

Supplemental table 1: Composition of the diets

	Chow diet (Teklad 2018, HARLAN)		HFHS diet	
Ingredients (g/100g)	Crude protein	19	Casein high nitrogen	20
	Fat (Soybean oil)	6.2	L-cysteine	0.18
	Carbohydrate	44	Sucrose FCC	26.9
	Crude fiber	3.5	Alphacel non nutritive bulk	5
	Insoluble fiber	15	Mineral mix	6.7
	Ash	5.3	Vitamin mix	1.4
			Lard	19.8
			Corn oil	19.8
Composition (kcal%)			Choline bitartrate	0.2
			Tert-butylhydroxytoluene (BHT)	0.03
	Protein	24		15
	Carbohydrates	58		19.6
	Lipids	18		65.4
Energy Density (kcal/g)	3.1		5.4	

Supplemental Table 2: Proanthocyanidin analysis of camu-camu extract by phloroglucinolysis. UPLC-ESI-MS-MS fragmentation, UV/Vis spectra.

Product number	UPLC Retention time (min)	Compound	[M] ⁻	MS fragments
1	2.59	(Epi)gallocatechin adduct	429	303, 261, 177, 125 ^b
2	2.95	Gallocatechin*	305	179, 125
3	3.72	(Epi)catechin adduct	413	287, 261, 245, 175, 161, 125
4	3.77	(Epi)gallocatechin gallate adduct	581	429 , 411, 319, 261
5	3.79	(Epi)gallocatechin adduct	429	303, 261, 177, 125
6	4.06	Epigallocatechin*	305	179, 125
7	4.44	Catechin*	289	245, 109
8	5.15	(Epi)catechin gallate adduct	565	439, 413 , 395, 169
9	5.15	(Epi)catechin adduct	413	287, 261, 245, 175, 161, 125
10	5.40	(Epi)gallocatechin gallate	457	331, 305, 287, 169 , 125
11	6.83	(epi)catechin gallate	441	331, 289, 169
Product number	HPLC Retention time (min)	Compound	mg/100g DW (average ± SD)	
1	2.55	(Epi)gallocatechin adduct	41.53 ± 1.11 ^a	
3+4+5	3.75	(Epi)catechin adduct + (Epi)gallocatechin gallate adduct + (Epi)gallocatechin adduct	1177.25 ± 5.47	
7	4.49	Catechin	6.87 ± 0.96	
8+9	5.13	(Epi)catechin gallate adduct + (Epi)catechin adduct	388.31 ± 5.25	
10	5.40	(Epi)gallocatechin gallate	167.40 ± 5.83	
11	6.82	(epi)catechin gallate	133.61 ± 14.03	
Total			1854.97 ± 6.53	

