

S1 Table. List of primers and PCR conditions used in this study.

Target	Primer sequence (5'-3')	Amplikon size	Mg (mM)	Annealing (°C)	Detection (°C)	Amount of template DNA for	Standard/reference organism for qPCR	Coverage (%)**	Original reference
Bacteria (qPCR)	F: 5'-TCCTACGGGAGGCGAGCT-3' R: 5'-GGACTACCCAGGGTATCTAATCTGTT-3'	466	3	50	82	0.5	<i>B. longum</i>	83.1**	[1]
Bacteria (16S rRNA gene V3-V4 amplicon sequencing)	F: 5'-CCTACGGGNGCGCAG-3' R: 5'-GACTACHVGGGTATCTAATCC-3'	444	-	-	-	-	-	95**	[2]
<i>Bacteroides-Prevotella-Porphyrionomus</i>	F: 5'-GGTGTGGCTAAGTGCCAT-3' R: 5'-CGGAYGTAAAGGGCCGTGC-3'	140	3	68	80	0.5	<i>B. fragilis</i>	95.8	[3]
<i>Bifidobacterium</i> spp.	F: 5'-TCGCTCYGGTGAAG-3' R: 5'-CCACATCCAGCTCCAC-3'	243	3	58	85	25	<i>B. longum</i>	93.9	[3]
<i>Clostridium coccooides-Eubacterium rectale</i> group (<i>Lachnospiraceae</i>)	F: 5'-CGTACTGACTAGAAGC-3' R: 5'-AGTTYATCTTGGCAAGC-3'	429	4	55	85	0.5	<i>R. prodansus</i>	85.9	[3]
<i>Escherichia coli</i> subgroup (<i>E. coli</i> , <i>Hafnia alvei</i> and <i>Shigella</i> spp.)	F: 5'-GTTAATACCTTGGCTATGA-3' R: 5'-ACCAGGATCTAATCTGTT-3'	340	3	60	85	25	<i>Escherichia coli</i> DSM 6897	90.6	[4]
Butyryl-CoA CoA transferase	F: 5'-GGGACATTCAGTGGAAAYWSITGGCAYATG-3' R: 5'-CCTGCCITTCACATTCACRAANGC-3'	530	3	53	82	25	-	-	[5]

*The coverage (i.e. the percentage of potentially covered taxa within the target) was estimated using the SILVA TestPrime tool with the sSUNR database version 132, allowing one mismatch during primer annealing to simulate realistic PCR behavior [2].

**Detailed breakdown of coverage for the targets at lower taxonomic levels is listed in S1 Table B.

S1 Table B.

Primers set	Target	Coverage (%)
Bacteria (qPCR)	<i>Bacteroides-Prevotella-Porphyrionomus</i>	93.7
	<i>Bifidobacterium</i> spp.	93.7
	<i>Clostridium coccooides-Eubacterium rectale</i> group (<i>Lachnospiraceae</i>)	95
	<i>Escherichia coli</i> subgroup (<i>E. coli</i> , <i>Hafnia alvei</i> and <i>Shigella</i> spp.)	94
Bacteria (16S rRNA gene V3-V4 amplicon sequencing)	<i>Bacteroides-Prevotella-Porphyrionomus</i>	95.7
	<i>Bifidobacterium</i> spp.	94.1
	<i>Clostridium coccooides-Eubacterium rectale</i> group (<i>Lachnospiraceae</i>)	95.9
	<i>Escherichia coli</i> subgroup (<i>E. coli</i> , <i>Hafnia alvei</i> and <i>Shigella</i> spp.)	95.1

References

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