

## **Supplementary Material - Tables**

### **Early life dietary intervention in dairy calves results in a long-term reduction in methane emissions**

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**Table S1.** Chemical composition of dietary ingredients fed to all calves (n=18)

	Hay	Starter Concentrate <sup>1</sup>	Concentrate <sup>2</sup>
Dry Matter, %	92.16	91.6	92
N, % DM	1.56	2.78	3.00
NDF, % DM	49.89	21.27	23.2
ADF, % DM	26.08	11.22	13.4
Starch, % DM		23.81	27

<sup>1</sup> Starter concentrate available from 4 weeks up to weaning at 11 weeks

<sup>2</sup> Concentrate supplied after weaning. This pelleted concentrate was also used to lure calves to GreenFeeds.

**Table S2.** Sequencing and amplicon size of primers used for MiSeq Illumina sequencing and quantitative PCR.

Target	Primer name	Sequence (5'-3')	Amplicon size (nt)	Usage	Reference <sup>1</sup>
Archaeal 16S rDNA	Arch349F	GYGCASCAGKCGMGA AW	457	Sequencing	Takai and Horikoshi (2000)
	Arch806R	GGACTACVSGGGTATCTAAT			
Bacterial V3-5 16S rDNA	V3_F357	CCTACGGGAGGCAGCAG	570	Sequencing	Muyzer et al. (1993)
	V5_R926	CCGTCAATTCMTTTRAGT			
Fungal ITS2	ITS3	GCATCGATGAAGAACGCAGC	330	Sequencing	White et al. (1990)
	ITS4	TCCTCCGCTTATTGATATGC			
Protozoal 18S rDNA	F566Euk	CAGCAGCCGCGGTAATTCC	660	Sequencing	Hadziavdic et al. (2007)
	R1200Euk	CCCGTGTTGAGTCAAATTAAGC			
Archaeal 16S rDNA	1406-1389R	AGGAATTGGCGGGGAGCAC	140	qPCR	Denman et al. (2007)
	896-915F	GAGGAAGGAGTGGACGACGGTA			
Bacterial 16S rDNA	520-F	AGCAGCCGCGGTAAT	280	qPCR	Edwards et al. (2008)
	799-R	CAGGGTATCTAATCCTGTT			

<sup>1</sup>Denman, S.E., Tomkins, N.W., and Mcsweeney, C.S. (2007). *FEMS Microbiology Ecology* 62, 313-322.

Edwards, J.E., Huws, S.A., Kim, E.J., and Kingston-Smith, A.H. (2008). *FEMS Microbiology Ecology* 63, 141-142.

Hadziavdic, K., Lekang, K., Lanzen, A., Jonassen, I., Thompson, E.M., and Troedsson, C. (2014). *PLOS ONE* 9, e87624.

Muyzer, G., De Waal, E.C., and Uitterlinden, A.G. (1993). *Applied and Environmental Microbiology* 59, 695-700.

Takai, K., and Horikoshi, K. (2000). *Applied and Environmental Microbiology* 66, 5066-5072.

White TJ, Bruns T, Lee S, Taylor JW: Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. PCR Protocols: A Guide to Methods and Applications. Edited by: Innis MA, Gelfand DH, Sninsky JJ, White TJ. 1990, New York: Academic Press Inc, 315-322.

**Table S3.** Ruminal fermentation parameters in calves supplemented with CONT or 3-NOP up to 60 weeks of age.

Parameter	Week 1 <sup>1</sup>		Week 4 <sup>2</sup>		Week 11 <sup>3</sup>		Week 14 <sup>2</sup>		Week 23 <sup>4</sup>		Week 60 <sup>3</sup>		SE	P-values		
	CONT	3NOP	CONT	3NOP	CONT	3NOP	CONT	3NOP	CONT	3NOP	CONT	3NOP		TRT	Week	TRT*Week
Total VFA, mmol/L	19.57	20.13	60.04	48.65	84.53	87.77	114.01	92.44	70.95	98.43	96.87	120.78	4.275	0.77	<0.001	0.22
Individual VFA, % of total																
Acetate (A)	82.11	78.81	77.35	80.24	72.98	62.97	69.08	70.60	65.90	68.52	73.94	72.41	2.973	0.88	<0.001	0.19
Propionate (P)	14.21	17.30	11.50	11.93	15.61	17.77	19.68	15.14	20.65	18.74	14.38	14.99	0.862	0.43	<0.001	0.29
Butyrate	2.28	2.26	8.59	5.89	9.49	15.82	8.95	11.23	10.53	10.12	10.20	11.05	0.610	0.20	<0.001	0.30
Isovalerate	0.94	1.09	1.33	1.20	0.70	1.56	0.70	1.04	1.07	1.01	0.43	0.43	0.055	0.12	0.013	0.28
Valerate	0.38	0.39	1.05	0.65	0.92	1.42	0.92	1.21	0.72	0.65	0.45	0.49	0.060	0.54	0.011	0.39
Caproate	0.09	0.15	0.19	0.09	0.18	0.37	0.18	0.19	0.26	0.18	0.13	0.13	0.015	0.44	0.003	0.70
A:P ratio	6.16	4.96	6.16	5.91	4.05	3.84	3.60	3.52	4.56	5.20	5.16	4.84	0.196	0.39	0.008	0.27
NH <sub>3</sub> , mM	2.54	2.23	14.60	12.15	1.28	1.31	2.28	2.16	4.32	3.06	1.44	1.43	0.470	0.51	0.003	0.44

<sup>1</sup> n=6 in CONT; n=9 in 3-NOP<sup>2</sup> n=8 in CONT; n=10 in 3-NOP<sup>3</sup> n=8 in CONT; n=9 in 3-NOP<sup>4</sup> n=7 in CONT; n=10 in 3-NOP

**Table S4.** Ruminal alpha diversity metrics in calves supplemented with CONT or 3-NOP up to 60 week of age.

	Week 1 <sup>1</sup>				Week 4 <sup>2</sup>				Week 11 <sup>3</sup>				Week 14 <sup>2</sup>				Week 23 <sup>4</sup>				Week 60 <sup>3</sup>			
	3NOP	CONT	SEM	P-value	3NOP	CONT	SEM	P-value	3NOP	CONT	SEM	P-value	3NOP	CONT	SEM	P-value	3NOP	CONT	SEM	P-value	3NOP	CONT	SEM	P-value
<b>Bacteria</b>																								
Shannon	2.41	2.51	0.126	0.643	3.34	3.70	0.144	0.171	4.46	4.62	0.072	0.102	4.42	4.84	0.102	0.031	4.69	4.76	0.075	0.847	4.03	4.46	0.129	0.124
Simpson	0.75	0.81	0.034	0.728	0.86	0.89	0.025	0.233	0.95	0.96	0.005	0.178	0.95	0.97	0.006	0.019	0.96	0.97	0.004	1.000	0.91	0.93	0.010	0.441
Richness	171	161	9.2	0.418	406	483	24.7	0.102	631	641	16.1	0.386	667	709	15.0	0.085	732	728	14.6	0.700	590	669	18.2	0.021
Evenness	0.47	0.50	0.024	0.817	0.56	0.60	0.023	0.200	0.69	0.72	0.011	0.178	0.68	0.74	0.014	0.031	0.71	0.72	0.011	0.923	0.63	0.68	0.017	0.248
<b>Archaea</b>																								
Shannon	0.40	0.50	0.133	0.754	2.28	2.69	0.082	0.015	2.99	2.93	0.074	0.700	2.95	2.98	0.058	0.825	3.10	3.26	0.046	0.178	3.64	3.60	0.031	0.630
Simpson	0.84	0.70	0.066	0.286	0.80	0.87	0.016	0.058	0.89	0.88	0.012	1.000	0.89	0.91	0.006	0.122	0.90	0.92	0.007	0.211	0.94	0.93	0.003	0.178
Richness	10	18	4.9	0.450	240	312	15.9	0.022	329	311	22.2	0.736	297	251	19.4	0.270	345	400	13.5	0.030	424	476	14.1	0.083
Evenness	0.14	0.23	0.063	0.490	0.42	0.47	0.012	0.070	0.52	0.51	0.009	1.000	0.52	0.54	0.008	0.038	0.53	0.54	0.007	0.564	0.60	0.58	0.004	0.083
<b>Anaerobic fungi</b>																								
Shannon					2.59	2.57	0.084	0.508	4.44	4.17	0.095	0.178	3.97	3.84	0.186	0.508	4.30	4.35	0.105	0.700	4.73	4.89	0.129	0.847
Simpson					0.72	0.73	0.005	0.965	0.95	0.94	0.006	0.211	0.91	0.89	0.021	0.310	0.96	0.96	0.005	0.847	0.97	0.98	0.004	0.248
Richness					524	439	67.2	0.566	723	433	77.1	0.068	560	573	60.5	0.895	691	600	65.1	0.847	735	699	68.6	0.773
Evenness					0.43	0.44	0.011	0.825	0.70	0.70	0.012	0.441	0.64	0.61	0.017	0.354	0.66	0.69	0.010	0.290	0.73	0.76	0.008	0.102
<b>Protozoa</b>																								
Shannon																	0.44	0.77	0.227	0.17	2.53	2.47	0.055	0.32
Simpson																	0.18	0.32	0.102	0.19	0.88	0.87	0.011	0.24
Richness																	15	21	4.5	0.23	41	42	1.2	0.64
Evenness																	0.16	0.24	0.061	0.23	0.68	0.66	0.015	0.24

