

## **Supplementary Materials**

### **Galactooligosaccharide (B-GOS) reduces branched short-chain fatty acids, ammonium and pH in a short-term colonic fermentation model**

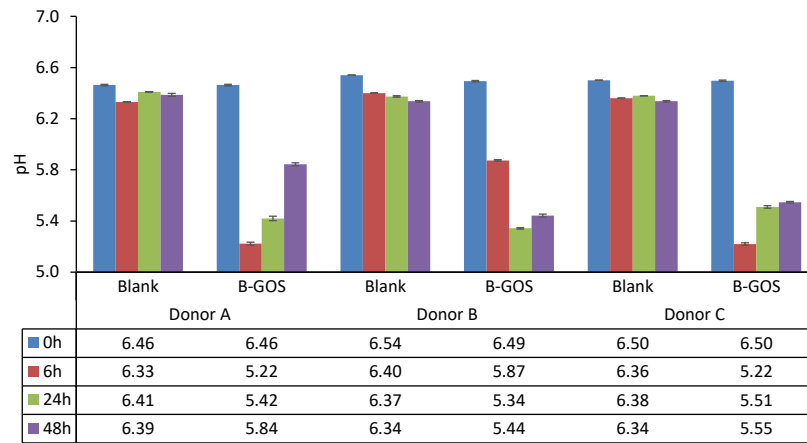
Massimo Marzorati, Jonas Ghyselinck, Pieter van den Abbeele, Aleksandra Maruszak, Lucien Harthoorn

