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Effects of fermented milk containing *Lacticaseibacillus paracasei* strain Shirota on constipation and gut microbiota: A randomised pilot study in Vietnam

V. Hoang Van, T. Dong Van, N. Nguyen Bao, U. Nguyen Quynh, C. Nguyen Thi Linh, C. Dao Xuan and T. Akiyama

Table S1. Schedule for data collection

	Week -4	**Week -2**	**Week 0**	**Week 2**	**Week 4**	**Week 6**
	Day 0	Day 14 ±1	Day 28 ±3	Day 42 ±3	Day 56 ±3	Day 70 ±3
	Initial visit/ Screening start	Screening end/ Baseline start	Baseline end/ Intervention start	Mid-intervention	Intervention end/ Washout start	Washout end
Informed consent	✓					
Inclusion/ Exclusion criteria	✓	✓				
Demographics	✓					
Medical history	✓	✓				
Concomitant medication assessment	✓	✓	✓	✓	✓	✓
Laboratory tests	✓[1]					
Pregnancy test	✓[2]					
Abdominal ultrasound	✓[3]					
Chest radiograph	✓[3]					
Physical examination	✓	✓	✓	✓	✓	✓
Compliance assessment (based on unused bottle collection and diary)				✓	✓	
Stool consistency (BSFS) and bowel habits diary	✓	✓	✓	✓	✓	✓
FFQ/CCQ			✓	✓	✓	✓
Stool samples for microbiota analysis			✓	✓	✓	✓
Safety, including AE assessment	✓	✓	✓	✓	✓	✓

[1] Biochemical tests and complete blood counts were performed. Laboratory tests were done at Week -4 or within 3 months before signing the ICF.

[2] Urine pregnancy test (using a quick stick) was performed on female participants of reproductive age before performing chest radiography.

[3] Abdominal ultrasound and chest radiography were done at Week -4 or within 3 months before signing the ICF.

FFQ, Food Frequency Questionnaire; CCQ, Chinese Constipation Questionnaire

Table S2. Investigational product compliance

Compliance percentage*	**Probiotic group n = 24**	
	Week 0 to Week 2 n (%)	**Week 2 to Week 4 n (%)**
100%	20 (83.3)	21 (87.5)
91–99%	3 (12.5)	3 (12.5)
81–89%	1 (4.2)	0 (0)

*Compliance percentage was calculated as [number of compliant days]/[the number of days from the previous visit] × 100%.

Table S3. Stool frequency and associated symptoms

Endpoints	**Intake period**								**Follow-up period**		
	Week 0		**Week 2**			**Week 4**			**Week 6**		
	Probiotic (n = 24)	**Control (n = 25)**	**Probiotic (n = 24)**	**Control (n = 25)**	***P****	**Probiotic (n = 24)**	**Control (n = 25)**	***P****	**Probiotic (n = 24)**	**Control (n = 25)**	***P****
Stool frequency with ideal stool (BSFS score 4), median [IQR]	1.5 [1.0, 2.0]	1.0 [1.0, 2.0]	2.0 [1.0, 2.0]	2.0 [1.0, 3.5]	0.629	2.0 [1.0, 4.0]	1.0 [1.0, 1.0]	0.287	3.0 [2.0, 3.0]	1.5 [1.3, 1.8]	0.130
Stool frequency with straining, median [IQR]	4.0 [3.0, 5.0]	4.0 [3.0, 5.0]	4.0 [3.0, 6.0]	4.0 [3.0, 5.0]	0.554	3.0 [2.0, 4.5]	4.0 [3.0, 5.0]	0.483	3.0 [3.0, 4.0]	4.0 [3.0, 5.0]	0.543
Stool frequency with sensation of remaining stool, median [IQR]	4.0 [2.0, 6.0]	2.0 [2.0, 3.0]	2.0 [1.8, 5.0]	2.5 [1.0, 5.0]	0.648	6.0 [2.0, 7.0]	2.0 [1.8, 5.0]	0.069	4.0 [3.0, 6.0]	4.0 [2.0, 4.3]	0.304
Stool frequency with sensation of anorectal blockage, median [IQR]	4.0 [2.8, 4.3]	3.0 [2.0, 5.0]	2.0 [1.5, 4.5]	4.0 [3.0, 4.3]	0.149	3.0 [1.8, 4.0]	4.0 [3.0, 4.3]	0.247	2.0 [1.8, 3.3]	4.0 [2.0, 6.0]	0.132
Stool frequency with manoeuvres, median [IQR]	3.0 [2.5, 3.5]	4.0 [2.8, 5.3]	1.0 [1.0, 1.5]	4.0 [2.0, 4.0]	0.083	1.0 [1.0, 2.5]	3.0 [2.0, 5.0]	0.285	2.0 [1.5, 3.0]	3.5 [1.5, 4.0]	0.593

**P*-value was estimated using the Mann–Whitney U test

BSFS, Bristol Stool Form Scale; IQR, interquartile range

Table S4. Change in constipation-related symptom scores (based on the CCQ) from Week 0 to Week 6

Endpoints	**Intake period**								**Follow-up period**		
	Week 0		**Week 2**			**Week 4**			**Week 6**		
	Probiotic (n = 24)	**Control (n = 25)**	**Probiotic (n = 24)**	**Control (n = 25)**	**_P_***	**Probiotic (n = 24)**	**Control (n = 25)**	**_P_***	**Probiotic (n = 24)**	**Control (n = 25)**	**_P_***
Proportion of individuals with a total CCQ score of ≥5, n (%)	24 (100)	22 (88.0)	18 (75.0)	23 (92.0)	0.138	11 (45.8)	24 (96.0)	**<0.001**	15 (62.5)	23 (92.0)	**0.018**
Total score, median [IQR]	10.5 [7.8, 13.0]	12.0 [9.0, 13.0]	8.0 [4.8, 10.3]	12.0 [9.0, 13.0]	**0.003**	4.0 [2.8, 7.3]	12.0 [9.0, 13.0]	**<0.001**	5.0 [3.0, 8.0]	12.0 [8.0, 14.0]	**<0.001**
False alarm, median [IQR]	2.0 [1.8, 3.0]	2.0 [1.0, 3.0]	2.0 [1.0, 2.0]	2.0 [2.0, 3.0]	0.156	1.0 [0.0, 1.0]	2.0 [2.0, 3.0]	**<0.001**	1.0 [0.0, 2.0]	2.0 [2.0, 3.0]	**<0.001**
Incomplete evacuation, median [IQR]	2.0 [1.0, 2.3]	2.0 [2.0, 3.0]	2.0 [0.8, 2.0]	2.0 [2.0, 3.0]	**0.032**	1.0 [0.0, 2.0]	2.0 [2.0, 3.0]	**<0.001**	1.0 [0.0, 2.0]	2.0 [2.0, 3.0]	**<0.001**
Lumpy or hard stool, median [IQR]	3.0 [2.0, 3.0]	3.0 [2.0, 3.0]	1.0 [1.0, 2.0]	3.0 [2.0, 3.0]	**0.001**	1.0 [1.0, 2.0]	3.0 [2.0, 3.0]	**<0.001**	1.0 [1.0, 2.0]	3.0 [2.0, 3.0]	**<0.001**
Abdominal bloating, median [IQR]	2.0 [1.8, 2.3]	2.0 [1.0, 2.0]	1.0 [1.0, 2.0]	2.0 [1.0, 2.0]	0.738	1.0 [0.0, 2.0]	2.0 [1.0, 3.0]	**0.007**	1.0 [0.0, 2.0]	2.0 [1.0, 2.0]	**0.023**
Individuals with number of defaecations ≤3 times/week, n (%)	12 (50.0)	16 (64.0)	9 (37.5)	17 (68.0)	**0.046**	4 (16.7)	18 (72.0)	**<0.001**	9 (37.5)	15 (60.0)	0.156
Patients with usage of laxatives, n (%)	0 (0)	0 (0)	0 (0)	0 (0)	NA	0 (0)	0 (0)	NA	0 (0)	1 (4)	1

**P*-values were estimated using Fisher's exact test for categorical variables or the Mann–Whitney U test for continuous variables.

CCQ, Chinese Constipation Questionnaire; IQR, interquartile range; NA, not available

Table S5. Mixed-effects logistic regression parameters for a total CCQ score of ≥5

	Participants having a total CCQ score ≥5		
Predictors	**Odds Ratios**	**CI**	***P***
Intercept	59.70	9.69–367.74	**<0.001**
Sex [Male vs. Female]	0.72	0.20–2.60	0.618
Week [Week 2 vs. Week 0]	0.30	0.07–1.29	0.106
Week [Week 4 vs. Week 0]	0.13	0.03–0.54	**0.006**
Group [Probiotic vs. Control]	0.20	0.06–0.65	**0.008**

CI, confidence interval

Table S6. Changes in alpha-diversity metrics

Metrics	**Groups**	**Baseline (n = 48)**	**Week 2 (n = 50)**	**Week 4 (n = 49)**	**Follow-up (n = 49)**
Observed ASVs	Probiotic	5217 (14.78)	4673 (13.83)	5127 (13.78)	5622 (14.44)
	Control	5183 (13.66)	5675 (13.51)	5971 (13.42)	5399 (13.59)
Chao 1	Probiotic	495.56 (141.94)	482.55 (124.12)	514.79 (126.55)	521.07 (127.14)
	Control	510.22 (147.48)	498.29 (147.66)	523.91 (203.22)	490.32 (139.59)
Shannon	Probiotic	6.25 (0.87)	5.68 (0.98)	6.17 (0.75)	6.21 (0.90)
	Control	6.26 (0.83)	6.03 (1.13)	6.04 (1.44)	6.05 (0.81)
Faith’s phylogenetic diversity	Probiotic	41.80 (11.93)	39.56 (9.74)	42.63 (10.51)	41.18 (10.10)
	Control	43.49 (11.84)	41.42 (9.44)	42.62 (13.33)	39.68 (9.58)

The results are expressed as the mean (standard deviation).

Table S7. Changes in beta-diversity metrics

Metrics	**Week 2 (n = 50)**	**Week 4 (n = 49)**	**Follow-up (n = 49)**
Bray–Curtis	0.009**	0.171	0.456
Jaccard	0.016*	0.101	0.113
Unweighted UniFrac	0.064†	0.259	0.456
Weighted UniFrac	0.347	0.299	0.663

The results are expressed as *p*-values based on permutational multivariate analysis of variance (999 permutations).

*P <0.05 vs. control

**P <0.01 vs. control

†P <0.10 vs. control.

Table S8. Microbiota log-fold change versus control at the phylum level

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 0	d__Bacteria.p__Desulfobacterota	1.469566301	0.454784437	0.00123208	0.01355291
Week 0	d__Bacteria.p__Proteobacteria	0.943748003	0.47528493	0.04707256	0.47072555
Week 0	d__Bacteria.p__Fusobacteriota	0.849874447	0.747759786	0.25572194	1
Week 0	d__Bacteria.__	0.262220787	0.336277769	0.43552369	1
Week 0	d__Bacteria.p__Firmicutes	0.224324484	0.353071281	0.52519898	1
Week 0	d__Bacteria.p__Synergistota	-0.00059377	0.468114081	0.99898794	1
Week 0	d__Bacteria.p__Bacteroidota	-0.031119	0.401227575	0.93817847	1
Week 0	d__Bacteria.p__Cyanobacteria	-0.13544574	0.436287891	0.75621848	1
Week 0	d__Bacteria.p__Patescibacteria	-0.19380189	0.31452905	0.53778543	1
Week 0	d__Bacteria.p__Verrucomicrobiota	-0.28645669	0.589674287	0.62711748	1
Week 0	d__Bacteria.p__Actinobacteriota	-0.59934427	0.398033756	0.13212817	1
Week 2	d__Bacteria.p__Fusobacteriota	1.364609568	0.665537932	0.04032679	0.40326791
Week 2	d__Bacteria.p__Proteobacteria	1.218107655	0.432200019	0.00482653	0.05309187
Week 2	d__Bacteria.p__Patescibacteria	0.256900927	0.276314703	0.35250554	1
Week 2	d__Bacteria.p__Firmicutes	0.226145868	0.351917196	0.52047653	1
Week 2	d__Bacteria.p__Synergistota	0.149766076	0.672241611	0.823702	1
Week 2	d__Bacteria.p__Actinobacteriota	0.111100885	0.483976383	0.81843487	1
Week 2	d__Bacteria.__	-0.05343448	0.356830277	0.88096376	1
Week 2	d__Bacteria.p__Cyanobacteria	-0.08051903	0.403016365	0.84164407	1
Week 2	d__Bacteria.p__Bacteroidota	-0.34432798	0.351593666	0.32741449	1
Week 2	d__Bacteria.p__Desulfobacterota	-0.377072	0.458200248	0.41054126	1
Week 2	d__Bacteria.p__Verrucomicrobiota	-0.88299366	0.59294057	0.13644067	1
Week 4	d__Bacteria.p__Fusobacteriota	0.586242707	0.68990269	0.39546579	1
Week 4	d__Bacteria.p__Cyanobacteria	0.473915724	0.465746646	0.30889673	1
Week 4	d__Bacteria.p__Proteobacteria	0.372894623	0.444302293	0.40131145	1
Week 4	d__Bacteria.p__Patescibacteria	0.187052793	0.269981567	0.48841284	1
Week 4	d__Bacteria.p__Campylobacterota	0.05267793	0.257401939	0.8378437	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 4	d__Bacteria.p__Actinobacteriota	0.004649213	0.447674297	0.99171391	1
Week 4	d__Bacteria.p__Verrucomicrobiota	-0.00169127	0.67363438	0.99799678	1
Week 4	d__Bacteria.__	-0.0084994	0.347660671	0.98049575	1
Week 4	d__Bacteria.p__Firmicutes	-0.15951907	0.348572102	0.64721412	1
Week 4	d__Bacteria.p__Desulfobacterota	-0.16450229	0.446740036	0.71270307	1
Week 4	d__Bacteria.p__Bacteroidota	-0.46802227	0.466017409	0.31523301	1
Week 4	d__Bacteria.p__Synergistota	-0.94966831	0.468655728	0.04272723	0.51272679
Follow-up	d__Bacteria.p__Fusobacteriota	0.750554818	0.679948671	0.26966237	1
Follow-up	d__Bacteria.p__Desulfobacterota	0.714492809	0.409100273	0.08072445	0.96869345
Follow-up	d__Bacteria.p__Verrucomicrobiota	0.384247222	0.60144041	0.52290211	1
Follow-up	d__Bacteria.p__Synergistota	0.198011617	0.481336849	0.68079504	1
Follow-up	d__Bacteria.p__Proteobacteria	0.172987064	0.442618809	0.69592565	1
Follow-up	d__Bacteria.p__Actinobacteriota	0.088465423	0.470619927	0.85089518	1
Follow-up	d__Bacteria.p__Campylobacterota	0.027257749	0.207989724	0.89573311	1
Follow-up	d__Bacteria.p__Firmicutes	-0.02212909	0.312606041	0.94356563	1
Follow-up	d__Bacteria.p__Cyanobacteria	-0.06812786	0.482540667	0.88772322	1
Follow-up	d__Bacteria.p__Patescibacteria	-0.18874703	0.327358655	0.56422616	1
Follow-up	d__Bacteria.p__Bacteroidota	-0.2167953	0.282514945	0.44285775	1
Follow-up	d__Bacteria.__	-0.39542459	0.289278112	0.17164545	1

Table S9. Microbiota log-fold change versus control at the class level

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 0	d__Bacteria.p__Desulfobacterota.c__Desulfovibrionia	1.424099519	0.513721387	0.00556918	0.10581437
Week 0	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria	0.915377464	0.478069232	0.05552589	0.99946598
Week 0	d__Bacteria.p__Fusobacteriota.c__Fusobacteriia	0.804761275	0.783576886	0.30440375	1
Week 0	d__Bacteria.p__Firmicutes.c__Negativicutes	0.509859083	0.516474145	0.32354858	1
Week 0	d__Bacteria.p__Actinobacteriota.c__Actinobacteria	0.450684397	0.55475195	0.4165581	1
Week 0	d__Bacteria.__.__	0.217107615	0.310635176	0.48460509	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia	0.155846811	0.280811002	0.57890269	1
Week 0	d__Bacteria.p__Firmicutes.__	0.147903267	0.245874116	0.54747997	1
Week 0	d__Bacteria.p__Firmicutes.c__Incertae_Sedis	0.092007774	0.253743305	0.71690238	1
Week 0	d__Bacteria.p__Firmicutes.c__Bacilli	-0.04124721	0.34925983	0.90598928	1
Week 0	d__Bacteria.p__Synergistota.c__Synergistia	-0.04570694	0.480911376	0.92428119	1
Week 0	d__Bacteria.p__Bacteroidota.c__Bacteroidia	-0.07623218	0.431599649	0.85980134	1
Week 0	d__Bacteria.p__Cyanobacteria.c__Cyanobacteriia	-0.12799746	0.435902483	0.76903466	1
Week 0	d__Bacteria.p__Verrucomicrobiota.c__Lentisphaeria	-0.12883169	0.275980347	0.64063244	1
Week 0	d__Bacteria.p__Verrucomicrobiota.c__Verrucomicrobiae	-0.23052281	0.622098123	0.71096752	1
Week 0	d__Bacteria.p__Patescibacteria.c__Saccharimonadia	-0.23891506	0.292987088	0.41481724	1
Week 0	d__Bacteria.p__Cyanobacteria.c__Vampirivibrionia	-0.29792287	0.296553737	0.31508139	1
Week 0	d__Bacteria.p__Proteobacteria.c__Alphaproteobacteria	-0.45087035	0.4703718	0.33779035	1
Week 0	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia	-0.69869585	0.379628107	0.0656986	1
Week 2	d__Bacteria.p__Fusobacteriota.c__Fusobacteriia	1.284038967	0.694568557	0.06450321	1
Week 2	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria	1.152270713	0.416491697	0.00566422	0.10195598
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli	0.898931721	0.479838267	0.06101239	1
Week 2	d__Bacteria.p__Actinobacteriota.c__Actinobacteria	0.812456053	0.540507245	0.1328039	1
Week 2	d__Bacteria.p__Firmicutes.__	0.381269452	0.271492038	0.16021508	1
Week 2	d__Bacteria.p__Patescibacteria.c__Saccharimonadia	0.176330326	0.261368673	0.49990314	1
Week 2	d__Bacteria.p__Proteobacteria.c__Alphaproteobacteria	0.122927931	0.435422928	0.77769933	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 2	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia	0.120089771	0.525936754	0.81938581	1
Week 2	d__Bacteria.p__Synergistota.c__Synergistia	0.069195475	0.675505581	0.91841133	1
Week 2	d__Bacteria.p__Firmicutes.c__Negativicutes	0.056716523	0.395118405	0.88586127	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia	-0.0870429	0.258114115	0.73594622	1
Week 2	d__Bacteria.p__Firmicutes.c__Incertae_Sedis	-0.13178298	0.300590257	0.66108618	1
Week 2	d__Bacteria.__.__	-0.13400508	0.34078078	0.69414994	1
Week 2	d__Bacteria.p__Cyanobacteria.c__Cyanobacteriia	-0.16192844	0.438321841	0.7118086	1
Week 2	d__Bacteria.p__Verrucomicrobiota.c__Lentisphaeria	-0.31314211	0.26377877	0.23517273	1
Week 2	d__Bacteria.p__Bacteroidota.c__Bacteroidia	-0.42489858	0.388921194	0.27461094	1
Week 2	d__Bacteria.p__Desulfobacterota.c__Desulfovibrionia	-0.4576426	0.49942703	0.35949107	1
Week 2	d__Bacteria.p__Verrucomicrobiota.c__Verrucomicrobiae	-0.84055616	0.632236328	0.18368413	1
Week 4	d__Bacteria.p__Fusobacteriota.c__Fusobacteriia	0.641431109	0.724474367	0.3759547	1
Week 4	d__Bacteria.p__Actinobacteriota.c__Actinobacteria	0.599356706	0.603581089	0.3207094	1
Week 4	d__Bacteria.p__Cyanobacteria.c__Cyanobacteriia	0.528431451	0.503208932	0.2936614	1
Week 4	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria	0.435434924	0.430915904	0.31226202	1
Week 4	d__Bacteria.p__Patescibacteria.c__Saccharimonadia	0.242241194	0.250796562	0.33410062	1
Week 4	d__Bacteria.p__Verrucomicrobiota.c__Verrucomicrobiae	0.118297398	0.708371142	0.8673707	1
Week 4	d__Bacteria.p__Campylobacterota.c__Campylobacteria	0.107866332	0.237890125	0.65023971	1
Week 4	d__Bacteria.p__Firmicutes.c__Incertae_Sedis	0.097870005	0.304933407	0.74824424	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia	0.076240182	0.320652712	0.81206291	1
Week 4	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia	0.050545926	0.45087103	0.91073834	1
Week 4	d__Bacteria.__.__	0.046689005	0.327556511	0.88665566	1
Week 4	d__Bacteria.p__Firmicutes.c__Bacilli	0.033205725	0.438800744	0.93967861	1
Week 4	d__Bacteria.p__Desulfobacterota.c__Desulfovibrionia	-0.10931389	0.483774682	0.82123227	1
Week 4	d__Bacteria.p__Cyanobacteria.c__Vampirivibrionia	-0.11480529	0.234459745	0.62437531	1
Week 4	d__Bacteria.p__Proteobacteria.c__Alphaproteobacteria	-0.14174867	0.413300735	0.73162299	1
Week 4	d__Bacteria.p__Firmicutes.__	-0.16582266	0.2827111	0.55750963	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 4	d__Bacteria.p__Verrucomicrobiota.c__Lentisphaeria	-0.16697108	0.223276665	0.45456787	1
Week 4	d__Bacteria.p__Bacteroidota.c__Bacteroidia	-0.41283387	0.490350368	0.39983492	1
Week 4	d__Bacteria.p__Synergistota.c__Synergistia	-0.89447991	0.475426555	0.05991399	1
Week 4	d__Bacteria.p__Firmicutes.c__Negativicutes	-1.04971739	0.39038297	0.00716787	0.14335749
Follow-up	d__Bacteria.p__Fusobacteriota.c__Fusobacteriia	0.7763612	0.718963542	0.28021616	1
Follow-up	d__Bacteria.p__Desulfobacterota.c__Desulfovibrionia	0.740299191	0.433578858	0.08774488	1
Follow-up	d__Bacteria.p__Verrucomicrobiota.c__Verrucomicrobiae	0.331420512	0.636438034	0.60254597	1
Follow-up	d__Bacteria.p__Verrucomicrobiota.c__Lentisphaeria	0.250532954	0.234078023	0.28448574	1
Follow-up	d__Bacteria.p__Proteobacteria.c__Alphaproteobacteria	0.232637506	0.443230437	0.5996749	1
Follow-up	d__Bacteria.p__Synergistota.c__Synergistia	0.223818	0.511588029	0.66175127	1
Follow-up	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria	0.194567803	0.440067275	0.65839373	1
Follow-up	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia	0.166270514	0.462654843	0.71930822	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia	0.11331422	0.296426995	0.70226342	1
Follow-up	d__Bacteria.p__Firmicutes.c__Negativicutes	0.082744071	0.448947703	0.85377285	1
Follow-up	d__Bacteria.p__Campylobacterota.c__Campylobacteria	0.053064131	0.188892472	0.7787699	1
Follow-up	d__Bacteria.p__Actinobacteriota.c__Actinobacteria	-0.02337324	0.632889429	0.97054002	1
Follow-up	d__Bacteria.p__Cyanobacteria.c__Cyanobacteriia	-0.04909215	0.483086754	0.91905686	1
Follow-up	d__Bacteria.p__Patescibacteria.c__Saccharimonadia	-0.16294065	0.306266667	0.59471067	1
Follow-up	d__Bacteria.p__Bacteroidota.c__Bacteroidia	-0.19098892	0.273114114	0.48436406	1
Follow-up	d__Bacteria.p__Firmicutes.c__Bacilli	-0.28423667	0.408625368	0.48668417	1
Follow-up	d__Bacteria.p__Cyanobacteria.c__Vampirivibrionia	-0.32647267	0.248923167	0.18967542	1
Follow-up	d__Bacteria.__.__	-0.3696182	0.264316115	0.16199463	1
Follow-up	d__Bacteria.p__Firmicutes.__	-0.46457048	0.237856303	0.05080111	0.96522104
Follow-up	d__Bacteria.p__Firmicutes.c__Incertae_Sedis	-0.61609417	0.290182946	0.03374352	0.67487042

