

Supplementary Materials:

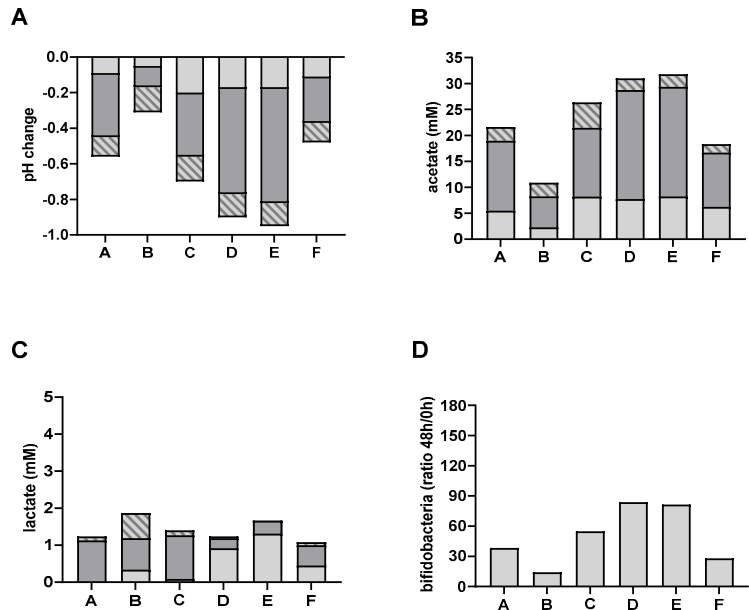


Figure S1. Metabolic activity of BB-12 in monoculture in presence of sterile fecal suspension of six donors (A, B, C, D, E and F) upon dosing starch as carbon source. Bars represents changes in pH (A), acetate (B; mM), lactate (C; mM) levels between 0 and 6h (light grey), 6h and 24h (dark grey) and 24h and 48h (stripes) as well as changes in *Bifidobacterium* numbers (D; expressed as the ratio of their absolute abundance as measured via qPCR at the end versus the beginning of the incubation (48h/0h)) (n=6). BB-12 = *Bifidobacterium animalis* subsp. *lactis*.

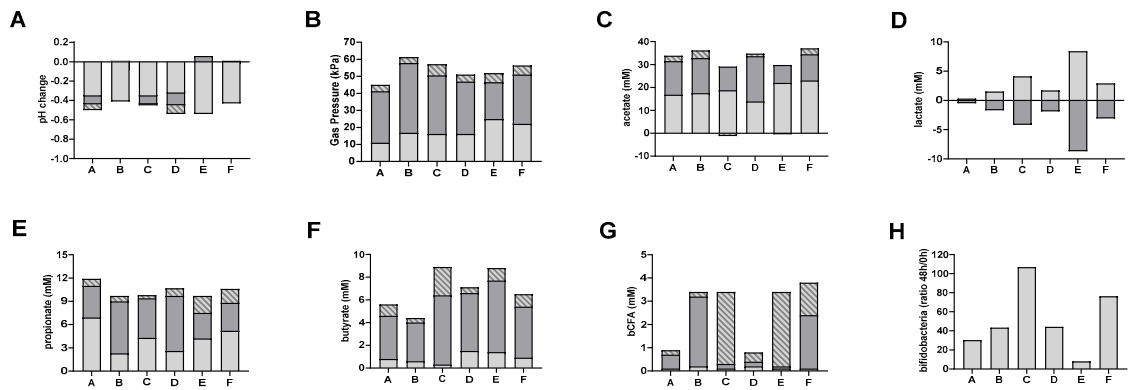


Figure S2. Metabolic activity of fecal microbiota of the six same donors as such (A, B, C, D, E and F) upon dosing starch as carbon source. Bars represents the changes in pH (A), gas production (B), acetate (C; mM), lactate (D; mM), propionate (E; mM), butyrate (F; mM) and bCFA (G; mM) levels between 0 and 6h (light grey), 6h and 24h (dark grey) and 24h and 48h (stripes) as well as changes in *Bifidobacterium* numbers (H; expressed as the ratio of their absolute abundance as measured via qPCR at the end versus the beginning of the incubation (48h/0h)) (n=6). BB-12 = *Bifidobacterium animalis* subsp. *lactis*.

Table S1. Changes in metabolic activity upon dosing BB-12 and/or seven fructans with short (OF1, OF2), intermediate (OF/IN1, OF/IN2) and high degree of polymerization (IN1, IN2 and IN3) to the complex microbiota of three human donors (C, D and F). The values represent differences for the three donors individually (as well as average values over the three donors) versus the respective reference (for fructans, the reference was the untreated blank, while for conditions with BB-12 addition this was the respective condition where BB-12 was not dosed). The data represent the changes between 0-48h (except for the intermediate metabolite lactate where it is the maximal value measured throughout the incubation). For optimal visualization, values indicating more pronounced fermentation are highlighted with grey shading (pH/bCFA <0 or gas/acetate/lactate/propionate/butyrate > 0), with significant changes being indicated in bold (n = 9; 3 values for each of the 3 donors).

