

Supplementary Materials

Supplementary Table S1A: Alpha Diversity Index by Time

Supplementary Table S1A: Alpha Diversity Index by Time							
	Week 0						
	DIET 1			DIET 2			p-value
	Median	Min	Max	Median	Min	Max	
Observed ASVs	931	477	1043	944.5	883	998	0.5737
Shannon Index	5.2910	4.6935	5.6325	5.4378	5.2185	5.7197	0.1605
Simpson Index	0.9855	0.9819	0.9915	0.9864	0.9827	0.9934	0.1949
	Week 4						
	DIET 1			DIET 2			p-value
	Median	Min	Max	Median	Min	Max	
Observed ASVs	947	840	1042	1116.5	1075	1173	0.0002
Shannon Index	5.3287	4.7586	5.5727	5.8203	5.6461	5.9144	0.0002
Simpson Index	0.9858	0.9538	0.9893	0.9932	0.9907	0.9942	0.0002
	Week 12						
	DIET 1			DIET 2			p-value
	Median	Min	Max	Median	Min	Max	
Observed ASVs	1035	958	1104	1107	1014	1157	0.0207
Shannon Index	5.4457	5.3138	5.6586	5.8946	5.7021	5.9963	0.0002
Simpson Index	0.9869	0.9826	0.9914	0.9940	0.9915	0.9947	0.0002
	Week 24						
	DIET 1			DIET 2			p-value
	Median	Min	Max	Median	Min	Max	
Observed ASVs	995	859	1133	1080	1044	1177	0.0148
Shannon Index	5.5636	5.3234	6.0780	5.7755	5.6106	6.0150	0.0830
Simpson Index	0.9904	0.9866	0.9954	0.9927	0.9910	0.9948	0.0499

Supplementary Table S1A: Alpha diversity index (Observed ASVs, Shannon and Simpson Index) for groups D1 and D2 at different time feeding. Significant differences established using the Wilcoxon signed-rank test ($p < 0.05$). p-values in bold style were statistically significant.

Supplementary Table S1B: Alpha Diversity Index by Diets

Supplementary Table S1B: Alpha Diversity Index by Diets

	DIET1				DIET2			
	Week 0	Week 4	Week 12	Week 24	Week 0	Week 4	Week 12	Week 24
<i>Observed ASVs - Median</i>	931	947	1035	995	945	1117	1107	1080
<i>Observed ASVs - Min</i>	477	840	958	859	883	1075	1014	1044
<i>Observed ASVs - Max</i>	1043	1042	1104	1133	998	1173	1157	1177
<i>p - value</i>		0.1357				0.0024		
<i>Shannon Index - Median</i>	5.2910	5.3287	5.4457	5.5636	5.4378	5.8203	5.8946	5.7755
<i>Shannon Index - Min</i>	4.6935	4.7586	5.3138	5.3234	5.2185	5.6461	5.7021	5.6106
<i>Shannon Index - Max</i>	5.6325	5.5727	5.6586	6.0780	5.7197	5.9144	5.9963	6.0150
<i>p - value</i>		0.0336				0.0022		
<i>Simpson Index - Median</i>	0.9855	0.9858	0.9869	0.9904	0.9864	0.9932	0.994	0.9927
<i>Simpson Index - Min</i>	0.98194	0.95383	0.98265	0.98658	0.9827	0.9907	0.9915	0.9910
<i>Simpson Index - Max</i>	0.99152	0.98933	0.99141	0.99537	0.9934	0.9942	0.9947	0.9948
<i>p - value</i>		0.05				0.0239		

Supplementary Table S1B: Alpha diversity index (Observed ASVs, Shannon and Simpson Index) for week 0, 4, 12 and 24 in the different diets. Significant differences established using the Friedman test ($p < 0.05$). p-values in bold style were statistically significant.

Supplementary Table S1C: Post hoc analysis for significant Friedman test

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Comparison	DIET 1			DIET 2		
	Observed ASVs p-value adj	Shannon p-value adj	Simpson p-value adj	Observed ASVs p-value adj	Shannon p-value adj	Simpson p-value adj
Week 0 - Week 4	-	1.000	1.000	0.047	0.094	0.328
Week 0 - Week 12	-	0.888	1.000	0.047	0.047	0.047
Week 0 - Week 24	-	0.654	0.328	0.047	0.047	0.654
Week 4 - Week 12	-	0.328	1.000	1.000	1.000	1.000
Week 4 - Week 24	-	0.047	0.047	1.000	1.000	1.000
Week 12 - Week 24	-	1.000	0.328	1.000	0.328	0.888

Supplementary Table S1C: Post hoc analysis for Alpha diversity index (Observed ASVs, Shannon and Simpson Index) with significant Friedman test for week 0, 4, 12 and 24 in the different diets. Significant differences established using the Wilcoxon signed-rank test ($p < 0.05$). p-values in bold style were statistically significant.

Supplementary Table S2: Relative abundance comparison at Phylum level

Supplementary Table 2: Relative abundance comparison at Phylum level

	Week 0						
	DIET1			DIET2			<i>p-value</i>
	Median	Min	Max	Median	Min	Max	
<i>Actinobacteriota</i>	0.0002	0.0000	0.0008	0.0000	0.0000	0.0001	0.0716
<i>Bacteroidota</i>	0.6699	0.5166	0.7285	0.6095	0.2582	0.7542	0.4948
<i>Campylobacterota</i>	0.0116	0.0039	0.0225	0.0234	0.0044	0.0380	0.1893
<i>Cyanobacteria</i>	0.0000	0.0000	0.0016	0.0001	0.0000	0.0007	0.8663
<i>Deferribacterota</i>	0.0025	0.0007	0.0089	0.0033	0.0008	0.0137	0.4942
<i>Desulfobacterota</i>	0.0058	0.0035	0.0131	0.0085	0.0047	0.0205	0.1715
<i>Firmicutes</i>	0.2196	0.1187	0.3808	0.2954	0.1348	0.6280	0.3720
<i>Patescibacteria</i>	0.0048	0.0001	0.0103	0.0061	0.0025	0.0128	0.4005
<i>Proteobacteria</i>	0.0831	0.0619	0.1505	0.0609	0.0417	0.0921	0.1893
<i>Verrucomicrobiota</i>	0.0000	0.0000	0.0009	0.0000	0.0000	0.0000	0.3816
	Week 4						
	DIET1			DIET2			<i>p-value</i>
	Median	Min	Max	Median	Min	Max	
<i>Actinobacteriota</i>	0.0001	0.0000	0.0007	0.0001	0.0000	0.0002	0.3575
<i>Bacteroidota</i>	0.6721	0.6152	0.7727	0.5529	0.4621	0.6716	0.0074
<i>Campylobacterota</i>	0.0129	0.0073	0.0270	0.0272	0.0107	0.0406	0.0156
<i>Cyanobacteria</i>	0.0000	0.0000	0.0002	0.0003	0.0001	0.0008	0.0099
<i>Deferribacterota</i>	0.0022	0.0001	0.0041	0.0127	0.0047	0.0222	0.0009
<i>Desulfobacterota</i>	0.0059	0.0020	0.0075	0.0207	0.0143	0.0353	0.0009
<i>Firmicutes</i>	0.2002	0.1173	0.2568	0.2924	0.2090	0.3813	0.0054
<i>Patescibacteria</i>	0.0126	0.0101	0.0241	0.0218	0.0072	0.0399	0.0831
<i>Proteobacteria</i>	0.0832	0.0718	0.1027	0.0617	0.0470	0.0735	0.0019
<i>Verrucomicrobiota</i>	0.0000	0.0000	0.0012	0.0001	0.0000	0.0006	0.2304
	Week 12						
	DIET1			DIET2			<i>p-value</i>
	Median	Min	Max	Median	Min	Max	
<i>Actinobacteriota</i>	0.0001	0.0000	0.0005	0.0000	0.0000	0.0001	0.0043
<i>Bacteroidota</i>	0.6603	0.6124	0.7147	0.5376	0.4350	0.6003	0.0009
<i>Campylobacterota</i>	0.0124	0.0050	0.0159	0.0179	0.0086	0.0352	0.0831
<i>Cyanobacteria</i>	0.0001	0.0000	0.0007	0.0002	0.0000	0.0012	0.3071
<i>Deferribacterota</i>	0.0015	0.0004	0.0047	0.0092	0.0033	0.0115	0.0019
<i>Desulfobacterota</i>	0.0058	0.0023	0.0110	0.0332	0.0214	0.0412	0.0009
<i>Firmicutes</i>	0.2157	0.1551	0.2395	0.3238	0.2568	0.4184	0.0009
<i>Patescibacteria</i>	0.0129	0.0119	0.0239	0.0146	0.0011	0.0185	0.8748
<i>Proteobacteria</i>	0.0967	0.0508	0.1428	0.0612	0.0520	0.0808	0.0181
<i>Verrucomicrobiota</i>	0.0002	0.0000	0.0011	0.0000	0.0000	0.0002	0.0823
	Week 24						
	DIET1			DIET2			<i>p-value</i>
	Median	Min	Max	Median	Min	Max	

<i>Actinobacteriota</i>	0.0002	0.0000	0.0004	0.0000	0.0000	0.0002	0.1524
<i>Bacteroidota</i>	0.6711	0.4880	0.7742	0.5430	0.4993	0.6844	0.2271
<i>Campylobacterota</i>	0.0159	0.0069	0.0256	0.0107	0.0020	0.0218	0.1893
<i>Cyanobacteria</i>	0.0005	0.0000	0.0010	0.0001	0.0000	0.0002	0.0127
<i>Deferribacterota</i>	0.0019	0.0002	0.0050	0.0045	0.0001	0.0082	0.2701
<i>Desulfobacterota</i>	0.0054	0.0010	0.0139	0.0163	0.0083	0.0311	0.0039
<i>Firmicutes</i>	0.1966	0.1298	0.4149	0.3025	0.2042	0.3722	0.1563
<i>Patescibacteria</i>	0.0149	0.0061	0.0200	0.0235	0.0159	0.0688	0.0100
<i>Proteobacteria</i>	0.0696	0.0413	0.1085	0.0763	0.0617	0.0879	0.5635
<i>Verrucomicrobiota</i>	0.0003	0.0000	0.0021	0.0000	0.0000	0.0010	0.3253

Supplementary Table S2: Relative abundance comparison between diet groups at Phylum level in the different weeks of study. Significant differences established using the Wilcoxon signed-rank test ($p < 0.05$). p-values in bold style were statistically significant.

