



Table S1. Relative abundances determined by 16S rRNA gen profiling at phylum and family level and ITS-region profiling of *Bifidobacterium* species after 24 h of incubation with different carbon sources and without any carbon source added (control) where p-value <0.1. Different letters indicate significant differences (p <0.05) among carbon sources and control after 24 hours of fermentation for the microorganisms considered. Information of relative levels at basal conditions (T0) for all groups is provided.

Group	Taxonomic rank	p-value	T0	T24								
			Control	Glucose	1-kestose	Actilight	GOS	Inulin	P95	Synergy1		
MOB	<u>Phylum</u>											
	Bacteroidetes	0.056	2.34 [1.44 - 4.56]	3.51 [1.63 - 6.24]	12.06 [5.52 - 15.29]	13.46 [6.89 - 24.72]	7.32 [3.77 - 15.47]	12.10 [5.31 - 20.90]	8.23 [2.23 - 10.63]	13.74 [4.88 - 14.79]	6.84 [2.84 - 18.05]	
	<u>Family</u>											
	Eggerthellaceae	0.013	0.57 [0.26 - 1.10]	1.02 [0.73 - 2.50] <sup>b</sup>	0.44 [0.28 - 0.69] <sup>a</sup>	0.36 [0.21 - 0.53] <sup>a</sup>	0.23 [0.13 - 0.41] <sup>a</sup>	0.33 [0.17 - 0.47] <sup>a</sup>	0.30 [0.16 - 0.79] <sup>a</sup>	0.35 [0.28 - 0.45] <sup>a</sup>	0.48 [0.27 - 0.55] <sup>a</sup>	
	Bacteroidaceae	0.081	1.48 [0.76 - 2.31]	1.79 [0.84 - 4.91]	5.53 [2.79 - 10.31]	10.89 [2.96 - 16.23]	5.25 [2.03 - 9.98]	8.78 [2.29 - 17.98]	4.85 [1.05 - 6.68]	10.85 [1.68 - 11.03]	4.68 [1.31 - 11.58]	
	Prevotellaceae	0.076	0.20 [0.05 - 0.38]	0.52 [0.17 - 1.01]	0.30 [0.12 - 0.72]	0.05 [0.02 - 0.18]	0.16 [0.04 - 0.71]	0.20 [0.12 - 0.39]	0.55 [0.25 - 1.41]	0.19 [0.02 - 0.37]	0.26 [0.14 - 0.69]	
	Tannerellaceae	0.012	0.14 [0.07 - 0.25]	0.16 [0.09 - 0.50] <sup>a</sup>	1.34 [0.82 - 2.80] <sup>b</sup>	1.37 [0.82 - 4.50] <sup>b</sup>	1.29 [0.67 - 3.11] <sup>b</sup>	1.02 [0.79 - 2.63] <sup>b</sup>	0.57 [0.22 - 1.51] <sup>b</sup>	0.98 [0.55 - 3.16] <sup>b</sup>	1.07 [0.45 - 3.07] <sup>b</sup>	
	<u>Bifidobacteria ITS</u>											