Endpoint	Donor	Blank	OF1		OF2		OF/IN1		OF/IN2		IN1		IN2		IN3	
		BB-12	-	BB-12	-	BB-12	-	BB-12	-	BB-12	-	BB-12	-	BB-12	-	BB-12
pH	C	0,00	-1,20	0,18	-1,27	0,11	-1,07	0,07	-0,77	0,09	-0,72	0,00	-0,83	0,07	-0,76	0,05
	D	-0,01	-0,79	-0,12	-0,78	-0,13	-0,90	-0,02	-0,72	-0,16	-0,76	-0,10	-0,80	-0,07	-0,77	-0,15
	F	0,01	-0,80	0,16	-0,86	0,08	-0,60	-0,01	-0,84	0,23	-0,57	0,01	-0,78	0,00	-0,79	0,12
	C/D/F	0,00	-0,93	0,07	-0,97	0,02	-0,86	0,01	-0,78	0,05	-0,68	-0,03	-0,80	0,00	-0,77	0,01
Gas (kPa)	C	2,6	1,1	9,6	0,8	5,2	13,3	1,2	42,2	4,5	40,3	3,0	42,3	0,6	39,6	3,6
	D	2,2	36,1	-5,1	28,7	4,0	36,1	0,0	60,0	-13,1	53,6	-5,2	50,5	-2,4	52,8	-8,3
	F	2,3	47,0	4,3	35,1	4,7	42,3	8,8	44,5	4,7	43,9	5,4	42,3	4,0	38,9	11,2
	C/D/F	2,4	28,1	2,9	21,5	4,6	30,6	3,3	48,9	-1,3	45,9	1,0	45,0	0,7	43,8	2,2
Acetate (mM)	C	0,3	17,4	0,7	16,6	0,5	23,0	-0,9	22,9	-8,5	22,3	-4,2	26,2	-10,1	25,5	-1,6
	D	0,8	20,6	2,1	19,1	6,1	23,7	5,2	24,1	6,2	26,4	3,4	29,6	-2,3	22,9	6,2
	F	0,6	23,2	-3,3	24,6	6,3	21,0	-1,3	23,7	1,4	25,1	-7,5	23,2	-0,1	25,1	-1,6
	C/D/F	0,6	20,4	-0,2	20,1	4,3	22,5	1,0	23,6	-0,3	24,6	-2,8	26,3	-4,2	24,5	1,0
Lactate (mM)	C	0,4	26,1	-0,3	24,6	0,8	24,5	-0,1	12,2	1,7	13,1	-0,8	13,9	0,3	16,0	-1,4
	D	0,1	5,0	0,0	6,5	-1,6	4,3	-1,1	2,9	-0,2	2,1	0,8	2,0	0,8	2,1	0,9
	F	-0,1	14,1	-2,4	14,1	-2,9	13,4	-2,3	8,4	-0,5	7,6	1,5	8,2	-0,6	9,3	0,0
	C/D/F	0,1	15,1	-0,9	15,1	-1,2	14,1	-1,2	7,8	0,3	7,6	0,5	8,1	0,2	9,2	-0,2
Propionate (mM)	C	0,6	-1,4	0,3	0,2	-0,2	-1,5	0,2	5,5	-0,3	5,3	0,1	3,5	0,7	2,1	0,8
	D	0,3	2,8	1,2	2,1	1,8	5,4	-0,1	4,6	2,4	6,1	0,5	7,3	-0,4	5,2	2,0
	F	0,4	-0,8	-0,3	-0,6	1,1	-1,0	0,3	2,9	1,5	5,1	-1,0	2,4	0,6	2,9	0,7
	C/D/F	0,4	0,2	0,4	0,6	0,9	1,0	0,1	4,3	1,2	5,5	-0,1	4,4	0,3	3,4	1,2
Butyrate (mM)	C	0,0	-3,8	0,1	-3,8	0,1	-3,8	0,1	2,5	3,3	3,5	1,5	2,1	2,2	2,7	0,8
	D	0,3	2,3	1,5	1,8	-0,3	0,9	1,7	8,5	-2,6	6,6	0,0	5,3	1,4	6,6	-1,2
	F	0,0	8,6	0,2	2,7	1,0	8,5	1,5	5,5	3,6	7,7	2,8	5,2	2,3	7,4	0,3
	C/D/F	0,1	2,4	0,6	0,2	0,3	1,9	1,1	5,5	1,4	5,9	1,4	4,2	1,9	5,6	-0,1
bCFA (mM)	C	0,1	-3,4	-0,1	-3,5	0,0	-3,5	0,1	-3,5	0,0	-3,5	0,0	-3,5	0,0	-3,5	0,0
	D	0,1	-0,6	0,1	-0,6	0,0	-0,5	0,0	-0,4	-0,1	-0,5	0,0	-0,5	0,0	-0,5	0,0
	F	0,2	-4,3	0,0	-4,5	0,1	-4,5	0,2	-4,2	0,2	-4,1	0,2	-4,3	0,2	-4,0	0,2
	C/D/F	0,1	-2,8	0,0	-2,8	0,0	-2,8	0,1	-2,7	0,0	-2,7	0,1	-2,8	0,1	-2,7	0,1

Table S2. Changes of microbial abundances at phylum level (log(cells/mL)) as detected via quantitative 16S-targeted Illumina sequencing at the end of the colonic incubation (48h) upon dosing BB-12 and/or seven fructans with short (OF1, OF2), intermediate (OF/IN1, OF/IN2) and high degree of polymerization (IN1, IN2 and IN3) to the complex microbiota of three human donors (C, D and F). The values represent average differences versus the respective reference (for fructans, the reference was the untreated blank, while for conditions with BB-12 addition this was the respective condition where BB-12 was not dosed) at the end of the colonic incubation for each of the three donors, together with averages over the three donors. For optimal visualization, increases due to treatment are highlighted with grey shading, with significant changes being indicated in bold (n = 3 per donor).