Data is presented as the mean ±SD

*Identified based on retention time

^a Catechin equivalents

^b Bold values represent the main fragments

Supplemental table 3: Primer sequences

Gene/Taxa	Forward	Reverse
Syber Green		
<i>Actb</i>	CTCTAGACTTCGAGCAGGAG	AGAGTACTTGCGCTCAGGAG
<i>Nr1h4</i>	CTGAGACTGGGTACCAGGG	CCATTCGCGGCTTCTTTGTC
<i>Nr0b2</i>	ACGATCCTCTTCAACCCAGA	AGGGCTCCAAGACTTCACAC
<i>Fabp6</i>	GGTCTTCCAGGAGACGTGAT	ACATTCTTTGCCAATGGTGA
<i>Slc51a</i>	TGTTCCAGGTGCTTGTCATCC	CCACTGTTAGCCAAGATGGAGAA
<i>Slc51b</i>	GATGCGGCTCCTTGAATTA	GGAGGAACATGCTTGTCATGAC
<i>Gpbar1</i>	CTGCTGGCTGCTTCTTCC	CACTGCCATGTAGCGTTCC
<i>Fgfr4</i>	GTACCCTCGGACCGCGGCACATAC	GCCGAAGCTGCTGCCGTTGATG
<i>Fgf15</i>	GAGGACCAAACGAACGAAATT	ACGTCCTTGATGGCAATCG
<i>Abcb11</i>	AAGCTACATCTGCCTTAGACACAGAA	CAATACAGGTCCGACCCTCTCT
<i>Cyp7a1</i>	AGCAACTAAACAACCTGCCAGTACTA	GTCCGGATATTCAAGGATGCA
<i>Cyp7b1</i>	TGAGGTTCTGAGGCTGTGCTC	TCCTGCACTTCTCGGATGATG
<i>Fiaf</i>	CAATGCCAAATTGCTCCAATT	TGGCCGTGGGCTCAGT
<i>Pgc1a</i>	CTGAGACCCTCGGGGAAC	AAACGTCAGTTCACAGGGAAG
<i>Ppara</i>	ATGCCAGTACTGCCGTTTCA	GGGCCTTGACCTTGTTTCATGT
<i>Pnpla2</i>	ACCAGCATCCAGTTCAACCT	ATCCCTGCTTGCACATCTCT
<i>Mgl1</i>	CTAATTCACCTCTGATCCT	AGGACAGAGTTGGTCACTTC
<i>Pparg2</i>	ACTGCCTATGAGCACTTCAC	CAATCGGATGGTTCTTCGGA
<i>Prdm16</i>	CAG CAC GGT GAA GCC ATT	GCG TGC ATC CGC TTG TG
<i>Ucp1</i>	ACTGCCACACCTCCAGTCATT	CTTTGCCTCACTCAGGATTGG
<i>Dio2</i>	GTCCGCAAATGACCCCTTT	CCCACCCACTCTCTGACTTTC
16S - 891F/1033R	TGGAGCATGTGGTTTAATTCTGA	TGCGGGACTTAACCCAACA
Firmicutes	CTGATGGAGCAACGCCGCGT	ACACYTAGYACTCATCGTTT
Bacteroidetes	CCGGAWTYATTGGGTTTAAAGGG	GGTAAGGTTCCTCGCGTA
<i>Lactobacillus</i>	TGGAAACAGRTGCTAATACCG	GTCCATTGTGGAAGATTCCC
<i>Bifidobacterium</i>	TCGCGTCYGGTGTGAAAG	CCACATCCAGCRTCCAC
<i>Barnesiella</i>	CCAAGTCGCGTGAAGGAAGA	ACGGAGTTAGCCGATGCTTT
<i>Turicibacter</i>	CCGCGGTAATACGTAGGTGG	ACGCATTCACCGCTACACA
<i>Allobaculum</i>	TTATGGCCTGGGCTACACAC	TTCTCGGATTGGCTTGCTT
<i>Akkermansia muciniphila</i>	CAG CAC GTG AAG GTG GGG AC	CCT TGC GGT TGG CTT CAG AT
TaqMan		
<i>Actb</i>	Mm01205647_g1	
<i>Nos2</i>	Mm00440483_m1	
<i>Adgre1</i>	Mm00802529_m1	

Supplemental table 4: Concentration of bile acids in plasma and faeces.

