

Effects of fructan and gluten on gut microbiota in individuals with self-reported non-celiac gluten/wheat sensitivity – a randomised controlled crossover trial, Herfindal AM *et al.*

Table S1. Content of muesli bars used for the 7-day gluten, FOS-fructan, and placebo challenges in g per 100 g. FOS, fructo-oligosaccharides.

Ingredient	Gluten	FOS-fructan	Placebo
Maple syrup	15.4	12.8	16.8
Rice malt	14.9	16.4	16.4
Quinoa flour	0	15.5	15.6
Soft brown sugar	14.1	15.4	15.4
Sesame seeds	6.8	7.7	7.7
Pecans	6.4	7.3	7.3
Quinoa flakes	4.6	5.4	5.4
Pepitas	4.6	5.4	5.4
Puffed quinoa	3.3	3.9	3.9
Macadamia oil	2.7	3.1	3.1
Rice puffs	2.5	3	3
Gluten flour*	15.2	0	0
White chia seeds	9.6	0	0
Fructose	0	0.2	0
Galacto-oligosaccharides (GOS)	0	0.1	0
Fructo-oligosaccharides (FOS)	0	3.8	0

* The gluten flour contained 75% gluten. Thus, 15.2 g gluten flour contained 11.4 g gluten.

Table S2. Primers modified with Illumina adapters used for index PCR during library preparation for gene sequencing of 16S rRNA [27]. Unique combination of forward and reverse primer was used for each sample. FOS, fructo-oligosaccharides.

Primer name	Sequence, 5' → 3'	Target gene (region)	Direction
F1	aatgatacggcgaccaccgagatctacactctttccctacacgacgctcttccgata tagtcaaCCTACGGGRBGCASCAG	16S rRNA (V3-V4)	Forward
F2	aatgatacggcgaccaccgagatctacactctttccctacacgacgctcttccgata tagttccCCTACGGGRBGCASCAG	16S rRNA (V3-V4)	Forward
F3	aatgatacggcgaccaccgagatctacactctttccctacacgacgctcttccgata tatgtcaCCTACGGGRBGCASCAG	16S rRNA (V3-V4)	Forward
F4	aatgatacggcgaccaccgagatctacactctttccctacacgacgctcttccgata tccgtccCCTACGGGRBGCASCAG	16S rRNA (V3-V4)	Forward
F5	aatgatacggcgaccaccgagatctacactctttccctacacgacgctcttccgata ttagagCCTACGGGRBGCASCAG	16S rRNA (V3-V4)	Forward
F6	aatgatacggcgaccaccgagatctacactctttccctacacgacgctcttccgata tgtccgcCCTACGGGRBGCASCAG	16S rRNA (V3-V4)	Forward
F7	aatgatacggcgaccaccgagatctacactctttccctacacgacgctcttccgata tgtgaaaCCTACGGGRBGCASCAG	16S rRNA (V3-V4)	Forward
F8	aatgatacggcgaccaccgagatctacactctttccctacacgacgctcttccgata tgtggccCCTACGGGRBGCASCAG	16S rRNA (V3-V4)	Forward
F9	aatgatacggcgaccaccgagatctacactctttccctacacgacgctcttccgata tgtttcgCCTACGGGRBGCASCAG	16S rRNA (V3-V4)	Forward
F10	aatgatacggcgaccaccgagatctacactctttccctacacgacgctcttccgata tcgtacgCCTACGGGRBGCASCAG	16S rRNA (V3-V4)	Forward
F11	aatgatacggcgaccaccgagatctacactctttccctacacgacgctcttccgata tgagtggCCTACGGGRBGCASCAG	16S rRNA (V3-V4)	Forward
F12	aatgatacggcgaccaccgagatctacactctttccctacacgacgctcttccgata tggtagcCCTACGGGRBGCASCAG	16S rRNA (V3-V4)	Forward
F13	aatgatacggcgaccaccgagatctacactctttccctacacgacgctcttccgata tactgatCCTACGGGRBGCASCAG	16S rRNA (V3-V4)	Forward
F14	aatgatacggcgaccaccgagatctacactctttccctacacgacgctcttccgata tatgagcCCTACGGGRBGCASCAG	16S rRNA (V3-V4)	Forward
F15	aatgatacggcgaccaccgagatctacactctttccctacacgacgctcttccgata tattcctCCTACGGGRBGCASCAG	16S rRNA (V3-V4)	Forward
F16	aatgatacggcgaccaccgagatctacactctttccctacacgacgctcttccgata tcaaaagCCTACGGGRBGCASCAG	16S rRNA (V3-V4)	Forward
R1	caagcagaagacggcatacagatCGTGATgtgactggagttcagacgtgt gctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R2	caagcagaagacggcatacagatACATCGgtgactggagttcagacgtgt gctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R3	caagcagaagacggcatacagatGCCTAAgtgactggagttcagacgtgt gctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R4	caagcagaagacggcatacagatTGGTCAGtgactggagttcagacgtgt gctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R5	caagcagaagacggcatacagatCACTCTgtgactggagttcagacgtgt gctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R6	caagcagaagacggcatacagatATTGGCgtgactggagttcagacgtgt gctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R7	caagcagaagacggcatacagatGATCTGgtgactggagttcagacgtgt gctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse

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R8	caagcagaagacggcatacagagatTCAAGTgtgactggagttcagacgtgt gctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R9	caagcagaagacggcatacagagatCTGATCgtgactggagttcagacgtgt gctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R10	caagcagaagacggcatacagagatAAGCTAgtgactggagttcagacgtgt gctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R11	caagcagaagacggcatacagagatTAGCCgtgactggagttcagacgtgt gctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R12	caagcagaagacggcatacagagatTACAAGgtgactggagttcagacgtgt gctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R13	caagcagaagacggcatacagagatTTGACTgtgactggagttcagacgtgt gctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R14	caagcagaagacggcatacagagatGGAAGTgtgactggagttcagacgtgt gctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R15	caagcagaagacggcatacagagatTGACATgtgactggagttcagacgtgt gctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R16	caagcagaagacggcatacagagatGGACGGgtgactggagttcagacgtg tgctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R17	caagcagaagacggcatacagagatCTCTACgtgactggagttcagacgtgt gctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R18	caagcagaagacggcatacagagatGCGGACgtgactggagttcagacgtgt gctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R19	caagcagaagacggcatacagagatTTTCACgtgactggagttcagacgtgt gctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R20	caagcagaagacggcatacagagatGGCCACgtgactggagttcagacgtgt gctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R21	caagcagaagacggcatacagagatCGAAACgtgactggagttcagacgtgt gctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R22	caagcagaagacggcatacagagatCGTACGgtgactggagttcagacgtgt gctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R23	caagcagaagacggcatacagagatCCACTCgtgactggagttcagacgtgt gctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R24	caagcagaagacggcatacagagatGCTACCgtgactggagttcagacgtgt gctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R25	caagcagaagacggcatacagagatATCAGTgtgactggagttcagacgtgt gctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R26	caagcagaagacggcatacagagatGCTCATgtgactggagttcagacgtgt gctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R27	caagcagaagacggcatacagagatAGGAATgtgactggagttcagacgtgt gctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R28	caagcagaagacggcatacagagatCTTTTGgtgactggagttcagacgtgt gctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse
R29	caagcagaagacggcatacagagatTAGTTGgtgactggagttcagacgtgt gctcttccgatctGGACTACYVGGGTATCTAAT	16S rRNA (V3-V4)	Reverse

Table S3. Changes in faecal α -diversity following the 7-day gluten, FOS-fructan, and placebo challenges ($n = 57$)*

	Gluten	FOS-fructan	Placebo	Challenge
	EMM (CI)	EMM (CI)	EMM (CI)	P value†
Observed number of OTUs	2.0 (-3.2,7.2)	-2.3 (-7.4,2.8)	2.0 (-3.2,7.2)	0.20
Chao1 index	3.6 (-3.4,11)	0.98 (-5.9,7.9)	3.9 (-3.1,11)	0.68
Shannon-Wiener index	0.059 (-0.013,0.13)	-0.031 (-0.10,0.040)	0.005 (-0.067,0.077)	0.11
Simpson index	0.004 (-0.001,0.008)	-0.002 (-0.006,0.002)	-0.000 (-0.004,0.004)	0.15
PD whole tree index	0.30 (-0.12,0.72)	0.001 (-0.41,0.41)	0.20 (-0.22,0.62)	0.42

*Changes in α -diversity indices from baseline to diet challenge follow-ups are presented as estimated marginal means (EMM) (95% confidence intervals [CI]) from linear mixed models with change values as response variable and baseline values, period, sequence, and diet challenge as explanatory variables. Change-values for each diet challenge were calculated for each participant by subtracting the baseline value from the follow-up value (i.e., positive value: increased, negative value: decreased). Among the fifty-seven participants included in the analyses, two participants only had α -diversity data from the FOS-fructan challenge, and one participant was missing α -diversity data from the gluten challenge. FOS, fructo-oligosaccharides.

† P value for the main effect of diet challenge from linear mixed model. Since no significant differences were found across diet challenges ($P \geq 0.05$), pairwise comparisons between three diet challenges were not performed.

Table S4. Summary statistics for faecal bacterial α -diversity at baseline ($n = 58$) and after the 7-day FOS-fructan ($n = 57$), gluten ($n = 54$), and placebo ($n = 55$) challenges. Summary statistics include means with SD, medians with 25th and 75th percentile, minimum value, and maximum value. The one participant that was missing baseline 16S data, and therefore excluded from all the other statistical analyses (see section 3.1 in main text), was not included in the summary statistics. FOS, fructo-oligosaccharides.

	Baseline/ diet challenge	Mean $\pm$ SD	Median [Q1,Q3]	Minimum	Maximum
Observed number of OTUs	Baseline	208 $\pm$ 45	204 [176,236]	97	301
Observed number of OTUs	FOS-fructan	205 $\pm$ 45	202 [181,240]	105	285
Observed number of OTUs	Gluten	209 $\pm$ 40	215 [179,236]	110	304
Observed number of OTUs	Placebo	208 $\pm$ 45	214 [168,235]	103	322
Chao1 index	Baseline	269 $\pm$ 57	272 [227,297]	126	391
Chao1 index	FOS-fructan	269 $\pm$ 55	260 [234,318]	160	365
Chao1 index	Gluten	272 $\pm$ 50	277 [236,305]	137	399
Chao1 index	Placebo	271 $\pm$ 59	277 [221,308]	152	424
Shannon-Wiener index	Baseline	5.40 $\pm$ 0.50	5.40 [5.12,5.77]	4.04	6.34
Shannon-Wiener index	FOS-fructan	5.35 $\pm$ 0.52	5.40 [5.02,5.74]	3.81	6.25
Shannon-Wiener index	Gluten	5.45 $\pm$ 0.45	5.52 [5.06,5.79]	4.43	6.43
Shannon-Wiener index	Placebo	5.38 $\pm$ 0.50	5.46 [5.00,5.80]	4.34	6.28
Simpson index	Baseline	0.95 $\pm$ 0.02	0.95 [0.94,0.96]	0.87	0.98
Simpson index	FOS-fructan	0.95 $\pm$ 0.03	0.95 [0.94,0.96]	0.80	0.98
Simpson index	Gluten	0.95 $\pm$ 0.02	0.96 [0.94,0.97]	0.90	0.98
Simpson index	Placebo	0.95 $\pm$ 0.02	0.95 [0.93,0.96]	0.86	0.98
PD whole tree index	Baseline	18 $\pm$ 3.68	18 [15,21]	11	26
PD whole tree index	FOS-fructan	18 $\pm$ 3.89	18 [15,22]	10	26
PD whole tree index	Gluten	18 $\pm$ 3.39	18 [16,21]	11	26
PD whole tree index	Placebo	18 $\pm$ 3.75	19 [15,21]	11	27

Table S5. Changes in faecal bacterial abundances following the 7-day gluten, FOS-fructan, and placebo challenges ($n = 57$)*

	Gluten	FOS-fructan	Placebo	Challenge
	EMM (CI)	EMM (CI)	EMM (CI)	P value†
<i>c_Actinobacteria</i>	0.037 (-0.069,0.14)	0.14 (0.038,0.25)	0.072 (-0.034,0.18)	0.23
<i>f_Bifidobacteriaceae</i>	0.033 (-0.074,0.14)	0.14 (0.033,0.24)	0.066 (-0.041,0.17)	0.24
<i>g_Bifidobacterium</i>	0.033 (-0.074,0.14)	0.14 (0.034,0.24)	0.065 (-0.041,0.17)	0.23
<i>g_Anaerostipes</i>	0.092 (-0.021,0.20)	0.15 (0.042,0.26)	0.044 (-0.068,0.16)	0.24
<i>g_Faecalibacterium</i>	0.044 (-0.12,0.21)	0.23 (0.065,0.39)	0.041 (-0.12,0.21)	0.10
<i>g_Sutterella</i>	0.018 (-0.079,0.11)	0.10 (0.005,0.20)	0.060 (-0.036,0.16)	0.14
<i>g_Lachnospiraceae NK4A136 group</i>	-0.041 (-0.13,0.046)	-0.090 (-0.18,-0.004)	-0.018 (-0.11,0.069)	0.21
<i>g_Subdoligranulum</i>	-0.049 (-0.14,0.044)	-0.11 (-0.20,-0.016)	-0.059 (-0.15,0.034)	0.53
<i>c_Bacilli</i>	-0.16 (-0.28,-0.029)	-0.043 (-0.17,0.081)	-0.091 (-0.22,0.035)	0.19
<i>o_Lactobacillales</i>	-0.15 (-0.28,-0.028)	-0.040 (-0.16,0.083)	-0.089 (-0.21,0.037)	0.18
<i>f_Streptococcaceae</i>	-0.16 (-0.28,-0.045)	-0.068 (-0.18,0.046)	-0.080 (-0.20,0.034)	0.15
<i>g_Streptococcus</i>	-0.14 (-0.25,-0.025)	-0.059 (-0.17,0.053)	-0.090 (-0.20,0.023)	0.27
<i>g_Phascolarctobacterium</i>	0.047 (0.002,0.093)	0.035 (-0.009,0.079)	0.008 (-0.038,0.053)	0.37
<i>g_Lachnospiraceae ND3007 group</i>	0.063 (0.004,0.12)	0.086 (0.028,0.14)	0.030 (-0.029,0.089)	0.25
<i>g_Enterorhabdus</i>	-0.044 (-0.080,-0.008)	-0.041 (-0.077,-0.005)	-0.039 (-0.075,-0.003)	0.94
<i>f_Erysipelotrichaceae</i>	-0.089 (-0.15,-0.026)	-0.070 (-0.13,-0.007)	-0.083 (-0.15,-0.020)	0.81
<i>g_Unknown Coriobacteriaceae</i>	-0.024 (-0.076,0.029)	-0.032 (-0.084,0.019)	-0.055 (-0.11,-0.003)	0.45
<i>g_Eubacterium ventriosum group</i>	0.023 (-0.058,0.11)	0.067 (-0.013,0.15)	0.083 (0.002,0.16)	0.39
<i>g_Roseburia</i>	0.044 (-0.060,0.15)	0.068 (-0.034,0.17)	0.14 (0.036,0.24)	0.30
<i>g_Ruminiclostridium5</i>	0.021 (-0.056,0.098)	-0.001 (-0.076,0.073)	-0.093 (-0.17,-0.017)	0.07
<i>g_Ruminiclostridium9</i>	0.026 (-0.004,0.056)	-0.004 (-0.034,0.025)	0.030 (0.000,0.060)	0.09
<i>g_Ruminococcaceae UCG-003</i>	0.040 (-0.018,0.097)	-0.001 (-0.057,0.055)	0.074 (0.018,0.13)	0.05

*Only the taxa that displayed notable change from baseline to follow-up for at least one diet challenge, but without significant difference across diet challenges are included in the table. For taxa with across-challenge differences, see section 3.4 and Table 2 in main text. Changes in bacterial abundances from baseline to diet challenge follow-ups are presented as estimated marginal means (EMM) (95% confidence intervals [CI]) from linear mixed models with change values as response variable and baseline values, period, sequence, and diet challenge as explanatory variables. Change-values for each diet challenge were calculated for each participant by subtracting the baseline value from the follow-up value (i.e., positive value: increased, negative value: decreased). Follow-up and baseline values were sqrt-transformed, i.e., a change value is the sqrt-transformed follow-up value minus the sqrt-transformed baseline value for a given participant/challenge. Of the fifty-seven participants included in the analyses, two participants only had abundance data from the FOS-fructan challenge, and one participant was missing abundance data from the gluten challenge. FOS, fructo-oligosaccharides.

† P value for the main effect of diet challenge from linear mixed model. Since no significant differences were found across diet challenges ($P \geq 0.05$), pairwise comparisons between the three diet challenges were not performed.

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Table S6. Summary statistics for faecal bacterial abundances (%) of at baseline (“B”; $n = 58$) and after the 7-day FOS-fructan (“F”; $n = 57$), gluten (“G”; $n = 54$), and placebo (“P”; $n = 55$) challenges. Summary statistics include means with SD, medians with 25th and 75th percentile, minimum value, maximum value, detection rate (i.e., in how many samples the taxon was detected out of total number of samples with 16S data). The one participant that was missing baseline 16S data, and therefore excluded from all the other statistical analyses (see section 3.1 in main text), was not included in the summary statistics. FOS, fructo-oligosaccharides.