Table S10. Microbiota log-fold change versus control at the order level

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 0	d__Bacteria.p__Desulfobacterota.c__Desulfovibrionia.o__Desulfovibrionales	1.347686575	0.547104478	0.01376618	0.56441333
Week 0	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales	1.049519851	0.676957437	0.12105793	1
Week 0	d__Bacteria.p__Fusobacteriota.c__Fusobacteriia.o__Fusobacteriales	0.728348331	0.805845639	0.36608498	1
Week 0	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Flavobacteriales	0.655714915	0.299237953	0.02843135	1
Week 0	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Veillonellales.Selenomonadales	0.355730993	0.727908835	0.62505221	1
Week 0	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Bifidobacteriales	0.351778652	0.599487183	0.55733852	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales	0.342396349	0.260751696	0.18914499	1
Week 0	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales	0.326865957	0.428820543	0.44591429	1
Week 0	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Actinomycetales	0.224327351	0.306079409	0.46361593	1
Week 0	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Pseudomonadales	0.218327636	0.264895897	0.40982499	1
Week 0	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Corynebacteriales	0.215946035	0.231207382	0.3503076	1
Week 0	d__Bacteria.__.__.__	0.14069467	0.330274344	0.6701127	1
Week 0	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Burkholderiales	0.132520883	0.474373933	0.77996892	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales	0.095503566	0.27182713	0.72533378	1
Week 0	d__Bacteria.p__Firmicutes.__.__	0.071490322	0.235940225	0.76188846	1
Week 0	d__Bacteria.p__Proteobacteria.c__Alphaproteobacteria.o__Caulobacterales	0.044523236	0.241121069	0.85350282	1
Week 0	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Micrococcales	0.030503559	0.227824739	0.89348919	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__uncultured	0.024494547	0.239786678	0.9186365	1
Week 0	d__Bacteria.p__Firmicutes.c__Incertae_Sedis.o__DTU014	0.01559483	0.241736592	0.94856282	1
Week 0	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales	-0.08713245	0.360934104	0.80923877	1
Week 0	d__Bacteria.p__Firmicutes.c__Bacilli.o__Izemoplasmatales	-0.11959931	0.283181542	0.67277579	1
Week 0	d__Bacteria.p__Synergistota.c__Synergistia.o__Synergistales	-0.12211989	0.508644784	0.81026146	1
Week 0	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Acidaminococcales	-0.15074294	0.429367739	0.72552743	1
Week 0	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales	-0.1528377	0.448653087	0.73336032	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales	-0.19067129	0.329332771	0.56261454	1
Week 0	d__Bacteria.p__Cyanobacteria.c__Cyanobacteriia.o__Chloroplast	-0.20441041	0.44438875	0.64552982	1
Week 0	d__Bacteria.p__Verrucomicrobiota.c__Lentisphaeria.o__Victivallales	-0.20524464	0.285219415	0.4717697	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 0	d__Bacteria.p__Firmicutes.c__Bacilli.o__Staphylococcales	-0.27044389	0.333917985	0.41799125	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridia_vadinBB60_group	-0.27979154	0.512497661	0.5851091	1
Week 0	d__Bacteria.p__Verrucomicrobiota.c__Verrucomicrobiae.o__Verrucomicrobiales	-0.30580035	0.639874309	0.63271647	1
Week 0	d__Bacteria.p__Patescibacteria.c__Saccharimonadia.o__Saccharimonadales	-0.315328	0.284017114	0.26689434	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales	-0.34575681	0.440784435	0.43279811	1
Week 0	d__Bacteria.p__Cyanobacteria.c__Vampirivibrionia.o__Gastranaerophilales	-0.37433582	0.297880508	0.2088752	1
Week 0	d__Bacteria.p__Firmicutes.c__Bacilli.o__RF39	-0.56660154	0.700470073	0.41857981	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Christensenellales	-0.63351332	0.552124557	0.25121215	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales	-0.74860308	0.612926072	0.22194994	1
Week 0	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales	-0.7751088	0.360970476	0.03177009	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridia_UCG.014	-0.80301678	0.709797899	0.25791556	1
Week 0	d__Bacteria.p__Proteobacteria.c__Alphaproteobacteria.o__Rhodospirillales	-0.81901262	0.489755161	0.09446717	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptococcales	-0.9661788	0.426000676	0.02332788	0.93311525
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Monoglobales	-0.97431228	0.469401305	0.03792644	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.__	-1.22563622	0.333925952	0.00024219	0.01017186
Week 2	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales	1.176364724	0.538591718	0.02895128	1
Week 2	d__Bacteria.p__Fusobacteriota.c__Fusobacteriia.o__Fusobacteriales	1.107692098	0.707087014	0.11721828	1
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales	0.887366356	0.638568851	0.1646451	1
Week 2	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Veillonellales.Selenomonadales	0.866297836	0.653268744	0.18480751	1
Week 2	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Micrococcales	0.729524091	0.387328222	0.05963565	1
Week 2	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Bifidobacteriales	0.468770909	0.607672241	0.44045765	1
Week 2	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Pseudomonadales	0.41916157	0.264589094	0.11314862	1
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.o__Bacillales	0.40031804	0.256747501	0.11895151	1
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales	0.397342742	0.370886298	0.28401971	1
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.o__Staphylococcales	0.321970716	0.507944459	0.52616571	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Monoglobales	0.20541465	0.560637204	0.71407037	1
Week 2	d__Bacteria.p__Firmicutes.__.__	0.204922583	0.259516447	0.42974251	1
Week 2	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Propionibacteriales	0.204390324	0.194067366	0.2922527	1

Timepoint	Taxon	Log-fold change (vs. control)	Standard error	*P*-value (raw)	*P*-value (Holm)
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__uncultured	0.114616256	0.268569113	0.66954953	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridia_UCG.014	0.042764733	0.699728814	0.95126671	1
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.__	0.018614711	0.181456118	0.91829219	1
Week 2	d__Bacteria.p__Patescibacteria.c__Saccharimonadia.o__Saccharimonadales	-1.6543E-05	0.255537941	0.99994835	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales	-0.00265137	0.348043976	0.99392184	1
Week 2	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Corynebacteriales	-0.02369407	0.212633711	0.91127427	1
Week 2	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.__	-0.02797277	0.182775113	0.878363	1
Week 2	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Flavobacteriales	-0.03835417	0.329996399	0.90747342	1
Week 2	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales	-0.0562571	0.486408796	0.90792355	1
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.o__RF39	-0.06743725	0.677739278	0.92073872	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales	-0.10385853	0.24174217	0.66746831	1
Week 2	d__Bacteria.p__Synergistota.c__Synergistia.o__Synergistales	-0.10715139	0.706033019	0.87937196	1
Week 2	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Burkholderiales	-0.16652193	0.528680641	0.75277957	1
Week 2	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Actinomycetales	-0.20579284	0.407417744	0.61347801	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridia_vadinBB60_group	-0.25357301	0.430203057	0.55557532	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales	-0.27268175	0.261891484	0.29778215	1
Week 2	d__Bacteria.p__Firmicutes.c__Incertae_Sedis.o__DTU014	-0.30812985	0.302544467	0.30845875	1
Week 2	d__Bacteria.__.__.__	-0.31035195	0.362457691	0.39186325	1
Week 2	d__Bacteria.p__Cyanobacteria.c__Cyanobacteriia.o__Chloroplast	-0.41515358	0.487527529	0.39446446	1
Week 2	d__Bacteria.p__Proteobacteria.c__Alphaproteobacteria.o__Rhodospirillales	-0.41941332	0.456201377	0.35790727	1
Week 2	d__Bacteria.p__Verrucomicrobiota.c__Lentisphaeria.o__Victivallales	-0.48948898	0.266481186	0.06623037	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales	-0.50630472	0.335047186	0.13075163	1
Week 2	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales	-0.60126542	0.420369619	0.1526236	1
Week 2	d__Bacteria.p__Desulfobacterota.c__Desulfovibrionia.o__Desulfovibrionales	-0.63398947	0.542170471	0.24226084	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales	-0.85901762	0.583514078	0.14098159	1
Week 2	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Acidaminococcales	-0.86219619	0.541962102	0.11163678	1
Week 2	d__Bacteria.p__Verrucomicrobiota.c__Verrucomicrobiae.o__Verrucomicrobiales	-1.00847789	0.666812287	0.13043557	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.__	-1.14928501	0.341993153	0.00077788	0.03267076

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptococcales	-1.35767839	0.348210008	9.6582E-05	0.00415303
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Christensenellales	-1.76022982	0.616790747	0.00431926	0.17708958
Week 4	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Bifidobacteriales	0.816761317	0.669459707	0.22245328	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Monoglobales	0.720136322	0.545800295	0.18703088	1
Week 4	d__Bacteria.p__Fusobacteriota.c__Fusobacteriia.o__Fusobacteriales	0.664110246	0.762211138	0.38359346	1
Week 4	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales	0.597920574	0.53087495	0.26004165	1
Week 4	d__Bacteria.p__Cyanobacteria.c__Cyanobacteriia.o__Chloroplast	0.551110589	0.538406312	0.3060261	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridia_UCG.014	0.543013935	0.713959783	0.446916	1
Week 4	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Burkholderiales	0.502240115	0.455810366	0.27052168	1
Week 4	d__Bacteria.p__Firmicutes.c__Bacilli.o__RF39	0.421946873	0.660248976	0.52277586	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales	0.397797156	0.544493111	0.46503418	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales	0.317720317	0.311485471	0.30772064	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__uncultured	0.281964203	0.303775871	0.35330479	1
Week 4	d__Bacteria.p__Patescibacteria.c__Saccharimonadia.o__Saccharimonadales	0.264920331	0.243916306	0.27742962	1
Week 4	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales	0.261619706	0.430631308	0.54350191	1
Week 4	d__Bacteria.p__Verrucomicrobiota.c__Verrucomicrobiae.o__Verrucomicrobiales	0.148490108	0.741604251	0.84130209	1
Week 4	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Micrococcales	0.147390913	0.314870155	0.63971264	1
Week 4	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Veillonellales.Selenomonadales	0.143676402	0.615868413	0.81553564	1
Week 4	d__Bacteria.p__Campylobacterota.c__Campylobacteria.o__Campylobacterales	0.130545469	0.233065563	0.57539529	1
Week 4	d__Bacteria.p__Firmicutes.c__Incertae_Sedis.o__DTU014	0.120549143	0.307792157	0.69531121	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales	0.117993741	0.283685544	0.67746016	1
Week 4	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.__	0.082687561	0.197567114	0.67556041	1
Week 4	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales	0.075559937	0.599066972	0.89962952	1
Week 4	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales	0.073225063	0.409359894	0.8580343	1
Week 4	d__Bacteria.__.__.__	0.069368143	0.357248552	0.84604016	1
Week 4	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Pseudomonadales	0.051017834	0.277272333	0.85401423	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptococcales	-0.02024845	0.446946878	0.96386506	1
Week 4	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Xanthomonadales	-0.02739189	0.240291714	0.90924229	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 4	d__Bacteria.p__Proteobacteria.c__Alphaproteobacteria.o__Caulobacterales	-0.05286582	0.201738703	0.79328214	1
Week 4	d__Bacteria.p__Desulfobacterota.c__Desulfovibrionia.o__Desulfovibrionales	-0.08663475	0.509294944	0.86492581	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Christensenellales	-0.08970079	0.546232133	0.86956005	1
Week 4	d__Bacteria.p__Cyanobacteria.c__Vampirivibrionia.o__Gastranaerophilales	-0.09212616	0.243939691	0.70568351	1
Week 4	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Corynebacteriales	-0.12650546	0.222596139	0.56981885	1
Week 4	d__Bacteria.p__Proteobacteria.c__Alphaproteobacteria.o__Rhodospirillales	-0.12962059	0.427552984	0.76176146	1
Week 4	d__Bacteria.p__Firmicutes.__.__	-0.14314352	0.290312918	0.62196573	1
Week 4	d__Bacteria.p__Verrucomicrobiota.c__Lentisphaeria.o__Victivallales	-0.14429194	0.226427909	0.52395984	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales	-0.16267542	0.290889064	0.57600117	1
Week 4	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Flavobacteriales	-0.1874943	0.350312311	0.59249745	1
Week 4	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Propionibacteriales	-0.18772449	0.229557253	0.41348988	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.__	-0.22301433	0.315809883	0.48008466	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales	-0.28325591	0.427987628	0.5080789	1
Week 4	d__Bacteria.p__Firmicutes.c__Bacilli.o__Staphylococcales	-0.30143291	0.471530162	0.5226503	1
Week 4	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales	-0.39027947	0.51788553	0.45108836	1
Week 4	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Actinomycetales	-0.59300579	0.406977609	0.14508965	1
Week 4	d__Bacteria.p__Synergistota.c__Synergistia.o__Synergistales	-0.87180077	0.490508967	0.07551246	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridia_vadinBB60_group	-0.90669618	0.452285385	0.04499521	1
Week 4	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Acidaminococcales	-1.69369899	0.545302826	0.0018965	0.08534266
Follow-up	d__Bacteria.p__Fusobacteriota.c__Fusobacteriia.o__Fusobacteriales	0.861883624	0.759422154	0.25640871	1
Follow-up	d__Bacteria.p__Desulfobacterota.c__Desulfovibrionia.o__Desulfovibrionales	0.825821616	0.472190174	0.0803053	1
Follow-up	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Burkholderiales	0.580447199	0.460213316	0.20721632	1
Follow-up	d__Bacteria.p__Verrucomicrobiota.c__Verrucomicrobiae.o__Verrucomicrobiales	0.417649877	0.674348587	0.53569355	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales	0.379103936	0.281707557	0.17838775	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales	0.371902204	0.29664462	0.20995249	1
Follow-up	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Veillonellales.Selenomonadales	0.365670918	0.653377872	0.57570985	1
Follow-up	d__Bacteria.p__Verrucomicrobiota.c__Lentisphaeria.o__Victivallales	0.336055378	0.237298721	0.15672568	1
Follow-up	d__Bacteria.p__Synergistota.c__Synergistia.o__Synergistales	0.309340424	0.537886345	0.56522117	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Follow-up	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales	0.251792938	0.428625386	0.55690629	1
Follow-up	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Pseudomonadales	0.249572418	0.298457972	0.40303889	1
Follow-up	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales	0.228997844	0.514601998	0.65631982	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridia_vadinBB60_group	0.181104531	0.478338578	0.70497631	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__uncultured	0.175975311	0.250324851	0.48206337	1
Follow-up	d__Bacteria.p__Proteobacteria.c__Alphaproteobacteria.o__Rhodospirillales	0.163489431	0.46594968	0.7256832	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales	0.156762283	0.552087527	0.77645282	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Christensenellales	0.142999433	0.509764085	0.77907796	1
Follow-up	d__Bacteria.p__Campylobacterota.c__Campylobacteria.o__Campylobacterales	0.138586555	0.190643797	0.46726286	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Monoglobales	0.138419294	0.553729953	0.80260578	1
Follow-up	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Bifidobacteriales	0.137543008	0.689298758	0.84183998	1
Follow-up	d__Bacteria.p__Proteobacteria.c__Alphaproteobacteria.o__Caulobacterales	0.132035269	0.205575015	0.52069598	1
Follow-up	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Flavobacteriales	0.106273723	0.388714345	0.78454729	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales	0.079113677	0.273562453	0.77242997	1
Follow-up	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Propionibacteriales	0.0502237	0.206186865	0.80755348	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales	0.038046951	0.444264457	0.93175234	1
Follow-up	d__Bacteria.p__Cyanobacteria.c__Cyanobacteriia.o__Chloroplast	0.036430271	0.482446531	0.93980773	1
Follow-up	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Micrococcales	0.008467186	0.18906429	0.96427893	1
Follow-up	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales	-0.05401535	0.594601133	0.92761735	1
Follow-up	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Actinomycetales	-0.06878694	0.369994527	0.85251267	1
Follow-up	d__Bacteria.p__Patescibacteria.c__Saccharimonadia.o__Saccharimonadales	-0.07741822	0.30543255	0.79990445	1
Follow-up	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Corynebacteriales	-0.09505964	0.161698397	0.55661123	1
Follow-up	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales	-0.10569852	0.271339415	0.69687411	1
Follow-up	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Acidaminococcales	-0.18494168	0.512940763	0.71843458	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridia_UCG.014	-0.18781216	0.699221481	0.78823612	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.__	-0.20164397	0.348218269	0.56253959	1
Follow-up	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales	-0.2138657	0.419419091	0.610115	1
Follow-up	d__Bacteria.p__Firmicutes.c__Bacilli.__	-0.220018	0.184060105	0.23194659	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Follow-up	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Xanthomonadales	-0.23593385	0.222052039	0.28800149	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptococcales	-0.23971179	0.422812216	0.57075072	1
Follow-up	d__Bacteria.p__Cyanobacteria.c__Vampirivibrionia.o__Gastranaerophilales	-0.24095024	0.249247646	0.33368893	1
Follow-up	d__Bacteria.__.__.__	-0.28409578	0.282520876	0.31462031	1
Follow-up	d__Bacteria.p__Firmicutes.c__Bacilli.o__Staphylococcales	-0.33919175	0.37088877	0.36043439	1
Follow-up	d__Bacteria.p__Firmicutes.__.__	-0.37904805	0.240985337	0.11573985	1
Follow-up	d__Bacteria.p__Firmicutes.c__Incertae_Sedis.o__DTU014	-0.53057175	0.287443225	0.06491668	1
Follow-up	d__Bacteria.p__Firmicutes.c__Bacilli.o__RF39	-0.76953049	0.735391209	0.29536565	1

Table S11. Microbiota log-fold change versus control at the family level

Timepoint	**Taxon**	**Log-fold change vs. control**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 0	d__Bacteria.p__Desulfobacterota.c__Desulfovibrionia.o__Desulfovibrionales.f__Desulfovibrionaceae	1.349302285	0.532716008	0.01131318	0.8824277
Week 0	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Pasteurellaceae	1.324515345	0.569871436	0.02011288	1
Week 0	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Enterobacteriaceae	1.047236587	0.707219061	0.13866493	1
Week 0	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.__	1.028382336	0.501687264	0.04037932	1
Week 0	d__Bacteria.p__Fusobacteriota.c__Fusobacteriia.o__Fusobacteriales.f__Fusobacteriaceae	0.80955022	0.795944967	0.30910909	1
Week 0	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Flavobacteriales.f__Flavobacteriaceae	0.565779601	0.317632616	0.07487342	1
Week 0	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Streptococcaceae	0.548219574	0.491508344	0.26468675	1
Week 0	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Burkholderiales.f__Comamonadaceae	0.536259518	0.47664434	0.26055824	1
Week 0	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Atopobiaceae	0.494790181	0.357564073	0.16642569	1
Week 0	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelatoclostridiaceae	0.429651732	0.315083581	0.17268973	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Anaerovoraceae	0.394879392	0.432636714	0.36138592	1
Week 0	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Bifidobacteriales.f__Bifidobacteriaceae	0.353394362	0.616569341	0.56653474	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae	0.344715296	0.254017804	0.17476478	1
Week 0	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Veillonellales.Selenomonadales.f__Veillonellaceae	0.343760469	0.691855657	0.61928262	1
Week 0	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__uncultured	0.30828766	0.195236344	0.11432493	1
Week 0	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Enterococcaceae	0.255355725	0.485759789	0.59910839	1
Week 0	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Porphyromonadaceae	0.242657615	0.345423066	0.48237117	1

Timepoint	**Taxon**	**Log-fold change vs. control**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 0	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Actinomycetales.f__Actinomycetaceae	0.225943061	0.319090079	0.47889216	1
Week 0	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Corynebacteriales.f__Corynebacteriaceae	0.217561746	0.247740675	0.37984421	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae	0.195543637	0.345305915	0.57119597	1
Week 0	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Pseudomonadales.f__Pseudomonadaceae	0.1636964	0.237517158	0.49069854	1
Week 0	d__Bacteria.__.__.__.__	0.142310381	0.350693306	0.68489158	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.__	0.11647874	0.456743158	0.79870748	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae	0.095684039	0.292247122	0.74335933	1
Week 0	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Marinifilaceae	0.094175424	0.552380726	0.86462475	1
Week 0	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Morganellaceae	0.081537399	0.224724607	0.71672999	1
Week 0	d__Bacteria.p__Firmicutes.__.__.__	0.073106033	0.259056761	0.77778952	1
Week 0	d__Bacteria.p__Proteobacteria.c__Alphaproteobacteria.o__Caulobacterales.f__Caulobacteraceae	0.046138946	0.241883754	0.84872269	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Butyricicoccaceae	0.040576252	0.376464095	0.9141682	1
Week 0	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Succinivibrionaceae	0.037910775	0.366201662	0.91754686	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__uncultured.f__uncultured	0.026110257	0.24023223	0.9134503	1
Week 0	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Burkholderiales.f__Oxalobacteraceae	0.021395406	0.484472826	0.96477508	1
Week 0	d__Bacteria.p__Firmicutes.c__Incertae_Sedis.o__DTU014.f__DTU014	0.01721054	0.249846758	0.94508165	1
Week 0	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Eggerthellaceae	0.012591993	0.390619015	0.97428385	1

Timepoint	**Taxon**	**Log-fold change vs. control**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 0	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Lactobacillaceae	0.002844735	0.648668128	0.99650089	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Anaerofustaceae	-0.00691865	0.231997239	0.97620892	1
Week 0	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Micrococcales.f__Micrococcaceae	-0.01365624	0.235908187	0.95383788	1
Week 0	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Burkholderiales.f__Sutterellaceae	-0.08064471	0.601500334	0.89334516	1
Week 0	d__Bacteria.p__Patescibacteria.c__Saccharimonadia.o__Saccharimonadales.f__Saccharimonadales	-0.08071616	0.198096108	0.68367048	1
Week 0	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Burkholderiales.f__Burkholderiaceae	-0.10690818	0.285256241	0.70782448	1
Week 0	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__uncultured	-0.11065606	0.558844582	0.8430383	1
Week 0	d__Bacteria.p__Firmicutes.c__Bacilli.o__Izemoplasmatales.f__Izemoplasmatales	-0.1179836	0.28913353	0.68323021	1
Week 0	d__Bacteria.p__Synergistota.c__Synergistia.o__Synergistales.f__Synergistaceae	-0.12050418	0.516641342	0.81557091	1
Week 0	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae	-0.13570625	0.664676168	0.83822146	1
Week 0	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Acidaminococcales.f__Acidaminococcaceae	-0.14912723	0.419093901	0.72196601	1
Week 0	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Bacteroidaceae	-0.14994859	0.488606354	0.75892681	1