	PLASMA						FAECES									
	Chow		HFHS		CC		P value Chow vs HFHS	P value HFHS vs CC	Chow		HFHS		CC		P value Chow vs HFHS	P value HFHS vs CC
	Concentration (ng/mL)	SEM	Concentration (ng/mL)	SEM	Concentration (ng/mL)	SEM			Concentration (ng/mL)	SEM	Concentration (ng/mL)	SEM	Concentration (ng/mL)	SEM		
α MCA	62.43	16.12	78.66	38.26	42.32	12.51	0.90	0.53	149.64	37.03	446.81	45.33	406.11	50.53	<0.01	0.76
HCA	6.00	2.01	1.76	1.29	0.39	0.21	0.11	0.43	4.52	0.87	4.07	0.61	8.49	2.96	0.79	0.32
CA	488.07	141.07	459.54	301.11	187.53	61.19	0.99	0.60	143.37	87.58	177.26	29.92	94.75	27.00	0.82	0.07
UDCA	83.46	13.93	45.90	17.10	43.89	9.19	0.15	0.98	6.75	2.84	27.11	4.00	19.48	4.30	<0.01	0.54
HDCA	56.14	11.53	11.46	1.69	14.14	3.12	<0.01	0.67	72.00	18.05	34.31	5.24	47.57	10.00	0.08	0.36
DCA	176.21	27.63	85.08	29.11	72.72	8.73	0.05	0.89	287.87	32.67	614.88	64.45	571.40	74.92	<0.01	0.78
CDCA	64.72	12.15	48.12	33.38	22.19	4.36	0.85	0.66	7.32	4.63	14.67	2.96	8.38	2.20	0.50	0.42
LCA	7.03	1.00	3.06	0.57	2.73	0.93	0.03	0.98	40.66	3.23	33.80	3.98	32.80	5.70	0.50	0.98

TCA	TUDCA	TDCA	TCDCA	GDCA	GCDCA	GCA	TLCA	GLCA	ωMCA	βMCA
33.60	45.99	17.04	-	-	2.28	1.00	-	-	501.62	535.56
6.07	9.04	3.40	-	-	1.25	0.27	-	-	71.69	119.57
322.27	163.97	174.50	-	-	5.34	0.87	-	-	322.61	713.98
42.38	25.87	56.64	-	-	1.61	0.26	-	-	90.84	387.47
211.17	111.37	59.18	-	-	4.55	0.13	-	-	317.36	351.57
27.18	19.49	11.41	-	-	2.62	0.09	-	-	66.63	81.01
<0.01	<0.01	0.04	-	-	0.45	0.91	-	-	0.32	0.77
0.05	0.41	0.09	-	-	0.91	0.04	-	-	0.96	0.53
109.62	4.12	2.57	3.05	-	-	0.75	0.15	-	606.46	514.31
85.16	2.10	0.47	1.76	-	-	0.57	0.07	-	73.73	105.69
512.57	20.78	21.75	22.59	0.05	-	1.79	3.66	-	760.20	1,088.31
275.59	7.44	7.99	10.02	0.03	-	0.39	0.72	-	118.54	202.29
173.52	9.95	14.74	8.55	-	-	0.71	3.17	-	966.86	722.48
46.30	2.15	3.21	1.75	-	-	0.16	0.70	-	126.23	86.19
0.30	0.07	0.06	0.09	0.35	-	0.34	<0.01	-	0.43	0.04
0.35	0.39	0.49	0.21	0.35	-	0.04	0.76	-	0.41	0.31

T ω MCA	T β MCA	T α MCA	GUDCA
277.38	132.98	-	370.92
115.28	45.39	-	105.72
3,143.89	645.20	0.17	1,753.21
1,316.53	144.59	0.17	362.41
474.26	191.20	0.17	767.22
143.76	56.61	0.17	167.97
0.05	<0.01	0.39	<0.01
0.06	0.04	1.00	0.05
296.07	467.62	69.05	-
183.81	281.84	43.29	-
518.29	1,553.28	223.36	0.02
105.65	738.89	84.50	0.02
421.32	567.09	88.35	0.04
146.86	137.73	20.36	0.04
0.51	0.25	0.39	0.61
0.80	0.41	0.45	0.89

