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Produktinformation

- Forschungsprodukte & Biochemikalien
- Zellkultur & Verbrauchsmaterial
- Diagnostik & molekulare Diagnostik
- Laborgeräte & Service

Weitere Information auf den folgenden Seiten!
See the following pages for more information!

Lieferung & Zahlungsart

siehe unsere Liefer- und Versandbedingungen

Zuschläge

- Mindermengenzuschlag
- Trockeneiszuschlag
- Gefahrgutzuschlag
- Expressversand

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ZYMO RESEARCH

Microbiomics
Made Simple™

Load N' Go™ ZymoBIOMICS™ DNA MagBead Kit

Automation ready: Rapid, high-throughput DNA extraction from any sample for microbial study and discovery

Highlights

- **Save Time and Focus on Discovery:** Pre-filled 96-deepwell reagent plates that offer multi-platform compatibility and reduce handing times by as much as 75%.
- **Validated Unbiased for Microbiome Measurements:** Unbiased cellular lysis validated using the **ZymoBIOMICS™ Microbial Community Standard**.
- **Inhibitor-Free DNA from Any Sample**: Isolate ultra-pure DNA, ready for any downstream application.
- **Certified Low Bioburden**: Boost your detection limit for low abundance microbes.

Catalog Numbers:
D4311

Scan with your smart-phone camera to view the online protocol/video.

tech@zymoresearch.com www.zymoresearch.com Toll Free: (888) 882-9682

Table of Contents

Product Contents

Load N' Go™ ZymoBIOMICS™ DNA MagBead Kit	Volume / Qty
Plate 1: Sample Plate	625 µl x 96
Plate 2: Binding Wash	500 µl x 96
Plate 3: ZymoBIOMICS™ MagWash 1	500 µl x 96
Plate 4: ZymoBIOMICS™ MagWash 2	900 µl x 96
Plate 5: ZymoBIOMICS™ MagWash 3	900 µl x 96
Plate 6: Elution Plate	50 µl x 96
DNA/RNA Shield™ (2x)	125 ml
96 Tip Combs[1] (For V-Bottom Deep Well Plate)	2 pc
Instruction Manual	1 pc

- **Materials/Equipment Needed (user provided)**
  - ✓ Sample Lysis Module
  - ✓ 96-well plate/block disruptor/pulverizer
  - ✓ Nuclease-free water
  - ✓ Centrifuge with microplate carriers
  - ✓ Vortex Mixer
  - ✓ Liquid handler or bead mover laboratory automation
- **Materials Available Separately (not provided)**
  - DNA/RNA Shield™ Lysis Tubes (Microbe) (R1103)
  - DNA/RNA Shield™ Fecal Collection Tube (R1101), (R1137, with beads)
  - DNA/RNA Shield™ Collection Tube w/ Swab (R1106)
  - ZymoBIOMICS™ Microbial Community Standard (D6300)
  - ZymoBIOMICS™ Microbial Community DNA Standard (D6305)
  - ZR BashingBead™ Lysis Tubes (S6012-50; 0.1 & 0.5 mm beads)
  - ZR-96 BashingBead™ Lysis Rack (Barcoded) (S6002-96-4, Single barcoded tubes), (S6002-96-5, Double barcoded tubes)
  - ZR-96 BashingBead™ Lysis Rack (S6002-96-3, 0.1 & 0.5 mm beads)

1 Compatible with platforms such as KingFisher™ Flex, KingFisher™ Apex, IsoPure™ 96, and Auto-Pure 96 systems.

Specifications

Sample Sources – Bacterial (including endospores), fungal, protozoan, algal, viral, mitochondrial, and host DNA is efficiently isolated from ≤ 100 mg of mammalian feces, ≤ 100 mg soil, and 5 – 20 mg (wet weight) of bacterial/fungal cells[1], biofilms, and water[2].

Binding Capacity – 5 µg DNA per prep.

Elution Volume – 50 µL **ZymoBIOMICS™ DNase/RNase Free Water**.

DNA Purity – High quality, inhibitor-free DNA is eluted with **ZymoBIOMICS™ DNase/RNase Free Water** and is suitable for all downstream applications including PCR and Next-Generation Sequencing.

