

Table S1: Primers used for the qPCR to quantitatively detect selected bacterial groups and species in the feces of cats fed diets with varying protein concentrations and qualities.

Bacterial group/species	Primer	Sequence	Base pairs	Temperature (°C)	Reference
<i>Bacteroides/Prevotella/Porphyromonas</i>	BPP1	5'-GGT GTC GGC TTA AGT GCC AT-3'	147	55	[1]
	BPP2	5'-CGG AYG TAA GGG CCG TGC-3'			
<i>Bifidobacterium spp.</i>	g-BIFID-F	5'-TCG CGT CYG GTG TGA AAG-3'	251	58	[1]
	g-BIFID-R	5'-CCA CAT CCA GCR TCC AC-3'			
<i>Clostridium coccoides cluster XIVa</i>	g-Ccoc-F	5'-AAA TGA CGG TAC CTG ACT AA-3'	455	60	[2]
	g-Ccoc-R	5'-CTT TGA GTT TCA TTC TTG CGA A-3'			
<i>Clostridium cluster I</i>	CI-F1	5'-TAC CHR AGG AGG AAG CCA C-3'	239	63	[3]
	CI-R2	5'-GTT CTT CCT AAT CTC TAC GCA T-3'			
<i>Clostridioides difficile</i>	Cdiff-16S-1f	5'-TTG AGC GAT TTA CTT CGG TAA	174	58	Developed in the Institute of Animal Nutrition, Freie Universität Berlin
	Cdiff-16S-1r	AGA-3'			
<i>Clostridium leptum cluster IV</i>	sg-Clept-F	5'-CCA TCC TGT ACT GGC TCA CCT-3'	253	60	[4]
	sg-Clept-R	5'-GCA CAA GCA GTG GAG T-3'			
<i>Clostridium perfringens</i>	Cpa1a	5'-AGG CGC TTA TTT GTG CTA CG-3'	90	48	Developed in the Institute of Animal Nutrition, Freie Universität Berlin
	Cpa1b	5'-TCA ATC TTT CCA TCC CAA GC-3'			
<i>Enterobacteriaceae</i>	EntqPCR3417f	5'-GTB TCD CCR CGC AGR C-3'	454	55	Developed in the Institute of Animal Nutrition, Freie Universität Berlin
	EntqPCR3852r	5'-TGC GYC TGG TRA TCT A-3'			
<i>Escherichia coli/Hafnia/Shigella</i>	Entero-F	5'-GTT AAT ACC TTT GCT CAT TGA-3'	354	55	[5]
	Entero-R	5'-ACC AGG GTA TCT AAT CCT GTT-3'			
<i>Lactobacillus spp.</i>	Lac1	5'-AGC AGT AGG GAA TCT TCC A-3'	351	58	[1]
	Lac2	5'-CAC CGC TAC ACA TGG AG-3'			
<i>Salmonella spp.</i>	QVR133	5'-GAA GCA GCG CCT GTA AAA TC-3'	20	60	Developed in the Institute of Animal Nutrition, Freie Universität Berlin
	QVR134	5'-TGG CTG TGG TGC AAA ATA TC-3'			

References cited in this Supplementary Material

1. Rinttilä, T.; Kassinen, A.; Malinen, E.; Krogius, L.; Palva, A. Development of an extensive set of 16S rDNA-targeted primers for quantification of pathogenic and indigenous bacteria in faecal samples by real-time PCR. *J. Appl. Microbiol.* **2004**, *97*, 1166–1177.
2. Matsuki, T.; Watanabe, K.; Fujimoto, J.; Miyamoto, Y.; Takada, T.; Matsumoto, K.; Oyaizu, H.; Tanaka, R. Development of 16S rRNA-gene-targeted group-specific primers for the detection and identification of predominant bacteria in human feces. *Appl. Environ. Microbiol.* **2002**, *68*, 5445–5451.
3. Song, Y.; Liu, C.; Finegold, S.M. Real-Time PCR quantitation of clostridia in feces of autistic children. *Appl. Environ. Microbiol.* **2004**, *70*, 6459–6465.
4. Matsuki, T.; Watanabe, K.; Fujimoto, J.; Takada, T.; Tanaka, R. Use of 16S rRNA gene-targeted group-specific primers for real-time PCR analysis of predominant bacteria in human feces. *Appl. Environ. Microbiol.* **2004**, *70*, 7220–7228.
5. Malinen, E.; Kassinen, A.; Rinttilä, T.; Palva, A. Comparison of real-time PCR with SYBR Green I or 5'-nuclease assays and dot-blot hybridization with rDNA-targeted oligonucleotide probes in quantification of selected faecal bacteria. *Microbiology* **2003**, *149*, 269–277.