Data is presented as the mean \pm SEM. Cholic acid (CA), Chenodeoxycholic acid (CDCA), Deoxycholic acid (DCA), Ursodeoxycholic acid (UDCA), Lithocholic acid (LCA) Tauro-Cholic acid (TCA), Tauro-Deoxycholic acid (TDCA), Tauro-ursodeoxycholic acid (TUDCA), Tauro-Lithocholic acid (TLCA) α -Murocholic acid (α MCA), β -Murocholic acid (β MCA), ω -Murocholic acid (ω MCA), Tauro- α -murocholic acid (T α MCA), Tauro- β -murocholic acid (T β MCA), Tauro- ω -murocholic acid (T ω MCA), Glycoursodeoxycholic acid (GUDCA), Glycodeoxycholic acid (GDCA), Glycocholic acid (GCA), Glycochenodeoxycholic acid (GCDCA), Glycolithocholic acid (GLCA), Hyocholic acid (HCA), Hyodeoxycholic acid (HDCA). P values calculated using one-way ANOVA with Bonferroni post-hoc test.

Supplemental table 5: Proportion of bile acids in plasma and faeces.

	PLASMA								FAECES							
	Chow		HFHS		CC		P value Chow vs HFHS	P value HFHS vs CC	Chow		HFHS		CC		P value Chow vs HFHS	P value HFHS vs CC
	Relative abundance (%)	SEM	Relative abundance (%)	SEM	Relative abundance (%)	SEM			Relative abundance (%)	SEM	Relative abundance (%)	SEM	Relative abundance (%)	SEM		
βMCA	13.69	1.76	5.41	1.43	10.52	1.86	<0.01	0.06	20.52	1.78	19.45	2.86	18.62	2.37	0.78	0.86
αMCA	1.64	0.29	0.65	0.14	1.07	0.17	<0.01	0.08	5.91	0.53	8.89	0.96	9.85	0.69	0.03	0.46
HCA	0.27	0.09	0.01	0.01	0.01	0.01	0.04	0.95	0.22	0.04	0.09	0.02	0.18	0.04	0.03	0.09
CA	13.19	2.03	3.46	1.12	4.21	0.85	<0.01	0.65	2.68	0.91	3.33	0.60	2.09	0.37	0.59	0.20
UDCA	2.48	0.38	0.55	0.12	1.37	0.31	<0.01	0.05	0.22	0.03	0.54	0.09	0.46	0.06	<0.01	0.66
HDCA	2.05	0.52	0.19	0.04	0.40	0.07	<0.01	0.05	4.80	1.85	0.72	0.12	1.12	0.18	0.07	0.09
DCA	5.80	0.97	1.10	0.23	2.44	0.38	<0.01	<0.01	14.60	1.71	12.31	1.44	14.01	1.33	0.39	0.48
CDCA	1.95	0.32	0.38	0.14	0.67	0.25	<0.01	0.16	0.17	0.06	0.29	0.07	0.19	0.03	0.28	0.29
LCA	0.27	0.04	0.05	0.02	0.08	0.04	<0.01	0.38	2.31	0.35	0.71	0.10	0.79	0.10	<0.01	0.31

GUDCA	TCA	TUDCA	TDCA	TCDCA	GDCA	GCDCA	GCA	TLCA	GLCA	ωMCA
10.44	1.08	1.48	0.61	-	-	0.04	0.03	-	-	17.90
1.35	0.11	0.25	0.11	-	-	0.02	0.01	-	-	2.29
22.43	5.17	2.80	1.82	-	-	0.07	0.01	-	-	3.96
2.16	0.72	0.50	0.15	-	-	0.03	0.01	-	-	0.79
21.06	6.83	3.35	1.72	-	-	0.09	0.00	-	-	9.63
1.88	0.76	0.40	0.18	-	-	0.04	0.00	-	-	1.75
<0.01	<0.01	0.03	0.00	-	-	0.41	0.20	-	-	<0.01
0.69	0.15	0.42	0.69	-	-	0.79	0.19	-	-	0.04
-	2.08	0.13	0.17	0.08	-	-	0.01	-	-	31.35
-	1.14	0.02	0.02	0.02	-	-	0.01	-	-	4.28
-	5.71	0.30	0.31	0.29	-	-	0.03	0.07	-	16.21
-	1.73	0.04	0.04	0.06	-	-	-	0.01	-	2.94
-	3.85	0.22	0.33	0.19	-	-	-	0.07	-	23.79
-	0.86	0.03	0.06	0.03	-	-	-	0.02	-	2.66
-	0.1	<0.01	<0.01	<0.01	-	-	0.05	<0.01	-	<0.01
-	0.39	0.19	0.79	0.21	-	-	-	0.88	-	0.08