	Mean±SD				Median[Q1,Q3]				Minimum				Maximum				Detected in			
	B	F	G	P	B	F	G	P	B	F	G	P	B	F	G	P	B	F	G	P
<i>k_Archaea</i>	0.17±0.30	0.16±0.34	0.23±0.49	0.19±0.35	0.00[0.00,0.22]	0.00[0.00,0.15]	0.01[0.00,0.31]	0.00[0.00,0.26]	0.00	0.00	0.00	0.00	1.1	1.9	2.9	1.4	26/58	25/57	28/54	24/55
<i>p_Euryarchaeota</i>	0.17±0.30	0.16±0.34	0.23±0.49	0.19±0.35	0.00[0.00,0.22]	0.00[0.00,0.15]	0.01[0.00,0.31]	0.00[0.00,0.26]	0.00	0.00	0.00	0.00	1.1	1.9	2.9	1.4	26/58	25/57	28/54	24/55
<i>c_Methanobacteria</i>	0.17±0.30	0.16±0.35	0.23±0.49	0.18±0.35	0.00[0.00,0.22]	0.00[0.00,0.15]	0.01[0.00,0.31]	0.00[0.00,0.21]	0.00	0.00	0.00	0.00	1.1	1.9	2.9	1.4	25/58	24/57	28/54	23/55
<i>o_Methanobacteriales</i>	0.17±0.30	0.16±0.35	0.23±0.49	0.18±0.35	0.00[0.00,0.22]	0.00[0.00,0.15]	0.01[0.00,0.31]	0.00[0.00,0.21]	0.00	0.00	0.00	0.00	1.1	1.9	2.9	1.4	25/58	24/57	28/54	23/55
<i>f_Methanobacteriaceae</i>	0.17±0.30	0.16±0.35	0.23±0.49	0.18±0.35	0.00[0.00,0.22]	0.00[0.00,0.15]	0.01[0.00,0.31]	0.00[0.00,0.21]	0.00	0.00	0.00	0.00	1.1	1.9	2.9	1.4	25/58	24/57	28/54	23/55
<i>g_Methanobrevibacter</i>	0.17±0.29	0.15±0.33	0.22±0.47	0.18±0.34	0.00[0.00,0.21]	0.00[0.00,0.15]	0.01[0.00,0.31]	0.00[0.00,0.21]	0.00	0.00	0.00	0.00	1.1	1.9	2.9	1.4	25/58	24/57	27/54	23/55
<i>g_Methanosphaera</i>	0.01±0.03	0.01±0.04	0.02±0.09	0.01±0.04	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	0.00	0.21	0.25	0.61	0.28	3/58	2/57	4/54	3/55
<i>c_Thermoplasmata</i>	0.00±0.00	0.00±0.01	0.00±0.00	0.00±0.02	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	0.00	0.01	0.03	0.00	0.11	2/58	4/57	0/54	3/55
<i>o_Thermoplasmatales</i>	0.00±0.00	0.00±0.01	0.00±0.00	0.00±0.02	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	0.00	0.01	0.03	0.00	0.11	2/58	4/57	0/54	3/55
<i>f_ThermoplasmatalesIncertaeSedis</i>	0.00±0.00	0.00±0.01	0.00±0.00	0.00±0.02	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	0.00	0.01	0.03	0.00	0.11	2/58	4/57	0/54	3/55
<i>g_Methanomassiliicoccus</i>	0.00±0.00	0.00±0.01	0.00±0.00	0.00±0.02	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	0.00	0.01	0.03	0.00	0.11	2/58	4/57	0/54	3/55
<i>k_Bacteria</i>	100±0.30	100±0.35	100±0.49	100±0.35	100[100,100]	100[100,100]	100[100,100]	100[100,100]	99	98	97	99	100	100	100	100	58/58	57/57	54/54	55/55
<i>p_Actinobacteria</i>	1.6±1.1	1.8±1.7	1.6±1.5	1.6±1.5	1.4[0.71,2.2]	1.4[0.67,2.5]	1.3[0.78,2.1]	1.2[0.62,1.9]	0.08	0.10	0.17	0.09	4.2	9.3	9.1	8.6	58/58	57/57	54/54	55/55
<i>c_Actinobacteria</i>	0.53±0.70	0.87±1.5	0.66±1.3	0.71±1.2	0.22[0.03,0.86]	0.33[0.05,0.97]	0.29[0.05,0.78]	0.30[0.03,0.77]	0.00	0.00	0.00	0.00	3.6	7.5	7.2	6.8	52/58	52/57	50/54	52/55
<i>o_Actinomycetales</i>	0.00±0.00	0.00±0.01	0.00±0.00	0.00±0.01	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	0.00	0.02	0.05	0.01	0.04	6/58	7/57	2/54	8/55
<i>f_Actinomycetales</i>	0.00±0.00	0.00±0.01	0.00±0.00	0.00±0.01	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	0.00	0.02	0.05	0.01	0.04	6/58	7/57	2/54	8/55
<i>g_Actinomyces</i>	0.00±0.00	0.00±0.00	0.00±0.00	0.00±0.01	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	0.00	0.02	0.02	0.01	0.04	5/58	7/57	2/54	7/55
<i>g_Arcanobacterium</i>	0.00±0.00	0.00±0.01	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[0.00,0.00]	0.00	0.00	0.00	0.00	0.01	0.04	0.00	0.00	1/58	1/57	0/54	0/55
<i>g_Varibaculum</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0/58	0/57	0/54	1/55
<i>o_Bifidobacteriales</i>	0.52±0.70	0.87±1.5	0.65±1.3	0.71±1.2	0.21[0.03,0.86]	0.32[0.04,0.97]	0.29[0.05,0.77]	0.30[0.03,0.77]	0.00	0.00	0.00	0.00	3.6	7.5	7.2	6.8	52/58	51/57	49/54	49/55
<i>f_Bifidobacteriaceae</i>	0.52±0.70	0.87±1.5	0.65±1.3	0.71±1.2	0.21[0.03,0.86]	0.32[0.04,0.97]	0.29[0.05,0.77]	0.30[0.03,0.77]	0.00	0.00	0.00	0.00	3.6	7.5	7.2	6.8	52/58	51/57	49/54	49/55
<i>g_Bifidobacterium</i>	0.52±0.70	0.87±1.5	0.65±1.3	0.70±1.2	0.21[0.02,0.86]	0.32[0.04,0.97]	0.29[0.05,0.77]	0.30[0.03,0.77]	0.00	0.00	0.00	0.00	3.6	7.5	7.2	6.8	52/58	51/57	49/54	49/55
<i>g_Scardovia</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0/58	0/57	0/54	2/55
<i>g_unknown_Bifidobacteriaceae</i>	0.00±0.00	0.00±0.00	0.00±0.01	0.00±0.02	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	0.00	0.02	0.01	0.05	0.11	1/58	2/57	2/54	1/55
<i>o_Corynebacteriales</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.00	0.02	0.01	0.00	0/58	2/57	3/54	0/55
<i>f_Corynebacteriaceae</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.00	0.02	0.01	0.00	0/58	2/57	3/54	0/55
<i>g_Corynebacterium</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0/58	1/57	3/54	0/55
<i>g_Corynebacterium1</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0/58	1/57	0/54	0/55
<i>o_Micrococcales</i>	0.00±0.00	0.00±0.00	0.00±0.01	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	0.00	0.00	0.00	0.01	0.02	0.02	0.02	3/58	4/57	6/54	4/55
<i>f_Micrococcaceae</i>	0.00±0.00	0.00±0.00	0.00±0.01	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	0.00	0.00	0.00	0.01	0.02	0.02	0.02	3/58	4/57	6/54	4/55
<i>g_Rothia</i>	0.00±0.00	0.00±0.00	0.00±0.01	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	0.00	0.00	0.00	0.01	0.02	0.02	0.02	3/58	4/57	6/54	4/55
<i>c_Coriobacteriia</i>	1.1±0.80	0.95±0.68	0.97±0.64	0.93±0.85	0.85[0.41,1.6]	0.75[0.50,1.4]	0.76[0.55,1.2]	0.70[0.47,1.1]	0.07	0.04	0.09	0.03	3.5	3.1	3.2	4.6	58/58	57/57	54/54	55/55

Effects of fructan and gluten on gut microbiota in individuals with self-reported non-celiac gluten/wheat sensitivity – a randomised controlled crossover trial, Herfindal AM *et al.*

<i>o_Coriobacteriales</i>	1.1±0.80	0.95±0.68	0.97±0.64	0.93±0.85	0.85[0.41,1.6]	0.75[0.50,1.4]	0.76[0.55,1.2]	0.70[0.47,1.1]	0.07	0.04	0.09	0.03	3.5	3.1	3.2	4.6	58/58	57/57	54/54	55/55
<i>f_Coriobacteriaceae</i>	1.1±0.80	0.95±0.68	0.97±0.64	0.93±0.85	0.85[0.41,1.6]	0.75[0.50,1.4]	0.76[0.55,1.2]	0.70[0.47,1.1]	0.07	0.04	0.09	0.03	3.5	3.1	3.2	4.6	58/58	57/57	54/54	55/55
<i>g_Atopobium</i>	0.00±0.01	0.00±0.00	0.00±0.00	0.00±0.01	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	0.00	0.04	0.01	0.02	0.04	6/58	4/57	3/54	5/55
<i>g_Collinsella</i>	0.31±0.46	0.33±0.39	0.33±0.44	0.31±0.49	0.15[0.02,0.39]	0.22[0.05,0.48]	0.24[0.03,0.43]	0.19[0.04,0.35]	0.00	0.00	0.00	0.00	2.6	1.7	2.4	3.1	49/58	46/57	44/54	43/55
<i>g_CoriobacteriaceaeUCG-002</i>	0.00±0.02	0.00±0.03	0.00±0.02	0.00±0.01	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	0.00	0.15	0.21	0.13	0.05	1/58	1/57	1/54	1/55
<i>g_CoriobacteriaceaeUCG-003</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.02	0.01	0.00	0.00	1/58	1/57	0/54	0/55
<i>g_Eggerthella</i>	0.03±0.09	0.02±0.05	0.04±0.09	0.03±0.06	0.01[0.00,0.02]	0.00[0.00,0.02]	0.01[0.00,0.03]	0.01[0.00,0.02]	0.00	0.00	0.00	0.00	0.53	0.21	0.55	0.32	32/58	26/57	29/54	32/55
<i>g_Enorma</i>	0.00±0.00	0.00±0.01	0.00±0.01	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	0.00	0.00	0.00	0.03	0.03	0.04	0.02	1/58	2/57	2/54	1/55
<i>g_Enterorhabdus</i>	0.24±0.30	0.19±0.18	0.18±0.14	0.19±0.17	0.15[0.06,0.28]	0.15[0.04,0.24]	0.16[0.06,0.25]	0.14[0.04,0.33]	0.00	0.00	0.00	0.00	1.7	0.91	0.55	0.78	52/58	49/57	48/54	47/55
<i>g_Gordonibacter</i>	0.01±0.02	0.01±0.02	0.01±0.01	0.01±0.02	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00	0.00	0.00	0.00	0.06	0.09	0.06	0.09	16/58	20/57	25/54	20/55
<i>g_Olsenella</i>	0.00±0.01	0.00±0.01	0.00±0.01	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	0.00	0.00	0.00	0.07	0.06	0.05	0.02	1/58	1/57	2/54	2/55
<i>g_Senegalimassilia</i>	0.05±0.10	0.04±0.08	0.06±0.15	0.05±0.08	0.00[0.00,0.03]	0.00[0.00,0.05]	0.00[0.00,0.04]	0.00[0.00,0.06]	0.00	0.00	0.00	0.00	0.41	0.35	0.99	0.31	26/58	27/57	24/54	27/55
<i>g_Slackia</i>	0.02±0.07	0.02±0.06	0.03±0.08	0.02±0.06	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.02]	0.00[0.00,0.01]	0.00	0.00	0.00	0.00	0.45	0.39	0.44	0.44	15/58	15/57	14/54	16/55
<i>g_unknown_Coriobacteriaceae</i>	0.38±0.40	0.33±0.41	0.33±0.34	0.32±0.53	0.30[0.06,0.55]	0.23[0.07,0.46]	0.23[0.08,0.47]	0.18[0.04,0.33]	0.00	0.00	0.00	0.00	1.6	2.5	1.7	3.6	53/58	51/57	50/54	50/55
<i>p_Bacteroidetes</i>	34±11	35±9.0	34±7.8	35±8.5	34[28,40]	34[27,40]	35[30,39]	34[28,41]	3.7	19	9.5	18	58	59	50	60	58/58	57/57	54/54	55/55
<i>c_Bacteroidia</i>	34±11	35±9.0	34±7.8	35±8.5	34[28,40]	34[27,40]	35[30,39]	34[28,41]	3.7	19	9.5	18	58	59	50	60	58/58	57/57	54/54	55/55
<i>o_Bacteroidales</i>	34±11	35±9.0	34±7.8	35±8.5	34[28,40]	34[27,40]	35[30,39]	34[28,41]	3.7	19	9.5	18	58	59	50	60	58/58	57/57	54/54	55/55
<i>f_Bacteroidaceae</i>	21±11	21±9.1	21±9.2	22±9.9	20[14,29]	19[15,26]	22[15,28]	22[13,28]	1.8	1.2	1.1	1.6	48	50	45	48	58/58	57/57	54/54	55/55
<i>g_Bacteroides</i>	21±11	21±9.1	21±9.2	22±9.9	20[14,29]	19[15,26]	22[15,28]	22[13,28]	1.8	1.2	1.1	1.6	48	50	45	48	58/58	57/57	54/54	55/55
<i>f_BacteroidalesS24-7group</i>	1.3±2.8	1.5±3.3	1.3±2.8	1.3±3.3	0.01[0.00,0.52]	0.02[0.00,0.94]	0.02[0.00,0.99]	0.01[0.00,0.51]	0.00	0.00	0.00	0.00	13	15	13	19	30/58	39/57	38/54	35/55
<i>g_unknown_BacteroidalesS24-7group</i>	1.3±2.8	1.5±3.3	1.3±2.8	1.3±3.3	0.01[0.00,0.52]	0.02[0.00,0.94]	0.02[0.00,0.99]	0.01[0.00,0.51]	0.00	0.00	0.00	0.00	13	15	13	19	30/58	39/57	38/54	35/55
<i>f_Porphyromonadaceae</i>	4.6±3.5	4.7±3.2	4.8±3.0	4.4±3.1	4.0[2.3,6.5]	4.1[2.5,5.8]	4.8[2.7,6.1]	3.9[2.2,5.7]	0.19	0.42	0.19	0.23	22	15	17	16	58/58	57/57	54/54	55/55
<i>g_Barnesiella</i>	0.94±1.5	0.90±1.2	1.0±1.3	0.92±1.2	0.48[0.01,1.1]	0.48[0.01,1.5]	0.48[0.01,1.5]	0.39[0.01,1.5]	0.00	0.00	0.00	0.00	8.1	6.7	4.9	5.8	44/58	49/57	44/54	42/55
<i>g_Butyricimonas</i>	0.21±0.33	0.20±0.34	0.27±0.40	0.21±0.30	0.02[0.00,0.45]	0.05[0.00,0.29]	0.04[0.00,0.46]	0.02[0.00,0.40]	0.00	0.00	0.00	0.00	1.7	2.0	1.7	1.3	31/58	32/57	34/54	33/55
<i>g_Coproacter</i>	0.05±0.13	0.04±0.08	0.04±0.11	0.05±0.12	0.00[0.00,0.02]	0.00[0.00,0.04]	0.00[0.00,0.02]	0.00[0.00,0.03]	0.00	0.00	0.00	0.00	0.62	0.37	0.62	0.65	23/58	22/57	20/54	19/55
<i>g_Dysgonomonas</i>	0.00±0.01	0.00±0.00	0.00±0.00	0.00±0.01	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	0.00	0.05	0.01	0.02	0.05	1/58	1/57	1/54	1/55
<i>g_Odoribacter</i>	0.50±0.43	0.48±0.37	0.52±0.37	0.48±0.37	0.40[0.18,0.63]	0.42[0.25,0.64]	0.50[0.28,0.70]	0.46[0.18,0.70]	0.00	0.00	0.00	0.00	2.1	1.5	2.1	1.4	57/58	53/57	50/54	50/55
<i>g_Parabacteroides</i>	3.0±2.5	3.1±2.6	3.0±2.4	2.8±2.2	2.4[1.2,4.1]	2.7[1.2,4.1]	2.6[1.3,4.0]	2.2[1.3,3.8]	0.01	0.00	0.00	0.00	12	12	12	9.4	58/58	56/57	53/54	53/55
<i>g_Porphyromonas</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.01	1/58	2/57	0/54	1/55
<i>f_Prevotellaceae</i>	1.6±4.5	2.5±6.7	1.8±4.6	2.5±6.5	0.02[0.00,0.96]	0.04[0.01,2.0]	0.02[0.01,1.0]	0.02[0.01,1.9]	0.00	0.00	0.00	0.00	27	39	21	41	39/58	44/57	44/54	43/55
<i>g_Alloprevotella</i>	0.08±0.29	0.15±0.56	0.05±0.17	0.20±0.90	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	0.00	1.7	2.8	0.97	6.0	10/58	12/57	11/54	10/55
<i>g_Paraprevotella</i>	0.26±1.1	0.34±1.0	0.31±1.1	0.42±1.6	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00	0.00	0.00	0.00	7.6	5.2	7.9	11	16/58	19/57	16/54	15/55
<i>g_Prevotella</i>	0.00±0.01	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]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.03	0.02	0.01	0.01	5/58	4/57	8/54	5/55
<i>g_Prevotella2</i>	0.02±0.18	0.08±0.61	0.19±1.4	0.06±0.44	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	0.00	1.3	4.6	10	3.3	2/58	6/57	5/54	5/55
<i>g_Prevotella6</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.01	0.01	0.01	0.00	1/58	1/57	3/54	0/55
<i>g_Prevotella7</i>	0.07±0.40	0.05±0.30	0.08±0.44	0.04±0.21	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	0.00	2.9	2.2	3.2	1.3	6/58	5/57	4/54	5/55
<i>g_Prevotella9</i>	1.1±4.1	1.7±5.9	1.1±3.8	1.6±5.3	0.00[0.00,0.01]	0.01[0.00,0.03]	0.01[0.00,0.03]	0.01[0.00,0.03]	0.00	0.00	0.00	0.00	24	32	19	31	22/58	33/57	30/54	30/55
<i>g_PrevotellaceaeNK3B31group</i>	0.08±0.36	0.12±0.48	0.05±0.21	0.07±0.31	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	0.00	2.3	3.0	1.2	1.9	6/58	6/57	6/54	5/55
<i>g_PrevotellaceaeUCG-001</i>	0.01±0.07	0.03±0.19	0.08±0.52	0.02±0.15	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	0.00	0.53	1.5	3.8	1.1	4/58	3/57	2/54	3/55
<i>g_unknown_Prevotellaceae</i>	0.01±0.04	0.02±0.09	0.01±0.06	0.01±0.04	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	0.00	0.23	0.66	0.44	0.25	2/58	6/57	3/54	4/55

Effects of fructan and gluten on gut microbiota in individuals with self-reported non-celiac gluten/wheat sensitivity – a randomised controlled crossover trial, Herfindal AM *et al.*