Bead Beating System – The innovative ZymoBIOMICS™ lysis system enables complete homogenization/disruption of the microbial cells walls and accurate microbial DNA analysis, free of bias. To ensure unbiased lysis, calibration of each bead-beating device is recommended by using the **ZymoBIOMICS™ Microbial Community Standard** (see Appendix C).

DNA Integrity – On average, post bead beating, genomic DNA is between 15-20 kb depending on the initial quality of the sample, making it amenable to Next-Generation Sequencing platforms requiring high molecular weight DNA. For optimal DNA integrity, collect samples in **DNA/RNA Shield™**.

Bioburden – A single preparation is guaranteed to contain less than 3 bacterial genomic copies per µl of eluate as determined by quantitative amplification of the 16S rRNA gene when eluted using 100 µl water.

1 This equates to approximately 2 x 10^8 bacterial cells and 2 x 10^7 yeast cells.
2 For water samples, filter using desired filter (not provided). Cut the filter into small pieces and place into ZR BashingBead™ Lysis Tube (0.1 & 0.5 mm). Alternatively, up to 250 µl water can be processed directly. See Page 18 for ordering information.

Product Description

The **Load N' Go™ ZymoBIOMICS™ DNA MagBead Kit** is intended for rapid, high-throughput DNA extraction from any sample for microbial study and discovery. The system features pre-loaded plate technology that reduces hands-on time on average by 75%. Simply prepare your sample, load the plates, and run the purification script on your laboratory automation platform of choice.

The ZymoBIOMICS™ innovative lysis system eliminates bias associated with unequal lysis efficiencies[1] of different organisms (*e.g.,* Gram negative/positive bacteria including endospores, fungi, protozoans, algae, etc.) making it ideal for microbial community profiling. Unbiased mechanical lysis of tough microbes is achieved by bead beating with the innovative ultra-high density BashingBeads™ and validated using the **ZymoBIOMICS™ Microbial Community Standard**[2], as shown in Figure 3 (page 5).

1 Chemical, enzymatic, and inferior lysis matrices lead to unrealistic representation of organisms in downstream metagenomic analyses that is not reflective of actual abundance.

2 For more information on the ZymoBIOMICS™ Microbial Community Standard & ZymoBIOMICS™ Microbial Community DNA Standard, see Appendix C. See Page 18 for ordering information.

Ultra-pure DNA from Inhibitor Rich Samples

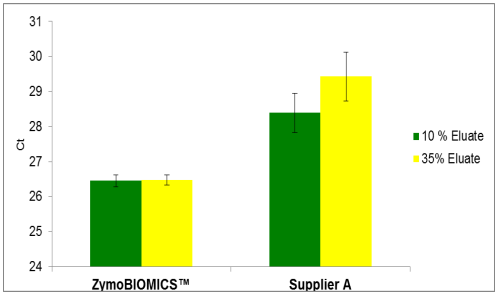


Figure 1.
The Load N' Go™ ZymoBIOMICS™ DNA MagBead Kit provides inhibitor-free DNA even when challenged with extremely inhibitor rich samples. Real-time PCR was used to evaluate eluates recovered using the Load N' Go™ ZymoBIOMICS™ DNA MagBead Kit, or Supplier A. Reaction volumes consisted of either 10% or 35% of the eluate from each kit to detect the presence of PCR inhibitors. Each reaction contained 10 ng of Brettanomyces DNA. Delayed amplification indicates PCR inhibition from inefficient inhibitor removal. N=8.