	T ω MCA	T β MCA	T α MCA
	6.05	3.25	-
	1.55	0.53	-
	24.64	7.48	-
	3.75	0.75	-
	11.92	4.59	-
	1.30	0.67	-
	<0.01	<0.01	
	<0.01	<0.01	
	5.49	8.24	1.12
	1.89	3.43	0.54
	9.21	18.56	2.98
	1.64	3.55	0.62
	8.99	13.21	1.99
	2.19	2.58	0.33
	0.19	0.07	0.05
	0.99	0.29	0.22

Data is presented as the mean \pm SEM. Cholic acid (CA), Chenodeoxycholic acid (CDCA), Deoxycholic acid (DCA), Ursodeoxycholic acid (UDCA), Lithocholic acid (LCA) Tauro-Cholic acid (TCA), Tauro-Deoxycholic acid (TDCA), Tauro-ursodeoxycholic acid (TUDCA), Tauro-Lithocholic acid (TLCA) α -Murocholic acid (α MCA), β -Murocholic acid (β MCA), ω -Murocholic acid (ω MCA), Tauro- α -murocholic acid (T α MCA), Tauro- β -murocholic acid (T β MCA), Tauro- ω -murocholic acid (T ω MCA), Glycoursodeoxycholic acid (GUDCA), Glycodeoxycholic acid (GDCA), Glycocholic acid (GCA), Glycochenodeoxycholic acid (GCDCA), Glycolithocholic acid (GLCA), Hyocholic acid (HCA), Hyodeoxycholic acid (HDCA). P values calculated using one-way ANOVA with Bonferroni post-hoc test.

Supplemental table 6: Taxonomic profile at phylum level of germ-free mice reconstituted with the fecal microbiota of vehicle- and camu camu-treated mice.

Days post-colonization	Phylum	HFHS receivers	SEM	CC receivers	SEM	<i>P</i> value
Day1	Other	4.80	0.64	4.30	1.56	0.79
Day1	Actinobacteria	0.84	0.06	1.99	1.18	0.43
Day1	Bacteroidetes	8.30	8.20	12.83	6.07	0.68
Day1	Firmicutes	84.73	8.11	69.21	7.67	0.24
Day1	Proteobacteria	0.00	0.00	0.02	0.02	0.42
Day1	Verrucomicrobia	1.33	1.18	11.65	6.04	0.23
Day1	F/B ratio	615	307	29.74	26.28	0.1
Day2	Other	5.48	0.46	3.45	0.76	0.06
Day2	Actinobacteria	0.93	0.16	2.57	1.17	0.24
Day2	Bacteroidetes	21.78	6.33	15.83	6.12	0.52
Day2	Firmicutes	70.81	6.09	41.42	5.41	0.01
Day2	Proteobacteria	0.37	0.39	0.32	0.32	0.90
Day2	Verrucomicrobia	0.10	0.01	35.15	10.38	0.02
Day2	F/B ratio	5.45	2.13	3.76	1.01	0.49
Day3	Other	3.98	0.62	3.84	0.93	0.90
Day3	Actinobacteria	1.38	0.47	2.53	0.93	0.32
Day3	Bacteroidetes	29.50	4.56	14.60	5.33	0.08
Day3	Firmicutes	45.00	6.73	56.01	11.51	0.45
Day3	Proteobacteria	0.43	0.39	0.01	0.01	0.36
Day3	Verrucomicrobia	19.72	11.52	23.01	10.79	0.84
Day3	F/B ratio	1.54	0.14	37.27	34.32	0.34