Phylum	Donor	Blank	OF1		OF2		OF/IN1		OF/IN2		IN1		IN2		IN3	
		BB-12	-	BB-12	-	BB-12	-	BB-12	-	BB-12	-	BB-12	-	BB-12	-	BB-12
Actinobacteria	C	0.10	0.38	0.17	0.39	0.03	0.45	0.05	0.69	-0.03	0.74	0.01	0.64	0.10	0.65	0.06
	D	0.35	0.73	0.45	0.81	0.40	0.62	0.40	0.37	0.73	0.31	0.60	0.24	0.77	0.44	0.59
	F	0.13	0.79	0.29	0.81	0.08	0.86	0.22	0.85	0.08	0.85	0.04	0.86	0.02	0.85	0.17
	C/D/F	0.19	0.63	0.30	0.67	0.17	0.64	0.22	0.64	0.26	0.63	0.22	0.58	0.30	0.65	0.27
Bacteroidetes	C	0.02	-0.59	0.03	-0.64	0.15	-0.63	0.06	0.24	0.08	0.33	0.03	0.20	0.04	-0.30	0.37
	D	-0.02	-0.54	-0.01	-0.47	0.00	-0.30	-0.11	-0.48	0.25	-0.35	0.04	-0.40	0.16	-0.31	0.15
	F	-0.04	-0.48	0.05	-0.45	0.10	-0.43	0.14	-0.03	0.12	0.28	0.00	0.04	-0.14	0.09	-0.12
	C/D/F	-0.01	-0.54	0.02	-0.52	0.09	-0.45	0.03	-0.09	0.15	0.09	0.02	-0.05	0.02	-0.17	0.13
Firmicutes	C	0.05	0.10	-0.04	0.38	-0.25	-0.05	-0.19	0.02	0.29	0.06	0.22	-0.16	0.26	-0.26	0.29
	D	-0.04	0.03	-0.01	0.00	-0.06	-0.10	0.09	0.32	0.06	0.39	-0.03	0.36	-0.07	0.36	-0.15
	F	0.01	0.18	-0.04	0.18	-0.01	0.19	-0.04	0.25	0.01	0.24	0.00	0.25	-0.01	0.23	-0.03
	C/D/F	0.01	0.10	-0.03	0.19	-0.11	0.01	-0.05	0.20	0.12	0.23	0.06	0.15	0.06	0.11	0.04
Proteobacteria	C	0.01	0.09	0.03	0.07	0.00	0.10	0.06	0.19	-0.06	0.14	0.01	0.09	0.06	0.10	-0.02
	D	-0.02	0.09	-0.24	0.09	-0.36	0.28	-0.19	0.38	-0.14	0.30	-0.03	0.41	-0.20	0.34	-0.08
	F	0.00	-0.30	-0.06	-0.37	-0.05	-0.26	-0.11	-0.32	-0.03	-0.30	-0.07	-0.36	-0.01	-0.24	-0.04
	C/D/F	0.00	-0.04	-0.09	-0.07	-0.14	0.04	-0.08	0.08	-0.08	0.05	-0.03	0.04	-0.05	0.07	-0.04
Verrucomicrobia	C	0.14	-0.62	0.05	-0.71	0.14	-0.69	-0.10	-0.72	0.37	-0.53	0.13	-0.60	0.30	-0.53	0.18
	D	0.01	0.14	-0.38	0.39	-0.48	0.22	0.13	0.29	0.04	0.41	-0.25	0.27	0.11	0.52	0.00
	F	0.25	0.17	0.27	0.38	0.51	0.60	-0.20	0.27	0.09	0.28	0.19	0.39	0.08	0.29	0.05
	C/D/F	0.14	-0.10	-0.02	0.02	0.06	0.04	-0.06	-0.05	0.17	0.05	0.03	0.02	0.16	0.09	0.08

Table S3. Changes of microbial abundances at family level (log(cells/mL)) as detected via quantitative 16S-targeted Illumina sequencing at the end of the colonic incubation (48h) upon dosing BB-12 and/or seven fructans with short (OF1, OF2), intermediate (OF/IN1, OF/IN2) and high degree of polymerization (IN1, IN2 and IN3) to the complex microbiota of donor C. The values represent average differences versus the respective reference (for fructans, the reference was the untreated blank, while for conditions with BB-12 addition this was the respective condition where BB-12 was not dosed) at the end of the colonic incubation. For optimal visualization, increases due to treatment are highlighted with grey shading, with significant changes being indicated in bold (n = 3).