Superior DNA Yield

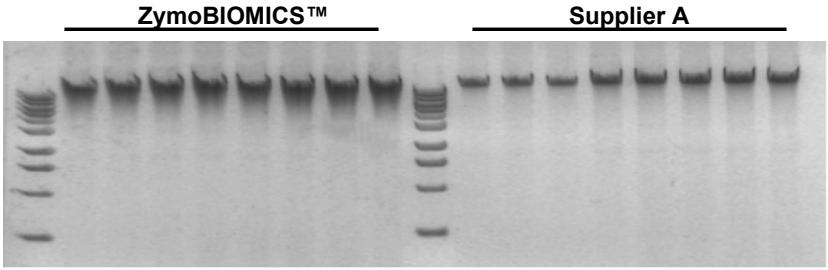


Figure 2.
The Load N' Go™ ZymoBIOMICS™ DNA MagBead Kit provides superior yields when compared to Supplier A. 80 mg of feces was processed using each kit according to the manufactures' recommended protocol. DNA was eluted using 100 µl ZymoBIOMICS™ DNase/RNase Free Water**.** 6 µl of each sample was analyzed in a 1.0% (w/v) agarose/ethidium bromide gel. Samples were processed in triplicate. Ladder is a 1Kb ladder, ZR 1 kb DNA Marker.

Bias-Free Microbial DNA Extraction Using Load N' Go™ ZymoBIOMICS™ MagBead DNA Kit Validated with the ZymoBIOMICS™ Microbial Community Standard

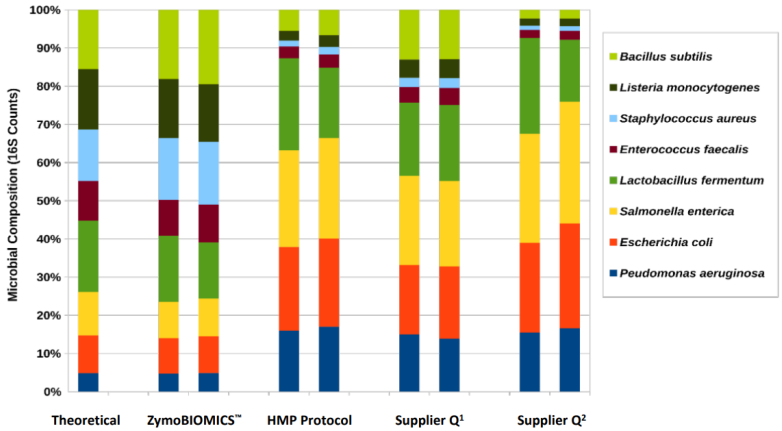


Figure 3.
The Load N' Go™ ZymoBIOMICS™ MagBead DNA Kit provides unbiased representation of the organisms extracted from the ZymoBIOMICS™ Microbial Community Standard. DNA was extracted from ZymoBIOMICS™ Microbial Community Standard using four different DNA extraction methods (ZymoBIOMICS™ MagBead DNA Kit, Human Microbiome Project Protocol, Supplier Q[1], and Supplier Q[2]) and analyzed using 16S rRNA gene sequencing. 16S rRNA genes were amplified with primers targeting v3-4 region and the amplicons were sequenced on Illumina® MiSeq™ (2 x 250 bp). Overlapping paired-end reads were assembled into complete amplicon sequences. The composition profile was determined based on sequence counts after mapping amplicon sequences to the known 16S rRNA genes of the eight different bacterial species.

Bias-Free Microbial DNA Extraction Using Load N' Go™ ZymoBIOMICS™ MagBead DNA Kit From Human Stool