Timepoint	**Taxon**	**Log-fold change vs. control**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Eubacteriaceae	-0.16362787	0.317830314	0.60667339	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Family_XI	-0.18949459	0.316573229	0.54945261	1
Week 0	d__Bacteria.p__Cyanobacteria.c__Cyanobacteriia.o__Chloroplast.f__Chloroplast	-0.20279469	0.458853978	0.6585188	1
Week 0	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.__	-0.21622347	0.43714331	0.6208625	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospirales	-0.24556444	0.281888199	0.38367703	1
Week 0	d__Bacteria.p__Firmicutes.c__Bacilli.o__Staphylococcales.f__Gemellaceae	-0.25258999	0.34937575	0.46969515	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__uncultured	-0.25855462	0.305271574	0.39701412	1
Week 0	d__Bacteria.p__Verrucomicrobiota.c__Lentisphaeria.o__Victivallales.f__Victivallaceae	-0.25921489	0.294520985	0.37879232	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridia_vadinBB60_group.f__Clostridia_vadinBB60_group	-0.27817583	0.519292877	0.59217837	1
Week 0	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Tannerellaceae	-0.29990102	0.490739349	0.54111962	1
Week 0	d__Bacteria.p__Verrucomicrobiota.c__Verrucomicrobiae.o__Verrucomicrobiales.f__Akkermansiaceae	-0.30418464	0.651180696	0.64040841	1

Timepoint	**Taxon**	**Log-fold change vs. control**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 0	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Rikenellaceae	-0.31681849	0.553033816	0.56673026	1
Week 0	d__Bacteria.p__Cyanobacteria.c__Vampirivibrionia.o__Gastranaerophilales.f__Gastranaerophilales	-0.37272011	0.303671275	0.21967973	1
Week 0	d__Bacteria.p__Patescibacteria.c__Saccharimonadia.o__Saccharimonadales.f__Saccharimonadaceae	-0.37943732	0.287627997	0.18710404	1
Week 0	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Veillonellales.Selenomonadales.f__Selenomonadaceae	-0.45561927	0.865082732	0.59841784	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Defluviitaleaceae	-0.52617109	0.398579054	0.18679587	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ethanoligenenaceae	-0.52855429	0.258800245	0.04111927	1
Week 0	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelotrichaceae	-0.52946519	0.538859855	0.32582125	1
Week 0	d__Bacteria.p__Firmicutes.c__Bacilli.o__RF39.f__RF39	-0.56498583	0.703390812	0.4218408	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Christensenellales.f__Christensenellaceae	-0.63189761	0.556590461	0.2562493	1
Week 0	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Barnesiellaceae	-0.70472438	0.74109616	0.34164415	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Clostridiaceae	-0.74698736	0.620799523	0.22887315	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridia_UCG.014.f__Clostridia_UCG.014	-0.80140107	0.716027295	0.26304094	1

Timepoint	**Taxon**	**Log-fold change vs. control**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 0	d__Bacteria.p__Proteobacteria.c__Alphaproteobacteria.o__Rhodospirillales.f__uncultured	-0.81739691	0.487520815	0.0936129	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__.Eubacterium._coprostanoligenes_group	-0.83978566	0.423163774	0.04719561	1
Week 0	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Muribaculaceae	-0.87255202	0.806767154	0.27945639	1
Week 0	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Coriobacteriaceae	-0.90375071	0.520160579	0.08230855	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Peptostreptococcaceae	-0.95679657	0.671034892	0.15391101	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptococcales.f__Peptococcaceae	-0.96456309	0.429786037	0.02481396	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Monoglobales.f__Monoglobaceae	-0.97269656	0.470095996	0.03853252	1
Week 0	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.__	-1.05850194	0.555663934	0.05678893	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__.Clostridium._methylpentosum_group	-1.09188635	0.402404672	0.00665959	0.52610767
Week 0	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Coriobacteriales_Incertae_Sedis	-1.1414467	0.40613945	0.00494677	0.39574161
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__UCG.010	-1.14381525	0.581242856	0.04908203	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.__.__	-1.22402051	0.34312789	0.00036076	0.02922133

Timepoint	**Taxon**	**Log-fold change vs. control**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 2	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Pasteurellaceae	1.444921278	0.682680126	0.0342987 2	1
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Streptococcaceae	1.224789697	0.714730057	0.0865949 4	1
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Lactobacillaceae	1.154330323	0.502374864	0.0215761 9	1
Week 2	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Enterobacteriaceae	1.088166774	0.624435585	0.0813964 2	1
Week 2	d__Bacteria.p__Fusobacteriota.c__Fusobacteriia.o__Fusobacteriales.f__Fusobacteriaceae	1.032618883	0.688118616	0.1334484 9	1
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.__	0.911973001	0.581662094	0.1169104 9	1
Week 2	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Veillonellales.Selenomonadales.f__Veillonellaceae	0.888047927	0.662638679	0.1801903 5	1
Week 2	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Micrococcales.f__Micrococcaceae	0.672184666	0.400623362	0.0933769 9	1
Week 2	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.__	0.593776751	0.429871254	0.1671898 9	1
Week 2	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Burkholderiales.f__Comamonadaceae	0.520277482	0.430544624	0.2268868 7	1
Week 2	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Atopobiaceae	0.513377609	0.367503992	0.1624344 1	1
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Carnobacteriaceae	0.489935961	0.423679213	0.2475240 3	1
Week 2	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Bifidobacteriales.f__Bifidobacteriaceae	0.411431484	0.622715595	0.5088013 3	1
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelatoclostridiaceae	0.373658917	0.390951941	0.3391900 2	1
Week 2	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Porphyromonadaceae	0.326071796	0.286836574	0.2556277 7	1
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.o__Bacillales.f__Bacillaceae	0.321694214	0.272602041	0.2379654 8	1
Week 2	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Pseudomonadales.f__Pseudomonadaceae	0.320185826	0.26874053	0.2334843 9	1

Timepoint	**Taxon**	**Log-fold change vs. control**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.o__Staphylococcales.f__Gemellaceae	0.28472812	0.520908574	0.58465424	1
Week 2	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__uncultured	0.268409885	0.312732998	0.39074245	1
Week 2	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Muribaculaceae	0.261988153	0.788042831	0.73954631	1
Week 2	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Eggerthellaceae	0.256460261	0.423934567	0.54521058	1
Week 2	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Burkholderiales.f__Neisseriaceae	0.249864801	0.253537566	0.3243717	1
Week 2	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__uncultured	0.238757979	0.503154473	0.63512755	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Anaerovoraceae	0.232468161	0.432407578	0.59084389	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Monoglobales.f__Monoglobaceae	0.148075226	0.562703085	0.79243509	1
Week 2	d__Bacteria.p__Firmicutes.__.__.__	0.147583159	0.274848011	0.59129331	1
Week 2	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Propionibacteriales.f__Propionibacteriaceae	0.1470509	0.212231587	0.48838522	1
Week 2	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Succinivibrionaceae	0.133980273	0.399268495	0.73719941	1
Week 2	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae	0.115076558	0.621266044	0.85304934	1
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelotrichaceae	0.065332336	0.478229852	0.89133683	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__uncultured.f__uncultured	0.057276832	0.26596159	0.82948858	1
Week 2	d__Bacteria.p__Patescibacteria.c__Saccharimonadia.o__Saccharimonadales.f__Saccharimonadaceae	-0.0133531	0.26558134	0.95990026	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridia_UCG.014.f__Clostridia_UCG.014	-0.01457469	0.694172671	0.98324903	1

Timepoint	**Taxon**	**Log-fold change vs. control**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 2	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Burkholderiales.f__Burkholderiaceae	-0.01853259	0.248387473	0.94052375	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Butyricicoccaceae	-0.01880661	0.478723203	0.96866322	1
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.__.__	-0.03872471	0.197141422	0.84427273	1
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.o__Staphylococcales.f__Staphylococcaceae	-0.06644792	0.205777593	0.7467624	1
Week 2	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.__.__	-0.08531219	0.188005711	0.64999116	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Anaerofustaceae	-0.09013324	0.272824019	0.74111939	1
Week 2	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Corynebacteriales.f__Corynebacteriaceae	-0.09792787	0.228674134	0.66847492	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Peptostreptococcaceae	-0.11282186	0.521993564	0.82888136	1
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.o__RF39.f__RF39	-0.12477668	0.680526016	0.85452083	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Family_XI	-0.13878802	0.366663603	0.70504734	1
Week 2	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Flavobacteriales.f__Flavobacteriaceae	-0.1414691	0.333382998	0.67131489	1
Week 2	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Veillonellales.Selenomonadales.f__Selenomonadaceae	-0.15233395	0.810612217	0.85093578	1

Timepoint	**Taxon**	**Log-fold change vs. control**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae	-0.16010258	0.248564785	0.51950537	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__.Eubacterium._coprostanoligenes_group	-0.16279005	0.530414216	0.75891098	1
Week 2	d__Bacteria.p__Synergistota.c__Synergistia.o__Synergistales.f__Synergistaceae	-0.16449082	0.720498391	0.81941191	1
Week 2	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Coriobacteriales_Incertae_Sedis	-0.22498635	0.458889598	0.62393275	1
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Aerococcaceae	-0.24460502	0.337273047	0.46830278	1
Week 2	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Actinomycetales.f__Actinomycetaceae	-0.26313227	0.427195319	0.53792549	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridia_vadinBB60_group.f__Clostridia_vadinBB60_group	-0.31091243	0.428066821	0.46764414	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__uncultured	-0.32867613	0.200103706	0.10048043	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae	-0.35054293	0.341400677	0.3045247	1
Week 2	d__Bacteria.p__Firmicutes.c__Incertae_Sedis.o__DTU014.f__DTU014	-0.36546928	0.312279481	0.24186918	1
Week 2	d__Bacteria.__.__.__.__	-0.36769137	0.374665825	0.32640299	1

Timepoint	**Taxon**	**Log-fold change vs. control**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 2	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Marinifilaceae	-0.44698547	0.583860782	0.44393305	1
Week 2	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Coriobacteriaceae	-0.45365612	0.582154768	0.43582031	1
Week 2	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Barnesiellaceae	-0.46065804	0.705428181	0.513744	1
Week 2	d__Bacteria.p__Cyanobacteria.c__Cyanobacteriia.o__Chloroplast.f__Chloroplast	-0.472493	0.480685108	0.32562839	1
Week 2	d__Bacteria.p__Proteobacteria.c__Alphaproteobacteria.o__Rhodospirillales.f__uncultured	-0.47675275	0.463335339	0.30349926	1
Week 2	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Bacteroidaceae	-0.48505861	0.500483795	0.33245567	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.__	-0.48513664	0.486851673	0.31901829	1
Week 2	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Burkholderiales.f__Sutterellaceae	-0.49298936	0.663713976	0.45761864	1
Week 2	d__Bacteria.p__Verrucomicrobiota.c__Lentisphaeria.o__Victivallales.f__Victivallaceae	-0.50029618	0.268316222	0.06224076	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Eubacteriaceae	-0.55928766	0.317403641	0.07805735	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ethanoligenenaceae	-0.60289408	0.204853955	0.00325003	0.25675226
Week 2	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Burkholderiales.f__Oxalobacteraceae	-0.60916634	0.424946282	0.15171107	1

Timepoint	**Taxon**	**Log-fold change vs. control**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 2	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.__	-0.66434019	0.526982027	0.20743477	1
Week 2	d__Bacteria.p__Desulfobacterota.c__Desulfovibrionia.o__Desulfovibrionales.f__Desulfovibrionaceae	-0.6913289	0.53755826	0.19842425	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae	-0.72040338	0.318484832	0.02369921	1
Week 2	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Rikenellaceae	-0.76255547	0.69424069	0.27202892	1
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Enterococcaceae	-0.7713962	0.665553932	0.24644443	1
Week 2	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Tannerellaceae	-0.80285138	0.560684891	0.15216903	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Clostridiaceae	-0.91893519	0.592651085	0.12100954	1
Week 2	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Acidaminococcales.f__Acidaminococcaceae	-0.91953561	0.529811134	0.08263612	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Defluviitaleaceae	-0.94841171	0.344372676	0.00588669	0.45916165
Week 2	d__Bacteria.p__Verrucomicrobiota.c__Verrucomicrobiae.o__Verrucomicrobiales.f__Akkermansiaceae	-1.06581732	0.660210326	0.1064493	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.__.__	-1.20662443	0.32972213	0.00025269	0.02046781
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__UCG.010	-1.22759979	0.555942038	0.02723427	1

Timepoint	**Taxon**	**Log-fold change vs. control**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptococcales.f__Peptococcaceae	-1.41501782	0.340016832	3.1601E-05	0.00262288
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__.Clostridium._methylpentosum_group	-1.62259613	0.421573093	0.00011865	0.00972893
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Christensenellales.f__Christensenellaceae	-1.81756924	0.601947869	0.00253209	0.20256755
Week 4	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Burkholderiales.f__Comamonadaceae	1.066175915	0.485443218	0.02807092	1
Week 4	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Lactobacillaceae	1.027964722	0.509575248	0.04366451	1
Week 4	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Pasteurellaceae	1.011787098	0.561087159	0.07134709	1
Week 4	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Veillonellales.Selenomonadales.f__Veillonellaceae	0.923050657	0.657790905	0.16053978	1
Week 4	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Porphyromonadaceae	0.883154082	0.408248618	0.03052002	1
Week 4	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Bifidobacteriales.f__Bifidobacteriaceae	0.837298527	0.68876084	0.22411473	1
Week 4	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae	0.795875454	0.723931697	0.2716027	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Monoglobales.f__Monoglobaceae	0.740673532	0.567199407	0.19160586	1
Week 4	d__Bacteria.p__Fusobacteriota.c__Fusobacteriia.o__Fusobacteriales.f__Fusobacteriaceae	0.70949181	0.746037522	0.34159749	1
Week 4	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelatoclostridiaceae	0.684986492	0.414741124	0.09861609	1
Week 4	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Enterobacteriaceae	0.621274474	0.561357774	0.26840838	1
Week 4	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Barnesiellaceae	0.601404222	0.774603338	0.43751118	1
Week 4	d__Bacteria.p__Cyanobacteria.c__Cyanobacteriia.o__Chloroplast.f__Chloroplast	0.571647799	0.539980408	0.28976128	1

Timepoint	**Taxon**	**Log-fold change vs. control**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridia_UCG.014.f__Clostridia_UCG.014	0.563551145	0.706835438	0.42528401	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Butyricicoccaceae	0.517255194	0.394479762	0.18977879	1
Week 4	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Eggerthellaceae	0.471118978	0.373679496	0.20739647	1
Week 4	d__Bacteria.p__Firmicutes.c__Bacilli.o__RF39.f__RF39	0.442484083	0.673309565	0.51106661	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Clostridiaceae	0.418334366	0.537899595	0.43673509	1
Week 4	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__uncultured	0.390660494	0.283893639	0.16879672	1
Week 4	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Enterococcaceae	0.351947661	0.679046079	0.60425095	1
Week 4	d__Bacteria.p__Patescibacteria.c__Saccharimonadia.o__Saccharimonadales.f__Saccharimonadaceae	0.346229207	0.255910942	0.17607847	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae	0.338971526	0.310529726	0.27501281	1
Week 4	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Burkholderiales.f__Neisseriaceae	0.308662157	0.253435728	0.2232578	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__uncultured.f__uncultured	0.302501413	0.308830531	0.32732994	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae	0.274916491	0.343350191	0.4233121	1
Week 4	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Carnobacteriaceae	0.274347613	0.386535781	0.47785301	1
Week 4	d__Bacteria.p__Campylobacterota.c__Campylobacteria.o__Campylobacterales.f__Campylobacteraceae	0.246656012	0.208965123	0.23785337	1
Week 4	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Pseudomonadales.f__Pseudomonadaceae	0.226605298	0.279473696	0.41746404	1
Week 4	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Morganellaceae	0.210352018	0.245628047	0.39178521	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Family_XI	0.170819772	0.382962332	0.65556222	1

Timepoint	**Taxon**	**Log-fold change vs. control**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 4	d__Bacteria.p__Verrucomicrobiota.c__Verrucomicrobiae.o__Verrucomicrobiales.f__Akkermansiaceae	0.169027318	0.744464926	0.82038846	1
Week 4	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Micrococcales.f__Micrococcaceae	0.153298895	0.320323143	0.63224046	1
Week 4	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Atopobiaceae	0.148561334	0.410236608	0.7172506	1
Week 4	d__Bacteria.p__Firmicutes.c__Incertae_Sedis.o__DTU014.f__DTU014	0.141086353	0.304649479	0.64328521	1
Week 4	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Muribaculaceae	0.114084494	0.796475042	0.88610321	1
Week 4	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.__.__	0.103224771	0.208380907	0.62034194	1
Week 4	d__Bacteria.__.__.__.__	0.089905353	0.377191362	0.81160596	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.__	0.082736193	0.410390041	0.84022647	1
Week 4	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Burkholderiales.f__Burkholderiaceae	0.041713745	0.223717082	0.85208595	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Anaerovoraceae	0.036708919	0.277738709	0.89484928	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__.Eubacterium._coprostanoligenes_group	0.01871452	0.437483784	0.9658788	1
Week 4	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Streptococcaceae	0.013535609	0.61775731	0.98251904	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptococcales.f__Peptococcaceae	0.000288761	0.431272671	0.99946577	1
Week 4	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Xanthomonadales.f__Xanthomonadaceae	-0.00685468	0.256577041	0.97868634	1
Week 4	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Burkholderiales.f__Sutterellaceae	-0.02661014	0.575764778	0.96313726	1
Week 4	d__Bacteria.p__Proteobacteria.c__Alphaproteobacteria.o__Caulobacterales.f__Caulobacteraceae	-0.03232861	0.211663679	0.87860665	1

Timepoint	**Taxon**	**Log-fold change vs. control**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 4	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.__	-0.0373281	0.511954865	0.94187545	1
Week 4	d__Bacteria.p__Desulfobacterota.c__Desulfovibrionia.o__Desulfovibrionales.f__Desulfovibrionaceae	-0.06609754	0.486314997	0.89188841	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Christensenellales.f__Christensenellaceae	-0.06916358	0.543114397	0.89866636	1
Week 4	d__Bacteria.p__Cyanobacteria.c__Vampirivibrionia.o__Gastranaerophilales.f__Gastranaerophilales	-0.07158895	0.262763165	0.7852786	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__uncultured	-0.07786871	0.232471926	0.73765554	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae	-0.0793074	0.353943302	0.82270431	1
Week 4	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.__	-0.08448922	0.551684928	0.87828188	1
Week 4	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Flavobacteriales.f__Flavobacteriaceae	-0.09804326	0.354892099	0.7823467	1
Week 4	d__Bacteria.p__Proteobacteria.c__Alphaproteobacteria.o__Rhodospirillales.f__uncultured	-0.10908338	0.436559229	0.8026873	1
Week 4	d__Bacteria.p__Firmicutes.__.__.__	-0.12260631	0.306549274	0.68918871	1
Week 4	d__Bacteria.p__Verrucomicrobiota.c__Lentisphaeria.o__Victivallales.f__Victivallaceae	-0.12375473	0.245574362	0.61430358	1
Week 4	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Coriobacteriaceae	-0.1255655	0.498784844	0.80123986	1

Timepoint	Taxon	Log-fold change vs. control	Standard error	*P*-value (raw)	*P*-value (Holm)
Week 4	d__Bacteria.p__Fusobacteriota.c__Fusobacteriia.o__Fusobacteriales.f__Leptotrichiaceae	-0.13433672	0.26113039	0.60694225	1
Week 4	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Corynebacteriales.f__Corynebacteriaceae	-0.153734	0.243383869	0.52761404	1
Week 4	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Propionibacteriales.f__Propionibacteriaceae	-0.16718728	0.256438796	0.51442838	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Peptostreptococcaceae	-0.17682001	0.535286487	0.74115228	1
Week 4	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Pseudomonadales.f__Moraxellaceae	-0.19098305	0.196173528	0.33028429	1
Week 4	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Marinifilaceae	-0.19586277	0.551152807	0.72231297	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.__.__	-0.20247712	0.301993384	0.50255903	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__UCG.010	-0.20326607	0.527964025	0.70023752	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Anaerofustaceae	-0.22082357	0.329915557	0.5032827	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospirales	-0.22180741	0.244212802	0.3637437	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Eubacteriaceae	-0.281714	0.381405691	0.46013757	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__.Clostridium._methylpentosum_group	-0.30136997	0.444569915	0.49784077	1

Timepoint	**Taxon**	**Log-fold change vs. control**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 4	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Rikenellaceae	-0.33869874	0.635879903	0.59427881	1
Week 4	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Coriobacteriales_Incertae_Sedis	-0.35988276	0.345577375	0.29769199	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ethanoligenenaceae	-0.38137635	0.217651692	0.07973385	1
Week 4	d__Bacteria.p__Firmicutes.c__Bacilli.o__Staphylococcales.f__Gemellaceae	-0.386624	0.472813887	0.41352358	1
Week 4	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Aerococcaceae	-0.43005049	0.390090392	0.27027128	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Defluviitaleaceae	-0.49010128	0.354887923	0.16727804	1
Week 4	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__uncultured	-0.5639893	0.503561554	0.26271346	1
Week 4	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.__	-0.57244746	0.590535469	0.33236054	1
Week 4	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Actinomycetales.f__Actinomycetaceae	-0.57246858	0.428236293	0.18128618	1
Week 4	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelotrichaceae	-0.64575276	0.476636719	0.17547772	1
Week 4	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Burkholderiales.f__Oxalobacteraceae	-0.68619178	0.473832936	0.14756884	1
Week 4	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Bacteroidaceae	-0.70484417	0.623903933	0.25858922	1

Timepoint	Taxon	Log-fold change vs. control	Standard error	*P*-value (raw)	*P*-value (Holm)
Week 4	d__Bacteria.p__Synergistota.c__Synergistia.o__Synergistales.f__Synergistaceae	-0.85126356	0.487557354	0.08081508	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridia_vadinBB60_group.f__Clostridia_vadinBB60_group	-0.88615897	0.454159494	0.05103248	1
Week 4	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Tannerellaceae	-0.91538618	0.477175264	0.05506744	1
Week 4	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Succinivibrionaceae	-1.07736556	0.519833052	0.03821676	1
Week 4	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Veillonellales.Selenomonadales.f__Selenomonadaceae	-1.11571805	0.751280265	0.13752025	1
Week 4	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Acidaminococcales.f__Acidaminococcaceae	-1.67316178	0.542614214	0.00204567	0.18001928
Follow-up	d__Bacteria.p__Desulfobacterota.c__Desulfovibrionia.o__Desulfovibrionales.f__Desulfovibrionaceae	0.831724467	0.467616863	0.07529796	1
Follow-up	d__Bacteria.p__Fusobacteriota.c__Fusobacteriia.o__Fusobacteriales.f__Fusobacteriaceae	0.68186692	0.782687371	0.38365216	1
Follow-up	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Morganellaceae	0.574997663	0.345888495	0.09643687	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.__	0.539626554	0.40511493	0.18284927	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__.Clostridium._methylpentosum_group	0.536118595	0.423846658	0.20591144	1
Follow-up	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Veillonellales.Selenomonadales.f__Veillonellaceae	0.528367204	0.679648517	0.43691548	1
Follow-up	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Burkholderiales.f__Sutterellaceae	0.516951133	0.526565179	0.32622699	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Butyricicoccaceae	0.500780142	0.412914689	0.22520888	1
Follow-up	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Porphyromonadaceae	0.481840491	0.358735859	0.17921942	1

