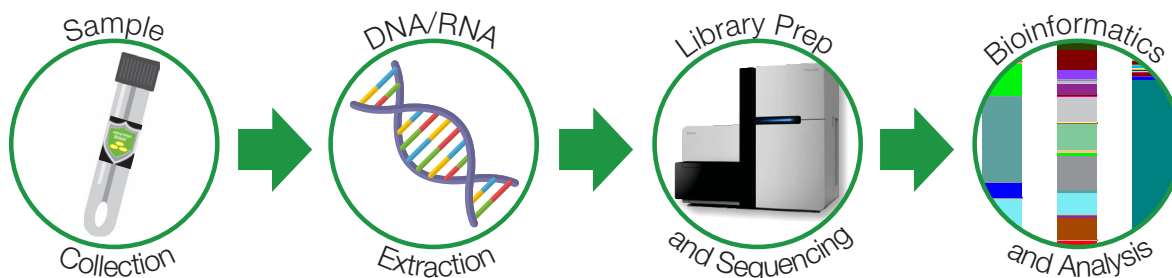


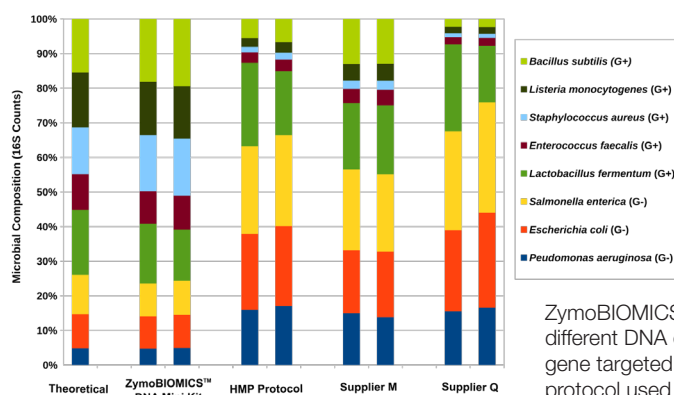


# ZymoBIOMICS™ Microbial Community Standards

## Standards for Optimizing Microbiomics Workflows



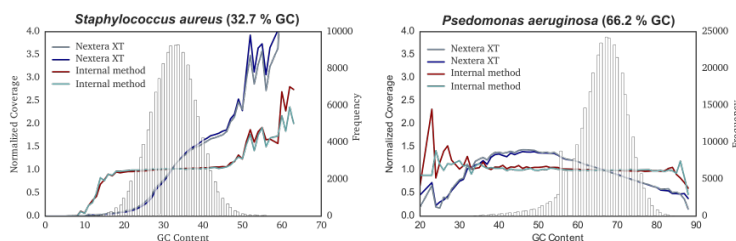
## Standardizing Microbiomics



**Does Your DNA Extraction Method Reflect Reality or is it Biased?**  
Evaluate Your Method.

ZymoBIOMICS™ Microbial Community Standard is the ideal way to compare different DNA extraction protocols. DNA samples were profiled by 16S rRNA gene targeted sequencing. HMP Protocol stands for the fecal DNA extraction protocol used by the Human Microbiome Project.

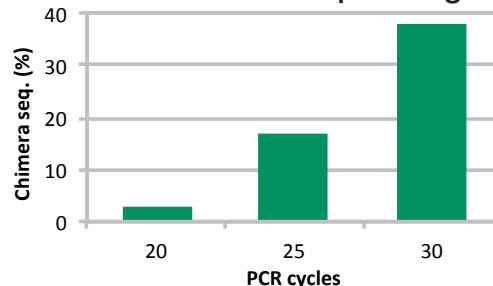
## Assess GC-Bias in Shotgun Metagenomics



Library preparation for shotgun metagenomic sequencing was performed in two different ways: one by Illumina Nextera® XT kit and one by an in-house method. Shotgun sequencing was performed on MiSeq with paired-end sequencing (2x150 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 with the average sequencing coverage of each genome.

Disclaimer: Illumina® and Nextera® are registered trademarks of Illumina, Inc.