**Table S1.** Absolute abundances (log(cells/mL)) of bacterial families at 24h of incubation.

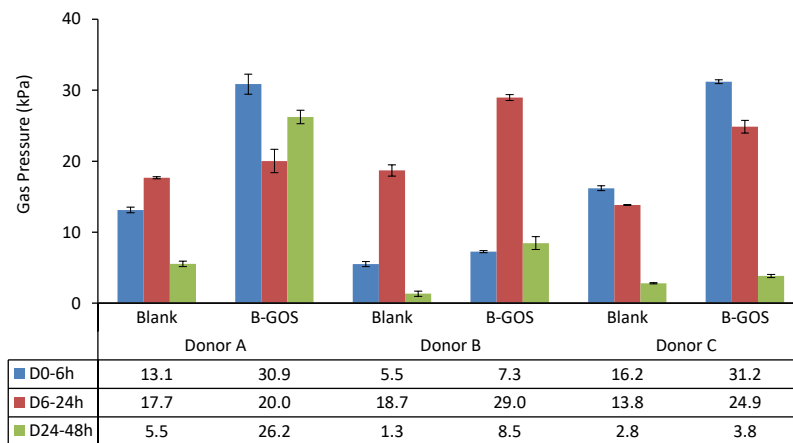
Phylum	Family	Donor A		Donor B		Donor C		Average	
		Blank	B-GOS	Blank	B-GOS	Blank	B-GOS	Blank	B-GOS
Actinobacteria	<i>Bifidobacteriaceae</i>	7.92	<b>8.73</b>	8.31	<b>8.58</b>	8.22	<b>8.95</b>	8.18	<b>8.78</b>
	<i>Coriobacteriaceae</i>	8.20	<b>8.31</b>	7.76	<b>8.48</b>	7.36	<b>7.69</b>	7.90	<b>8.27</b>
	<i>Eggerthellaceae</i>	<b>6.93</b>	<b>6.58</b>	8.28	<b>8.34</b>	<b>8.17</b>	<b>8.01</b>	8.06	8.03
	<i>Propionibacteriaceae</i>	<LOQ	<LOQ	<LOQ	<LOQ	<LOQ	<LOQ	<LOQ	<LOQ
<i>Bacteria_u_p</i>	<i>Bacteria_u_f</i>	<LOQ	<LOQ	<LOQ	<LOQ	<LOQ	<LOQ	<LOQ	<LOQ
Bacteroidetes	<i>Bacteroidaceae</i>	<b>8.74</b>	<b>8.50</b>	8.79	<b>8.93</b>	<b>9.00</b>	<b>8.93</b>	8.86	8.83
	<i>Bacteroidales_u_f</i>	<LOQ	<LOQ	<LOQ	<LOQ	<LOQ	<LOQ	<LOQ	<LOQ
	<i>Barnesiellaceae</i>	<b>6.44</b>	<LOQ	<b>6.84</b>	<b>6.64</b>	7.06	<b>7.20</b>	6.85	<b>6.88</b>
	<i>Odoribacteraceae</i>	7.08	<b>6.85</b>	6.71	<b>6.47</b>	<b>7.14</b>	<b>6.60</b>	7.02	6.67
	<i>Porphyromonadaceae</i>	<b>7.46</b>	<b>6.98</b>	<b>6.69</b>	<LOQ	<b>6.80</b>	6.49	<b>7.13</b>	<b>6.71</b>
	<i>Prevotellaceae</i>	6.74	<b>7.17</b>	<LOQ	<LOQ	<LOQ	<LOQ	6.56	<b>6.83</b>
	<i>Rikenellaceae</i>	<b>8.33</b>	8.22	<b>8.10</b>	<b>7.98</b>	8.38	<b>8.49</b>	8.29	8.28
	<i>Tannerellaceae</i>	<b>7.97</b>	<b>7.44</b>	<b>7.55</b>	<b>7.19</b>	7.97	<b>8.08</b>	<b>7.87</b>	<b>7.74</b>
<i>Euryarchaeota</i>	<i>Methanobacteriaceae</i>	<LOQ	<LOQ	<LOQ	<LOQ	6.65	6.59	6.51	6.49
Firmicutes	<i>Acidaminococcaceae</i>	<LOQ	<LOQ	7.27	<b>7.75</b>	7.84	<b>7.91</b>	7.48	<b>7.67</b>
	<i>Christensenellaceae</i>	<LOQ	<b>6.65</b>	<LOQ	<b>6.55</b>	<LOQ	<LOQ	<LOQ	6.55