Timepoint	**Taxon**	**Log-fold change vs. control**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Peptostreptococcaceae	0.46202029	0.504312067	0.35959364	1
Follow-up	d__Bacteria.p__Verrucomicrobiota.c__Verrucomicrobiae.o__Verrucomicrobiales.f__Akkermansiaceae	0.423552728	0.681928028	0.53452685	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae	0.384475047	0.288524717	0.18267789	1
Follow-up	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Burkholderiales.f__Comamonadaceae	0.381266555	0.546978319	0.48577686	1
Follow-up	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Marinifilaceae	0.363654058	0.454846233	0.42399482	1
Follow-up	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Coriobacteriaceae	0.356585817	0.525731635	0.49760314	1
Follow-up	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Pseudomonadales.f__Pseudomonadaceae	0.354923002	0.284270987	0.21183427	1
Follow-up	d__Bacteria.p__Synergistota.c__Synergistia.o__Synergistales.f__Synergistaceae	0.315243275	0.536566228	0.55685467	1
Follow-up	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Streptococcaceae	0.309078464	0.555367266	0.57784869	1
Follow-up	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Eggerthellaceae	0.305152784	0.414784779	0.46191971	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__uncultured	0.225557559	0.201943945	0.2640236	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae	0.218401467	0.339535022	0.52007037	1
Follow-up	d__Bacteria.p__Verrucomicrobiota.c__Lentisphaeria.o__Victivallales.f__Victivallaceae	0.215103128	0.23475501	0.35951602	1
Follow-up	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Barnesiellaceae	0.213460917	0.657095013	0.74529045	1
Follow-up	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae	0.188920465	0.734376993	0.7969837	1
Follow-up	d__Bacteria.p__Campylobacterota.c__Campylobacteria.o__Campylobacterales.f__Campylobacteraceae	0.188433898	0.18078232	0.29726111	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridia_vadinBB60_group.f__Clostridia_vadinBB60_group	0.187007382	0.478248322	0.69577824	1

Timepoint	**Taxon**	**Log-fold change vs. control**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__uncultured.f__uncultured	0.181878162	0.245357836	0.4585254	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae	0.178143404	0.205850284	0.38681777	1
Follow-up	d__Bacteria.p__Proteobacteria.c__Alphaproteobacteria.o__Rhodospirillales.f__uncultured	0.169392282	0.477383413	0.7227133	1
Follow-up	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Atopobiaceae	0.167286882	0.32890054	0.61101543	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Clostridiaceae	0.162665134	0.560469263	0.7716401	1
Follow-up	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.__	0.161388018	0.469623149	0.73110628	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Christensenellales.f__Christensenellaceae	0.148902285	0.50485385	0.76803867	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Monoglobales.f__Monoglobaceae	0.144322145	0.565436179	0.79853745	1
Follow-up	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Bifidobacteriales.f__Bifidobacteriaceae	0.14344586	0.701441548	0.83796161	1
Follow-up	d__Bacteria.p__Proteobacteria.c__Alphaproteobacteria.o__Caulobacterales.f__Caulobacteraceae	0.13793812	0.201008326	0.49256753	1
Follow-up	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Pasteurellaceae	0.137390607	0.550618645	0.80295823	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Anaerovoraceae	0.117981761	0.332013664	0.72232581	1
Follow-up	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Flavobacteriales.f__Flavobacteriaceae	0.112176574	0.399944734	0.77910912	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Eubacteriaceae	0.111736698	0.439270269	0.79921057	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__.Eubacterium._coprostanoligenes_group	0.072752028	0.390508868	0.85220905	1
Follow-up	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Propionibacteriales.f__Propionibacteriaceae	0.056126551	0.206454259	0.78573005	1
Follow-up	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Carnobacteriaceae	0.052176852	0.260547944	0.84127868	1

Timepoint	**Taxon**	**Log-fold change vs. control**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Follow-up	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__uncultured	0.047311479	0.268708344	0.86023895	1
Follow-up	d__Bacteria.p__Cyanobacteria.c__Cyanobacteriia.o__Chloroplast.f__Chloroplast	0.042333122	0.486712342	0.93068923	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ethanoligenenaceae	0.032014701	0.223767107	0.88623369	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Anaerofustaceae	0.005556101	0.23111775	0.9808206	1
Follow-up	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelatoclostridiaceae	-0.00036003	0.415078865	0.99930793	1
Follow-up	d__Bacteria.p__Patescibacteria.c__Saccharimonadia.o__Saccharimonadales.f__Saccharimonadaceae	-0.02428135	0.306895533	0.93693775	1
Follow-up	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Burkholderiales.f__Burkholderiaceae	-0.03823352	0.235112455	0.87081921	1
Follow-up	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Enterobacteriaceae	-0.06264486	0.600665725	0.91693732	1
Follow-up	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Actinomycetales.f__Actinomycetaceae	-0.06288409	0.374267932	0.8665684	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Family_XI	-0.0745747	0.357962186	0.83497035	1
Follow-up	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Burkholderiales.f__Oxalobacteraceae	-0.08526272	0.459453308	0.85277861	1
Follow-up	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Succinivibrionaceae	-0.09758099	0.370932934	0.79249732	1
Follow-up	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__uncultured	-0.10293603	0.511763713	0.8405893	1

Timepoint	**Taxon**	**Log-fold change vs. control**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__UCG.010	-0.14489148	0.523051204	0.78177086	1
Follow-up	d__Bacteria.p__Firmicutes.c__Bacilli.o__Staphylococcales.f__Staphylococcaceae	-0.15132467	0.188936476	0.42317285	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospirales	-0.15230018	0.293881956	0.60429368	1
Follow-up	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Micrococcales.f__Micrococcaceae	-0.17410351	0.18006773	0.33360507	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Defluviitaleaceae	-0.17450531	0.424001039	0.680656	1
Follow-up	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Acidaminococcales.f__Acidaminococcaceae	-0.17903883	0.509628425	0.72535393	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridia_UCG.014.f__Clostridia_UCG.014	-0.18190931	0.694249875	0.79330385	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.__.__	-0.19574111	0.344313063	0.56969721	1
Follow-up	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Aerococcaceae	-0.21191036	0.306599448	0.48946277	1
Follow-up	d__Bacteria.p__Firmicutes.c__Bacilli.__.__	-0.21411515	0.177598076	0.22796544	1
Follow-up	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Xanthomonadales.f__Xanthomonadaceae	-0.23003099	0.217648913	0.29056172	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptococcales.f__Peptococcaceae	-0.23380894	0.41644282	0.57449552	1

Timepoint	**Taxon**	**Log-fold change vs. control**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Follow-up	d__Bacteria.p__Cyanobacteria.c__Vampirivibrionia.o__Gastranaerophilales.f__Gastranaerophilales	-0.23504739	0.248124793	0.34348845	1
Follow-up	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Lactobacillaceae	-0.23728853	0.495699819	0.63215633	1
Follow-up	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Rikenellaceae	-0.24190016	0.503160068	0.63068577	1
Follow-up	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Bacteroidaceae	-0.25975221	0.28609374	0.36391683	1
Follow-up	d__Bacteria.__.__.__.__	-0.27819293	0.287240916	0.33279454	1
Follow-up	d__Bacteria.p__Firmicutes.c__Bacilli.o__Staphylococcales.f__Gemellaceae	-0.29485904	0.381352232	0.43940792	1
Follow-up	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelotrichaceae	-0.29938501	0.514271045	0.56046287	1
Follow-up	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Pseudomonadales.f__Moraxellaceae	-0.3168702	0.212316956	0.13558398	1
Follow-up	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Tannerellaceae	-0.32518581	0.354951111	0.35959215	1
Follow-up	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.__	-0.34054689	0.539412681	0.5278254	1
Follow-up	d__Bacteria.p__Firmicutes.__.__.__	-0.3731452	0.238475145	0.11765018	1
Follow-up	d__Bacteria.p__Firmicutes.c__Incertae_Sedis.o__DTU014.f__DTU014	-0.5246689	0.293452632	0.07378943	1

Timepoint	**Taxon**	**Log-fold change vs. control**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Follow-up	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Coriobacteriales_Incertae_Sedis	-0.57901629	0.421390926	0.16942315	1
Follow-up	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Enterococcaceae	-0.64580577	0.42881758	0.13206328	1
Follow-up	d__Bacteria.p__Firmicutes.c__Bacilli.o__RF39.f__RF39	-0.76362763	0.730870641	0.29610657	1
Follow-up	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Muribaculaceae	-0.76663006	0.791742119	0.33290329	1
Follow-up	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.__	-0.92599439	0.621522315	0.13625549	1
Follow-up	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Veillonellales.Selenomonadales.f__Selenomonadaceae	-1.05732992	0.806796974	0.19001732	1

Table S12. Microbiota log-fold change versus control at the genus level

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 0	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelatoclostridiaceae.g__Catenibacterium	1.612128569	0.650879856	0.01325494	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Lachnospira	1.377785984	0.45577218	0.00250306	0.55317716
Week 0	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Pasteurellaceae.g__Haemophilus	1.366797494	0.562074218	0.01502803	1
Week 0	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelotrichaceae.g__Holdemania	1.337983137	0.413631081	0.0012176	0.2703063
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__uncultured	1.245811101	0.606022354	0.0398097	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Lachnospiraceae_UCG.004	1.206413454	0.541032425	0.02575835	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__.Ruminococcus._gnavus_group	1.122987534	0.840113499	0.18131754	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__.Ruminococcus._torques_group	1.117443441	0.464299471	0.01609607	1
Week 0	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Veillonellales.Selenomonadales.f__Veillonellaceae.g__Dialister	1.107456604	0.865377966	0.20063748	1
Week 0	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Enterobacteriaceae.__	1.105923922	0.764065688	0.14777934	1
Week 0	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelatoclostridiaceae.g__Erysipelatoclostridium	1.09200107	0.600524985	0.06900138	1
Week 0	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.g__Prevotella	1.089058606	0.72003122	0.13040269	1
Week 0	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.__.__	1.036366799	0.494773263	0.03620392	1
Week 0	d__Bacteria.p__Desulfobacterota.c__Desulfovibrionia.o__Desulfovibrionales.f__Desulfovibrionaceae.g__Bilophila	1.016650305	0.481383227	0.03469199	1
Week 0	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Enterobacteriaceae.g__Escherichia.Shigella	1.00710163	0.720597879	0.16223571	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Lachnospiraceae_UCG.003	0.971532822	0.347005593	0.00511404	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 0	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Eggerthellaceae.g__un-cultured	0.944446048	0.355607161	0.00791043	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Roseburia	0.933754147	0.552396553	0.09095733	1
Week 0	d__Bacteria.p__Desulfobacterota.c__Desulfovibrionia.o__Desulfovibrionales.f__Desulfovibrionaceae.g__Desulfovibrio	0.93131805	0.683924175	0.17328404	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__UC5.1.2E3	0.903786353	0.527701495	0.08677053	1
Week 0	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Veillonellales.Selenomonadales.f__Veillonellaceae.g__Veillonella	0.890616739	0.603923094	0.14028816	1
Week 0	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.g__Prevotellaceae_NK3B31_group	0.880510928	0.559282391	0.11540462	1
Week 0	d__Bacteria.p__Fusobacteriota.c__Fusobacteriia.o__Fusobacteriales.f__Fusobacteriaceae.g__Fusobacterium	0.817534683	0.780438277	0.29485392	1
Week 0	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Enterobacteriaceae.g__Kluyvera	0.811023779	0.37475417	0.03045293	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Agathobacter	0.790516865	0.564355142	0.16129075	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Lachnospiraceae_NK4A136_group	0.782828593	0.510266122	0.12499091	1
Week 0	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Enterobacteriaceae.g__Klebsiella	0.761521294	0.855271147	0.37325876	1
Week 0	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Eggerthellaceae.g__Eggerthella	0.747661976	0.377746096	0.04778548	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Sellimonas	0.710858883	0.546299635	0.19318136	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Lachnoclostridium	0.602789719	0.404701249	0.13636407	1
Week 0	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Flavobacteriales.f__Flavobacteriaceae.g__uncultured	0.579327873	0.348958767	0.09688199	1
Week 0	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Streptococcaceae.g__Streptococcus	0.557481466	0.487290695	0.25260584	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Howardella	0.552047295	0.423746462	0.19265078	1

Timepoint	Taxon	Log-fold change (vs. control)	Standard error	*P*-value (raw)	*P*-value (Holm)
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Fournierella	0.545418778	0.351846522	0.12110286	1
Week 0	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelotrichaceae.g__.Clostridium._innocuum_group	0.540202109	0.534450653	0.31213062	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.g__Oscillibacter	0.500120922	0.551066439	0.36411547	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Anaerosporobacter	0.487906932	0.595427347	0.41254505	1
Week 0	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Lactobacillaceae.g__Lacticaseibacillus	0.444979737	0.278697144	0.11034539	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Negativibacillus	0.432474594	0.524221005	0.40937997	1
Week 0	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.g__Prevotella_9	0.429080214	0.895073145	0.63166828	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Lachnospiraceae_UCG.010	0.429050476	0.511069626	0.40118053	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Faecalibacterium	0.41256777	0.48198272	0.39200861	1
Week 0	d__Bacteria.p__Desulfobacterota.c__Desulfovibrionia.o__Desulfovibrionales.f__Desulfovibrionaceae.g__uncultured	0.407142316	0.259231389	0.11628142	1
Week 0	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Burkholderiales.f__Sutterellaceae.g__Parasutterella	0.398286561	0.622513459	0.52230007	1
Week 0	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Burkholderiales.f__Comamonadaceae.g__Comamonas	0.395597374	0.468935735	0.39888916	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Tyzzerella	0.392250309	0.695735391	0.57289544	1
Week 0	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Atopobiaceae.g__Olsenella	0.389650867	0.343704914	0.25692944	1
Week 0	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Bifidobacteriales.f__Bifidobacteriaceae.g__Bifidobacterium	0.37185026	0.627985117	0.55376201	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.g__UCG.003	0.369943348	0.577508009	0.52179192	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Butyricicoccaceae.g__UCG.009	0.365857691	0.275301375	0.18386935	1

Timepoint	Taxon	Log-fold change (vs. control)	Standard error	*P*-value (raw)	*P*-value (Holm)
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Anaerovoracaceae.g__Mogibacterium	0.353514535	0.303168173	0.24358718	1
Week 0	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Actinomycetales.f__Actinomycetaceae.g__Actinomyces	0.344007125	0.288590523	0.23325143	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.g__Flavonifractor	0.325198112	0.441114915	0.46098944	1
Week 0	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__uncultured.g__uncultured	0.316272124	0.190330854	0.09657363	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Lachnospiraceae_ND3007_group	0.311792728	0.498277526	0.53148477	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Subdoligranulum	0.295100336	0.661632741	0.655584	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Lachnospiraceae_UCG.008	0.294716582	0.493750079	0.55057799	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Anaerotruncus	0.276978669	0.392850161	0.48077965	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Moryella	0.274032368	0.551951309	0.61955633	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.g__Oscillospira	0.26397172	0.474515021	0.57800721	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.g__UCG.002	0.263851809	0.618318108	0.66957962	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__.Eubacterium._ventriosum_group	0.257360935	0.497561842	0.60498576	1
Week 0	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Porphyromonadaceae.g__Porphyromonas	0.250642079	0.336555061	0.45643599	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.g__Colidextribacter	0.246297355	0.560775129	0.66051027	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.g__Pseudoflavonifractor	0.242789549	0.316714325	0.44332623	1
Week 0	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Enterococcaceae.g__Enterococcus	0.237923655	0.467557009	0.61084647	1
Week 0	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Corynebacteriales.f__Corynebacteriaceae.g__Corynebacterium	0.225546209	0.251025964	0.36892036	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptococcales.f__Peptococcaceae.__	0.212661973	0.283872899	0.45376979	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Lachnospiraceae_FCS020_group	0.20617049	0.467440091	0.65916745	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__.Ruminococcus._gauvreauii_group	0.20064545	0.534238936	0.70723474	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Peptostreptococcaceae.g__Intestinibacter	0.183572395	0.501934257	0.71456659	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Butyricicoccaceae.g__Butyricicoccus	0.180906518	0.353150387	0.60846569	1
Week 0	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Muribaculaceae.g__CAG.873	0.16998981	0.434442653	0.69558843	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__uncultured	0.169934453	0.415946619	0.68287088	1
Week 0	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Morganellaceae.g__Proteus	0.164178507	0.204095654	0.42115479	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Eisenbergiella	0.162845949	0.553453363	0.76857751	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Phocea	0.161290912	0.461693947	0.7268296	1
Week 0	d__Bacteria.__.__.__.__.__	0.150294844	0.379719643	0.69224906	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__.Eubacterium._xylanophilum_group	0.145161969	0.527620699	0.78321973	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Anaerovoracaceae.g__.Eubacterium._brachy_group	0.128267463	0.352486681	0.71593785	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.__.__	0.124463204	0.456920437	0.78531771	1
Week 0	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Lactobacillaceae.g__Lactiplantibacillus	0.124078699	0.287954944	0.66654383	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Incertae_Sedis	0.109299071	0.326886607	0.738105	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 0	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.__	0.108215659	0.462757943	0.81510191	1
Week 0	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Lactobacillaceae.g__Ligilactobacillus	0.106300835	0.358416486	0.76678362	1
Week 0	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Eggerthellaceae.g__Gordonibacter	0.097030967	0.305921328	0.7511099	1
Week 0	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelotrichaceae.g__Dielma	0.086927481	0.40793948	0.83125742	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Christensenellales.f__Christensenellaceae.g__Christensenella	0.084666806	0.328583986	0.79666026	1
Week 0	d__Bacteria.p__Firmicutes.__.__.__.__	0.081090496	0.27531354	0.76834628	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__.Eubacterium._hallii_group	0.06321725	0.409430588	0.87729211	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.g__UCG.005	0.054115382	0.406674104	0.89413946	1
Week 0	d__Bacteria.p__Patescibacteria.c__Saccharimonadia.o__Saccharimonadales.f__Saccharimonadaceae.g__TM7x	0.052090486	0.181292963	0.77386143	1
Week 0	d__Bacteria.p__Synergistota.c__Synergistia.o__Synergistales.f__Synergistaceae.g__Cloacibacillus	0.048031758	0.477965756	0.91995369	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Dorea	0.046570893	0.362127373	0.8976713	1
Week 0	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Streptococcaceae.g__Lactococcus	0.046455818	0.53704127	0.93106637	1
Week 0	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Atopobiaceae.g__Atopobium	0.044493754	0.211620159	0.83347029	1
Week 0	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Rikenellaceae.g__Rikenellaceae_RC9_gut_group	0.044125578	0.942975551	0.96267743	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.__	0.038809902	0.269349408	0.88543132	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Peptostreptococcaceae.g__Terrisporobacter	0.03492644	0.472046539	0.94101882	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__uncultured.f__uncultured.g__uncultured	0.034094721	0.234045821	0.88417763	1
Week 0	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Burkholderiales.f__Oxalobacteraceae.g__Oxalobacter	0.02937987	0.505119093	0.9536178	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__.Eubacterium._eligens_group	0.0289093	0.575965871	0.9599688	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Coprococcus	0.025253322	0.583968328	0.96550676	1
Week 0	d__Bacteria.p__Firmicutes.c__Incertae_Sedis.o__DTU014.f__DTU014.g__DTU014	0.025195004	0.266712367	0.92473973	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Christensenellales.f__Christensenellaceae.g__Christensenellaceae	0.013911705	0.191137851	0.9419783	1
Week 0	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Rikenellaceae.__	0.012210789	0.21856035	0.95544602	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Anaerofustaceae.g__Anaerofustis	0.001065815	0.218743409	0.99611237	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Family_XI.g__Fenollaria	-0.00209925	0.219142922	0.99235689	1
Week 0	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Micrococcales.f__Micrococcaceae.g__Rothia	-0.00567178	0.23044685	0.98036437	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__DTU089	-0.00593828	0.461308543	0.98972936	1
Week 0	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Marinifilaceae.g__Odoribacter	-0.00666621	0.619389428	0.99141289	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__UBA1819	-0.01650859	0.282532695	0.95340553	1
Week 0	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Lactobacillaceae.g__Leuconostoc	-0.02111915	0.290177019	0.94198101	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Anaerovoracaceae.__	-0.03128534	0.480787025	0.94811739	1
Week 0	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.g__Prevotellaceae_UCG.003	-0.04637481	0.33205449	0.88892845	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae. g__.Eubacterium._fissicatena_group	-0.0477934	0.354436656	0.89273579	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__ Anaerovoracaceae. g__Family_XIII_AD3011_group	-0.05087707	0.448228346	0.90962859	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__ Lachnospiraceae_UCG.001	-0.06262384	0.564938301	0.91173469	1
Week 0	d__Bacteria.p__Patescibacteria.c__Saccharimonadia.o__Saccharimonadales.f__Saccharimonadales. g__Saccharimonadales	-0.07273169	0.193535031	0.70706087	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Christensenellales.f__Christensenellaceae.g__ Catabacter	-0.07646553	0.218893541	0.72684346	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__ Peptostreptococcaceae. g__uncultured	-0.08032842	0.201989853	0.69086207	1
Week 0	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Barnesiellaceae.g__Coprobacter	-0.08926734	0.716815404	0.90089309	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Harryflintia	-0.08933952	0.300785966	0.76645107	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Marvinbryantia	-0.09520435	0.432112152	0.82561942	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 0	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Marinifilaceae.g__Sanguibacteroides	-0.09542206	0.406909339	0.81459336	1
Week 0	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Burkholderiales.f__Sutterellaceae.g__Sutterella	-0.09739324	0.616656064	0.87450589	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Oribacterium	-0.10179842	0.236008551	0.66622581	1
Week 0	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__uncultured.g__uncultured	-0.1026716	0.554817909	0.85318623	1
Week 0	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Burkholderiales.f__Burkholderiaceae.g__Ralstonia	-0.10743624	0.253424217	0.67161079	1
Week 0	d__Bacteria.p__Firmicutes.c__Bacilli.o__Izemoplasmatales.f__Izemoplasmatales.g__Izemoplasmatales	-0.10999914	0.285986318	0.700511	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Blautia	-0.12176732	0.300751007	0.68556756	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.g__NK4A214_group	-0.12297468	0.523671732	0.81433942	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Candidatus_Soleaferrea	-0.12383584	0.326527069	0.7045012	1
Week 0	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Acidaminococcales.f__Acidaminococcaceae.g__Phascolarctobacterium	-0.12531584	0.461644403	0.78604083	1
Week 0	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Bacteroidaceae.g__Bacteroides	-0.14196413	0.492275846	0.77305336	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Eubacteriaceae.g__Eubacterium	-0.1556434	0.307537958	0.61279001	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__GCA.900066755	-0.16422162	0.361231152	0.6493852	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Anaerovoracaceae.g__Family_XIII_UCG.001	-0.17558472	0.383110706	0.6467274	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__CAG.56	-0.17881528	0.563895213	0.75116219	1
Week 0	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Eggerthellaceae.g__Slackia	-0.18306298	0.419276889	0.66238989	1
Week 0	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Lactobacillaceae.g__Weissella	-0.18656133	0.616638153	0.76223596	1
Week 0	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Coriobacteriales_Incertae_Sedis.g__Raoultibacter	-0.18662203	0.239312061	0.43549266	1
Week 0	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.g__Prevotella_7	-0.1877186	0.428764832	0.66152221	1
Week 0	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Burkholderiales.f__Sutterellaceae.__	-0.18887471	0.539034405	0.72604262	1
Week 0	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelatoclostridiaceae.g__Coprobacillus	-0.19205292	0.4583609	0.67521661	1
Week 0	d__Bacteria.p__Cyanobacteria.c__Cyanobacteriia.o__Chloroplast.f__Chloroplast.g__Chloroplast	-0.19481023	0.484090597	0.68737116	1
Week 0	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.__.__	-0.208239	0.438412609	0.63479833	1
Week 0	d__Bacteria.p__Verrucomicrobiota.c__Lentisphaeria.o__Victivallales.f__Victivallaceae.g__Victivallaceae	-0.21157355	0.263508373	0.42202667	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.g__Intestinimonas	-0.21506143	0.466093323	0.64450246	1
Week 0	d__Bacteria.p__Synergistota.c__Synergistia.o__Synergistales.f__Synergistaceae.g__Synergistes	-0.22977924	0.458576689	0.61632152	1
Week 0	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Tannerellaceae.g__Parabacteroides	-0.23743012	0.490077481	0.62804904	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospirales.g__Hydrogenoanaerobacterium	-0.23757998	0.292417649	0.41652315	1
Week 0	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Succinivibrionaceae.g__Succinivibrio	-0.24184203	0.334891977	0.47020266	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.g__uncultured	-0.2438882	0.489439052	0.61827157	1
Week 0	d__Bacteria.p__Firmicutes.c__Bacilli.o__Staphylococcales.f__Gemellaceae.g__Gemella	-0.24460552	0.344030328	0.47708431	1
Week 0	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Enterobacteriaceae.g__Citrobacter	-0.24780927	0.70959791	0.72692047	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__uncultured.g__uncultured	-0.25057016	0.314108011	0.42503315	1
Week 0	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelotrichaceae.g__Faecalitalea	-0.26445944	0.476160758	0.57862145	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.__	-0.26609568	0.585123848	0.64927606	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridia_vadinBB60_group.f__Clostridia_vadinBB60_group.g__Clostridia_vadinBB60_group	-0.27019137	0.541555541	0.61783773	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Anaerovoracaceae.g__.Eubacterium._nodatum_group	-0.29558238	0.443508244	0.50511442	1
Week 0	d__Bacteria.p__Verrucomicrobiota.c__Verrucomicrobiae.o__Verrucomicrobiales.f__Akkermansiaceae.g__Akkermansia	-0.29620018	0.681126506	0.66365818	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Fusicatenibacter	-0.29962757	0.411600769	0.46664005	1
Week 0	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Eggerthellaceae.g__Adlercreutzia	-0.32927432	0.432674123	0.44664421	1
Week 0	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelotrichaceae.g__Holdemanella	-0.34420484	0.759075829	0.65022294	1
Week 0	d__Bacteria.p__Patescibacteria.c__Saccharimonadia.o__Saccharimonadales.f__Saccharimonadaceae.g__Saccharimonadaceae	-0.3506734	0.281886632	0.21349117	1
Week 0	d__Bacteria.p__Cyanobacteria.c__Vampirivibrionia.o__Gastranaerophilales.f__Gastranaerophilales.g__Gastranaerophilales	-0.36473564	0.314139203	0.24561597	1
Week 0	d__Bacteria.p__Desulfobacterota.c__Desulfovibrionia.o__Desulfovibrionales.f__Desulfovibrionaceae.g__Mailhella	-0.36475534	0.313173605	0.24413781	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Anaerostipes	-0.37069854	0.401350458	0.35568	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Family_XI.g__Parvimonas	-0.37655425	0.261401245	0.14971976	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Frisingicoccus	-0.39314189	0.341209183	0.24923809	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Tuzzerella	-0.40617524	0.360082917	0.25931792	1
Week 0	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Veillonellales.Selenomonadales.f__Veillonellaceae.g__Veillonellaceae	-0.4268232	0.36189638	0.23823607	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.__	-0.44843893	0.368973407	0.22422529	1
Week 0	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Eggerthellaceae.g__Senegalimassilia	-0.4754387	0.543498681	0.3816967	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Defluviitaleaceae.g__Defluviitaleaceae_UCG.011	-0.51818663	0.39643565	0.19117396	1
Week 0	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Rikenellaceae.g__Alistipes	-0.52010349	0.604815659	0.38982366	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ethanoligenenaceae.g__Acetanaerobacterium	-0.52056982	0.253458233	0.03998844	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Butyricicoccaceae.g__UCG.008	-0.52426063	0.340512087	0.123652	1
Week 0	d__Bacteria.p__Firmicutes.c__Bacilli.o__RF39.f__RF39.g__RF39	-0.55700137	0.725027855	0.44233972	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Anaerofilum	-0.5937798	0.335498745	0.07675345	1
Week 0	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Tannerellaceae.__	-0.60182892	0.58669923	0.30499161	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 0	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Veillonellales.Selenomonadales.f__Selenomonadaceae.g__Megamonas	-0.60796024	0.872016329	0.48568449	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Ruminococcus	-0.61345381	0.545712673	0.26095647	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Christensenellales.f__Christensenellaceae.g__Christensenellaceae_R.7_group	-0.63339215	0.646206137	0.327002	1
Week 0	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.g__Prevotellaceae_UCG.001	-0.6465835	0.64929243	0.31933379	1
Week 0	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Marinifilaceae.g__Butyricimonas	-0.65677249	0.561921295	0.24248502	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Catenibacillus	-0.65755669	0.22764049	0.00386991	0.85138102
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Paludicola	-0.6622579	0.340678153	0.05190268	1
Week 0	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Lactobacillaceae.g__Lactobacillus	-0.66346263	0.419513569	0.11376271	1
Week 0	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Eggerthellaceae.__	-0.67674145	0.340662854	0.04697305	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Incertae_Sedis	-0.70178366	0.572379956	0.22016854	1
Week 0	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Acidaminococcales.f__Acidaminococcaceae.g__Acidaminococcus	-0.70959312	0.579652009	0.22088777	1
Week 0	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Veillonellales.Selenomonadales.f__Veillonellaceae.__	-0.73567412	0.4567285	0.10723485	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Clostridiaceae.g__Clostridium_sensu_stricto_1	-0.74149636	0.61485113	0.22782634	1
Week 0	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelatoclostridiaceae.g__Erysipelotrichaceae_UCG.003	-0.75694531	0.583677735	0.19468113	1
Week 0	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.g__Paraprevotella	-0.76877183	0.613249022	0.20998574	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__.Eubacterium._siraeum_group	-0.78061168	0.728071618	0.28364668	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Hungatella	-0.78780396	0.625783241	0.20806331	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Christensenellales.f__Christensenellaceae.g__uncultured	-0.78785034	0.363724732	0.03030645	1
Week 0	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.g__Alloprevotella	-0.78941677	0.814238903	0.33228834	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptococcales.f__Peptococcaceae.g__Peptococcus	-0.78947258	0.37025927	0.03298913	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridia_UCG.014.f__Clostridia_UCG.014.g__Clostridia_UCG.014	-0.7934166	0.730692535	0.27754893	1
Week 0	d__Bacteria.p__Proteobacteria.c__Alphaproteobacteria.o__Rhodospirillales.f__uncultured.g__uncultured	-0.80941245	0.497960016	0.10406528	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Peptostreptococcaceae.g__Romboutsia	-0.81022444	0.603708569	0.17957046	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__.Eubacterium._coprostanoligenes_group	-0.8318012	0.41724981	0.04620313	1