Supplementary Table S3: Relative abundance comparison at Genus level

Supplementary Table S3: Relative abundance comparison at Genus level

	Week 0						
	DIET1			DIET2			p-value
	Median	Min	Max	Median	Min	Max	
<i>Alloprevotella</i>	0.1255	0.0311	0.1729	0.1140	0.0069	0.1544	0.4948
<i>Lachnoanaerobaculum</i>	0.0185	0.0001	0.0636	0.0209	0.0114	0.0478	0.7929
<i>Helicobacter</i>	0.0243	0.0111	0.0609	0.0441	0.0150	0.0660	0.1278
<i>Rikenellaceae RC9 gut group</i>	0.0205	0.0090	0.0486	0.0333	0.0061	0.0649	0.6365
<i>Candidatus Saccharimonas</i>	0.0130	0.0001	0.0271	0.0121	0.0084	0.0381	0.7132
<i>Bacteroides</i>	0.1537	0.0947	0.5134	0.1527	0.0790	0.2466	1.0000
<i>Prevotellaceae UCG-001</i>	0.0759	0.0030	0.1472	0.0748	0.0251	0.1799	0.7132
<i>Flavonifractor</i>	0.0079	0.0008	0.0120	0.0082	0.0055	0.0124	0.8748
<i>Colidextribacter</i>	0.0221	0.0034	0.0376	0.0253	0.0140	0.0320	0.7132
<i>Parasutterella</i>	0.0271	0.0088	0.0787	0.0133	0.0005	0.0443	0.0520
<i>Odoribacter</i>	0.0193	0.0000	0.0658	0.0290	0.0181	0.0690	0.1893
<i>Lachnospiraceae NK4A136 group</i>	0.1739	0.0040	0.3049	0.1499	0.1063	0.3421	0.9581
<i>Intestinimonas</i>	0.0108	0.0008	0.0169	0.0107	0.0077	0.0147	1.0000
<i>Mucispirillum</i>	0.0090	0.0020	0.0168	0.0084	0.0027	0.0215	0.9581
<i>Oscillospira</i>	0.0031	0.0001	0.0067	0.0025	0.0017	0.0038	0.5635
<i>Muribaculum</i>	0.0285	0.0079	0.0914	0.0262	0.0004	0.0680	0.7132
<i>Herbinix</i>	0.0129	0.0008	0.0400	0.0125	0.0073	0.0460	0.3184
<i>Negativibacillus</i>	0.0052	0.0017	0.0089	0.0055	0.0018	0.0104	0.7132
<i>Parabacteroides</i>	0.0238	0.0040	0.0407	0.0120	0.0001	0.0195	0.0831
<i>Alistipes</i>	0.0207	0.0029	0.0497	0.0186	0.0137	0.1007	0.7132
<i>Ruminococcus gnavus group</i>	0.0048	0.0005	0.0067	0.0052	0.0018	0.0121	0.4309
<i>Oscillibacter</i>	0.0069	0.0002	0.0107	0.0090	0.0040	0.0186	0.0831
<i>Ligilactobacillus</i>	0.0046	0.0017	0.0224	0.0055	0.0007	0.0109	0.7929
<i>Anaerotruncus</i>	0.0008	0.0000	0.0060	0.0010	0.0000	0.0085	0.8335
<i>Eubacterium xylanophilum group</i>	0.0040	0.0001	0.0138	0.0038	0.0020	0.0100	0.8748
<i>Prevotella 7</i>	0.0014	0.0002	0.0045	0.0007	0.0002	0.0038	0.7132
<i>Harryflintia</i>	0.0016	0.0001	0.0034	0.0027	0.0006	0.0044	0.1563
<i>Desulfovibrio</i>	0.0023	0.0002	0.0039	0.0031	0.0011	0.0036	0.4948
<i>Tuzzerella</i>	0.0031	0.0000	0.0060	0.0041	0.0008	0.0061	0.4309
<i>Anaeroplasma</i>	0.0028	0.0000	0.0128	0.0046	0.0016	0.0208	0.0831
<i>Butyricicoccaceae UCG-009</i>	0.0020	0.0000	0.0063	0.0030	0.0005	0.0036	0.3184
<i>Erysipelatoclostridium</i>	0.0009	0.0003	0.1317	0.0002	0.0000	0.0027	0.0831
<i>Ruminococcaceae UCG-001</i>	0.0004	0.0000	0.0043	0.0000	0.0000	0.0014	0.2620
<i>Lachnoclostridium</i>	0.0064	0.0021	0.0111	0.0095	0.0050	0.0238	0.1893
<i>Ruminococcaceae Incertae Sedis</i>	0.0024	0.0006	0.0051	0.0033	0.0014	0.0054	0.3184
<i>Butyricicoccus</i>	0.0021	0.0002	0.0078	0.0016	0.0000	0.0028	0.4309
<i>Stomatobaculum</i>	0.0002	0.0000	0.0053	0.0003	0.0000	0.0006	0.9575
<i>Prevotellaceae NK3B31 group</i>	0.0000	0.0000	0.0029	0.0000	0.0000	0.0004	1.0000
<i>Lactobacillus</i>	0.0005	0.0000	0.0163	0.0001	0.0000	0.0010	0.1179
<i>Eubacterium eligens group</i>	0.0002	0.0000	0.0019	0.0019	0.0004	0.0060	0.0136
<i>Lachnospiraceae GCA-900066575</i>	0.0109	0.0018	0.0229	0.0065	0.0015	0.0189	0.4309
<i>Rikenella</i>	0.0032	0.0000	0.0142	0.0042	0.0008	0.0152	0.6365

<i>Ruminococcus</i>	0.0005	0.0000	0.0058	0.0000	0.0000	0.0032	0.2976
<i>Acetatifactor</i>	0.0032	0.0000	0.0144	0.0065	0.0008	0.0152	0.5635
<i>Lactobacillaceae HT002</i>	0.0000	0.0000	0.0084	0.0000	0.0000	0.0002	0.8360
<i>Angelakisella</i>	0.0007	0.0001	0.0022	0.0006	0.0002	0.0013	0.7132
<i>Lachnospiraceae ASF356</i>	0.0038	0.0009	0.0202	0.0051	0.0000	0.0108	0.8748
<i>Lachnospiraceae UCG-006</i>	0.0029	0.0004	0.0041	0.0016	0.0009	0.0087	0.9581
<i>Oscillospiraceae UCG-003</i>	0.0005	0.0000	0.0016	0.0004	0.0000	0.0020	0.8745
<i>Eubacterium siraeum group</i>	0.0011	0.0000	0.0220	0.0027	0.0005	0.0096	0.5635
<i>Ruminococcaceae UBA1819</i>	0.0000	0.0000	0.0003	0.0000	0.0000	0.0000	0.1709
<i>Dubosiella</i>	0.0009	0.0000	0.0166	0.0003	0.0000	0.0015	0.2445
<i>Paludicola</i>	0.0013	0.0000	0.0024	0.0006	0.0001	0.0016	0.0661
<i>Lachnospiraceae FCS020 group</i>	0.0008	0.0001	0.0026	0.0015	0.0004	0.0117	0.1893
<i>Anaerosporebacter</i>	0.0007	0.0000	0.0055	0.0000	0.0000	0.0012	0.1389
<i>Bilophila</i>	0.0002	0.0000	0.0007	0.0004	0.0000	0.0007	0.3973
<i>Lachnospiraceae UCG-001</i>	0.0008	0.0000	0.0046	0.0007	0.0002	0.0080	0.7130
<i>Escherichia-Shigella</i>	0.0008	0.0004	0.0057	0.0000	0.0000	0.0002	0.0007
<i>Oscillospiraceae UCG-002</i>	0.0002	0.0000	0.0005	0.0004	0.0000	0.0009	0.1550
<i>Shuttleworthia</i>	0.0007	0.0000	0.0043	0.0017	0.0000	0.0041	0.7923
<i>Eubacterium nodatum group</i>	0.0017	0.0002	0.0044	0.0023	0.0010	0.0032	0.5635
<i>Oscillospiraceae V9D2013 group</i>	0.0003	0.0000	0.0009	0.0004	0.0000	0.0008	0.8335
<i>Oscillospiraceae NK4A214 group</i>	0.0004	0.0000	0.0007	0.0003	0.0000	0.0010	1.0000
<i>Anaerovorax</i>	0.0000	0.0000	0.0007	0.0000	0.0000	0.0007	1.0000
<i>Roseburia</i>	0.0017	0.0002	0.0070	0.0027	0.0008	0.0092	0.2271
<i>Lachnospiraceae UCG-003</i>	0.0000	0.0000	0.0024	0.0001	0.0000	0.0068	0.5009
<i>Ureaplasma</i>	0.0005	0.0000	0.0053	0.0015	0.0000	0.0112	0.3649
<i>Faecalibaculum</i>	0.0000	0.0000	0.0089	0.0000	0.0000	0.0000	0.0764
<i>Christensenellaceae R-7 group</i>	0.0004	0.0000	0.0020	0.0002	0.0000	0.0008	0.3973
<i>Anaerostipes</i>	0.0001	0.0000	0.0004	0.0001	0.0000	0.0005	0.4761
<i>Mobilitalea</i>	0.0005	0.0001	0.0022	0.0006	0.0003	0.0014	0.5635
<i>Lachnospiraceae A2</i>	0.0005	0.0003	0.0016	0.0013	0.0002	0.0052	0.1278
<i>Akkermansia</i>	0.0000	0.0000	0.0036	0.0000	0.0000	0.0000	0.3816
<i>Peptococcus</i>	0.0008	0.0000	0.0021	0.0011	0.0007	0.0018	0.5635
<i>Eubacterium fissicatena group</i>	0.0005	0.0000	0.0016	0.0007	0.0000	0.0014	1.0000
<i>Tyzzereella</i>	0.0004	0.0000	0.0033	0.0000	0.0000	0.0007	0.1480
<i>Lachnospiraceae UCG-009</i>	0.0003	0.0000	0.0031	0.0001	0.0000	0.0011	0.3514
<i>Monoglobus</i>	0.0004	0.0000	0.0022	0.0001	0.0000	0.0005	0.2497
<i>Anaerovoracaceae Family XIII UCG-001</i>	0.0002	0.0000	0.0006	0.0001	0.0000	0.0005	0.5465
<i>Marvinbryantia</i>	0.0003	0.0000	0.0018	0.0001	0.0000	0.0005	0.2202
<i>Salmonella</i>	0.0000	0.0000	0.0020	0.0000	0.0000	0.0001	0.2697
<i>Lactococcus</i>	0.0008	0.0000	0.0041	0.0001	0.0000	0.0006	0.0569
<i>Anaerovoracaceae Family XIII AD3011 group</i>	0.0001	0.0000	0.0012	0.0001	0.0000	0.0009	0.9553
<i>Lachnospiraceae UCG-004</i>	0.0003	0.0000	0.0009	0.0003	0.0000	0.0011	0.7509
<i>Veillonella</i>	0.0002	0.0000	0.0004	0.0000	0.0000	0.0004	0.1480
<i>Merdibacter</i>	0.0000	0.0000	0.0003	0.0000	0.0000	0.0002	0.3342
<i>Lachnospiraceae UC5-1-2E3</i>	0.0000	0.0000	0.0003	0.0002	0.0000	0.0006	0.0380
<i>Olsenella</i>	0.0003	0.0000	0.0007	0.0000	0.0000	0.0001	0.0298