<sup>1</sup> n=6 in CONT; n=9 in 3-NOP

<sup>2</sup> n=8 in CONT; n=10 in 3-NOP

<sup>3</sup> n=8 in CONT; n=9 in 3-NOP

<sup>4</sup> n=7 in CONT; n=10 in 3-NOP

**Table S5.** Faecal alpha diversity metrics in calves supplemented with CONT or 3NOP up to 60 week of age.

	Week 1 <sup>1</sup>				Week 4 <sup>2</sup>				Week 11 <sup>2</sup>				Week 14 <sup>3</sup>				Week 23 <sup>4</sup>				Week 60 <sup>2</sup>			
	3NOP	CONT	SEM	P-value	3NOP	CONT	SEM	P-value	3NOP	CONT	SEM	P-value	3NOP	CONT	SEM	P-value	3NOP	CONT	SEM	P-value	3NOP	CONT	SEM	P-value
<b>Bacteria</b>																								
Shannon	2.96	3.01	0.097	1.000	4.21	4.11	0.094	0.56	4.25	4.11	0.067	0.42	4.68	4.71	0.029	0.57	4.53	4.42	0.038	0.18	2.96	3.01	0.097	1
Simpson	0.87	0.86	0.016	0.441	0.95	0.94	0.007	0.70	0.95	0.94	0.005	0.91	0.97	0.97	0.002	0.45	0.96	0.95	0.002	0.054	0.87	0.86	0.016	0.44
Richness	239	257	14.9	0.386	490	494	11.6	0.56	527	525	13.8	1	563	555	10.9	0.76	456	463	6.8	0.50	239	257	14.9	0.39
Evenness	0.54	0.55	0.014	1.000	0.68	0.66	0.014	0.63	0.68	0.66	0.009	0.42	0.74	0.75	0.004	0.45	0.74	0.72	0.006	0.068	0.54	0.55	0.014	1
<b>Anaerobic fungi</b>																								
Shannon					1.04	0.95	0.239	0.69	1.69	1.41	0.353	0.72	3.78	3.69	0.135	0.89	4.08	4.17	0.148	1	1.04	0.95	0.239	0.69
Simpson					0.79	0.82	0.048	0.69	0.86	0.76	0.048	0.35	0.94	0.92	0.009	0.89	0.95	0.94	0.008	0.50	0.79	0.82	0.048	0.69
Richness					30	23	9.8	0.58	156	47	44.2	0.55	422	385	43.3	0.69	358	393	51.5	0.92	30	23	9.8	0.58
Evenness					0.33	0.38	0.084	0.69	0.33	0.38	0.072	0.81	0.63	0.66	0.017	0.31	0.72	0.72	0.010	0.85	0.33	0.38	0.084	0.69

<sup>1</sup> n=6 in CONT; n=9 in 3-NOP

<sup>2</sup> n=8 in CONT; n=9 in 3-NOP

<sup>3</sup> n=6 in CONT; n=9 in 3-NOP

<sup>4</sup> n=8 in CONT; n=10 in 3-NOP

**Table S6.** Relative abundance of ruminal taxa in calves aged 1, 4, 11, 14, 23 and 60 weeks, as affected by dietary supplementation of 3NOP.

Taxa	Week 1 <sup>1</sup>		Week 4 <sup>2</sup>		Week 11 <sup>3</sup>		Week 14 <sup>2</sup>		Week 23 <sup>4</sup>		Week 60 <sup>3</sup>		P-value						
	CONT	3NOP	CONT	3NOP	CONT	3NOP	CONT	3NOP	CONT	3NOP	CONT	3NOP	1	4	11	14	23	60	
<b>Archaea</b>																			
<i>Methanobrevibacter</i>	0.68	0.12	62.18	61.41	59.61	56.56	51.12	58.27	52.48	53.04	58.41	53.36	0.262	0.632	0.48	0.057	0.966	0.103	
<i>M. boviskoreani</i> clade	0.00	0.00	0.00	0.20	0.00	0.00	0.00	0.00	1.02	0.11	1.28	1.89	NA	0.315	NA	NA	0.301	0.678	
<i>M. gottschalkii</i> clade	0.21	0.01	49.31	34.66	43.81	39.77	30.67	44.26	36.60	40.60	42.45	40.90	0.177	0.083	0.59	0.012	0.352	0.686	
<i>M. oralis</i>	0.00	0.00	0.20	0.14	0.37	0.15	0.13	0.19	0.22	0.16	1.34	1.22	NA	0.041	0.117	0.182	0.267	0.285	
<i>M. ruminantium</i> clade	0.00	0.03	9.97	21.44	12.45	13.18	16.75	11.24	11.18	8.56	8.84	4.88	0.421	0.077	0.847	0.237	0.321	0.024	
<i>M. smithii</i>	0.00	0.00	0.01	0.01	0.02	0.01	0.02	0.02	0.03	0.02	0.05	0.03	NA	0.394	0.247	0.994	0.227	0.149	
Methanobrevibacter unclassified	0.00	0.00	0.46	0.45	1.07	0.36	0.37	0.44	0.63	0.45	1.69	1.32	NA	0.933	0.026	0.696	0.203	0.131	
<i>Methanosphaera</i>	0.00	0.42	7.33	10.68	7.33	6.02	7.03	9.45	7.49	6.03	3.10	2.20	0.435	0.426	0.438	0.297	0.39	0.217	
Methanobacteriaceae -F	0.00	0.00	0.01	0.03	0.02	0.01	0.01	0.02	0.02	0.04	0.06	0.04	NA	0.022	0.166	0.399	0.097	0.26	
Methanococcales-o	0.05	0.13	0.14	0.11	0.04	0.14	0.36	0.01	0.30	0.06	0.20	0.07	0.414	0.819	0.409	0.234	0.331	0.36	
<i>Methanomicrobium mobile</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.90	3.35	NA	NA	NA	NA	NA	0.036	
Methanomassiliococcaceae																			
<i>Group5</i>	0.00	0.00	0.00	0.00	0.01	0.01	0.01	0.01	0.03	0.02	0.04	0.04	NA	0.132	0.83	0.471	0.133	0.999	
<i>Group8</i>	0.00	0.00	0.03	0.02	2.72	0.84	4.07	4.20	4.06	2.63	1.46	3.79	NA	0.647	0.087	0.934	0.444	<0.001	
<i>Group9</i>	0.00	0.00	7.30	0.83	6.11	9.84	4.52	5.34	5.87	5.94	7.14	8.83	NA	0.002	0.187	0.626	0.985	0.231	
<i>Group10</i>	0.00	0.00	7.47	5.70	8.24	9.95	8.29	6.75	6.93	4.26	6.46	5.04	NA	0.711	0.636	0.749	0.305	0.319	
<i>Group11</i>	0.00	0.03	5.88	10.56	1.26	0.72	0.63	0.98	0.50	0.42	0.23	0.17	0.435	0.281	0.498	0.637	0.823	0.55	
<i>Group12</i>	0.00	0.00	0.87	3.15	7.86	9.04	12.22	7.07	4.47	8.05	3.28	3.04	NA	0.376	0.652	0.036	0.141	0.73	
Methanomassiliococcaceae unclassified	0.00	0.00	6.60	4.26	5.80	3.89	7.56	6.49	14.21	13.36	15.08	16.09	0.48	0.497	0.244	0.793	0.747	0.631	
Euryarchaeota	92.25	99.28	2.17	3.25	0.79	2.97	3.23	1.38	2.82	3.88	3.15	3.40	0.772	0.519	0.244	0.793	0.159	0.437	
<b>Bacteria</b>																			
Actinobacteria	3.53	5.17	0.88	0.48	0.82	0.82	1.31	0.93	1.71	0.86	1.45	0.63	0.628	0.1	0.989	0.279	0.079	0.043	
<i>Actinomyces</i>	2.49	1.43	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.338	0.749	NA	NA	NA	NA	
<i>Atopobium</i>	0.00	0.00	0.17	0.09	0.13	0.09	0.11	0.08	0.12	0.10	0.09	0.04	NA	0.155	0.406	0.421	0.635	0.049	
<i>Collinsella</i>	0.52	3.41	0.04	0.06	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.405	0.711	NA	0.387	0.42	NA	