Timepoint	Taxon	Log-fold change (vs. control)	Standard error	*P*-value (raw)	*P*-value (Holm)
	.g__.Eubacterium._coprostanoligenes_group				
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Peptostreptococcaceae.__	-0.83905445	0.741350874	0.2577222	1
Week 0	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Eggerthellaceae.g__Enterorhabdus	-0.84358409	0.439274062	0.05480677	1
Week 0	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Barnesiellaceae.g__Barnesiella	-0.85739817	0.804484398	0.28652603	1
Week 0	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Tannerellaceae.g__Tannerellaceae	-0.8753283	0.395236435	0.02678098	1
Week 0	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Coriobacteriaceae.g__Collinsella	-0.89576625	0.529527969	0.09071624	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__.Eubacterium._ruminantium_group	-0.90057129	0.617644121	0.14481994	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptococcales.f__Peptococcaceae.g__uncultured	-0.95012265	0.453772549	0.03627511	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Monoglobales.f__Monoglobaceae.g__Monoglobus	-0.9647121	0.465008993	0.03802274	1
Week 0	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Veillonellales.Selenomonadales.f__Veillonellaceae.g__Megasphaera	-0.99100556	0.737852928	0.17924166	1
Week 0	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Muribaculaceae.g__Muribaculaceae	-1.0030773	0.803523167	0.21190329	1
Week 0	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.__.__	-1.05051747	0.557540107	0.05953783	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__.Clostridium._methylpentosum_group.g__.Clostridium._methylpentosum_group	-1.08390189	0.406548468	0.00767352	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__UCG.010.g__UCG.010	-1.13583079	0.601052359	0.05879316	1
Week 0	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Coriobacteriales_Incertae_Sedis.g__uncultured	-1.18204152	0.449355942	0.00852534	1
Week 0	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelotrichaceae.g__Turicibacter	-1.18779771	0.675649062	0.07874583	1
Week 0	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.g__uncultured	-1.1920973	0.559359819	0.03307419	1
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.__.__.__	-1.21603605	0.358807037	0.0007012	0.15636807
Week 0	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__CAG.352	-1.73882309	0.47544604	0.00025494	0.05710651
Week 2	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Enterobacteriaceae.g__Klebsiella	2.479930916	0.843282846	0.0032736	0.7038238
Week 2	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Pasteurellaceae.g__Haemophilus	1.738587666	0.63762713	0.00639804	1
Week 2	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Enterobacteriaceae.__	1.38317196	0.658294774	0.03562835	1
Week 2	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Veillonellales.Selenomonadales.f__Veillonellaceae.g__Veillonella	1.376105146	0.729225004	0.05914971	1
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Lactobacillaceae.g__Lacticaseibacillus	1.25166807	0.36699118	0.00064815	0.14518551
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Streptococcaceae.g__Streptococcus	1.228868893	0.728600241	0.0916772	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Agathobacter	1.224107781	0.533416499	0.02174205	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__.Ruminococcus._gnavus_group	1.138907024	0.850258953	0.18041363	1

Timepoint	Taxon	Log-fold change (vs. control)	Standard error	*P*-value (raw)	*P*-value (Holm)
Week 2	d__Bacteria.p__Fusobacteriota.c__Fusobacteriia.o__Fusobacteriales.f__Fusobacteriaceae.g__Fusobacterium	1.103376554	0.675560858	0.10241121	1
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.__.__	0.982730673	0.586915726	0.09405235	1
Week 2	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Enterobacteriaceae.g__Citrobacter	0.981318918	0.575520773	0.08817628	1
Week 2	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.g__Prevotellaceae_NK3B31_group	0.946766519	0.595541454	0.11188947	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Tyzzerella	0.919765223	0.64522898	0.15401661	1
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelatoclostridiaceae.g__Catenibacterium	0.898621744	0.736755198	0.22257789	1
Week 2	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.g__Prevotella_9	0.87416593	0.886633012	0.32416312	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__CAG.56	0.859170204	0.624807764	0.16910191	1
Week 2	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Barnesiellaceae.g__Coprobacter	0.855592011	0.653535479	0.19047523	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Subdoligranulum	0.838011558	0.659336953	0.20373173	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Lachnospiraceae_UCG.004	0.773428504	0.533782369	0.14734917	1
Week 2	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Micrococcales.f__Micrococcaceae.g__Rothia	0.742942338	0.408917858	0.06924011	1
Week 2	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Eggerthellaceae.g__Eggerthella	0.735883047	0.438491848	0.09330538	1
Week 2	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Veillonellales.Selenomonadales.f__Veillonellaceae.g__Dialister	0.72468592	0.710697173	0.30787876	1
Week 2	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Eggerthellaceae.g__uncultured	0.674867934	0.362069978	0.06233354	1
Week 2	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.__.__	0.664534423	0.443977934	0.13445219	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Anaerovoracaceae.__	0.628037709	0.497562572	0.20686654	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Lachnospiraceae_UCG.003	0.623717537	0.405686975	0.12418671	1
Week 2	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Burkholderiales.f__Comamonadaceae.g__Comamonas	0.621603792	0.458506408	0.17519002	1
Week 2	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.g__Prevotella	0.582558116	0.743059548	0.43304056	1
Week 2	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Enterobacteriaceae.g__Escherichia.Shigella	0.579997004	0.768037895	0.45014868	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Roseburia	0.57705527	0.468500437	0.21805855	1
Week 2	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Enterobacteriaceae.g__Kluyvera	0.566145763	0.378256769	0.13446524	1
Week 2	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Atopobiaceae.g__Olsenella	0.515367832	0.338444093	0.12781972	1
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Carnobacteriaceae.g__Granulicatella	0.514918121	0.441677261	0.24368546	1
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelatoclostridiaceae.g__Erysipelotrichaceae_UCG.003	0.507489542	0.569339607	0.37273325	1
Week 2	d__Bacteria.p__Synergistota.c__Synergistia.o__Synergistales.f__Synergistaceae.g__Pyramidobacter	0.484269363	0.668052877	0.46851537	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Anaerosporobacter	0.465374786	0.553419112	0.40039925	1
Week 2	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Bifidobacteriales.f__Bifidobacteriaceae.g__Bifidobacterium	0.465321455	0.637567579	0.46548882	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__.Ruminococcus._torques_group	0.444604104	0.443352664	0.31594643	1
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Lactobacillaceae.g__Limosilactobacillus	0.412874162	0.413885762	0.31849478	1
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.o__Bacillales.f__Bacillaceae.g__Bacillus	0.408577832	0.290787946	0.16000004	1
Week 2	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Porphyromonadaceae.g__Porphyromonas	0.396829468	0.307704746	0.19717442	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Streptococcaceae.g__Lactococcus	0.382157589	0.403724381	0.34385263	1
Week 2	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.__	0.381853714	0.503181254	0.44792491	1
Week 2	d__Bacteria.p__Desulfobacterota.c__Desulfovibrionia.o__Desulfovibrionales.f__ Desulfovibrionaceae.g__uncultured	0.374210452	0.31931092	0.24122465	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__.Ruminococcus._gauvreauii_ group	0.362824587	0.538865854	0.50074913	1
Week 2	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__ Succinivibrionaceae.g__ Succinatimonas	0.357243639	0.299177368	0.23244416	1
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Lactobacillaceae.g__Ligilactobacillus	0.357074787	0.403832877	0.37658056	1
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.o__Staphylococcales.f__Gemellaceae.g__Gemella	0.355485791	0.529277662	0.50181081	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.g__Colidextribacter	0.351129096	0.45408081	0.43935996	1
Week 2	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__uncultured.g__ uncultured	0.339167556	0.306241357	0.2680704	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__UC5.1.2E3	0.319394444	0.432861928	0.4605954	1
Week 2	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Burkholderiales.f__Sutterellaceae.g__Parasutterella	0.318870099	0.526978007	0.54511797	1
Week 2	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Muribaculaceae.g__ Muribaculaceae	0.314234415	0.784408495	0.6887143	1
Week 2	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__uncultured.g__uncultured	0.309515651	0.487388357	0.52539624	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Butyricicoccaceae.g__Butyricicoccus	0.300999734	0.487798086	0.53719644	1
Week 2	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Pseudomonadales.f__ Pseudomonadaceae.g__ Pseudomonas	0.279808989	0.255845594	0.27410258	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__ Lachnospiraceae_UCG.008	0.278670381	0.468163176	0.55168173	1
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Lactobacillaceae.g__Weissella	0.267787989	0.473673962	0.57184087	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.__	0.258757497	0.299396164	0.38744257	1
Week 2	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Burkholderiales.f__Sutterellaceae.__	0.25162396	0.503452232	0.61721796	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__.Eubacterium._hallii_group	0.242828203	0.352554605	0.4909695	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Howardella	0.231465275	0.421856746	0.58322358	1
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelotrichaceae.g__Holdemanella	0.220579801	0.814648673	0.78657041	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Monoglobales.f__Monoglobaceae.g__Monoglobus	0.218832897	0.556567467	0.69418428	1
Week 2	d__Bacteria.p__Firmicutes.__.__.__.__	0.21834083	0.29376716	0.45733366	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Hungatella	0.206901696	0.769116323	0.78792027	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Peptostreptococcaceae.g__Peptostreptococcus	0.206768423	0.232667783	0.37417227	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Lachnoclostridium	0.206515728	0.360342724	0.56657076	1
Week 2	d__Bacteria.p__Patescibacteria.c__Saccharimonadia.o__Saccharimonadales.f__Saccharimonadaceae.g__TM7a	0.201178022	0.195323169	0.30302164	1
Week 2	d__Bacteria.p__Synergistota.c__Synergistia.o__Synergistales.f__Synergistaceae.g__Cloacibacillus	0.1963487	0.619310588	0.75121022	1
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelatoclostridiaceae.g__Erysipelatoclostridium	0.195737267	0.572434049	0.73239714	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__uncultured	0.185722384	0.50090839	0.71080798	1
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelatoclostridiaceae.g__UCG.004	0.185589916	0.320455665	0.56249214	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__.Eubacterium._ventriosum_group	0.169965387	0.518175566	0.74290612	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Dorea	0.163982019	0.474206454	0.72949076	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Sellimonas	0.14828975	0.551198362	0.7879054	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__uncultured.f__uncultured.g__uncultured	0.128034503	0.269463858	0.63468337	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Christensenellales.f__Christensenellaceae.g__Christensenella	0.117583846	0.30231749	0.69731935	1
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelotrichaceae.g__.Clostridium._innocuum_group	0.116413269	0.558398394	0.83485647	1
Week 2	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Atopobiaceae.g__Atopobium	0.111343595	0.235123269	0.63581789	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Anaerostipes	0.111087244	0.375246284	0.76720089	1
Week 2	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.g__Prevotellaceae_UCG.001	0.100994428	0.612442458	0.86901926	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__.Eubacterium._eligens_group	0.089037609	0.50837727	0.86096899	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Family_XI.g__Fenollaria	0.085608257	0.214129186	0.68930587	1
Week 2	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Muribaculaceae.g__CAG.873	0.082810583	0.327182118	0.80018907	1
Week 2	d__Bacteria.p__Patescibacteria.c__Saccharimonadia.o__Saccharimonadales.f__Saccharimonadaceae.g__Saccharimonadaceae	0.065089103	0.242649451	0.788512	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridia_UCG.014.f__Clostridia_UCG.014.g__Clostridia_UCG.014	0.05618298	0.682830382	0.93442441	1
Week 2	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Corynebacteriales.f__Corynebacteriaceae.g__Corynebacterium	0.052808318	0.237178343	0.82380608	1
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.__.__.__	0.032032958	0.208944173	0.87815484	1
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelotrichaceae.g__Dielma	0.018340483	0.359928778	0.95936069	1

Timepoint	Taxon	Log-fold change (vs. control)	Standard error	*P*-value (raw)	*P*-value (Holm)
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Fournierella	0.017990731	0.359338715	0.96006962	1
Week 2	d__Bacteria.p__Desulfobacterota.c__Desulfovibrionia.o__Desulfovibrionales.f__Desulfovibrionaceae.g__Bilophila	0.009894111	0.45147579	0.98251573	1
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.o__Staphylococcales.f__Staphylococcaceae.g__Staphylococcus	0.004309755	0.211607543	0.98375082	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__.Eubacterium._xylanophilum_group	0.004181975	0.439086163	0.99240085	1
Week 2	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.__.__.__	-0.01455452	0.2052735	0.9434749	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Anaerofustaceae.g__Anaerofustis	-0.01937557	0.262100644	0.94107075	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Anaerovoracaceae.g__Family_XIII_AD3011_group	-0.01946548	0.457602283	0.96606983	1
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Lactobacillaceae.g__Leuconostoc	-0.02067754	0.303809478	0.94573718	1
Week 2	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Flavobacteriales.f__Flavobacteriaceae.g__uncultured	-0.02110672	0.342838431	0.95090954	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Lachnospiraceae_UCG.001	-0.02460554	0.586504936	0.9665363	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Blautia	-0.02462458	0.32230423	0.93909955	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.__	-0.02602982	0.588689075	0.96473177	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 2	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.g__Paraprevotella	-0.04995452	0.626978363	0.93649571	1
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.o__RF39.f__RF39.g__RF39	-0.054019	0.679835057	0.93666755	1
Week 2	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Marinifilaceae.g__Sanguibacteroides	-0.06631521	0.363201618	0.85512356	1
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelotrichaceae.g__Faecalitalea	-0.07064349	0.456769424	0.87709018	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.g__Flavonifractor	-0.07175018	0.391217169	0.85448227	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Peptostreptococcaceae.__	-0.0791656	0.601843587	0.89534933	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__.Eubacterium._coprostanoligenes_group.g__.Eubacterium._coprostanoligenes_group	-0.09203238	0.520543225	0.85966498	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Incertae_Sedis	-0.09807718	0.392270178	0.80256836	1
Week 2	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Succinivibrionaceae.g__Succinivibrio	-0.10586915	0.323788616	0.74369061	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Family_XI.g__Parvimonas	-0.1084162	0.378643543	0.77462701	1
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelotrichaceae.g__Holdemania	-0.11276175	0.403752153	0.78002644	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptococcales.f__Peptococcaceae.__	-0.11472211	0.283270024	0.68548334	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Lachnospiraceae_UCG.010	-0.12071249	0.356370339	0.73481491	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__GCA.900066755	-0.12427475	0.330487382	0.70689104	1
Week 2	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Actinomycetales.f__Actinomycetaceae.g__Actinomyces	-0.12532751	0.420862244	0.76586537	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Family_XI.g__Peptoniphilus	-0.12699386	0.198778895	0.52290756	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Peptostreptococcaceae.g__Terrisporobacter	-0.13357703	0.405545866	0.74187158	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Frisingicoccus	-0.15078233	0.257372638	0.55797484	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Anaerovoracaceae.g__Mogibacterium	-0.15646611	0.206528473	0.44869007	1
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Aerococcaceae.g__Abiotrophia	-0.17384735	0.333891381	0.60259642	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Lachnospiraceae_NK4A136_group	-0.17759862	0.432643113	0.68144155	1
Week 2	d__Bacteria.p__Desulfobacterota.c__Desulfovibrionia.o__Desulfovibrionales.f__Desulfovibrionaceae.g__Mailhella	-0.18881567	0.273188219	0.48946753	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Peptostreptococcaceae.g__Intestinibacter	-0.19636598	0.444682347	0.65878803	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 2	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Rikenellaceae.g__Rikenellaceae_RC9_gut_group	-0.19900477	0.882241267	0.82153799	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Anaerovoracaceae.g__.Eubacterium._nodatum_group	-0.2102599	0.370274199	0.57013738	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Tuzzerella	-0.21544979	0.336780344	0.52234564	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.g__uncultured	-0.22524026	0.416723717	0.58885045	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.g__Oscillibacter	-0.22895222	0.535812931	0.66916171	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Paludicola	-0.23780819	0.317505456	0.45386365	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridia_vadinBB60_group.f__Clostridia_vadinBB60_group.g__Clostridia_vadinBB60_group	-0.24015476	0.447242359	0.59128983	1
Week 2	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.g__Prevotella_7	-0.25737404	0.437618086	0.55644854	1
Week 2	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Coriobacteriales_Incertae_Sedis.g__Raoultibacter	-0.25776701	0.341514801	0.45038369	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__uncultured.g__uncultured	-0.25791846	0.208078255	0.21515067	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Lachnospiraceae_ND3007_group	-0.25831733	0.458160029	0.57288029	1