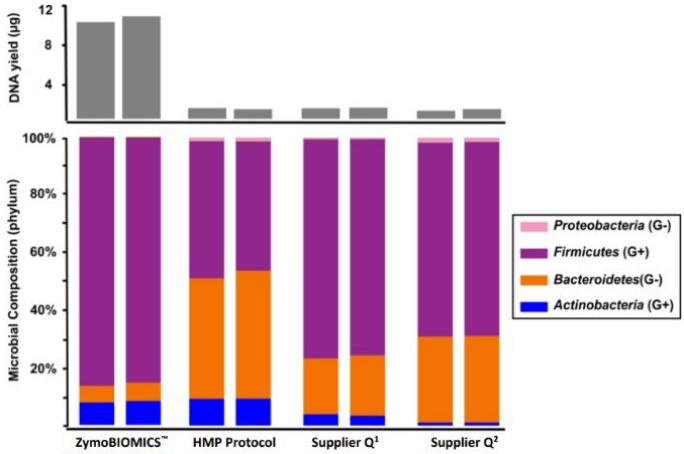


Figure 4.
The Load N' Go™ ZymoBIOMICS™ MagBead DNA Kit reliably isolates DNA from even the toughest to lyse Gram-positive organisms, enabling unbiased analyses of microbial community compositions. There is a significant increase in yield and Gram-positive bacterial abundance when DNA was isolated using the ZymoBIOMICS™ MagBead DNA Kit. Correlated with the DNA yield results, it can be concluded that unbiased DNA isolation was achieved. DNA was extracted from 200 µl of human feces suspended in PBS (10 % m/v) using four different DNA extraction methods (ZymoBIOMICS™ MagBead DNA Kit, Human Microbiome Project Protocol, Supplier Q^1, and Supplier Q^2) and analyzed using 16S rRNA gene sequencing. 16S rRNA genes were amplified with primers targeting v3-4 region and the amplicons were sequenced on Illumina® MiSeq™ (2 x 250 bp). Overlapping paired-end reads were assembled into complete amplicon sequences. Amplicon sequences were profiled with Qiime using Greengenes 16S rRNA gene database (gg_13_8).

Protocol

The protocol consists of: (I) Loading Scripts, (II) Sample Preparation, and (III) Purification.

(I) Loading Scripts

Contact **automation@zymoresearch.com** to obtain the script and other reference materials related to this **Load N' Go™ ZymoBIOMICS™ MagBead DNA Kit** on your automation platform.

Examples of popular systems that are compatible include, but are not limited to:

- ✓ AllSheng Auto-Pure 96
- ✓ Accuris IsoPure™ 96
- ✓ Thermo Scientific™ KingFisher™ Flex
- ✓ Thermo Scientific™ KingFisher™ Apex
- ✓ Tecan Fluent®
- ✓ Hamilton Microlab® Star™
- ✓ Opentrons™ OT-2

If you are unsure about compatibility, reach out to **automation@zymoresearch.com** for verification.

(II) Sample Preparation

1. Add sample to the **BashingBead™ Lysis Module**[1] using the Sample Input Table:
   a. If using **ZymoBIOMICS™ BashingBead™ Lysis Rack (0.1 & 0.5 mm)** add 550 µl **DNA/RNA Shield™ (1x).**[2]
   Remove cover before bead beating, secure clamp directly to the lysis tube caps.

   When using the **ZymoBIOMICS™ BashingBead™ Lysis Rack (0.1 & 0.5 mm)**, it is recommended to seal the rack with the provided sealing foils. Seal the foils to the rack using a heat sealing device set at 180°C for 4 seconds. Refer to Appendix E, Page 17, for more detailed guidance.

   b. If using **ZR BashingBead™ Lysis Tubes (0.1 & 0.5 mm),** add 750 µl **DNA/RNA Shield™ (1x).**[2]

Table 1: Sample Input

Sample Type	Maximum Input
Feces	100 mg
Soil	100 mg
Liquid Samples[3] and Swab Collections[4]	250 µl
Cells (Suspended in PBS)	5-20 mg (wet weight) (2×10^8 bacterial and 2×10^7 yeast cells)
Samples in DNA/RNA Shield™	≤ 800 µl

1 ZR BashingBead™ Lysis Modules sold separately. See Page 18 for ordering information.
2 DNA/RNA Shield™ provided in the kit is 2x concentration; dillute using an equal volume of nuclease-free water (not provided) to the DNA/RNA Shield™ (2x) concentrate (1:1) and mix well.
3 For water samples, filter using desired filter (not provided). Cut the filter into small pieces and place into ZR BashingBead™ Lysis Tubes (0.1 & 0.5 mm).
4 Swabs can also be cut or broken and placed directly in bead beating tube.

(II) Sample Preparation (continued)

2. Secure a bead beater fitted with the appropriate holder assembly for your bead beating module and process using optimized beat beating conditions (speed and time) for your device (see Appendix D)[1].

