

Supplementary information for “**Accurate Microbiome Sequencing with Synthetic Long Read Sequencing**”

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Supplementary Table 1. Bacterial species in the ATCC-gut and ATCC-oral mock community samples.

Species	Strain	System	Genome Size (Mb)	16S rRNA gene copies	Expected proportion (%)
<i>Bacteroides fragilis</i>	ATCC 25285	Gut	5.2	6	8.0
<i>Bacteroides vulgatus</i>	ATCC 8482	Gut	5.2	7	9.3
<i>Clostridioides difficile</i>	ATCC 9689	Gut	4.3	12	16.0
<i>Enterobacter cloacae</i>	ATCC 13047	Gut	5.6	8	10.7
<i>Escherichia coli</i>	ATCC 700926	Gut	4.6	7	9.3
<i>Salmonella enterica subsp. enterica</i>	ATCC 9150	Gut	2.7	7	9.3
<i>Bifidobacterium adolescentis</i>	ATCC 15703	Gut	2.0	5	6.7
<i>Enterococcus faecalis</i>	ATCC 700802	Gut	3.2	4	5.3
<i>Lactobacillus plantarum</i>	ATCC BAA-793	Gut	3.3	5	6.7
<i>Helicobacter pylori</i>	ATCC 700392	Gut	1.7	2	2.7
<i>Yersinia enterocolitica</i>	ATCC 27729	Gut	4.6	7	9.3
<i>Fusobacterium nucleatum subsp. nucleatum</i>	ATCC 25586	Gut	2.2	5	6.7
<i>Schaalia odontolytica</i>	ATCC 17982	Oral	2.4	3	11.5
<i>Prevotella melaninogenica</i>	ATCC 25845	Oral	1.8	4	15.4
<i>Fusobacterium nucleatum subsp. nucleatum</i>	ATCC 25586	Oral	2.2	5	19.2
<i>Streptococcus mitis</i>	ATCC 49456	Oral	1.9	4	15.4
<i>Veillonella parvula</i>	ATCC 17745	Oral	2.2	4	15.4
<i>Haemophilus parainfluenzae</i>	ATCC 33392	Oral	2.1	6	23.1

Supplementary Table 2. Mapping Zymo-Loop and Zymo-V3V4 to references provided by Zymo Research.

Species	Genome size (Mb)	GC content (%)	16S rRNA gene copies	Gram stain	Expected proportion (%)	Zymo-Loop 16S (%)	Zymo-V3V4 (%)
<i>Bacillus subtilis</i>	4.0	43.9	10	+	17.4	21.0	15.6
<i>Enterococcus faecalis</i>	2.8	37.5	4	+	9.9	9.7	9.0
<i>Escherichia coli</i>	4.9	46.7	7	-	10.1	10.9	11.9
<i>Lactobacillus fermentum</i>	1.9	52.4	5	+	18.4	11.3	15.7
<i>Listeria monocytogenes</i>	3.0	38.0	6	+	14.1	17.4	12.6
<i>Pseudomonas aeruginosa</i>	6.8	66.2	4	-	4.2	4.2	8.0
<i>Salmonella enterica</i>	4.8	52.2	7	-	10.4	11.2	12.0
<i>Staphylococcus aureus</i>	2.7	32.9	6	+	15.5	14.3	15.2