## Track PCR Chimera in 16S rRNA Gene Sequencing

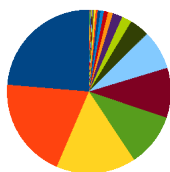


PCR chimera increases with increasing PCR cycle number in the library preparation process of 16S rRNA gene targeted sequencing. 20 ng ZymoBIOMICS™ Microbial Community DNA Standard was used as a template. The PCR reaction was performed with ZymoTag™ master mix and with primers that target v34 region of 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.

# Optimize your Microbiomics Workflows



## Reduce Noise in Your 16S rRNA Gene Seq. with the ZymoBIOMICS™ Microbial Community DNA Standard

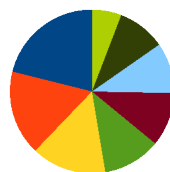


**Before**

Noise and bias



Optimized Workflow



**After**

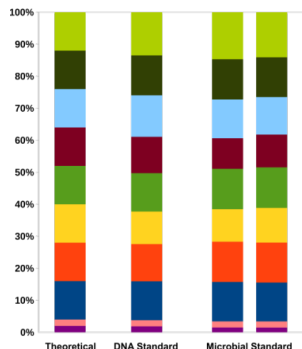
True composition of the standard

## Accurate Characterization

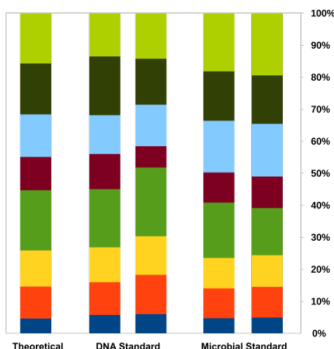
Species	GC %	Gram Stain	gDNA Abun. (%)
<i>Pseudomonas aeruginosa</i>	66.2	-	12
<i>Escherichia coli</i>	56.8	-	12
<i>Salmonella enterica</i>	52.2	-	12
<i>Lactobacillus fermentum</i>	52.8	+	12
<i>Enterococcus faecalis</i>	37.5	+	12
<i>Staphylococcus aureus</i>	32.7	+	12
<i>Listeria monocytogenes</i>	38.0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

### Accurate Composition

gDNA by Shotgun Sequencing



16S Counts by 16S Sequencing



For reliable evaluation of shotgun sequencing and 16S rRNA gene sequencing.

- Well defined and characterized standards composed of 5 Gram-Positive and 3 Gram-Negative bacteria plus 2 yeast species with wide GC range (15%-85%)
- Quality control for Microbiomics workflows (16S rRNA seq. and Shotgun seq.)
- Impurities are less than 0.01%

### Negligible Impurity (<0.01%)

Species	mOTU counts	mOTU Abun. (%)
<i>Bacillus subtilis</i>	9048	11.86
<i>Enterococcus faecalis</i>	11322	14.84
<i>Escherichia coli</i>	6994	9.17
<i>Lactobacillus fermentum</i>	17081	22.39
<i>Listeria monocytogenes</i>	11454	15.01
<i>Pseudomonas aeruginosa</i>	4484	5.88
<i>Salmonella enterica</i>	7939	10.41
<i>Staphylococcus aureus</i>	7960	10.43
<i>Propionibacterium acnes</i> (contaminant)	1	0.0013

Microbial composition was profiled with shotgun metagenomic sequencing (178 million reads). Taxonomy identification was performed with mOTU (<http://www.bork.embl.de/software/mOTU/>)

## Liste des standards ZymoBIOMICS

Référence	Désignation	Conditionnement
ZD6300	ZymoBIOMICS Microbial Community Standard (Microbial Standard)	10 preps
ZD6305	ZymoBIOMICS Microbial Community DNA Standard	200 ng
ZD6306	ZymoBIOMICS Microbial Community DNA Standard	2000 ng

**Nous contacter**



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### Service technique

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Instrumentation : 01 30 85 92 88 - [instrum@ozyne.fr](mailto:instrum@ozyne.fr)



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