<i>Mycoplasma</i>	0.0000	0.0000	0.0027	0.0004	0.0000	0.0027	0.0249
<i>Lachnospiraceae AC2044 group</i>	0.0000	0.0000	0.0013	0.0000	0.0000	0.0000	0.1709
<i>Coriobacteriaceae UCG-002</i>	0.0001	0.0000	0.0008	0.0000	0.0000	0.0002	0.0847
Week 4							
	DIET1			DIET2			p-value
	Median	Min	Max	Median	Min	Max	
<i>Alloprevotella</i>	0.1146	0.0341	0.2013	0.0735	0.0258	0.1415	0.1036
<i>Lachnoanaerobaculum</i>	0.0194	0.0080	0.0347	0.0311	0.0161	0.0393	0.1893
<i>Helicobacter</i>	0.0410	0.0253	0.0704	0.0790	0.0246	0.1059	0.0313
<i>Rikenellaceae RC9 gut group</i>	0.0297	0.0090	0.0679	0.0302	0.0119	0.0442	0.7132
<i>Candidatus Saccharimonas</i>	0.0421	0.0263	0.0833	0.0597	0.0264	0.0858	0.3720
<i>Bacteroides</i>	0.1040	0.0654	0.1211	0.0865	0.0508	0.1449	0.3184
<i>Prevotellaceae UCG-001</i>	0.0910	0.0218	0.1158	0.0438	0.0140	0.0930	0.0406
<i>Flavonifractor</i>	0.0074	0.0038	0.0161	0.0169	0.0075	0.0342	0.0136
<i>Colidextribacter</i>	0.0363	0.0229	0.0790	0.0396	0.0303	0.0553	0.7132
<i>Parasutterella</i>	0.0479	0.0208	0.1005	0.0318	0.0222	0.0475	0.1563
<i>Odoribacter</i>	0.0139	0.0049	0.0308	0.0178	0.0090	0.0302	0.4948
<i>Lachnospiraceae NK4A136 group</i>	0.1649	0.0816	0.2491	0.1811	0.1119	0.1995	0.3720
<i>Intestinimonas</i>	0.0169	0.0068	0.0275	0.0167	0.0092	0.0234	0.9581
<i>Mucispirillum</i>	0.0062	0.0002	0.0144	0.0296	0.0107	0.0580	0.0028
<i>Oscillospira</i>	0.0028	0.0014	0.0089	0.0092	0.0051	0.0183	0.0074
<i>Muribaculum</i>	0.0476	0.0172	0.0951	0.0190	0.0117	0.0778	0.0181
<i>Herbinix</i>	0.0040	0.0022	0.0408	0.0062	0.0018	0.0217	0.7929
<i>Negativibacillus</i>	0.0033	0.0015	0.0073	0.0109	0.0064	0.0138	0.0019
<i>Parabacteroides</i>	0.0149	0.0063	0.0468	0.0195	0.0083	0.0365	0.7132
<i>Alistipes</i>	0.0092	0.0056	0.0216	0.0222	0.0070	0.0299	0.0313
<i>Ruminococcus gnavus group</i>	0.0061	0.0036	0.0154	0.0034	0.0020	0.0062	0.0181
<i>Oscillibacter</i>	0.0040	0.0014	0.0089	0.0104	0.0080	0.0233	0.0019
<i>Ligilactobacillus</i>	0.0068	0.0015	0.0158	0.0052	0.0022	0.0107	0.4309
<i>Anaerotruncus</i>	0.0004	0.0002	0.0011	0.0104	0.0061	0.0241	0.0009
<i>Eubacterium xylanophilum group</i>	0.0060	0.0022	0.0109	0.0049	0.0028	0.0090	0.8748
<i>Prevotella 7</i>	0.0010	0.0003	0.0033	0.0007	0.0002	0.0014	0.5635
<i>Harryflintia</i>	0.0011	0.0004	0.0025	0.0035	0.0019	0.0058	0.0039
<i>Desulfovibrio</i>	0.0145	0.0036	0.0211	0.0078	0.0046	0.0135	0.0313
<i>Tuzzerella</i>	0.0059	0.0038	0.0131	0.0082	0.0036	0.0142	0.2701
<i>Anaeroplasma</i>	0.0005	0.0004	0.0069	0.0008	0.0004	0.0038	0.7929
<i>Butyricicoccaceae UCG-009</i>	0.0029	0.0022	0.0047	0.0039	0.0017	0.0088	0.3720
<i>Erysipelatoclostridium</i>	0.0002	0.0000	0.0018	0.0002	0.0000	0.0010	0.9575
<i>Ruminococcaceae UCG-001</i>	0.0016	0.0000	0.0127	0.0011	0.0000	0.0119	1.0000
<i>Lachnoclostridium</i>	0.0059	0.0016	0.0117	0.0039	0.0023	0.0068	0.4948
<i>Ruminococcaceae Incertae Sedis</i>	0.0038	0.0023	0.0083	0.0063	0.0041	0.0081	0.1036
<i>Butyricoccus</i>	0.0037	0.0029	0.0074	0.0020	0.0011	0.0052	0.0181
<i>Stomatobaculum</i>	0.0014	0.0000	0.0053	0.0019	0.0009	0.0080	0.4309
<i>Prevotellaceae NK3B31 group</i>	0.0000	0.0000	0.0000	0.0003	0.0000	0.0188	0.0015
<i>Lactobacillus</i>	0.0006	0.0002	0.0033	0.0017	0.0002	0.0197	0.2271

<i>Eubacterium eligens</i> group	0.0003	0.0000	0.0028	0.0019	0.0007	0.0067	0.0180
<i>Lachnospiraceae</i> GCA-900066575	0.0069	0.0036	0.0114	0.0025	0.0005	0.0036	0.0014
<i>Rikenella</i>	0.0024	0.0007	0.0034	0.0027	0.0018	0.0051	0.2271
<i>Ruminococcus</i>	0.0017	0.0009	0.0059	0.0053	0.0020	0.0061	0.0313
<i>Acetatifactor</i>	0.0054	0.0006	0.0148	0.0052	0.0013	0.0353	0.9581
<i>Lactobacillaceae</i> HT002	0.0003	0.0000	0.0013	0.0008	0.0000	0.0038	0.2630
<i>Angelakisella</i>	0.0007	0.0002	0.0038	0.0013	0.0004	0.0022	0.3720
<i>Lachnospiraceae</i> ASF356	0.0009	0.0002	0.0192	0.0060	0.0031	0.0183	0.0181
<i>Lachnospiraceae</i> UCG-006	0.0041	0.0024	0.0141	0.0016	0.0011	0.0045	0.0313
<i>Oscillospiraceae</i> UCG-003	0.0008	0.0002	0.0019	0.0006	0.0003	0.0019	0.5635
<i>Eubacterium siraeum</i> group	0.0009	0.0000	0.0041	0.0083	0.0042	0.0098	0.0009
<i>Ruminococcaceae</i> UBA1819	0.0000	0.0000	0.0000	0.0007	0.0000	0.0049	0.0015
<i>Dubosiella</i>	0.0031	0.0006	0.0055	0.0008	0.0001	0.0070	0.1278
<i>Paludicola</i>	0.0014	0.0002	0.0046	0.0027	0.0017	0.0074	0.0313
<i>Lachnospiraceae</i> FCS020 group	0.0003	0.0002	0.0019	0.0002	0.0000	0.0005	0.0822
<i>Anaerosporebacter</i>	0.0003	0.0000	0.0013	0.0002	0.0000	0.0013	0.8739
<i>Bilophila</i>	0.0036	0.0006	0.0066	0.0013	0.0007	0.0022	0.0239
<i>Lachnospiraceae</i> UCG-001	0.0017	0.0005	0.0059	0.0015	0.0004	0.0076	0.7132
<i>Escherichia-Shigella</i>	0.0019	0.0011	0.0046	0.0031	0.0021	0.0048	0.1893
<i>Oscillospiraceae</i> UCG-002	0.0002	0.0000	0.0007	0.0007	0.0003	0.0013	0.0074
<i>Shuttleworthia</i>	0.0000	0.0000	0.0002	0.0012	0.0006	0.0029	0.0007
<i>Eubacterium nodatum</i> group	0.0017	0.0012	0.0023	0.0045	0.0019	0.0064	0.0019
<i>Oscillospiraceae</i> V9D2013 group	0.0001	0.0000	0.0004	0.0010	0.0002	0.0016	0.0036
<i>Oscillospiraceae</i> NK4A214 group	0.0008	0.0000	0.0014	0.0007	0.0005	0.0012	0.5635
<i>Anaerovorax</i>	0.0009	0.0002	0.0017	0.0000	0.0000	0.0012	0.0113
<i>Roseburia</i>	0.0015	0.0002	0.0042	0.0050	0.0019	0.0106	0.0136
<i>Lachnospiraceae</i> UCG-003	0.0000	0.0000	0.0014	0.0002	0.0000	0.0008	0.2497
<i>Ureaplasma</i>	0.0000	0.0000	0.0000	0.0000	0.0000	0.0002	0.0764
<i>Faecalibaculum</i>	0.0004	0.0000	0.0066	0.0000	0.0000	0.0005	0.1448
<i>Christensenellaceae</i> R-7 group	0.0010	0.0002	0.0023	0.0009	0.0003	0.0019	0.9581
<i>Anaerostipes</i>	0.0004	0.0000	0.0008	0.0004	0.0001	0.0009	0.8748
<i>Mobilitalea</i>	0.0005	0.0000	0.0012	0.0000	0.0000	0.0007	0.0136
<i>Lachnospiraceae</i> A2	0.0017	0.0004	0.0062	0.0008	0.0002	0.0015	0.0239
<i>Akkermansia</i>	0.0000	0.0000	0.0049	0.0002	0.0000	0.0017	0.3318
<i>Peptococcus</i>	0.0011	0.0005	0.0027	0.0029	0.0009	0.0046	0.0181
<i>Eubacterium fissicatena</i> group	0.0010	0.0002	0.0036	0.0000	0.0000	0.0002	0.0008
<i>Tyzzerella</i>	0.0000	0.0000	0.0002	0.0014	0.0002	0.0046	0.0008
<i>Lachnospiraceae</i> UCG-009	0.0000	0.0000	0.0003	0.0001	0.0000	0.0017	0.5069
<i>Monoglobus</i>	0.0002	0.0000	0.0015	0.0008	0.0002	0.0013	0.1025
<i>Anaerovoracaceae</i> Family XIII UCG-001	0.0007	0.0002	0.0015	0.0004	0.0002	0.0012	0.1893
<i>Marvinbryantia</i>	0.0003	0.0000	0.0028	0.0001	0.0000	0.0002	0.1957
<i>Salmonella</i>	0.0001	0.0000	0.0004	0.0000	0.0000	0.0007	0.8622
<i>Lactococcus</i>	0.0000	0.0000	0.0009	0.0000	0.0000	0.0000	0.0764
<i>Anaerovoracaceae</i> Family XIII AD3011 group	0.0011	0.0005	0.0028	0.0006	0.0000	0.0016	0.0406
<i>Lachnospiraceae</i> UCG-004	0.0004	0.0000	0.0005	0.0002	0.0000	0.0009	0.4240
<i>Veillonella</i>	0.0004	0.0002	0.0013	0.0000	0.0000	0.0000	0.0004