<i>f_Rikenellaceae</i>	4.8±3.7	4.8±4.3	5.1±3.1	4.5±3.0	4.0[2.2,5.9]	3.8[2.2,6.6]	4.4[3.2,6.8]	4.0[2.2,6.2]	0.05	0.12	0.41	0.18	22	28	13	13	58/58	57/57	54/54	55/55
<i>g_Alistipes</i>	4.5±3.6	4.6±4.3	4.8±3.0	4.2±2.6	3.8[2.2,5.8]	3.7[2.1,5.8]	4.3[2.6,6.6]	3.6[2.2,6.0]	0.04	0.12	0.40	0.10	22	28	13	12	58/58	57/57	54/54	55/55
<i>g_Rikenella</i>	0.01±0.05	0.01±0.05	0.01±0.04	0.01±0.09	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	0.00	0.41	0.34	0.30	0.65	2/58	1/57	2/54	1/55
<i>g_RikenellaceaeRC9gutgroup</i>	0.24±1.2	0.19±1.1	0.30±1.5	0.28±1.5	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	0.00	8.4	8.4	9.6	10	9/58	7/57	10/54	10/55
<i>g_unknown_Bacteroidales</i>	0.01±0.08	0.01±0.03	0.02±0.11	0.01±0.06	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	0.00	0.52	0.12	0.79	0.41	4/58	4/57	6/54	4/55
<i>f_unknown_Bacteroidales</i>	0.01±0.08	0.01±0.03	0.02±0.11	0.01±0.06	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	0.00	0.52	0.12	0.79	0.41	4/58	4/57	6/54	4/55
<i>c_Flavobacteriia</i>	0.02±0.06	0.02±0.07	0.03±0.14	0.02±0.05	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	0.00	0.30	0.38	0.93	0.26	9/58	7/57	7/54	7/55
<i>o_Flavobacteriales</i>	0.02±0.06	0.02±0.07	0.03±0.14	0.02±0.05	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	0.00	0.30	0.38	0.93	0.26	9/58	7/57	7/54	7/55
<i>f_Flavobacteriaceae</i>	0.02±0.06	0.02±0.07	0.03±0.14	0.02±0.05	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	0.00	0.30	0.38	0.93	0.26	9/58	7/57	7/54	7/55
<i>g_Bergeyella</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	1/58	0/57	0/54	0/55
<i>g_unknown_Flavobacteriaceae</i>	0.02±0.06	0.02±0.07	0.03±0.14	0.02±0.05	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	0.00	0.30	0.38	0.93	0.26	8/58	7/57	7/54	7/55
<i>p_Cyanobacteria</i>	0.11±0.26	0.06±0.14	0.07±0.13	0.06±0.08	0.01[0.00,0.06]	0.00[0.00,0.07]	0.01[0.00,0.07]	0.01[0.00,0.09]	0.00	0.00	0.00	0.00	1.5	0.84	0.65	0.34	29/58	27/57	30/54	30/55
<i>c_Chloroplast</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.02	0.01	0.02	0.01	4/58	1/57	7/54	3/55
<i>o_Nicotianaotophora</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.02	0.01	0.01	0.01	4/58	1/57	6/54	3/55
<i>f_Nicotianaotophora</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.02	0.01	0.01	0.01	4/58	1/57	6/54	3/55
<i>g_Nicotianaotophora</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.02	0.01	0.01	0.01	4/58	1/57	6/54	3/55
<i>g_unknown_Chloroplast</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0/58	0/57	2/54	0/55
<i>f_unknown_Chloroplast</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0/58	0/57	2/54	0/55
<i>o_unknown_Chloroplast</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0/58	0/57	2/54	0/55
<i>c_Melainabacteria</i>	0.11±0.26	0.06±0.14	0.06±0.13	0.06±0.08	0.00[0.00,0.06]	0.00[0.00,0.07]	0.01[0.00,0.07]	0.01[0.00,0.09]	0.00	0.00	0.00	0.00	1.5	0.84	0.65	0.34	26/58	26/57	28/54	28/55
<i>o_Gastranaerophilales</i>	0.11±0.26	0.06±0.14	0.06±0.13	0.06±0.08	0.00[0.00,0.06]	0.00[0.00,0.07]	0.01[0.00,0.07]	0.01[0.00,0.09]	0.00	0.00	0.00	0.00	1.5	0.84	0.65	0.34	26/58	26/57	28/54	28/55
<i>g_unknown_Gastranaerophilales</i>	0.11±0.26	0.06±0.14	0.06±0.13	0.06±0.08	0.00[0.00,0.06]	0.00[0.00,0.07]	0.01[0.00,0.07]	0.01[0.00,0.09]	0.00	0.00	0.00	0.00	1.5	0.84	0.65	0.34	26/58	26/57	28/54	28/55
<i>f_unknown_Gastranaerophilales</i>	0.11±0.26	0.06±0.14	0.06±0.13	0.06±0.08	0.00[0.00,0.06]	0.00[0.00,0.07]	0.01[0.00,0.07]	0.01[0.00,0.09]	0.00	0.00	0.00	0.00	1.5	0.84	0.65	0.34	26/58	26/57	28/54	28/55
<i>p_Firmicutes</i>	61±11	60±9.2	60±8.7	60±8.3	59[55,67]	61[55,66]	60[55,67]	63[56,65]	32	27	43	35	91	76	81	81	58/58	57/57	54/54	55/55
<i>c_Bacilli</i>	1.0±2.6	0.81±1.9	0.59±1.5	0.96±3.4	0.29[0.09,0.62]	0.28[0.10,0.48]	0.16[0.07,0.48]	0.15[0.11,0.32]	0.01	0.02	0.01	0.01	16	11	8.5	22	58/58	57/57	54/54	55/55
<i>o_Bacillales</i>	0.00±0.01	0.00±0.01	0.00±0.01	0.01±0.04	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	0.00	0.06	0.04	0.03	0.32	10/58	8/57	5/54	3/55
<i>f_Bacillaceae</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0/58	1/57	0/54	0/55
<i>g_Bacillus</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0/58	1/57	0/54	0/55
<i>f_FamilyXI_in_Bacillales</i>	0.00±0.01	0.00±0.01	0.00±0.01	0.01±0.04	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	0.00	0.04	0.04	0.03	0.29	7/58	5/57	4/54	3/55
<i>g_Gemella</i>	0.00±0.01	0.00±0.01	0.00±0.01	0.01±0.04	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	0.00	0.04	0.04	0.03	0.29	7/58	5/57	4/54	3/55
<i>f_Staphylococcaceae</i>	0.00±0.01	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]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.06	0.01	0.01	0.03	5/58	2/57	2/54	1/55
<i>g_Staphylococcus</i>	0.00±0.01	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]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.06	0.01	0.01	0.03	5/58	2/57	2/54	1/55
<i>o_Lactobacillales</i>	1.0±2.6	0.81±1.9	0.58±1.5	0.95±3.3	0.28[0.09,0.62]	0.28[0.10,0.48]	0.16[0.07,0.48]	0.14[0.11,0.32]	0.01	0.02	0.01	0.01	16	11	8.5	22	58/58	57/57	54/54	55/55
<i>f_Carnobacteriaceae</i>	0.01±0.02	0.01±0.02	0.01±0.01	0.01±0.05	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.13	0.11	0.04	0.33	22/58	19/57	16/54	9/55
<i>g_Carnobacterium</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0/58	1/57	0/54	0/55
<i>g_Granulicatella</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.01	1/58	1/57	0/54	1/55
<i>g_unknown_Carnobacteriaceae</i>	0.01±0.02	0.01±0.02	0.01±0.01	0.01±0.04	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.13	0.11	0.04	0.32	21/58	17/57	16/54	9/55
<i>f_Enterococcaceae</i>	0.09±0.44	0.03±0.09	0.06±0.39	0.03±0.14	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	0.00	2.9	0.50	2.9	0.99	14/58	13/57	7/54	9/55
<i>g_Enterococcus</i>	0.09±0.44	0.03±0.09	0.06±0.39	0.03±0.14	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	0.00	2.9	0.50	2.9	0.99	14/58	13/57	7/54	9/55
<i>f_Lactobacillaceae</i>	0.02±0.04	0.10±0.47	0.02±0.06	0.05±0.18	0.00[0.00,0.02]	0.00[0.00,0.02]	0.00[0.00,0.02]	0.00[0.00,0.02]	0.00	0.00	0.00	0.00	0.26	3.1	0.38	1.2	28/58	23/57	26/54	27/55

Effects of fructan and gluten on gut microbiota in individuals with self-reported non-celiac gluten/wheat sensitivity – a randomised controlled crossover trial, Herfindal AM *et al.*

<i>g_Lactobacillus</i>	0.02±0.04	0.10±0.47	0.02±0.06	0.05±0.18	0.00[0.00,0.02]	0.00[0.00,0.02]	0.00[0.00,0.02]	0.00[0.00,0.02]	0.00	0.00	0.00	0.00	0.26	3.1	0.38	1.2	28/58	23/57	25/54	27/55
<i>g_Pediococcus</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0/58	0/57	1/54	0/55
<i>f_Leuconostocaceae</i>	0.00±0.01	0.00±0.00	0.00±0.00	0.00±0.01	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	0.00	0.03	0.01	0.01	0.06	4/58	2/57	2/54	3/55
<i>g_Leuconostoc</i>	0.00±0.01	0.00±0.00	0.00±0.00	0.00±0.01	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	0.00	0.03	0.01	0.01	0.06	4/58	2/57	2/54	3/55
<i>f_Streptococcaceae</i>	0.91±2.3	0.67±1.7	0.49±1.4	0.86±3.1	0.22[0.08,0.57]	0.22[0.07,0.41]	0.15[0.05,0.43]	0.13[0.09,0.30]	0.00	0.01	0.00	0.01	14	11	8.1	20	57/58	57/57	53/54	55/55
<i>g_Lactococcus</i>	0.07±0.32	0.02±0.06	0.01±0.03	0.07±0.27	0.00[0.00,0.02]	0.00[0.00,0.01]	0.00[0.00,0.00]	0.00[0.00,0.01]	0.00	0.00	0.00	0.00	2.4	0.29	0.15	1.8	20/58	17/57	12/54	20/55
<i>g_Streptococcus</i>	0.85±2.3	0.65±1.7	0.48±1.4	0.79±3.0	0.22[0.08,0.48]	0.19[0.07,0.37]	0.14[0.05,0.43]	0.12[0.08,0.29]	0.00	0.01	0.00	0.01	14	11	8.1	20	57/58	57/57	53/54	55/55
<i>c_Clostridia</i>	57±11	56±9.5	57±9.0	57±8.9	56[49,64]	58[51,63]	57[50,65]	58[51,63]	29	20	36	33	85	73	75	74	58/58	57/57	54/54	55/55
<i>o_Clostridiales</i>	57±11	56±9.5	57±9.0	57±8.9	56[49,64]	58[51,63]	57[50,65]	58[51,63]	29	20	36	33	85	73	75	74	58/58	57/57	54/54	55/55
<i>f_Christensenellaceae</i>	1.4±1.6	1.1±1.2	1.4±1.5	1.4±1.4	0.90[0.31,2.1]	0.73[0.24,1.8]	1.00[0.33,2.3]	1.0[0.31,1.9]	0.00	0.00	0.00	0.01	7.3	5.9	8.2	6.4	57/58	56/57	53/54	55/55
<i>g_ChristensenellaceaeR-7group</i>	1.4±1.6	1.1±1.2	1.4±1.5	1.3±1.4	0.89[0.29,2.0]	0.71[0.23,1.7]	0.98[0.29,2.3]	0.91[0.20,1.9]	0.00	0.00	0.00	0.01	7.2	5.9	8.2	6.4	57/58	56/57	53/54	55/55
<i>g_unknown_Christensenellaceae</i>	0.03±0.04	0.03±0.02	0.04±0.05	0.04±0.06	0.02[0.00,0.04]	0.02[0.01,0.04]	0.03[0.01,0.05]	0.02[0.00,0.05]	0.00	0.00	0.00	0.00	0.19	0.11	0.26	0.36	40/58	46/57	43/54	41/55
<i>f_Clostridiaceae1</i>	0.10±0.28	0.10±0.12	0.08±0.11	0.08±0.11	0.03[0.00,0.07]	0.05[0.01,0.15]	0.03[0.00,0.10]	0.04[0.01,0.07]	0.00	0.00	0.00	0.00	2.0	0.41	0.48	0.60	41/58	46/57	38/54	43/55
<i>g_Clostridiumsensustricto1</i>	0.10±0.28	0.10±0.12	0.08±0.11	0.08±0.11	0.03[0.00,0.07]	0.05[0.01,0.15]	0.03[0.00,0.10]	0.04[0.01,0.07]	0.00	0.00	0.00	0.00	2.0	0.41	0.48	0.60	41/58	46/57	38/54	43/55
<i>g_Clostridiumsensustricto3</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.01	0.00	0.01	0.01	1/58	0/57	1/54	1/55
<i>f_ClostridialesvadinBB60group</i>	0.35±0.75	0.18±0.38	0.34±0.79	0.28±0.58	0.10[0.01,0.28]	0.07[0.01,0.20]	0.06[0.01,0.26]	0.06[0.01,0.25]	0.00	0.00	0.00	0.00	4.2	2.5	4.7	2.9	48/58	44/57	46/54	44/55
<i>g_unknown_ClostridialesvadinBB60group</i>	0.35±0.75	0.18±0.38	0.34±0.79	0.28±0.58	0.10[0.01,0.28]	0.07[0.01,0.20]	0.06[0.01,0.26]	0.06[0.01,0.25]	0.00	0.00	0.00	0.00	4.2	2.5	4.7	2.9	48/58	44/57	46/54	44/55
<i>f_Defluviitaleaceae</i>	0.02±0.06	0.02±0.03	0.02±0.04	0.02±0.03	0.01[0.00,0.03]	0.01[0.00,0.03]	0.01[0.00,0.03]	0.01[0.00,0.03]	0.00	0.00	0.00	0.00	0.41	0.13	0.26	0.12	34/58	34/57	34/54	35/55
<i>g_DefluviitaleaceaeUCG-011</i>	0.02±0.06	0.02±0.03	0.02±0.04	0.02±0.03	0.01[0.00,0.03]	0.01[0.00,0.03]	0.01[0.00,0.03]	0.01[0.00,0.03]	0.00	0.00	0.00	0.00	0.41	0.13	0.26	0.12	34/58	34/57	34/54	35/55
<i>f_Eubacteriaceae</i>	0.00±0.01	0.00±0.01	0.00±0.01	0.00±0.01	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	0.00	0.05	0.02	0.07	0.03	8/58	13/57	12/54	11/55
<i>g_Anaerofustis</i>	0.00±0.01	0.00±0.01	0.00±0.01	0.00±0.01	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	0.00	0.04	0.02	0.03	0.03	7/58	12/57	11/54	9/55
<i>g_Eubacterium</i>	0.00±0.01	0.00±0.00	0.00±0.01	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	0.00	0.00	0.00	0.05	0.02	0.04	0.03	1/58	2/57	2/54	2/55
<i>f_FamilyXI_in_Clostridiales</i>	0.00±0.01	0.00±0.01	0.00±0.01	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	0.00	0.00	0.00	0.04	0.03	0.03	0.02	8/58	4/57	9/54	9/55
<i>g_Anaerococcus</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.01	0.01	0.01	0.01	5/58	1/57	2/54	1/55
<i>g_Ezakiella</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.01	1/58	0/57	0/54	4/55
<i>g_Finegoldia</i>	0.00±0.00	0.00±0.00	0.00±0.01	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	0.00	0.00	0.00	0.01	0.01	0.03	0.01	1/58	1/57	5/54	1/55
<i>g_Murdochella</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0/58	0/57	2/54	1/55
<i>g_Parvimonas</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.02	0.01	0.01	0.01	2/58	2/57	1/54	3/55
<i>g_Peptoniphilus</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.02	0.02	0.00	0.00	2/58	1/57	0/54	0/55
<i>f_FamilyXIII</i>	0.17±0.15	0.14±0.10	0.18±0.14	0.15±0.11	0.14[0.08,0.22]	0.12[0.06,0.19]	0.16[0.08,0.22]	0.13[0.08,0.21]	0.00	0.00	0.00	0.00	0.76	0.45	0.57	0.48	56/58	54/57	53/54	51/55
<i>g_[Eubacterium]brachygroup</i>	0.01±0.02	0.01±0.02	0.01±0.02	0.01±0.01	0.00[0.00,0.01]	0.00[0.00,0.02]	0.00[0.00,0.02]	0.00[0.00,0.02]	0.00	0.00	0.00	0.00	0.08	0.14	0.08	0.07	22/58	26/57	26/54	23/55
<i>g_[Eubacterium]nodatumgroup</i>	0.01±0.03	0.00±0.01	0.01±0.03	0.01±0.01	0.00[0.00,0.00]	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00	0.00	0.00	0.00	0.16	0.02	0.16	0.03	10/58	14/57	15/54	18/55
<i>g_FamilyXIIID3011group</i>	0.11±0.12	0.08±0.08	0.11±0.10	0.10±0.09	0.08[0.03,0.13]	0.06[0.04,0.12]	0.08[0.04,0.14]	0.08[0.04,0.13]	0.00	0.00	0.00	0.00	0.66	0.36	0.43	0.47	55/58	52/57	52/54	51/55
<i>g_FamilyXIIICUG-001</i>	0.05±0.04	0.04±0.04	0.05±0.04	0.03±0.03	0.04[0.00,0.07]	0.03[0.01,0.06]	0.04[0.02,0.07]	0.03[0.01,0.05]	0.00	0.00	0.00	0.00	0.15	0.17	0.14	0.13	43/58	43/57	45/54	44/55
<i>g_FamilyXIIICUG-002</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.02	0.02	0.01	0.01	4/58	1/57	1/54	3/55
<i>g_Mogibacterium</i>	0.00±0.00	0.00±0.00	0.00±0.01	0.00±0.01	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	0.00	0.02	0.00	0.05	0.05	3/58	0/57	3/54	3/55
<i>g_unknown_FamilyXIII</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.02	0.01	0.03	0.01	1/58	2/57	3/54	2/55
<i>f_Gracilibacteraceae</i>	0.00±0.02	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]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.13	0.01	0.02	0.00	1/58	1/57	2/54	0/55
<i>g_Lutispora</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0/58	0/57	1/54	0/55
<i>g_unknown_Gracilibacteraceae</i>	0.00±0.02	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]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.13	0.01	0.02	0.00	1/58	1/57	1/54	0/55

Effects of fructan and gluten on gut microbiota in individuals with self-reported non-celiac gluten/wheat sensitivity – a randomised controlled crossover trial, Herfindal AM *et al.*