Phylum	Family	Blank	OF1		OF2		OF/IN1		OF/IN2		IN1		IN2		IN3	
		BB-12	-	BB-12	-	BB-12	-	BB-12	-	BB-12	-	BB-12	-	BB-12	-	BB-12
Actinobacteria	<i>Bifidobacteriaceae</i>	0.40	1.31	0.14	1.34	0.03	1.35	0.00	1.47	0.02	1.59	-0.03	1.47	0.07	1.40	0.15
	<i>Coriobacteriaceae</i>	0.21	0.24	0.15	-0.01	0.41	0.25	-0.01	0.07	0.08	0.29	0.24	0.13	0.30	0.20	0.11
	<i>Eggerthellaceae</i>	0.05	-0.37	0.18	-0.46	-0.01	-0.19	0.18	0.33	-0.13	0.24	0.07	0.22	0.12	0.33	-0.10
Bacteroidetes	<i>Bacteroidaceae</i>	0.02	-0.85	0.06	-0.96	0.30	-0.77	0.05	0.31	0.08	0.40	0.03	0.26	0.03	-0.30	0.41
	<i>Marinifilaceae</i>	0.14	-0.52	0.03	-0.53	0.00	-0.53	0.00	-0.20	-0.04	-0.36	-0.13	-0.27	0.20	-0.37	0.19
	<i>Muribaculaceae</i>	0.31	0.28	0.09	0.36	-0.13	0.08	0.27	0.22	-0.48	0.31	-0.03	0.18	0.30	0.38	0.11
	<i>Prevotellaceae</i>	0.00	0.52	0.25	1.32	-0.11	0.43	-0.05	0.70	-0.24	0.17	0.13	1.04	-0.15	0.13	0.38
	<i>Rikenellaceae</i>	0.01	0.15	-0.02	0.00	0.08	-0.01	0.03	-0.21	0.12	-0.19	0.20	-0.12	0.16	-0.25	0.23
	<i>Tannerellaceae</i>	-0.04	-1.66	-0.03	-1.70	0.03	-1.67	0.00	-1.28	0.25	-1.25	0.03	-1.15	0.10	-1.22	0.00
Firmicutes	<i>Enterococcaceae</i>	0.10	0.76	0.18	0.94	-0.08	0.84	-0.23	0.59	-0.12	0.54	0.20	0.44	0.05	0.22	0.27
	<i>Erysipelotrichaceae</i>	-0.05	-0.43	0.11	-0.44	0.14	-0.49	0.17	-0.81	0.87	0.23	0.09	-0.68	1.02	-0.70	1.38
	<i>Lachnospiraceae</i>	0.03	-0.52	-0.03	-0.44	-0.04	-0.76	0.03	-0.10	-0.08	0.00	-0.22	-0.21	0.17	-0.28	0.29
	<i>Lactobacillaceae</i>	0.00	2.48	-0.08	2.83	-0.39	2.29	-0.29	0.03	-0.03	0.00	0.00	0.60	-0.60	1.57	-1.57
	<i>Ruminococcaceae</i>	0.06	-1.19	0.12	-1.13	0.17	-1.04	-0.16	-0.04	0.48	-0.04	0.51	-0.42	0.14	-0.95	0.65
	<i>Streptococcaceae</i>	0.40	1.19	0.22	1.06	0.63	1.35	-0.07	1.62	0.57	1.56	0.30	1.22	0.79	0.86	0.79
	<i>Veillonellaceae</i>	0.07	-0.40	0.02	-0.25	0.10	-0.32	0.07	0.24	0.02	0.15	0.20	0.15	0.21	-0.05	0.16
Proteobacteria	<i>Burkholderiaceae</i>	0.02	0.09	0.05	0.11	0.00	0.16	-0.21	0.17	0.03	0.06	0.06	0.03	0.28	-0.01	0.29
	<i>Desulfovibrionaceae</i>	0.15	-0.33	0.18	-0.34	0.01	0.13	0.09	0.30	-0.13	0.11	0.39	0.21	-0.04	0.36	-0.64
	<i>Enterobacteriaceae</i>	0.01	0.09	0.03	0.07	0.00	0.10	0.06	0.19	-0.06	0.14	0.01	0.09	0.05	0.10	-0.01
Verrucomicrobia	<i>Akkermansiaceae</i>	0.14	-0.62	0.05	-0.71	0.14	-0.69	-0.10	-0.72	0.37	-0.53	0.13	-0.60	0.30	-0.53	0.18

Table S4. Changes of microbial abundances at family level (log(cells/mL)) as detected via quantitative 16S-targeted Illumina sequencing at the end of the colonic incubation (48h) upon dosing BB-12 and/or seven fructans with short (OF1, OF2), intermediate (OF/IN1, OF/IN2) and high degree of polymerization (IN1, IN2 and IN3) to the complex microbiota of donor D. The values represent average differences versus the respective reference (for fructans, the reference was the untreated blank, while for conditions with BB-12 addition this was the respective condition where BB-12 was not dosed) at the end of the colonic incubation. For optimal visualization, increases due to treatment are highlighted with grey shading, with significant changes being indicated in bold (n = 3).

Phylum	Family	Blank	OF1		OF2		OF/IN1		OF/IN2		IN1		IN2		IN3	
		BB-12	-	BB-12	-	BB-12	-	BB-12	-	BB-12	-	BB-12	-	BB-12	-	BB-12
Actinobacteria	<i>Bifidobacteriaceae</i>	0.91	1.37	0.46	1.47	0.41	0.83	0.82	0.77	0.97	0.34	1.17	0.37	1.26	0.52	1.10
	<i>Coriobacteriaceae</i>	-0.29	-0.27	0.04	0.30	-0.43	-0.03	-0.21	-0.04	-0.03	-0.54	0.15	-0.55	0.27	-0.11	0.02
	<i>Eggerthellaceae</i>	-0.09	0.05	0.41	-0.02	0.42	0.57	-0.17	0.19	0.23	0.33	0.06	0.23	0.17	0.43	0.12
Bacteroidetes	<i>Bacteroidaceae</i>	0.00	-1.32	-0.09	-1.20	-0.13	-0.77	-0.12	-1.00	0.27	-0.63	0.07	-0.61	0.12	-0.58	0.07
	<i>Marinifilaceae</i>	0.12	0.14	0.25	0.08	0.30	0.63	-0.35	-0.05	0.37	0.01	0.02	0.01	0.26	0.19	0.09
	<i>Muribaculaceae</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	<i>Prevotellaceae</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	<i>Rikenellaceae</i>	-0.16	1.08	0.00	1.15	0.03	1.16	-0.07	1.04	0.24	1.06	-0.02	0.96	0.18	1.10	0.19
	<i>Tannerellaceae</i>	-0.11	-0.85	-0.05	-0.94	0.05	-0.31	-0.28	-0.59	0.29	-0.66	0.21	-0.70	0.29	-0.56	0.21
Firmicutes	<i>Enterococcaceae</i>	0.00	1.34	-0.02	0.03	1.14	0.00	0.87	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	<i>Erysipelotrichaceae</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	-0.03	0.00	0.00	0.00	0.00	0.14	-0.14
	<i>Lachnospiraceae</i>	-0.01	-0.31	-0.18	-0.11	-0.42	-0.11	0.04	0.43	0.11	0.45	-0.02	0.52	-0.23	0.43	-0.06
	<i>Lactobacillaceae</i>	0.00	1.46	0.67	0.16	2.05	0.56	0.48	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	<i>Ruminococcaceae</i>	-0.07	0.06	-0.20	0.03	-0.24	-0.25	0.05	0.12	-0.02	0.27	-0.07	0.09	0.14	0.23	-0.33
	<i>Streptococcaceae</i>	0.01	1.59	-0.03	1.32	0.48	1.15	0.15	0.40	0.79	0.64	0.16	0.57	0.25	0.85	0.23
	<i>Veillonellaceae</i>	0.17	1.20	-0.05	1.41	-0.35	1.79	-0.19	1.93	-0.08	1.92	0.00	1.94	-0.03	2.02	-0.13
Proteobacteria	<i>Burkholderiaceae</i>	0.14	1.06	-0.22	0.97	-0.33	1.12	0.06	1.55	-0.16	1.44	-0.07	1.45	-0.16	1.45	-0.07
	<i>Desulfovibrionaceae</i>	-0.07	-0.02	-0.22	0.26	-0.35	0.08	0.09	-0.02	-0.20	-0.13	0.21	-0.11	-0.07	0.04	-0.03
	<i>Enterobacteriaceae</i>	-0.06	-0.19	-0.26	-0.12	-0.36	0.10	-0.47	-0.25	-0.08	-0.26	0.04	0.05	-0.26	-0.13	-0.09
Verrucomicrobia	<i>Akkermansiaceae</i>	0.01	0.14	-0.38	0.39	-0.48	0.22	0.13	0.29	0.04	0.41	-0.25	0.27	0.11	0.52	0.00