Relative abundance (%), except for F/B – Firmicutes to Bacteroidetes - ratio (total counts of Firmicutes/total counts Bacteroidetes). Data is presented as the mean \pm SEM. *P* value calculated using Student's t-test. F/B – Firmicutes to Bacteroidetes ratio (total counts of Firmicutes/total counts Bacteroidetes)

Supplemental table 7: Taxonomic profile at genus level of germ-free mice reconstituted with the fecal microbiota of vehicle- and camu camu-treated mice.

	DAY1					DAY2					DAY3				
	HFHS receivers	SEM	CC receivers	SEM	P value	HFHS receivers	SEM	CC receivers	SEM	P value	HFHS receivers	SEM	CC receivers	SEM	P value
Other	4.80	0.64	4.17	1.62	0.74	5.48	0.46	3.45	0.76	0.06	3.98	0.62	3.84	0.93	0.90
<i>Bifidobacterium</i>	0.09	0.08	1.07	1.07	0.45	0.00	0.00	2.01	1.24	0.18	0.55	0.42	1.48	0.96	0.43
<i>Adlercreutzia</i>	0.75	0.06	0.92	0.28	0.62	0.93	0.16	0.57	0.16	0.14	0.83	0.29	1.05	0.27	0.59
<i>Barnesiella</i>	0.19	0.14	5.91	4.27	0.31	5.78	2.17	10.22	4.54	0.41	11.31	4.90	11.07	4.59	0.97
S24-7_g	8.11	8.06	6.92	5.48	0.91	16.00	4.30	5.61	1.66	0.07	18.19	8.00	3.53	1.11	0.16
Bacillales_f_g	0.04	0.03	0.01	0.01	0.45	0.01	0.01	0.00	0.00	0.26	0.00	0.00	0.00	0.00	0.23
Lactobacillales_f_g	0.27	0.06	0.18	0.07	0.36	0.07	0.03	0.10	0.03	0.48	0.03	0.01	0.12	0.06	0.23
Lactobacillales_f_g_2	0.69	0.07	0.38	0.11	0.09	0.26	0.04	0.25	0.04	0.73	0.18	0.09	0.33	0.07	0.23
Enterococcaceae_g	39.65	4.92	34.82	10.94	0.72	29.03	6.49	18.34	3.27	0.19	15.19	5.92	23.02	3.88	0.32
Enterococcaceae_g_2	0.54	0.36	0.27	0.07	0.53	0.60	0.38	0.13	0.05	0.28	0.10	0.06	0.19	0.09	0.48
<i>Enterococcus</i>	3.40	0.36	2.27	0.24	0.07	2.04	0.43	1.58	0.31	0.41	1.15	0.34	1.96	0.47	0.22
<i>Lactobacillus</i>	3.72	3.15	1.32	0.28	0.53	7.39	6.31	0.93	0.40	0.36	1.93	1.52	1.30	0.81	0.73
<i>Lactococcus</i>	1.30	0.60	1.94	0.51	0.46	1.80	0.76	1.38	0.34	0.64	1.68	0.68	1.95	0.36	0.74
<i>Turicibacter</i>	8.96	1.77	0.68	0.34	0.04	0.57	0.34	0.40	0.26	0.72	0.05	0.01	0.11	0.05	0.35
Clostridiales_f_g	0.13	0.03	0.04	0.01	0.08	0.01	0.01	0.04	0.02	0.20	0.01	0.01	0.03	0.02	0.55
Clostridiales_f_g_2	0.05	0.01	0.18	0.16	0.51	1.74	0.87	0.71	0.41	0.33	2.64	1.05	1.12	0.86	0.31