<i>f_Lachnospiraceae</i>	28±7.1	29±6.2	28±7.3	28±6.3	28[23,31]	28[25,33]	27[23,31]	28[24,31]	10	15	11	13	49	47	53	44	58/58	57/57	54/54	55/55
<i>g_[Bacteroides]pectinophilusgroup</i>	0.02±0.07	0.05±0.25	0.04±0.13	0.07±0.27	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	0.00	0.34	1.8	0.62	1.6	5/58	10/57	7/54	11/55
<i>g_[Eubacterium]halliigroup</i>	1.3±0.77	1.3±0.77	1.4±0.73	1.3±0.71	1.2[0.75,1.8]	1.3[0.80,1.6]	1.2[0.99,1.7]	1.3[0.87,1.6]	0.01	0.07	0.19	0.19	4.0	4.5	3.9	4.4	58/58	57/57	54/54	55/55
<i>g_[Eubacterium]rectalegroup</i>	4.4±3.6	4.9±3.8	4.2±2.9	4.6±2.8	3.6[1.7,5.8]	4.3[2.2,6.1]	3.9[1.6,6.6]	4.1[2.2,6.4]	0.20	0.36	0.27	0.44	17	18	11	11	58/58	57/57	54/54	55/55
<i>g_[Eubacterium]ruminantiumgroup</i>	0.38±1.2	0.27±0.98	0.22±0.85	0.29±0.96	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00	0.00	0.00	0.00	6.6	6.4	5.3	4.6	20/58	23/57	19/54	16/55
<i>g_[Eubacterium]ventriosumgroup</i>	0.48±1.5	0.59±1.5	0.32±0.37	0.39±0.51	0.19[0.08,0.37]	0.20[0.07,0.49]	0.19[0.09,0.44]	0.28[0.10,0.51]	0.00	0.00	0.00	0.00	11	8.8	1.6	3.3	55/58	55/57	52/54	54/55
<i>g_[Eubacterium]xylanophilumgroup</i>	0.32±0.35	0.29±0.37	0.46±0.49	0.32±0.37	0.19[0.04,0.55]	0.15[0.01,0.43]	0.29[0.07,0.63]	0.23[0.04,0.50]	0.00	0.00	0.00	0.00	1.4	1.7	1.8	1.8	50/58	47/57	47/54	48/55
<i>g_[Ruminococcus]torquesgroup</i>	1.5±1.2	1.4±0.94	1.8±1.2	1.3±0.79	1.3[0.64,2.1]	1.2[0.73,1.7]	1.6[0.85,2.5]	1.2[0.82,1.7]	0.15	0.12	0.14	0.19	6.1	4.2	5.3	3.5	58/58	57/57	54/54	55/55
<i>g_Anaerospobacter</i>	0.03±0.07	0.03±0.04	0.03±0.04	0.05±0.15	0.01[0.00,0.04]	0.01[0.00,0.04]	0.00[0.00,0.04]	0.01[0.00,0.05]	0.00	0.00	0.00	0.00	0.41	0.18	0.14	1.0	29/58	33/57	26/54	30/55
<i>g_Anaerostipes</i>	1.5±1.4	1.9±1.3	1.8±1.4	1.7±1.7	1.4[0.53,1.9]	1.7[0.87,2.5]	1.4[0.76,2.6]	1.2[0.47,2.4]	0.05	0.25	0.09	0.02	8.7	5.1	6.3	8.9	58/58	57/57	54/54	55/55
<i>g_Blautia</i>	3.9±2.2	4.0±1.8	3.9±2.1	4.0±2.6	3.3[2.3,5.2]	3.9[2.5,5.1]	3.2[2.3,5.1]	3.6[2.5,4.3]	0.15	1.4	1.3	1.4	11	8.6	11	19	58/58	57/57	54/54	55/55
<i>g_Butyrvibrio</i>	0.10±0.41	0.10±0.42	0.06±0.40	0.16±0.77	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	0.00	2.7	2.3	2.9	5.4	9/58	12/57	7/54	11/55
<i>g_Coproccocus1</i>	0.29±0.17	0.26±0.11	0.25±0.12	0.25±0.11	0.24[0.18,0.34]	0.26[0.17,0.34]	0.24[0.17,0.33]	0.25[0.17,0.32]	0.01	0.01	0.00	0.01	0.79	0.47	0.50	0.60	58/58	57/57	53/54	55/55
<i>g_Coproccocus2</i>	0.79±1.5	0.59±1.0	0.62±0.95	0.93±1.7	0.03[0.00,0.84]	0.02[0.00,1.0]	0.05[0.00,1.1]	0.03[0.01,1.2]	0.00	0.00	0.00	0.00	6.0	4.3	3.3	7.9	37/58	39/57	39/54	43/55
<i>g_Coproccocus3</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0/58	0/57	0/54	2/55
<i>g_Eisenbergiella</i>	0.12±0.20	0.08±0.07	0.09±0.14	0.09±0.09	0.07[0.05,0.11]	0.06[0.03,0.11]	0.07[0.02,0.11]	0.06[0.03,0.10]	0.00	0.00	0.00	0.00	1.5	0.32	0.94	0.48	57/58	53/57	53/54	53/55
<i>g_Fusicatenibacter</i>	1.3±0.74	1.7±0.98	1.4±0.89	1.3±0.85	1.2[0.67,1.9]	1.5[1.0,2.5]	1.2[0.94,1.7]	1.2[0.73,1.9]	0.01	0.01	0.02	0.00	3.2	4.6	3.9	3.9	58/58	57/57	54/54	54/55
<i>g_Howardella</i>	0.01±0.02	0.00±0.02	0.00±0.02	0.00±0.02	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	0.00	0.14	0.13	0.10	0.11	5/58	5/57	5/54	4/55
<i>g_Lachnoanaerobaculum</i>	0.00±0.00	0.00±0.00	0.00±0.00	0.00±0.01	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	0.00	0.01	0.00	0.00	0.08	1/58	0/57	0/54	1/55
<i>g_Lachnoclostridium</i>	1.6±1.3	1.6±1.5	1.8±1.8	1.8±1.9	1.1[0.78,1.7]	1.3[0.86,1.6]	1.2[0.88,1.9]	1.2[0.81,1.9]	0.43	0.49	0.55	0.32	6.3	8.9	11	11	58/58	57/57	54/54	55/55
<i>g_Lachnospira</i>	1.5±1.6	1.6±1.4	1.3±1.2	1.6±1.3	1.2[0.42,2.0]	1.3[0.53,2.6]	0.99[0.39,2.0]	1.4[0.49,2.3]	0.01	0.00	0.00	0.05	8.9	5.2	6.2	6.7	58/58	55/57	53/54	55/55
<i>g_LachnospiraceaeFCS020group</i>	0.17±0.11	0.17±0.15	0.19±0.21	0.19±0.14	0.16[0.09,0.23]	0.13[0.09,0.26]	0.15[0.11,0.22]	0.17[0.09,0.24]	0.00	0.00	0.01	0.00	0.52	0.73	1.5	0.59	56/58	54/57	54/54	54/55
<i>g_LachnospiraceaeFE2018group</i>	0.02±0.03	0.03±0.06	0.03±0.03	0.03±0.06	0.01[0.00,0.03]	0.01[0.00,0.04]	0.02[0.00,0.04]	0.01[0.00,0.04]	0.00	0.00	0.00	0.00	0.16	0.44	0.15	0.32	40/58	37/57	37/54	34/55
<i>g_LachnospiraceaeNC2004group</i>	0.52±0.79	0.63±0.84	0.57±0.70	0.56±0.91	0.26[0.05,0.61]	0.33[0.06,0.79]	0.35[0.10,0.83]	0.28[0.09,0.64]	0.00	0.00	0.00	0.00	3.6	3.5	3.7	5.4	51/58	51/57	50/54	52/55
<i>g_LachnospiraceaeND3007group</i>	0.50±0.46	0.62±0.52	0.58±0.49	0.53±0.48	0.42[0.13,0.77]	0.44[0.24,0.85]	0.49[0.24,0.76]	0.44[0.20,0.63]	0.00	0.00	0.01	0.00	2.5	2.5	2.2	2.4	57/58	56/57	54/54	54/55
<i>g_LachnospiraceaeNK4A136group</i>	1.0±0.89	0.81±0.66	0.94±0.87	0.97±0.89	0.72[0.37,1.4]	0.62[0.33,1.2]	0.68[0.37,1.3]	0.73[0.44,1.2]	0.00	0.01	0.01	0.00	3.8	3.2	3.6	5.2	57/58	57/57	54/54	54/55
<i>g_LachnospiraceaeNK4B4group</i>	0.03±0.14	0.03±0.09	0.04±0.15	0.04±0.12	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	0.00	1.0	0.45	0.90	0.48	11/58	13/57	11/54	8/55
<i>g_LachnospiraceaeUCG-001</i>	0.62±0.59	0.72±0.70	0.63±0.65	0.66±0.64	0.40[0.13,0.97]	0.48[0.21,1.1]	0.41[0.13,0.87]	0.50[0.17,0.97]	0.00	0.00	0.00	0.00	2.5	2.8	2.6	3.1	55/58	54/57	51/54	53/55
<i>g_LachnospiraceaeUCG-003</i>	0.08±0.41	0.08±0.31	0.03±0.13	0.02±0.06	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	0.00	3.1	1.9	0.95	0.32	9/58	7/57	7/54	6/55
<i>g_LachnospiraceaeUCG-004</i>	0.42±0.39	0.43±0.35	0.43±0.39	0.39±0.28	0.37[0.13,0.57]	0.33[0.20,0.63]	0.34[0.18,0.59]	0.39[0.14,0.57]	0.00	0.00	0.00	0.00	2.2	1.8	1.9	1.5	54/58	55/57	49/54	52/55
<i>g_LachnospiraceaeUCG-008</i>	0.04±0.05	0.03±0.03	0.03±0.04	0.04±0.04	0.02[0.01,0.04]	0.02[0.01,0.04]	0.02[0.01,0.05]	0.03[0.01,0.05]	0.00	0.00	0.00	0.00	0.28	0.13	0.17	0.26	48/58	45/57	44/54	46/55
<i>g_LachnospiraceaeUCG-010</i>	0.02±0.02	0.02±0.02	0.02±0.02	0.02±0.02	0.01[0.00,0.02]	0.01[0.00,0.02]	0.01[0.00,0.02]	0.02[0.01,0.03]	0.00	0.00	0.00	0.00	0.10	0.06	0.09	0.08	39/58	39/57	36/54	42/55
<i>g_Marvinbryantia</i>	0.07±0.07	0.05±0.04	0.07±0.08	0.06±0.07	0.04[0.01,0.08]	0.03[0.02,0.07]	0.04[0.02,0.08]	0.04[0.01,0.08]	0.00	0.00	0.00	0.00	0.28	0.17	0.34	0.37	49/58	51/57	48/54	43/55
<i>g_Oribacterium</i>	0.01±0.02	0.01±0.02	0.01±0.02	0.01±0.02	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.01]	0.01[0.00,0.01]	0.00	0.00	0.00	0.00	0.13	0.16	0.11	0.17	25/58	20/57	22/54	32/55
<i>g_Pseudobutyrvibrio</i>	0.05±0.10	0.04±0.08	0.03±0.05	0.04±0.07	0.00[0.00,0.06]	0.00[0.00,0.06]	0.00[0.00,0.04]	0.00[0.00,0.05]	0.00	0.00	0.00	0.00	0.45	0.43	0.22	0.28	23/58	22/57	24/54	22/55
<i>g_Roseburia</i>	0.73±0.89	0.89±1.1	0.72±0.53	1.0±1.1	0.54[0.26,0.91]	0.54[0.29,0.88]	0.56[0.32,1.1]	0.67[0.39,1.3]	0.01	0.03	0.06	0.02	5.9	6.2	2.4	5.7	58/58	57/57	54/54	55/55
<i>g_Sellimonas</i>	0.08±0.33	0.06±0.23	0.07±0.16	0.05±0.13	0.00[0.00,0.05]	0.00[0.00,0.04]	0.00[0.00,0.05]	0.00[0.00,0.05]	0.00	0.00	0.00	0.00	2.5	1.7	0.97	0.69	28/58	25/57	26/54	27/55
<i>g_Shuttleworthia</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.02	0.03	0.01	0.01	1/58	2/57	1/54	2/55
<i>g_Stomatobaculum</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	2/58	0/57	0/54	0/55
<i>g_Tyzzerella</i>	0.01±0.05	0.02±0.06	0.02±0.09	0.02±0.08	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	0.00	0.34	0.42	0.65	0.52	13/58	13/57	7/54	10/55

Effects of fructan and gluten on gut microbiota in individuals with self-reported non-celiac gluten/wheat sensitivity – a randomised controlled crossover trial, Herfindal AM *et al.*

<i>g_Tyzzerella3</i>	0.09±0.16	0.08±0.14	0.08±0.16	0.09±0.15	0.00[0.00,0.13]	0.01[0.00,0.10]	0.01[0.00,0.08]	0.01[0.00,0.12]	0.00	0.00	0.00	0.00	0.67	0.59	0.82	0.72	28/58	29/57	28/54	30/55
<i>g_Tyzzerella4</i>	0.37±0.39	0.41±0.38	0.40±0.32	0.38±0.34	0.28[0.13,0.52]	0.32[0.16,0.55]	0.34[0.19,0.60]	0.32[0.16,0.55]	0.00	0.00	0.00	0.00	2.2	2.2	1.5	1.8	51/58	54/57	50/54	51/55
<i>g_unknown_Lachnospiraceae</i>	3.4±2.0	3.1±2.1	3.2±2.1	3.1±1.7	2.7[2.1,4.4]	2.6[1.6,4.2]	2.5[1.8,3.9]	2.7[1.9,3.7]	0.75	0.47	0.59	0.74	9.3	9.7	9.4	11	58/58	57/57	54/54	55/55
<i>f_Peptococcaceae</i>	0.10±0.12	0.09±0.11	0.09±0.09	0.09±0.11	0.05[0.00,0.14]	0.05[0.01,0.13]	0.08[0.00,0.14]	0.05[0.00,0.13]	0.00	0.00	0.00	0.00	0.44	0.56	0.38	0.50	42/58	43/57	40/54	40/55
<i>g_Peptococcus</i>	0.02±0.05	0.02±0.04	0.02±0.04	0.02±0.04	0.00[0.00,0.02]	0.00[0.00,0.03]	0.00[0.00,0.03]	0.00[0.00,0.04]	0.00	0.00	0.00	0.00	0.23	0.17	0.15	0.17	25/58	25/57	26/54	24/55
<i>g_unknown_Peptococcaceae</i>	0.07±0.10	0.07±0.10	0.07±0.08	0.06±0.10	0.03[0.00,0.10]	0.02[0.00,0.11]	0.04[0.00,0.14]	0.02[0.00,0.10]	0.00	0.00	0.00	0.00	0.34	0.49	0.32	0.50	41/58	39/57	35/54	33/55
<i>f_Peptostreptococcaceae</i>	0.16±0.37	0.15±0.22	0.14±0.28	0.15±0.19	0.07[0.02,0.15]	0.05[0.03,0.15]	0.07[0.02,0.17]	0.08[0.03,0.15]	0.00	0.00	0.00	0.00	2.5	1.1	2.0	0.94	52/58	47/57	51/54	50/55
<i>g_Intestinibacter</i>	0.05±0.12	0.06±0.11	0.07±0.16	0.06±0.12	0.01[0.00,0.05]	0.02[0.00,0.06]	0.03[0.01,0.07]	0.02[0.01,0.05]	0.00	0.00	0.00	0.00	0.82	0.55	1.1	0.71	38/58	38/57	41/54	44/55
<i>g_Peptoclostridium</i>	0.11±0.27	0.09±0.17	0.07±0.14	0.09±0.16	0.03[0.01,0.09]	0.03[0.00,0.07]	0.02[0.01,0.08]	0.04[0.01,0.09]	0.00	0.00	0.00	0.00	1.7	0.92	0.85	0.93	47/58	42/57	42/54	44/55
<i>g_Peptostreptococcus</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.01	0.00	0.01	0.00	1/58	0/57	1/54	0/55
<i>f_Ruminococcaceae</i>	27±7.5	26±6.4	27±7.0	26±8.0	26[23,32]	26[22,31]	28[23,32]	27[23,31]	4.0	1.9	2.3	1.6	44	36	42	39	58/58	57/57	54/54	55/55
<i>g_[Eubacterium]coprostanoligenesgroup</i>	1.1±1.3	0.76±0.77	0.95±0.87	0.94±0.93	0.62[0.31,1.5]	0.51[0.25,1.1]	0.67[0.35,1.4]	0.68[0.32,1.2]	0.00	0.00	0.00	0.00	7.9	3.5	4.5	3.9	55/58	56/57	50/54	50/55
<i>g_Acetanaerobacterium</i>	0.00±0.01	0.00±0.00	0.00±0.01	0.00±0.01	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	0.00	0.04	0.02	0.03	0.02	11/58	6/57	11/54	10/55
<i>g_Anaerofilum</i>	0.01±0.01	0.00±0.01	0.01±0.01	0.00±0.01	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.05	0.04	0.03	0.02	19/58	15/57	19/54	13/55
<i>g_Anaerotruncus</i>	0.28±0.25	0.23±0.24	0.29±0.29	0.31±0.31	0.24[0.09,0.40]	0.19[0.06,0.29]	0.21[0.10,0.39]	0.27[0.07,0.39]	0.00	0.00	0.01	0.00	1.3	1.3	1.3	1.7	55/58	53/57	54/54	53/55
<i>g_Butyricoccus</i>	0.62±0.39	0.68±0.46	0.64±0.44	0.63±0.38	0.54[0.33,0.88]	0.58[0.30,0.94]	0.60[0.37,0.82]	0.54[0.34,0.83]	0.04	0.10	0.07	0.12	1.8	2.4	2.7	2.2	58/58	57/57	54/54	55/55
<i>g_CandidatusSoleaferrea</i>	0.01±0.01	0.01±0.01	0.01±0.01	0.01±0.01	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00	0.00	0.00	0.00	0.04	0.05	0.07	0.04	22/58	23/57	24/54	23/55
<i>g_Caproiciproducens</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0/58	1/57	0/54	0/55
<i>g_Faecalibacterium</i>	12±5.8	13±5.1	12±5.8	12±5.5	12[7.8,16]	13[9.4,17]	12[7.3,16]	12[7.2,16]	0.08	0.10	0.16	0.06	24	26	27	22	58/58	57/57	54/54	55/55
<i>g_Flavinifractor</i>	0.09±0.17	0.07±0.11	0.06±0.08	0.05±0.06	0.04[0.01,0.08]	0.03[0.01,0.11]	0.03[0.01,0.08]	0.03[0.01,0.07]	0.00	0.00	0.00	0.00	0.97	0.70	0.42	0.28	45/58	47/57	45/54	48/55
<i>g_Hydrogenoanaerobacterium</i>	0.01±0.03	0.01±0.02	0.01±0.03	0.01±0.02	0.00[0.00,0.00]	0.00[0.00,0.00]	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00	0.00	0.00	0.00	0.16	0.12	0.16	0.12	14/58	13/57	21/54	16/55
<i>g_Intestinimonas</i>	0.01±0.03	0.01±0.02	0.01±0.02	0.01±0.02	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.14	0.11	0.09	0.10	21/58	16/57	13/54	13/55
<i>g_Oscillibacter</i>	0.03±0.05	0.02±0.03	0.03±0.04	0.03±0.04	0.01[0.00,0.03]	0.01[0.00,0.03]	0.01[0.00,0.04]	0.01[0.00,0.06]	0.00	0.00	0.00	0.00	0.31	0.18	0.14	0.13	36/58	34/57	29/54	31/55
<i>g_Oscillospira</i>	0.02±0.04	0.01±0.03	0.01±0.02	0.01±0.02	0.00[0.00,0.02]	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00	0.00	0.00	0.00	0.27	0.19	0.13	0.09	22/58	19/57	14/54	18/55
<i>g_Papillibacter</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.01	0.01	0.01	0.00	3/58	1/57	1/54	0/55
<i>g_Ruminiclostridium</i>	0.01±0.02	0.01±0.02	0.01±0.02	0.01±0.01	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00	0.00	0.00	0.00	0.12	0.08	0.10	0.04	23/58	22/57	18/54	27/55
<i>g_Ruminiclostridium1</i>	0.01±0.02	0.01±0.02	0.01±0.01	0.01±0.02	0.00[0.00,0.00]	0.00[0.00,0.00]	0.00[0.00,0.00]	0.00[0.00,0.01]	0.00	0.00	0.00	0.00	0.10	0.07	0.05	0.13	14/58	10/57	13/54	16/55
<i>g_Ruminiclostridium5</i>	0.59±0.91	0.59±0.85	0.61±0.70	0.40±0.42	0.28[0.14,0.50]	0.26[0.13,0.82]	0.33[0.18,0.74]	0.26[0.14,0.52]	0.02	0.01	0.02	0.02	4.2	5.4	3.2	1.9	58/58	57/57	54/54	55/55
<i>g_Ruminiclostridium6</i>	0.49±1.1	0.55±1.1	0.75±1.3	0.52±1.1	0.02[0.00,0.27]	0.01[0.00,0.52]	0.02[0.00,0.77]	0.02[0.00,0.43]	0.00	0.00	0.00	0.00	4.1	4.0	4.6	6.0	39/58	37/57	39/54	35/55
<i>g_Ruminiclostridium9</i>	0.15±0.12	0.14±0.10	0.17±0.12	0.17±0.12	0.11[0.07,0.21]	0.11[0.09,0.18]	0.15[0.09,0.24]	0.14[0.09,0.24]	0.00	0.00	0.00	0.00	0.61	0.42	0.56	0.53	55/58	55/57	53/54	54/55
<i>g_RuminococcaceaeNK4A214group</i>	0.67±1.2	0.43±0.49	0.64±0.69	0.52±0.67	0.33[0.11,0.69]	0.22[0.11,0.56]	0.39[0.10,1.1]	0.30[0.09,0.64]	0.00	0.00	0.00	0.00	7.5	2.1	2.8	3.7	52/58	51/57	52/54	50/55
<i>g_RuminococcaceaeUCG-002</i>	1.5±1.1	1.3±0.91	1.6±1.1	1.4±1.1	1.4[0.66,2.0]	1.2[0.65,2.0]	1.3[0.83,2.3]	1.1[0.73,2.0]	0.01	0.00	0.01	0.01	4.9	3.6	4.6	4.4	58/58	56/57	54/54	55/55
<i>g_RuminococcaceaeUCG-003</i>	0.32±0.37	0.29±0.28	0.35±0.36	0.40±0.40	0.22[0.04,0.50]	0.20[0.11,0.35]	0.27[0.08,0.49]	0.23[0.10,0.61]	0.00	0.00	0.00	0.00	1.4	1.2	1.8	1.5	54/58	53/57	50/54	51/55
<i>g_RuminococcaceaeUCG-004</i>	0.11±0.20	0.09±0.12	0.10±0.15	0.09±0.12	0.04[0.00,0.14]	0.06[0.00,0.15]	0.05[0.00,0.17]	0.03[0.00,0.14]	0.00	0.00	0.00	0.00	1.3	0.54	0.80	0.51	38/58	37/57	31/54	34/55
<i>g_RuminococcaceaeUCG-005</i>	0.29±0.45	0.21±0.24	0.27±0.52	0.24±0.30	0.16[0.06,0.33]	0.12[0.07,0.31]	0.16[0.06,0.33]	0.14[0.04,0.33]	0.00	0.00	0.00	0.00	2.5	1.1	3.8	1.4	56/58	52/57	51/54	52/55
<i>g_RuminococcaceaeUCG-007</i>	0.00±0.01	0.00±0.01	0.00±0.01	0.00±0.01	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	0.00	0.06	0.10	0.02	0.05	10/58	9/57	10/54	12/55
<i>g_RuminococcaceaeUCG-008</i>	0.00±0.00	0.00±0.01	0.00±0.01	0.00±0.01	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	0.00	0.01	0.03	0.05	0.05	4/58	6/57	4/54	3/55
<i>g_RuminococcaceaeUCG-009</i>	0.01±0.01	0.02±0.03	0.01±0.02	0.01±0.02	0.00[0.00,0.01]	0.00[0.00,0.02]	0.00[0.00,0.01]	0.00[0.00,0.02]	0.00	0.00	0.00	0.00	0.05	0.14	0.09	0.09	28/58	27/57	20/54	25/55
<i>g_RuminococcaceaeUCG-010</i>	0.32±0.46	0.30±0.47	0.31±0.45	0.29±0.46	0.18[0.02,0.44]	0.17[0.01,0.36]	0.21[0.02,0.40]	0.14[0.01,0.46]	0.00	0.00	0.00	0.00	2.9	2.7	2.6	3.0	49/58	46/57	45/54	43/55
<i>g_RuminococcaceaeUCG-011</i>	0.00±0.01	0.00±0.01	0.00±0.01	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	0.00	0.00	0.00	0.07	0.05	0.03	0.02	7/58	4/57	7/54	3/55

Effects of fructan and gluten on gut microbiota in individuals with self-reported non-celiac gluten/wheat sensitivity – a randomised controlled crossover trial, Herfindal AM *et al.*

