Table S3. Comparative mock community composition.

Species	Zymo Theoretical Composition (%) Genomic DNA	Zymo Measured Composition (%) Genomic DNA *	Study QC Measurements Measured Composition (%) Genomic DNA **
Pseudomonas aeruginosa	12	14.7	11.8
Escherichia coli	12	12.6	15.2
Salmonella enterica	12	12.1	15.16
Lactobacillus fermentum	12	9.5	13.2
Enterococcus faecalis	12	12.6	8.1
Staphylococcus aureus	12	10.2	10
Listeria monocytogenes	12	12.6	9.1
Bacillus subtillis	12	12.3	16.74
Saccharomyces cerevisiae	2	1.9	n/a - 0
Cryptococcus neoformans	2	1.5	n/a - 0

Shotgun sequencing was performed using the Illumina® MiSeq™ (2x150bp) and with sequencing library prepared with Kapa HyperPlus. The composition in terms of genomic DNA abundance was calculated by summarizing the raw sequencing reads mapped to the genome of each strain.

*** 16S rRNA Amplicon - Illumina MiSeq (2x 250bp) and Sequencing Library prepared with Schloss Primers - 2 step PCR approach and Sequences at the Genomics Facility at Cornell University.*