Table S1: The qPCR analysis details

		Universal	Methanobrevibacter genus	Human b-actin
Primers	Forward	TCCTACGGGAGGCAGCAGT	TGGGAAACTGGGGATAATACTG	TCACCCACACTGTGCCCATCTACGA
	Reverse	GGACTACCAGGGTATCTAATCCTGTT	AATGAAAAGCCATCCCGTTAAG	CAGCGGAACCGCTCATTGCCAATGG
Assay conditions	PCR product (bp)	466	282	259
	MgCl2 (mM)	3	3	3
	Detection temp.(°C)	82	86	88
	Annealing temp (°C)	50	54	56
	amount of tempate (ng)	0.5	25	25
	Standard	*B. Longum* 16S gene	*M. smithii* 16S gene	Human genomic DNA
Average detection	CT value of the 10^7 standard	13.01	15.5	17.67
	RSq	0.998	0.998	0.998
	Slope	-3.704	-3.499	-3.465
	Efficiency %	86.44	93.1	94.82
	Reference	Nadkarni et al., 2003	Ufnaret al., 2006	Heid et al., 1996

Table S2: Significant correlations between the bacterial abundances and FSP activity

Phylum/Firmicute class	Genus-like group	Correlation with FSP activity
Bacilli	*Gemella*	0.30
	Lactobacillus plantarum et rel.	-0.29
	Weissella et rel.	-0.31
Clostridium cluster III	*Clostridium thermocellum et rel.*	-0.30
Clostridium cluster IV	*Anaerotruncus colihominis et rel.*	-0.31
	Clostridium leptum et rel.	-0.31
	Eubacterium siraeum et rel.	-0.32
	Faecalibacterium prausnitzii et rel.	-0.40
Clostridium cluster IV	*Ruminococcus callidus et rel.*	-0.40
Clostridium cluster IX	*Phascolarctobacterium faecium et rel.*	-0.37
Clostridium cluster XIVa	*Clostridium sphenoides et rel.*	0.30
	Dorea formicigenerans et rel.	0.45
	Eubacterium ventriosum et rel.	-0.31
	Lachnobacillus bovis et rel.	-0.34
Uncultured Mollicutes	Uncultured *Mollicutes*	-0.35

et rel. = and relatives