Coriobacteriaceae-F	0.00	0.05	0.01	0.01	0.04	0.02	0.03	0.03	0.04	0.05	0.05	0.03	0.469	0.896	0.284	0.943	0.253	0.161
Corynebacterium-F	0.08	0.03	0.01	0.00	0.00	0.00	0.14	0.00	0.01	0.00	0.00	0.00	0.253	0.276	0.648	0.273	0.237	NA
<i>Denitrobacterium</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.01	0.00	0.00	NA	0.562	0.989	0.637	0.926	0.595
<i>Eggerthella</i>	0.02	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.897	0.648	NA	NA	NA	NA
<i>Enterorhabdus</i>	0.00	0.00	0.02	0.03	0.02	0.03	0.01	0.03	0.01	0.02	0.02	0.01	0.435	0.405	0.165	0.178	0.276	0.306
<i>Olsenella</i>	0.00	0.00	0.57	0.26	0.62	0.63	0.99	0.75	1.49	0.65	1.19	0.49	0.234	0.15	0.969	0.461	0.061	0.07
<i>Paraeggerthella</i>	0.26	0.07	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.197	NA	NA	NA	NA	NA
<i>Senegalimassilia</i>	0.01	0.02	0.02	0.01	0.02	0.02	0.02	0.01	0.04	0.02	0.07	0.04	0.617	0.51	0.837	0.308	0.272	0.124
<i>Trueperella</i>	0.14	0.12	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.851	0.276	NA	NA	NA	NA
Bacteroidetes	49.43	61.97	52.01	55.63	37.98	41.87	35.13	35.75	43.62	47.19	39.13	39.39	0.253	0.651	0.338	0.897	0.476	0.954
<i>Alistipes</i>	0.12	0.05	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.459	0.558	NA	0.387	NA	NA
<i>Alloprevotella</i>	13.26	5.28	0.99	1.47	0.07	0.04	0.08	0.04	0.04	0.04	0.01	0.00	0.07	0.442	0.236	0.024	0.981	0.498
Bacteroidales_BS11_gut_group-F	0.00	0.00	12.99	17.03	0.26	0.16	0.62	0.16	1.42	1.56	1.18	1.26	0.435	0.7	0.065	0.029	0.791	0.919
Bacteroidales_RF16-F	0.00	0.00	4.04	1.21	5.37	8.14	4.64	5.19	13.07	12.02	20.26	20.64	0.28	0.249	0.35	0.786	0.83	0.926
<i>Bacteroidales_S24-7_group</i>	0.06	0.00	0.63	0.81	0.50	2.70	0.58	0.66	0.61	0.41	1.43	0.77	0.237	0.669	0.352	0.761	0.166	0.011
Bacteroidales-O	0.22	0.01	3.94	4.21	3.55	8.70	3.25	2.81	0.16	0.14	0.15	0.20	0.024	0.925	0.019	0.729	0.758	0.206
<i>Bacteroides</i>	21.77	47.19	0.29	0.32	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.101	0.898	0.434	0.352	0.632	0.962
Bacteroidetes unclassified	0.00	0.00	0.50	0.09	0.19	0.23	0.14	0.13	0.09	0.25	0.12	0.07	NA	0.291	0.838	0.866	0.339	0.178
<i>Barnesiella</i>	0.02	0.01	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.405	0.335	NA	NA	NA	NA
<i>Bergeyella</i>	0.01	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.534	NA	NA	0.387	0.244	NA
<i>Butyricimonas</i>	3.06	0.79	0.04	0.14	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.12	0.319	NA	NA	NA	NA
<i>Capnocytophaga</i>	0.12	0.05	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.445	NA	NA	0.387	NA	NA
Marinilabiaceae-F	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.03	0.01	NA	0.276	0.543	0.684	0.147	0.469
<i>Odoribacter</i>	0.43	0.16	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.027	0.46	NA	NA	NA	NA
<i>Parabacteroides</i>	1.69	0.82	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.298	0.082	NA	0.387	NA	NA
<i>Phocaeicola</i>	0.00	0.00	1.03	0.39	0.11	0.54	0.11	0.14	0.07	0.07	0.09	0.04	0.234	0.074	0.021	0.582	0.978	0.145
Porphyromonadaceae-F	0.10	z	0.03	0.06	0.00	0.00	0.00	0.00	0.01	0.00	0.02	0.03	0.234	0.396	0.291	0.387	0.091	0.518
<i>Porphyromonas</i>	6.62	1.40	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.112	0.062	NA	NA	NA	NA
<i>Prevotella</i>	0.87	3.73	20.78	20.89	19.58	12.91	13.25	18.32	18.50	24.85	9.77	10.73	0.294	0.964	0.037	0.9	0.03	0.661
<i>Prevotella_7</i>	0.02	0.34	0.07	0.10	0.10	0.08	4.46	0.18	0.03	0.04	0.00	0.00	0.35	0.7	0.357	0.279	0.488	0.304
<i>Prevotella_9</i>	0.01	0.44	0.00	0.19	0.00	0.00	0.09	0.00	0.00	0.00	0.00	0.00	0.313	0.293	NA	0.136	NA	NA
Prevotellaceae-F	0.90	0.66	2.46	1.94	5.01	3.57	5.04	4.26	3.45	1.93	1.73	1.56	0.623	0.522	0.379	0.702	0.07	0.577



<i>Rikenellaceae_RC9_gut_group</i>	0.05	0.25	4.17	6.64	3.20	4.76	2.84	3.77	6.12	5.86	4.30	4.05	0.335	0.408	0.181	0.303	0.856	0.802
Rikenellaceae-F	0.00	0.00	0.03	0.07	0.02	0.04	0.02	0.06	0.04	0.02	0.03	0.01	0.435	0.347	0.196	0.197	0.553	0.095
Cyanobacteria																		
Gastranaerophilales-O	0.00	0.00	0.47	0.25	5.78	4.45	6.79	3.65	8.25	6.66	4.48	3.91	0.234	0.326	0.466	0.062	0.411	0.531
Elusimicrobia																		
Elusimicrobia-C	0.00	0.00	0.00	0.00	0.01	0.02	0.00	0.00	0.02	0.02	0.07	0.02	NA	0.228	0.621	0.637	0.524	0.251
Fibrobacteres																		
<i>Fibrobacter</i>	0.00	0.25	1.99	6.67	3.73	3.47	7.78	5.90	9.09	6.20	20.75	31.46	0.165	0.126	0.826	0.43	0.04	0.013
Firmicutes	17.10	16.95	28.70	22.04	40.88	38.06	37.24	38.61	20.17	23.10	23.58	15.01	0.987	0.22	0.52	0.745	0.256	0.065
<i>Acetitomaculum</i>	0.01	0.00	5.12	0.65	2.00	1.46	1.83	0.99	0.81	0.61	1.02	0.41	0.449	0.187	0.357	0.103	0.35	0.116
<i>Acidaminococcus</i>	0.00	0.00	0.02	0.01	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.435	0.627	NA	0.387	NA	NA
<i>Anaerotruncus</i>	0.01	0.02	0.02	0.01	0.03	0.03	0.02	0.03	0.06	0.04	0.09	0.02	0.423	0.407	0.512	0.326	0.179	4E-04
<i>Anaerovorax</i>	0.00	0.00	0.02	0.02	0.02	0.01	0.02	0.01	0.02	0.01	0.03	0.03	NA	0.928	0.413	0.135	0.024	0.793
<i>Asteroleplasma</i>	0.01	0.01	0.03	0.23	0.09	0.06	0.10	0.16	0.09	0.13	0.14	0.17	0.834	0.408	0.565	0.593	0.682	0.569
<i>Blautia</i>	0.11	0.05	0.02	0.10	0.02	0.01	0.02	0.01	0.02	0.01	0.04	0.02	0.261	0.271	0.577	0.391	0.483	0.141
<i>Butyricoccus</i>	0.15	0.10	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.714	0.269	NA	0.387	NA	NA
<i>Butyrivibrio</i>	0.52	0.47	0.92	0.42	2.15	1.74	2.34	1.91	1.29	1.22	1.07	0.78	0.943	0.038	0.563	0.372	0.811	0.37
<i>Catenisphaera</i>	0.00	0.00	0.04	0.05	0.01	0.00	0.01	0.00	0.01	0.00	0.00	0.00	0.234	0.989	0.187	0.552	0.039	0.828
<i>Cellulosilyticum</i>	0.05	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.08	NA	NA	NA	NA	NA
<i>Christensenellaceae_R-7_group</i>	0.02	0.01	3.28	1.54	3.03	2.09	2.19	1.99	2.63	2.85	3.40	1.95	0.384	0.122	0.109	0.71	0.736	0.027
Christensenellaceae-F	0.00	0.00	0.02	0.00	0.01	0.01	0.01	0.01	0.01	0.01	0.02	0.01	NA	0.006	0.937	0.558	0.466	0.14
Clostridiales																		
<i>Family_XIII_AD3011_group</i>	0.00	0.00	0.11	0.05	0.03	0.03	0.02	0.03	0.05	0.03	0.05	0.01	NA	0.071	0.982	0.383	0.332	0.047
<i>Clostridiales_Eubacterium_nodatum_group</i>	0.00	0.00	0.03	0.03	0.03	0.02	0.02	0.02	0.02	0.02	0.02	0.01	NA	0.928	0.7	0.766	0.915	0.241
<i>Clostridiales_vadinBB60-F</i>	0.17	0.43	0.46	0.54	0.67	0.49	0.64	1.10	0.75	0.75	1.25	1.37	0.329	0.792	0.327	0.391	0.985	0.667
Clostridiales-O	0.06	0.04	0.03	0.12	0.40	0.08	0.15	0.20	0.03	0.10	0.08	0.04	0.663	0.474	0.288	0.58	0.015	0.004
<i>Clostridium_sensu_stricto_1</i>	0.01	0.02	0.02	1.05	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.755	0.051	NA	0.276	0.42	0.148
<i>Clostridium_sensu_stricto_2</i>	0.02	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.574	NA	NA	NA	NA	NA
<i>Coprococcus_1</i>	0.00	0.00	0.04	0.05	0.05	0.03	0.02	0.02	0.02	0.04	0.02	0.01	NA	0.879	0.14	0.599	0.105	0.297
<i>Coprococcus_2</i>	0.00	0.00	0.86	0.62	0.56	0.65	0.23	0.34	0.04	0.09	0.01	0.02	NA	0.679	0.789	0.313	0.438	0.495
<i>Defluviitaleaceae_UCG-011</i>	0.00	0.00	0.04	0.01	0.08	0.04	0.05	0.02	0.04	0.03	0.02	0.01	NA	0.008	0.049	0.02	0.415	0.111
<i>Dialister</i>	0.00	0.07	0.00	0.06	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.435	0.369	NA	NA	NA	NA