	<i>B. animalis</i> subsp <i>lactis</i>	0.020	1.07 [0.45 - 1.39]	0.59 [0.47 - 1.23] <sup>c</sup>	0.15 [0.02 - 0.57] <sup>b</sup>	0.31 [0.12 - 0.73] <sup>bc</sup>	0.24 [0.09 - 0.63] <sup>abc</sup>	0.05 [0.00 - 0.10] <sup>a</sup>	0.57 [0.16 - 1.09] <sup>bc</sup>	0.40 [0.11 - 0.65] <sup>abc</sup>	0.37 [0.20 - 0.43] <sup>bc</sup>	
	<i>B. crudilactis</i>	0.022	2.12 [0.82 - 3.03]	1.62 [0.93 - 2.41] <sup>c</sup>	0.29 [0.12 - 1.52] <sup>ab</sup>	0.50 [0.20 - 2.14] <sup>abc</sup>	0.49 [0.32 - 1.04] <sup>ab</sup>	0.09 [0.06 - 0.12] <sup>a</sup>	1.15 [0.41 - 2.61] <sup>bc</sup>	0.45 [0.25 - 1.54] <sup>abc</sup>	0.49 [0.30 - 1.27] <sup>bc</sup>	
NW	<u>Phylum</u>											
	Fusobacteria	0.04	0.01 [0.00 - 0.04]	0.02 [0.00 - 0.05] <sup>b</sup>	0.01 [0.00 - 0.01] <sup>ab</sup>	0.00 [0.00 - 0.00] <sup>a</sup>	0.00 [0.00 - 0.01] <sup>a</sup>	0.00 [0.00 - 0.01] <sup>ab</sup>	0.00 [0.00 - 0.01] <sup>a</sup>	0.00 [0.00 - 0.00] <sup>a</sup>	0.00 [0.00 - 0.00] <sup>a</sup>	
	<u>Family</u>											
	Fusobacteriaceae	0.03	0.01 [0.00 - 0.04]	0.02 [0.00 - 0.05] <sup>b</sup>	0.01 [0.00 - 0.01] <sup>ab</sup>	0.00 [0.00 - 0.00] <sup>a</sup>	0.00 [0.00 - 0.00] <sup>a</sup>	0.00 [0.00 - 0.01] <sup>ab</sup>	0.00 [0.00 - 0.01] <sup>a</sup>	0.00 [0.00 - 0.00] <sup>a</sup>	0.00 [0.00 - 0.00] <sup>a</sup>	
	Others	0.02	0.19 [0.16 - 0.41]	0.33 [0.23 - 0.78] <sup>b</sup>	0.13 [0.08 - 0.24] <sup>a</sup>	0.12 [0.05 - 0.24] <sup>a</sup>	0.14 [0.10 - 0.26] <sup>a</sup>	0.18 [0.11 - 0.27] <sup>ab</sup>	0.13 [0.07 - 0.24] <sup>a</sup>	0.10 [0.05 - 0.13] <sup>a</sup>	0.10 [0.06 - 0.20] <sup>a</sup>	
	<u>Bifidobacteria ITS</u>											
<i>B. breve</i>	0.01	0.29 [0.03 - 0.59]	0.51 [0.33 - 1.10] <sup>b</sup>	0.00 [0.00 - 0.27] <sup>a</sup>	0.10 [0.00 - 0.27] <sup>a</sup>	0.11 [0.00 - 0.29] <sup>a</sup>	0.00 [0.00 - 0.12] <sup>a</sup>	0.00 [0.00 - 0.09] <sup>a</sup>	0.19 [0.02 - 0.27] <sup>ab</sup>	0.00 [0.00 - 0.27] <sup>a</sup>		

Table S2. Absolute levels (mean  $\pm$  SD) (Log UFC/mL) of fecal microbial groups and some *Bifidobacterium* species determined by qPCR at basal conditions (T0) and after 24 hours of incubation with different carbon sources. The comparison of both population groups for each carbon source is shown with “\*” (p<0.05).