<i>g_RuminococcaceaeUCG-013</i>	0.51±0.46	0.52±0.41	0.56±0.43	0.48±0.35	0.44[0.22,0.60]	0.42[0.30,0.64]	0.50[0.25,0.73]	0.43[0.22,0.57]	0.00	0.01	0.00	0.01	2.1	2.1	2.6	1.7	56/58	57/57	53/54	55/55
<i>g_RuminococcaceaeUCG-014</i>	1.4±2.0	1.1±1.2	1.1±1.2	1.3±1.4	0.74[0.05,1.8]	0.71[0.06,1.7]	0.90[0.03,1.7]	0.95[0.02,2.0]	0.00	0.00	0.00	0.00	9.6	4.4	5.1	5.8	54/58	49/57	49/54	49/55
<i>g_Ruminococcus1</i>	1.2±1.5	0.90±1.1	1.1±1.4	1.1±1.7	0.83[0.03,1.7]	0.52[0.03,1.4]	0.61[0.07,1.3]	0.42[0.03,1.5]	0.00	0.00	0.00	0.00	7.7	5.0	6.1	7.3	55/58	49/57	49/54	49/55
<i>g_Ruminococcus2</i>	0.07±0.35	0.03±0.19	0.04±0.30	0.04±0.25	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	0.00	2.2	1.4	2.2	1.9	6/58	2/57	2/54	3/55
<i>g_Subdoligranulum</i>	2.4±1.9	2.1±1.4	2.3±1.7	2.2±1.5	1.9[1.2,3.2]	1.9[0.97,2.8]	2.0[1.1,3.0]	1.9[1.1,3.1]	0.03	0.01	0.01	0.04	9.2	5.7	9.3	6.6	58/58	57/57	54/54	55/55
<i>g_unknown_Ruminococcaceae</i>	2.7±2.9	2.2±2.0	2.8±2.0	2.8±2.8	1.9[1.2,3.1]	1.8[0.71,2.9]	2.1[1.0,4.3]	2.4[1.1,3.6]	0.27	0.07	0.04	0.09	18	9.5	8.2	17	58/58	57/57	54/54	55/55
<i>f_Syntrophomonadaceae</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.01	0.00	0.02	0.01	1/58	0/57	2/54	3/55
<i>g_Syntrophomonas</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.01	0.00	0.02	0.01	1/58	0/57	2/54	3/55
<i>o_Thermoanaerobacterales</i>	0.01±0.01	0.01±0.01	0.01±0.01	0.01±0.02	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00	0.00	0.00	0.00	0.05	0.06	0.08	0.10	19/58	14/57	18/54	17/55
<i>f_Thermoanaerobacteraceae</i>	0.01±0.01	0.01±0.01	0.01±0.01	0.01±0.02	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00	0.00	0.00	0.00	0.05	0.06	0.08	0.10	19/58	14/57	18/54	17/55
<i>g_Gelria</i>	0.01±0.01	0.01±0.01	0.01±0.01	0.01±0.02	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00	0.00	0.00	0.00	0.05	0.06	0.08	0.10	19/58	14/57	18/54	17/55
<i>c_Erysipelotrichia</i>	1.0±1.1	0.81±0.81	0.76±0.69	0.77±0.65	0.64[0.36,1.2]	0.57[0.36,0.93]	0.53[0.26,1.1]	0.64[0.28,0.91]	0.04	0.03	0.04	0.05	4.9	4.5	2.6	2.6	58/58	57/57	54/54	55/55
<i>o_Erysipelotrichales</i>	1.0±1.1	0.81±0.81	0.76±0.69	0.77±0.65	0.64[0.36,1.2]	0.57[0.36,0.93]	0.53[0.26,1.1]	0.64[0.28,0.91]	0.04	0.03	0.04	0.05	4.9	4.5	2.6	2.6	58/58	57/57	54/54	55/55
<i>f_Erysipelotrichaceae</i>	1.0±1.1	0.81±0.81	0.76±0.69	0.77±0.65	0.64[0.36,1.2]	0.57[0.36,0.93]	0.53[0.26,1.1]	0.64[0.28,0.91]	0.04	0.03	0.04	0.05	4.9	4.5	2.6	2.6	58/58	57/57	54/54	55/55
<i>g_[Clostridium]innocuumgroup</i>	0.09±0.56	0.01±0.01	0.01±0.02	0.02±0.08	0.00[0.00,0.02]	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00	0.00	0.00	0.00	4.3	0.06	0.08	0.60	24/58	22/57	23/54	16/55
<i>g_Catenibacterium</i>	0.01±0.09	0.01±0.07	0.02±0.12	0.02±0.11	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	0.00	0.66	0.50	0.86	0.79	1/58	2/57	3/54	2/55
<i>g_Catenisphaera</i>	0.00±0.00	0.00±0.00	0.00±0.01	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	0.00	0.00	0.00	0.00	0.01	0.05	0.03	0/58	2/57	1/54	2/55
<i>g_Coprobacillus</i>	0.01±0.06	0.00±0.01	0.00±0.01	0.00±0.01	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	0.00	0.45	0.05	0.09	0.09	9/58	2/57	7/54	3/55
<i>g_Dielma</i>	0.01±0.02	0.00±0.01	0.00±0.01	0.01±0.01	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	0.00	0.09	0.06	0.03	0.06	10/58	11/57	10/54	11/55
<i>g_Erysipelatoclostridium</i>	0.04±0.08	0.02±0.03	0.03±0.08	0.03±0.08	0.02[0.00,0.05]	0.01[0.00,0.03]	0.02[0.00,0.03]	0.01[0.00,0.03]	0.00	0.00	0.00	0.00	0.50	0.17	0.58	0.56	37/58	36/57	38/54	35/55
<i>g_ErysipelotrichaceaeUCG-003</i>	0.39±0.37	0.41±0.34	0.35±0.33	0.37±0.36	0.32[0.14,0.56]	0.27[0.15,0.65]	0.31[0.11,0.47]	0.24[0.12,0.54]	0.00	0.00	0.00	0.00	2.2	1.6	1.4	1.8	54/58	55/57	52/54	51/55
<i>g_ErysipelotrichaceaeUCG-004</i>	0.00±0.00	0.00±0.01	0.00±0.02	0.00±0.02	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	0.00	0.03	0.04	0.16	0.12	2/58	4/57	3/54	4/55
<i>g_ErysipelotrichaceaeUCG-007</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.01	5/58	0/57	0/54	2/55
<i>g_Faecalicoccus</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.02	0.00	0.01	0.01	1/58	0/57	1/54	2/55
<i>g_Faecalitalea</i>	0.01±0.03	0.01±0.03	0.01±0.02	0.01±0.03	0.00[0.00,0.01]	0.00[0.00,0.00]	0.00[0.00,0.00]	0.00[0.00,0.01]	0.00	0.00	0.00	0.00	0.12	0.20	0.11	0.17	18/58	13/57	13/54	15/55
<i>g_Holdemanela</i>	0.29±0.81	0.19±0.55	0.19±0.48	0.19±0.45	0.00[0.00,0.11]	0.00[0.00,0.07]	0.00[0.00,0.13]	0.00[0.00,0.05]	0.00	0.00	0.00	0.00	4.2	3.3	2.5	1.8	24/58	22/57	24/54	18/55
<i>g_Holdemania</i>	0.01±0.02	0.01±0.01	0.02±0.02	0.01±0.02	0.01[0.00,0.02]	0.00[0.00,0.01]	0.01[0.00,0.03]	0.01[0.00,0.02]	0.00	0.00	0.00	0.00	0.08	0.05	0.09	0.06	30/58	26/57	35/54	28/55
<i>g_Solobacterium</i>	0.04±0.26	0.03±0.18	0.04±0.24	0.03±0.22	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	0.00	2.0	1.4	1.7	1.6	4/58	5/57	4/54	3/55
<i>g_Turicibacter</i>	0.04±0.08	0.04±0.08	0.03±0.05	0.04±0.07	0.01[0.00,0.04]	0.00[0.00,0.03]	0.01[0.00,0.04]	0.01[0.00,0.07]	0.00	0.00	0.00	0.00	0.41	0.37	0.20	0.44	29/58	26/57	29/54	30/55
<i>g_unknown_Erysipelotrichaceae</i>	0.06±0.41	0.08±0.59	0.05±0.34	0.05±0.32	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00	0.00	0.00	0.00	3.1	4.4	2.5	2.4	22/58	18/57	16/54	18/55
<i>c_Negativicutes</i>	1.9±1.8	1.7±1.3	2.0±1.7	2.0±1.8	1.3[0.84,2.2]	1.3[0.70,2.6]	1.5[0.81,2.6]	1.4[0.87,2.4]	0.02	0.00	0.04	0.18	9.9	5.3	7.3	8.7	58/58	56/57	54/54	55/55
<i>o_Selenomonadales</i>	1.9±1.8	1.7±1.3	2.0±1.7	2.0±1.8	1.3[0.84,2.2]	1.3[0.70,2.6]	1.5[0.81,2.6]	1.4[0.87,2.4]	0.02	0.00	0.04	0.18	9.9	5.3	7.3	8.7	58/58	56/57	54/54	55/55
<i>f_Acidaminococcaceae</i>	0.60±0.77	0.69±0.89	0.68±0.80	0.58±0.71	0.30[0.01,0.88]	0.53[0.01,0.87]	0.44[0.01,1.1]	0.45[0.01,0.89]	0.00	0.00	0.00	0.00	3.8	3.5	3.6	3.5	48/58	45/57	41/54	45/55
<i>g_Acidaminococcus</i>	0.07±0.30	0.05±0.20	0.08±0.30	0.09±0.31	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	0.00	2.1	1.4	1.8	2.0	12/58	8/57	12/54	10/55
<i>g_Phascolartobacterium</i>	0.50±0.63	0.61±0.84	0.57±0.66	0.46±0.54	0.26[0.00,0.83]	0.33[0.00,0.80]	0.36[0.00,1.1]	0.18[0.01,0.82]	0.00	0.00	0.00	0.00	3.0	3.5	2.6	2.1	42/58	41/57	38/54	42/55
<i>g_Succiniclacticum</i>	0.03±0.18	0.04±0.19	0.03±0.13	0.03±0.15	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	0.00	1.3	1.3	0.87	0.89	4/58	3/57	3/54	4/55
<i>f_Veillonellaceae</i>	1.3±1.9	1.0±1.4	1.3±1.8	1.4±1.9	0.53[0.03,1.8]	0.14[0.02,1.9]	0.22[0.01,2.0]	0.52[0.02,2.2]	0.00	0.00	0.00	0.00	9.9	5.2	7.0	7.2	56/58	53/57	44/54	51/55
<i>g_Allisonella</i>	0.02±0.08	0.02±0.09	0.03±0.13	0.03±0.14	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	0.00	0.52	0.45	0.80	0.95	8/58	7/57	11/54	8/55
<i>g_Dialister</i>	1.1±1.7	0.83±1.3	1.1±1.6	1.1±1.5	0.03[0.01,1.7]	0.02[0.00,1.4]	0.03[0.00,1.8]	0.33[0.00,1.8]	0.00	0.00	0.00	0.00	7.8	4.2	7.0	5.4	45/58	40/57	37/54	41/55
<i>g_Megamonas</i>	0.04±0.32	0.04±0.31	0.11±0.79	0.13±0.96	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	0.00	2.4	2.3	5.8	7.2	4/58	3/57	2/54	4/55

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<i>g_Megasphaera</i>	0.04±0.32	0.03±0.15	0.02±0.13	0.02±0.14	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	0.00	2.4	0.89	0.88	0.97	2/58	4/57	2/54	4/55
<i>g_Mitsuokella</i>	0.03±0.24	0.02±0.14	0.02±0.14	0.05±0.36	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	0.00	1.8	1.0	1.0	2.7	1/58	4/57	2/54	2/55
<i>g_Selenomonas3</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0/58	0/57	0/54	1/55
<i>g_unknown_Veillonellaceae</i>	0.00±0.01	0.01±0.05	0.00±0.03	0.00±0.02	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	0.00	0.04	0.31	0.22	0.17	2/58	2/57	1/54	1/55
<i>g_Veillonella</i>	0.08±0.17	0.07±0.20	0.04±0.11	0.12±0.67	0.01[0.00,0.05]	0.01[0.00,0.04]	0.01[0.00,0.03]	0.01[0.00,0.05]	0.00	0.00	0.00	0.00	0.94	1.4	0.69	5.0	33/58	37/57	32/54	37/55
<i>p_Fusobacteria</i>	0.00±0.01	0.00±0.01	0.00±0.02	0.02±0.14	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	0.00	0.07	0.08	0.08	1.1	7/58	6/57	6/54	7/55
<i>c_Fusobacteriia</i>	0.00±0.01	0.00±0.01	0.00±0.02	0.02±0.14	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	0.00	0.07	0.08	0.08	1.1	7/58	6/57	6/54	7/55
<i>o_Fusobacteriales</i>	0.00±0.01	0.00±0.01	0.00±0.02	0.02±0.14	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	0.00	0.07	0.08	0.08	1.1	7/58	6/57	6/54	7/55
<i>f_Fusobacteriaceae</i>	0.00±0.01	0.00±0.01	0.00±0.02	0.02±0.14	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	0.00	0.06	0.08	0.08	1.0	5/58	5/57	5/54	6/55
<i>g_Fusobacterium</i>	0.00±0.01	0.00±0.01	0.00±0.02	0.02±0.14	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	0.00	0.06	0.08	0.08	1.0	5/58	5/57	5/54	6/55
<i>f_Leptotrichiaceae</i>	0.00±0.01	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]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.06	0.03	0.01	0.01	3/58	2/57	1/54	2/55
<i>g_Leptotrichia</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.01	2/58	0/57	0/54	1/55
<i>g_Sneathia</i>	0.00±0.01	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]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.06	0.03	0.01	0.01	1/58	2/57	1/54	1/55
<i>p_Lentisphaerae</i>	0.04±0.16	0.01±0.03	0.04±0.18	0.02±0.06	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.02]	0.00[0.00,0.02]	0.00	0.00	0.00	0.00	1.1	0.14	1.3	0.28	18/58	19/57	17/54	20/55
<i>c_Lentisphaeria</i>	0.04±0.16	0.01±0.03	0.04±0.18	0.02±0.06	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.02]	0.00[0.00,0.02]	0.00	0.00	0.00	0.00	1.1	0.14	1.3	0.28	18/58	19/57	17/54	20/55
<i>o_Victivallales</i>	0.04±0.16	0.01±0.03	0.04±0.18	0.02±0.06	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.02]	0.00[0.00,0.02]	0.00	0.00	0.00	0.00	1.1	0.14	1.3	0.28	18/58	19/57	17/54	20/55
<i>f_vadinBE97</i>	0.02±0.09	0.01±0.02	0.02±0.09	0.01±0.04	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	0.00	0.67	0.14	0.62	0.28	5/58	6/57	6/54	5/55
<i>g_unknown_vadinBE97</i>	0.02±0.09	0.01±0.02	0.02±0.09	0.01±0.04	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	0.00	0.67	0.14	0.62	0.28	5/58	6/57	6/54	5/55
<i>f_Victivallaceae</i>	0.02±0.07	0.01±0.02	0.03±0.10	0.01±0.03	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00	0.00	0.00	0.00	0.47	0.09	0.64	0.17	16/58	16/57	15/54	19/55
<i>g_unknown_Victivallaceae</i>	0.01±0.06	0.00±0.00	0.01±0.09	0.00±0.02	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	0.00	0.47	0.00	0.63	0.15	2/58	0/57	3/54	3/55
<i>g_Victivallis</i>	0.01±0.04	0.01±0.02	0.01±0.04	0.01±0.02	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00	0.00	0.00	0.00	0.25	0.09	0.26	0.10	15/58	16/57	14/54	17/55
<i>p_Proteobacteria</i>	3.1±3.9	3.1±3.3	3.2±3.8	2.8±3.0	1.9[0.97,3.5]	2.0[1.1,3.5]	2.2[1.0,3.3]	1.8[0.86,3.3]	0.12	0.15	0.07	0.17	26	15	22	15	58/58	57/57	54/54	55/55
<i>c_Alphaproteobacteria</i>	0.50±1.4	0.55±1.4	0.49±0.98	0.43±0.94	0.02[0.00,0.42]	0.01[0.00,0.62]	0.02[0.00,0.39]	0.01[0.00,0.44]	0.00	0.00	0.00	0.00	9.5	9.6	4.5	5.0	37/58	35/57	32/54	33/55
<i>o_Rhodospirillales</i>	0.50±1.4	0.55±1.4	0.49±0.98	0.43±0.94	0.02[0.00,0.42]	0.01[0.00,0.62]	0.02[0.00,0.39]	0.01[0.00,0.44]	0.00	0.00	0.00	0.00	9.5	9.6	4.5	5.0	36/58	34/57	32/54	32/55
<i>f_Rhodospirillaceae</i>	0.50±1.4	0.55±1.4	0.49±0.98	0.43±0.94	0.02[0.00,0.42]	0.01[0.00,0.62]	0.02[0.00,0.39]	0.01[0.00,0.44]	0.00	0.00	0.00	0.00	9.5	9.6	4.5	5.0	36/58	34/57	32/54	32/55
<i>g_unknown_Rhodospirillaceae</i>	0.50±1.4	0.55±1.4	0.49±0.98	0.43±0.94	0.02[0.00,0.42]	0.01[0.00,0.62]	0.02[0.00,0.39]	0.01[0.00,0.44]	0.00	0.00	0.00	0.00	9.5	9.6	4.5	5.0	36/58	34/57	32/54	32/55
<i>o_Rickettsiales</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.01	1/58	2/57	0/54	1/55
<i>f_Mitochondria</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.01	1/58	2/57	0/54	1/55
<i>g_unknown_Mitochondria</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.01	1/58	2/57	0/54	1/55
<i>c_Betaproteobacteria</i>	1.1±1.0	1.4±2.1	1.1±0.89	1.2±1.1	0.89[0.29,1.6]	0.84[0.43,1.7]	1.0[0.31,1.7]	1.0[0.46,1.7]	0.00	0.00	0.00	0.00	5.2	13	3.9	6.1	54/58	53/57	53/54	53/55
<i>o_Burkholderiales</i>	1.1±1.0	1.4±2.1	1.1±0.89	1.2±1.1	0.89[0.29,1.6]	0.84[0.43,1.7]	1.0[0.31,1.7]	1.0[0.46,1.7]	0.00	0.00	0.00	0.00	5.2	13	3.9	6.1	54/58	53/57	53/54	53/55
<i>f_Alcaligenaceae</i>	1.1±1.0	1.4±2.1	1.1±0.88	1.2±1.1	0.89[0.27,1.6]	0.84[0.43,1.7]	1.0[0.30,1.7]	0.97[0.46,1.7]	0.00	0.00	0.00	0.00	5.2	13	3.9	6.1	54/58	53/57	53/54	53/55
<i>g_Parasutterella</i>	0.44±0.71	0.37±0.55	0.43±0.66	0.42±0.58	0.09[0.01,0.48]	0.05[0.00,0.58]	0.07[0.00,0.89]	0.07[0.01,0.95]	0.00	0.00	0.00	0.00	2.6	2.0	2.2	2.0	44/58	41/57	40/54	42/55
<i>g_Sutterella</i>	0.68±0.99	1.0±2.2	0.67±0.90	0.76±1.2	0.24[0.01,1.1]	0.32[0.01,0.96]	0.27[0.01,1.2]	0.29[0.01,0.87]	0.00	0.00	0.00	0.00	5.2	13	3.8	6.1	47/58	47/57	46/54	46/55
<i>f_Oxalobacteraceae</i>	0.02±0.03	0.01±0.02	0.02±0.04	0.02±0.03	0.00[0.00,0.02]	0.00[0.00,0.03]	0.00[0.00,0.03]	0.00[0.00,0.03]	0.00	0.00	0.00	0.00	0.10	0.06	0.18	0.10	23/58	21/57	23/54	22/55
<i>g_Oxalobacter</i>	0.01±0.03	0.01±0.02	0.02±0.04	0.02±0.03	0.00[0.00,0.02]	0.00[0.00,0.03]	0.00[0.00,0.02]	0.00[0.00,0.03]	0.00	0.00	0.00	0.00	0.10	0.06	0.18	0.10	20/58	18/57	20/54	19/55
<i>g_unknown_Oxalobacteraceae</i>	0.00±0.01	0.00±0.01	0.00±0.01	0.00±0.01	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	0.00	0.03	0.03	0.04	0.04	3/58	3/57	3/54	3/55
<i>o_Neisseriales</i>	0.00±0.00	0.00±0.00	0.00±0.00	0.00±0.01	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	0.00	0.00	0.02	0.00	0.09	0/58	1/57	0/54	1/55
<i>f_Neisseriaceae</i>	0.00±0.00	0.00±0.00	0.00±0.00	0.00±0.01	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	0.00	0.00	0.02	0.00	0.09	0/58	1/57	0/54	1/55
<i>g_Eikenella</i>	0.00±0.00	0.00±0.00	0.00±0.00	0.00±0.01	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	0.00	0.00	0.02	0.00	0.07	0/58	1/57	0/54	1/55