Optional Stopping Point: *Following Step 2 is the best stopping point if breaking up the work is needed. Samples post lysis can be stored for several hours at room temperature or can be stored at –80°C for long term storage.*

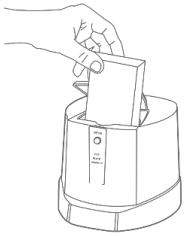
3. Centrifuge the **BashingBead™ Lysis Module**:
    a. If using **ZR BashingBead™ Lysis Tubes (0.1 & 0.5 mm)**, centrifuge at ≥ 10,000 x *g* for 1 minute.
    b. If using **ZymoBIOMICS™ BashingBead™ Lysis Rack (0.1 & 0.5 mm)**, centrifuge at ≥ 4,000 x *g* for 5 minutes.

1 For optimal lysis efficiency and unbiased profiling all bead beater devices beyond those validated by Zymo Research should be calibrated using the ZymoBIOMICS™ Microbial Community Standard. See Appendix C. See Page 18 for ordering information.

(III) Purification

✓ Perform all steps at room temperature (20-30°C)

1. **Spin down elution plate.**



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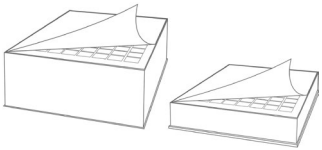
2. **Remove foil seals from all plates.**



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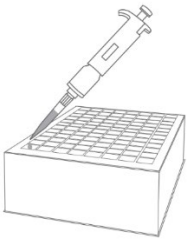
3. **Load 200 µL of prepped sample[1] into each well of sample plate.**



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4. **Run extraction script**

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1 If using < 200 µl sample, increase the total sample input volume to 200 µl using DNA/RNA Shield™ (1x).

Appendices

Appendix A: FAQ

Question	Suggested Solutions
How do I avoid background contamination?	- Clean workspace, centrifuge, and pipettes with 10% bleach to routinely to avoid contamination. - If use of kit is in an exposed environment without proper filtration. Check pipettes, pipette tips, microcentrifuge tubes, workspace, etc. for contamination.
How do I fix low DNA yield?	Lysis Method - Bead beating devices that oscillate in a single dimension (only vertically or only horizontally) have been observed to inefficiently lyse very recalcitrant species. Devices that oscillate three-dimensionally or in a figure-8 motion often lyse microbes efficiently. Input - Consult Table 1 on Page 8 for information on your particular input limit based on sample.
How do I know if my automation instrument is compatible?	Examples of popular systems that are compatible include, but are not limited to: - AllSheng Auto-Pure 96 - Accuris IsoPure™ 96 - Thermo Scientific™ KingFisher™ Flex - Thermo Scientific™ KingFisher™ Apex - Tecan Fluent® - Hamilton Microlab® Star™ - Opentrons™ OT-2 If you are unsure about compatibility, reach out to automation@zymoresearch.com for verification.
How do I get scripts for this kit on my automation platform?	Please contact automation@zymoresearch.com to send a request for scripts and additional reference material.

For any other technical assistance, please email automation@zymoresearch.com

Appendix B: Sample Collection

For high quality reproducible metagenomic data, **DNA/RNA Shield™** is recommended for sample collection to avoid bias or erroneous results due to compositional changes from nucleic acid degradation or microbial growth. DNA/RNA Shield™ provides an unbiased molecular snapshot of the sample at the time of collection by preserving nucleic acids at ambient temperature and inactivating organisms including infectious agents. Samples can be stored and transported easily and safely with DNA/RNA Shield™ and is ideal for applications such as PCR, 16S rRNA gene sequencing, and shotgun metagenomic sequencing. DNA/RNA Shield™ can preserve nucleic acids in nearly any sample including feces, soil, saliva, blood, and tissues.

DNA/RNA Shield™ - Lysis Tube (Microbe) – Simply add sample, seal, and store at ambient temperature. The Lysis Tube is immediately ready for bead beating, thereby streamlining the collection to extraction transition. (Cat. No. **R1103**)

DNA/RNA Shield™ – Fecal Collection Tube – The collection device is specifically designed for easy collection and stabilization of feces. Includes a scoop built for collecting 1 gram of feces (or any other sample such as saliva or soil). (Cat. No. **R1101** & **R1137**)

DNA/RNA Shield™ – Swab Collection Tube – Easy collection of biological samples; swab has breakable tip to allow for easy sample collection and removes the need to dispose of a potentially biohazardous swab material. (Cat. No. **R1106** & **R1107**).