<i>Merdibacter</i>	0.0000	0.0000	0.0003	0.0001	0.0000	0.0004	0.4328
<i>Lachnospiraceae UC5-1-2E3</i>	0.0002	0.0000	0.0006	0.0002	0.0000	0.0004	0.5968
<i>Olsenella</i>	0.0003	0.0000	0.0017	0.0000	0.0000	0.0005	0.1389
<i>Mycoplasma</i>	0.0000	0.0000	0.0000	0.0000	0.0000	0.0003	0.0764
<i>Lachnospiraceae AC2044 group</i>	0.0000	0.0000	0.0000	0.0001	0.0000	0.0004	0.0325
<i>Coriobacteriaceae UCG-002</i>	0.0000	0.0000	0.0010	0.0000	0.0000	0.0003	0.5656
Week 12							
	DIET1			DIET2			p-value
	Median	Min	Max	Median	Min	Max	
<i>Alloprevotella</i>	0.0677	0.0351	0.2073	0.0382	0.0253	0.0781	0.0661
<i>Lachnoanaerobaculum</i>	0.0174	0.0044	0.0261	0.0224	0.0078	0.0471	0.1563
<i>Helicobacter</i>	0.0377	0.0185	0.0488	0.0532	0.0155	0.0774	0.1563
<i>Rikenellaceae RC9 gut group</i>	0.0218	0.0095	0.0346	0.0288	0.0098	0.0466	0.1036
<i>Candidatus Saccharimonas</i>	0.0472	0.0288	0.0888	0.0335	0.0024	0.0627	0.052
<i>Bacteroides</i>	0.0739	0.0337	0.2251	0.0772	0.0505	0.2352	0.7132
<i>Prevotellaceae UCG-001</i>	0.0467	0.0213	0.2070	0.0541	0.0254	0.1131	0.9581
<i>Flavonifractor</i>	0.0176	0.0092	0.0260	0.0223	0.0142	0.0265	0.1893
<i>Colidextribacter</i>	0.0402	0.0323	0.0503	0.0485	0.0361	0.0650	0.0661
<i>Parasutterella</i>	0.1050	0.0196	0.1580	0.0380	0.0086	0.0571	0.0239
<i>Odoribacter</i>	0.0173	0.0052	0.0624	0.0232	0.0132	0.0380	0.1278
<i>Lachnospiraceae NK4A136 group</i>	0.1571	0.1080	0.1956	0.2291	0.1457	0.3176	0.0074
<i>Intestinimonas</i>	0.0190	0.0110	0.0417	0.0197	0.0111	0.0297	0.7929
<i>Mucispirillum</i>	0.0052	0.0018	0.0118	0.0208	0.0112	0.0321	0.0014
<i>Oscillospira</i>	0.0054	0.0025	0.0102	0.0076	0.0008	0.0147	0.0831
<i>Muribaculum</i>	0.0467	0.0210	0.0843	0.0232	0.0043	0.0441	0.0181
<i>Herbinix</i>	0.0065	0.0019	0.0275	0.0067	0.0012	0.0170	0.7929
<i>Negativibacillus</i>	0.0036	0.0009	0.0106	0.0108	0.0016	0.0161	0.0239
<i>Parabacteroides</i>	0.0122	0.0026	0.0467	0.0102	0.0053	0.0393	0.4309
<i>Alistipes</i>	0.0142	0.0068	0.0459	0.0149	0.0063	0.0574	0.6365
<i>Ruminococcus gnavus group</i>	0.0021	0.0009	0.0050	0.0024	0.0009	0.0040	1.0000
<i>Oscillibacter</i>	0.0071	0.0021	0.0106	0.0124	0.0040	0.0170	0.0181
<i>Ligilactobacillus</i>	0.0204	0.0025	0.0358	0.0028	0.0004	0.0041	0.0039
<i>Anaerotruncus</i>	0.0000	0.0000	0.0007	0.0071	0.0008	0.0228	0.0008
<i>Eubacterium xylanophilum group</i>	0.0082	0.0042	0.0196	0.0063	0.0021	0.0133	0.2271
<i>Prevotella 7</i>	0.0008	0.0000	0.0047	0.0011	0.0000	0.0029	0.5624
<i>Harryflintia</i>	0.0015	0.0005	0.0040	0.0037	0.0012	0.0057	0.0136
<i>Desulfovibrio</i>	0.0088	0.0048	0.0351	0.0136	0.0061	0.0285	0.372
<i>Tuzzerella</i>	0.0044	0.0030	0.0091	0.0142	0.0065	0.0210	0.0054
<i>Anaeroplasma</i>	0.0028	0.0013	0.0046	0.0016	0.0008	0.0026	0.0831
<i>Butyricocccaceae UCG-009</i>	0.0028	0.0013	0.0062	0.0021	0.0011	0.0132	0.7929
<i>Erysipelatoclostridium</i>	0.0000	0.0000	0.0011	0.0000	0.0000	0.0002	0.4066
<i>Ruminococcaceae UCG-001</i>	0.0002	0.0000	0.0046	0.0003	0.0000	0.0037	0.9575
<i>Lachnoclostridium</i>	0.0050	0.0023	0.0083	0.0055	0.0012	0.0129	0.8748
<i>Ruminococcaceae Incertae Sedis</i>	0.0024	0.0013	0.0064	0.0032	0.0018	0.0048	0.4309
<i>Butyricoccus</i>	0.0032	0.0019	0.0095	0.0021	0.0012	0.0037	0.0313

<i>Stomatobaculum</i>	0.0024	0.0000	0.0075	0.0033	0.0006	0.0051	0.7132
<i>Prevotellaceae NK3B31 group</i>	0.0000	0.0000	0.0040	0.0000	0.0000	0.0009	0.7001
<i>Lactobacillus</i>	0.0025	0.0003	0.0051	0.0014	0.0000	0.0028	0.2271
<i>Eubacterium eligens group</i>	0.0004	0.0000	0.0060	0.0004	0.0000	0.0021	1.0000
<i>Lachnospiraceae GCA-900066575</i>	0.0059	0.0026	0.0185	0.0028	0.0022	0.0077	0.1278
<i>Rikenella</i>	0.0020	0.0003	0.0043	0.0040	0.0014	0.0083	0.0181
<i>Ruminococcus</i>	0.0001	0.0000	0.0094	0.0004	0.0000	0.0009	0.7059
<i>Acetatifactor</i>	0.0083	0.0034	0.0121	0.0061	0.0037	0.0366	0.6365
<i>Lactobacillaceae HT002</i>	0.0013	0.0002	0.0029	0.0004	0.0000	0.0019	0.1893
<i>Angelakisella</i>	0.0011	0.0002	0.0020	0.0007	0.0002	0.0024	0.4309
<i>Lachnospiraceae ASF356</i>	0.0012	0.0000	0.0025	0.0066	0.0001	0.0193	0.0313
<i>Lachnospiraceae UCG-006</i>	0.0041	0.0013	0.0084	0.0018	0.0007	0.0022	0.0661
<i>Oscillospiraceae UCG-003</i>	0.0016	0.0008	0.0054	0.0010	0.0006	0.0016	0.0406
<i>Eubacterium siraeum group</i>	0.0001	0.0000	0.0019	0.0000	0.0000	0.0003	0.1105
<i>Ruminococcaceae UBA1819</i>	0.0000	0.0000	0.0000	0.0002	0.0000	0.0021	0.0046
<i>Dubosiella</i>	0.0030	0.0000	0.0095	0.0002	0.0000	0.0026	0.0122
<i>Paludicola</i>	0.0015	0.0006	0.0037	0.0013	0.0002	0.0017	0.4309
<i>Lachnospiraceae FCS020 group</i>	0.0009	0.0003	0.0022	0.0003	0.0000	0.0009	0.0181
<i>Anaerospobacter</i>	0.0015	0.0002	0.0031	0.0002	0.0000	0.0005	0.0100
<i>Bilophila</i>	0.0012	0.0000	0.0044	0.0034	0.0012	0.0116	0.1036
<i>Lachnospiraceae UCG-001</i>	0.0010	0.0000	0.0113	0.0009	0.0003	0.0021	0.7929
<i>Escherichia-Shigella</i>	0.0001	0.0000	0.0005	0.0003	0.0000	0.0076	0.1222
<i>Oscillospiraceae UCG-002</i>	0.0004	0.0002	0.0018	0.0010	0.0003	0.0038	0.1563
<i>Shuttleworthia</i>	0.0011	0.0000	0.0092	0.0010	0.0001	0.0047	0.9581
<i>Eubacterium nodatum group</i>	0.0026	0.0015	0.0057	0.0028	0.0005	0.0062	1.0000
<i>Oscillospiraceae V9D2013 group</i>	0.0005	0.0000	0.0011	0.0006	0.0002	0.0012	0.8748
<i>Oscillospiraceae NK4A214 group</i>	0.0007	0.0003	0.0022	0.0008	0.0003	0.0018	0.9581
<i>Anaerovorax</i>	0.0006	0.0000	0.0015	0.0019	0.0008	0.0045	0.0101
<i>Roseburia</i>	0.0031	0.0014	0.0042	0.0038	0.0014	0.0086	0.3184
<i>Lachnospiraceae UCG-003</i>	0.0000	0.0000	0.0000	0.0008	0.0000	0.0050	0.0046
<i>Ureaplasma</i>	0.0002	0.0000	0.0008	0.0000	0.0000	0.0000	0.0128
<i>Faecalibaculum</i>	0.0017	0.0002	0.0175	0.0000	0.0000	0.0000	0.0004
<i>Christensenellaceae R-7 group</i>	0.0012	0.0006	0.0029	0.0004	0.0000	0.0032	0.0239
<i>Anaerostipes</i>	0.0003	0.0000	0.0008	0.0001	0.0000	0.0008	0.1827
<i>Mobilitalea</i>	0.0003	0.0001	0.0022	0.0001	0.0000	0.0008	0.1250
<i>Lachnospiraceae A2</i>	0.0014	0.0008	0.0020	0.0016	0.0002	0.0044	0.7132
<i>Akkermansia</i>	0.0005	0.0000	0.0030	0.0000	0.0000	0.0005	0.0728
<i>Peptococcus</i>	0.0024	0.0008	0.0036	0.0030	0.0023	0.0057	0.0831
<i>Eubacterium fissicatena group</i>	0.0007	0.0002	0.0019	0.0000	0.0000	0.0003	0.0034
<i>Tyzzarella</i>	0.0000	0.0000	0.0006	0.0013	0.0003	0.0048	0.0015
<i>Lachnospiraceae UCG-009</i>	0.0005	0.0000	0.0018	0.0001	0.0000	0.0002	0.0111
<i>Monoglobus</i>	0.0009	0.0000	0.0031	0.0002	0.0000	0.0012	0.155
<i>Anaerovoracaceae Family XIII UCG-001</i>	0.0008	0.0002	0.0010	0.0005	0.0000	0.0014	0.4948
<i>Marvinbryantia</i>	0.0000	0.0000	0.0005	0.0000	0.0000	0.0008	0.8360
<i>Salmonella</i>	0.0001	0.0000	0.0006	0.0002	0.0000	0.0038	0.7840
<i>Lactococcus</i>	0.0000	0.0000	0.0005	0.0000	0.0000	0.0000	0.0764