<i>Dielma</i>	0.01	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.482	NA	NA	NA	NA	NA
<i>Dorea</i>	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.275	0.877	NA	0.387	NA	NA
Enterococcaceae-F	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.482	NA	NA	NA	NA	NA
<i>Enterococcus</i>	0.01	7.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.428	0.276	NA	NA	NA	NA
<i>Erysipelatoclostridium</i>	0.06	0.05	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.735	NA	NA	NA	NA	NA
<i>Erysipelotrichaceae_UCG-002</i>	0.00	0.00	1.72	4.28	0.16	0.37	1.10	1.15	0.00	0.00	0.00	0.00	NA	0.502	0.528	0.948	0.42	NA
<i>Erysipelotrichaceae_UCG-004</i>	0.26	0.01	0.30	0.24	0.61	0.52	0.74	1.75	1.41	1.30	3.07	2.57	0.169	0.761	0.579	0.309	0.79	0.195
Erysipelotrichaceae-F	0.00	0.00	0.06	0.03	0.05	0.04	0.03	0.03	0.03	0.03	0.02	0.01	0.488	0.263	0.211	0.955	0.911	0.243
<i>Eubacterium</i>	0.02	0.01	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.181	0.412	NA	NA	NA	NA
<i>Gemella</i>	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.818	NA	NA	NA	NA	NA
<i>Granulicatella</i>	0.13	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.391	0.387	NA	NA	NA	NA
Halanaerobiales-O	0.00	0.00	0.02	0.10	0.04	0.03	0.02	0.03	0.01	0.04	0.00	0.00	NA	0.248	0.231	0.457	0.429	NA
<i>Helcococcus</i>	0.05	0.06	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.846	0.453	0.362	NA	NA	NA
<i>Howardella</i>	0.00	0.03	0.01	0.01	0.02	0.01	0.02	0.02	0.02	0.03	0.01	0.02	0.105	0.326	0.386	0.479	0.229	0.475
<i>Kandleria</i>	0.00	0.00	0.14	0.18	0.05	0.03	0.03	0.02	0.00	0.00	0.00	0.00	NA	0.834	0.303	0.699	0.259	NA
<i>Lachnobacterium</i>	0.00	0.00	0.01	0.00	0.00	0.00	0.02	0.01	0.00	0.01	0.00	0.00	NA	0.333	0.912	0.258	0.602	0.129
<i>Lachnoclostridium</i>	1.15	0.52	0.05	0.08	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.069	0.566	0.188	0.856	0.027	0.176
<i>Lachnoclostridium_10</i>	0.00	0.00	0.04	0.01	0.03	0.02	0.04	0.02	0.05	0.03	0.15	0.07	NA	0.103	0.341	0.263	0.485	0.178
<i>Lachnoclostridium_12</i>	0.00	0.00	0.00	0.00	0.02	0.02	0.03	0.04	0.00	0.01	0.00	0.00	NA	0.276	0.917	0.777	0.182	0.66
<i>Lachnoclostridium_5</i>	0.51	0.16	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.162	NA	0.304	0.276	0.244	0.592
<i>Lachnospira</i>	0.00	0.00	0.00	0.03	0.02	0.00	0.02	0.03	0.00	0.01	0.00	0.00	NA	0.224	0.299	0.368	0.37	NA
<i>Lachnospiraceae_AC2044_group</i>	0.00	0.01	0.20	0.05	0.82	0.28	0.61	0.89	0.57	0.61	0.84	0.40	0.388	0.198	6E-04	0.349	0.858	0.092
<i>Lachnospiraceae_Bacteroides_pectinophilus_group</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.08	0.00	0.00	0.00	NA	NA	NA	NA	0.238	0.304
<i>Lachnospiraceae_Eubacterium_cellulosolvens_group</i>	0.00	0.00	0.06	0.02	0.16	0.05	0.22	0.22	0.02	0.03	0.01	0.01	NA	0.285	0.085	0.954	0.64	0.708
<i>Lachnospiraceae_Eubacterium_eligens_group</i>	0.01	0.01	0.01	0.01	0.07	0.01	0.06	0.05	0.00	0.01	0.00	0.00	0.471	0.962	0.141	0.853	0.322	NA
<i>Lachnospiraceae_Eubacterium_hallii_group</i>	0.00	0.00	0.07	0.32	0.10	0.09	0.14	0.13	0.08	0.07	0.09	0.04	NA	0.313	0.709	0.807	0.733	0.054
<i>Lachnospiraceae_Eubacterium_rectale_group</i>	0.00	0.00	0.02	0.01	0.09	0.03	0.10	0.11	0.02	0.01	0.03	0.02	NA	0.074	0.022	0.907	0.636	0.164