Effects of fructan and gluten on gut microbiota in individuals with self-reported non-celiac gluten/wheat sensitivity – a randomised controlled crossover trial, Herfindal AM *et al.*

<i>g_Neisseria</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0/58	0/57	0/54	1/55
<i>o_Nitrosomonadales</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.03	0.00	0.01	0.00	1/58	0/57	1/54	0/55
<i>f_Nitrosomonadaceae</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.03	0.00	0.01	0.00	1/58	0/57	1/54	0/55
<i>g_Nitrosomonas</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.03	0.00	0.01	0.00	1/58	0/57	1/54	0/55
<i>c_Deltaproteobacteria</i>	0.28±0.29	0.23±0.26	0.30±0.30	0.22±0.23	0.20[0.07,0.39]	0.15[0.07,0.31]	0.18[0.09,0.45]	0.13[0.05,0.30]	0.00	0.00	0.00	0.00	1.4	1.3	1.1	1.1	50/58	50/57	50/54	49/55
<i>o_Desulfovibrionales</i>	0.28±0.29	0.23±0.26	0.30±0.30	0.22±0.23	0.20[0.07,0.39]	0.15[0.07,0.31]	0.18[0.09,0.45]	0.13[0.05,0.30]	0.00	0.00	0.00	0.00	1.4	1.3	1.1	1.1	50/58	50/57	50/54	49/55
<i>f_Desulfovibrionaceae</i>	0.28±0.29	0.23±0.26	0.30±0.30	0.22±0.23	0.20[0.07,0.39]	0.15[0.07,0.31]	0.18[0.09,0.45]	0.13[0.05,0.30]	0.00	0.00	0.00	0.00	1.4	1.3	1.1	1.1	50/58	50/57	50/54	49/55
<i>g_Bilophila</i>	0.21±0.21	0.17±0.19	0.23±0.25	0.17±0.19	0.15[0.05,0.28]	0.11[0.04,0.27]	0.15[0.05,0.31]	0.10[0.03,0.25]	0.00	0.00	0.00	0.00	0.99	0.92	1.1	0.81	49/58	46/57	49/54	48/55
<i>g_Desulfovibrio</i>	0.07±0.18	0.06±0.18	0.08±0.17	0.05±0.12	0.01[0.00,0.04]	0.00[0.00,0.04]	0.02[0.00,0.05]	0.00[0.00,0.03]	0.00	0.00	0.00	0.00	1.0	1.2	0.77	0.62	30/58	28/57	30/54	25/55
<i>c_Epsilonproteobacteria</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.01	0.02	0.01	0.00	4/58	6/57	1/54	0/55
<i>o_Campylobacteriales</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.01	0.02	0.01	0.00	4/58	6/57	1/54	0/55
<i>f_Campylobacteraceae</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.01	0.02	0.01	0.00	4/58	6/57	1/54	0/55
<i>g_Campylobacter</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.01	0.02	0.01	0.00	4/58	6/57	1/54	0/55
<i>c_Gammaproteobacteria</i>	1.2±3.6	0.92±2.5	1.3±3.6	0.95±2.8	0.14[0.05,0.66]	0.14[0.05,0.50]	0.14[0.03,0.26]	0.08[0.04,0.34]	0.00	0.00	0.01	0.01	25	14	22	15	56/58	55/57	54/54	55/55
<i>o_Aeromonadales</i>	0.04±0.27	0.03±0.24	0.13±0.96	0.28±1.9	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	0.00	2.1	1.8	7.1	14	4/58	4/57	9/54	8/55
<i>f_Succinivibrionaceae</i>	0.04±0.27	0.03±0.24	0.13±0.96	0.28±1.9	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	0.00	2.1	1.8	7.1	14	4/58	4/57	9/54	8/55
<i>g_Succinivibrio</i>	0.04±0.27	0.03±0.24	0.13±0.96	0.28±1.9	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	0.00	2.1	1.8	7.1	14	4/58	4/57	9/54	8/55
<i>o_Alteromonadales</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00	1/58	0/57	0/54	0/55
<i>f_Pseudoalteromonadaceae</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00	1/58	0/57	0/54	0/55
<i>g_Pseudoalteromonas</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00	1/58	0/57	0/54	0/55
<i>o_Enterobacteriales</i>	1.1±3.7	0.72±2.5	1.0±3.4	0.52±1.9	0.08[0.02,0.31]	0.07[0.02,0.21]	0.05[0.01,0.17]	0.04[0.01,0.12]	0.00	0.00	0.00	0.00	25	14	22	11	49/58	52/57	50/54	47/55
<i>f_Enterobacteriaceae</i>	1.1±3.7	0.72±2.5	1.0±3.4	0.52±1.9	0.08[0.02,0.31]	0.07[0.02,0.21]	0.05[0.01,0.17]	0.04[0.01,0.12]	0.00	0.00	0.00	0.00	25	14	22	11	49/58	52/57	50/54	47/55
<i>g_Escherichia-Shigella</i>	0.86±3.5	0.68±2.4	0.90±2.9	0.42±1.6	0.04[0.01,0.18]	0.04[0.02,0.17]	0.03[0.01,0.17]	0.02[0.01,0.08]	0.00	0.00	0.00	0.00	24	14	17	9.3	48/58	51/57	49/54	43/55
<i>g_Klebsiella</i>	0.14±0.58	0.04±0.14	0.12±0.62	0.10±0.39	0.00[0.00,0.00]	0.00[0.00,0.00]	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00	0.00	0.00	0.00	4.2	0.72	4.3	2.1	14/58	11/57	14/54	17/55
<i>g_Proteus</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00	1/58	0/57	0/54	0/55
<i>g_unknown_Enterobacteriaceae</i>	0.07±0.36	0.00±0.02	0.00±0.03	0.01±0.03	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	0.00	2.5	0.16	0.20	0.18	6/58	4/57	3/54	5/55
<i>o_Oceanospirillales</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.01	0.01	0.01	0.03	1/58	1/57	1/54	1/55
<i>f_Halomonadaceae</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.01	0.01	0.01	0.03	1/58	1/57	1/54	1/55
<i>g_Halomonas</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.01	0.01	0.01	0.03	1/58	1/57	1/54	1/55
<i>o_Pasteurellales</i>	0.11±0.24	0.16±0.45	0.10±0.22	0.15±0.34	0.02[0.01,0.08]	0.02[0.00,0.19]	0.02[0.00,0.08]	0.03[0.01,0.08]	0.00	0.00	0.00	0.00	1.5	3.2	0.87	1.9	44/58	36/57	33/54	44/55
<i>f_Pasteurellaceae</i>	0.11±0.24	0.16±0.45	0.10±0.22	0.15±0.34	0.02[0.01,0.08]	0.02[0.00,0.19]	0.02[0.00,0.08]	0.03[0.01,0.08]	0.00	0.00	0.00	0.00	1.5	3.2	0.87	1.9	44/58	36/57	33/54	44/55
<i>g_Actinobacillus</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.01	0.01	0.01	0.00	1/58	2/57	1/54	0/55
<i>g_Aggregatibacter</i>	0.00±0.00	0.00±0.00	0.00±0.01	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	0.00	0.00	0.00	0.01	0.01	0.08	0.00	1/58	1/57	2/54	0/55
<i>g_Haemophilus</i>	0.11±0.24	0.16±0.45	0.10±0.21	0.15±0.34	0.02[0.01,0.08]	0.02[0.00,0.19]	0.02[0.00,0.08]	0.03[0.01,0.08]	0.00	0.00	0.00	0.00	1.5	3.2	0.86	1.9	44/58	36/57	33/54	44/55
<i>g_unknown_Pasteurellaceae</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.01	0/58	1/57	0/54	1/55
<i>o_Pseudomonadales</i>	0.00±0.00	0.00±0.02	0.00±0.02	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	0.00	0.00	0.00	0.00	0.13	0.15	0.01	0/58	3/57	3/54	1/55
<i>f_Pseudomonadaceae</i>	0.00±0.00	0.00±0.02	0.00±0.02	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	0.00	0.00	0.00	0.00	0.13	0.15	0.01	0/58	3/57	3/54	1/55
<i>g_Pseudomonas</i>	0.00±0.00	0.00±0.02	0.00±0.02	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	0.00	0.00	0.00	0.00	0.13	0.15	0.01	0/58	3/57	3/54	1/55
<i>p_Saccharibacteria</i>	0.00±0.01	0.00±0.01	0.00±0.01	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	0.00	0.00	0.00	0.04	0.02	0.03	0.02	13/58	9/57	10/54	10/55
<i>g_CandidatusSaccharimonas</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[0.00,0.00]	0.00[0.00,0.00]	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0/58	0/57	1/54	1/55

Effects of fructan and gluten on gut microbiota in individuals with self-reported non-celiac gluten/wheat sensitivity – a randomised controlled crossover trial, Herfindal AM *et al.*

<i>g_unknown_Saccharibacteria</i>	0.00±0.01	0.00±0.01	0.00±0.01	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	0.00	0.00	0.00	0.04	0.02	0.03	0.02	13/58	9/57	9/54	9/55
<i>f_unknown_Saccharibacteria</i>	0.00±0.01	0.00±0.01	0.00±0.01	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	0.00	0.00	0.00	0.04	0.02	0.03	0.02	13/58	9/57	10/54	10/55
<i>o_unknown_Saccharibacteria</i>	0.00±0.01	0.00±0.01	0.00±0.01	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	0.00	0.00	0.00	0.04	0.02	0.03	0.02	13/58	9/57	10/54	10/55
<i>c_unknown_Saccharibacteria</i>	0.00±0.01	0.00±0.01	0.00±0.01	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	0.00	0.00	0.00	0.04	0.02	0.03	0.02	13/58	9/57	10/54	10/55
<i>p_Synergistetes</i>	0.01±0.03	0.00±0.01	0.00±0.02	0.00±0.01	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	0.00	0.22	0.05	0.16	0.06	6/58	5/57	4/54	6/55
<i>c_Synergistia</i>	0.01±0.03	0.00±0.01	0.00±0.02	0.00±0.01	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	0.00	0.22	0.05	0.16	0.06	6/58	5/57	4/54	6/55
<i>o_Synergistales</i>	0.01±0.03	0.00±0.01	0.00±0.02	0.00±0.01	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	0.00	0.22	0.05	0.16	0.06	6/58	5/57	4/54	6/55
<i>f_Synergistaceae</i>	0.01±0.03	0.00±0.01	0.00±0.02	0.00±0.01	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	0.00	0.22	0.05	0.16	0.06	6/58	5/57	4/54	6/55
<i>g_Cloacibacillus</i>	0.01±0.03	0.00±0.01	0.00±0.02	0.00±0.01	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	0.00	0.22	0.05	0.16	0.06	6/58	5/57	4/54	6/55
<i>p_Tenericutes</i>	0.36±0.67	0.34±0.91	0.26±0.50	0.28±0.54	0.06[0.00,0.43]	0.06[0.00,0.32]	0.04[0.00,0.37]	0.02[0.00,0.42]	0.00	0.00	0.00	0.00	2.9	5.6	3.1	3.4	34/58	37/57	39/54	34/55
<i>c_Mollicutes</i>	0.36±0.67	0.34±0.91	0.26±0.50	0.28±0.54	0.06[0.00,0.43]	0.06[0.00,0.32]	0.04[0.00,0.37]	0.02[0.00,0.42]	0.00	0.00	0.00	0.00	2.9	5.6	3.1	3.4	34/58	37/57	39/54	34/55
<i>o_Anaeroplasmatales</i>	0.07±0.35	0.15±0.79	0.04±0.15	0.06±0.29	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	0.00	2.3	4.5	0.79	2.0	4/58	5/57	7/54	8/55
<i>f_Anaeroplasmataceae</i>	0.07±0.35	0.15±0.79	0.04±0.15	0.06±0.29	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	0.00	2.3	4.5	0.79	2.0	4/58	5/57	7/54	8/55
<i>g_Anaeroplasma</i>	0.07±0.35	0.15±0.79	0.04±0.15	0.06±0.29	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	0.00	2.3	4.5	0.79	2.0	4/58	5/57	7/54	8/55
<i>o_MollicutesRF9</i>	0.22±0.49	0.09±0.13	0.10±0.16	0.11±0.17	0.00[0.00,0.14]	0.01[0.00,0.13]	0.01[0.00,0.15]	0.00[0.00,0.21]	0.00	0.00	0.00	0.00	2.6	0.47	0.80	0.69	28/58	31/57	33/54	27/55
<i>g_unknown_MollicutesRF9</i>	0.22±0.49	0.09±0.13	0.10±0.16	0.11±0.17	0.00[0.00,0.14]	0.01[0.00,0.13]	0.01[0.00,0.15]	0.00[0.00,0.21]	0.00	0.00	0.00	0.00	2.6	0.47	0.80	0.69	28/58	31/57	33/54	27/55
<i>f_unknown_MollicutesRF9</i>	0.22±0.49	0.09±0.13	0.10±0.16	0.11±0.17	0.00[0.00,0.14]	0.01[0.00,0.13]	0.01[0.00,0.15]	0.00[0.00,0.21]	0.00	0.00	0.00	0.00	2.6	0.47	0.80	0.69	28/58	31/57	33/54	27/55
<i>o_NB1-n</i>	0.08±0.20	0.10±0.24	0.12±0.41	0.11±0.25	0.00[0.00,0.08]	0.00[0.00,0.07]	0.00[0.00,0.06]	0.00[0.00,0.07]	0.00	0.00	0.00	0.00	1.3	1.1	2.8	1.2	25/58	27/57	24/54	25/55
<i>g_unknown_NB1-n</i>	0.08±0.20	0.10±0.24	0.12±0.41	0.11±0.25	0.00[0.00,0.08]	0.00[0.00,0.07]	0.00[0.00,0.06]	0.00[0.00,0.07]	0.00	0.00	0.00	0.00	1.3	1.1	2.8	1.2	25/58	27/57	24/54	25/55
<i>f_unknown_NB1-n</i>	0.08±0.20	0.10±0.24	0.12±0.41	0.11±0.25	0.00[0.00,0.08]	0.00[0.00,0.07]	0.00[0.00,0.06]	0.00[0.00,0.07]	0.00	0.00	0.00	0.00	1.3	1.1	2.8	1.2	25/58	27/57	24/54	25/55
<i>g_unknown_Bacteria</i>	0.00±0.03	0.00±0.01	0.00±0.03	0.00±0.02	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	0.00	0.22	0.07	0.20	0.14	3/58	1/57	1/54	1/55
<i>f_unknown_Bacteria</i>	0.00±0.03	0.00±0.01	0.00±0.03	0.00±0.02	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	0.00	0.22	0.07	0.20	0.14	3/58	1/57	1/54	1/55
<i>o_unknown_Bacteria</i>	0.00±0.03	0.00±0.01	0.00±0.03	0.00±0.02	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	0.00	0.22	0.07	0.20	0.14	3/58	1/57	1/54	1/55
<i>c_unknown_Bacteria</i>	0.00±0.03	0.00±0.01	0.00±0.03	0.00±0.02	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	0.00	0.22	0.07	0.20	0.14	3/58	1/57	1/54	1/55
<i>p_unknown_Bacteria</i>	0.00±0.03	0.00±0.01	0.00±0.03	0.00±0.02	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	0.00	0.22	0.07	0.20	0.14	3/58	1/57	1/54	1/55
<i>p_Verrucomicrobia</i>	0.19±0.45	0.18±0.29	0.16±0.22	0.16±0.35	0.05[0.00,0.21]	0.08[0.01,0.23]	0.08[0.01,0.30]	0.04[0.00,0.10]	0.00	0.00	0.00	0.00	3.0	1.4	0.83	1.8	39/58	43/57	42/54	39/55
<i>c_Opitutae</i>	0.00±0.01	0.00±0.01	0.00±0.02	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	0.00	0.00	0.00	0.04	0.03	0.11	0.03	4/58	4/57	4/54	3/55
<i>o_Opitutae</i>	0.00±0.01	0.00±0.01	0.00±0.02	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	0.00	0.00	0.00	0.04	0.03	0.11	0.03	4/58	4/57	4/54	3/55
<i>g_unknown_Opitutae</i>	0.00±0.01	0.00±0.01	0.00±0.02	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	0.00	0.00	0.00	0.04	0.03	0.11	0.03	4/58	4/57	4/54	3/55
<i>f_unknown_Opitutae</i>	0.00±0.01	0.00±0.01	0.00±0.02	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	0.00	0.00	0.00	0.04	0.03	0.11	0.03	4/58	4/57	4/54	3/55
<i>c_Verrucomicrobiae</i>	0.19±0.45	0.18±0.29	0.16±0.22	0.15±0.35	0.05[0.00,0.20]	0.08[0.00,0.23]	0.07[0.01,0.29]	0.04[0.00,0.10]	0.00	0.00	0.00	0.00	3.0	1.4	0.83	1.8	39/58	41/57	41/54	39/55
<i>o_Verrucomicrobiales</i>	0.19±0.45	0.18±0.29	0.16±0.22	0.15±0.35	0.05[0.00,0.20]	0.08[0.00,0.23]	0.07[0.01,0.29]	0.04[0.00,0.10]	0.00	0.00	0.00	0.00	3.0	1.4	0.83	1.8	39/58	41/57	41/54	39/55
<i>f_Verrucomicrobiaceae</i>	0.19±0.45	0.18±0.29	0.16±0.22	0.15±0.35	0.05[0.00,0.20]	0.08[0.00,0.23]	0.07[0.01,0.29]	0.04[0.00,0.10]	0.00	0.00	0.00	0.00	3.0	1.4	0.83	1.8	39/58	41/57	41/54	39/55
<i>g_Akkermansia</i>	0.19±0.45	0.18±0.29	0.16±0.22	0.15±0.35	0.05[0.00,0.20]	0.08[0.00,0.23]	0.07[0.01,0.29]	0.04[0.00,0.10]	0.00	0.00	0.00	0.00	3.0	1.4	0.83	1.8	39/58	41/57	41/54	39/55
<i>k_Unassigned</i>	0.01±0.01	0.00±0.01	0.00±0.01	0.00±0.01	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00	0.00	0.00	0.00	0.04	0.06	0.03	0.02	20/58	14/57	15/54	16/55
<i>g_unknown_Unassigned</i>	0.01±0.01	0.00±0.01	0.00±0.01	0.00±0.01	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00	0.00	0.00	0.00	0.04	0.06	0.03	0.02	20/58	14/57	15/54	16/55
<i>f_unknown_Unassigned</i>	0.01±0.01	0.00±0.01	0.00±0.01	0.00±0.01	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00	0.00	0.00	0.00	0.04	0.06	0.03	0.02	20/58	14/57	15/54	16/55
<i>o_unknown_Unassigned</i>	0.01±0.01	0.00±0.01	0.00±0.01	0.00±0.01	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00	0.00	0.00	0.00	0.04	0.06	0.03	0.02	20/58	14/57	15/54	16/55
<i>c_unknown_Unassigned</i>	0.01±0.01	0.00±0.01	0.00±0.01	0.00±0.01	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00	0.00	0.00	0.00	0.04	0.06	0.03	0.02	20/58	14/57	15/54	16/55
<i>p_unknown_Unassigned</i>	0.01±0.01	0.00±0.01	0.00±0.01	0.00±0.01	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00[0.00,0.01]	0.00	0.00	0.00	0.00	0.04	0.06	0.03	0.02	20/58	14/57	15/54	16/55

Table S7. Summary statistics for faecal SCFA at baseline ($n = 56$) and after the 7-day FOS-fructan ($n = 55$), gluten ($n = 52$), and placebo ($n = 53$) challenges. Summary statistics for SCFA concentrations (“conc”, mmol/kg faeces) and proportional levels (“%”, of total SCFA concentration) include means with SD, medians with 25th and 75th percentile, minimum value, maximum value, detection rate (i.e., in how many samples the SCFA was detected out of total number of samples analysed for SCFA). The three participants that were missing baseline SCFA data, and therefore excluded from all the other statistical analyses (see section 3.1 in main text), were not included in the summary statistics. FOS, fructo-oligosaccharides; SCFA, short-chain fatty acids.

