



ZYMO RESEARCH
The Beauty of Science is to Make Things Simple

The Complete Microbiomics Solution

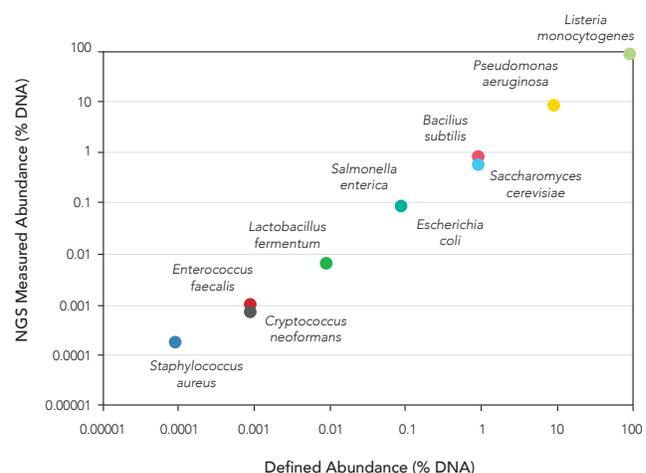


ZymoBIOMICS® Microbial Community Standard II (Log Distribution)

- **Assess Detection Limit:** Log distributed abundance enables reliable positive identification down to 100 microbes.
- **Accurate Composition:** Cross-validated with multiple measurements.
- **Microbiome QC:** Quality control for microbiome profiling and pathogen identification.

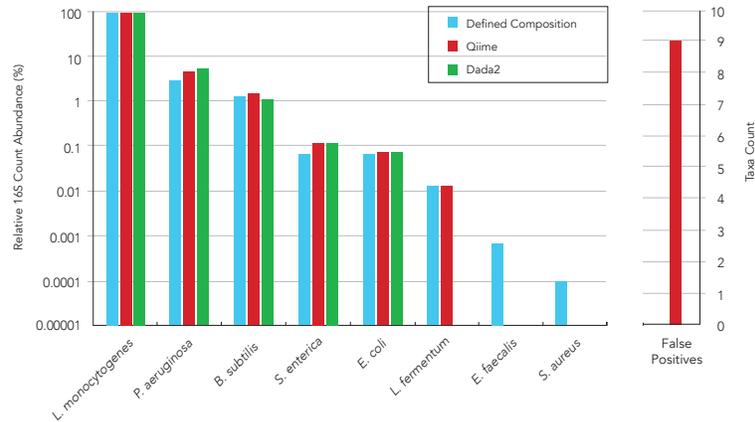
Accurate Composition with Log Distribution

NGS analysis of the ZymoBIOMICS® Microbial Community Standard II (Log Distribution) agrees with the defined composition. DNA was extracted using the ZymoBIOMICS® DNA Miniprep kit. The library was prepared with an internal method and sequenced using an Illumina® MiSeq™. Abundance was inferred by mapping raw sequencing reads against reference genomes.



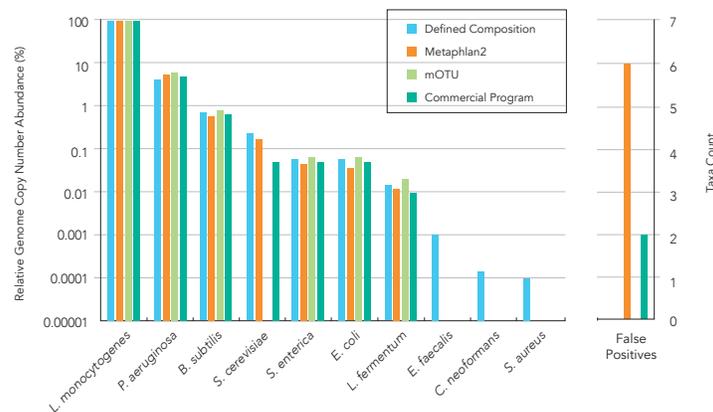
ZymoBIOMICS® Microbial Community Standard II (Log Distribution) Accuracy and Detection Limit Assessment

Assess Performance of 16S Sequencing



The 16S sequencing results from the ZymoBIOMICS® Microbial Community Standard II (Log Distribution) were analyzed using Qiime 1.9.0 and Dada2 analysis pipelines. DNA was extracted using the ZymoBIOMICS® DNA Miniprep kit. A library of 16S V3-V4 region was prepared with the *Quick-16S™* NGS Library Prep kit. Sequencing was performed using an Illumina® MiSeq™ generating 93,762 paired-end reads (2 x 300 bp). Dada2 showed no false positives. The Qiime pipeline predicted 9 false positives, but had a lower detection limit identifying the presence of *L. fermentum* while Dada2 did not.

Assess Performance of Shotgun Metagenomic Sequencing



The shotgun sequencing data of the ZymoBIOMICS® Microbial Community Standard II (Log Distribution) were analyzed using three different bioinformatics pipelines, MetaPhlan2, mOTU, and a commercial program. The library prepared with an internal method was sequenced using an Illumina® MiSeq™. The three analysis pipelines had similar detection limits down to a relative genome copy number abundance of ~0.01% (*L. fermentum* abundance). MetaPhlan2 and the commercial program led to false positives; while the mOTU pipeline made no false predictions, it was unable to detect yeast.

Product	Cat. No.	Size
ZymoBIOMICS® Microbial Community Standard II (Log Distribution)	D6310	10 preps
ZymoBIOMICS® Microbial Community DNA Standard II (Log Distribution)	D6311	220 ng
Human HCT116 DKO Non-Methylated DNA	D5014-1	5 µg

