

Supplementary Table S1. Significant OTUs identified in SIMPER analysis of female pre- versus post-treatment. These mean relative abundances are displayed in Supplementary Figure S1A.

Comparison	Phylum	Class	Order	Family	Genus	OTU	Pre-treatment (%)	Post-treatment (%)	Variation Explained (%)	Adjusted P
Low Fat	Bacteroidetes	Bacteroidia	Bacteroidales	S24-7	unclassified	Otu00007	1.83	10.57	8.52	0.087
	Bacteroidetes	Bacteroidia	Bacteroidales	S24-7	unclassified	Otu00011	7.61	2.78	4.17	0.073
	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	unclassified	Otu00015	5.15	0.90	3.78	0.046
	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	<i>Alistipes</i>	Otu00023	0.13	7.75	6.40	0.036
High Fat	Bacteroidetes	Bacteroidia	Bacteroidales	S24-7	unclassified	Otu00006	16.12	0.53	10.04	0.036
	Tenericutes	Mollicutes	Anaeroplasmatales	Anaeroplasmataceae	<i>Anaeroplasma</i>	Otu00008	6.78	0.00	4.36	0.036
	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Ruminiclostridium</i>	Otu00010	0.74	7.17	4.16	0.036
	Bacteroidetes	Bacteroidia	Bacteroidales	S24-7	unclassified	Otu00011	11.35	0.08	7.25	0.036
	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	<i>Lactococcus</i>	Otu00012	0.03	7.96	5.13	0.036
Saccharin	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	<i>Akkermansia</i>	Otu00002	4.96	23.23	11.88	0.036
	Bacteroidetes	Bacteroidia	Bacteroidales	S24-7	unclassified	Otu00006	11.39	0.06	7.29	0.036
	Bacteroidetes	Bacteroidia	Bacteroidales	S24-7	unclassified	Otu00007	1.90	1.39	4.91	0.036
	Bacteroidetes	Bacteroidia	Bacteroidales	S24-7	unclassified	Otu00011	7.09	0.08	4.51	0.036
	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	<i>Lactococcus</i>	Otu00012	0.00	7.47	4.85	0.036
	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	unclassified	Otu00015	5.25	0.00	3.37	0.036
Stevia	Bacteroidetes	Bacteroidia	Bacteroidales	S24-7	unclassified	Otu00006	13.00	0.05	8.28	0.036
	Tenericutes	Mollicutes	Anaeroplasmatales	Anaeroplasmataceae	<i>Anaeroplasma</i>	Otu00008	10.30	0.01	6.58	0.036
	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Ruminiclostridium</i>	Otu00010	1.33	8.67	4.72	0.036
	Bacteroidetes	Bacteroidia	Bacteroidales	S24-7	unclassified	Otu00011	6.92	0.08	4.37	0.036
	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	<i>Lactococcus</i>	Otu00012	0.00	8.92	5.73	0.036
	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	<i>NK4A136</i>	Otu00014	0.00	8.32	5.35	0.036
	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	unclassified	Otu00015	6.61	0.01	4.21	0.036

Supplementary Table S2. Significant OTUs identified in SIMPER analysis of male pre- versus post-treatment samples. These mean relative abundances are displayed in Supplementary Figure S1B.

Comparison	Phylum	Class	Order	Family	Genus	OTU	Pre-treatment (%)	Post-treatment (%)	Variation Explained (%)	Adjusted P
Low Fat	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	<i>Bacteroides</i>	Otu00003	9.73	4.51	4.08	0.094
	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	unclassified	Otu00013	9.82	0.00	7.36	0.045
	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	<i>NK4A136</i>	Otu00033	0.08	4.22	3.12	0.045
High Fat	Bacteroidetes	Bacteroidia	Bacteroidales	S24-7	unclassified	Otu00001	0.01	6.98	4.41	0.045
	Bacteroidetes	Bacteroidia	Bacteroidales	S24-7	unclassified	Otu00004	5.14	11.21	3.83	0.045
	Bacteroidetes	Bacteroidia	Bacteroidales	S24-7	unclassified	Otu00005	10.59	0.66	6.29	0.045
	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Ruminiclostridium</i>	Otu00010	1.14	5.12	2.52	0.045
	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	unclassified	Otu00012	0.43	7.25	4.32	0.045
	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	<i>Lactococcus</i>	Otu00014	0.00	6.74	4.27	0.045
Saccharin	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	<i>Bacteroides</i>	Otu00003	7.33	2.91	2.96	0.046
	Bacteroidetes	Bacteroidia	Bacteroidales	S24-7	unclassified	Otu00004	4.98	10.29	3.57	0.046
	Bacteroidetes	Bacteroidia	Bacteroidales	S24-7	unclassified	Otu00005	20.91	0.72	13.55	0.046
	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Ruminiclostridium</i>	Otu00010	1.92	8.28	4.46	0.089
	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	<i>Lactococcus</i>	Otu00014	0.00	3.32	2.23	0.046
Stevia	Bacteroidetes	Bacteroidia	Bacteroidales	S24-7	unclassified	Otu00005	11.74	0.24	7.37	0.046
	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Ruminiclostridium</i>	Otu00010	1.08	6.66	3.61	0.046
	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	unclassified	Otu00012	0.38	6.62	4.03	0.046
	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	unclassified	Otu00013	14.02	0.91	8.40	0.046
	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	<i>Lactococcus</i>	Otu00014	0.00	9.09	5.87	0.046
	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	<i>Lactobacillus</i>	Otu00018	0.05	6.99	4.47	0.046

Supplementary Table S3. Significant OTUs identified in SIMPER analysis of female post-treatment samples. These mean relative abundances are displayed in Fig 6A. "Left/right treatment" refer to the order in which are presented in the "Comparison" column. For example, in the "Low Fat vs. High Fat" comparison, the left treatment is low fat while the right treatment is high fat.

