

S1 Table. Sequences of the primers and detection limits of each bacterium

Target bacteria	Primer	Sequence (5' - 3')	Detection limits (Log ₁₀ /g feces)	Reference No.
<i>Clostridium coccooides</i> group	g-Ccoc-F	AAATGACGGTACCTGACTAA	5.0	1
	g-Ccoc-R	CTTTGAGTTTCATTCTTGGCAA		
<i>Clostridium leptum</i> subgroup	sg-Clept-F	GCACAAGCAGTGGAGT	5.0	1
	sg-Clept-R3	CTTCCTCCGTTTTGTCAA		
<i>Bacteroides fragilis</i> group	g-Bfra-F2	AYAGCCTTCGAAAGRAAGAT	5.0	2
	g-Bfra-R	CCAGTATCAACTGCAATTTTA		
<i>Bifidobacterium</i>	g-Bifid-F	CTCCTGGAAACGGGTGG	5.0	3
	g-Bifid-R	GGTGTCTTCCCGATATCTACA		
<i>Atopobium</i> cluster	g-Atopo-F	GGGTTGAGAGACCGACC	5.9	1
	g-Atopo-R	CGGRGCTTCTTCTGCAGG		
<i>Prevotella</i>	g-Prevo-F	CACRGTAAACGATGGATGCC	5.1	1
	g-Prevo-R	GGTCGGGTTGCAGACC		
<i>Enterobacteriaceae</i>	En-Isu-3F	TGCCGTAAC TTCGGGAGAAGGCA	3.9	7
	En-Isu-3'R	TCAAGGACCAGTGTTCAGTGC		
<i>Enterococcus</i>	g-Encoc-F	ATCAGAGGGGATAACACTT	3.0	5
	g-Encoc-R	ACTCTCATCCTTGTCTTCTC		
<i>Staphylococcus</i>	g-Staph-F	TTTGGGCTACACACGTGCTACAATGGACAA	3.0	5
	g-Staph-R	AACAAC TTTATGGGATTTGCWTGA		
<i>Streptococcus</i>	g-Str-F	AGCTTAGAAGCAGCTATTCATTC	3.0	8
	g-Str-R	GGATACACCTTTCGGTCTCTC		
<i>Clostridium difficile</i>	Cd-Isu-F	GGGAGCTTCCCATACGGGTTG	2.4	4
	Cd-Isu-R	TTGATGCCTCAATGCTTGGGC		
<i>Clostridium perfringens</i>	s-Clper-F	GGGGGTTTCAACACCTCC	2.3	5
	CIPER-R	GCAAGGGATGTCAAGTGT		
<i>Lactobacillus gasseri</i> subgroup	sg-Lgas-F	GATGCATAGCCGAGTTGAGAGACTGAT	2.7	5
	sg-Lgas-R	TAAAGGCCAGTTACTACCTCTATCC		
<i>Lactobacillus reuteri</i> subgroup	sg-Lreu-F	GAACGCAYTGGCCCAA	3.0	5
	sg-Lreu-R	TCCATTGTGGCCGATCAGT		
<i>Lactobacillus ruminis</i> subgroup	sg-Lrum-F	CACCGAATGCTTGCAYTACC	2.3	5
	sg-Lrum-R	GCCGCGGGTCCATCCAAAA		
<i>Lactobacillus plantarum</i> subgroup	sg-Lpla-F	CTCTGGTATTGATTGGTGCTTGCAT	2.6	5
	sg-Lpla-R	GTTCCGCACTCACTCAAATGTAATA		
<i>Lactobacillus sakei</i> subgroup	sg-Lsak-F	CATAAAACCTAMCACC GCATGG	2.9	5
	sg-Lsak-R	TCAGTTACTATCAGATACRTTCTTCTC		
<i>Lactobacillus casei</i> subgroup	sg-Lcas-F	ACCGCATGGTTCTTGGC	3.5	5
	sg-Lcas-R	CCGACAACAGTTACTCTGGC		
<i>Lactobacillus brevis</i>	s-Lbre-F	ATTTTGTGTTGAAAGGTGGCTTCGG	2.6	5
	s-Lbre-R	ACCCTTGAACAGTTACTCTCAAAGG		
<i>Lactobacillus fermentum</i>	LFer-1	CCTGATTGATTTTGGTCGCCAAC	4.0	5
	LFer-2	ACGTATGAACAGTTACTCTCATACGT		

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