	<i>Clostridiaceae</i>	<b>7.18</b>	6.99	<b>6.86</b>	<LOQ	6.88	6.91	7.00	6.84
	<i>Clostridiales_u_f</i>	<b>7.63</b>	<b>6.96</b>	<b>7.84</b>	<b>7.20</b>	<b>7.47</b>	<b>7.21</b>	<b>7.67</b>	<b>7.14</b>
	<i>Enterococcaceae</i>	<LOQ	<LOQ	7.04	<b>7.74</b>	6.75	<b>7.48</b>	6.81	<b>7.47</b>
	<i>Erysipelotrichaceae</i>	<LOQ	<LOQ	<b>6.49</b>	<LOQ	<b>6.52</b>	<LOQ	<b>6.48</b>	<LOQ
	<i>Eubacteriaceae</i>	6.75	<b>6.88</b>	<b>7.09</b>	<b>6.58</b>	6.78	<b>7.32</b>	6.90	<b>7.03</b>
	<i>Lachnospiraceae</i>	<b>7.99</b>	<b>7.82</b>	8.18	<b>8.01</b>	8.19	<b>8.27</b>	8.13	8.07
	<i>Lactobacillaceae</i>	<LOQ	<b>6.49</b>	<LOQ	<b>6.93</b>	<LOQ	<LOQ	<LOQ	<b>6.68</b>
	<i>Leuconostocaceae</i>	<LOQ	<LOQ	<LOQ	<LOQ	<LOQ	<LOQ	<LOQ	<LOQ
	<i>Oscillospiraceae</i>	<b>7.26</b>	<b>6.43</b>	<b>7.32</b>	<b>6.87</b>	<b>7.45</b>	<b>6.99</b>	<b>7.35</b>	<b>6.83</b>
	<i>Peptostreptococcaceae</i>	<LOQ	<LOQ	7.88	7.95	<b>7.67</b>	7.11	7.62	7.55
	<i>Ruminococcaceae</i>	<b>7.89</b>	<b>7.55</b>	<b>7.89</b>	<b>7.32</b>	7.66	<b>7.99</b>	<b>7.83</b>	7.71
	<i>Selenomonadaceae</i>	<LOQ	<LOQ	<b>7.35</b>	<LOQ	7.56	<b>8.07</b>	7.31	<b>7.61</b>
	<i>Streptococcaceae</i>	8.15	<b>8.76</b>	<LOQ	<LOQ	<LOQ	<LOQ	7.69	<b>8.28</b>
	<i>Veillonellaceae</i>	7.42	<b>7.44</b>	6.69	<b>7.23</b>	<LOQ	<LOQ	7.05	<b>7.20</b>
Proteobacteria	<i>Burkholderiales_u_f</i>	<LOQ	<LOQ	<b>6.68</b>	<LOQ	<LOQ	<b>6.58</b>	<b>6.53</b>	6.48
	<i>Desulfovibrionaceae</i>	<LOQ	<LOQ	<b>7.23</b>	<b>6.88</b>	<b>7.44</b>	<b>7.10</b>	7.20	6.88
	<i>Enterobacteriaceae</i>	<b>8.37</b>	<b>8.14</b>	<LOQ	<LOQ	7.90	<b>8.11</b>	8.02	7.95
	<i>Sutterellaceae</i>	<b>6.65</b>	<LOQ	<b>6.97</b>	<LOQ	<b>7.74</b>	<b>7.49</b>	<b>7.36</b>	7.08

