

**SUPPLEMENTARY MATERIALS**

**Table S1.** Counts of reads, OTUs and Good's coverage index per sample.

	Sample 1			Sample 2			Sample 3			Sample 4		
	TEHC	TEHC Normalized	16S- Amplicon	TEHC	TEHC Normalized	16S- Amplicon	TEHC	TEHC Normalized	16S- Amplicon	TEHC	TEHC Normalized	16S- Amplicon
Raw reads	1,144,928	-	563,114	727,571	-	564,542	1,235,085	-	508,936	1,044,957	-	697,643
Filtered reads	847,125	475,231	475,231	531,323	489,748	489,748	945,679	446,346	446,346	797,226	601,577	601,577
16S mapping reads	-	300235	323506	-	315252	350801	-	316794	354840	-	380515	389125
% Reads mapped	-	63	68	-	64	72	-	71	79	-	63	65
OTUs	-	11046	4981	-	10058	5340	-	9032	4036	-	10178	4641
Good's coverage index	-	0.9932619	0.9944545	-	0.9945789	0.9944612	-	0.9934879	0.995412	-	0.9949805	0.9954616

BEI MOCK MICROBIOME			
	TEHC	TEHC Normalized	16S- Amplicon
Raw reads	5,345,638	-	136,184
Filtered reads	4,591,609	56,879	56,879
16S mapping reads	-	38,427	42,261
% Reads mapped	-	68	74
OTUs	-	1,940	634
Good's coverage index	-	99.73857	99.29722

**Table S2.** Relative abundance (%) of genera identified among the most abundant exclusively with one sequencing strategy.

<b>Fecal Sample</b>	<b>Genus</b>	<b>TEHC</b>	<b>16S-AMP</b>
1	<i>Phascolarctobacterium</i>	0.99	1.85
	<i>Pseudobutyrvibrio</i>	0.72	1.55
2	<i>Fibrobacter</i>	1.47	0.92
	BF311	0.77	1.62
	<i>Solibacillus</i>	0.99	1.26
3	<i>Blautia</i>	1.37	0.95
	<b><i>Lysinibacillus</i></b>	<b>8.43</b>	<b>0.17</b>
	<i>Parabacteroides</i>	0.95	1.29
	<i>Streptococcus</i>	1.01	0.86
	<i>Clostridium</i>	1.17	0.68
4	<b><i>Lysinibacillus</i></b>	<b>1.45</b>	<b>0.04</b>
	<i>Paludibacter</i>	0.98	1.82
	<i>Phascolarctobacterium</i>	0.95	1.46
	<i>Wautersiella</i>	0.90	1.11
	YRC22	0.42	1.37

**Table S3.** Relative abundance (%) of species identified among the most abundant exclusively with one sequencing strategy.

Fecal Sample	Genus	TEHC	16S-AMP
1	<i>F. succinogenes</i>	2.12600	2.90505
	<i>F. succinogenes</i>	1.44710	0.91590
2	<i>C. variabile</i>	0.85551	1.27850
	<i>S. luteaciae</i>	5.88386	6.65819
	<b><i>L. boronitolerans</i></b>	<b>8.41399</b>	<b>0.17191</b>
3	<i>B. muralis</i>	0.94383	1.11318
	<i>B. uniformis</i>	1.40628	2.39404
4	<i>A. lwoffii</i>	<b>1.41308</b>	<b>0.00026</b>
	<i>L. boronitolerans</i>	<b>1.44751</b>	<b>0.00694</b>

**Table S4.** Relative abundance (%) of expected species identified with 16S-amplicon sequencing and TEHC.

<b>Species</b>	<b>16S-Amplicon</b>	<b>TEHC</b>	<b>Expected</b>
<i>Helicobacter pylori</i>	12.19	5.96	5
<i>Neisseria cinerea</i>	7.17	4.38	5
<i>Staphylococcus aureus</i>	5.81	4.03	5
<i>Staphylococcus epidermidis</i>	4.28	2.88	5
<i>Propionibacterium acnes</i>	0.36	3.72	5
<i>Rhodobacter sphaeroides</i>	2.49	2.56	5