

Zymo Quick-16S NGS Library Prep Kit

The Zymo Quick 16S NGS Library Prep Kit is a rapid protocol targeting the V3-V4 hypervariable regions of bacterial and archaeal 16S rRNA genes. Up to 384 unique combinatorial indices are available enabling highly multiplexed sequencing runs. Recommended read depth is $\geq 100,000$ reads per library using a PE300 sequencing configuration. Data deliverables include demultiplexed FASTQ files and outputs from the nf-core/ampliseq analysis pipeline.

When submitting samples for library preparation using the Zymo Quick-16S NGS Library Prep Kit, please follow these guidelines:

DNA Sample Concentration	0.5 – 5 ng/ μ L
DNA Sample Volume	5 μ L
DNA Sample Buffer	10mM Tris-Cl pH 7.5- 8.5. Must be free of EDTA
A260/A280 Ratio	1.8 – 2.0
A260/A230 Ratio	2.0 – 2.2

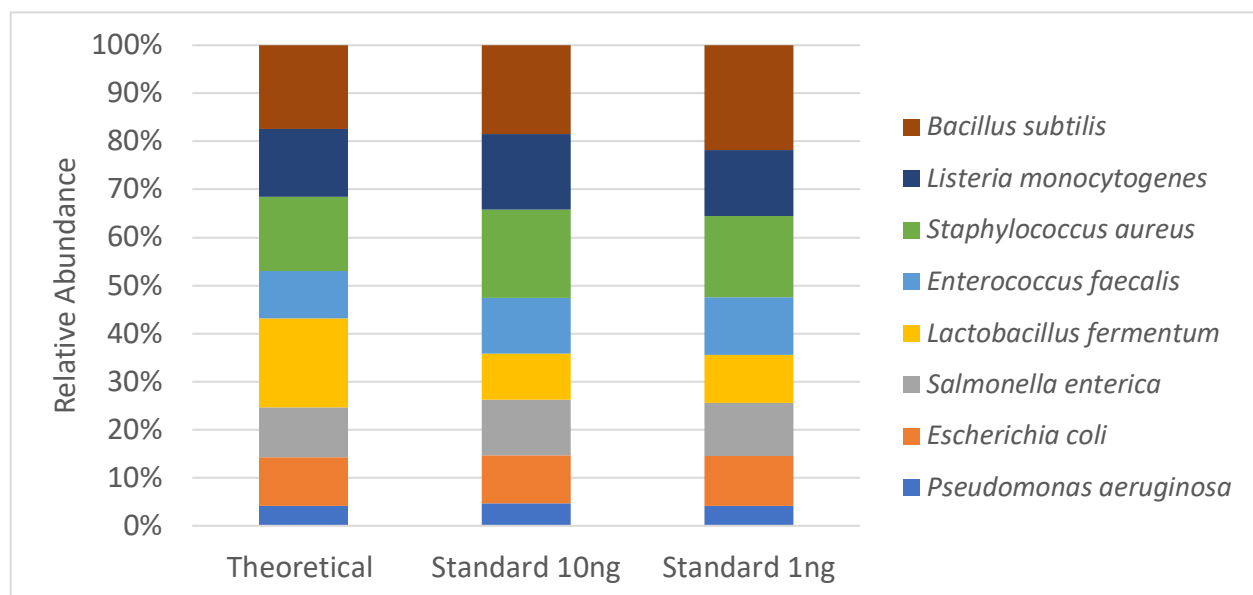


Figure 1. In a pilot study, a microbial community standard with known content was used for library preparation with 10 ng and 1 ng of input mass. All expected bacterial species were detected at both input levels in relative abundances similar to the theoretical values based on genomic content of the standard.

References

1. <https://www.zymoresearch.com/products/quick-16s-plus-ngs-library-prep-kit>
2. <https://nf-co.re/ampliseq>