Condition	Group	<i>Lactobacillus</i> - group	<i>Akkermansia</i>	<i>Bacteroides</i> group	<i>Faecalibacterium</i>	<i>Bifidobacterium</i>	<i>B.longum</i>	<i>B.catenulatum</i>	<i>B.adolescentis</i>	Enterobacteria	<i>Clostridium</i> cluster XIVa	Total
T0	MOB	<b>4.56 <math>\pm</math> 0.96*</b>	<b>3.18 <math>\pm</math> 0.39*</b>	<b>6.71 <math>\pm</math> 0.88*</b>	<b>4.79 <math>\pm</math> 0.81*</b>	<b>6.37 <math>\pm</math> 0.45*</b>	<b>5.60 <math>\pm</math> 0.32*</b>	<b>5.34 <math>\pm</math> 1.10*</b>	4.80 $\pm$ 0.67	<b>7.41 <math>\pm</math> 1.27*</b>	6.77 $\pm$ 0.62	<b>8.36 <math>\pm</math> 0.58*</b>
	NW	<b>3.63 <math>\pm</math> 0.83</b>	<b>4.66 <math>\pm</math> 1.39</b>	<b>7.04 <math>\pm</math> 0.92</b>	<b>5.37 <math>\pm</math> 0.84</b>	<b>6.96 <math>\pm</math> 0.48</b>	<b>5.85 <math>\pm</math> 0.48</b>	<b>6.80 <math>\pm</math> 0.70</b>	5.15 $\pm$ 0.90	<b>7.90 <math>\pm</math> 0.98</b>	6.62 $\pm$ 0.70	<b>8.66 <math>\pm</math> 0.54</b>
Control	MOB	4.20 $\pm$ 1.32	3.17 $\pm$ 0.41	5.99 $\pm$ 1.01	4.18 $\pm$ 0.67	6.40 $\pm$ 0.61	5.47 $\pm$ 0.31	5.47 $\pm$ 1.24	5.05 $\pm$ 0.81	6.80 $\pm$ 1.32	5.80 $\pm$ 0.75	7.87 $\pm$ 0.61
	NW	3.82 $\pm$ 1.01	4.39 $\pm$ 1.28	6.39 $\pm$ 0.96	4.75 $\pm$ 0.63	6.78 $\pm$ 0.47	5.70 $\pm$ 0.45	6.97 $\pm$ 0.56	5.16 $\pm$ 0.90	7.84 $\pm$ 0.92	6.71 $\pm$ 0.54	8.15 $\pm$ 0.65
Glucose	MOB	4.67 $\pm$ 1.45	<b>3.23 <math>\pm</math> 0.45*</b>	7.42 $\pm$ 0.77	<b>5.04 <math>\pm</math> 0.80*</b>	7.06 $\pm$ 0.83	6.52 $\pm$ 0.82	5.67 $\pm$ 1.34	<b>5.69 <math>\pm</math> 0.70*</b>	7.16 $\pm$ 1.35	<b>5.41 <math>\pm</math> 1.45*</b>	8.26 $\pm$ 0.77
	NW	3.88 $\pm$ 1.00	<b>4.53 <math>\pm</math> 1.41</b>	7.36 $\pm$ 0.72	<b>5.83 <math>\pm</math> 0.56</b>	7.65 $\pm$ 0.43	6.70 $\pm$ 0.27	7.40 $\pm$ 1.01	<b>6.67 <math>\pm</math> 0.63</b>	7.84 $\pm$ 0.94	<b>6.85 <math>\pm</math> 0.42</b>	8.72 $\pm$ 0.39
1-kestose	MOB	5.20 $\pm$ 1.62	<b>3.00 <math>\pm</math> 0.00*</b>	8.13 $\pm$ 0.51	5.59 $\pm$ 0.60	7.37 $\pm$ 0.76	6.66 $\pm$ 1.27	6.40 $\pm$ 1.42	5.86 $\pm$ 0.67	7.79 $\pm$ 0.98	6.43 $\pm$ 1.19	8.91 $\pm$ 0.40
	NW	3.93 $\pm$ 1.16	<b>4.82 <math>\pm</math> 1.31</b>	7.67 $\pm$ 0.52	5.98 $\pm$ 0.56	7.48 $\pm$ 0.46	6.49 $\pm$ 0.53	7.43 $\pm$ 0.88	6.50 $\pm$ 0.62	7.96 $\pm$ 1.00	6.90 $\pm$ 0.34	8.90 $\pm$ 0.33