Timepoint	Taxon	Log-fold change (vs. control)	Standard error	*P*-value (raw)	*P*-value (Holm)
Week 2	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Eggerthellaceae.g__Gordonibacter	-0.27003719	0.3715053	0.46730372	1
Week 2	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Eggerthellaceae.g__Senegalimassilia	-0.27996892	0.560102256	0.61717843	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Moryella	-0.28139157	0.498800219	0.57266103	1
Week 2	d__Bacteria.p__Firmicutes.c__Incertae_Sedis.o__DTU014.f__DTU014.g__DTU014	-0.29471161	0.318412086	0.35467123	1
Week 2	d__Bacteria.__.__.__.__.__	-0.2969337	0.399424962	0.45723775	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Coprococcus	-0.3013179	0.530767284	0.57023701	1
Week 2	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Eggerthellaceae.__	-0.30354787	0.30939172	0.3265376	1
Week 2	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Veillonellales.Selenomonadales.f__Selenomonadaceae.g__Megamonas	-0.30649973	0.83237295	0.71270619	1
Week 2	d__Bacteria.p__Verrucomicrobiota.c__Lentisphaeria.o__Victivallales.f__Victivallaceae.g__Victivallaceae	-0.30696964	0.238941826	0.19889557	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Anaerovoracaceae.g__.Eubacterium._brachy_group	-0.30750548	0.313892506	0.32725784	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Eisenbergiella	-0.32124322	0.525142051	0.54071884	1
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelotrichaceae.g__Faecalicoccus	-0.32579025	0.26270476	0.21492423	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 2	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Coriobacteriales_Incertae_Sedis.g__uncultured	-0.33026147	0.474205687	0.48614585	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Marvinbryantia	-0.33116747	0.426234192	0.4371816	1
Week 2	d__Bacteria.p__Verrucomicrobiota.c__Lentisphaeria.o__Victivallales.f__Victivallaceae.g__Victivallis	-0.33516376	0.24002715	0.16260681	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Fusicatenibacter	-0.36241089	0.455679004	0.42642704	1
Week 2	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Veillonellales.Selenomonadales.f__Veillonellaceae.__	-0.37274217	0.391011196	0.3404495	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Lachnospiraceae_FCS020_group	-0.37869979	0.448290448	0.39824242	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Butyricicoccaceae.g__UCG.008	-0.37902014	0.320812264	0.23742835	1
Week 2	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Coriobacteriaceae.g__Collinsella	-0.38289845	0.583450313	0.51165316	1
Week 2	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Marinifilaceae.g__Butyricimonas	-0.39481177	0.605932112	0.51467372	1
Week 2	d__Bacteria.p__Cyanobacteria.c__Cyanobacteriia.o__Chloroplast.f__Chloroplast.g__Chloroplast	-0.40173533	0.489052814	0.41138662	1
Week 2	d__Bacteria.p__Proteobacteria.c__Alphaproteobacteria.o__Rhodospirillales.f__uncultured.g__uncultured	-0.40599508	0.482265403	0.39987198	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Anaerotruncus	-0.41032179	0.535166502	0.4432492	1
Week 2	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Eggerthellaceae.g__Enterorhabdus	-0.41052448	0.448748032	0.36028519	1
Week 2	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Eggerthellaceae.g__Adlercreutzia	-0.41213285	0.438912039	0.34773724	1
Week 2	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Bacteroidaceae.g__Bacteroides	-0.41430093	0.508785853	0.41547692	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.__.__	-0.41437897	0.483249762	0.39117742	1
Week 2	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Eggerthellaceae.g__Slackia	-0.42813268	0.407650958	0.29360627	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Butyricicoccaceae.g__UCG.009	-0.43813037	0.291373285	0.13266538	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Anaerofilum	-0.44164495	0.300245199	0.1413053	1
Week 2	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Veillonellales.Selenomonadales.f__Veillonellaceae.g__Veillonellaceae	-0.45636617	0.398572093	0.25220799	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Eubacteriaceae.g__Eubacterium	-0.48852999	0.325666583	0.13359045	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.g__Oscillospira	-0.50679597	0.469250901	0.28013744	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__DTU089	-0.5257232	0.454654045	0.24755242	1
Week 2	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Tannerellaceae.g__Tannerellaceae	-0.53080229	0.386414336	0.16954696	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ethanoligenenaceae.g__Acetanaerobacterium	-0.53213641	0.208112222	0.01055888	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Lachnospira	-0.54014034	0.508780093	0.28840001	1
Week 2	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.g__Alloprevotella	-0.5645558	0.731617129	0.44031896	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Peptostreptococcaceae.g__Romboutsia	-0.57768539	0.469390459	0.21842987	1
Week 2	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.__.__	-0.59358252	0.533560655	0.26592622	1
Week 2	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Rikenellaceae.g__Alistipes	-0.60115579	0.702261221	0.39198188	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__.Eubacterium._ruminantium_group	-0.62112943	0.594689582	0.29627265	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Anaerovoracaceae.g__Family_XIII_UCG.001	-0.63060799	0.433533261	0.1457861	1
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Lactobacillaceae.g__Lactobacillus	-0.63406064	0.28436018	0.02576205	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Harryflintia	-0.63752043	0.313233188	0.04182168	1

Timepoint	Taxon	Log-fold change (vs. control)	Standard error	*P*-value (raw)	*P*-value (Holm)
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Catenibacillus	-0.64273049	0.217729133	0.00315751	0.68394379
Week 2	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Tannerellaceae.g__Parabacteroides	-0.64435517	0.559066191	0.24909261	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__UBA1819	-0.65786435	0.375693771	0.07993465	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.g__UCG.005	-0.66645817	0.467676354	0.15414523	1
Week 2	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Burkholderiales.f__Oxalobacteraceae.g__Oxalobacter	-0.67038333	0.438410201	0.12623384	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Phocea	-0.67222825	0.391522756	0.08598679	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__uncultured	-0.68182414	0.458179545	0.1367204	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.__	-0.6835922	0.417316122	0.1014075	1
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Enterococcaceae.g__Enterococcus	-0.70063853	0.673944992	0.29852211	1
Week 2	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Burkholderiales.f__Sutterellaceae.g__Sutterella	-0.7075066	0.694966128	0.3086567	1
Week 2	d__Bacteria.p__Synergistota.c__Synergistia.o__Synergistales.f__Synergistaceae.g__Synergistes	-0.70955368	0.397790109	0.07446611	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Negativibacillus	-0.71205528	0.570663194	0.21211603	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptococcales.f__Peptococcaceae.g__Peptococcus	-0.73125997	0.330744745	0.02703933	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.g__UCG.003	-0.74419822	0.572137979	0.19335018	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.g__Pseudoflavonifractor	-0.75985314	0.257356623	0.00315181	0.68394379
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelatoclostridiaceae.g__Coprobacillus	-0.76744236	0.592095668	0.19492523	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Faecalibacterium	-0.81289884	0.518236883	0.11674456	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__.Eubacterium._fissicatena_group	-0.82875034	0.326778191	0.01120867	1
Week 2	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Barnesiellaceae.g__Barnesiella	-0.84894668	0.718140837	0.23714813	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Defluviitaleaceae.g__Defluviitaleaceae_UCG.011	-0.87765404	0.33731288	0.00927092	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Candidatus_Soleaferrea	-0.8815681	0.271364343	0.00115954	0.25741691
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.g__Intestinimonas	-0.91999048	0.507367041	0.06979108	1
Week 2	d__Bacteria.p__Desulfobacterota.c__Desulfovibrionia.o__Desulfovibrionales.f__Desulfovibrionaceae.g__Desulfovibrio	-0.92289085	0.583666544	0.11383337	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__.Eubacterium._siraeum_group	-0.9269461	0.630821869	0.14171726	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 2	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Acidaminococcales.f__Acidaminococcaceae.g__Phascolarctobacterium	-0.94030342	0.552078986	0.0885298	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Incertae_Sedis	-0.96004736	0.317883187	0.00252669	0.55334585
Week 2	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Marinifilaceae.g__Odoribacter	-0.96457882	0.580035945	0.09631967	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Christensenellales.f__Christensenellaceae.g__uncultured	-0.97823154	0.324678868	0.00258747	0.56406821
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.g__UCG.002	-0.98360273	0.550451513	0.07395338	1
Week 2	d__Bacteria.p__Verrucomicrobiota.c__Verrucomicrobiae.o__Verrucomicrobiales.f__Akkermansiaceae.g__Akkermansia	-0.99505965	0.673014604	0.13927099	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Ruminococcus	-0.99631943	0.544403067	0.06723296	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Clostridiaceae.g__Clostridium_sensu_stricto_1	-0.99981208	0.568080659	0.07841076	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.g__NK4A214_group	-1.00405364	0.579986527	0.08342195	1
Week 2	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Veillonellales.Selenomonadales.f__Veillonellaceae.g__Megasphaera	-1.03369151	0.637071393	0.10468184	1
Week 2	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelotrichaceae.g__Turicibacter	-1.07850418	0.405828075	0.00787133	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.__.__.__	-1.13586676	0.336026314	0.00072409	0.16147227
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptococcales.f__Peptococcaceae.g__uncultured	-1.14353234	0.359104485	0.00145054	0.32057022
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__UCG.010.g__UCG.010	-1.15684212	0.543354278	0.03324804	1
Week 2	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.g__uncultured	-1.30381399	0.617378416	0.03469885	1
Week 2	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Tannerellaceae.__	-1.31580174	0.579104126	0.02307846	1
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__.Clostridium._methylpentosum_group.g__.Clostridium._methylpentosum_group	-1.55183846	0.424464047	0.00025619	0.05764192
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__CAG.352	-1.57550287	0.546821773	0.00396164	0.84779143
Week 2	d__Bacteria.p__Firmicutes.c__Clostridia.o__Christensenellales.f__Christensenellaceae.g__Christensenellaceae_R.7_group	-1.97008941	0.63611397	0.00195444	0.42997638
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Lachnospiraceae_UCG.004	1.811523553	0.45067176	5.8295E-05	0.01369937
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__.Eubacterium._eligens_group	1.500106476	0.538570473	0.00534702	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Agathobacter	1.33322469	0.553578589	0.01602372	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Lachnospiraceae_UCG.001	1.313189296	0.582731109	0.02422713	1
Week 4	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Veillonellales.Selenomonadales.f__Veillonellaceae.g__Veillonella	1.117023553	0.590681504	0.05861421	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Lachnospiraceae_NK4A136_group	1.112705382	0.555243259	0.04507047	1
Week 4	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.g__Prevotella_9	1.104340053	0.873877497	0.20632907	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Subdoligranulum	1.09194458	0.602211152	0.06979706	1
Week 4	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Pasteurellaceae.g__Haemophilus	1.062243178	0.573207092	0.06385975	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Lachnospiraceae_ND3007_group	1.05525362	0.438683803	0.01615038	1
Week 4	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelatoclostridiaceae.g__Catenibacterium	1.050502691	0.751724223	0.16227602	1
Week 4	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Enterobacteriaceae.__	1.028865891	0.7429298	0.16609029	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Anaerosporobacter	1.022570805	0.586314334	0.08114761	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__UC5.1.2E3	1.006838449	0.465390795	0.03050845	1
Week 4	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Burkholderiales.f__Comamonadaceae.g__Comamonas	0.938059126	0.50023225	0.06075872	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__.Eubacterium._ventriosum_group	0.913697548	0.556904684	0.10086566	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__.Eubacterium._xylanophilum_group	0.896633315	0.518948941	0.08402639	1
Week 4	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Enterobacteriaceae.g__Klebsiella	0.892089969	0.794808537	0.26169408	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Roseburia	0.876852899	0.50652301	0.08343009	1
Week 4	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Barnesiellaceae.g__Barnesiella	0.84899221	0.770515991	0.27052736	1
Week 4	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Porphyromonadaceae.g__Porphyromonas	0.81632399	0.42148029	0.05276952	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Lachnospiraceae_UCG.010	0.781403193	0.370592206	0.03498554	1
Week 4	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Bifidobacteriales.f__Bifidobacteriaceae.g__Bifidobacterium	0.780180826	0.700309198	0.2652569	1
Week 4	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Eggerthellaceae.g__uncultured	0.761636707	0.417599341	0.06817542	1
Week 4	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Lactobacillaceae.g__Lacticaseibacillus	0.702803579	0.352724002	0.04631591	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.g__Colidextribacter	0.698753067	0.423981542	0.09933743	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Monoglobales.f__Monoglobaceae.g__Monoglobus	0.673843439	0.556648001	0.2260726	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__CAG.56	0.67040177	0.565995015	0.2362287	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Lachnospira	0.655195928	0.616533544	0.2879138	1
Week 4	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Veillonellales.Selenomonadales.f__Veillonellaceae.g__Dialister	0.654136372	0.80563	0.41681669	1
Week 4	d__Bacteria.p__Fusobacteriota.c__Fusobacteriia.o__Fusobacteriales.f__Fusobacteriaceae.g__Fusobacterium	0.642661717	0.744143696	0.38779347	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Ruminococcus	0.641944341	0.584837985	0.27235965	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Lachnospiraceae_UCG.008	0.609689256	0.470283351	0.19482752	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__.Eubacterium._siraeum_group	0.593436666	0.641727647	0.35509676	1
Week 4	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.g__Prevotellaceae_NK3B31_group	0.568823129	0.666743235	0.3935835	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Lachnospiraceae_UCG.003	0.564066527	0.462835726	0.222951	1
Week 4	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Enterobacteriaceae.g__Kluyvera	0.552351345	0.405624083	0.17328244	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 4	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.g__Prevotellaceae_UCG.001	0.543010053	0.422110075	0.19829717	1
Week 4	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Lactobacillaceae.g__Weissella	0.532896152	0.513319847	0.29920644	1
Week 4	d__Bacteria.p__Cyanobacteria.c__Cyanobacteriia.o__Chloroplast.f__Chloroplast.g__Chloroplast	0.504817706	0.551260509	0.35979718	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridia_UCG.014.f__Clostridia_UCG.014.g__Clostridia_UCG.014	0.496721052	0.706665948	0.48211317	1
Week 4	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Enterobacteriaceae.g__Citrobacter	0.463382832	0.644454077	0.47212146	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Peptostreptococcaceae.g__Intestinibacter	0.460710253	0.460119596	0.31668967	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Family_XI.g__Fenollaria	0.43842112	0.27635499	0.11263911	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Anaerostipes	0.420880461	0.438150743	0.33676153	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Peptostreptococcaceae.__	0.41869096	0.543676818	0.44123464	1
Week 4	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Eggerthellaceae.g__Senegalimassilia	0.387690259	0.546108447	0.47775721	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Anaerovoracaceae.__	0.381576353	0.401763515	0.34223746	1
Week 4	d__Bacteria.p__Desulfobacterota.c__Desulfovibrionia.o__Desulfovibrionales.f__Desulfovibrionaceae.g__uncultured	0.379047224	0.267132596	0.15591422	1
Week 4	d__Bacteria.p__Firmicutes.c__Bacilli.o__RF39.f__RF39.g__RF39	0.37565399	0.672931311	0.57668374	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__.Ruminococcus._torques_group	0.367604498	0.438850487	0.40222553	1
Week 4	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Eggerthellaceae.g__Adlercreutzia	0.349552273	0.380008228	0.35764881	1

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Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Clostridiaceae.g__Clostridium_sensu_stricto_1	0.342476475	0.538625058	0.5248842	1
Week 4	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelatoclostridiaceae.g__UCG.004	0.341886746	0.310129412	0.2702877	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Butyricicoccaceae.g__Butyricicoccus	0.341844835	0.412867885	0.40768391	1
Week 4	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Burkholderiales.f__Sutterellaceae.__	0.337459736	0.462661008	0.4657639	1
Week 4	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Enterobacteriaceae.g__Escherichia.Shigella	0.329165095	0.641519705	0.60787992	1
Week 4	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__uncultured.g__uncultured	0.323830401	0.291370476	0.26639436	1
Week 4	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Marinifilaceae.g__Odoribacter	0.314729356	0.597972481	0.59866069	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Butyricicoccaceae.g__UCG.008	0.304024993	0.238210137	0.20185335	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Dorea	0.30046187	0.416589003	0.47076007	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Fusicatenibacter	0.296869296	0.397022554	0.45461753	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptococcales.f__Peptococcaceae.__	0.289608968	0.285399975	0.31022611	1
Week 4	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Enterococcaceae.g__Enterococcus	0.285117568	0.685527628	0.6774761	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__.Eubacterium._hallii_group	0.252861366	0.413705117	0.54105951	1
Week 4	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.g__Prevotella	0.249205727	0.738263763	0.73569743	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__uncultured.f__uncultured.g__uncultured	0.235671321	0.311704252	0.44960514	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Anaerovoracaceae.g__Mogibacterium	0.215652985	0.191724615	0.26067128	1

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Week 4	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Barnesiellaceae.g__Coprobacter	0.214480358	0.660286836	0.74531044	1
Week 4	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Atopobiaceae.g__Olsenella	0.210729481	0.391758861	0.59064188	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Lachnoclostridium	0.210069222	0.310733101	0.49901276	1
Week 4	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Carnobacteriaceae.g__Granulicatella	0.207517521	0.397673721	0.60178968	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Tyzzerella	0.206249024	0.708824425	0.77107169	1
Week 4	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Veillonellales.Selenomonadales.f__Veillonellaceae.__	0.191374194	0.327493895	0.55897842	1
Week 4	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.__	0.188074188	0.463600786	0.68497675	1
Week 4	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Streptococcaceae.g__Lactococcus	0.184206411	0.406778837	0.65066275	1
Week 4	d__Bacteria.p__Campylobacterota.c__Campylobacteria.o__Campylobacterales.f__Campylobacteraceae.g__Campylobacter	0.179825919	0.212706743	0.397878	1
Week 4	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelotrichaceae.g__Dielma	0.177092778	0.453397306	0.69609979	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__.Ruminococcus._gauvreauii_group	0.175668633	0.58588638	0.76430381	1
Week 4	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Eggerthellaceae.g__Eggerthella	0.172673913	0.445843871	0.69853648	1
Week 4	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Pseudomonadales.f__Pseudomonadaceae.g__Pseudomonas	0.159775205	0.286159832	0.57661051	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.g__UCG.002	0.159308717	0.480478447	0.74021951	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Howardella	0.143548549	0.418078241	0.73133268	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Coprococcus	0.139135855	0.568582287	0.80668359	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 4	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Lactobacillaceae.g__Ligilactobacillus	0.135959392	0.468982831	0.77189067	1
Week 4	d__Bacteria.p__Patescibacteria.c__Saccharimonadia.o__Saccharimonadales.f__Saccharimonadaceae.g__TM7a	0.134560174	0.199814416	0.50067647	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Anaerovoracaceae.g__Family_XIII_UCG.001	0.118993603	0.420018844	0.77694275	1
Week 4	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Burkholderiales.f__Neisseriaceae.g__Neisseria	0.116163727	0.235981409	0.622537	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.g__UCG.003	0.116037102	0.598896046	0.84637034	1
Week 4	d__Bacteria.p__Patescibacteria.c__Saccharimonadia.o__Saccharimonadales.f__Saccharimonadaceae.g__Saccharimonadaceae	0.114110513	0.263303014	0.66473803	1
Week 4	d__Bacteria.p__Desulfobacterota.c__Desulfovibrionia.o__Desulfovibrionales.f__Desulfovibrionaceae.g__Mailhella	0.111686248	0.318751414	0.72604853	1
Week 4	d__Bacteria.p__Verrucomicrobiota.c__Verrucomicrobiae.o__Verrucomicrobiales.f__Akkermansiaceae.g__Akkermansia	0.102197226	0.767204318	0.89402943	1
Week 4	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Muribaculaceae.g__CAG.873	0.094176881	0.339697484	0.78159775	1
Week 4	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Micrococcales.f__Micrococcaceae.g__Rothia	0.086468803	0.331521398	0.79422808	1
Week 4	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Morganellaceae.g__Proteus	0.08018837	0.21801996	0.71302022	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Faecalibacterium	0.079527382	0.443329636	0.85763418	1
Week 4	d__Bacteria.p__Firmicutes.c__Incertae_Sedis.o__DTU014.f__DTU014.g__DTU014	0.07425626	0.318502811	0.81565144	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Fournierella	0.062444612	0.346433928	0.85695654	1

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Week 4	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.g__Prevotella_7	0.049794652	0.455407994	0.91293223	1
Week 4	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.__.__.__	0.036394679	0.225431822	0.87174349	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Sellimonas	0.024194531	0.498360672	0.96127932	1
Week 4	d__Bacteria.__.__.__.__.__	0.02307526	0.402090476	0.95423594	1
Week 4	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Muribaculaceae.g__Muribaculaceae	0.021616828	0.799020724	0.97841654	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.__.__	0.0159061	0.395904972	0.96795236	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Oribacterium	0.010815735	0.28409665	0.96963138	1
Week 4	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelatoclostridiaceae.g__Coprobacillus	0.009423451	0.548790133	0.98629994	1
Week 4	d__Bacteria.p__Desulfobacterota.c__Desulfovibrionia.o__Desulfovibrionales.f__Desulfovibrionaceae.g__Bilophila	0.002248992	0.436477953	0.99588885	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Blautia	-0.00383572	0.321725777	0.99048759	1
Week 4	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Coriobacteriales_Incertae_Sedis.g__Raoultibacter	-0.00634636	0.274145031	0.98153091	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__uncultured	-0.0245749	0.459281857	0.95732777	1
Week 4	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Enterobacteriaceae.g__Pseudocitrobacter	-0.03658941	0.380629261	0.92341834	1
Week 4	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Burkholderiales.f__Sutterellaceae.g__Parasutterella	-0.03892275	0.594408578	0.94779066	1