The intensity of shading is a measure for the abundance of a family in the different conditions per donor/average. Values in bold represent a statistically significant difference in abundance between blank and B-GOS using unpaired t-tests on technical replicates (n=3) for within donor comparisons and using paired t-tests for across donor comparisons. B-GOS = Bimuno® galactooligosaccharide.

(a)

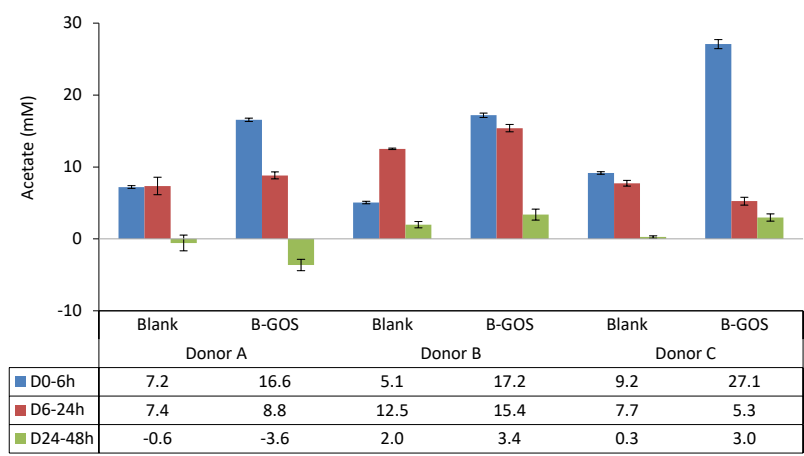


(b)

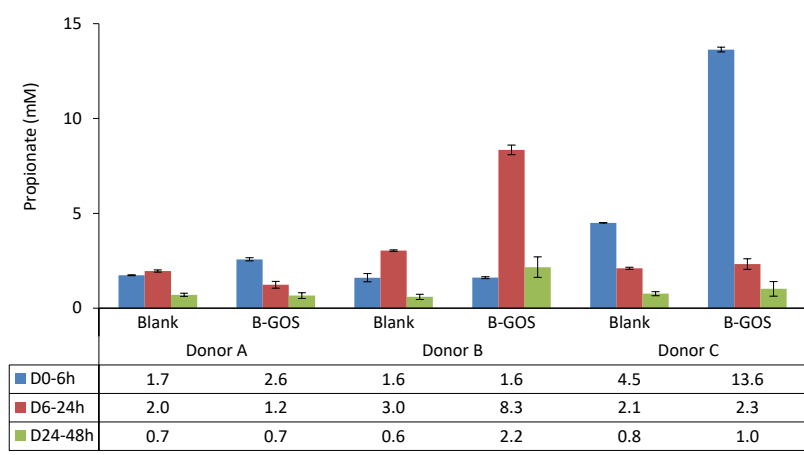


**Figure S1.** Overall microbial community activity (acidification and gas production) shown as (a) pH and (b) gas pressure for individual donors. Measurements were collected in triplicate. Error bars represent standard deviation. B-GOS = Bimuno® galactooligosaccharide.