<i>Anaerovoracaceae</i> Family XIII AD3011 group	0.0011	0.0006	0.0022	0.0004	0.0001	0.0016	0.052
<i>Lachnospiraceae</i> UCG-004	0.0004	0.0002	0.0007	0.0003	0.0000	0.0017	0.9581
<i>Veillonella</i>	0.0007	0.0000	0.0015	0.0000	0.0000	0.0000	0.0015
<i>Merdibacter</i>	0.0000	0.0000	0.0000	0.0000	0.0000	0.0002	0.3816
<i>Lachnospiraceae</i> UC5-1-2E3	0.0002	0.0000	0.0006	0.0001	0.0000	0.0004	0.2630
<i>Olsenella</i>	0.0002	0.0000	0.0015	0.0000	0.0000	0.0000	0.0046
<i>Mycoplasma</i>	0.0000	0.0000	0.0003	0.0000	0.0000	0.0000	0.3816
<i>Lachnospiraceae</i> AC2044 group	0.0000	0.0000	0.0000	0.0001	0.0000	0.0011	0.0128
<i>Coriobacteriaceae</i> UCG-002	0.0000	0.0000	0.0005	0.0000	0.0000	0.0002	0.2143
Week 24							
	DIET1			DIET2			p-value
	Median	Min	Max	Median	Min	Max	
<i>Alloprevotella</i>	0.0792	0.0043	0.1869	0.0584	0.0248	0.1891	0.8748
<i>Lachnoanaerobaculum</i>	0.0085	0.0022	0.0237	0.0265	0.0103	0.1028	0.0074
<i>Helicobacter</i>	0.0451	0.0119	0.0702	0.0283	0.0065	0.0655	0.1036
<i>Rikenellaceae</i> RC9 gut group	0.0376	0.0138	0.1366	0.0171	0.0053	0.0288	0.0661
<i>Candidatus Saccharimonas</i>	0.0438	0.0121	0.0573	0.0617	0.0366	0.2069	0.0181
<i>Bacteroides</i>	0.1807	0.0824	0.4089	0.1238	0.0299	0.1990	0.1278
<i>Prevotellaceae</i> UCG-001	0.0548	0.0108	0.1315	0.0352	0.0000	0.0733	0.2701
<i>Flavonifractor</i>	0.0145	0.0071	0.0181	0.0167	0.0112	0.0214	0.2271
<i>Colidextribacter</i>	0.0340	0.0192	0.0519	0.0396	0.0248	0.0511	0.5635
<i>Parasutterella</i>	0.0396	0.0047	0.0820	0.0504	0.0368	0.0716	0.2271
<i>Odoribacter</i>	0.0180	0.0065	0.0298	0.0091	0.0054	0.0196	0.0831
<i>Lachnospiraceae</i> NK4A136 group	0.1037	0.0276	0.2714	0.1476	0.0969	0.1740	0.2271
<i>Intestinimonas</i>	0.0151	0.0091	0.0501	0.0223	0.0098	0.0329	0.7929
<i>Mucispirillum</i>	0.0057	0.0010	0.0128	0.0116	0.0004	0.0227	0.3720
<i>Oscillospira</i>	0.0045	0.0028	0.0155	0.0053	0.0034	0.0108	0.6365
<i>Muribaculum</i>	0.0319	0.0178	0.1109	0.0331	0.0146	0.0504	0.9581
<i>Herbinix</i>	0.0018	0.0004	0.0222	0.0057	0.0013	0.0090	0.2271
<i>Negativibacillus</i>	0.0013	0.0000	0.0056	0.0087	0.0054	0.0144	0.0014
<i>Parabacteroides</i>	0.0301	0.0132	0.1131	0.0172	0.0028	0.0436	0.1036
<i>Alistipes</i>	0.0223	0.0125	0.0381	0.0102	0.0034	0.0232	0.0074
<i>Ruminococcus gnavus</i> group	0.0029	0.0012	0.0086	0.0043	0.0021	0.0148	0.2701
<i>Oscillibacter</i>	0.0080	0.0054	0.0147	0.0103	0.0080	0.0153	0.1893
<i>Ligilactobacillus</i>	0.0033	0.0007	0.0129	0.0142	0.0054	0.1214	0.0074
<i>Anaerotruncus</i>	0.0001	0.0000	0.0003	0.0052	0.0010	0.0155	0.0009
<i>Eubacterium xylanophilum</i> group	0.0061	0.0008	0.0109	0.0067	0.0021	0.0168	0.3184
<i>Prevotella</i> 7	0.0016	0.0005	0.0032	0.0003	0.0000	0.0019	0.0308
<i>Harryflintia</i>	0.0015	0.0004	0.0029	0.0047	0.0015	0.0087	0.0039
<i>Desulfovibrio</i>	0.0098	0.0013	0.0233	0.0115	0.0071	0.0323	0.2271
<i>Tuzzerella</i>	0.0061	0.0022	0.0106	0.0058	0.0034	0.0179	0.4948
<i>Anaeroplasma</i>	0.0026	0.0013	0.0128	0.0005	0.0001	0.0022	0.0028
<i>Butyricoccaceae</i> UCG-009	0.0019	0.0004	0.0028	0.0041	0.0012	0.0117	0.0136
<i>Erysipelatoclostridium</i>	0.0014	0.0000	0.0066	0.0000	0.0000	0.0019	0.1783
<i>Ruminococcaceae</i> UCG-001	0.0000	0.0000	0.0003	0.0025	0.0000	0.0193	0.0924

<i>Lachnoclostridium</i>	0.0078	0.0021	0.0224	0.0088	0.0027	0.0144	1.0000
<i>Ruminococcaceae Incertae Sedis</i>	0.0028	0.0019	0.0070	0.0073	0.0028	0.0100	0.0239
<i>Butyricoccus</i>	0.0040	0.0015	0.0156	0.0027	0.0006	0.0063	0.3184
<i>Stomatobaculum</i>	0.0015	0.0000	0.0102	0.0008	0.0000	0.0142	0.4619
<i>Prevotellaceae NK3B31 group</i>	0.0007	0.0000	0.0406	0.0000	0.0000	0.0020	0.0550
<i>Lactobacillus</i>	0.0002	0.0000	0.0014	0.0147	0.0023	0.0438	0.0009
<i>Eubacterium eligens group</i>	0.0001	0.0000	0.0057	0.0002	0.0000	0.0025	0.7059
<i>Lachnospiraceae GCA-900066575</i>	0.0065	0.0035	0.0148	0.0041	0.0029	0.0067	0.0661
<i>Rikenella</i>	0.0013	0.0000	0.0061	0.0028	0.0011	0.0106	0.1278
<i>Ruminococcus</i>	0.0016	0.0000	0.0050	0.0024	0.0005	0.0065	0.2701
<i>Acetatifactor</i>	0.0036	0.0002	0.0077	0.0044	0.0021	0.0070	0.6365
<i>Lactobacillaceae HT002</i>	0.0001	0.0000	0.0005	0.0059	0.0013	0.0136	0.0009
<i>Angelakisella</i>	0.0010	0.0002	0.0055	0.0007	0.0002	0.0018	0.4948
<i>Lachnospiraceae ASF356</i>	0.0001	0.0000	0.0119	0.0223	0.0075	0.0337	0.0018
<i>Lachnospiraceae UCG-006</i>	0.0034	0.0009	0.0110	0.0021	0.0012	0.0061	0.3720
<i>Oscillospiraceae UCG-003</i>	0.0021	0.0003	0.0089	0.0009	0.0001	0.0029	0.1278
<i>Eubacterium siraeum group</i>	0.0011	0.0000	0.0037	0.0006	0.0000	0.0050	0.7923
<i>Ruminococcaceae UBA1819</i>	0.0000	0.0000	0.0000	0.0004	0.0000	0.0075	0.0325
<i>Dubosiella</i>	0.0028	0.0003	0.0795	0.0011	0.0000	0.0020	0.1893
<i>Paludicola</i>	0.0009	0.0000	0.0022	0.0014	0.0010	0.0029	0.1563
<i>Lachnospiraceae FCS020 group</i>	0.0007	0.0000	0.0035	0.0001	0.0000	0.0007	0.1706
<i>Anaerosporeobacter</i>	0.0002	0.0000	0.0012	0.0001	0.0000	0.0005	0.3514
<i>Bilophila</i>	0.0035	0.0005	0.0070	0.0009	0.0006	0.0031	0.0661
<i>Lachnospiraceae UCG-001</i>	0.0006	0.0000	0.0017	0.0011	0.0000	0.0089	0.2687
<i>Escherichia-Shigella</i>	0.0006	0.0002	0.0022	0.0006	0.0000	0.0085	0.9581
<i>Oscillospiraceae UCG-002</i>	0.0003	0.0000	0.0024	0.0008	0.0002	0.0054	0.1278
<i>Shuttleworthia</i>	0.0000	0.0000	0.0003	0.0000	0.0000	0.0001	1.0000
<i>Eubacterium nodatum group</i>	0.0016	0.0006	0.0071	0.0083	0.0021	0.0123	0.0054
<i>Oscillospiraceae V9D2013 group</i>	0.0004	0.0000	0.0017	0.0002	0.0000	0.0014	0.5283
<i>Oscillospiraceae NK4A214 group</i>	0.0004	0.0002	0.0008	0.0011	0.0006	0.0017	0.0014
<i>Anaerovorax</i>	0.0006	0.0000	0.0012	0.0024	0.0010	0.0031	0.0014
<i>Roseburia</i>	0.0031	0.0006	0.0050	0.0044	0.0008	0.0069	0.1893
<i>Lachnospiraceae UCG-003</i>	0.0000	0.0000	0.0014	0.0003	0.0000	0.0119	0.0535
<i>Ureaplasma</i>	0.0001	0.0000	0.0003	0.0000	0.0000	0.0002	0.2716
<i>Faecalibaculum</i>	0.0000	0.0000	0.0017	0.0000	0.0000	0.0005	0.9491
<i>Christensenellaceae R-7 group</i>	0.0004	0.0000	0.0029	0.0020	0.0013	0.0070	0.0136
<i>Anaerostipes</i>	0.0001	0.0000	0.0003	0.0004	0.0000	0.0008	0.0486
<i>Mobilitalea</i>	0.0003	0.0000	0.0014	0.0001	0.0000	0.0003	0.1706
<i>Lachnospiraceae A2</i>	0.0010	0.0001	0.0033	0.0007	0.0004	0.0016	0.7929
<i>Akkermansia</i>	0.0009	0.0000	0.0071	0.0000	0.0000	0.0026	0.3253
<i>Peptococcus</i>	0.0014	0.0000	0.0026	0.0028	0.0015	0.0065	0.0054
<i>Eubacterium fissicatena group</i>	0.0006	0.0000	0.0026	0.0004	0.0002	0.0011	1.0000
<i>Tyzzera</i>	0.0000	0.0000	0.0000	0.0001	0.0000	0.0014	0.0325
<i>Lachnospiraceae UCG-009</i>	0.0002	0.0000	0.0010	0.0000	0.0000	0.0006	0.3695
<i>Monoglobus</i>	0.0001	0.0000	0.0017	0.0012	0.0004	0.0019	0.0178
<i>Anaerovoracaceae Family XIII UCG-001</i>	0.0004	0.0001	0.0010	0.0014	0.0003	0.0020	0.0054

