resolution metagenomic assembly using PacBio HiFi sequencing—enabling complete genome reconstruction from complex microbiomes. Our comprehensive workflow includes mechanical lysis-based extraction of high-molecular-weight DNA, long-read sequencing. Our bioinformatics pipeline includes quality filtering, contig assembly, binning, MAG taxonomy, and pathway profiling, all optimized for PacBio HiFi data.

As a PacBio Certified Service Provider, we offer end-to-end expertise and validated methods to help you uncover the functional and taxonomic complexity of your microbiome samples with confidence and clarity.

- ✓ Unbiased HMW DNA extraction with mechanical lysis
- ✓ Comprehensive assembly, binning & profiling
- ✓ High-resolution assembly from complex sample

One Hundred High-Quality MAGs from Fecal Reference Assembled by PacBio HiFi Sequencing

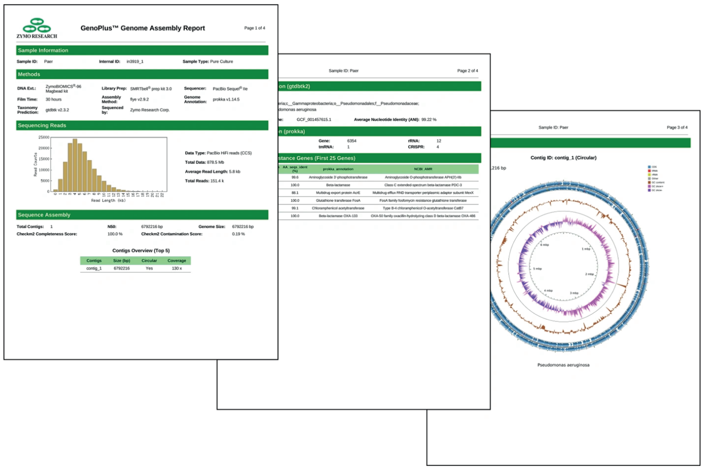


HiFi Reads >Q20	Mean Read Length	High-Quality MAGs
1,792,146 reads	10,318 bp	100 MAGs

In this study, DNA from ZymoBIOMICS™ Fecal Reference (D6323) was extracted and sequenced using PacBio HiFi Sequencing. The assembly of this dataset produced 100 high-quality metagenome assembled genomes (MAGs) using our bioinformatics pipeline.

Long-read Bacterial Whole Genome Assembly

Simplifying Genome Assembly Interpretation



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GenoPlus™ Genome Assembly Report

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Sample Information

Sample ID: Paer **Internal ID:** in3919_1 **Sample Type:** Pure Culture

Methods

DNA Ext.: ZymoBIOMICS®-96 Magbead kit
Library Prep: SMRTbell® prep kit 3.0
Sequencer: PacBio Sequel® IIe
Film Time: 30 hours
Assembly Method: flye v2.9.2
Genome Annotation: prokka v1.14.5
Taxonomy Prediction: gtdbtk v2.3.2
Sequenced by: Zymo Research Corp.

Sequencing Reads

Data Type: PacBio HiFi reads (CCS)
Total Data: 878.5 Mb
Average Read Length: 5.8 kb
Total Reads: 151.4 k

Sequence Assembly

Total Contigs: 1
N50: 6792216 bp
Genome Size: 6792216 bp
Checkm2 Completeness Score: 100.0 %
Checkm2 Contamination Score: 0.19 %

Contigs Overview (Top 5)

Contigs	Size (bp)	Circular	Coverage
contig_1	6792216	Yes	130 x

Sample ID: Paer

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on (gtdbtk2)

eria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;
domonas aeruginosa

e: GCF_001457615.1 **Average Nucleotide Identity (ANI):** 99.22 %

n (prokka)

Gene: 6354 **rRNA:** 12
tmRNA: 1 **CRISPR:** 4

stance Genes (First 25 Genes)

AA_seqs_ident (%)	prokka_annotation	NCBI_AMR
99.6	Aminoglycoside 3'-phosphotransferase	Aminoglycoside O-phosphotransferase APH(3')-IIb
100.0	Beta-lactamase	Class C extended-spectrum beta-lactamase PDC-3
88.1	Multidrug export protein AcrE	Multidrug efflux RND transporter periplasmic adaptor subunit MexX
100.0	Glutathione transferase FosA	FosA family fosfomycin resistance glutathione transferase
99.1	Chloramphenicol acetyltransferase	Type B-4 chloramphenicol O-acetyltransferase CatB7
100.0	Beta-lactamase OXA-133	OXA-50 family oxacillin-hydrolyzing class D beta-lactamase OXA-486

Sample ID: Paer

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Contig ID: contig_1 (Circular)

Pseudomonas aeruginosa

Our comprehensive, user-friendly report includes sequence read distribution, assembly summary, taxonomy prediction, genome annotation, antimicrobial resistance gene identification, and a circular genome map—providing clear, actionable insights at every step.

