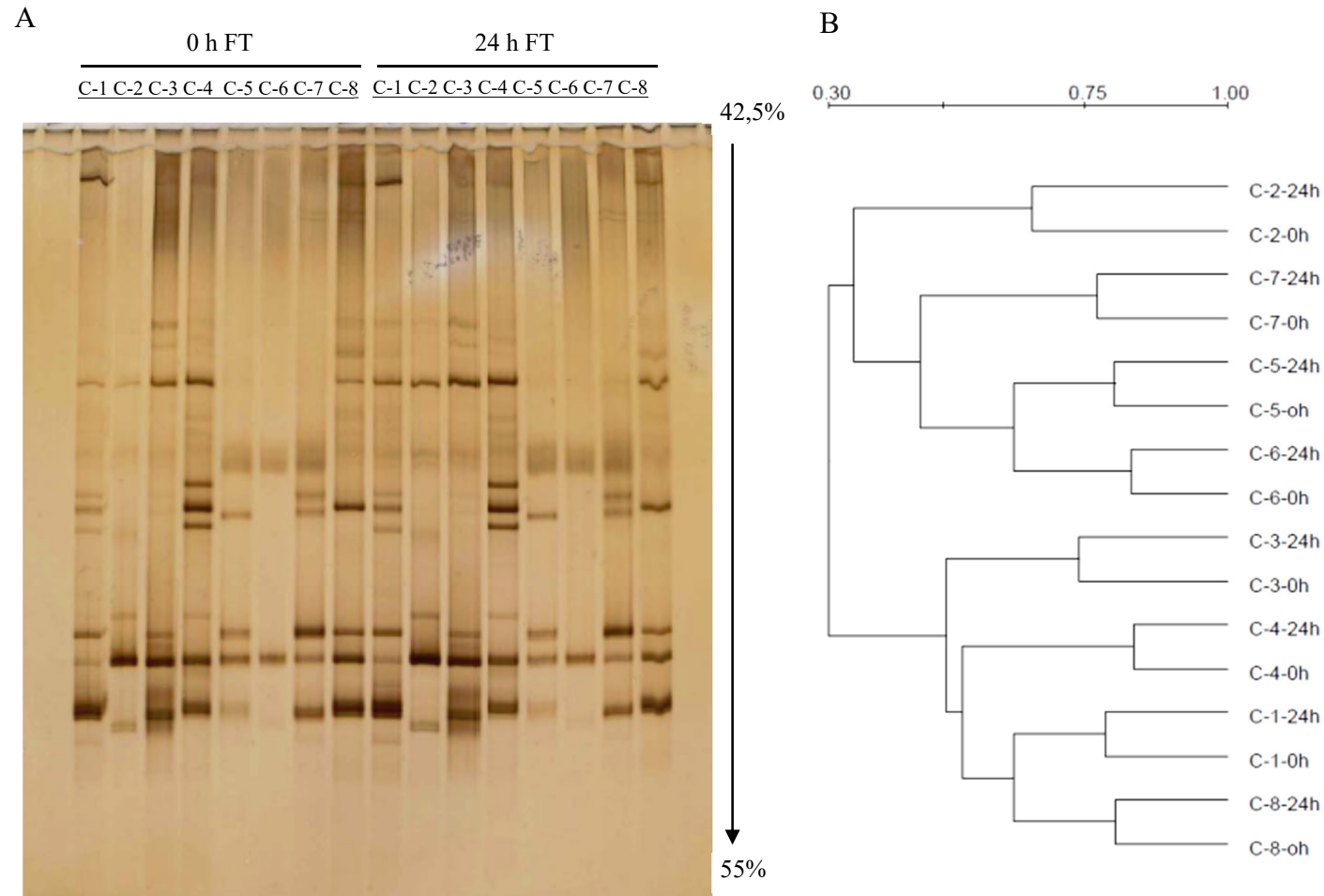


Supplemental Figure 1. A) DGGE profiles and B) dendrogram of the *Bifidobacterium* population from faecal samples from eight infants



Faecal control samples from infants at 0 and 24 h of fermentation. Cluster analysis of DGGE pattern profiles was performed using the Dice similarity coefficient and the unweighted-pair group method by means of arithmetic average clustering algorithm (UPGMA). Vertical arrow shows the direction and concentration of the denaturing gradient.

