Table S1 - Primers and conditions used for the determinations of several bacterial groups in faeces by qPCR. Ef: Efficiency obtained for each pair of primers.

Primers	Sequences (5'-3')	Standard	Dynamic Range (UFC mL^{-1})	*Primers* (nM)	Ta (°C)	Ef (%)	Reference
Lactobacillus-F	AGCAGTAGGGAATCTTCCA	*Lactobacillus fermentum* Lf2	$6x10^8$-$2x10^5$	200	55	73	Echarri et al.. (2011)
Lactobacillus-R	CATGGAGTTCCACTGTCCTC						
Bifidobacterium-F	GATTCTGGCTCAGGATGAACGC	*Bifidobacterium animalis* subsp. *lactis* INL1	$4x10^9$-$4x10^4$	200	60	90	Gueimonde, Tölkkö, & Korpimaki (2004)
Bifidobacterium-R	CTGATAGGACGCGACCCCAT						
B. animalis-F	ACCAACCTGCCCTGTGCACCG	*Bifidobacterium animalis* subsp. *lactis* INL1	$4x10^9$-$4x10^4$	200	60	92	Rinne et al. (2005)
B. animalis-R	CCATCACCCCGCCAACAAGCT						
B. breve-F	AATGCCGGATGCTCCATCACAC	*Bifidobacterium breve* 110	$1x10^9$-$1x10^5$	200	63	80	Gueimonde, Debor, Tölkkö, Jokisalo, & Salminen (2006)
B. breve-R	GCCTTGCTCCCTAACAAAAGAGG						
C. leptum-F	GCACAAGCAGTGGAGT	*Faecalibacterium prausnitzii* JCM 31915	$1x10^5$-32	200	54	83	Matsuki, Watanabe, Fujimoto, Takada, & Tanaka (2004)
C. leptum-R	CTTCCTCCGTTTTGTCAA						
B. catenulatum-F	GCCGGATGCTCCGACTCCT	*Bifidobacterium pseudocatenulatum* ATCC 27919	$8x10^4$-26	200	55	81	Gueimonde et al. (2006)
B. catenulatum-R	ACCCGAAGGCTTGCTCCCGAT						
C. coccoides-F	AAATGACGGTACCTGACTAA	*Blautia coccoides* ATCC 29236	$2x10^5$-700	300	55	65	Matsuki et al. (2002)
C. coccoides-R	CTTTGAGTTTCATTCTTGCGAA						
B. bifidum-F	TGACCGACCTGCCCCATGCT	*Bifidobacterium bifidum* ATCC 35914	$2x10^8$-$2x10^3$	100	60	88	Gueimonde et al. (2006)
B. bifidum-R	CCCATCCCACGCCGATAGAAT						
Staphylococcus-F	ACGGTCTTGCTGTCACTTATA	*Staphylococcus aureus* 76	$2x10^8$-$2x10^3$	300	56	102	Matsuda Tsuji, Asahara, Kado, & Nomoto (2007)
Staphylococcus-R	TACACATATGTTCTTCCCTAATAA						
Enterobacteriaceae-F	CATTGACGTTACCCGCAGAAGAAGC	*Escherichia coli* EC101	$2x10^8$-$2x10^3$	300	60	95	Bartosch, Fite, Macfarlane, & McMurdo (2004)
Enterobacteriaceae-R	CTCTACGAGACTCAAGCTTGC						
Streptococcus-F	GTACAGTTGCTTCAGGACGTATC	*Streptococcus thermophilus* SC 42	$1.5x10^8$-$1.5x10^5$	200	60	81	Picard et al. (2004)
Streptococcus-R	ACGTTCGATTTCATCACGTTG						
Universal-F	AGAGTTTGATCCTGGCTCAG	*Lactobacillus fermentum* Lf2	$3x10^8$-$1x10^6$	200	58	70	Kullen, Sanozky-Dawes, Crowell, & Klaenhammer (2000)
Universal-R	GGCTGCTGGCACGTAGTTAG						

References:

Bartosch, S., Fite, A., Macfarlane, G. T., & McMurdo, M. E. T. (2004). Characterization of bacterial communities in feces from healthy elderly volunteers and hospitalized elderly patients by using real-time PCR and effects of antibiotic treatment on the fecal microbiota. *Applied and Environmental Microbiology*, *70*(6), 3575-3581.

Echarri, P. P., Graciá, C. M., Berruezo, G. R., Vives, I., Ballesta, M., Solís, G., Morillas, I. V., Reyes-Gavilán, C., Margolles, A., & Gueimonde, M. (2011). Assessment of intestinal microbiota of full-term breast-fed infants from two different geographical locations. *Early Human Development*, *87*(7), 511-513.

Gueimonde, M., Debor, L., Tölkkö, S., Jokisalo, E., & Salminen, S. (2006). Quantitative assessment of faecal bifidobacterial populations by real-time PCR using lanthanide probes. *Journal of Applied Microbiology*, *102*(4), 1116-1122.

Gueimonde, M., Tolkko, S., & Korpimaki, T. (2004). New real-time quantitative PCR procedure for quantification of bifidobacteria in human fecal samples. *Applied and Environmental Microbiology*, *70*(7), 4165-4169.

Kullen, M. J., Sanozky-Dawes, R. B., Crowell, D. C., & Klaenhammer, T. R. (2000). Use of the DNA sequence of variable regions of the 16S rRNA gene for rapid and accurate identification of bacteria in the *Lactobacillus acidophilus* complex. *Journal of Applied Microbiology*, *89*(3), 511-516.

Matsuda, K., Tsuji, H., Asahara, T., Kado, Y., & Nomoto, K. (2007). Sensitive quantitative detection of commensal bacteria by rRNA-targeted reverse transcription-PCR. *Applied and Environmental Microbiology*, *73*(1), 32-39.

Matsuki, T., Watanabe, K., Fujimoto, J., Miyamoto, Y., Takada, T., Matsumoto, K., Oyaizu, H., & Tanaka, R. (2002). Development of 16S rRNA-gene-targeted group-specific primers for the detection and identification of predominant bacteria in human feces. *Applied and Environmental Microbiology*, *68*(11), 5445-51.

Matsuki, T., Watanabe, K., Fujimoto, J., Takada, T., & Tanaka, R. (2004). Use of 16S rRNA gene-targeted group-specific primers for real-time PCR analysis of predominant bacteria in human feces. *Applied and Environmental Microbiology*, *70*(12), 7220-7228.

Picard, F. J., Ke, D., Boudreau, D. K., Boissinot, M., Huletsky, A., Richard, D., Ouellette, M., Roy, P. H., & Bergeron, M. G. (2004). Use of tuf sequences for genus-specific PCR detection and phylogenetic analysis of 28 streptococcal species. *Journal of Clinical Microbiology*, *42*(8), 3686-3695.

Rinne, M. M., Gueimonde, M., Kalliomäki, M., Hoppu, U., Salminen, S. J., & Isolauri, E. (2005). Similar bifidogenic effects of prebiotic-supplemented partially hydrolyzed infant formula and breastfeeding on infant gut microbiota. *FEMS Immunology & Medical Microbiology*, *43*(1), 59-65.