Appendix C: Community Standards

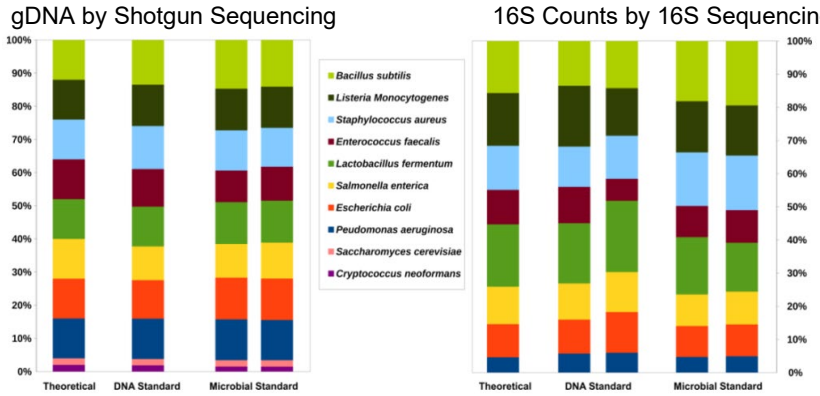
The **ZymoBIOMICS™ Microbial Community Standard** (Cat. No. **D6300**) is a mock microbial community of defined and well characterized composition making it the perfect control for all microbiome profiling and metagenomics analyses.

It is ideal for assessing bias of DNA extraction methods since it contains three easy-to-lyse Gram-negative bacteria (*e.g. Escherichia coli*), five tough-to-lyse Gram-positive bacteria (*e.g. Listeria monocytogenes*), and two tough-to-lyse yeasts (*e.g. Saccharomyces cerevisiae*).

Bead Beating Device Calibration Protocol:
Zymo Research suggests calibrating bead beating devices with the ZymoBIOMICS™ Microbial Community Standard to ensure bias free microbial extraction. For vortex adapters and vortex lysis we suggest a time course ranging from 10-45 minutes with the vortex at maximum speed. For high-speed cell disruptors such as the MP FastPrep™-24 we suggest a time course at maximum speed with a range of 3-10 minutes. The resulting DNA should be evaluated by quantifying DNA yield and changes in microbial profile at each time point. The bead beating time that yields a profile that closely matches the theoretical composition should become standard operating procedure for the bead beating device.

ZymoBIOMICS™ Microbial Community DNA Standard (Cat. No. **D6305**) is a mixture of genomic DNA extracted from pure cultures of eight bacterial and two fungal strains. Genomic DNA from each culture was quantified before mixing. The ZymoBIOMICS™ Microbial Community Standard allows for assessment of bias from library preparation, sequencing, and bioinformatics analysis.
It serves perfectly as a microbial standard for benchmarking the performance of microbiome or metagenomics analyses, including those provided by a 3rd party.

Accurate Composition for Reliable Use to Evaluate Shotgun Sequencing and 16S rRNA Sequencing



Species	Avg. GC (%)	Gram Stain	gDNA Abun. (%)
Pseudomonas aeruinosa	66.2	-	12
Escherichia coli	56.8	-	12
Salmonella enterica	52.2	-	12
Lactobacillus fermentum	52.8	+	12
Enterococcus faecalis	37.5	+	12
Syaphylococcus aureus	32.7	+	12
Listeria monocytogenes	38.0	+	12
Bacillus subtilis	43.8	+	12
Saccharomyces cerevisiae	38.4	Yeast	2
Cryptococcus neoformans	48.2	Yeast	2

Figure 5.

Characterization of the microbial composition of the two ZymoBIOMICS™ standards with shotgun metagenomic sequencing (left, upper panel) and 16S rRNA gene targeted sequencing (right, upper panel). The measured composition of the two standards agrees with the theoretical/designed composition. “DNA Standard” represents ZymoBIOMICS™ Microbial Community DNA Standard (DNA version) and “Microbial Standard” represents ZymoBIOMICS™ Microbial Community Standard (cellular version). Genomic DNA composition by shotgun sequencing was calculated based on counting the amounts of raw reads mapped to each genome. 16S composition by 16S rRNA gene targeted sequencing was calculated based on counting the amount of 16S raw reads mapped to each genome.