Supplemental Table 1. β -GOS composition after purification by size-exclusion chromatography (SEC)

β-GOS purified by SEC	
Structures	% (w/w)
β -Gal-(1-4)- β -Gal-(1-4)-Glc	15.8
β -Gal-(1-6)- β -Gal-(1-4)-Glc	5.3
β -Gal-(1-4)- β -Gal-(1-6)-Glc	3.2
β -Gal-(1-4)- β -Gal-(1-2)-Glc	3.2
β -Gal-(1-6)- β -Gal-(1-2)-Glc	1.8
Unknown DP3	5.9
DP4 + DP5 + DP6	64.8

Supplemental Table 2. PCR primers based on 16S rRNA sequences used for quantitative PCR for bacterial groups.

<i>Target bacterial group</i>	<i>Primer</i>	<i>Oligonucleotide Sequence (5'–3')</i>	<i>PCR product size (bp)</i>	<i>Annealing Temp (°C)</i>	<i>References</i>
<i>All bacteria</i>	F-Eub 338 R-Eub 518	ACTCCTACGGGAGGCAGCAG ATTACCGCGGCTGCTGG	200	60	Guo <i>et al.</i> (2008)
<i>Bacteroides</i>	F-AllBac 296 R-AllBac 412	GAGAGGAAGGTCCCCCAC CGCTACTTGGCTGGTTCAG	106	60	Layton <i>et al.</i> (2006)
<i>Bifidobacteria</i>	F-Bifido R-Bifido	CGCGTCYGGTGTGAAAG CCCCACATCCAGCATCCA	244	60	Delroisse <i>et al.</i> (2008)
<i>Clostridium coccoides / Eubacterium rectale group</i>	F-g-Ccoc R-g-Ccoc	AAATGACGGTACCTGACTAA CTTTGAGTTTCATTCTTGCGAA	440	50	Matsuki <i>et al.</i> (2004a)
<i>Clostridium leptum subgroup</i>	F-sg-Clept R3-sg-Clept	GCACAAGCAGTGGAGT CTTCCTCCGTTTTGTCAA	239	50	Matsuki <i>et al.</i> (2004a)
<i>Lactobacilli</i>	F-Lacto R-Lacto	GAGGCAGCAGTAGGGAATCTTC GGCCAGTTACTACCTCTATCCTTCTTC	126	60	Delroisse <i>et al.</i> (2008)
<i>Enterobacteria</i>	F-Ent R-Ent	ATGGCTGTCGTCAGCTCGT CCTACTTCTTTTGCAACCCACTC	385	60	Castillo <i>et al.</i> (2006)

Supplemental Table 3. PCR primers based on 16S rRNA sequences used for quantitative PCR for Bifidobacteria species.

<i>Target bacterial group</i>	<i>Primer</i>	<i>Oligonucleotide Sequence (5'–3')</i>	<i>PCR product size (bp)</i>	<i>Annealing Temp (°C)</i>	<i>References</i>
<i>Bifidobacterium adolescentis</i>	BiADO-1a BiADO-2	CTCCAGTTGGATGCATGTC CGAAGGCTTGCTCCCAGT	279	55	Matsuki <i>et al.</i> (2004b)
<i>Bifidobacterium bifidum</i>	BiBIF-1 BiBIF-2	CCACATGATCGCATGTGATTG CCGAAGGCTTGCTCCCCAAA	278	55	Matsuki <i>et al.</i> (2004b)
<i>Bifidobacterium catenulatum/pseudo-catenulatum</i>	BiCATg-1 BiCATg-2	CGGATGCTCCGACTCCT CGAAGGCTTGCTCCCGAT	285	55	Matsuki <i>et al.</i> (2004b)
<i>Bifidobacterium infantis</i>	BiINF-1 BiINF-2	TTCCAGTTGATCGCATGGTC GGAAACCCCATCTCTGGGAT	828	55	Matsuki <i>et al.</i> (2004b)
<i>Bifidobacterium longum</i>	BiLON-1 BiLON-2	TTCCAGTTGATCGCATGGTC GGGAAGCCGTATCTCTACGA	829	55	Matsuki <i>et al.</i> (2004b)
<i>Bifidobacterium breve</i>	BiBRE-1 BiBRE-2	CCGGATGCTCCATCACAC ACAAAGTGCCTTGCTCCCT	288	55	Matsuki <i>et al.</i> (2004b)
<i>Faecalis prausnitzii</i>	JFF-F-praust-up JFF-F-praust-rp	TTAACACAATAAGTAATCCACCTGG ACCTTCCTCCGTTTTGTCAAC	314	60	

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