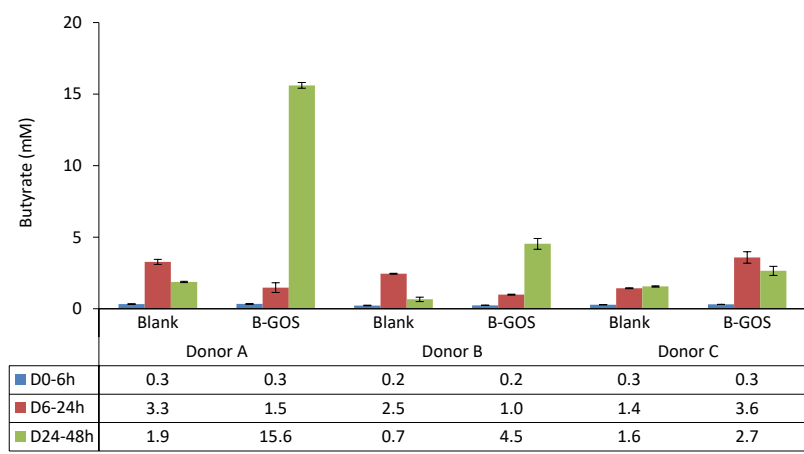
(a)



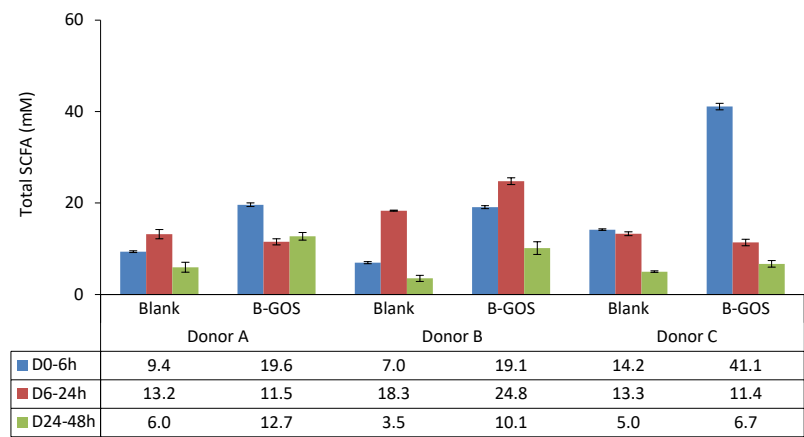
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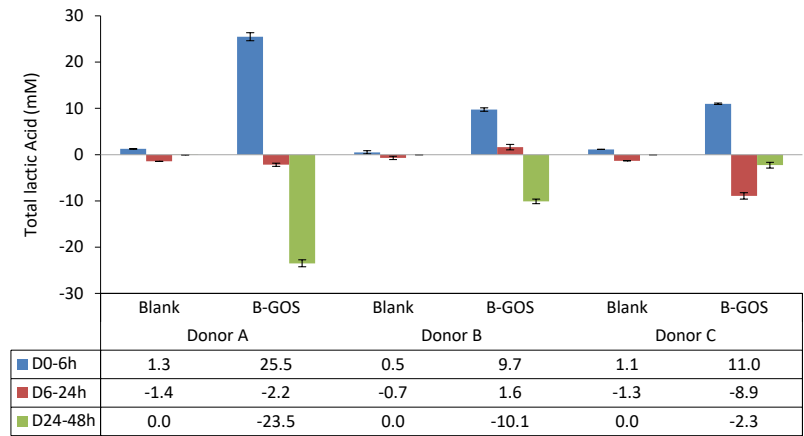
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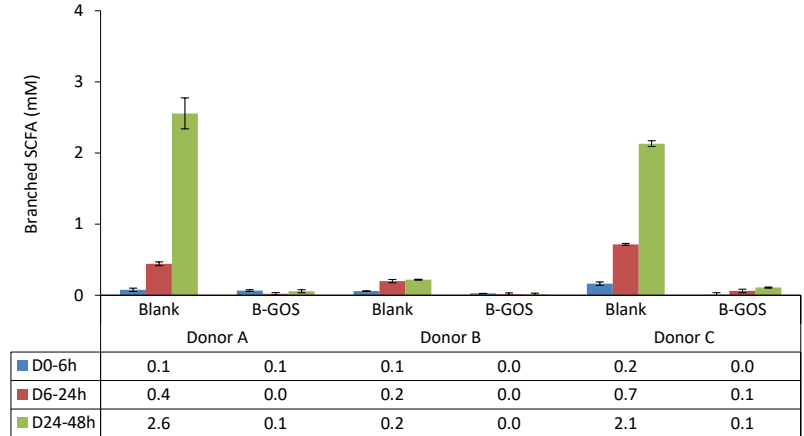
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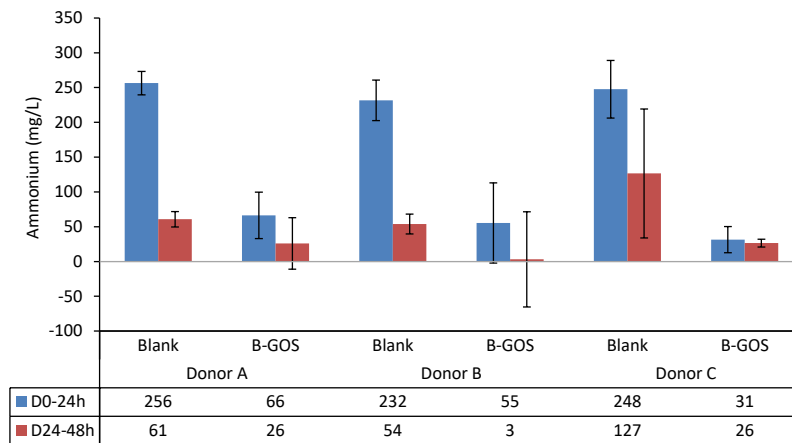
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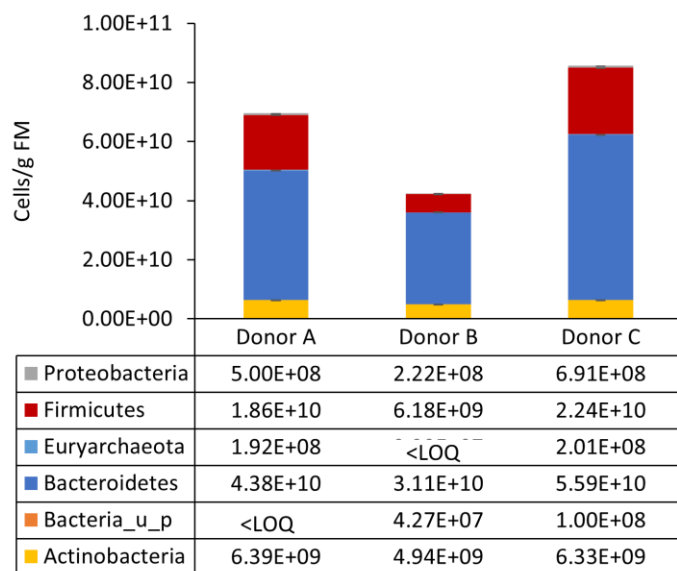
(f)



**(g)**



**Figure S2.** Microbial metabolic activity (a) acetate, (b) propionate, (c) butyrate, (d) total SCFA, (e) lactate, (f) branched SCFA, and (g) ammonium for individual donors. Measurements were collected in triplicate. Error bars represent standard deviation. B-GOS = Bimuno® galactooligosaccharide; SCFA = short-chain fatty acid.



**Figure S3.** Representation of major phyla in the fecal microbiota of each donor at 0h. Samples were assayed in triplicate. B-GOS = Bimuno® galactooligosaccharide; FM = fecal matter; LOQ = limit of quantification.