<i>Lachnospiraceae_Eubacterium_ruminantium_group</i>	0.00	0.00	0.12	0.30	0.34	0.53	0.69	0.38	0.10	0.17	0.12	0.08	0.435	0.333	0.462	0.135	0.187	0.314
<i>Lachnospiraceae_Eubacterium_ventriosum_group</i>	0.00	0.00	0.01	0.00	0.03	0.01	0.03	0.04	0.05	0.06	0.10	0.04	NA	0.608	0.015	0.455	0.59	0.029
<i>Lachnospiraceae_Eubacterium_xylanophilum_group</i>	0.00	0.00	0.00	0.01	0.04	0.02	0.06	0.03	0.03	0.04	0.01	0.01	NA	0.389	0.086	0.014	0.608	0.814
<i>Lachnospiraceae_NC2004_group</i>	0.00	0.00	0.00	0.00	0.00	0.03	0.01	0.01	0.00	0.01	0.00	0.00	NA	NA	0.362	0.693	0.14	0.362
<i>Lachnospiraceae_ND3007_group</i>	0.00	0.00	0.00	0.00	0.07	0.01	0.04	0.04	0.05	0.08	0.46	0.34	NA	0.626	0.12	0.98	0.492	0.341
<i>Lachnospiraceae_NK3A20_group</i>	0.00	0.00	3.66	2.09	2.48	1.65	1.39	1.51	0.93	0.82	0.78	0.39	0.071	0.331	0.3	0.849	0.627	0.111
<i>Lachnospiraceae_NK4A136_group</i>	0.01	0.02	0.38	0.44	0.74	3.48	0.48	0.79	0.25	0.26	0.31	0.26	0.469	0.796	0.349	0.247	0.897	0.662
<i>Lachnospiraceae_Ruminococcus_gaureauii_group</i>	0.00	0.00	0.23	0.28	0.18	0.08	0.22	0.12	0.28	0.19	0.13	0.10	NA	0.778	0.011	0.031	0.118	0.391
<i>Lachnospiraceae_Ruminococcus_torques_group</i>	0.00	0.08	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.319	0.249	0.177	0.754	NA	NA
<i>Lachnospiraceae_UCG-001</i>	0.00	0.00	0.01	0.01	0.13	0.13	0.04	0.08	0.01	0.02	0.00	0.00	NA	0.99	0.99	0.229	0.185	0.304
<i>Lachnospiraceae_UCG-006</i>	0.00	0.00	0.01	0.01	0.05	0.03	0.05	0.04	0.05	0.05	0.12	0.04	0.435	0.717	0.181	0.368	0.883	0.044
<i>Lachnospiraceae_UCG-008</i>	0.00	0.00	0.04	0.02	0.06	0.06	0.04	0.04	0.04	0.04	0.06	0.03	NA	0.084	0.996	0.852	0.552	0.054
<i>Lachnospiraceae_UCG-009</i>	0.00	0.02	0.03	0.02	0.08	0.03	0.03	0.04	0.05	0.03	0.13	0.05	0.234	0.627	0.163	0.765	0.248	0.109
<i>Lachnospiraceae_XPB1014_group</i>	0.00	0.00	0.76	0.68	0.23	1.16	0.42	0.48	1.41	0.33	0.73	0.28	0.234	0.847	0.108	0.834	0.237	0.103
Lachnospiraceae-F	4.46	0.18	0.90	0.33	1.05	0.72	0.95	0.77	0.62	0.45	1.21	0.74	0.233	0.082	0.111	0.388	0.103	0.258
Lactobacillales-O	0.04	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.525	NA	NA	NA	NA	NA
<i>Lactobacillus</i>	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.258	0.74	0.514	0.387	NA	NA
<i>Marvinbryantia</i>	0.00	0.00	0.02	0.01	0.04	0.04	0.03	0.03	0.04	0.05	0.02	0.03	NA	0.215	0.721	0.406	0.645	0.463
<i>Megasphaera</i>	0.00	0.19	0.03	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.435	0.609	NA	NA	NA	NA
<i>Mogibacterium</i>	0.00	0.01	0.06	0.03	0.04	0.02	0.01	0.02	0.07	0.06	0.05	0.06	0.435	0.242	0.153	0.670	0.591	0.761
<i>Moryella</i>	0.00	0.00	0.08	0.14	0.07	0.02	0.03	0.03	0.07	0.03	0.05	0.04	NA	0.348	0.008	0.538	0.009	0.711
<i>Negativicoccus</i>	1.89	2.32	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.838	NA	NA	NA	NA	NA
<i>Oribacterium</i>	0.00	0.00	0.02	0.04	0.06	0.04	0.54	0.84	0.03	0.07	0.02	0.01	NA	0.492	0.374	0.702	0.396	0.247
<i>Oscillospira</i>	0.00	0.02	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00	0.00	0.421	0.128	0.187	0.202	0.247	NA
<i>Papillibacter</i>	0.00	0.00	0.04	0.05	0.01	0.01	0.02	0.01	0.03	0.02	0.13	0.06	NA	0.892	0.563	0.054	0.904	0.292
<i>Parvimonas</i>	0.85	0.34	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.484	0.452	NA	NA	0.244	0.304
<i>Peptococcus</i>	0.03	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.347	0.276	NA	NA	NA	NA
<i>Peptoniphilus</i>	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.102	NA	NA	NA	NA	NA

<i>Peptostreptococcus</i>	0.11	0.05	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.147	0.387	NA	0.387	NA	NA
<i>Phascolarctobacterium</i>	0.47	0.43	0.02	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.880	0.873	NA	NA	NA	NA
<i>Pseudobutyrvibrio</i>	0.00	0.03	0.38	0.20	0.84	0.67	0.90	0.62	0.59	0.53	0.72	0.57	0.198	0.015	0.446	0.215	0.645	0.529
<i>Romboutsia</i>	0.01	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.01	0.00	0.02	0.01	0.078	0.480	0.705	0.326	0.026	0.717
<i>Roseburia</i>	0.01	0.00	0.41	0.17	0.56	0.41	0.65	1.38	0.11	0.14	0.12	0.09	0.234	0.188	0.259	0.441	0.507	0.427
<i>Ruminiclostridium_1</i>	0.00	0.00	0.02	0.00	0.01	0.01	0.02	0.01	0.04	0.02	0.06	0.03	NA	0.107	0.498	0.113	0.228	0.086
<i>Ruminiclostridium_6</i>	0.00	0.00	0.03	0.02	0.02	0.02	0.01	0.01	0.02	0.01	0.00	0.01	0.435	0.694	0.504	0.400	0.444	0.231
<i>Ruminiclostridium_9</i>	0.01	0.01	0.18	0.35	8.68	8.13	7.88	9.20	1.48	5.01	0.03	0.02	0.526	0.272	0.862	0.668	0.052	0.654
<i>Ruminococcaceae_NK4A214_group</i>	0.13	0.11	1.87	1.86	2.39	3.12	2.15	2.67	1.05	1.13	1.04	0.60	0.907	0.990	0.338	0.488	0.797	0.049
<i>Ruminococcaceae_UCG-001</i>	0.00	0.00	0.14	0.02	0.08	0.10	0.10	0.06	0.02	0.02	0.02	0.01	NA	0.161	0.739	0.435	0.894	0.519
<i>Ruminococcaceae_UCG-002</i>	0.01	0.02	0.14	0.34	0.05	0.07	0.06	0.07	0.05	0.03	0.04	0.05	0.688	0.182	0.073	0.704	0.569	0.559
<i>Ruminococcaceae_UCG-004</i>	0.02	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.464	0.126	0.391	0.812	0.727	0.988
<i>Ruminococcaceae_UCG-005</i>	0.00	0.02	0.16	0.09	0.12	0.10	0.12	0.07	0.05	0.07	0.14	0.09	0.471	0.168	0.335	0.184	0.481	0.207
<i>Ruminococcaceae_UCG-009</i>	0.00	0.00	0.05	0.03	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.234	0.580	0.129	0.104	0.559	NA
<i>Ruminococcaceae_UCG-010</i>	0.00	0.00	0.35	0.14	0.29	0.23	0.19	0.36	0.56	0.40	0.82	0.59	0.136	0.173	0.469	0.281	0.141	0.071
<i>Ruminococcaceae_UCG-011</i>	0.00	0.00	0.01	0.00	0.06	0.02	0.04	0.02	0.08	0.08	0.33	0.04	NA	0.061	0.029	0.078	0.906	0.302
<i>Ruminococcaceae_UCG-012</i>	0.00	0.00	0.01	0.02	0.01	0.01	0.03	0.02	0.08	0.07	0.06	0.03	NA	0.613	0.520	0.387	0.794	0.070
<i>Ruminococcaceae_UCG-013</i>	0.00	0.00	0.02	0.03	0.01	0.01	0.02	0.04	0.04	0.04	0.03	0.02	0.692	0.319	0.554	0.403	0.928	0.194
<i>Ruminococcaceae_UCG-014</i>	0.01	0.00	1.43	1.15	6.06	4.57	5.38	3.74	1.78	1.83	1.19	0.53	0.260	0.658	0.087	0.039	0.948	0.004
<i>Ruminococcaceae_V9D2013_group</i>	0.00	0.00	0.01	0.01	0.01	0.02	0.01	0.02	0.01	0.00	0.01	0.01	NA	0.772	0.838	0.120	0.791	0.668
<i>Ruminococcaceae-F</i>	3.68	1.29	0.27	0.23	0.61	0.58	0.39	0.44	0.20	0.26	0.18	0.14	0.442	0.300	0.830	0.610	0.358	0.379
<i>Ruminococcus_1</i>	0.11	0.76	0.39	0.39	0.92	0.86	0.73	0.76	0.27	0.60	0.34	0.22	0.417	0.968	0.858	0.855	0.017	0.356
<i>Ruminococcus_2</i>	0.00	0.00	0.60	0.55	0.87	0.84	0.50	0.39	0.43	0.77	0.10	0.07	0.206	0.857	0.912	0.483	0.222	0.352
<i>Saccharofermentans</i>	0.00	0.00	1.19	0.18	1.65	1.36	1.37	1.11	0.47	0.75	1.49	1.00	NA	0.036	0.736	0.383	0.149	0.381
<i>Schwartzia</i>	0.00	0.00	0.00	0.01	0.01	0.00	0.01	0.01	0.01	0.01	0.03	0.01	NA	0.762	0.347	0.788	0.515	0.038
<i>Selenomonas</i>	0.00	0.00	0.00	0.14	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	NA	0.098	0.304	0.464	NA	NA
<i>Selenomonas_1</i>	0.00	0.00	0.06	0.08	0.21	0.28	0.19	0.15	0.16	0.13	0.21	0.08	0.435	0.736	0.433	0.464	0.587	0.126
<i>Sharpea</i>	0.00	0.00	0.40	0.22	0.00	0.00	0.11	0.39	0.00	0.00	0.00	0.00	NA	0.578	0.125	0.520	NA	NA
<i>Shuttleworthia</i>	0.00	0.00	0.02	0.01	0.07	0.08	0.10	0.06	0.01	0.01	0.01	0.01	NA	0.735	0.794	0.279	0.504	0.501
<i>Staphylococcus</i>	0.00	0.02	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.463	0.329	0.574	NA	0.610	NA
<i>Streptococcus</i>	1.63	1.41	0.01	0.01	0.02	0.01	0.03	0.02	0.01	0.01	0.02	0.01	0.898	0.672	0.365	0.866	0.249	0.273
<i>Subdoligranulum</i>	0.02	0.00	0.02	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.095	0.935	NA	NA	NA	NA