Clostridiaceae_g	0.25	0.02	0.19	0.08	0.55	0.06	0.03	0.11	0.03	0.28	0.03	0.02	0.11	0.06	0.24
Clostridiaceae_g_2	1.33	0.35	1.81	0.83	0.63	1.43	0.23	2.27	1.07	0.48	1.36	0.37	2.54	1.13	0.38
<i>Clostridium</i>	0.01	0.01	0.04	0.04	0.60	0.36	0.29	0.71	0.63	0.64	1.87	1.08	0.03	0.02	0.19
SMB53	0.02	0.02	0.01	0.01	0.57	0.01	0.00	0.02	0.01	0.26	0.01	0.01	0.01	0.00	0.68
Lachnospiraceae_g	0.00	0.00	0.00	0.00	0.53	0.00	0.00	0.00	0.00	0.37	0.06	0.04	0.00	0.00	0.21
Lachnospiraceae_g_2	0.01	0.01	0.95	0.92	0.42	2.16	1.23	1.17	0.46	0.49	3.09	1.16	0.80	0.27	0.14
<i>Coprococcus</i>	0.00	0.00	0.01	0.00	0.78	0.56	0.30	0.01	0.01	0.15	0.49	0.20	0.02	0.01	0.11
<i>Dorea</i>	0.00	0.00	0.01	0.00	0.30	0.01	0.01	0.03	0.03	0.45	0.13	0.09	0.01	0.00	0.30
<i>Ruminococcus</i>	0.02	0.01	0.22	0.21	0.44	0.66	0.35	0.52	0.25	0.74	1.37	0.44	0.52	0.24	0.15
rc4-4	0.00	0.00	0.18	0.18	0.42	0.00	0.00	0.20	0.07	0.05	0.26	0.23	0.24	0.14	0.96
Peptostreptococcaceae_g	3.71	1.12	5.02	2.34	0.65	1.61	0.95	2.75	0.87	0.40	0.75	0.54	2.18	1.11	0.30
Ruminococcaceae_g	0.00	0.00	0.08	0.08	0.43	0.46	0.34	0.05	0.03	0.29	0.63	0.36	0.43	0.34	0.70
Ruminococcaceae_g_2	0.12	0.09	0.39	0.39	0.56	1.32	0.59	0.57	0.28	0.30	1.10	0.59	0.62	0.15	0.47
<i>Oscillospira</i>	0.00	0.00	0.06	0.06	0.44	0.19	0.09	0.11	0.07	0.51	0.28	0.10	0.13	0.06	0.26
<i>Ruminococcus</i>	0.03	0.01	0.03	0.01	0.74	0.10	0.04	0.03	0.02	0.16	0.19	0.07	0.04	0.02	0.13
Erysipelotrichaceae_g	11.71	3.76	9.97	1.25	0.70	8.68	2.67	5.80	2.20	0.43	5.49	1.02	12.83	4.66	0.21
<i>Allobaculum</i>	7.91	1.82	7.74	5.28	0.98	9.88	1.91	3.13	1.57	0.03	4.53	1.69	4.92	3.27	0.92
<i>Clostridium</i>	0.83	0.20	0.27	0.12	0.09	0.14	0.05	0.15	0.05	0.79	0.13	0.03	0.23	0.10	0.42
<i>Coprobacillus</i>	0.03	0.02	0.14	0.09	0.32	0.16	0.06	0.10	0.04	0.43	0.28	0.09	0.22	0.17	0.79
<i>Pseudomonas</i>	0.00	0.00	0.02	0.02	0.42	0.39	0.39	0.32	0.32	0.90	0.43	0.39	0.01	0.01	0.36
<i>Akkermansia</i>	1.33	1.18	11.65	6.04	0.23	0.10	0.01	36.22	10.11	0.02	19.72	11.52	23.01	10.79	0.84

Relative abundance (%). Data is presented as the mean \pm SEM. P value calculated using Student's t-test.