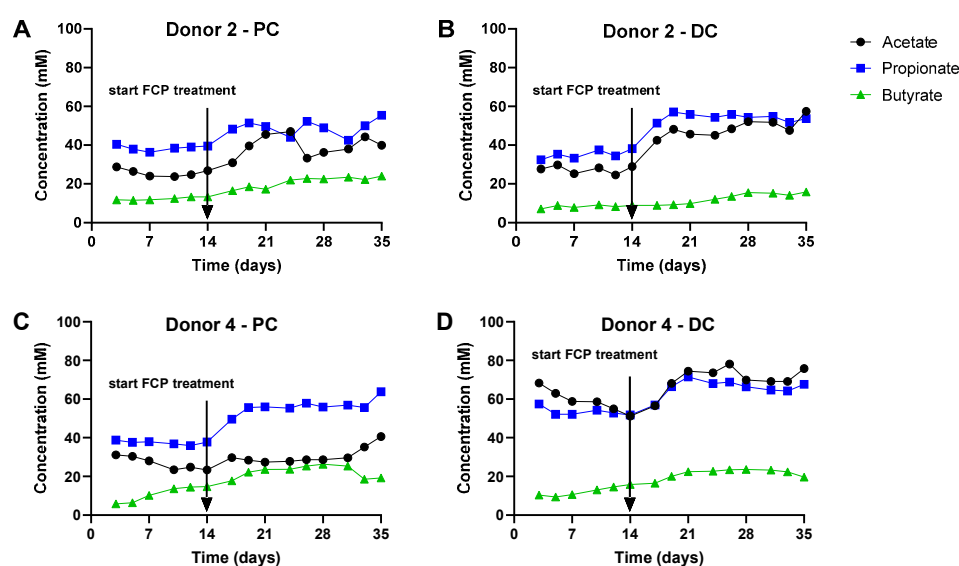


**Figure S1.** Effect of FCP on average ( $\pm$  SD) levels of acetate (A), propionate (B), butyrate (C), bCFA (D), total SCFA (E) and *Bifidobacteriaceae* (F), upon incubation with human faecal microbiota derived from 5 different human donors. All conditions were tested in technical duplicate. The data is presented as the average ( $\pm$  SD) for each of the different test conditions ( $n = 2$ ). Statistical differences due to treatment were indicated by \*/\*\*/\*\* (0.01 < adjusted p-value < 0.05/0.001 < adjusted p-value < 0.01/ adjusted p-value < 0.001).



**Figure S2.** Effect of fermentation of FCP on SCFA levels (mM) in the simulated proximal colon (A/C) and distal colon (B/D) during both the control (Days 0–14) and treatment period (Days 14–35) of the triple-M-SHIME for donors 2 (A/B) and 4 (C/D). Arrows indicate the start of the FCP treatment.

**Table S1.** Effect of FCP on microbial composition (families belonging to specific phyla) in the simulated mucus (as estimated via 16S rRNA gene profiling (%)) of the simulated proximal and distal colon of the triple-M-SHIME. The data is presented as the difference between the value obtained at the end of the treatment period (TR: Day 35) and the end of the control period (C: Day 14) (n = 1). An increase (indicated in bold when > 2 %) thus reflects a stimulation of a given family by repeated FCP treatment, while a decrease (indicated by underlining when < -2 %) suggests a decrease due to FCP treatment.