<i>Succiniclasticum</i>	0.00	0.00	0.11	0.19	0.09	0.12	0.12	0.09	0.18	0.10	0.42	0.09	NA	0.182	0.508	0.371	0.097	0.072
<i>Syntrophococcus</i>	0.00	0.00	0.03	0.04	0.01	0.01	0.02	0.01	0.01	0.01	0.02	0.01	NA	0.745	0.384	0.105	0.634	0.116
<i>Tyzzerella</i>	0.04	0.21	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.512	NA	NA	NA	NA	NA
<i>Tyzzerella_3</i>	0.01	0.00	0.02	0.01	0.01	0.02	0.03	0.03	0.02	0.02	0.00	0.00	0.266	0.466	0.499	0.984	0.429	0.412
<i>Tyzzerella_4</i>	0.01	0.05	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.517	0.276	NA	NA	NA	0.362
<i>Veillonella</i>	0.03	0.06	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.485	0.105	NA	NA	NA	NA
<i>Veillonellaceae_UCG-001</i>	0.00	0.00	0.01	0.01	0.02	0.01	0.02	0.01	0.03	0.02	0.09	0.03	NA	0.901	0.451	0.655	0.445	0.067
Veillonellaceae-F	0.00	0.00	0.01	0.02	0.04	0.03	0.08	0.05	0.00	0.01	0.01	0.01	NA	0.488	0.695	0.361	0.416	0.437
Fusobacteria	2.44	1.31	0.01	0.01	0.00	0.00	0.02	0.00	0.00	0.00	0.01	0.00	0.368	0.155	0.829	0.281	0.356	0.120
<i>Caviibacter</i>	0.00	0.00	0.01	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.234	0.118	0.862	0.264	0.759	0.993
<i>Fusobacterium</i>	2.43	1.28	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.364	0.934	0.840	0.714	0.244	0.055
<i>Leptotrichia</i>	0.01	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.594	0.450	NA	NA	NA	0.304
Lentisphaerae	0.00	0.00	0.04	0.02	0.02	0.02	0.06	0.03	0.18	0.18	0.62	0.41	0.435	0.393	0.912	0.370	0.995	0.186
Oligosphaeraceae-F	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.02	0.01	NA	NA	0.869	0.387	0.022	0.113
vadinBE97-F	0.00	0.00	0.03	0.02	0.02	0.02	0.06	0.03	0.17	0.17	0.55	0.36	0.435	0.437	0.980	0.337	0.997	0.155
Victivallaceae-F	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.02	0.04	0.05	NA	0.241	0.435	0.211	0.317	0.739
Proteobacteria	25.77	9.38	11.33	8.73	6.85	6.68	4.55	8.16	9.90	9.69	3.04	2.98	0.021	0.614	0.961	0.189	0.938	0.930
<i>Acinetobacter</i>	0.23	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.035	0.500	0.310	0.276	NA	0.362
<i>Actinobacillus</i>	0.25	0.36	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.719	0.981	NA	0.276	NA	0.647
Alphaproteobacteria-C	0.01	0.00	0.02	0.01	0.04	0.09	0.04	0.07	0.14	0.13	0.03	0.02	0.397	0.233	0.221	0.237	0.886	0.492
<i>Alysiella</i>	0.02	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.059	0.244	NA	NA	NA	NA
Betaproteobacteria-C	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.294	0.170	NA	NA	NA	NA
Bradymonadales-O	0.00	0.00	0.00	0.02	0.01	0.00	0.01	0.00	0.00	0.01	0.00	0.01	NA	0.382	0.182	0.169	0.306	0.236
<i>Campylobacter</i>	0.02	0.05	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.384	0.851	0.153	0.035	NA	NA
Comamonadaceae-F	0.08	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.138	0.276	NA	NA	NA	NA
<i>Comamonas</i>	16.08	1.91	0.01	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.037	0.068	0.318	0.276	0.244	NA
<i>Escherichia-Shigella</i>	0.03	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.778	0.387	NA	NA	NA	0.304
<i>Gallibacterium</i>	4.85	5.58	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.749	0.387	NA	0.387	NA	NA
<i>Mannheimia</i>	0.07	0.16	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.530	0.282	NA	NA	NA	NA
<i>Moraxella</i>	0.04	0.11	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.606	NA	NA	0.387	NA	NA
<i>Neisseria</i>	0.06	0.07	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.746	NA	NA	0.276	NA	NA
Neisseriaceae-F	0.07	0.08	0.02	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.940	0.441	NA	0.276	0.420	NA