Zymo Research's Bacterial Whole Genome Assembly service uses PacBio HiFi sequencing to generate highly accurate, contiguous assemblies from isolates. Our end-to-end workflow includes mechanical lysis-based extraction of high-molecular-weight DNA, long-read library prep, and optimized de novo assembly with full genome annotation—resolving full chromosomes, plasmids, and repetitive regions. Each project includes a detailed Genome Assembly Report with quality metrics, taxonomic classification, AMR gene detection, and a circular genome map, supported by expert bioinformatic consultation.

- ✓ High quality HMW DNA extraction even from hard-to-lyse Bacterial
- ✓ Complete genome reconstruction and annotation
- ✓ Comprehensive and user-friendly report

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Complete & Custom Solutions for Any Industrial Partners

Zymo Research delivers end-to-end microbiome sequencing services customized for clinical, consumer, and environmental applications. From sample collection to advanced bioinformatics, our workflows provide high-resolution insights—even from low-input or complex samples.

Whether you're developing diagnostics, wellness products, or agricultural solutions, our platform adapts to your sample types, timelines, and regulatory needs. With ultra-clean reagents, validated pipelines, and expert support, we minimize noise and false positives—ensuring reliable, actionable data.

Scalable infrastructure enables fast turnaround times without compromising quality. We also offer white-labeled kits, branded reports, and expert consultation to help you bring microbiome science confidently to market.

All-in-One Microbiome Pipeline: From Sample to Result

Microbiome Standards

Sample Collection

DNA/RNA Extraction

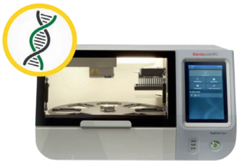
Library Preparation

NGS Analysis

Zymo Research offers complete, customizable microbiome analysis tailored to your needs—covering everything from sample collection and library prep to sequencing and bioinformatics. Enjoy a seamless, one-stop solution for high-quality, end-to-end microbiome insights.

High-Throughput Automated Workflows for Fast, Reliable Results

Our advanced, fully automated workflows leverage state-of-theart technology to ensure exceptional scalability, superior data quality, and turnaround times as fast as one week.

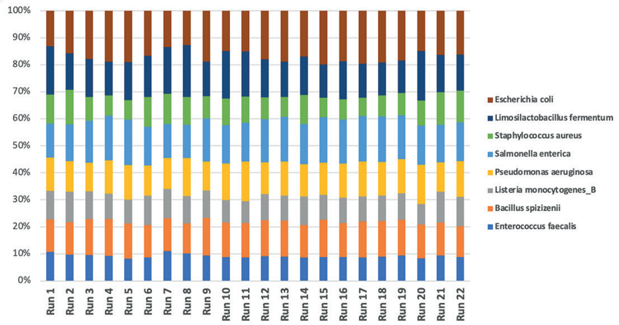


DNA and RNA Extraction

Library Preparation

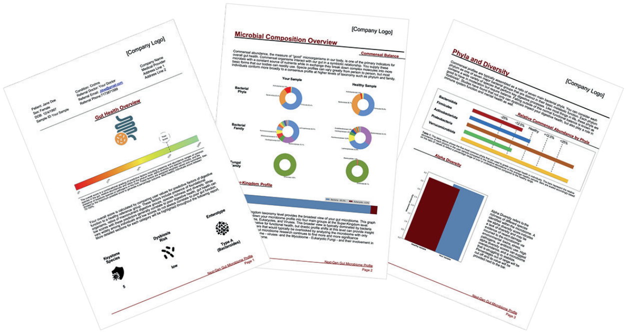
Sequencing

Excellent Reproducibility Across Runs



Our rigorously validated workflows ensure consistent, high-accuracy results. Microbial profiles from 25 independent runs of the ZymoBIOMICS Community Standard (D6300) demonstrate the reproducibility and reliability of our platform.

Custom Bioinformatic Reports for Actionable Insights



Our expert team delivers clear, tailored bioinformatic reports designed to make complex data easy to interpret—empowering you to act with confidence on every result.

Sample Collection & Kit Design

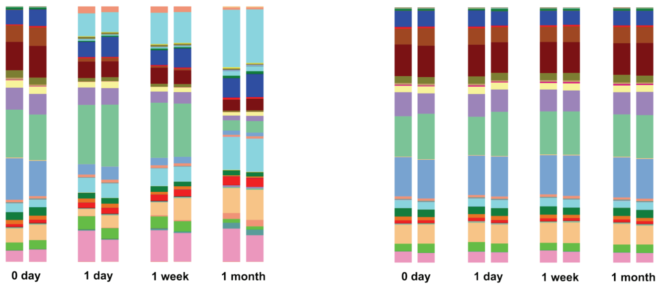
Zymo Research's comprehensive catalog offers a way to partner with a single company for all your service and product needs. With Zymo Research, a variety of sample collection devices can be seamlessly paired with customizable Direct-to-Consumer kits. With our DNA/RNA Shield™ collection reagent, samples can be safely collected, stored, and shipped at ambient temperature without worrying about their stability.