Table S5. Changes of microbial abundances at family level (log(cells/mL)) as detected via quantitative 16S-targeted Illumina sequencing at the end of the colonic incubation (48h) upon dosing BB-12 and/or seven fructans with short (OF1, OF2), intermediate (OF/IN1, OF/IN2) and high degree of polymerization (IN1, IN2 and IN3) to the complex microbiota of donor F. The values represent average differences versus the respective reference (for fructans, the reference was the untreated blank, while for conditions with BB-12 addition this was the respective condition where BB-12 was not dosed) at the end of the colonic incubation. For optimal visualization, increases due to treatment are highlighted with grey shading, with significant changes being indicated in bold (n = 3).

Phylum	Family	Blank	OF1		OF2		OF/IN1		OF/IN2		IN1		IN2		IN3	
		BB-12	-	BB-12	-	BB-12	-	BB-12	-	BB-12	-	BB-12	-	BB-12	-	BB-12
Actinobacteria	<i>Bifidobacteriaceae</i>	0.29	0.93	0.26	0.97	0.07	0.98	0.22	0.94	0.16	1.03	0.07	0.99	0.05	0.99	0.14
	<i>Coriobacteriaceae</i>	-0.21	0.46	0.76	0.19	0.61	0.66	0.49	0.42	0.18	0.21	0.38	0.37	0.23	0.39	0.50
	<i>Eggerthellaceae</i>	-0.03	0.69	0.23	0.71	0.06	0.79	0.15	0.85	-0.06	0.69	-0.02	0.78	-0.03	0.78	0.16
Bacteroidetes	<i>Bacteroidaceae</i>	-0.11	-0.28	0.07	-0.30	0.09	-0.21	0.18	0.30	0.13	0.65	0.00	0.37	-0.16	0.42	-0.14
	<i>Marinifilaceae</i>	0.06	-0.18	-0.19	-0.53	0.43	-0.26	0.07	-0.16	0.05	-0.33	-0.08	-0.02	0.03	0.00	-0.22
	<i>Muribaculaceae</i>	-0.04	0.02	-0.25	0.21	0.00	-0.08	-0.16	0.01	-0.22	-0.46	-0.10	0.02	0.05	-0.14	-0.08
	<i>Prevotellaceae</i>	-0.04	-0.68	-0.04	-0.47	0.35	-0.66	0.00	-0.62	-0.06	-0.72	-0.13	-0.69	0.06	-0.86	0.15
	<i>Rikenellaceae</i>	-0.05	-0.68	0.06	-0.50	-0.09	-0.70	0.04	-0.74	-0.02	-0.77	0.10	-0.65	-0.15	-0.60	-0.09
	<i>Tannerellaceae</i>	0.05	-0.98	0.11	-0.98	0.06	-0.85	0.12	-0.84	0.16	-0.89	0.00	-0.80	0.03	-0.74	-0.01
Firmicutes	<i>Enterococcaceae</i>	0.07	0.90	-0.58	0.93	-0.09	0.71	-0.42	0.42	-0.32	0.23	-0.24	0.23	0.03	0.30	-0.05
	<i>Erysipelotrichaceae</i>	-0.08	-0.14	-0.42	-0.15	-0.32	-0.07	-0.42	0.00	0.19	-0.28	0.43	0.22	-0.01	-0.24	0.22
	<i>Lachnospiraceae</i>	0.00	0.07	0.01	0.01	0.00	0.12	-0.02	0.24	0.06	0.28	-0.01	0.21	0.02	0.20	-0.01
	<i>Lactobacillaceae</i>	0.00	2.46	-0.24	2.77	-0.06	2.29	-0.10	0.73	-0.33	0.23	-0.12	1.12	-0.43	0.98	0.00
	<i>Ruminococcaceae</i>	0.05	0.26	-0.06	0.06	0.20	0.20	0.02	0.24	-0.16	0.05	0.05	0.34	-0.11	0.31	-0.24
	<i>Streptococcaceae</i>	-0.01	1.37	-0.35	1.47	-0.24	1.35	-0.35	1.32	-0.27	1.02	-0.24	1.22	-0.05	1.22	-0.14
	<i>Veillonellaceae</i>	0.01	-0.58	0.20	-0.41	0.14	-0.35	0.03	-0.08	0.13	-0.22	0.33	-0.06	0.08	-0.18	0.14
Proteobacteria	<i>Burkholderiaceae</i>	0.04	0.01	0.14	-0.04	0.11	0.02	0.10	0.04	0.14	0.04	0.08	0.00	0.16	0.02	0.21
	<i>Desulfovibrionaceae</i>	-0.02	-0.52	0.08	-0.36	0.00	-0.45	0.15	-0.57	0.11	-0.61	-0.01	-0.65	0.23	-0.64	0.21
	<i>Enterobacteriaceae</i>	-0.02	-0.49	-0.49	-0.58	-0.41	-0.42	-0.51	-0.55	-0.48	-0.52	-0.37	-0.61	-0.44	-0.38	-0.46
Verrucomicrobia	<i>Akkermansiaceae</i>	0.25	0.17	0.27	0.38	0.51	0.60	-0.20	0.27	0.09	0.28	0.19	0.39	0.08	0.29	0.05