<i>Parasutterella</i>	0.00	0.01	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.435	0.176	NA	NA	NA	NA	
Pasteurellaceae-F	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.422	0.387	NA	NA	NA	NA	
<i>Pseudomonas</i>	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	NA	0.276	0.663	0.783	NA	0.304	
<i>Psychrobacter</i>	0.05	0.07	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.645	0.202	NA	0.276	NA	NA	
Rhodocyclaceae-F	3.90	0.82	2.45	0.41	0.01	0.01	0.02	0.00	0.00	0.00	0.00	0.00	0.365	0.327	0.521	0.011	0.033	0.583	
Rhodospirillaceae-F	0.00	0.00	2.95	0.59	6.10	6.33	3.12	7.49	8.86	7.92	2.81	2.70	0.234	0.101	0.948	0.122	0.723	0.873	
Rickettsiales-O	0.00	0.00	0.00	0.00	0.02	0.01	0.00	0.08	0.11	0.08	0.11	0.11	NA	0.906	0.896	0.281	0.478	0.985	
<i>Ruminobacter</i>	0.00	0.00	0.04	0.05	0.01	0.03	0.01	0.10	0.10	0.06	0.02	0.03	NA	0.790	0.095	0.354	0.493	0.175	
<i>Sphingomonas</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.02	0.234	0.105	NA	0.368	0.233	0.280	
<i>Stenotrophomonas</i>	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	NA	0.116	0.267	0.387	0.420	0.757	
<i>Succinimonas</i>	0.00	0.00	0.00	0.00	0.01	0.01	0.64	0.01	0.01	0.01	0.00	0.02	NA	0.276	0.724	0.281	0.972	0.042	
<i>Succinivibrio</i>	0.00	0.01	5.62	6.13	0.00	0.01	0.01	0.02	0.01	0.14	0.02	0.01	0.349	0.907	0.084	0.568	0.378	0.704	
<i>Succinivibrionaceae_UCG-001</i>	0.00	0.00	0.04	0.06	0.56	0.03	0.59	0.23	0.00	0.41	0.00	0.00	NA	0.804	0.096	0.251	0.395	NA	
<i>Succinivibrionaceae_UCG-002</i>	0.00	0.00	0.02	0.64	0.07	0.06	0.07	0.10	0.64	0.91	0.01	0.02	NA	0.392	0.747	0.580	0.749	0.644	
Succinivibrionaceae-F	0.00	0.00	0.07	0.76	0.00	0.00	0.00	0.04	0.00	0.00	0.00	0.00	0.435	0.284	NA	0.407	NA	NA	
<i>Sutterella</i>	0.00	0.05	0.00	0.01	0.00	0.03	0.00	0.01	0.01	0.00	0.00	0.01	0.260	0.481	0.091	0.927	0.330	0.602	
Saccharibacteria	0.00	0.00	0.00	0.00	0.05	0.04	0.09	0.03	0.06	0.05	0.07	0.03	NA	0.784	0.556	0.025	0.359	0.060	
Spirochaetae	1.41	4.90	3.75	5.64	1.92	2.60	4.86	5.19	4.66	4.52	4.52	4.24	0.510	0.521	0.067	0.814	0.910	0.841	
<i>Sphaerochaeta</i>	0.02	0.80	0.28	2.30	0.09	0.14	0.08	0.17	0.19	0.14	0.38	0.25	0.436	0.125	0.458	0.328	0.264	0.012	
<i>Spirochaeta_2</i>	0.00	0.00	0.01	0.00	0.01	0.00	0.00	0.00	0.03	0.02	0.03	0.02	NA	0.223	0.125	0.698	0.521	0.258	
Spirochaetaceae-F	0.00	0.00	0.02	0.00	0.00	0.01	0.00	0.00	0.05	0.02	0.01	0.01	NA	0.276	0.212	0.214	0.294	0.482	
<i>Treponema</i>	1.39	4.10	3.44	3.34	1.82	2.46	4.78	5.02	4.40	4.34	4.10	3.96	0.608	0.970	0.101	0.860	0.963	0.924	
Tenericutes	0.18	0.02	0.52	0.40	1.55	1.35	1.52	1.22	1.70	1.14	1.83	1.57	0.071	0.423	0.465	0.314	0.080	0.351	
Anaeroplasma	0.06	0.00	0.09	0.09	0.34	0.16	0.39	0.30	0.84	0.47	0.65	0.88	0.237	0.933	0.045	0.251	0.018	0.173	
Mollicutes-C	0.12	0.01	0.43	0.31	1.20	1.19	1.13	0.93	0.87	0.67	1.19	0.69	0.133	0.338	0.935	0.396	0.329	0.010	
Verrucomicrobia	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.08	0.02	0.02	0.02	0.173	0.300	0.697	0.950	0.159	0.904	
<b>Anaerobic Fungi</b>																			
<i>Anaeromyces</i>	0.00	15.98	0.00	0.16	0.00	0.00	0.00	0.00	0.00	0.00	23.59	4.73	0.356	0.335	NA	NA	NA	0.670	
<i>Caecomycetes</i>	34.67	24.97	59.78	77.99	67.88	64.29	86.95	70.85	27.34	25.82	14.62	12.82	0.738	0.191	0.783	0.209	0.856	0.614	
<i>Cyllamyces</i>	0.00	0.00	0.15	1.64	0.00	4.17	0.00	5.62	29.70	30.06	8.48	17.14	NA	0.165	0.362	0.387	0.977	0.513	
<i>Neocallimastigaceae-F</i>	17.19	58.22	36.04	15.15	21.37	13.27	6.12	18.97	38.56	36.57	19.79	17.95	0.194	0.083	0.404	0.293	0.778	0.262	

<i>Neocallimastix</i>	23.61	0.00	0.07	0.40	0.00	0.01	0.11	0.01	0.74	0.83	0.86	0.70	0.356	0.370	0.185	0.289	0.867	0.613	
<i>Orpinomyces</i>	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.51	26.20	40.74	NA	0.396	NA	NA	0.420	0.876	
<i>Piromyces</i>	24.53	0.83	3.95	4.66	10.75	18.26	6.82	4.54	3.66	6.21	6.47	5.92	0.370	0.840	0.526	0.494	0.527	0.178	
<b>Protozoa</b>																			
<i>Dasytricha</i>	-	-	-	-	-	-	-	-	5.82	0.14	5.79	5.36	-	-	-	-	0.172	0.883	
<i>Diplodinium</i>	-	-	-	-	-	-	-	-	0.88	4.32	9.19	14.52	-	-	-	-	0.187	0.092	
<i>Entodinium</i>	-	-	-	-	-	-	-	-	88.70	94.34	33.05	40.10	-	-	-	-	0.257	0.308	
<i>Eremoplastron</i>	-	-	-	-	-	-	-	-	0.16	0.70	1.87	1.64	-	-	-	-	0.498	0.806	
<i>Eudiplodinium</i>	-	-	-	-	-	-	-	-	0.02	0.02	6.26	6.69	-	-	-	-	0.405	0.893	
<i>Isotricha</i>	-	-	-	-	-	-	-	-	0.00	0.00	5.14	3.83	-	-	-	-	0.861	0.555	
<i>Ophryoscolex</i>	-	-	-	-	-	-	-	-	3.61	0.18	19.56	12.77	-	-	-	-	0.036	0.222	
<i>Polyplastron</i>	-	-	-	-	-	-	-	-	0.35	0.15	3.08	3.34	-	-	-	-	0.098	0.825	
Trichostomatia -C	-	-	-	-	-	-	-	-	0.46	0.15	16.06	11.75	-	-	-	-	0.023	0.100	

Taxa are presented at the highest taxonomic level at which they were classified, F- family, O- order, C-class; P-values represent pairwise comparisons between CONT and 3NOP, within each week. Only taxa that were present at >0.01 in at least one group in a least one week are shown.

<sup>1</sup> n=6 in CONT; n=9 in 3-NOP

<sup>2</sup> n=8 in CONT; n=10 in 3-NOP

<sup>3</sup> n=8 in CONT; n=9 in 3-NOP

<sup>4</sup> n=7 in CONT; n=10 in 3-NOP

Table S7. Protozoa concentration in the rumen fluid of calves at 60 weeks of age as affected by dietary supplementation of 3-NOP.

	CONT	3NOP	SEM	P-value
Total protozoa, log <sub>10</sub> cells/mL	4.96	4.96	0.076	0.98
Entodiniomorphs, log <sub>10</sub> cells/mL				
Small (<100 µm)	4.92	4.93	0.077	0.92
Large (>100 µm)	3.64	3.48	0.173	0.36
Holotrichs, log <sub>10</sub> cells/mL				
Dasytricha	3.11	3.20	0.165	0.58
Isotricha	2.54	2.51	0.270	0.93

N= 8 in CONT; n= 9 in 3-NOP



**Table S8.** Relative abundance of faecal taxa in calves aged 1, 4, 11, 14, 23, and 60 weeks, as affected by dietary supplementation of 3-NOP.