Actilight	MOB	4.78 $\pm$ 1.47	<b>3.15 <math>\pm</math> 0.28*</b>	7.67 $\pm$ 0.75	5.26 $\pm$ 0.84	7.09 $\pm$ 0.82	6.14 $\pm$ 1.02	6.37 $\pm$ 1.39	5.64 $\pm$ 0.56	7.26 $\pm$ 1.47	6.26 $\pm$ 1.03	8.55 $\pm$ 0.62
	NW	3.58 $\pm$ 0.73	<b>4.55 <math>\pm</math> 1.36</b>	7.44 $\pm$ 0.44	5.65 $\pm$ 0.52	7.45 $\pm$ 0.43	6.40 $\pm$ 0.40	6.67 $\pm$ 0.77	6.33 $\pm$ 0.62	7.44 $\pm$ 0.95	6.32 $\pm$ 0.74	8.68 $\pm$ 0.39
GOS	MOB	4.93 $\pm$ 1.44	<b>3.00 <math>\pm</math> 0.00*</b>	<b>8.17 <math>\pm</math> 0.55*</b>	5.81 $\pm$ 0.46	7.84 $\pm$ 0.52	7.13 $\pm$ 1.03	6.69 $\pm$ 1.64	6.62 $\pm$ 0.55	8.12 $\pm$ 0.66	6.49 $\pm$ 1.03	8.95 $\pm$ 0.41
	NW	3.81 $\pm$ 1.00	<b>4.66 <math>\pm</math> 1.38</b>	<b>7.48 <math>\pm</math> 0.56</b>	5.75 $\pm$ 0.42	7.82 $\pm$ 0.58	6.75 $\pm$ 0.33	6.97 $\pm$ 0.86	6.92 $\pm$ 0.57	7.82 $\pm$ 0.94	6.79 $\pm$ 0.40	8.70 $\pm$ 0.33
Inulin	MOB	4.50 $\pm$ 1.01	<b>3.15 <math>\pm</math> 0.29*</b>	7.12 $\pm$ 1.01	5.19 $\pm$ 0.82	6.79 $\pm$ 0.92	5.71 $\pm$ 0.54	<b>5.85 <math>\pm</math> 1.04*</b>	5.43 $\pm$ 0.82	7.44 $\pm$ 1.29	6.32 $\pm$ 1.10	8.48 $\pm$ 0.69
	NW	3.66 $\pm$ 0.82	<b>4.58 <math>\pm</math> 1.38</b>	7.21 $\pm$ 0.38	5.73 $\pm$ 0.73	7.40 $\pm$ 0.60	6.27 $\pm$ 0.62	<b>7.01 <math>\pm</math> 0.59</b>	5.85 $\pm$ 0.87	8.01 $\pm$ 0.54	6.84 $\pm$ 0.52	8.63 $\pm$ 0.44
P95	MOB	4.87 $\pm$ 1.46	<b>3.00 <math>\pm</math> 0.00*</b>	7.99 $\pm$ 0.58	5.45 $\pm$ 0.38	7.04 $\pm$ 0.88	6.49 $\pm$ 1.36	6.17 $\pm$ 1.41	5.50 $\pm$ 0.68	8.12 $\pm$ 0.34	6.26 $\pm$ 1.34	8.88 $\pm$ 0.28
	NW	3.90 $\pm$ 1.02	<b>4.62 <math>\pm</math> 1.33</b>	7.50 $\pm$ 0.47	5.73 $\pm$ 0.33	7.39 $\pm$ 0.52	6.30 $\pm$ 0.45	7.25 $\pm$ 0.88	6.39 $\pm$ 0.61	7.90 $\pm$ 0.93	6.84 $\pm$ 0.37	8.76 $\pm$ 0.24
Synergy1	MOB	4.91 $\pm$ 1.28	<b>3.21 <math>\pm</math> 0.39*</b>	7.58 $\pm$ 0.82	5.28 $\pm$ 0.91	6.98 $\pm$ 0.76	6.04 $\pm$ 0.81	6.15 $\pm$ 1.39	5.67 $\pm$ 0.62	7.34 $\pm$ 1.40	6.34 $\pm$ 1.18	8.56 $\pm$ 0.69
	NW	3.75 $\pm$ 0.99	<b>4.58 <math>\pm</math> 1.40</b>	7.20 $\pm$ 0.44	5.46 $\pm$ 0.55	7.41 $\pm$ 0.56	6.27 $\pm$ 0.51	7.48 $\pm$ 1.31	6.23 $\pm$ 0.68	7.91 $\pm$ 0.86	6.63 $\pm$ 0.50	8.60 $\pm$ 0.36

Table S3. Median and interquartile range of relative *Bifidobacterium* species assessed by ITS-region sequencing at time 0, before the faecal cultures in NW and MOB microbiota. Bifidobacterial species were filtered by minimum abundance of 1%. “\*” shows differences between both population groups (p-value <0.05).