Preserve Microbiome Profile at Ambient Temperature

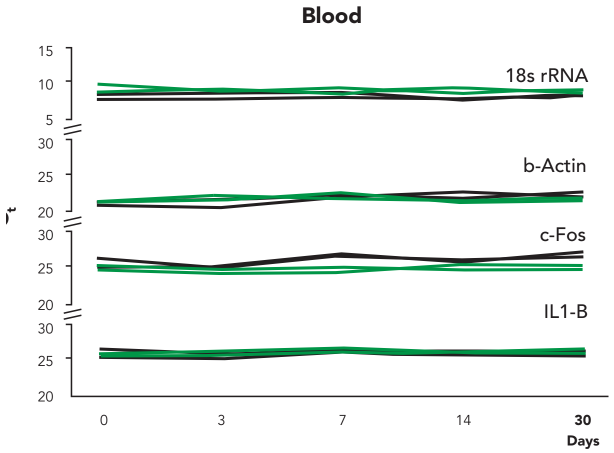
Microbial Composition of Stool is Unchanged After One Month at Ambient Temperature with DNA/RNA Shield™

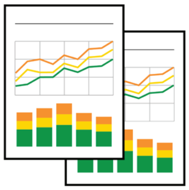
Without DNA/RNA Shield™ - Composition Changes

With DNA/RNA Shield™ - Accurate Composition



RNA Integrity is Maintained Over One Month with DNA/RNA Shield™





Customizable & User-friendly Report

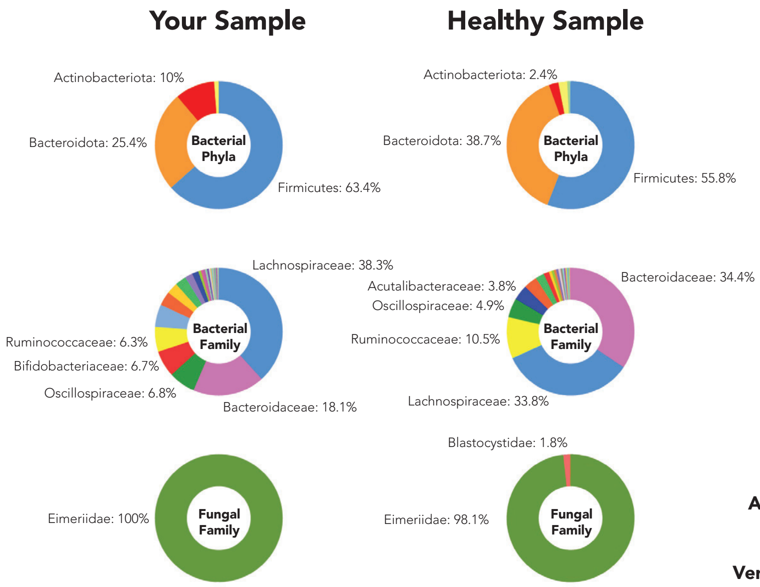
At Zymo Research's Microbiome Sequencing Service, we pride ourselves on our ability to tailor bioinformatic analysis and reports to meet the unique needs of any customers. Leveraging cutting-edge technology and expertise, we craft customized reports that provide actionable insights into microbiome composition, function, and potential implications for specific objectives. Our reports simplify NGS data interpretation, empower your clients with data-driven insights .

Customizable
Data Reports

Automatically
Generated Plots

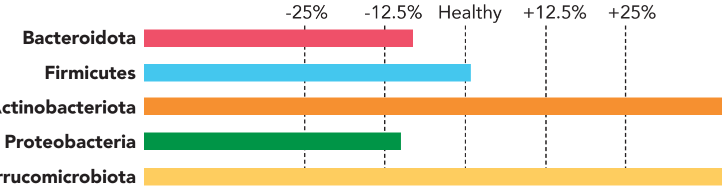
Detect Pathogens,
Antibiotic Resistance, Etc

Simplify NGS Data Interpretation for Your Clients



Species	Role	Abundance
Agathobacter rectalis	⁘	0.14%
Phocaeicola vulgatus	⁘	0.08%
Bifidobacterium adolescentis	⁘	0.06%
Acidaminococcus intestini	⁘	0.05%
Fusicatenibacter saccharivorans	⁘	0.04%
Faecalibacterium prausnitzii	🛡	0.03%
Bacteroides ovatus	⁘	0.03%
Bacteroides uniformis	⁘	0.02%
Bacteroides thetaiotaomicron	🛡	0.02%
Collinsella aerofaciens	⁘	0.02%

🛡 Keystone ✹ Pathogen ⁘ Commensal



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