Taxa	Week 1 <sup>1</sup>		Week 4 <sup>2</sup>		Week 11 <sup>2</sup>		Week 14 <sup>3</sup>		Week 23 <sup>4</sup>		Week 60 <sup>2</sup>		P-value					
	CONT	3NOP	CONT	3NOP	CONT	3NOP	CONT	3NOP	CONT	3NOP	CONT	3NOP	1	4	11	14	23	60
<b>Archaea</b>																		
Archaea unclassified	63.91	81.77	41.85	78.45	42.30	14.83	26.27	13.77	16.61	18.49	13.91	15.60	0.54	0.016	0.009	0.061	0.70	0.23
Euryarchaeota unclassified	20.94	17.99	21.99	14.90	26.12	62.96	33.25	73.13	41.10	52.77	45.00	49.27	0.92	0.52	0.019	0.001	0.068	0.21
<i>Methanobrevibacter_boviskoreani_c</i> <i>lade</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	NA	NA	NA	NA	NA	0.36
<i>Methanobrevibacter_gottschalkii_cl</i> <i>ade</i>	15.07	0.01	18.12	0.68	16.31	10.75	12.96	3.83	19.46	11.89	16.52	13.65	0.22	0.016	0.47	0.014	0.13	0.38
<i>Methanobrevibacter_oralis</i>	0.02	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.01	0.01	0.05	0.03	0.22	0.33	0.28	0.41	0.97	0.43
<i>Methanobrevibacter_ruminantium_c</i> <i>lade</i>	0.04	0.00	5.09	0.24	3.73	8.86	15.64	3.68	6.31	5.61	10.11	5.71	0.22	0.17	0.28	0.006	0.64	0.021
<i>Methanobrevibacter_smithii</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	NA	NA	NA	0.41	0.97	NA
<i>Methanobrevibacter_unclassified</i>	0.02	0.02	0.02	0.01	0.04	0.03	0.04	0.32	0.62	0.38	0.65	0.98	0.81	0.43	0.70	0.20	0.49	0.42
<i>Methanosphaera</i>	0.00	0.00	2.57	1.52	2.08	0.81	7.34	1.56	1.29	0.68	0.58	0.26	NA	0.72	0.25	0.094	0.33	0.17
Methanococcales-o	0.00	0.02	7.24	0.00	8.54	1.42	4.48	3.03	4.99	3.43	4.59	3.97	0.48	0.33	0.18	0.57	0.40	0.42
<i>Methanomassiliicoccaceae_Group10</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	NA	NA	NA	NA	0.39	0.30
<i>Methanomassiliicoccaceae_Group11</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	NA	NA	NA	NA	0.53	NA
<i>Methanomassiliicoccaceae_Group12</i>	0.00	0.00	0.01	0.03	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.482	0.37	0.37	0.41	NA	0.11
<i>Methanomassiliicoccaceae_Group3</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.01	0.04	0.05	NA	NA	NA	NA	0.046	0.71
<i>Methanomassiliicoccaceae_Group8</i>	0.00	0.18	0.00	0.00	0.02	0.32	0.00	0.38	5.04	3.55	2.73	3.14	0.48	NA	0.38	0.28	0.44	0.68
<i>Methanomassiliicoccaceae_Group9</i>	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.00	3.32	2.09	4.39	5.15	NA	NA	0.98	NA	0.33	0.51
<i>Methanomassiliicoccaceae_unclasifi</i> <i>ed</i>	0.00	0.00	3.11	4.17	0.83	0.00	0.02	0.01	0.60	0.42	0.82	0.93	NA	0.77	0.30	0.56	0.50	0.54
<b>Bacteria</b>																		
Bacteria_unclassified	0.16	0.07	0.01	0.05	0.01	0.01	0.01	0.01	0.06	0.05	0.10	0.08	0.59	0.044	0.89	0.33	0.21	0.50
Actinobacteria	12.07	7.22	0.21	0.08	0.07	0.03	0.05	0.05	0.09	0.10	0.10	0.07	0.60	0.30	0.39	0.98	0.70	0.85
Bacteroidetes	37.54	28.97	58.99	41.58	44.66	43.75	49.06	46.28	44.28	40.14	41.80	39.91	0.52	0.059	0.79	0.48	0.037	0.48
Cyanobacteria	0.00	0.00	1.11	0.15	0.79	1.08	0.08	0.08	0.57	0.76	0.32	0.41	NA	0.22	0.56	0.96	0.44	0.22
Elusimicrobia	0.00	0.00	0.00	0.00	0.06	0.04	0.01	0.01	0.01	0.01	0.02	0.04	NA	0.13	0.59	0.74	0.64	0.16

Fibrobacteres	0.00	0.00	0.00	0.00	0.40	0.00	0.00	0.00	0.01	0.02	0.00	0.00	NA	NA	0.31	0.83	0.50	NA	
Firmicutes	38.65	29.36	34.55	30.86	50.78	52.63	44.34	49.64	52.73	56.44	55.09	57.38	0.425	0.52	0.51	0.097	0.067	0.49	
Fusobacteria	0.22	9.62	1.30	19.06	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.15	0.027	0.36	NA	NA	NA	
Lentisphaerae	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.02	0.04	0.08	0.11	NA	NA	0.37	0.58	0.15	0.46	
Proteobacteria	11.22	24.74	2.91	8.07	0.87	0.89	0.51	0.86	0.68	0.79	0.37	0.44	0.16	0.006	0.96	0.46	0.66	0.75	
Saccharibacteria	0.00	0.00	0.00	0.00	0.01	0.00	0.01	0.01	0.01	0.02	0.02	0.01	NA	0.30	0.61	0.84	0.17	0.052	
Spirochaetae	0.00	0.00	0.00	0.00	1.55	0.86	5.47	2.33	0.87	0.83	1.66	1.07	NA	NA	0.33	0.12	0.82	0.68	
Tenericutes	0.15	0.00	0.92	0.15	0.80	0.56	0.45	0.69	0.65	0.78	0.40	0.41	0.48	0.070	0.49	0.16	0.28	0.67	
Verrucomicrobia	0.00	0.00	0.00	0.00	0.00	0.15	0.00	0.02	0.01	0.03	0.05	0.07	NA	NA	0.097	0.16	0.13	0.55	
<b>Anaerobic Fungi</b>																			
<i>Anaeromyces</i>	-	-	-	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.34	-	-	NA	NA	NA	0.19	
<i>Caecomycetes</i>	-	-	-	-	19.77	22.19	49.75	75.64	64.01	43.09	33.35	39.86	-	-	0.93	0.41	0.12	0.58	
<i>Cyllamyces</i>	-	-	-	-	0.00	0.00	0.00	0.00	9.40	28.36	18.24	9.82	-	-	NA	NA	0.13	0.34	
<i>Neocallimastix</i>	-	-	-	-	0.00	0.00	0.00	0.00	0.04	0.00	0.01	0.03	-	-	NA	NA	0.30	0.25	
<i>Orpinomyces</i>	-	-	-	-	0.00	0.00	0.00	0.01	0.00	0.00	1.25	0.76	-	-	MA	0.45	NA	0.65	
<i>Piromyces</i>	-	-	-	-	0.00	0.31	0.00	0.36	0.53	0.51	1.54	3.29	-	-	0.39	0.24	0.97	0.31	
<i>Neocallimastigaceae-F</i>	-	-	-	-	80.23	77.49	50.25	24.00	26.03	28.04	4.19	6.25	-	-	0.91	0.41	0.86	0.36	

<sup>1</sup> n=6 in CONT; n=9 in 3-NOP

<sup>2</sup> n=8 in CONT; n=9 in 3-NOP

<sup>3</sup> n=6 in CONT; n=9 in 3-NOP

<sup>4</sup> n=8 in CONT; n=10 in 3-NOP

**Table S9.** Discriminant plasma metabolites identified by untargeted LC-ToF/MS in 14 weeks old calves, as affected by dietary supplementation of 3-NOP

Metabolite	VIP	Rt (min)	FC <sup>1</sup>	P- value	ID level <sup>2</sup>	Ion species	Exact mass	Formula	$\Delta m/z^3$ (ppm)
Methionine	2.47	3.5	0.84	0.024	1	[M+H] <sup>+</sup>	150.0586	C5 H12 O2 N S	1.840
Leu/isol	6.96	3.6	0.93	0.082	1	[M+H] <sup>+</sup>	132.1020	C6 H14 O2 N	0.940
Tyrosine	2.31	3.6	0.87	0.020	1	[M+H] <sup>+</sup>	182.0812	C9 H12 O3 N	0.410
Phenylalanine	2.16	9.7	0.94	0.056	1	[M+H] <sup>+</sup>	166.0862	C9 H12 O2 N	-0.070
Tryptophane	3.14	10.3	0.89	0.151	2	[M+H] <sup>+</sup>	205.0969	C11 H13 O2 N2	-1.191
Glycocholic acid	6.34	13.3	0.49	0.076	2*	[M+H] <sup>+</sup>	466.3160	C26 H44 O6 N	-0.696
	1.22	13.3	0.36	0.082		[M+NH4] <sup>+</sup>	483.3430	C26 H47 O6 N2	0.365
	1.65	13.3	0.50	0.088		[M+Na] <sup>+</sup>	488.2979	C26 H43 O6 N Na	-0.838
	3.59	14.4	0.56	0.014		[M+H-3H2O]	355.2626	C24 H35 O2	-1.624
	6.38	14.4	0.54	0.015		[M+H-2H2O]	373.2732	C24 H37 O3	-1.504
	2.45	14.4	0.54	0.015		[M-H2O+H] <sup>+</sup>	391.2836	C24 H39 O4	-1.549
	1.00	14.4	0.67	0.133		[M+NH4]	426.3209	C24 H44 O5 N	-1.290
Cholic acid	1.94	14.4	0.62	0.022	2*	[M+Na]	431.2764	C24 H40 O5 Na	-1.010
Lyso PC(16:1)	1.13	15.6	0.82	0.217	2	[M+H] <sup>+</sup>	494.3239	C24 H49 O7 N P	-0.436
Lyso PE(18:2)	1.76	15.9	0.76	0.052	2	[M+H] <sup>+</sup>	478.2925	C23 H45 O7 N P	-0.660

<sup>1</sup> Fold change ratio of the average value of treated to that of control.

<sup>2</sup> Identification level: 1 based on retention time, accurate mass and fragmentation pattern compared to analytical standard; 2 obtained by querying in-house database: based on retention time and accurate mass match, and for 2\* also adducts pattern.

<sup>3</sup> Mass error, measured relatively to the theoretical exact mass.