Comparison	Phylum	Class	Order	Family	Genus	OTU	Left Treatment (%)	Right Treatment (%)	Variation Explained (%)	Adjust
Low Fat vs. High Fat	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	<i>Bacteroides</i>	Otu00003	2.26	8.62	4.04	0.038
	Bacteroidetes	Bacteroidia	Bacteroidales	S24-7	unclassified	Otu00004	1.12	9.47	5.31	0.038
	Bacteroidetes	Bacteroidia	Bacteroidales	S24-7	unclassified	Otu00006	6.57	0.53	3.82	0.038
	Tenericutes	Mollicutes	Anaeroplasmatales	Anaeroplasmataceae	<i>Anaeroplasma</i>	Otu00008	6.10	0.00	3.87	0.038
	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Ruminiclostridium</i>	Otu00010	0.81	7.17	4.04	0.038
	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	unclassified	Otu00012	0.37	7.96	4.82	0.038
	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	<i>Lactococcus</i>	Otu00014	0.00	6.07	3.85	0.038
Low Fat vs. Saccharin	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	<i>Akkermansia</i>	Otu00002	0.37	23.23	14.18	0.038
	Bacteroidetes	Bacteroidia	Bacteroidales	S24-7	unclassified	Otu00006	6.57	0.06	4.01	0.038
	Tenericutes	Mollicutes	Anaeroplasmatales	Anaeroplasmataceae	<i>Anaeroplasma</i>	Otu00008	6.10	0.00	3.76	0.038
	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	unclassified	Otu00012	0.37	7.47	4.40	0.038
Low Fat vs. Stevia	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	<i>Akkermansia</i>	Otu00002	0.37	7.15	4.22	0.098
	Bacteroidetes	Bacteroidia	Bacteroidales	S24-7	unclassified	Otu00004	1.12	9.16	4.98	0.038
	Bacteroidetes	Bacteroidia	Bacteroidales	S24-7	unclassified	Otu00006	6.57	0.05	4.02	0.038
	Tenericutes	Mollicutes	Anaeroplasmatales	Anaeroplasmataceae	<i>Anaeroplasma</i>	Otu00008	6.10	0.01	3.76	0.038
	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Ruminiclostridium</i>	Otu00010	0.81	8.67	4.87	0.038
	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	unclassified	Otu00012	0.37	8.92	5.29	0.038
	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	<i>Lactococcus</i>	Otu00014	0.00	8.32	5.15	0.038
Saccharin vs. Stevia	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	<i>Akkermansia</i>	Otu00002	23.23	7.15	18.85	0.069
	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	<i>Lactococcus</i>	Otu00014	3.08	8.32	6.04	0.038

Supplementary Table S4. Significant OTUs identified in SIMPER analysis of male post-treatment samples. These mean relative abundances are displayed in Fig 6B. "Left/right treatment" refer to the order in which treatments are presented in the "Comparison" column. For example, in the "Low Fat vs. High Fat" comparison, the left treatment is low fat while the right treatment is high fat.

Comparison	Phylum	Class	Order	Family	Genus	OTU	Left Treatment (%)	Right Treatment (%)	Variation Explained (%)	Adjusted P
Low Fat vs. High Fat	Bacteroidetes	Bacteroidia	S24-7	S24-7	unclassified	Otu00004	1.32	11.21	6.14	0.060
	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Ruminiclostridium</i>	Otu00010	0.81	5.12	2.67	0.060
	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	unclassified	Otu00012	0.37	7.25	4.28	0.060
	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	<i>Lactococcus</i>	Otu00014	0.00	6.74	4.20	0.060
	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	<i>NK4A136</i>	Otu00033	4.22	0.21	2.51	0.060
Low Fat vs. Saccharin	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	<i>Akkermansia</i>	Otu00002	0.01	5.45	3.49	0.060
	Bacteroidetes	Bacteroidia	S24-7	S24-7	unclassified	Otu00004	1.32	10.29	5.74	0.060
	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Ruminiclostridium</i>	Otu00010	0.81	8.28	4.78	0.060
	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	<i>Lactococcus</i>	Otu00014	0.00	3.32	2.12	0.060
	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	<i>NK4A136</i>	Otu00033	4.22	0.31	2.52	0.099
Low Fat vs. Stevia	Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	<i>Akkermansia</i>	Otu00002	0.01	6.93	4.34	0.060
	Bacteroidetes	Bacteroidia	S24-7	S24-7	unclassified	Otu00004	1.32	8.40	4.44	0.060
	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Ruminiclostridium</i>	Otu00010	0.81	6.66	3.68	0.060
	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	unclassified	Otu00012	0.37	6.62	3.93	0.060
	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	<i>Lactococcus</i>	Otu00014	0.00	9.09	5.72	0.060
	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	<i>Lactobacillus</i>	Otu00018	0.05	6.99	4.36	0.060
Saccharin vs. Stevia	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	<i>NK4A136</i>	Otu00033	4.22	0.28	2.50	0.079
	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	<i>Lactococcus</i>	Otu00014	3.32	9.09	6.77	0.080