Use ZymoBIOMICS™ Microbial Standards for assessing GC-Bias in Shotgun Metagenomics

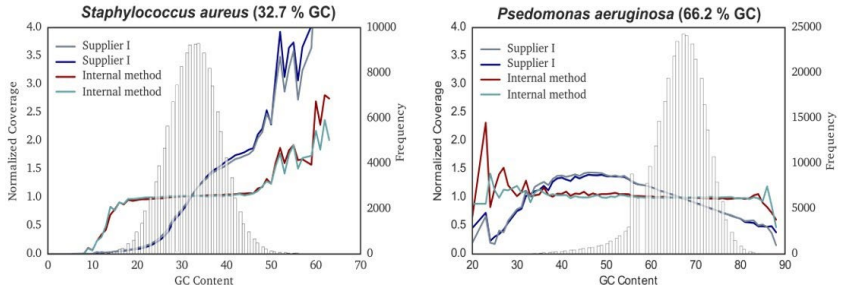


Figure 6.
Library preparation for shotgun metagenomic sequencing was performed in two different ways: one by supplier I and one by an in-house method. Shotgun sequencing was performed on Illumina® MiSeq™ with paired-end sequencing (2 x 150 bp). Raw reads were mapped to the 10 microbial genomes to evaluate the potential effect of GC content on sequencing coverage. Normalized coverage was calculated by normalization by the average sequencing coverage of each genome.

Perfect for tracking PCR Chimera in 16S rRNA Gene Sequencing

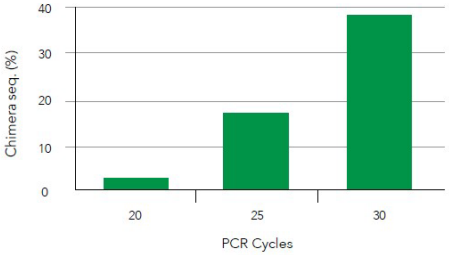


Figure 7.
PCR chimera increases with PCR cycle number in the library preparation process of 16S rRNA gene targeted sequencing. 20 ng ZymoBIOMICS™ Microbial Community Standard was used a template. The PCR reaction was performed with ZymoBIOMICS™ PCR Premix and with primers that target the v3-v4 region of 16S rRNA gene. Chimera rate in percentage was determined with Uchime and using the 16S rRNA gene of the 8 bacterial strains in the standard as reference PCR.

Appendix D: Optimized Lysis Protocols

The following conditions with different mechanical lysis machines were validated with minimum bias using the **ZymoBIOMICS™ Microbial Community Standard**.

1 Vortex Genie with 2ml BashingBead™ Tubes

Recommended for ease of use and accessibility

Use Microtube Adaptor (Scientific Industries, Inc. Cat. No. S5001-7)

1. 40 minutes of continuous bead beating (max of 18 tubes per adaptor)

2 Bertin Precellys Evolution with 2 ml BashingBead™ Tubes

Recommended for ease of use and ultra-high speed.

1. 1 minute on at 9,000 RPM
2. 2 minutes rest
3. Repeat cycle 4 times for a total of 4 minutes of bead beating

3 MP Fastprep-24™ (Classic & 5G) with 2 ml BashingBead™ Tubes

Maximum of 20 tubes. The weight of > 20 tubes may cause a system error.

1. 1 minute on at 6.5 m/s
2. 5 minutes rest
3. Repeat cycle 5 times for a total of 5 minutes of bead beating

4 Omni Bead Ruptor Elite with 2 ml BashingBead™ Tubes

1. 1 minute on at 6 m/s
2. 5 minutes rest
3. Repeat cycle 3 times for a total of 3 minutes of bead beating

5 Biospec Mini-BeadBeater-16 with 2 ml BashingBead™ Tubes

1. 1 minute at maximum speed
2. 5 minutes rest
3. Repeat cycle 5 times for a total of 5 minutes of bead beating

6 Biospec Mini-BeadBeater-96 with 2 ml BashingBead™ Tubes

1. 5 minutes on at Max RPM
2. 5 minutes rest
3. Repeat cycle 4 times for a total of 20 minutes of bead beating

7 Biospec Mini-BeadBeater-96 with 96 well lysis rack

1. 5 minutes on at Max RPM
2. 5 minutes rest
3. Repeat cycle 8 times for a total of 40 minutes of bead beating

✕ TissueLyser II

No tested conditions yielded accurate profiles. This device is not validated by Zymo Research for microbiome research.