ITS-sequencing	MOB	NW
Richness	12.50 [12.00 - 13.00]*	10.00 [8.00 - 11.00]
<i>B. adolescentis</i>	42.79 [31.21 - 59.79]*	28.76 [7.77 - 79.96]
<i>B. animalis</i> subsp <i>lactis</i>	1.07 [0.45 - 1.39]*	0.39 [0.10 - 1.08]
<i>B. bifidum</i>	1.25 [0.76 - 1.66]	0.53 [0.05 - 3.61]
<i>B. breve</i>	3.30 [1.97 - 4.50]*	0.29 [0.03 - 0.59]
<i>B. catenulatum</i>	1.15 [0.61 - 2.73]*	0.06 [0.00 - 3.15]
<i>B. choerinum</i>	0.50 [0.26 - 1.44]*	0.00 [0.00 - 0.53]
<i>B. crudilactis</i>	2.12 [0.82 - 3.03]*	15.54 [2.90 - 38.77]
<i>B. dentium</i>	3.20 [2.10 - 3.81]*	0.48 [0.06 - 3.60]
<i>B. longum</i> subsp <i>longum</i>	22.29 [15.27 - 24.92]*	12.72 [6.91 - 46.09]
<i>B. mongoliense</i>	0.11 [0.06 - 0.31]*	1.85 [0.30 - 5.28]
<i>B. pseudocatenulatum</i>	6.90 [2.95 - 12.98]*	1.32 [0.22 - 2.45]
Others	6.63 [2.67 - 9.78]	2.32 [0.29 - 3.88]

Table S4. Statistical tests carried out studying each variable independly in each population group. K-W means Kruskal-Wallis test

Analysis	Variable	MOB	NW	Comparision between populations
16S rRNA gene profiling	All taxonomic ranks	K-W	K-W	MANN WHITNEY U
Bifidobacterial ITS	All species	K-W	K-W	MANN WHITNEY U
Microbiota composition by qPCR	<i>Lactobacillus</i> group	K-W	K-W	MANN WHITNEY U
	<i>Akkermansia</i>	K-W	K-W	MANN WHITNEY U
	<i>Bacteroides</i> group	K-W	K-W	MANN WHITNEY U
	<i>Faecalibacterium</i> spp.	ANOVA	ANOVA	T-STUDENT
	<i>Bifidobacteirum</i> spp.	ANOVA	ANOVA	T-STUDENT
	Enterobacteria	K-W	K-W	MANN WHITNEY U
	<i>Clostridium</i> cluster XIVa	K-W	ANOVA	MANN WHITNEY U
	Total bacteria	K-W	ANOVA	MANN WHITNEY U
	<i>B. longum</i>	K-W	ANOVA	MANN WHITNEY U
	<i>B. catenulatum</i>	ANOVA	ANOVA	T-STUDENT
<i>B. adolescentis</i>	ANOVA	ANOVA	T-STUDENT	
Gas	Cumulative gas	ANOVA	ANOVA	T-STUDENT
pH-Increments respect to time 0	$\Delta$ pH	K-W	K-W	MANN WHITNEY U
SCFA-Increments respect to time 0	Acetate	K-W	K-W	MANN WHITNEY U
	Propionate	ANOVA	K-W	MANN WHITNEY U
	Butyrate	K-W	K-W	MANN WHITNEY U
	BSCFA	K-W	K-W	MANN WHITNEY U
	Total SCFA	K-W	K-W	MANN WHITNEY U
Interaction with HT29-AUC	FS	K-W	K-W	MANN WHITNEY U
	IM	K-W	K-W	MANN WHITNEY U