<i>Marvinbryantia</i>	0.0000	0.0000	0.0005	0.0000	0.0000	0.0002	0.4066
<i>Salmonella</i>	0.0002	0.0000	0.0004	0.0000	0.0000	0.0002	0.0496
<i>Lactococcus</i>	0.0000	0.0000	0.0002	0.0000	0.0000	0.0000	0.1709
<i>Anaerovoracaceae Family XIII AD3011 group</i>	0.0007	0.0002	0.0018	0.0011	0.0003	0.0026	0.2271
<i>Lachnospiraceae UCG-004</i>	0.0002	0.0000	0.0006	0.0007	0.0002	0.0010	0.0101
<i>Veillonella</i>	0.0001	0.0000	0.0011	0.0000	0.0000	0.0002	0.0535
<i>Merdibacter</i>	0.0000	0.0000	0.0002	0.0000	0.0000	0.0014	0.3342
<i>Lachnospiraceae UC5-1-2E3</i>	0.0000	0.0000	0.0005	0.0001	0.0000	0.0005	0.7723
<i>Olsenella</i>	0.0002	0.0000	0.0006	0.0000	0.0000	0.0007	0.2976
<i>Mycoplasma</i>	0.0000	0.0000	0.0000	0.0000	0.0000	0.0006	0.3816
<i>Lachnospiraceae AC2044 group</i>	0.0000	0.0000	0.0000	0.0003	0.0000	0.0009	0.0046
<i>Coriobacteriaceae UCG-002</i>	0.0002	0.0000	0.0005	0.0000	0.0000	0.0002	0.0402
<i>Faecalibacterium</i>	0.0003	0.0000	0.0006	0.0000	0.0000	0.0004	0.0496

Supplementary Table S3: Relative abundance comparison between diet groups at Genus level in the different weeks of study. Significant differences established using the Wilcoxon signed-rank test ($p < 0.05$). p-values in bold style were statistically significant.

Supplementary Table S4: Blood metabolic parameters comparison**Supplementary Table S4: Blood metabolic parameters comparison**

	DIET 1		DIET 2		p-value
	Mean	SD	Mean	SD	
Body weight (g)	34.6	3.0	49.6	5.0	0.0039
VAT weight (g)	1.3	0.2	2.5	0.3	0.0007
Glucose (mg/dL)	169	34	187	18	0.3882
Cholesterol (mg/dL)	128	13	214	11	5.641e-05
Triglycerides (mg/dL)	78	14	113	11	0.0095
HDL-c (mg/dL)	101	11	178	9	4.011e-05
LDL-c (mg/dL)	12	2	14	7	0.4952
AST (UI/L)	71	38	87	33	0.5497
ALT (UI/L)	15	7	19	13	0.6066
Leptin (pg/mL)	13286	9891	51042	1421	0.0042
Adiponectin (ng/mL)	3266	534	3209	180	0.8505

Supplementary Table S4: Body and VAT weight and Blood metabolic parameters comparison for groups D1 and D2 at week 24 of feeding. Significant differences established using two-tailed Student's t-test ($p < 0.05$). p-values in bold style were statistically significant.

Abbreviations: SD: standard deviation, VAT: visceral adipose tissue, HDL-c: high-density lipoprotein cholesterol, LDL-c: low-density lipoprotein cholesterol, AST: aspartate aminotransferase, ALT: alanine aminotransferase

Supplementary Table S5: Immune cells population in TAV comparison

Supplementary Table S5: Immune cells population in TAV comparison

<i>Parameter</i>	DIET 1		DIET 2		p-value
	Mean	SD	Mean	SD	
% CD11b+	32.7	11.5	5.5	3.1	0.0150
% CD11b+ CD36+	48.9	16.8	20.0	6.8	0.0336
% CD11b+ F4/80+	31.3	12.0	10.9	5.7	0.0342
% CD11b+ F4/80+ CD36+	55.8	9.3	32.9	6.0	0.0086
% CD11b+ F4/80+ CD206- CD11c+	40.0	9.7	21.7	5.0	0.0233
MFI CD11b+ F4/80+ CD206- CD11c+ ROS	46.8	14.9	16.4	4.6	0.0221
% CD11b+ F4/80+ CD206+ CD11c+	24.1	8.1	13.6	1.8	0.0221
% CD11b+ F4/80+ CD206- CD11c-	0.3	0.2	0.3	0.2	1.0000
% CD11b+ F4/80+ CD206- CD11c-	12.7	7.8	5.7	2.8	0.1717
MFI CD11b+ F4/80+ ROS	46.4	15.7	15.5	3.9	0.0258
MFI CD11b+ ROS	37.0	14.8	8.2	2.6	0.0281
% CD11b-	41.2	11.5	35.1	5.3	0.3869
% CD11b- CD36+	35.6	20.7	3.9	2.2	0.0540
% Leukocytes CD36+	42.4	18.9	6.4	4.1	0.0288
MFI Leukocytes ROS	34.4	11.9	3.5	2.1	0.0126

Supplementary Table S5: Comparison immune cells population in VAT for D1 and D2 groups at week 24 of feeding. Significant differences established using two-tailed Student's t test ($p < 0.05$). p-values in bold style were statistically significant.

Abbreviations: SD: standard deviation range, CD: cluster of differentiation, ROS: reactive oxygen species.

Supplementary Table S6: variables showing significant correlation**Supplementary Table S6: variables showing significant correlation**

Genus	Variable	r	p-value
<i>Candidatus Saccharimonas</i>	Body Weight	0,74	0,0365
<i>Negativibacillus</i>	Body Weight	0,77	0,0245
<i>Anaerotruncus</i>	Body Weight	0,9	0,0023
<i>Harryflintia</i>	Body Weight	0,72	0,0445
<i>Butyricicoccaceae UCG-009</i>	Body Weight	0,72	0,0431
<i>Ruminococcaceae Incertae Sedis</i>	Body Weight	0,71	0,0476
<i>Alistipes</i>	Body Weight	-0,73	0,0414
<i>Lactobacillus</i>	Body Weight	0,85	0,0074
<i>Lachnospiraceae GCA-900066575</i>	Body Weight	-0,78	0,021
<i>Lactobacillaceae HT002</i>	Body Weight	0,82	0,0133
<i>Lachnospiraceae ASF356</i>	Body Weight	0,85	0,0081
<i>Anaerovorax</i>	Body Weight	0,92	0,0012
<i>Peptococcus</i>	Body Weight	0,77	0,0252
<i>Anaerostipes</i>	Body Weight	0,78	0,0233
<i>Monoglobus</i>	Body Weight	0,77	0,0268
<i>Lachnospiraceae UCG-004</i>	Body Weight	0,77	0,0248
<i>Lachnospiraceae AC2044 group</i>	Body Weight	0,79	0,0199
<i>Negativibacillus</i>	VAT Weight	0,81	0,014
<i>Anaerotruncus</i>	VAT Weight	0,87	0,0054
<i>Harryflintia</i>	VAT Weight	0,71	0,0479
<i>Ruminococcaceae Incertae Sedis</i>	VAT Weight	0,73	0,0394
<i>Alistipes</i>	VAT Weight	-0,73	0,0416
<i>Lactobacillus</i>	VAT Weight	0,89	0,0033
<i>Lachnospiraceae GCA-900066575</i>	VAT Weight	-0,79	0,0207
<i>Lactobacillaceae HT002</i>	VAT Weight	0,84	0,0087
<i>Lachnospiraceae ASF356</i>	VAT Weight	0,85	0,0071
<i>Anaerovorax</i>	VAT Weight	0,88	0,0037
<i>Peptococcus</i>	VAT Weight	0,76	0,0274
<i>Anaerostipes</i>	VAT Weight	0,8	0,0171
<i>Monoglobus</i>	VAT Weight	0,75	0,0324
<i>Lachnospiraceae UCG-004</i>	VAT Weight	0,78	0,0237
<i>Lachnospiraceae AC2044 group</i>	VAT Weight	0,73	0,0418
<i>Muribaculum</i>	Glucose	0,71	0,0485
<i>Odoribacter</i>	Glucose	-0,79	0,0195
<i>Anaeroplasma</i>	Glucose	-0,85	0,0075
<i>Prevotellaceae NK3B31 group</i>	Glucose	-0,75	0,0315
<i>Eubacterium eligens group</i>	Glucose	-0,8	0,0179
<i>Angelakisella</i>	Glucose	-0,83	0,011
<i>Lachnospiraceae FCS020 group</i>	Glucose	-0,82	0,0127
<i>Bilophila</i>	Glucose	-0,87	0,0052
<i>Negativibacillus</i>	Cholesterol	0,81	0,0159
<i>Ligilactobacillus</i>	Cholesterol	0,87	0,0045
<i>Ruminococcaceae Incertae Sedis</i>	Cholesterol	0,78	0,0232