✕ TissueLyser LT

No tested conditions yielded accurate profiles. This device is not validated by Zymo Research for microbiome research.

✕ Retsch Mixer Mill MM 400

No tested conditions yielded accurate profiles. This device is not validated by Zymo Research for microbiome research.

Appendix E: BashingBead™ Lysis Racks

1. Remove all strip caps and use a Kimwipe™ to wipe away any residual beads found on the tops of the tubes.
2. Transfer samples into individual lysis rack tubes according to the sample input guide found in Section II, Step 1 of the main protocol (Page 8).
3. Cover the top of the lysis rack tubes with a Kimwipe™ and press down gently to remove any residual liquid.
4. Place the lysis rack on the sealing device stage.
5. Center a sealing foil on top of the lysis rack, such that all tubes are covered by the foil with a slight overhang along each edge.
6. Set heat sealing device to 180°C and allow the device adequate time to reach the target temperature.
7. Press the sealer down onto the foil for 4 seconds to seal the rack.

Note: *At no point should a roller (or similar) be used to press down the foil, as it can damage the bond between the sealing foil and lysis rack, causing leakage.*

8. Allow the sealed lysis rack to cool to room temperature before loading onto a mechanical lysis device.

Note: *Placing a rubber or silicone mat between the sealing foil and mounting clamp is recommended to protect the sealing foil from becoming worn or damaged by the clamp during mechanical lysis.*

9. Proceed with Section II, step 2 of the main protocol (Page 9).

Ordering Information

Product Description	Catalog No.	Size
Load N' Go™ ZymoBIOMICS™ DNA MagBead Kit	D4311	96 Preps
ZR BashingBead™ Lysis Tubes (0.1 & 0.5 mm)	S6012-50	50 Tubes
ZR-96 BashingBead™ Lysis Rack (0.5 mm & 0.1 mm)	S6002-96-3	1 x 96
ZR-96 BashingBead™ Lysis Rack (Single barcoded Tubes)	S6002-96-4	1 x 96
ZR-96 BashingBead™ Lysis Rack (Double barcoded Tubes)	S6002-96-5	1 x 96
DNA/RNA Shield™	R1100-250	250 ml
DNA/RNA Shield™ (2x)	R1200-125	125 ml
DNA/RNA Shield™ Lysis Tubes (Microbe)	R1103	50 Pack
DNA/RNA Shield™ Fecal Collection Tube	R1101	10 Pack
DNA/RNA Shield™ Collection Tube w/ Swab	R1106	10 Pack
ZymoBIOMICS™ Microbial Community Standard	D6300	10 Preps
ZymoBIOMICS™ Microbial Community DNA Standard	D6305	200 ng
ZR 1 kb DNA Marker	M5003-200	400 µl
96 Deep Well Plate (V-Bottom 2.2 ml)	C2018-5	5 Plates
96 Deep Well Plate (V-Bottom 2.2 ml)	C2018-50	50 Plates

Notes

Notes

100% satisfaction guarantee on all Zymo Research products, or your money back.

Zymo Research is committed to simplifying your research with quality products and services. If you are dissatisfied with this product for any reason, please call 1(888) 882-9682.

Integrity of kit components is guaranteed for up to one year from date of purchase.
Reagents are routinely tested on a lot-to-lot basis to ensure they provide the highest performance and reliability.

This product is for research use only and should only be used by trained professionals. It is not for use in diagnostic procedures. Some reagents included with this kit are irritants. Wear protective gloves and eye protection. Follow the safety guidelines and rules enacted by your research institution or facility.

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