Phylum	Family	Proximal colon			Distal colon		
		Donor 2	Donor 3	Donor 4	Donor 2	Donor 3	Donor 4
Actinobacteria	Bifidobacteriaceae	<u>-13.1%</u>	0.0%	<u>-34.8%</u>	<b>6.1%</b>	0.4%	<b>4.6%</b>
	Coriobacteriaceae	0.1%	0.8%	0.0%	<b>2.6%</b>	0.2%	<b>2.5%</b>
Bacteroidetes	Bacteroidaceae	<b>22.4%</b>	<b>6.1%</b>	0.6%	1.5%	<u>-7.4%</u>	<u>-7.8%</u>
	Bacteroidales_S24-7_group	0.0%	0.0%	0.0%	0.0%	<b>4.9%</b>	2.0%
	Porphyromonadaceae	0.0%	0.4%	0.0%	1.3%	<u>-2.2%</u>	0.1%
	Prevotellaceae	0.0%	<b>5.3%</b>	<b>16.7%</b>	0.0%	<b>2.4%</b>	<b>3.3%</b>
	Rikenellaceae	0.0%	0.1%	0.0%	-0.5%	0.1%	0.4%
Firmicutes	Acidaminococcaceae	<b>9.4%</b>	-1.7%	<b>10.5%</b>	<b>4.2%</b>	<b>3.6%</b>	<b>2.3%</b>
	Christensenellaceae	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%
	Clostridiaceae_1	-0.4%	-0.3%	-0.4%	-0.4%	0.6%	-0.7%
	Erysipelotrichaceae	0.0%	0.0%	0.0%	0.4%	0.4%	<b>3.6%</b>
	Eubacteriaceae	0.0%	0.0%	0.0%	-0.8%	<b>2.1%</b>	0.3%
	Lachnospiraceae	<u>-20.2%</u>	<b>3.4%</b>	1.5%	<b>7.5%</b>	<b>7.6%</b>	<u>-3.3%</u>
	Ruminococcaceae	0.0%	0.0%	0.0%	0.2%	0.9%	1.5%
Proteobacteria	Veillonellaceae	<b>6.8%</b>	<u>-11.3%</u>	<b>2.3%</b>	-0.5%	-0.5%	1.2%
	Victivallaceae	0.0%	0.0%	0.0%	-0.1%	0.3%	0.8%
	Alcaligenaceae	0.0%	-0.2%	0.5%	0.0%	0.3%	0.3%
	Campylobacteraceae	-0.4%	0.0%	0.0%	0.0%	0.0%	0.0%
	Desulfovibrionaceae	0.0%	0.7%	0.0%	-1.2%	-0.9%	-1.8%
	Enterobacteriaceae	<u>-3.9%</u>	-1.6%	<b>4.2%</b>	0.1%	0.5%	-0.2%
	Pseudomonadaceae	-0.7%	<u>-2.2%</u>	-0.5%	0.8%	-0.1%	-0.1%
Synergistetes	Rhodospirillaceae	0.0%	0.1%	0.0%	0.3%	0.2%	1.5%
	Xanthomonadaceae	-0.4%	-0.1%	-0.6%	0.0%	0.0%	-0.1%
Synergistetes	Synergistaceae	0.0%	0.3%	0.0%	<u>-21.0%</u>	<u>-12.8%</u>	<u>-11.4%</u>
Verrucomicrobia	Verrucomicrobiaceae	0.0%	0.0%	0.0%	-0.1%	-0.4%	0.9%

**Table S2.** Microbial composition (families belonging to specific phyla) in the lumen (as estimated via 16S rRNA gene profiling (%)) of the simulated proximal and distal colon of the triple-M-SHIME during the control period (Day 14) (n = 1).

Phylum	Family	Proximal colon			Distal colon		
		Donor 2	Donor 3	Donor 4	Donor 2	Donor 3	Donor 4
Actinobacteria	Bifidobacteriaceae	22.5%	2.0%	1.8%	0.4%	1.8%	0.6%
	Coriobacteriaceae	0.0%	0.0%	0.0%	0.2%	0.3%	0.1%
Bacteroidetes	Bacteroidaceae	19.2%	1.0%	0.0%	45.3%	39.6%	43.8%
	Bacteroidales_S24-7_group	0.0%	0.0%	0.0%	0.0%	0.2%	0.2%
	Porphyromonadaceae	0.0%	0.0%	0.0%	2.5%	1.4%	3.6%
	Prevotellaceae	0.0%	34.6%	27.8%	0.0%	8.1%	5.2%
	Rikenellaceae	0.0%	0.0%	0.0%	0.2%	0.2%	0.1%
Firmicutes	Acidaminococcaceae	1.8%	4.1%	5.4%	1.3%	1.8%	1.6%
	Christensenellaceae	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Clostridiaceae_1	0.1%	0.8%	1.7%	0.0%	0.0%	0.0%
	Erysipelotrichaceae	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	Eubacteriaceae	0.0%	0.0%	0.0%	0.1%	0.3%	0.2%