	Baseline/ diet challenge	Mean ± SD	Median [Q1,Q3]	Minimum	Maximum	Detected in
Total SCFA, conc	Baseline	54 ± 22	51 [35,68]	15	111	56/56
Total SCFA, conc	FOS-fructan	58 ± 22	57 [41,69]	13	110	55/55
Total SCFA, conc	Gluten	57 ± 24	54 [41,72]	20	114	52/52
Total SCFA, conc	Placebo	57 ± 20	56 [41,72]	19	112	53/53
Acetic acid, conc	Baseline	31 ± 12	31 [24,38]	11	72	56/56
Acetic acid, conc	FOS-fructan	34 ± 14	32 [24,38]	6.1	68	55/55
Acetic acid, conc	Gluten	33 ± 15	32 [22,38]	9.7	65	52/52
Acetic acid, conc	Placebo	32 ± 12	30 [23,42]	9.2	62	53/53
Butyric acid, conc	Baseline	9.9 ± 7.2	8.3 [5.0,12]	1.0	33	56/56
Butyric acid, conc	FOS-fructan	11 ± 6.7	9.3 [6.7,14]	2.5	41	55/55
Butyric acid, conc	Gluten	11 ± 5.6	9.7 [5.4,14]	1.3	22	52/52
Butyric acid, conc	Placebo	11 ± 5.0	11 [6.6,14]	1.9	24	53/53
Propionic acid, conc	Baseline	8.1 ± 3.5	7.5 [5.1,11]	2.0	16	56/56
Propionic acid, conc	FOS-fructan	9.0 ± 4.1	8.7 [6.2,10]	2.7	24	55/55
Propionic acid, conc	Gluten	9.0 ± 4.7	7.4 [6.2,11]	2.7	25	52/52
Propionic acid, conc	Placebo	9.0 ± 4.3	8.4 [6.0,12]	3.4	23	53/53
Valeric acid, conc	Baseline	1.3 ± 0.70	1.1 [0.78,1.6]	0.08	4.0	56/56
Valeric acid, conc	FOS-fructan	1.3 ± 0.56	1.2 [0.91,1.7]	0.08	2.5	55/55
Valeric acid, conc	Gluten	1.4 ± 0.63	1.2 [0.94,1.7]	0.20	3.3	52/52
Valeric acid, conc	Placebo	1.3 ± 0.58	1.2 [0.87,1.7]	0.19	2.5	53/53
Iso-valeric acid, conc	Baseline	1.9 ± 1.3	1.5 [1.1,2.2]	0.40	9.1	56/56
Iso-valeric acid, conc	FOS-fructan	1.7 ± 0.95	1.5 [1.1,2.1]	0.22	5.6	55/55
Iso-valeric acid, conc	Gluten	1.8 ± 1.1	1.6 [1.2,2.2]	0.20	6.6	52/52
Iso-valeric acid, conc	Placebo	1.8 ± 0.91	1.6 [1.3,2.3]	0.31	4.9	53/53
Iso-butyric acid, conc	Baseline	1.2 ± 0.78	1.0 [0.78,1.6]	0.41	5.4	56/56
Iso-butyric acid, conc	FOS-fructan	1.2 ± 0.62	1.0 [0.79,1.5]	0.27	4.2	55/55
Iso-butyric acid, conc	Gluten	1.2 ± 0.63	1.2 [0.79,1.3]	0.24	4.0	52/52
Iso-butyric acid, conc	Placebo	1.2 ± 0.53	1.0 [0.82,1.6]	0.38	3.2	53/53
Caproic acid, conc	Baseline	0.46 ± 0.67	0.22 [0.00,0.60]	0.00	3.5	39/56
Caproic acid, conc	FOS-fructan	0.44 ± 0.49	0.36 [0.00,0.68]	0.00	2.2	35/55
Caproic acid, conc	Gluten	0.46 ± 0.69	0.29 [0.00,0.68]	0.00	4.2	31/52
Caproic acid, conc	Placebo	0.45 ± 0.56	0.22 [0.00,0.74]	0.00	2.7	33/53
Iso-caproic acid, conc	Baseline	0.00 ± 0.02	0.00 [0.00,0.00]	0.00	0.14	2/56

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Iso-caproic acid, conc	FOS-fructan	0.00 ± 0.01	0.00 [0.00,0.00]	0.00	0.07	2/55
Iso-caproic acid, conc	Gluten	0.00 ± 0.02	0.00 [0.00,0.00]	0.00	0.12	1/52
Iso-caproic acid, conc	Placebo	0.01 ± 0.02	0.00 [0.00,0.00]	0.00	0.11	3/53
Acetic acid, %	Baseline	59 ± 8.4	59 [52,65]	36	81	56/56
Acetic acid, %	FOS-fructan	58 ± 7.1	58 [54,62]	36	75	55/55
Acetic acid, %	Gluten	57 ± 7.1	58 [52,63]	43	69	52/52
Acetic acid, %	Placebo	57 ± 6.5	57 [52,62]	43	73	53/53
Butyric acid, %	Baseline	17 ± 6.4	17 [12,20]	5.5	31	56/56
Butyric acid, %	FOS-fructan	19 ± 6.0	17 [14,23]	8.3	42	55/55
Butyric acid, %	Gluten	18 ± 4.5	17 [16,21]	5.4	29	52/52
Butyric acid, %	Placebo	18 ± 4.4	19 [15,22]	7.3	27	53/53
Propionic acid, %	Baseline	15 ± 3.1	15 [13,17]	7.0	22	56/56
Propionic acid, %	FOS-fructan	15 ± 3.5	15 [13,17]	8.8	22	55/55
Propionic acid, %	Gluten	16 ± 3.4	15 [13,18]	7.7	25	52/52
Propionic acid, %	Placebo	16 ± 3.6	16 [13,19]	7.4	25	53/53
Valeric acid, %	Baseline	2.4 ± 0.82	2.5 [2.0,2.9]	0.22	3.7	56/56
Valeric acid, %	FOS-fructan	2.3 ± 0.85	2.3 [1.8,2.8]	0.16	3.8	55/55
Valeric acid, %	Gluten	2.5 ± 0.91	2.6 [2.0,3.0]	0.22	4.2	52/52
Valeric acid, %	Placebo	2.4 ± 0.87	2.6 [1.7,3.0]	0.24	4.3	53/53
Iso-valeric acid, %	Baseline	3.6 ± 1.6	3.6 [2.3,4.7]	0.56	8.6	56/56
Iso-valeric acid, %	FOS-fructan	3.2 ± 1.6	3.1 [2.1,4.4]	0.28	6.8	55/55
Iso-valeric acid, %	Gluten	3.6 ± 1.8	3.7 [2.0,4.6]	0.21	7.6	52/52
Iso-valeric acid, %	Placebo	3.4 ± 1.6	3.4 [2.1,4.7]	0.39	8.2	53/53
Iso-butyric acid, %	Baseline	2.4 ± 0.96	2.4 [1.7,3.1]	0.51	5.1	56/56
Iso-butyric acid, %	FOS-fructan	2.2 ± 0.93	2.1 [1.6,2.7]	0.34	5.0	55/55
Iso-butyric acid, %	Gluten	2.4 ± 0.98	2.4 [1.5,3.1]	0.25	4.5	52/52
Iso-butyric acid, %	Placebo	2.3 ± 0.93	2.2 [1.5,3.0]	0.48	5.0	53/53
Caproic acid, %	Baseline	0.85 ± 1.00	0.58 [0.00,1.3]	0.00	3.9	39/56
Caproic acid, %	FOS-fructan	0.85 ± 0.92	0.77 [0.00,1.5]	0.00	3.9	35/55
Caproic acid, %	Gluten	0.86 ± 0.98	0.90 [0.00,1.4]	0.00	4.2	31/52
Caproic acid, %	Placebo	0.84 ± 0.94	0.64 [0.00,1.4]	0.00	4.8	33/53
Iso-caproic acid, %	Baseline	0.01 ± 0.03	0.00 [0.00,0.00]	0.00	0.15	2/56
Iso-caproic acid, %	FOS-fructan	0.00 ± 0.02	0.00 [0.00,0.00]	0.00	0.11	2/55
Iso-caproic acid, %	Gluten	0.00 ± 0.02	0.00 [0.00,0.00]	0.00	0.12	1/52
Iso-caproic acid, %	Placebo	0.01 ± 0.03	0.00 [0.00,0.00]	0.00	0.12	3/53

Table S8. Summary statistics for faecal NGAL/LCN2 concentrations (ng/g faeces) at baseline ($n = 58$) and after the 7-day FOS-fructan ($n = 56$), gluten ($n = 54$), and placebo ($n = 54$) challenges. Summary statistics include means with SD, medians with 25th and 75th percentile, minimum value, and maximum value. The one participant that was missing baseline NGAL/LCN2 data, and therefore excluded from all the other statistical analyses (see section 3.1), was not included in the summary statistics. FOS, fructo-oligosaccharides; NGAL/LCN2, neutrophil gelatinase-associated lipocalin.

Baseline/diet challenge	Mean $\pm$ SD	Median [Q1,Q3]	Minimum	Maximum
Baseline	291 $\pm$ 225	266 [166,391]	3.7	1302
FOS-fructan	336 $\pm$ 219	314 [206,408]	21	1228
Gluten	324 $\pm$ 252	305 [175,409]	8.6	1494
Placebo	330 $\pm$ 346	263 [178,368]	13	2244

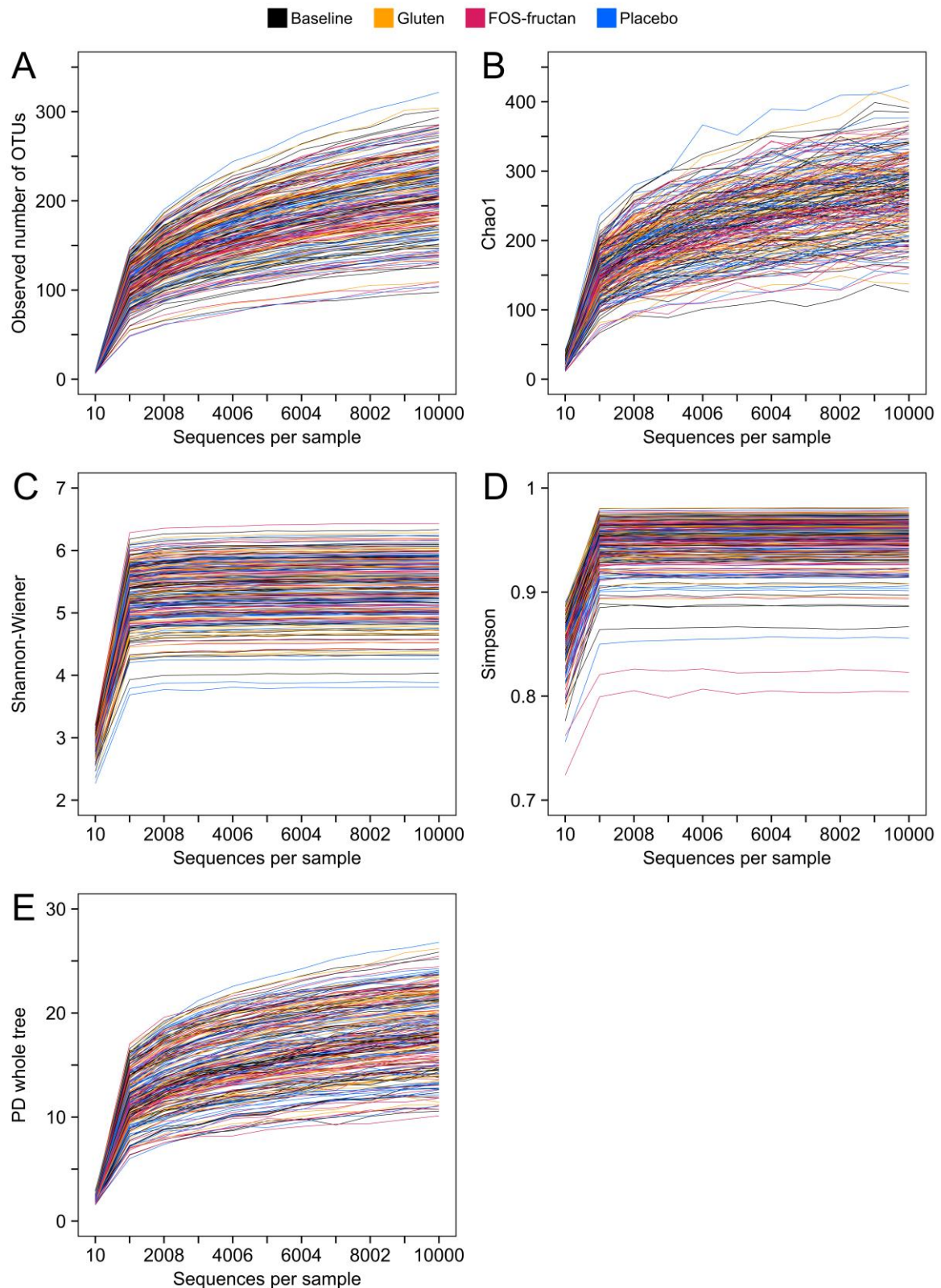


Fig. S1. Rarefaction curves. Relationship between the different measures of α -diversity and sequencing depth (sequences per sample) in faecal samples collected at baseline and after each diet challenge (FOS-fructan, gluten, placebo). **(A)** Number of observed OTUs, **(B)** Chao1, **(C)** Shannon-Wiener, **(D)** Simpson, and **(E)** PD whole tree index of α -diversity. Each line represents one faecal sample from one participant. The α -diversity for one sample at one sequencing depth is the mean α -diversity from ten rarefying iterations. FOS, fructo-oligosaccharides; OTU, operational taxonomic unit.

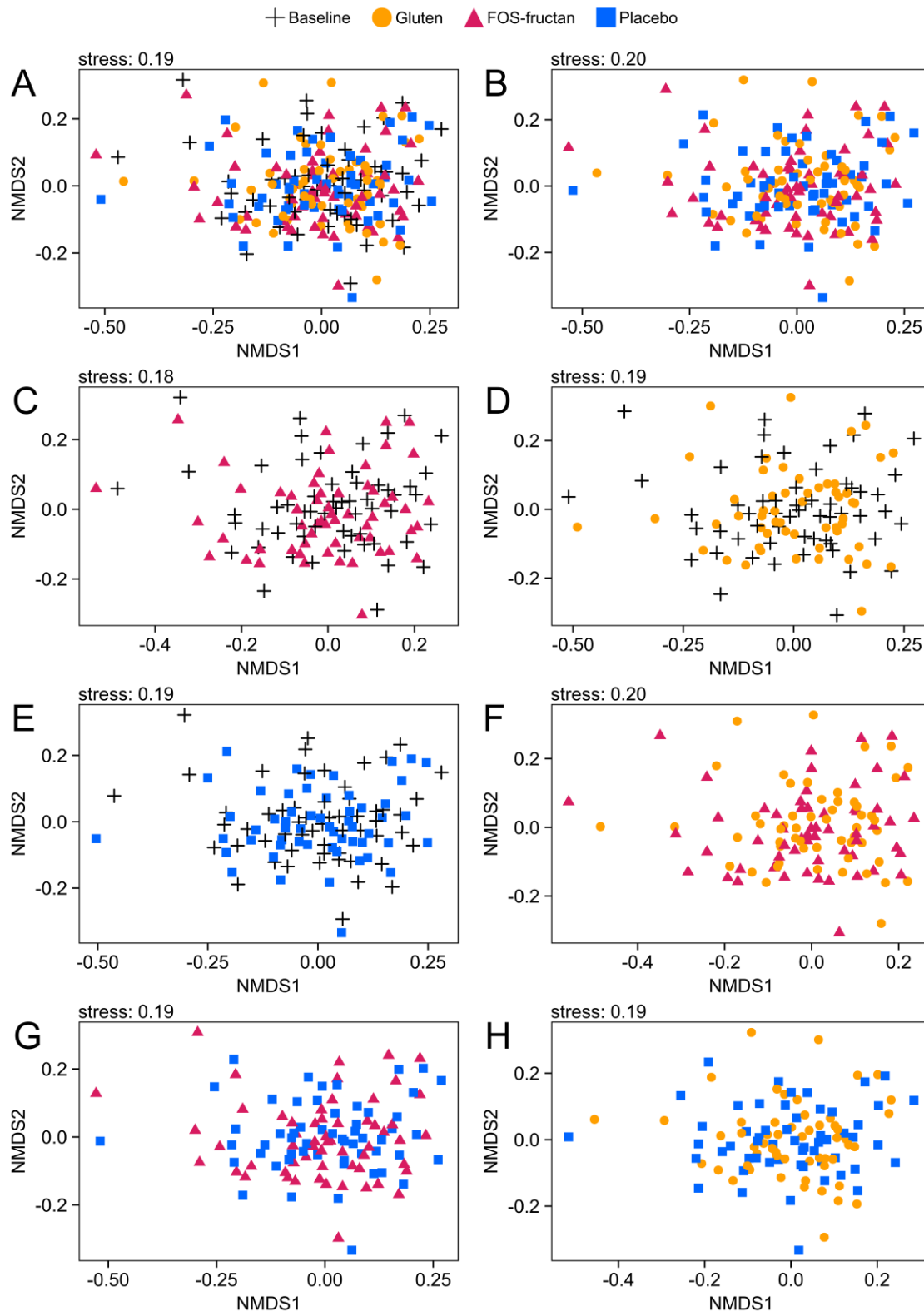


Fig. S2. Ordination plots from non-metric multidimensional scaling (NMDS) of binary Jaccard β -diversity distances between samples from (A) baseline and all diet challenges ($n = 227$), (B) gluten, FOS-fructan, and placebo challenge ($n = 169$), (C) baseline and FOS-fructan challenge ($n = 116$), (D) baseline and gluten challenge ($n = 113$), (E) baseline and placebo challenge ($n = 114$), (F) gluten and FOS-fructan challenges ($n = 113$), (G) FOS-fructan and placebo challenges ($n = 114$), and (H) gluten and placebo challenges ($n = 111$). Each symbol represents one sample from one participant at a given time point (baseline or diet challenge follow-up). FOS, fructo-oligosaccharides.

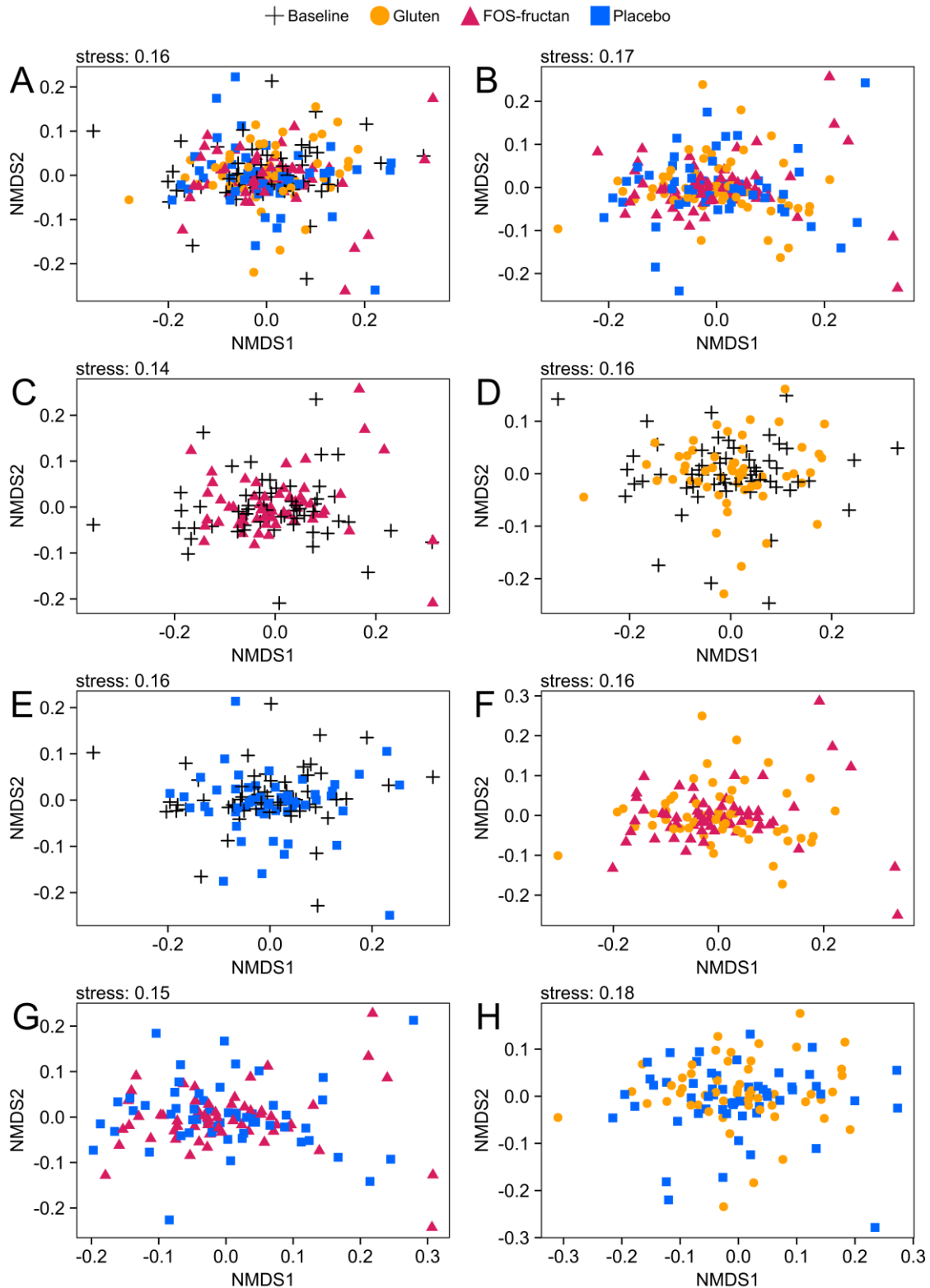


Fig. S3. Ordination plots from non-metric multidimensional scaling (NMDS) of weighted Unifrac β -diversity distances between samples from (A) baseline and all the diet challenges ($n = 227$), (B) gluten, FOS-fructan, and placebo challenge ($n = 169$), (C) baseline and FOS-fructan challenge ($n = 116$), (D) baseline and gluten challenge ($n = 113$), (E) baseline and placebo challenge ($n = 114$), (F) gluten and FOS-fructan challenges ($n = 113$), (G) FOS-fructan and placebo challenges ($n = 114$), and (H) gluten and placebo challenges ($n = 111$). Each symbol represents one sample from one participant at a given time point (baseline or diet challenge follow-up). FOS, fructo-oligosaccharides.