<i>Lactobacillus</i>	Cholesterol	0,89	0,0034
<i>Lachnospiraceae</i> GCA-900066575	Cholesterol	-0,73	0,0387
<i>Lactobacillaceae</i> HT002	Cholesterol	0,8	0,0177
<i>Lachnospiraceae</i> ASF356	Cholesterol	0,76	0,0302
<i>Peptococcus</i>	Cholesterol	0,75	0,033
<i>Christensenellaceae</i> R-7 group	Cholesterol	0,74	0,0347
<i>Anaerostipes</i>	Cholesterol	0,86	0,0061
<i>Lachnospiraceae</i> UCG-004	Cholesterol	0,72	0,0438
<i>Lachnoanaerobaculum</i>	Triglycerides	0,74	0,0361
<i>Rikenellaceae</i> RC9 gut group	Triglycerides	-0,74	0,0368
<i>Negativibacillus</i>	Triglycerides	0,98	1.25E-05
<i>Ligilactobacillus</i>	Triglycerides	0,71	0,0479
<i>Harryflintia</i>	Triglycerides	0,82	0,0126
<i>Lactobacillus</i>	Triglycerides	0,88	0,0044
<i>Lactobacillaceae</i> HT002	Triglycerides	0,86	0,0065
<i>Oscillospiraceae</i> UCG-003	Triglycerides	-0,75	0,0308
<i>Oscillospiraceae</i> NK4A214 group	Triglycerides	0,72	0,0459
<i>Peptococcus</i>	Triglycerides	0,72	0,0444
<i>Christensenellaceae</i> R-7 group	Triglycerides	0,8	0,0181
<i>Lachnospiraceae</i> UCG-004	Triglycerides	0,88	0,0044
<i>Negativibacillus</i>	HDL-c	0,8	0,0172
<i>Ligilactobacillus</i>	HDL-c	0,9	0,0021
<i>Ruminococcaceae</i> Incertae Sedis	HDL-c	0,74	0,0371
<i>Alistipes</i>	HDL-c	-0,72	0,0455
<i>Lactobacillus</i>	HDL-c	0,88	0,0038
<i>Lachnospiraceae</i> GCA-900066575	HDL-c	-0,72	0,0432
<i>Lactobacillaceae</i> HT002	HDL-c	0,8	0,0171
<i>Eubacterium nodatum</i> group	HDL-c	0,72	0,0432
<i>Peptococcus</i>	HDL-c	0,78	0,0233
<i>Christensenellaceae</i> R-7 group	HDL-c	0,77	0,0269
<i>Anaerostipes</i>	HDL-c	0,85	0,008
<i>Lachnospiraceae</i> UCG-004	HDL-c	0,72	0,0419
<i>Ruminococcaceae</i> Incertae Sedis	LDL-c	0,75	0,033
<i>Alloprevotella</i>	AST	0,86	0,0063
<i>Odoribacter</i>	AST	-0,73	0,0382
<i>Escherichia-Shigella</i>	AST	0,81	0,0147
<i>Oscillospiraceae</i> V9D2013 group	AST	-0,81	0,0139
<i>Escherichia-Shigella</i>	ALT	0,83	0,01
<i>Christensenellaceae</i> R-7 group	ALT	0,79	0,0191
<i>Rikenellaceae</i> RC9 gut group	Leptin	-0,72	0,0444
<i>Negativibacillus</i>	Leptin	0,83	0,0099
<i>Ligilactobacillus</i>	Leptin	0,82	0,0127
<i>Anaerotruncus</i>	Leptin	0,72	0,0454
<i>Ruminococcaceae</i> Incertae Sedis	Leptin	0,73	0,0395
<i>Alistipes</i>	Leptin	-0,77	0,0255
<i>Lactobacillus</i>	Leptin	0,89	0,0028

<i>Lachnospiraceae</i> GCA-900066575	Leptin	-0,76	0,0276
<i>Lactobacillaceae</i> HT002	Leptin	0,83	0,0107
<i>Eubacterium nodatum</i> group	Leptin	0,72	0,0425
<i>Lachnospiraceae</i> ASF356	Leptin	0,78	0,0235
<i>Anaerovorax</i>	Leptin	0,8	0,0183
<i>Peptococcus</i>	Leptin	0,85	0,0069
<i>Christensenellaceae</i> R-7 group	Leptin	0,76	0,03
<i>Anaerostipes</i>	Leptin	0,79	0,019
<i>Lachnospiraceae</i> UCG-004	Leptin	0,83	0,0105
<i>Eubacterium xylanophilum</i> group	Adiponectin	0,71	0,048
<i>Lachnospiraceae</i> FCS020 group	Adiponectin	0,82	0,0125
<i>Eubacterium fissicatena</i> group	Adiponectin	0,78	0,0211
<i>Salmonella</i>	Adiponectin	0,81	0,0157

Genus	Inmune cells variable	r	p-value
<i>Lachnoanaerobaculum</i>	% CD11b+	-0,76	0,0291
<i>Rikenellaceae</i> RC9 gut group	% CD11b+	0,88	0,0038
<i>Negativibacillus</i>	% CD11b+	-0,8	0,0162
<i>Ligilactobacillus</i>	% CD11b+	-0,74	0,0346
<i>Parabacteroides</i>	% CD11b+	0,79	0,0191
<i>Alistipes</i>	% CD11b+	0,78	0,0216
<i>Lactobacillus</i>	% CD11b+	-0,8	0,0179
<i>Lactobacillaceae</i> HT002	% CD11b+	-0,75	0,0337
<i>Eubacterium nodatum</i> group	% CD11b+	-0,77	0,0248
<i>Anaerovorax</i>	% CD11b+	-0,77	0,0241
<i>Peptococcus</i>	% CD11b+	-0,84	0,0087
<i>Christensenellaceae</i> R-7 group	% CD11b+	-0,73	0,0391
<i>Anaerostipes</i>	% CD11b+	-0,73	0,0383
<i>Lachnospiraceae</i> UCG-004	% CD11b+	-0,83	0,0106
<i>Anaerovoracaceae</i> Family XIII UCG-001	% CD11b+	-0,79	0,0202
<i>Lachnoanaerobaculum</i>	% CD11b+ CD36+	-0,74	0,0359
<i>Rikenellaceae</i> RC9 gut group	% CD11b+ CD36+	0,91	0,0019
<i>Bacteroides</i>	% CD11b+ CD36+	0,84	0,0096
<i>Parabacteroides</i>	% CD11b+ CD36+	0,89	0,0028
<i>Desulfovibrio</i>	% CD11b+ CD36+	-0,71	0,0484
<i>Butyricicoccaceae</i> UCG-009	% CD11b+ CD36+	-0,74	0,0371
<i>Tuzzerella</i>	% CD11b+ CD36+	-0,75	0,0303
<i>Eubacterium nodatum</i> group	% CD11b+ CD36+	-0,72	0,0452
<i>Anaerovorax</i>	% CD11b+ CD36+	-0,78	0,0222
<i>Peptococcus</i>	% CD11b+ CD36+	-0,74	0,0369
<i>Monoglobus</i>	% CD11b+ CD36+	-0,74	0,0342
<i>Lachnospiraceae</i> UCG-004	% CD11b+ CD36+	-0,74	0,0364
<i>Anaerovoracaceae</i> Family XIII UCG-001	% CD11b+ CD36+	-0,8	0,0162
<i>Lachnoanaerobaculum</i>	% CD11b+ F4/80+	-0,76	0,0271
<i>Rikenellaceae</i> RC9 gut group	% CD11b+ F4/80+	0,92	0,001
<i>Bacteroides</i>	% CD11b+ F4/80+	0,77	0,0255

<i>Negativibacillus</i>	% CD11b+ F4/80+	-0,74	0,0362
<i>Parabacteroides</i>	% CD11b+ F4/80+	0,85	0,0072
<i>Alistipes</i>	% CD11b+ F4/80+	0,87	0,005
<i>Eubacterium nodatum group</i>	% CD11b+ F4/80+	-0,82	0,0125
<i>Anaerovorax</i>	% CD11b+ F4/80+	-0,75	0,0311
<i>Peptococcus</i>	% CD11b+ F4/80+	-0,83	0,0101
<i>Anaerostipes</i>	% CD11b+ F4/80+	-0,72	0,0462
<i>Lachnospiraceae UCG-004</i>	% CD11b+ F4/80+	-0,82	0,0135
<i>Anaerovoracaceae Family XIII UCG-001</i>	% CD11b+ F4/80+	-0,85	0,0069
<i>Rikenellaceae RC9 gut group</i>	% CD11b+ F4/80+ CD36+	0,86	0,0067
<i>Bacteroides</i>	% CD11b+ F4/80+ CD36+	0,71	0,0477
<i>Negativibacillus</i>	% CD11b+ F4/80+ CD36+	-0,76	0,0279
<i>Oscillibacter</i>	% CD11b+ F4/80+ CD36+	-0,72	0,0446
<i>Anaerotruncus</i>	% CD11b+ F4/80+ CD36+	-0,79	0,02
<i>Parabacteroides</i>	% CD11b+ F4/80+ CD36+	0,78	0,0235
<i>Harryflintia</i>	% CD11b+ F4/80+ CD36+	-0,74	0,0378
<i>Butyricicoccaceae UCG-009</i>	% CD11b+ F4/80+ CD36+	-0,75	0,0329
<i>Ruminococcaceae Incertae Sedis</i>	% CD11b+ F4/80+ CD36+	-0,79	0,0209
<i>Alistipes</i>	% CD11b+ F4/80+ CD36+	0,71	0,048
<i>Lactobacillus</i>	% CD11b+ F4/80+ CD36+	-0,79	0,0199
<i>Tuzzerella</i>	% CD11b+ F4/80+ CD36+	-0,71	0,0481
<i>Lactobacillaceae HT002</i>	% CD11b+ F4/80+ CD36+	-0,74	0,0352
<i>Lachnospiraceae ASF356</i>	% CD11b+ F4/80+ CD36+	-0,78	0,0231
<i>Anaerovorax</i>	% CD11b+ F4/80+ CD36+	-0,88	0,0039
<i>Peptococcus</i>	% CD11b+ F4/80+ CD36+	-0,73	0,0408
<i>Anaerostipes</i>	% CD11b+ F4/80+ CD36+	-0,77	0,0252
<i>Monoglobus</i>	% CD11b+ F4/80+ CD36+	-0,76	0,0292
<i>Lachnospiraceae UCG-004</i>	% CD11b+ F4/80+ CD36+	-0,77	0,0262
<i>Anaerovoracaceae Family XIII UCG-001</i>	% CD11b+ F4/80+ CD36+	-0,72	0,0452
<i>Rikenellaceae RC9 gut group</i>	% CD11b+ F4/80+ CD206- CD11c+	0,72	0,0433
<i>Negativibacillus</i>	% CD11b+ F4/80+ CD206- CD11c+	-0,79	0,0202
<i>Anaerotruncus</i>	% CD11b+ F4/80+ CD206- CD11c+	-0,71	0,0495
<i>Alistipes</i>	% CD11b+ F4/80+ CD206- CD11c+	0,9	0,0025
<i>Lactobacillus</i>	% CD11b+ F4/80+ CD206- CD11c+	-0,71	0,0494
<i>Lachnospiraceae GCA-900066575</i>	% CD11b+ F4/80+ CD206- CD11c+	0,81	0,0156
<i>Eubacterium nodatum group</i>	% CD11b+ F4/80+ CD206- CD11c+	-0,72	0,0446
<i>Lachnospiraceae ASF356</i>	% CD11b+ F4/80+ CD206- CD11c+	-0,84	0,0097
<i>Anaerovorax</i>	% CD11b+ F4/80+ CD206- CD11c+	-0,78	0,0222
<i>Peptococcus</i>	% CD11b+ F4/80+ CD206- CD11c+	-0,78	0,0231
<i>Anaerostipes</i>	% CD11b+ F4/80+ CD206- CD11c+	-0,76	0,0279
<i>Lachnospiraceae UCG-004</i>	% CD11b+ F4/80+ CD206- CD11c+	-0,8	0,016
<i>Lachnoanaerobaculum</i>	MFI CD11b+ F4/80+ CD206- CD11c+ ROS	-0,71	0,0492
<i>Negativibacillus</i>	MFI CD11b+ F4/80+ CD206- CD11c+ ROS	-0,83	0,0114
<i>Ligilactobacillus</i>	MFI CD11b+ F4/80+ CD206- CD11c+ ROS	-0,79	0,021
<i>Anaeroplasma</i>	MFI CD11b+ F4/80+ CD206- CD11c+ ROS	0,77	0,0245
<i>Alistipes</i>	MFI CD11b+ F4/80+ CD206- CD11c+ ROS	0,79	0,0188