Table S6. Changes of microbial abundances at OTU level (log(cells/mL)) as detected via quantitative 16S-targeted Illumina sequencing at the end of the colonic incubation (48h) upon dosing BB-12 and/or seven fructans with short (OF1, OF2), intermediate (OF/IN1, OF/IN2) and high degree of polymerization (IN1, IN2 and IN3) to the complex microbiota of donor C. The values represent average differences versus the respective reference (for fructans, the reference was the untreated blank, while for conditions with BB-12 addition this was the respective condition where BB-12 was not dosed) at the end of the colonic incubation. For optimal visualization, increases due to treatment are highlighted with grey shading, with significant changes being indicated in bold (n = 3).

Phylum	Family	OTU#	Related species	Blank	OF1		OF2		OF/IN1		OF/IN2		IN1		IN2		IN3	
				BB-12	-	BB-12	-	BB-12	-	BB-12	-	BB-12	-	BB-12	-	BB-12	-	BB-12
Actinobacteria	Bifidobacteriaceae	2	<i>Bifidobacterium adolescentis</i>	0.04	1.34	0.03	1.37	-0.04	1.29	0.00	1.50	-0.04	1.62	-0.06	1.50	0.01	1.43	0.11
		5	<i>Bifidobacterium animalis</i>	1.96	0.00	2.62	0.00	2.31	0.00	2.40	0.00	2.40	0.00	2.28	0.00	2.38	0.00	2.32
		21	<i>Bifidobacterium longum</i>	-0.04	0.32	0.01	0.26	0.10	0.17	-0.02	0.53	-0.03	0.57	0.02	0.44	0.13	0.42	-0.01
	Coriobacteriaceae	20	<i>Collinsella aerofaciens</i>	0.21	0.24	0.15	-0.01	0.41	0.23	0.00	0.07	0.06	0.27	0.24	0.10	0.33	0.20	0.11
	Eggerthellaceae	4	<i>Senegalimassilia</i> sp.	0.05	-0.39	0.19	-0.47	-0.03	-0.20	0.19	0.33	-0.14	0.25	0.07	0.22	0.11	0.33	-0.11
		7	<i>Ellagibacter isourolithinifaciens</i>	0.25	-0.02	-0.13	0.27	-0.09	-0.06	0.06	0.17	-0.16	0.41	-0.26	0.71	-0.53	0.22	0.04
Bacteroidetes	Bacteroidaceae	9	<i>Bacteroides caccae</i>	0.05	-0.76	0.07	-1.09	0.34	-0.70	0.18	1.52	0.08	1.51	0.01	1.15	0.28	0.31	0.82
		6	<i>Bacteroides dorei</i>	0.00	-1.06	0.03	-1.16	0.34	-0.83	-0.08	-0.50	0.03	-0.51	-0.13	-0.48	0.02	-0.73	0.20
		11	<i>Bacteroides uniformis</i>	0.02	-0.81	0.05	-0.93	0.31	-0.75	0.12	0.23	0.07	0.40	-0.01	0.34	-0.08	-0.21	0.28
	Rikenellaceae	13	<i>Alistipes onderdonkii</i>	0.00	1.40	0.46	2.48	-0.45	1.46	-0.51	0.03	-0.03	0.00	0.00	0.21	-0.21	0.22	-0.22
Firmicutes	Lactobacillaceae	19	<i>Lactobacillus fermentum</i>	0.00	2.41	-0.22	2.52	-0.36	2.16	-0.27	0.00	0.00	0.00	0.00	0.37	-0.37	1.56	-1.56
	Lachnospiraceae	10	<i>Blautia faecis</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
		23	<i>butyrate-producing</i> SR1/5	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
		16	<i>Dorea longicatena</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
		17	<i>Clostridium boltea</i> /clostridioforme	0.00	0.07	0.18	0.00	0.00	0.19	-0.13	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00
	Ruminococcaceae	12	<i>Faecalibacterium prausnitzii</i>	0.06	-1.07	0.16	-0.77	-0.03	-0.82	-0.13	-0.12	0.05	-0.07	0.05	-0.58	0.04	-0.87	0.34
		8	<i>Faecalibacterium prausnitzii</i>	0.02	0.00	0.05	-0.01	0.21	0.11	-0.12	1.91	0.55	1.87	0.57	1.48	0.08	0.51	0.93
	Veillonellaceae	18	<i>Dialister succinatiphilus</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria	Burkholderiaceae	3	<i>Sutterella wadsworthensis</i>	-0.01	0.34	-0.30	0.03	0.36	0.28	-0.02	1.62	-0.04	1.62	-0.07	1.52	0.05	0.85	0.73
	Enterobacteriaceae	1	<i>Escherichia coli</i>	0.01	0.09	0.03	0.07	0.00	0.10	0.06	0.19	-0.06	0.14	0.01	0.09	0.05	0.10	-0.01

