# Precise Microbiome Standards

ZymoBIOMICS® Microbial Community Standard

- **Microbiome Standard:** Mock microbial community of well-defined composition.
- **Identify Bias:** Contains both tough-to-lyse and easy-to-lyse organisms.
- **Accurate Characterization:** Ideal for validation, optimization, and quality control of complete microbiome workflows.

Defined Microbial Community

Species	Avg. GC (%)	Gram Stain	gDNA Abun. (%)
Pseudomonas aeruginosa	66.2	-	12
Escherichia coli	56.8	-	12
Salmonella enterica	52.2	-	12
Lactobacillus fermentum	52.8	+	12
Enterococcus faecalis	37.5	+	12
Staphylococcus 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
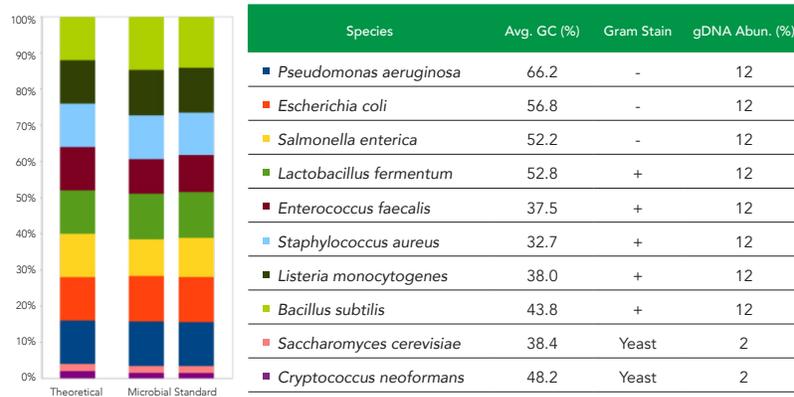
The ZymoBIOMICS® Microbial Community Standard contains three easy-to-lyse bacteria, five tough-to-lyse bacteria, and two tough-to-lyse yeasts.

Identify and Eliminate Bias

- *Bacillus subtilis* (G+)
- *Listeria monocytogenes* (G+)
- *Staphylococcus aureus* (G+)
- *Enterococcus faecalis* (G+)
- *Lactobacillus fermentum* (G+)
- *Salmonella enterica* (G-)
- *Escherichia coli* (G-)
- *Pseudomonas aeruginosa* (G-)
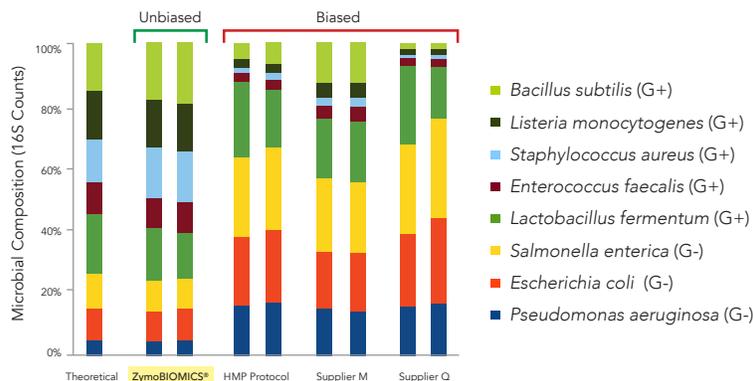
The ZymoBIOMICS® Microbial Community Standard was used to compare different DNA extraction protocols. DNA samples were profiled by 16S rRNA gene targeted sequencing.

Product	Cat. No.	Size
ZymoBIOMICS® Microbial Community Standard	D6300	10 preps

Precise Microbiome Controls

## ZymoBIOMICS® Microbial Community DNA Standard

- **Microbiome DNA Standard:** Eight bacteria and two yeast genomes.
- **Identify Bias in Library Prep Methods:** The DNA has a wide GC range of 15% - 85%.
- **Accurate Composition:** Ideal for validation, optimization, and quality control of microbiome workflows.

Address & Reduce PCR Chimera
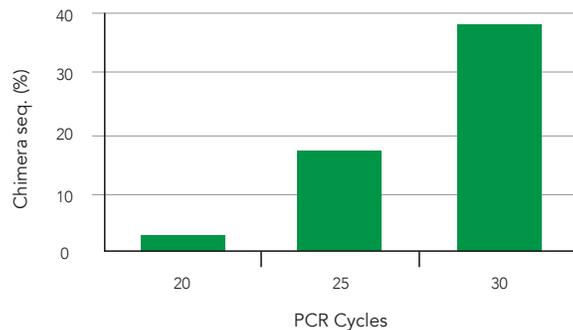
The occurrence of PCR chimera increases with the number of PCR cycles during 16S library preparation. The ZymoBIOMICS® Microbial Community DNA Standard can be used as a positive control to optimize the number of cycles needed in a prep.

Assess GC Bias
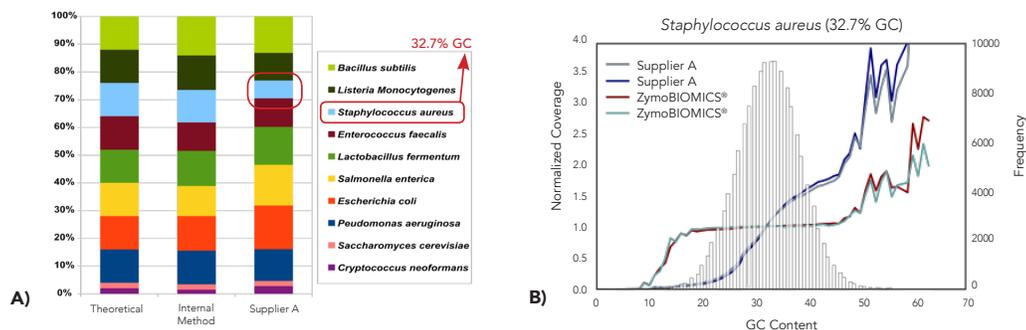
Assess GC bias in library preparations. A) Compared to the ZymoBIOMICS® services, Supplier A's shotgun metagenomic sequencing was biased due to GC content variation. **B)** Coverage of the 10 microbial genomes was normalized to evaluate the effects of GC content.

Product	Cat. No.	Size
ZymoBIOMICS® Microbial Community DNA Standard	D6305 D6306	200 ng 2,000 ng

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