Timepoint	Taxon	Log-fold change (vs. control)	Standard error	*P*-value (raw)	*P*-value (Holm)
Week 4	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Burkholderiales.f__Sutterellaceae.g__Sutterella	-0.04351972	0.569497866	0.93908678	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__.Eubacterium._coprostanoligenes_group.g__.Eubacterium._coprostanoligenes_group	-0.04811557	0.418170919	0.908396	1
Week 4	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Lactobacillaceae.g__Leuconostoc	-0.04811886	0.382051094	0.89977249	1
Week 4	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelotrichaceae.g__Holdemania	-0.04878346	0.410583212	0.9054219	1
Week 4	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Streptococcaceae.g__Streptococcus	-0.05685658	0.620549059	0.92699756	1
Week 4	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelatoclostridiaceae.g__Erysipelatoclostridium	-0.06015679	0.535314417	0.91052485	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Anaerovoracaceae.g__.Eubacterium._brachy_group	-0.07177921	0.424189639	0.8656276	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Christensenellales.f__Christensenellaceae.g__Christensenellaceae_R.7_group	-0.07376339	0.5903133	0.90055811	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Anaerofilum	-0.08896884	0.283369416	0.75354557	1
Week 4	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Rikenellaceae.__	-0.09033139	0.214441177	0.6735792	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Incertae_Sedis	-0.09041055	0.405277814	0.82347099	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 4	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Xanthomonadales.f__Xanthomonadaceae.g__Vulcaniibacterium	-0.09442061	0.248872985	0.70439624	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.g__UCG.005	-0.1020696	0.506659467	0.84034202	1
Week 4	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.__.__	-0.10415819	0.519019049	0.84094661	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Peptostreptococcaceae.g__Romboutsia	-0.10940765	0.378580912	0.77258589	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Family_XI.g__Peptoniphilus	-0.11435764	0.225310866	0.61176552	1
Week 4	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Atopobiaceae.g__Atopobium	-0.12084583	0.268811126	0.65303016	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Candidatus_Soleaferrea	-0.13753262	0.248517077	0.57998053	1
Week 4	d__Bacteria.p__Cyanobacteria.c__Vampirivibrionia.o__Gastranaerophilales.f__Gastranaerophilales.g__Gastranaerophilales	-0.13841904	0.279602109	0.62055974	1
Week 4	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Flavobacteriales.f__Flavobacteriaceae.g__uncultured	-0.14073469	0.371189475	0.70458008	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__uncultured.g__uncultured	-0.1446988	0.239760467	0.54616679	1
Week 4	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Corynebacteriales.f__Corynebacteriaceae.g__Corynebacterium	-0.14639129	0.231903826	0.52787144	1
Week 4	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.__.__	-0.15131931	0.560337637	0.7871216	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 4	d__Bacteria.p__Proteobacteria.c__Alphaproteobacteria.o__Rhodospirillales.f__uncultured.g__uncultured	-0.17591348	0.446530738	0.6936135	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.g__Pseudoflavonifractor	-0.1840769	0.244996259	0.4524446	1
Week 4	d__Bacteria.p__Firmicutes.__.__.__.__	-0.1894364	0.322281258	0.55666763	1
Week 4	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Coriobacteriaceae.g__Collinsella	-0.1922873	0.507380286	0.70470224	1
Week 4	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Succinivibrionaceae.g__Succinatimonas	-0.19894657	0.265970294	0.45445838	1
Week 4	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelatoclostridiaceae.g__Erysipelotrichaceae_UCG.003	-0.21040979	0.655323306	0.74815141	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Frisingicoccus	-0.21380487	0.269817749	0.4281247	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Lachnospiraceae_FCS020_group	-0.21516821	0.402709712	0.59313329	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Tuzzerella	-0.21532132	0.441682806	0.62590251	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__uncultured	-0.22806266	0.571718592	0.68996158	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.g__NK4A214_group	-0.23779737	0.58276399	0.6832363	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptococcales.f__Peptococcaceae.g__Peptococcus	-0.25118007	0.425695943	0.55516	1

Timepoint	Taxon	Log-fold change (vs. control)	Standard error	*P*-value (raw)	*P*-value (Holm)
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__ Peptostreptococcaceae.g__Peptostreptococcus	-0.25528061	0.31690861	0.42051168	1
Week 4	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Pseudomonadales.f__Moraxellaceae.g__Acinetobacter	-0.25781314	0.195257283	0.18670932	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.__.__.__	-0.26930721	0.298071198	0.36626079	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Eisenbergiella	-0.2694995	0.577902123	0.64097138	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__UCG.010.g__UCG.010	-0.27009617	0.525905576	0.60754356	1
Week 4	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.g__Paraprevotella	-0.27131489	0.657848905	0.68002621	1
Week 4	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelatoclostridiaceae.g__Candidatus_Stoquefichus	-0.27143514	0.194737446	0.16336237	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Anaerofustaceae.g__Anaerofustis	-0.28765366	0.322630258	0.37261315	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospirales.g__Hydrogenoanaerobacterium	-0.28863751	0.260364114	0.26760634	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.g__Oscillibacter	-0.28867625	0.469906864	0.53899958	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.__	-0.29342817	0.360877135	0.41616236	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 4	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelotrichaceae.g__Erysipelotrichaceae_UCG.006	-0.30662935	0.322685046	0.34198857	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Christensenellales.f__Christensenellaceae.g__Catabacter	-0.3082336	0.34636227	0.37351057	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Family_XI.g__Parvimonas	-0.31544926	0.353799048	0.3726043	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.g__Flavonifractor	-0.31566717	0.426457369	0.45917377	1
Week 4	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Marinifilaceae.g__Sanguibacteroides	-0.31863425	0.40583092	0.43237125	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.g__Oscillospira	-0.34269825	0.466515548	0.46258846	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Incertae_Sedis	-0.34787819	0.33842314	0.30397874	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Marvinbryantia	-0.34815467	0.455774385	0.44494172	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Eubacteriaceae.g__Eubacterium	-0.3485441	0.37352829	0.35076164	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Angelakisella	-0.35908899	0.227266994	0.11409967	1
Week 4	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelotrichaceae.g__Solobacterium	-0.36370764	0.248734368	0.14367733	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__.Clostridium._methylpentosum_group.g__.Clostridium._methylpentosum_group	-0.36820006	0.435788427	0.39816357	1

Timepoint	Taxon	Log-fold change (vs. control)	Standard error	*P*-value (raw)	*P*-value (Holm)
Week 4	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Eggerthellaceae.__	-0.36948969	0.292739845	0.20688486	1
Week 4	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Eggerthellaceae.g__Gordonibacter	-0.37091134	0.276087003	0.17912366	1
Week 4	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelotrichaceae.g__Turicibacter	-0.37513328	0.487457554	0.44155431	1
Week 4	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Tannerellaceae.g__Tannerellaceae	-0.37547015	0.313103268	0.23045427	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Catenibacillus	-0.40407893	0.283904496	0.1546516	1
Week 4	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Lactobacillaceae.g__Limosilactobacillus	-0.40767432	0.312001686	0.19133453	1
Week 4	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Marinifilaceae.g__Butyricimonas	-0.41613495	0.634180557	0.51170999	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Peptostreptococcaceae.g__Peptoclostridium	-0.41619936	0.405913593	0.30520289	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptococcales.f__Peptococcaceae.g__uncultured	-0.41785267	0.364599361	0.25177041	1
Week 4	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Lactobacillaceae.g__Lactobacillus	-0.43040332	0.382202579	0.26011767	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Butyricicoccaceae.g__UCG.009	-0.43862323	0.248915225	0.07804582	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 4	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Rikenellaceae.g__Alistipes	-0.43882441	0.629720418	0.48589296	1
Week 4	d__Bacteria.p__Desulfobacterota.c__Desulfovibrionia.o__Desulfovibrionales.f__Desulfovibrionaceae.g__Desulfovibrio	-0.44579372	0.581975676	0.44367594	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ethanoligenenaceae.g__Acetanaerobacterium	-0.44820644	0.217682717	0.03949524	1
Week 4	d__Bacteria.p__Firmicutes.c__Bacilli.o__Staphylococcales.f__Gemellaceae.g__Gemella	-0.45345409	0.481715966	0.34653535	1
Week 4	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.g__Alloprevotella	-0.45725637	0.745028188	0.5393847	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__GCA.900066575	-0.46186201	0.242789632	0.05713017	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__UBA1819	-0.47770401	0.313895005	0.12804436	1
Week 4	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Aerococcaceae.g__Abiotrophia	-0.49688058	0.39641593	0.21004838	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Anaerovoracaceae.g__Family_XIII_AD3011_group	-0.49877795	0.364717924	0.17144614	1
Week 4	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Coriobacteriales_Incertae_Sedis.g__uncultured	-0.52301086	0.418507706	0.2114076	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Anaerovoracaceae.g__.Eubacterium._nodatum_group	-0.52614728	0.421099119	0.2114962	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Defluviitaleaceae.g__Defluviitaleaceae_UCG.011	-0.55693137	0.358701182	0.12051078	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.__	-0.56189939	0.388330264	0.14790739	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.g__Intestinimonas	-0.5704958	0.348773191	0.10189789	1
Week 4	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Actinomycetales.f__Actinomycetaceae.g__Actinomyces	-0.57386615	0.430856752	0.18288692	1
Week 4	d__Bacteria.p__Synergistota.c__Synergistia.o__Synergistales.f__Synergistaceae.g__Synergistes	-0.57643706	0.455015413	0.20520831	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Phocea	-0.58263654	0.398537777	0.14375887	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Moryella	-0.59044436	0.494652283	0.2326128	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__.Eubacterium._ruminantium_group	-0.59278245	0.73574489	0.4204215	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__DTU089	-0.60124901	0.443307339	0.17501	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Christensenellales.f__Christensenellaceae.g__Christensenella	-0.60277586	0.273599617	0.0275855	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__.Ruminococcus._gnavus_group	-0.61510278	0.78194363	0.43149665	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 4	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Rikenellaceae.g__Rikenellaceae_RC9_gut_group	-0.61732539	0.842818439	0.46389176	1
Week 4	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__uncultured.g__uncultured	-0.63081939	0.492801084	0.20052087	1
Week 4	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Eggerthellaceae.g__Enterorhabdus	-0.63345038	0.439904838	0.1498755	1
Week 4	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.__.__	-0.63927755	0.608145362	0.29317041	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__GCA.900066755	-0.64293906	0.32958847	0.05108883	1
Week 4	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelotrichaceae.g__Faecalitalea	-0.66907789	0.468665066	0.15339987	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Christensenellales.f__Christensenellaceae.g__uncultured	-0.67179413	0.332635311	0.04342369	1
Week 4	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelotrichaceae.g__Faecalicoccus	-0.67284138	0.262447569	0.01035578	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.g__uncultured	-0.67888173	0.406690874	0.09506152	1
Week 4	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Burkholderiales.f__Oxalobacteraceae.g__Oxalobacter	-0.69112041	0.482615206	0.15213467	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__.Eubacterium._fissicatena_group	-0.73709652	0.428965606	0.08573982	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 4	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Bacteroidaceae.g__Bacteroides	-0.77167426	0.618474924	0.21213911	1
Week 4	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelotrichaceae.g__.Clostridium._innocuum_group	-0.78557834	0.489362289	0.10842552	1
Week 4	d__Bacteria.p__Synergistota.c__Synergistia.o__Synergistales.f__Synergistaceae.g__Cloacibacillus	-0.79320824	0.468298534	0.0903016	1
Week 4	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Tannerellaceae.g__Parabacteroides	-0.79802054	0.473698782	0.09205454	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Negativibacillus	-0.79963351	0.59937474	0.18216689	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.__	-0.81467362	0.483183803	0.09178554	1
Week 4	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Veillonellales.Selenomonadales.f__Veillonellaceae.g__Veillonellaceae	-0.84192231	0.338436762	0.01285794	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Hungatella	-0.86575591	0.590410679	0.14254964	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Harryflintia	-0.87083362	0.28809619	0.00250515	0.5811956
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Peptostreptococcaceae.g__Terrisporobacter	-0.92846462	0.408943353	0.02318338	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Anaerotruncus	-0.94566562	0.397348657	0.0173155	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridia_vadinBB60_group.f__Clostridia_vadinBB60_group.g__Clostridia_vadinBB60_group	-0.95298906	0.462793552	0.03947414	1
Week 4	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Eggerthellaceae.g__Slackia	-0.96299294	0.373168436	0.0098633	1
Week 4	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Succinivibrionaceae.g__Succinivibrio	-1.01807201	0.508804696	0.04540217	1
Week 4	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Paludicola	-1.09436397	0.322318838	0.00068557	0.16042447
Week 4	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelotrichaceae.g__Holdemanella	-1.10884976	0.835331593	0.18436429	1
Week 4	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Veillonellales.Selenomonadales.f__Veillonellaceae.g__Megasphaera	-1.19883663	0.689050598	0.08188741	1
Week 4	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Veillonellales.Selenomonadales.f__Selenomonadaceae.g__Megamonas	-1.2525237	0.76722513	0.10256633	1
Week 4	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Tannerellaceae.__	-1.39163622	0.556259023	0.01235716	1
Week 4	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.g__uncultured	-1.5346971	0.535384056	0.00414992	0.95863233
Week 4	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Acidaminococcales.f__Acidaminococcaceae.g__Phascolarctobacterium	-1.78716015	0.570216912	0.00172337	0.40154629
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Lachnospiraceae_ND3007_group	1.63260626	0.435195186	0.00017583	0.03938495
Follow-up	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Veillonellales.Selenomonadales.f__Veillonellaceae.g__Veillonella	1.625543404	0.594688093	0.00626768	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Lachnospiraceae_UCG.004	1.588203644	0.524648227	0.00246848	0.54800353
Follow-up	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.g__Prevotella	1.3442851	0.88404601	0.1283589	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__.Eubacterium._ventriosum_group	1.290093501	0.428003298	0.00257646	0.56939781
Follow-up	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelatoclostridiaceae.g__Catenibacterium	1.125356329	0.712473473	0.11421998	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Lachnospiraceae_UCG.001	1.100538396	0.484818474	0.02320753	1
Follow-up	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Burkholderiales.f__Sutterellaceae.g__Parasutterella	1.043430135	0.631114359	0.098267	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__CAG.56	1.002357093	0.625540294	0.10907025	1
Follow-up	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Eggerthellaceae.g__uncultured	0.971672437	0.377304176	0.01001524	1
Follow-up	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Veillonellales.Selenomonadales.f__Veillonellaceae.g__Dialister	0.952438289	0.831376791	0.25195421	1
Follow-up	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.g__Prevotella_9	0.944026502	0.854405383	0.26920597	1
Follow-up	d__Bacteria.p__Desulfobacterota.c__Desulfovibrionia.o__Desulfovibrionales.f__Desulfovibrionaceae.g__Desulfovibrio	0.942934954	0.543725247	0.08288044	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Lachnospiraceae_UCG.008	0.942443963	0.448798615	0.03573534	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Tyzzerella	0.921850918	0.629547249	0.14310988	1
Follow-up	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Barnesiellaceae.g__Coprobacter	0.883829634	0.606757733	0.14521485	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Lachnoclostridium	0.866831513	0.443068688	0.05041488	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__uncultured	0.864726002	0.552604793	0.11762556	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Anaerovoracaceae.g__Family_XIII_UCG.001	0.783735132	0.415872859	0.05948999	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Agathobacter	0.747286274	0.477603761	0.11766325	1
Follow-up	d__Bacteria.p__Desulfobacterota.c__Desulfovibrionia.o__Desulfovibrionales.f__Desulfovibrionaceae.g__Bilophila	0.746572825	0.418266876	0.07427433	1
Follow-up	d__Bacteria.p__Fusobacteriota.c__Fusobacteriia.o__Fusobacteriales.f__Fusobacteriaceae.g__Fusobacterium	0.687614757	0.782250178	0.3793896	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Roseburia	0.670933236	0.384642616	0.08110628	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Lachnospira	0.628966887	0.543212158	0.24691872	1
Follow-up	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Burkholderiales.f__Sutterellaceae.__	0.624235351	0.565492854	0.26964589	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Peptostreptococcaceae.g__Intestinibacter	0.615511449	0.47458141	0.19464615	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.g__UCG.002	0.614776403	0.44565896	0.16774765	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Lachnospiraceae_UCG.010	0.608816981	0.395624104	0.12383424	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Lachnospiraceae_FCS020_group	0.604256448	0.430563826	0.1604954	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Subdoligranulum	0.592326566	0.533104222	0.26652978	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Butyricicoccaceae.g__Butyricicoccus	0.572771391	0.401549995	0.15375257	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.__.__	0.545374391	0.416231588	0.19010563	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__.Clostridium._methylpentosum_group.g__.Clostridium._methylpentosum_group	0.541866432	0.413017317	0.18953017	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Anaerofilum	0.535407663	0.349069582	0.12507552	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.g__NK4A214_group	0.530769968	0.450868163	0.23910864	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Anaerosporobacter	0.525392852	0.551662296	0.34090364	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__uncultured	0.523016586	0.389246135	0.17905659	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Peptostreptococcaceae.__	0.521803436	0.641963597	0.41631896	1
Follow-up	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Marinifilaceae.g__Odoribacter	0.519919123	0.572697226	0.36396122	1
Follow-up	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Porphyromonadaceae.g__Porphyromonas	0.487588328	0.364942119	0.1815263	1
Follow-up	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Enterobacteriaceae.g__Citrobacter	0.469509051	0.5937976	0.42912567	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Anaerovoracaceae.__	0.448970975	0.488288114	0.35784475	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.g__Colidextribacter	0.448788368	0.428866642	0.29535238	1
Follow-up	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelatoclostridiaceae.g__Coprobacillus	0.439038043	0.52757617	0.40530767	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Fusicatenibacter	0.436806277	0.505990117	0.38798883	1
Follow-up	d__Bacteria.p__Verrucomicrobiota.c__Verrucomicrobiae.o__Verrucomicrobiales.f__Akkermansiaceae.g__Akkermansia	0.429300566	0.690803948	0.53430315	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Sellimonas	0.421991638	0.521424839	0.41833983	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Coprococcus	0.410408136	0.492535115	0.40470003	1
Follow-up	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Streptococcaceae.g__Streptococcus	0.402944224	0.572486466	0.4815266	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Follow-up	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Morganellaceae.g__Proteus	0.395883542	0.292340087	0.17567629	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Lachnospiraceae_UCG.003	0.374524376	0.455449042	0.4108954	1
Follow-up	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelotrichaceae.g__Holdemania	0.366716594	0.382543992	0.33774722	1
Follow-up	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Coriobacteriaceae.g__Collinsella	0.362928432	0.529178645	0.49281812	1
Follow-up	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Marinifilaceae.g__Butyricimonas	0.358064594	0.520279398	0.49131678	1
Follow-up	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelotrichaceae.g__Turicibacter	0.336491108	0.482208748	0.4852947	1
Follow-up	d__Bacteria.p__Desulfobacterota.c__Desulfovibrionia.o__Desulfovibrionales.f__Desulfovibrionaceae.g__uncultured	0.330855304	0.266184424	0.21388436	1
Follow-up	d__Bacteria.p__Synergistota.c__Synergistia.o__Synergistales.f__Synergistaceae.g__Pyramidobacter	0.304261644	0.397484491	0.44399294	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Tuzzerella	0.295669974	0.365234626	0.41820786	1
Follow-up	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelotrichaceae.g__Dielma	0.26780923	0.357298655	0.45353248	1
Follow-up	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Eggerthellaceae.g__Eggerthella	0.264406639	0.380124687	0.4866927	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.g__Oscillibacter	0.264037869	0.3588488	0.46185764	1
Follow-up	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Pseudomonadales.f__Pseudomonadaceae.g__Pseudomonas	0.253797949	0.277839333	0.3609953	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Anaerovoracaceae.g__.Eubacterium._nodatum_group	0.25265134	0.345550365	0.46468366	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Family_XI.g__Fenollaria	0.245279962	0.230551617	0.28738167	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Dorea	0.232669027	0.367669865	0.52685087	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__uncultured.g__uncultured	0.231305397	0.202541305	0.2534474	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__GCA.900066575	0.221888586	0.25356509	0.38153285	1
Follow-up	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Atopobiaceae.g__Olsenella	0.217752035	0.30688239	0.47797589	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Lachnospiraceae_NK4A136_group	0.217572842	0.41392971	0.59914704	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Negativibacillus	0.205224998	0.49189434	0.67652219	1
Follow-up	d__Bacteria.p__Campylobacterota.c__Campylobacteria.o__Campylobacterales.f__Campylobacteraceae.g__Campylobacter	0.194181736	0.183417239	0.28974163	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridia_vadinBB60_group.f__Clostridia_vadinBB60_group.g__Clostridia_vadinBB60_group	0.19275522	0.489570532	0.6937855	1
Follow-up	d__Bacteria.p__Proteobacteria.c__Alphaproteobacteria.o__Caulobacterales.f__Caulobacteraceae.g__Brevundimonas	0.187630449	0.195966455	0.33833408	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__uncultured.f__uncultured.g__uncultured	0.187625999	0.246345464	0.44627625	1
Follow-up	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Barnesiellaceae.g__Barnesiella	0.187473328	0.796889489	0.81400976	1
Follow-up	d__Bacteria.p__Proteobacteria.c__Alphaproteobacteria.o__Rhodospirillales.f__uncultured.g__uncultured	0.17514012	0.48780337	0.7195664	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Phocea	0.169520237	0.403825221	0.67464168	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.g__Pseudoflavonifractor	0.169475756	0.309260393	0.58368955	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Clostridiaceae.g__Clostridium_sensu_stricto_1	0.168559353	0.563389912	0.76479681	1
Follow-up	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.__.__	0.167135856	0.481872648	0.72870662	1

Timepoint	Taxon	Log-fold change (vs. control)	Standard error	*P*-value (raw)	*P*-value (Holm)
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Monoglobales.f__Monoglobaceae.g__Monoglobus	0.150069982	0.554167271	0.7865428	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Howardella	0.149777456	0.383066689	0.69580036	1
Follow-up	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Bifidobacteriales.f__Bifidobacteriaceae.g__Bifidobacterium	0.148878039	0.709354476	0.83376274	1
Follow-up	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.g__Paraprevotella	0.143647202	0.746464285	0.84740006	1
Follow-up	d__Bacteria.p__Verrucomicrobiota.c__Lentisphaeria.o__Victivallales.f__Victivallaceae.g__Victivallis	0.143608371	0.229127487	0.53081534	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Anaerovoracaceae.g__.Eubacterium._brachy_group	0.125628266	0.343421894	0.71450446	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Faecalibacterium	0.124767017	0.442481963	0.77796586	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Eubacteriaceae.g__Eubacterium	0.117484536	0.433286549	0.78627764	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Oribacterium	0.094222353	0.243442328	0.69872528	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Incertae_Sedis	0.085503819	0.338686849	0.80068795	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.g__UCG.005	0.082894678	0.471768818	0.86052148	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__.Eubacterium._coprostanoligenes_group.g__.Eubacterium._coprostanoligenes_group	0.078499866	0.381014389	0.83676856	1
Follow-up	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Pasteurellaceae.g__Haemophilus	0.076292044	0.573990534	0.89426048	1
Follow-up	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Enterobacteriaceae.__	0.072959118	0.62650033	0.90729192	1
Follow-up	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Lactobacillaceae.g__Lactobacillus	0.072292507	0.332515531	0.82788812	1
Follow-up	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Eggerthellaceae.g__Senegalimassilia	0.069558006	0.599818317	0.90768018	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Follow-up	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Tannerellaceae.g__Tannerellaceae	0.065510303	0.355552746	0.85381798	1
Follow-up	d__Bacteria.p__Patescibacteria.c__Saccharimonadia.o__Saccharimonadales.f__Saccharimonadaceae.g__TM7x	0.061672486	0.202922137	0.76118738	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.__	0.058090153	0.305077534	0.84898699	1
Follow-up	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__uncultured.g__uncultured	0.053059316	0.270759777	0.84463792	1
Follow-up	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Carnobacteriaceae.g__Granulicatella	0.051501745	0.253747519	0.83916276	1
Follow-up	d__Bacteria.p__Cyanobacteria.c__Cyanobacteriia.o__Chloroplast.f__Chloroplast.g__Chloroplast	0.04808096	0.498951841	0.92323154	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Christensenellales.f__Christensenellaceae.g__Christensenellaceae_R.7_group	0.043583954	0.548642224	0.93668292	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__.Eubacterium._eligens_group	0.040879019	0.563026717	0.94211979	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.g__UCG.003	0.03792728	0.486238897	0.937827	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ethanoligenenaceae.g__Acetanaerobacterium	0.037762539	0.211117191	0.85803975	1
Follow-up	d__Bacteria.p__Synergistota.c__Synergistia.o__Synergistales.f__Synergistaceae.g__Cloacibacillus	0.028317521	0.510116647	0.95573069	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Christensenellales.f__Christensenellaceae.g__Catabacter	0.026019731	0.21247034	0.90253244	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Anaerofustaceae.g__Anaerofustis	0.011303939	0.223113107	0.95959278	1
Follow-up	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelatoclostridiaceae.g__Erysipelatoclostridium	0.008546803	0.564001024	0.98790942	1
Follow-up	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Burkholderiales.f__Comamonadaceae.g__Comamonas	0.00625834	0.558418408	0.99105809	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Lactonifactor	0.00411277	0.226215238	0.98549463	1