Table S7. Changes of microbial abundances at family level (log(cells/mL)) as detected via quantitative 16S-targeted Illumina sequencing at the end of the colonic incubation (48h) upon dosing BB-12 and/or seven fructans with short (OF1, OF2), intermediate (OF/IN1, OF/IN2) and high degree of polymerization (IN1, IN2 and IN3) to the complex microbiota of donor D. The values represent average differences versus the respective reference (for fructans, the reference was the untreated blank, while for conditions with BB-12 addition this was the respective condition where BB-12 was not dosed) at the end of the colonic incubation. For optimal visualization, increases due to treatment are highlighted with grey shading, with significant changes being indicated in bold (n = 3).

Phylum	Family	OTU#	Related species	Blank	OF1		OF2		OF/IN1		OF/IN2		IN1		IN2		IN3	
				BB-12	-	BB-12	-	BB-12	-	BB-12	-	BB-12	-	BB-12	-	BB-12	-	BB-12
Actinobacteria	Bifidobacteriaceae	2	<i>Bifidobacterium adolescentis</i>	-0.05	1.39	-0.75	1.48	-0.65	0.83	-0.42	0.81	-0.50	0.35	-0.15	0.40	-0.17	0.54	-0.32
		5	<i>Bifidobacterium animalis</i>	2.31	0.00	3.24	0.00	3.28	0.00	3.07	0.00	3.17	0.00	2.93	0.00	3.05	0.00	3.04
		21	<i>Bifidobacterium longum</i>	-0.08	1.15	-0.68	1.33	-0.76	0.68	-0.56	0.10	-0.08	-0.01	0.00	-0.03	-0.27	0.00	-0.25
	Coriobacteriaceae	20	<i>Collinsella aerofaciens</i>	-0.29	-0.27	0.04	0.30	-0.43	-0.03	-0.21	-0.04	-0.03	-0.54	0.15	-0.55	0.27	-0.11	0.02
	Eggerthellaceae	4	<i>Senegalimassilia sp.</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
		7	<i>Ellagibacter isourolithinifaciens</i>	-0.12	0.71	0.62	0.53	0.75	1.38	-0.19	0.70	0.39	0.92	0.11	0.85	0.25	1.06	0.22
Bacteroidetes	Bacteroidaceae	9	<i>Bacteroides caccae</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
		6	<i>Bacteroides dorei</i>	0.02	-1.54	0.04	-1.40	-0.01	-0.77	-0.11	-1.22	0.50	-0.64	0.11	-0.60	0.15	-0.57	0.12
		11	<i>Bacteroides uniformis</i>	-0.03	-0.69	-0.24	-0.67	-0.24	-0.83	-0.05	0.22	-0.25	0.07	-0.26	-0.40	0.05	-0.09	-0.44
	Rikenellaceae	13	<i>Alistipes onderdonkii</i>	-0.20	1.33	0.10	1.43	0.15	1.52	-0.08	1.36	0.30	1.36	0.01	1.29	0.22	1.41	0.21
Firmicutes	Lactobacillaceae	19	<i>Lactobacillus fermentum</i>	0.00	0.96	0.77	0.00	2.09	0.33	0.38	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	Lachnospiraceae	10	<i>Blautia faecis</i>	0.36	-1.24	0.00	-1.17	-0.08	-0.52	-0.44	0.68	0.13	1.33	-0.45	1.08	-0.40	1.18	-0.21
		23	<i>butyrate-producing SR1/5</i>	-0.04	-0.17	0.00	-0.17	0.00	0.09	-0.26	-0.17	0.00	-0.17	0.00	-0.17	0.00	-0.17	0.00
		16	<i>Dorea longicatena</i>	-0.47	-0.95	0.00	-0.95	0.00	-0.95	0.00	-0.95	0.07	-0.93	0.00	-0.95	0.09	-0.92	0.00
		17	<i>Clostridium bolteae/clostridioforme</i>	-0.17	-1.55	-0.20	-1.19	-0.42	-0.52	-0.01	0.89	-0.07	0.51	0.29	0.88	-0.20	0.57	0.02
	Ruminococcaceae	12	<i>Faecalibacterium prausnitzii</i>	-0.05	0.01	-0.35	-0.04	-0.40	-0.27	-0.01	-0.23	0.41	-0.12	0.22	-0.21	-0.02	-0.30	0.04
		8	<i>Faecalibacterium prausnitzii</i>	-0.18	-0.43	-0.59	-0.09	-0.63	-0.37	0.08	0.78	-0.12	0.94	0.09	0.50	0.83	0.73	-0.69
	Veillonellaceae	18	<i>Dialister succinatiphilus</i>	0.17	1.20	-0.05	1.41	-0.35	1.79	-0.19	1.93	-0.08	1.92	0.00	1.94	-0.03	2.02	-0.13
Proteobacteria	Burkholderiaceae	3	<i>Sutterella wadsworthensis</i>	0.14	1.06	-0.22	0.97	-0.33	1.12	0.06	1.55	-0.16	1.44	-0.07	1.45	-0.16	1.45	-0.07
	Enterobacteriaceae	1	<i>Escherichia coli</i>	-0.06	-0.19	-0.26	-0.12	-0.36	0.10	-0.47	-0.26	-0.08	-0.26	0.04	0.05	-0.26	-0.13	-0.09

Table S8. Changes of microbial abundances at family level (log(cells/mL)) as detected via quantitative 16S-targeted Illumina sequencing at the end of the colonic incubation (48h) upon dosing BB-12 and/or seven fructans with short (OF1, OF2), intermediate (OF/IN1, OF/IN2) and high degree of polymerization (IN1, IN2 and IN3) to the complex microbiota of donor F. The values represent average differences versus the respective reference (for fructans, the reference was the untreated blank, while for conditions with BB-12 addition this was the respective condition where BB-12 was not dosed) at the end of the colonic incubation. For optimal visualization, increases due to treatment are highlighted with grey shading, with significant changes being indicated in bold (n = 3).