	<i>Lachnospiraceae</i>	8.6%	1.9%	0.2%	19.7%	18.3%	15.4%
	<i>Ruminococcaceae</i>	0.0%	0.0%	0.0%	0.5%	0.5%	0.3%
	<i>Veillonellaceae</i>	37.1%	43.6%	49.6%	10.3%	10.1%	12.2%
<i>Lentisphaerae</i>	<i>Victivallaceae</i>	0.0%	0.0%	0.0%	0.4%	0.3%	0.3%
	<i>Alcaligenaceae</i>	0.0%	0.4%	0.0%	0.3%	0.2%	0.1%
	<i>Campylobacteraceae</i>	0.1%	0.0%	0.0%	0.0%	0.0%	0.0%
	<i>Desulfovibrionaceae</i>	0.0%	0.0%	0.0%	0.7%	1.5%	2.4%
<i>Proteobacteria</i>	<i>Enterobacteriaceae</i>	6.5%	2.6%	4.7%	0.1%	0.1%	0.2%
	<i>Pseudomonadaceae</i>	1.9%	8.2%	4.7%	4.2%	3.2%	5.2%
	<i>Rhodospirillaceae</i>	0.0%	0.0%	0.0%	0.1%	0.2%	0.4%
	<i>Xanthomonadaceae</i>	2.0%	0.8%	4.3%	0.1%	0.1%	0.3%
<i>Synergistetes</i>	<i>Synergistaceae</i>	0.0%	0.0%	0.0%	11.2%	7.0%	7.4%
<i>Verrucomicrobia</i>	<i>Verrucomicrobiaceae</i>	0.0%	0.0%	0.0%	2.1%	4.7%	0.1%

**Table S2.** Microbial composition (families belonging to specific phyla) in the simulated mucus (as estimated via 16S rRNA gene profiling (%)) of the simulated proximal and distal colon of the triple-M-SHIME during the control period (Day 14) (n = 1).

Phylum	Family	Proximal colon			Distal colon		
		Donor 2	Donor 3	Donor 4	Donor 2	Donor 3	Donor 4
<i>Actinobacteria</i>	<i>Bifidobacteriaceae</i>	43.2%	42.0%	60.4%	2.4%	6.9%	2.0%
	<i>Coriobacteriaceae</i>	0.0%	0.3%	0.0%	0.6%	1.3%	0.6%
<i>Bacteroidetes</i>	<i>Bacteroidaceae</i>	6.3%	0.5%	0.0%	12.5%	21.2%	16.9%
	<i>Bacteroidales_S24-7_group</i>	0.0%	0.0%	0.0%	0.0%	1.0%	1.1%
	<i>Porphyromonadaceae</i>	0.0%	0.0%	0.0%	1.5%	3.2%	2.0%
	<i>Prevotellaceae</i>	0.0%	7.2%	3.1%	0.0%	0.4%	0.3%
	<i>Rikenellaceae</i>	0.0%	0.0%	0.0%	1.7%	0.5%	1.6%
<i>Firmicutes</i>	<i>Acidaminococcaceae</i>	1.6%	16.7%	6.8%	0.9%	2.4%	2.1%
	<i>Christensenellaceae</i>	0.0%	0.0%	0.0%	0.3%	0.1%	0.0%
	<i>Clostridiaceae_1</i>	0.9%	0.5%	1.5%	0.9%	0.1%	1.2%
	<i>Erysipelotrichaceae</i>	0.0%	0.0%	0.0%	0.3%	0.1%	0.2%
	<i>Eubacteriaceae</i>	0.0%	0.0%	0.0%	2.5%	0.4%	1.0%
	<i>Lachnospiraceae</i>	26.3%	4.9%	0.8%	33.3%	22.6%	37.2%
	<i>Ruminococcaceae</i>	0.0%	0.0%	0.0%	3.2%	1.9%	3.2%
	<i>Veillonellaceae</i>	15.8%	21.5%	23.9%	4.2%	5.4%	4.1%
<i>Lentisphaerae</i>	<i>Victivallaceae</i>	0.0%	0.0%	0.0%	0.6%	0.2%	0.3%
	<i>Alcaligenaceae</i>	0.0%	1.7%	0.2%	0.4%	0.4%	0.2%
	<i>Campylobacteraceae</i>	0.5%	0.0%	0.0%	0.0%	0.0%	0.0%
	<i>Desulfovibrionaceae</i>	0.0%	0.0%	0.0%	2.1%	2.0%	2.5%
<i>Proteobacteria</i>	<i>Enterobacteriaceae</i>	4.2%	2.3%	1.7%	0.1%	0.1%	0.5%
	<i>Pseudomonadaceae</i>	0.7%	2.2%	0.8%	0.0%	0.2%	0.1%
	<i>Rhodospirillaceae</i>	0.0%	0.0%	0.0%	0.1%	0.2%	0.4%
	<i>Xanthomonadaceae</i>	0.4%	0.1%	0.8%	0.0%	0.0%	0.1%
<i>Synergistetes</i>	<i>Synergistaceae</i>	0.0%	0.2%	0.0%	31.1%	28.3%	21.8%
<i>Verrucomicrobia</i>	<i>Verrucomicrobiaceae</i>	0.0%	0.0%	0.0%	0.2%	0.5%	0.0%