Timepoint	Taxon	Log-fold change (vs. control)	Standard error	*P*-value (raw)	*P*-value (Holm)
Follow-up	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Propionibacteriales.f__Propionibacteriaceae.g__Cutibacterium	0.004112124	0.20333133	0.98386488	1
Follow-up	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Acidaminococcales.f__Acidaminococcaceae.g__Phascolarctobacterium	0.002483012	0.52668948	0.99623849	1
Follow-up	d__Bacteria.p__Synergistota.c__Synergistia.o__Synergistales.f__Synergistaceae.g__Synergistes	0.000657113	0.41467434	0.99873563	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Anaerostipes	0.00010859	0.419859559	0.99979364	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Anaerotruncus	-0.00057728	0.474363573	0.99902901	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Fournierella	-0.00807415	0.348245313	0.98150252	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__GCA.900066755	-0.01654425	0.331175399	0.96015733	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptococcales.f__Peptococcaceae.g__Peptococcus	-0.02116061	0.42793383	0.96056203	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Candidatus_Soleaferrea	-0.02344099	0.267200911	0.93009291	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__.Eubacterium._xylanophilum_group	-0.02616974	0.509832587	0.9590625	1
Follow-up	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Enterobacteriaceae.g__ Escherichia.Shigella	-0.02988466	0.70829776	0.96634545	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Peptostreptococcaceae.g__ Terrisporobacter	-0.03945867	0.306754545	0.89764827	1

Timepoint	Taxon	Log-fold change (vs. control)	Standard error	*P*-value (raw)	*P*-value (Holm)
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__UC5.1.2E3	-0.03971352	0.421023345	0.92485007	1
Follow-up	d__Bacteria.p__Patescibacteria.c__Saccharimonadia.o__Saccharimonadales.f__Saccharimonadaceae.g__ Saccharimonadaceae	-0.04052226	0.276729582	0.88357981	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Moryella	-0.04747964	0.461500746	0.91805745	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptococcales.f__Peptococcaceae.__	-0.0490196	0.296270437	0.86858541	1
Follow-up	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Actinomycetales.f__Actinomycetaceae.g__Actinomyces	-0.05713625	0.366558354	0.87613376	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Christensenellales.f__Christensenellaceae.g__Christensenella	-0.06039316	0.325004583	0.85258398	1
Follow-up	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Lactobacillaceae.g__Lacticaseibacillus	-0.06200883	0.231224483	0.78856394	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__.Eubacterium._hallii_group	-0.07041874	0.464428608	0.87948314	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.g__Oscillospira	-0.08805911	0.458419633	0.84766952	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__.Ruminococcus._gnavus_group	-0.08980595	0.893850953	0.91997053	1
Follow-up	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Coriobacteriales_Incertae_Sedis.g__ Raoultibacter	-0.09130639	0.290879931	0.75359914	1

Timepoint	Taxon	Log-fold change (vs. control)	Standard error	*P*-value (raw)	*P*-value (Holm)
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Blautia	-0.09339137	0.331900225	0.77841598	1
Follow-up	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__uncultured.g__uncultured	-0.09718819	0.501030482	0.84619421	1
Follow-up	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelotrichaceae.g__uncultured	-0.09741792	0.154505455	0.52835805	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Harryflintia	-0.09843384	0.248038391	0.69147867	1
Follow-up	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Lactobacillaceae.g__Lactiplantibacillus	-0.10008466	0.209666849	0.63311226	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.g__Flavonifractor	-0.102243	0.378978083	0.78732485	1
Follow-up	d__Bacteria.p__Actinobacteriota.c__Actinobacteria.o__Micrococcales.f__Micrococcaceae.g__Rothia	-0.10397816	0.183327494	0.57059756	1
Follow-up	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Lactobacillaceae.g__Ligilactobacillus	-0.10410274	0.448627818	0.8165015	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Family_XI.g__Parvimonas	-0.12591306	0.316438319	0.69069866	1
Follow-up	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Veillonellales.Selenomonadales.f__Veillonellaceae.g__Veillonellaceae	-0.12611746	0.430250182	0.76942594	1
Follow-up	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Veillonellales.Selenomonadales.f__Veillonellaceae.__	-0.12616715	0.350772419	0.71908362	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__UCG.010.g__UCG.010	-0.13914364	0.525888479	0.79132707	1
Follow-up	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Eggerthellaceae.g__Adlercreutzia	-0.13971974	0.43525049	0.74820285	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Butyricicoccaceae.g__UCG.009	-0.14801113	0.309408107	0.63238787	1
Follow-up	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Burkholderiales.f__Sutterellaceae.g__Sutterella	-0.15529691	0.66389347	0.81504832	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Ruminococcus	-0.15802422	0.572400403	0.7824921	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__.Ruminococcus._torques_group	-0.16348687	0.32274582	0.61247065	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Defluviitaleaceae.g__Defluviitaleaceae_UCG.011	-0.16875748	0.425323039	0.69153352	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Peptostreptococcaceae.g__Romboutsia	-0.16913857	0.472695834	0.72048032	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Clostridia_UCG.014.f__Clostridia_UCG.014.g__Clostridia_UCG.014	-0.17616147	0.698307184	0.80083291	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Christensenellales.f__Christensenellaceae.g__uncultured	-0.18092097	0.380523179	0.63446398	1
Follow-up	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Eggerthellaceae.g__Gordonibacter	-0.18341599	0.291975263	0.52987936	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Follow-up	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Rikenellaceae.g__Rikenella	-0.18361639	0.228339297	0.42131706	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.__.__.__	-0.18999328	0.349719553	0.58694168	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__UBA1819	-0.19655208	0.434423289	0.65094938	1
Follow-up	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Flavobacteriales.f__Flavobacteriaceae.g__uncultured	-0.1998885	0.393652845	0.61160861	1
Follow-up	d__Bacteria.p__Firmicutes.c__Bacilli.__.__.__	-0.20836731	0.17120258	0.22357361	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospirales.g__Hydrogenoanaerobacterium	-0.21361226	0.293301873	0.46642891	1
Follow-up	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelotrichaceae.g__Faecalicoccus	-0.21575162	0.240586918	0.36984056	1
Follow-up	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Rikenellaceae.g__Alistipes	-0.2201061	0.498199469	0.65863165	1
Follow-up	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Eggerthellaceae.g__Slackia	-0.2223754	0.450796183	0.62180432	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Marvinbryantia	-0.22544682	0.436434665	0.60545993	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.__	-0.2279973	0.365200036	0.53242533	1
Follow-up	d__Bacteria.p__Cyanobacteria.c__Vampirivibrionia.o__Gastranaerophilales.f__Gastranaerophilales.g__Gastranaerophilales	-0.22929955	0.252787422	0.36436211	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__DTU089	-0.23264077	0.442046808	0.59869308	1
Follow-up	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.__	-0.2448012	0.45407065	0.58980006	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__.Ruminococcus._gauvreauii_group	-0.2452057	0.564281358	0.66389265	1
Follow-up	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Bacteroidaceae.g__Bacteroides	-0.25400437	0.272863285	0.35191299	1
Follow-up	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Tannerellaceae.g__Parabacteroides	-0.25759893	0.345387119	0.45577212	1
Follow-up	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Burkholderiales.f__Oxalobacteraceae.g__Oxalobacter	-0.25987063	0.478121662	0.58676902	1
Follow-up	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelotrichaceae.g__.Clostridium._innocuum_group	-0.26401815	0.43029101	0.5394926	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__.Eubacterium._siraeum_group	-0.26904159	0.629435496	0.66906388	1
Follow-up	d__Bacteria.__.__.__.__.__	-0.27244509	0.312595991	0.38345033	1
Follow-up	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Aerococcaceae.g__Abiotrophia	-0.28081917	0.309449287	0.3641528	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Hungatella	-0.28384817	0.651476851	0.66305474	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Peptostreptococcaceae.g__ Peptoclostridium	-0.28567648	0.28202816	0.31109073	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__.Eubacterium._fissicatena_group	-0.28901073	0.343910161	0.40070267	1
Follow-up	d__Bacteria.p__Firmicutes.c__Bacilli.o__Staphylococcales.f__Gemellaceae.g__Gemella	-0.2891112	0.378532088	0.44500472	1
Follow-up	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Eggerthellaceae.__	-0.30181868	0.351780551	0.39090665	1
Follow-up	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Succinivibrionaceae.g__Succinivibrio	-0.3175741	0.331528032	0.33810802	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Incertae_Sedis	-0.33479848	0.370238567	0.36584816	1
Follow-up	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.__.__	-0.33479905	0.554831864	0.54622643	1
Follow-up	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.g__Prevotellaceae_NK3B31_group	-0.33675374	0.606201776	0.57854294	1
Follow-up	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Marinifilaceae.g__Sanguibacteroides	-0.34169178	0.470478411	0.46767662	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.g__uncultured	-0.34213163	0.414554393	0.40920144	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Anaerovoracaceae.g__Mogibacterium	-0.35769654	0.222685541	0.10821121	1
Follow-up	d__Bacteria.p__Firmicutes.__.__.__.__	-0.36739736	0.250071601	0.14178704	1
Follow-up	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Pseudomonadales.f__Moraxellaceae.g__Acinetobacter	-0.36888463	0.204798302	0.07166988	1

Timepoint	Taxon	Log-fold change (vs. control)	Standard error	*P*-value (raw)	*P*-value (Holm)
Follow-up	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelotrichaceae.g__Faecalitalea	-0.38553541	0.524218344	0.46206661	1
Follow-up	d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Enterobacteriaceae.g__Klebsiella	-0.38697781	0.843842694	0.64652863	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospiraceae.g__Intestinimonas	-0.40039481	0.473546373	0.39781836	1
Follow-up	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Coriobacteriales_Incertae_Sedis.g__uncultured	-0.4022896	0.457013553	0.37871984	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Anaerovoracaceae.g__Family_XIII_ AD3011_group	-0.41969749	0.377238839	0.26590127	1
Follow-up	d__Bacteria.p__Desulfobacterota.c__Desulfovibrionia.o__Desulfovibrionales.f__Desulfovibrionaceae.g__Mailhella	-0.44956477	0.38171235	0.23889311	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Peptococcales.f__Peptococcaceae.g__uncultured	-0.46359737	0.386188885	0.22996772	1
Follow-up	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Lactobacillaceae.g__Weissella	-0.51347015	0.428449142	0.23074617	1
Follow-up	d__Bacteria.p__Firmicutes.c__Incertae_Sedis.o__DTU014.f__DTU014.g__DTU014	-0.51892106	0.306240879	0.09017286	1
Follow-up	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.g__Prevotella_7	-0.52650407	0.579592252	0.36366468	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.__	-0.55781223	0.580170998	0.33632005	1

Timepoint	Taxon	Log-fold change (vs. control)	Standard error	*P*-value (raw)	*P*-value (Holm)
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae.g__Paludicola	-0.56032806	0.348826452	0.10820289	1
Follow-up	d__Bacteria.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Eggerthellaceae.g__Enterorhabdus	-0.56576776	0.439899063	0.1983974	1
Follow-up	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Muribaculaceae.g__CAG.873	-0.57157837	0.390808347	0.14358942	1
Follow-up	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Lactobacillaceae.g__Leuconostoc	-0.60893864	0.21478209	0.00458047	1
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__Eisenbergiella	-0.62706893	0.594811247	0.2917768	1
Follow-up	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Rikenellaceae.g__Rikenellaceae_RC9_gut_group	-0.68520311	0.9516144	0.47149864	1
Follow-up	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Streptococcaceae.g__Lactococcus	-0.69870133	0.34186993	0.0409769	1
Follow-up	d__Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Enterococcaceae.g__Enterococcus	-0.70711785	0.4423268	0.10990236	1
Follow-up	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.g__Alloprevotella	-0.72664103	0.85040829	0.39284941	1
Follow-up	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.g__Prevotellaceae_UCG.001	-0.73439152	0.549859901	0.18168086	1
Follow-up	d__Bacteria.p__Firmicutes.c__Bacilli.o__RF39.f__RF39.g__RF39	-0.7578798	0.740101674	0.30582527	1

Timepoint	**Taxon**	**Log-fold change (vs. control)**	**Standard error**	***P*-value (raw)**	***P*-value (Holm)**
Follow-up	d__Bacteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__.Eubacterium._ruminantium_group	-0.76200121	0.674054037	0.25827615	1
Follow-up	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Muribaculaceae.g__Muribaculaceae	-0.77233559	0.800037109	0.33435717	1
Follow-up	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelatoclostridiaceae.g__Erysipelotrichaceae_UCG.003	-0.87197767	0.655170821	0.18321648	1
Follow-up	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Tannerellaceae.__	-0.91002586	0.627273966	0.14684587	1
Follow-up	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.__.__	-0.92024655	0.623729381	0.14010666	1
Follow-up	d__Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipelotrichaceae.g__Holdemanella	-0.98238226	0.840656227	0.24256896	1
Follow-up	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Veillonellales.Selenomonadales.f__Selenomonadaceae.g__Megamonas	-1.11134913	0.819530657	0.17507372	1
Follow-up	d__Bacteria.p__Firmicutes.c__Negativicutes.o__Veillonellales.Selenomonadales.f__Veillonellaceae.g__Megasphaera	-1.38046008	0.761933002	0.07001916	1
Follow-up	d__Bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.g__uncultured	-1.95449029	0.550163529	0.0003815	0.08507416

Table S13. Summary of overall adverse events, severity, outcome, causality, and actions taken in the investigational product—Safety Analysis Set

Adverse event, n (%) [E][1]	**Probiotic (n = 24)**	**Control (n = 27)**
Participants who reported at least one AE	2 (8.3) [2]	2 (7.4) [2]
Seriousness		
Yes	0 (0) [0]	1 (3.7) [1]
Outcome		
Resolved	2 (8.3) [2]	2 (7.4) [2]
Resolving	0 (0) [0]	0 (0) [0]
Resolved with sequelae	0 (0) [0]	0 (0) [0]
Death	0 (0) [0]	0 (0) [0]
Severity of adverse event		
Mild	2 (8.3) [2]	1 (3.7) [1]
Moderate	0 (0) [0]	0 (0) [0]
Severe	0 (0) [0]	1 (3.7) [1]
Action taken		
None	2 (8.3) [2]	1 (3.7) [1]
Delayed	0 (0) [0]	0 (0) [0]
Withdraw	0 (0) [0]	1 (3.7) [1]
Relationship with IP		
Yes	0 (0) [0]	0 (0) [0]
Relationship with study procedures		
Yes	0 (0) [0]	0 (0) [0]

[1] Adverse events were reported as participant count (percentage of participants) [event count].

AE, adverse event; IP, investigational product

Table S14. Summary of adverse events by terminology

Adverse event, n (%) [E][1]	**Probiotic (n = 24)**	**Control (n = 27)**
Bleeding haemorrhoids[2]		1 (3.7) [1]
Eye pain	1 (4.2) [1]	
Headache	1 (4.2) [1]	
Leg joint pain		1 (3.7) [1]

[1] Adverse events are reported as participant count (percentage of participants) [event count].

[2] Serious adverse event resulting in study withdrawal.

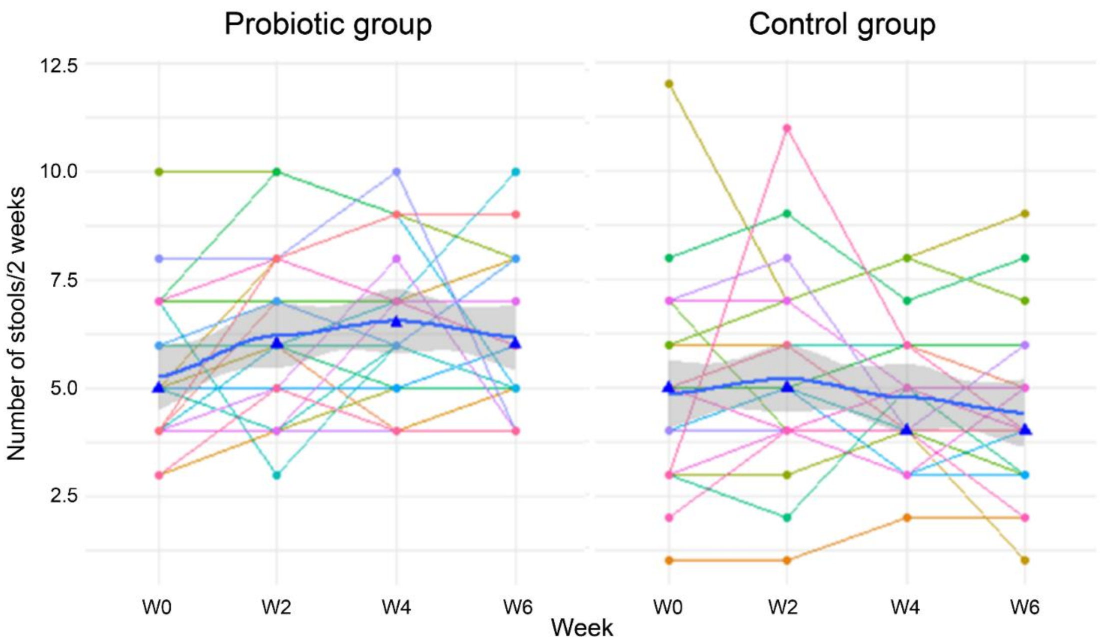

Figure S1. Stool frequency every 2 weeks, from Week 0 to Week 6
Note: Median frequency

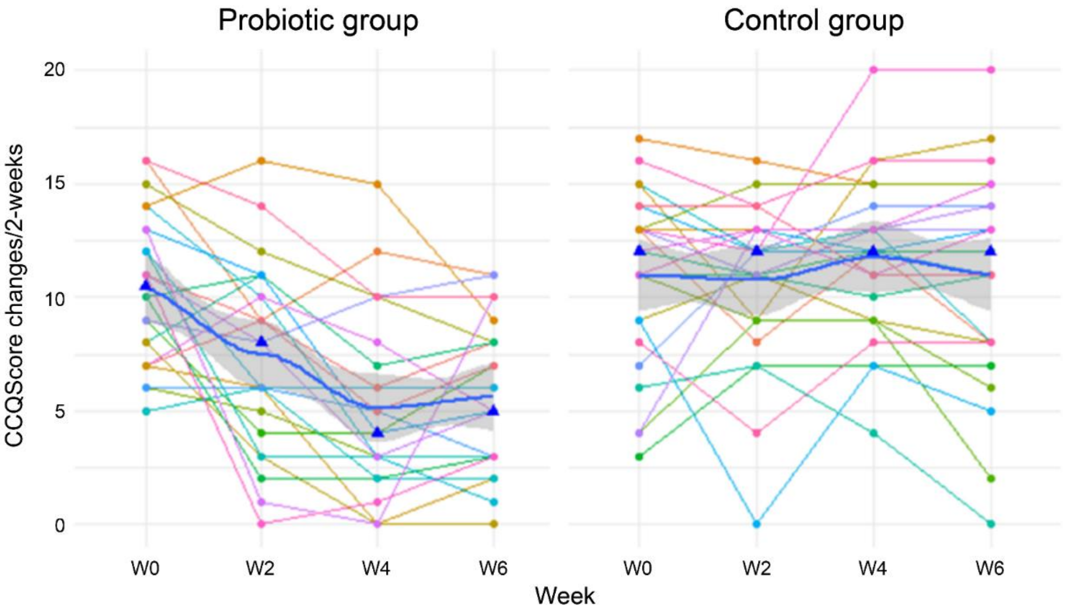

Figure S2. Changes in CCQ scores every 2 weeks from Week 0 to Week 6

Note: Median Chinese Constipation Questionnaire (CCQ) score.

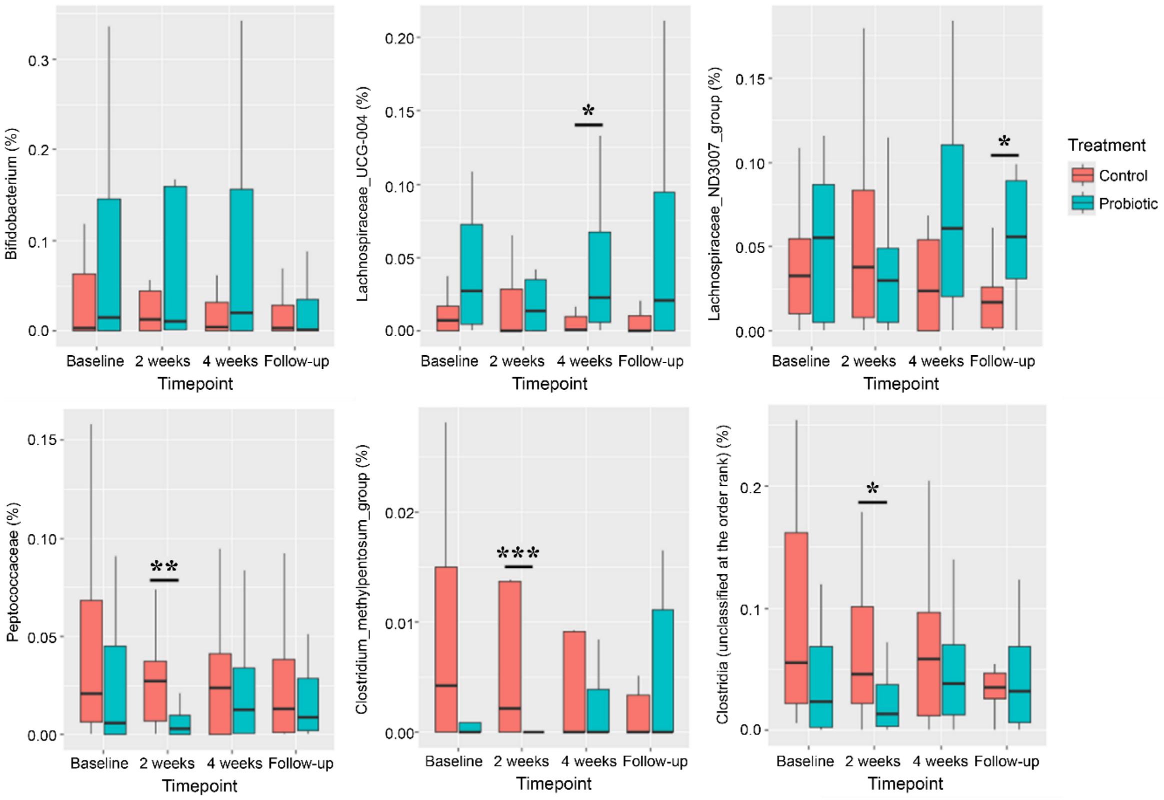

Figure S3. Changes in the relative abundance of *Bifidobacterium* and bacterial groups identified by ANCOM-BC

Outliers are not shown for descriptive purposes. **P* <0.05, ***P* <0.01, ****P* <0.001 vs. control (ANCOM-BC).