Phylum	Family	OTU#	Related species	Blank	OF1		OF2		OF/IN1		OF/IN2		IN1		IN2		IN3	
				BB-12	-	BB-12	-	BB-12	-	BB-12	-	BB-12	-	BB-12	-	BB-12	-	BB-12
Actinobacteria	Bifidobacteriaceae	2	<i>Bifidobacterium adolescentis</i>	-0.20	0.72	0.01	0.69	-0.10	0.84	0.04	0.95	-0.01	1.06	-0.05	0.99	-0.09	0.98	-0.02
		5	<i>Bifidobacterium animalis</i>	2.29	0.00	3.12	0.00	2.86	0.00	3.07	0.00	2.85	0.00	2.71	0.00	2.72	0.00	2.83
		21	<i>Bifidobacterium longum</i>	-0.09	1.48	-0.28	1.58	-0.27	1.42	-0.38	0.88	-0.37	0.72	-0.26	1.02	-0.28	1.02	-0.32
	Coriobacteriaceae	20	<i>Collinsella aerofaciens</i>	-0.22	0.45	0.76	0.18	0.62	0.65	0.50	0.41	0.18	0.20	0.38	0.36	0.23	0.38	0.51
	Eggerthellaceae	4	<i>Senegalimassilia</i> sp.	-0.01	0.37	0.26	0.48	0.12	0.40	0.19	0.68	-0.06	0.46	-0.04	0.49	0.02	0.53	0.21
		7	<i>Ellagibacter isourolithinifaciens</i>	-0.01	1.42	0.21	1.37	0.01	1.57	0.13	1.47	-0.06	1.35	0.01	1.49	-0.04	1.46	0.11
Bacteroidetes	Bacteroidaceae	9	<i>Bacteroides caccae</i>	-0.10	-0.44	0.06	-0.36	0.09	-0.13	0.18	0.93	0.19	1.48	-0.04	1.11	-0.25	1.07	-0.21
		6	<i>Bacteroides dorei</i>	-0.18	-0.26	0.13	-0.51	0.19	-0.22	0.27	-0.09	-0.04	-0.45	-0.02	-0.31	0.05	-0.08	-0.08
		11	<i>Bacteroides uniformis</i>	-0.08	-0.67	0.21	-0.54	0.00	-0.55	0.22	-0.23	0.07	-0.11	0.18	-0.28	0.00	-0.21	0.00
	Rikenellaceae	13	<i>Alistipes onderdonkii</i>	-0.04	-0.83	0.06	-0.61	-0.13	-0.85	-0.03	-0.93	-0.07	-0.97	0.11	-0.85	-0.18	-0.78	-0.10
Firmicutes	Lactobacillaceae	19	<i>Lactobacillus fermentum</i>	0.00	2.44	-0.26	2.75	-0.06	2.27	-0.10	0.54	-0.24	0.05	-0.05	1.05	-0.46	0.87	0.01
	Lachnospiraceae	10	<i>Blautia faecis</i>	-0.04	0.32	0.00	0.33	-0.01	0.37	-0.16	0.67	0.02	0.70	0.00	0.58	0.04	0.55	-0.01
		23	<i>butyrate-producing SR1/5</i>	0.05	0.22	0.03	0.42	-0.08	0.49	-0.14	0.83	0.12	0.93	-0.04	1.07	0.00	0.87	-0.13
		16	<i>Dorea longicatena</i>	0.07	0.16	0.14	-0.28	0.23	0.06	0.16	0.25	0.34	0.44	-0.08	0.04	0.16	0.22	0.04
		17	<i>Clostridium bolteae/clostridioforme</i>	-0.02	-0.07	0.29	-1.22	0.35	0.06	0.28	-0.05	0.05	0.11	-0.11	-0.18	0.09	0.20	0.02
	Ruminococcaceae	12	<i>Faecalibacterium prausnitzii</i>	0.15	-0.28	0.31	-0.47	0.34	-0.19	0.18	-0.35	0.47	-0.12	0.17	-0.14	0.15	-0.19	0.28
		8	<i>Faecalibacterium prausnitzii</i>	0.17	1.19	-0.17	0.97	0.23	1.11	-0.02	1.15	-0.27	0.87	0.07	1.29	-0.15	1.23	-0.37
	Veillonellaceae	18	<i>Dialister succinatiphilus</i>	0.01	-0.58	0.20	-0.41	0.13	-0.35	0.03	-0.08	0.13	-0.22	0.33	-0.06	0.07	-0.18	0.14
Proteobacteria	Burkholderiaceae	3	<i>Sutterella wadsworthensis</i>	0.04	0.01	0.14	-0.04	0.11	0.02	0.10	0.03	0.15	0.04	0.09	0.00	0.15	0.02	0.21
	Enterobacteriaceae	1	<i>Escherichia coli</i>	-0.02	-0.49	-0.49	-0.58	-0.41	-0.42	-0.51	-0.55	-0.48	-0.52	-0.37	-0.61	-0.44	-0.37	-0.46