

Table S2. Summary of the control mock community and respective amplicon sequence variants identified by DNA sequencing

Mock Community	Identification (lowest taxonomic resolution)	Mock Community (% Relative Abundance)	After sequencing (Raw sequence counts)	After sequencing (% Relative Abundance)
<i>Pseudomonas aeruginosa</i>	<i>Pseudomonas</i> (genus)	4.2	11375	14.4
<i>Escherichia coli</i>	<i>Escherichia- Shigella</i> (genus)	10.1	9622	12.2
<i>Salmonella enterica</i>	Enterobacteriaceae (family)	10.4	10748	13.6
<i>Lactobacillus fermentum</i>	<i>Lactobacillus fermentum</i> (species)	18.4	20347	25.8
<i>Enterococcus faecalis</i>	<i>Enterococcus</i> (genus)	9.9	1542	1.95
<i>Staphylococcus aureus</i>	<i>Staphylococcus</i> (genus)	15.5	8521	10.8

<i>Listeria monocytogenes</i>	<i>Listeria</i> (genus)	14.1	2410	3.1
<i>Bacillus subtilis</i>	<i>Bacillus</i> (genus)	17.4	14370	18.2

Eight organisms were included in the commercial mock community used as a positive control. The taxonomic identity and lowest level of taxonomic resolution correlating to each organism are listed. We also report the relative abundance of each organism specified in the product, as compared to the raw sequence counts and relative abundance of each organism from our data after DNA isolation and 16S rRNA gene amplicon sequencing.