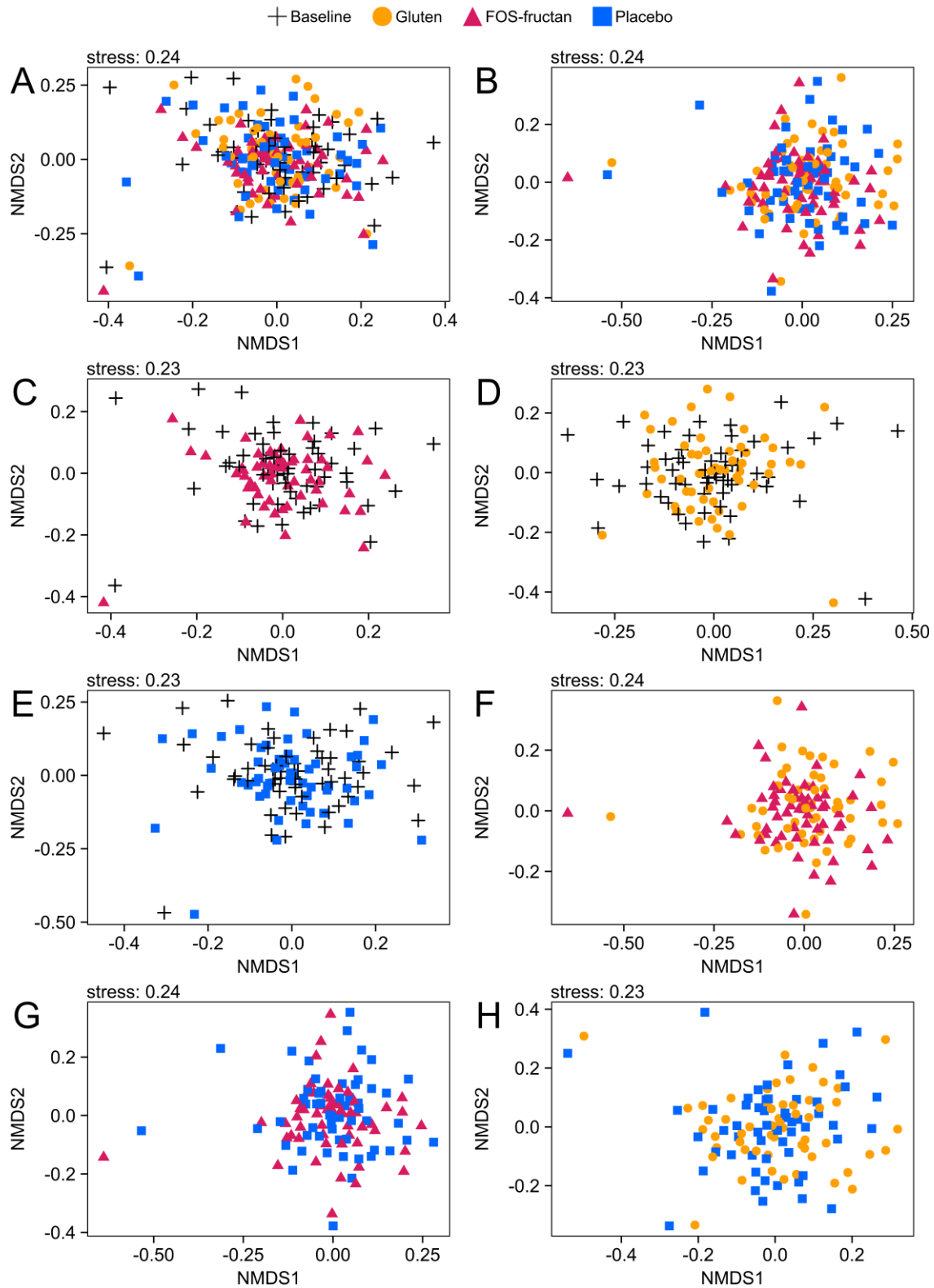


Fig. S4. Ordination plots from non-metric multidimensional scaling (NMDS) of Bray-Curtis β -diversity distances between samples from (A) baseline and all diet challenges ($n = 227$), (B) gluten, FOS-fructan, and placebo challenge ($n = 169$; same as shown in Figure 3 in the main text), (C) baseline and FOS-fructan challenge ($n = 116$), (D) baseline and gluten challenge ($n = 113$), (E) baseline and placebo challenge ($n = 114$), (F) gluten and FOS-fructan challenges ($n = 113$), (G) FOS-fructan and placebo challenges ($n = 114$), and (H) gluten and placebo challenges ($n = 111$). Each symbol represents one sample from one participant at a given time point (baseline or diet challenge follow-up). FOS, fructo-oligosaccharides.

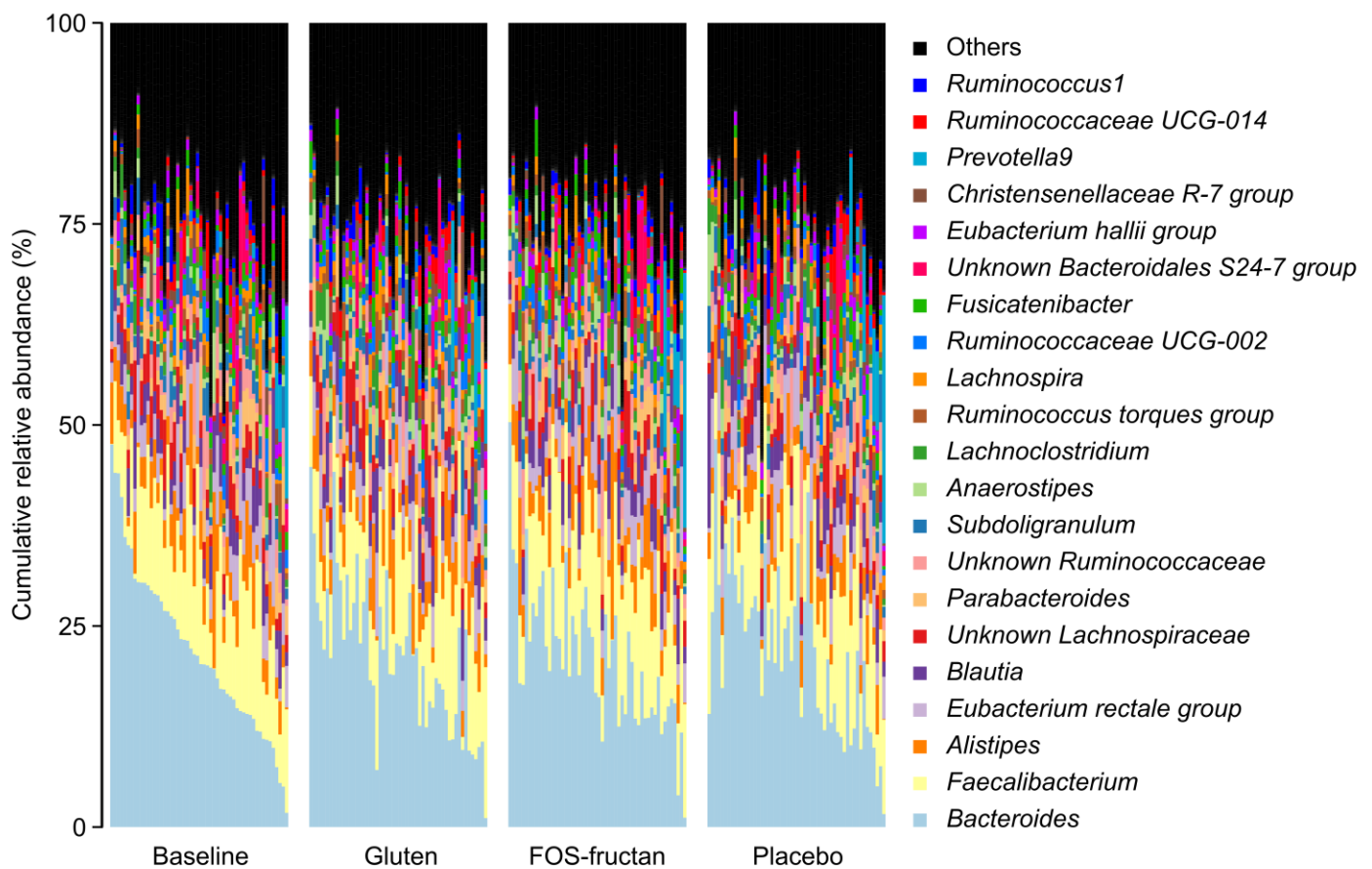


Fig. S5. Faecal relative abundances (%) of bacterial genera at baseline and after the 7-day gluten, FOS-fructan, and placebo challenges. Only participants with 16S data on all four timepoints are included in the figure. One bar represents one participant at a given time point. Participant bars are ordered according to abundance of *Bacteroides* at baseline. Taxa are ordered according to mean overall abundance. Genera with mean overall abundance $\leq 1\%$ are displayed as "Others". FOS, fructo-oligosaccharides.

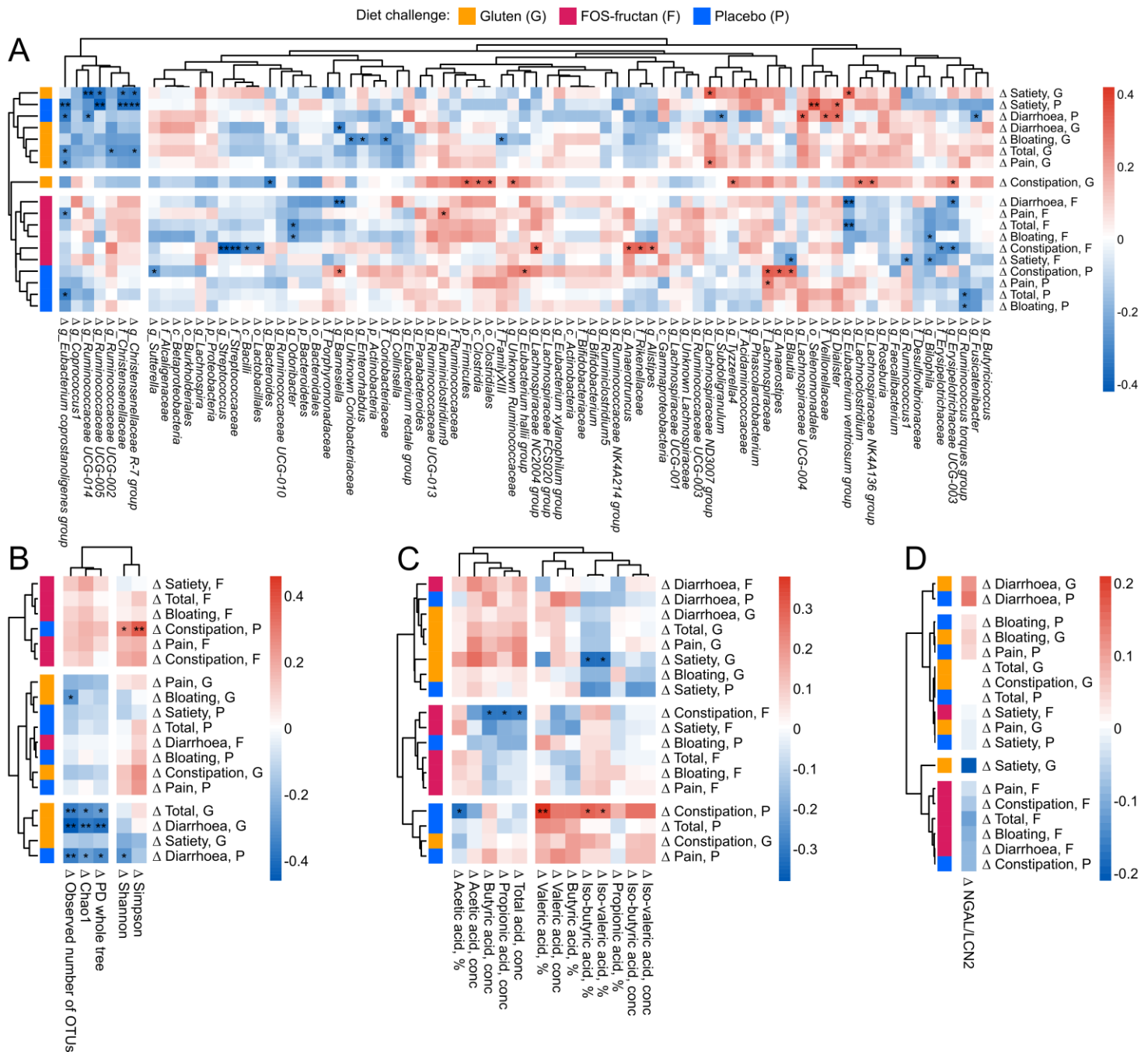
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Fig. S6. Correlograms illustrating Spearman's rank correlation coefficients (Rho) between changes ("Δ") in gastrointestinal symptoms (GSRs-IBS total, pain, bloating, constipation, diarrhoea, and satiety dimension scores) and changes in faecal **(A)** taxa abundances ($0.37 \leq \text{Rho} \leq -0.42$), **(B)** α-diversity ($0.37 \leq \text{Rho} \leq -0.45$), **(C)** SCFA ($0.38 \leq \text{Rho} \leq -0.33$), and **(D)** NGAL/LCN2 (ng/g faeces; $0.15 \leq \text{Rho} \leq -0.21$) following the 7-day gluten, FOS-fructan, and placebo challenges. Colour scale indicates strength and direction of the correlations. Significant correlations (not adjusted for multiple testing) are marked with asterisk (* $P < 0.05$, ** $P < 0.01$). Positive correlation indicates that increased values of the faecal outcome are associated with increased GSRs-IBS scores, while negative correlation indicates that reduced values of the faecal outcome are associated with increased GSRs-IBS scores. (A) A taxon was excluded from the correlation analysis if the median relative abundance $\geq 0.1\%$ for at least one timepoint (baseline or after diet challenge) or if the taxon was detected in less than 50% of the samples from all timepoints (baseline and after each diet challenge). (C) Both SCFA concentrations ("conc", mmol/kg faeces) and proportional levels ("%", of total SCFA concentration) are used in the analysis. FOS, fructo-oligosaccharides; GSRs-IBS, gastrointestinal symptom rating scale IBS version; IBS, irritable bowel syndrome; NGAL/LCN2, neutrophil gelatinase-associated lipocalin/lipocalin 2; SCFA, short-chain fatty acids.

Supplementary method description

OTU tables used for α - and β -diversity

β -diversities were calculated through QIIME default script (core_diversity_analyses.py) based on one single normalized OTU table, while α -diversities were calculated as mean diversity based on OTU tables from ten rarefying iterations.

β -diversity

Non-metric multidimensional scaling (NMDS) of Jaccard, Bray-Curtis, and weighted UniFrac distances was performed using the metaMDS() function from the *vegan* package (k=2, autotransform=FALSE, try=100) [32]. To the previous.best argument, ordination output from the cmdscale() function (k=2) from the *stats* package [33] was used. The goodness of fit of the NMDS ordinations (compliance between the Euclidian ordination distances and the original pairwise distances) were evaluated by the stress value and Shepherd's plot. Shepherd's plots were made using the stressplot() function from the *vegan* package. Stress > 0.2 was considered poor, 0.1-0.2 was considered fair, 0.05-0.1 was considered good, and stress < 0.05 was considered excellent. Global permutation based multivariate ANOVA (PERMANOVA) was performed using the adonis2() function from the *vegan* package, with permutations = 999.

Linear mixed models

Linear mixed models were fitted using the lmer() function (REML=F) from the *lmerTest* package (version 3.1-3) [36], which builds on the *lme4* package (version 1.1-31) [37]. *P* values for effect of diet challenges were obtained using the anova() function on the lmerModLmerTest model object (Type III Analysis of Variance Table with Satterthwaite's method; ddf="Satterthwaite", type=3). Estimated marginal means (EMM) with 95% confidence intervals from linear mixed models for the gluten, FOS-fructan, and placebo challenges were obtained using the ls_means() function from the *lmerTest* package. Significant differences across diet challenges ($P < 0.05$) were followed by pairwise comparison of the three diet challenges (placebo vs. gluten, placebo vs. FOS-fructan, gluten vs. FOS-fructan) using the diffslmeans() function from the *lmerTest* package. The three *P* values from pairwise comparisons for each faecal response were adjusted using the Bonferroni method (p.adjust()) function from the *stats* package [33]).

Assumptions of the described linear mixed models were evaluated in the following manner:

- (1) The normality of the model residuals (marginal and conditional) was assessed using normal QQ plot together with histogram and Shapiro-Wilk normality test. Normal QQ plot was made using the ggqqplot() function from the *ggpubr* package [38]. Histogram was made using the plotNormalHistogram() function from the *rcompanion* package [39]. The shapiro_test() function from the *rstatix* package [40] was used to perform Shapiro-Wilk normality test.

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- (2) Constant variance of the model residuals (marginal and conditional) was assessed by plotting the residuals against fitted values.
- (3) Presence of influential values (participants) was assessed using the `influence()` and `cooks.distance()` functions from the *influence.ME* package (version 0.9-9) [41].

Spearman's correlation analysis

To evaluate the associations between faecal outcomes (changes/baseline levels) and change in GSRS-IBS scores, we computed Spearman's rank correlation coefficients. Spearman's correlation was preferred over parametric alternative (Pearson's correlation) due to its less stringent assumptions. Considering the large number of correlation tests conducted, we deemed it impractical to thoroughly examine if the assumptions for performing Pearson correlation were met for all variables. By utilizing either Spearman's (or Pearson's) correlation, we are only able to determine the strength and direction of the association between two variables, and it should be noted that a significant association does not necessarily imply a cause-and-effect relationship between faecal outcomes and symptom responses.

Spearman's rank correlation coefficients (Rho) and corresponding *P* values were calculated using the `corr.test()` function from the *psych* package [42]. *P* value adjustment using the Benjamini-Hochberg method was performed using the argument `adjust = "BH"` in the `corr.test()` function. Rho's were visualized in correlograms with hierarchical clustering using the `pheatmap()` function from the *pheatmap* package with default clustering options (`clustering_distance_rows = "euclidean"`, `clustering_distance_cols = "euclidean"`, `clustering_method = "complete"`) [43].