<i>Lactobacillus</i>	MFI CD11b+ F4/80+ CD206- CD11c+ ROS	-0,84	0,0092
<i>Lachnospiraceae</i> GCA-900066575	MFI CD11b+ F4/80+ CD206- CD11c+ ROS	0,81	0,0147
<i>Lactobacillaceae</i> HT002	MFI CD11b+ F4/80+ CD206- CD11c+ ROS	-0,8	0,0178
<i>Eubacterium nodatum</i> group	MFI CD11b+ F4/80+ CD206- CD11c+ ROS	-0,71	0,0483
<i>Lachnospiraceae</i> ASF356	MFI CD11b+ F4/80+ CD206- CD11c+ ROS	-0,73	0,0412
<i>Lachnospiraceae</i> FCS020 group	MFI CD11b+ F4/80+ CD206- CD11c+ ROS	0,71	0,0493
<i>Bilophila</i>	MFI CD11b+ F4/80+ CD206- CD11c+ ROS	0,73	0,0385
<i>Anaerovorax</i>	MFI CD11b+ F4/80+ CD206- CD11c+ ROS	-0,74	0,0343
<i>Peptococcus</i>	MFI CD11b+ F4/80+ CD206- CD11c+ ROS	-0,92	0,0011
<i>Christensenellaceae</i> R-7 group	MFI CD11b+ F4/80+ CD206- CD11c+ ROS	-0,81	0,0141
<i>Lachnospiraceae</i> UCG-004	MFI CD11b+ F4/80+ CD206- CD11c+ ROS	-0,9	0,0022
<i>Rikenellaceae</i> RC9 gut group	% CD11b+ F4/80+ CD206+ CD11c+	0,74	0,0344
<i>Negativibacillus</i>	% CD11b+ F4/80+ CD206+ CD11c+	-0,9	0,0022
<i>Harryflintia</i>	% CD11b+ F4/80+ CD206+ CD11c+	-0,77	0,0264
<i>Lachnospiraceae</i> ASF356	% CD11b+ F4/80+ CD206+ CD11c+	-0,73	0,0392
<i>Lachnospiraceae</i> UCG-004	% CD11b+ F4/80+ CD206+ CD11c+	-0,74	0,0364
<i>Lachnospiraceae</i> FCS020 group	% CD11b+ F4/80+ CD206- CD11c-	0,9	0,0025
<i>Bilophila</i>	% CD11b+ F4/80+ CD206- CD11c-	0,77	0,0248
<i>Salmonella</i>	% CD11b+ F4/80+ CD206- CD11c-	0,93	8.00E-04
<i>Negativibacillus</i>	MFI CD11b+ F4/80+ ROS	-0,75	0,0308
<i>Ligilactobacillus</i>	MFI CD11b+ F4/80+ ROS	-0,8	0,0166
<i>Anaeroplasma</i>	MFI CD11b+ F4/80+ ROS	0,77	0,0239
<i>Alistipes</i>	MFI CD11b+ F4/80+ ROS	0,75	0,0327
<i>Lactobacillus</i>	MFI CD11b+ F4/80+ ROS	-0,83	0,0112
<i>Lachnospiraceae</i> GCA-900066575	MFI CD11b+ F4/80+ ROS	0,82	0,0136
<i>Lactobacillaceae</i> HT002	MFI CD11b+ F4/80+ ROS	-0,79	0,0208
<i>Eubacterium nodatum</i> group	MFI CD11b+ F4/80+ ROS	-0,74	0,0346
<i>Lachnospiraceae</i> FCS020 group	MFI CD11b+ F4/80+ ROS	0,8	0,0173
<i>Bilophila</i>	MFI CD11b+ F4/80+ ROS	0,78	0,0213
<i>Oscillospiraceae</i> NK4A214 group	MFI CD11b+ F4/80+ ROS	-0,72	0,0435
<i>Anaerovorax</i>	MFI CD11b+ F4/80+ ROS	-0,74	0,0375
<i>Peptococcus</i>	MFI CD11b+ F4/80+ ROS	-0,94	6.00E-04
<i>Christensenellaceae</i> R-7 group	MFI CD11b+ F4/80+ ROS	-0,82	0,0132
<i>Lachnospiraceae</i> UCG-004	MFI CD11b+ F4/80+ ROS	-0,86	0,0064
<i>Lachnoanaerobaculum</i>	MFI CD11b+ ROS	-0,71	0,0484
<i>Negativibacillus</i>	MFI CD11b+ ROS	-0,74	0,0344
<i>Ligilactobacillus</i>	MFI CD11b+ ROS	-0,8	0,0164
<i>Anaeroplasma</i>	MFI CD11b+ ROS	0,75	0,0308
<i>Alistipes</i>	MFI CD11b+ ROS	0,79	0,0209
<i>Lactobacillus</i>	MFI CD11b+ ROS	-0,81	0,0156
<i>Lachnospiraceae</i> GCA-900066575	MFI CD11b+ ROS	0,81	0,0149
<i>Lactobacillaceae</i> HT002	MFI CD11b+ ROS	-0,77	0,0255
<i>Eubacterium nodatum</i> group	MFI CD11b+ ROS	-0,81	0,0152
<i>Lachnospiraceae</i> FCS020 group	MFI CD11b+ ROS	0,8	0,0169
<i>Bilophila</i>	MFI CD11b+ ROS	0,78	0,0231
<i>Oscillospiraceae</i> NK4A214 group	MFI CD11b+ ROS	-0,74	0,0343

<i>Anaerovorax</i>	MFI CD11b+ ROS	-0,75	0,0315
<i>Peptococcus</i>	MFI CD11b+ ROS	-0,96	2.00E-04
<i>Christensenellaceae R-7 group</i>	MFI CD11b+ ROS	-0,79	0,0201
<i>Lachnospiraceae UCG-004</i>	MFI CD11b+ ROS	-0,86	0,0062
<i>Lachnospiraceae NK4A136 group</i>	% CD11b-	0,81	0,014
<i>Herbinix</i>	% CD11b-	0,76	0,0275
<i>Anaeroplasm</i>	% CD11b-	0,75	0,0323
<i>Prevotellaceae NK3B31 group</i>	% CD11b-	0,83	0,0111
<i>Lachnospiraceae GCA-900066575</i>	% CD11b-	0,8	0,0162
<i>Angelakisella</i>	% CD11b-	0,79	0,0197
<i>Anaerospiribacter</i>	% CD11b-	0,79	0,0206
<i>Marvinbryantia</i>	% CD11b-	0,85	0,0082
<i>Rikenellaceae RC9 gut group</i>	% CD11b- CD36+	0,89	0,0033
<i>Bacteroides</i>	% CD11b- CD36+	0,72	0,0431
<i>Negativibacillus</i>	% CD11b- CD36+	-0,83	0,0108
<i>Parabacteroides</i>	% CD11b- CD36+	0,86	0,0065
<i>Harryflintia</i>	% CD11b- CD36+	-0,72	0,0425
<i>Lactobacillus</i>	% CD11b- CD36+	-0,72	0,0444
<i>Lachnospiraceae UCG-004</i>	% CD11b- CD36+	-0,73	0,0387
<i>Lachnoanaerobaculum</i>	% Leukocytes CD36+	-0,71	0,0465
<i>Rikenellaceae RC9 gut group</i>	% Leukocytes CD36+	0,89	0,0029
<i>Bacteroides</i>	% Leukocytes CD36+	0,75	0,0309
<i>Negativibacillus</i>	% Leukocytes CD36+	-0,81	0,0157
<i>Parabacteroides</i>	% Leukocytes CD36+	0,87	0,0055
<i>Harryflintia</i>	% Leukocytes CD36+	-0,71	0,048
<i>Lactobacillus</i>	% Leukocytes CD36+	-0,76	0,0285
<i>Lactobacillaceae HT002</i>	% Leukocytes CD36+	-0,71	0,0469
<i>Anaerovorax</i>	% Leukocytes CD36+	-0,72	0,0439
<i>Monoglobus</i>	% Leukocytes CD36+	-0,72	0,0432
<i>Lachnospiraceae UCG-004</i>	% Leukocytes CD36+	-0,75	0,0307
<i>Anaerovoracaceae Family XIII UCG-001</i>	% Leukocytes CD36+	-0,73	0,0418
<i>Negativibacillus</i>	MFI Leukocytes ROS	-0,8	0,017
<i>Ligilactobacillus</i>	MFI Leukocytes ROS	-0,85	0,0071
<i>Anaeroplasm</i>	MFI Leukocytes ROS	0,77	0,0245
<i>Alistipes</i>	MFI Leukocytes ROS	0,82	0,0131
<i>Lactobacillus</i>	MFI Leukocytes ROS	-0,84	0,0094
<i>Lachnospiraceae GCA-900066575</i>	MFI Leukocytes ROS	0,82	0,0118
<i>Lactobacillaceae HT002</i>	MFI Leukocytes ROS	-0,79	0,0207
<i>Eubacterium nodatum group</i>	MFI Leukocytes ROS	-0,81	0,0158
<i>Lachnospiraceae FCS020 group</i>	MFI Leukocytes ROS	0,74	0,0366
<i>Bilophila</i>	MFI Leukocytes ROS	0,77	0,0245
<i>Oscillospiraceae NK4A214 group</i>	MFI Leukocytes ROS	-0,71	0,0484
<i>Anaerovorax</i>	MFI Leukocytes ROS	-0,74	0,0356
<i>Peptococcus</i>	MFI Leukocytes ROS	-0,91	0,0015
<i>Christensenellaceae R-7 group</i>	MFI Leukocytes ROS	-0,77	0,0241
<i>Anaerostipes</i>	MFI Leukocytes ROS	-0,73	0,0412

Lachnospiraceae UCG-004

MFI Leukocytes ROS

-0,84 0,0086

Supplementary Table S6: Correlation between body weight, blood metabolic parameters and immune cells present in VAT with bacterial genera of gut microbiota showing significant correlation. Correlation significant established using the Pearson test (Significant p-value<0.05 was consider).

Abbreviations: CD: cluster of differentiation, VAT: visceral adipose tissue, HDL-c: high-density lipoprotein cholesterol, LDL-c: low-density lipoprotein cholesterol, AST: aspartate aminotransferase, ALT: alanine aminotransferase, ROS: reactive oxygen species, MFI: median fluorescence intensity.