



Table S1. Libraries concentrations measured with Picogreen.

Sample barcode	Animal	ng/uL
193281	199A	80.24
193282	1340A	65.00
193283	1844A	86.09
193284	1717A	38.52
193285	1719A	77.64
193286	1711A	69.72
193287	1718A	49.84
193288	66A	39.54
193289	63A	44.11
193290	68A	45.64
193291	1259A	49.77
193292	965A	70.99
193293	100A	93.02
193294	1842A	84.88
193295	1846A	87.97
193296	1841A	40.65
193297	1713A	82.38
193298	1362A	18.40
193299	1257A	98.72
193300	1258A	47.41
193301	199B	64.32
193302	1340B	62.17
193303	1844B	98.65
193304	1717B	79.46
193305	1719B	93.65
193306	1711B	73.33
193307	1718B	107.97
193308	66B	34.87
193309	63B	63.05
193310	68B	64.08
193311	1259B	80.31
193312	965B	81.75
193313	100B	75.45
193314	1842B	44.98
193315	1846B	92.81
193316	1841B	89.55
193317	1713B	95.59
193318	1362B	87.76
193319	1257B	83.92
193320	1258B	75.71

Table S2. Number of sequences, average length, total Mb, and average quality after trimming.

Group	Animal Num.	Num. Seq	Av. Length	Total Mb	Av. Qual
CON	199	52868	403.52	21.33	37.51
	1340	48964	403.09	19.74	37.38
	1844	44267	405.16	17.94	37.44
	1717	51646	404.58	20.89	37.48
	1719	53744	400.61	21.53	37.37
ALG20	1711	57193	404.6	23.14	37.5
	1718	61984	403.99	25.04	37.46
	66	54085	405.63	21.94	37.45
	63	50066	407.55	20.4	37.46
	68	59904	403.54	24.17	37.5
ALG40	1259	52494	405.53	21.29	37.39
	965	53123	407.55	21.65	37.58
	100	47204	403.61	19.05	37.37
	1842	47633	403.97	19.24	37.3
	1846	43895	395.29	17.35	37.19
ALG60	1841	49339	405.16	19.99	37.36
	1713	47898	399	19.11	37.19
	1362	47504	403.64	19.17	37.47
	1257	91883	399.51	36.71	37.26
	1258	48478	402.26	19.5	37.36
CON	199	51667	402.48	20.79	37.22
	1340	51613	402.49	20.77	37.28
	1844	49443	402.54	19.9	37.32
	1717	54387	403.88	21.97	37.46
	1719	51376	402.72	20.69	37.44
ALG20	1711	52586	403.93	21.24	37.37
	1718	117337	400.75	47.02	37.25
	66	50358	405.21	20.41	37.5
	63	49665	404.43	20.09	37.46
	68	57118	405.53	23.16	37.4
ALG40	1259	50855	404.44	20.57	37.27
	965	56080	401.83	22.53	37.36
	100	51283	404.67	20.75	37.28
	1842	60596	406.08	24.61	37.47
	1846	51023	404.15	20.62	37.42
ALG60	1841	50358	407.2	20.51	37.61
	1713	47381	402.35	19.06	37.38
	1362	47890	402.67	19.28	37.35
	1257	49454	402.37	19.9	37.26
	1258	46574	402.42	18.74	37.39

Table S3. Relative abundance of identified phyla, unmapped bacteria, and no-clustered sequences (no-hit) in the liquid of rumen of the four dietary treatments (CON, ALG20, ALG40, and ALG60) on two sampling points (20th and 40th experimental day).

Phylum	Treatment (T)					Sampling time (S)			Effect ‡		
	CON	ALG20	ALG40	ALG60	SEM†	20	40	SEM†	T	S	T x S
Actinobacteria	0.125 ^a	0.083 ^{ab}	0.076 ^b	0.055 ^b	0.014	0.072 ^a	0.096 ^b	0.008	0.021	0.011	0.324
Bacteroidetes	18.86 ^t	21.91	22.50 ^t	18.92	1.360	19.89	21.19	0.875	0.099	0.272	0.046
Firmicutes	15.66 ^a	12.35 ^b	10.07 ^b	11.19 ^b	0.933	12.82	11.81	0.550	0.004	0.126	0.058
Chloroflexi	0.063 ^a	0.179 ^b	0.141 ^b	0.222 ^b	0.028	0.168	0.134	0.020	0.007	0.297	0.025
Elusimicrobia	0.387	0.147	0.271	0.327	0.058	0.197 ^a	0.368 ^b	0.035	0.056	0.001	0.079
Euryarchaeota	0.106	0.131	0.053	0.078	0.024	0.087	0.097	0.017	0.163	0.662	0.007
Fibrobacteres	1.642	1.792	1.441	1.186	0.269	2.151	0.879	0.151	0.439	<0.001	0.361
Fusobacteria	0.029	0.022	0.015	0.008	0.006	0.021	0.016	0.004	0.116	0.418	0.033
Lentisphaerae	0.162	0.179	0.121	0.174	0.051	0.164	0.154	0.035	0.850	0.788	0.123
Proteobacteria	2.437 ^a	4.762 ^b	5.576 ^b	3.539 ^{ab}	0.654	4.670	3.487	0.423	0.019	0.075	0.025
Spirochaetes	1.291	0.777	0.770	0.860	0.184	1.112 ^a	0.736 ^b	0.120	0.185	0.030	0.234
Synergistetes	1.133 ^a	3.287 ^b	3.288 ^b	2.397 ^b	0.454	2.280	2.772	0.277	0.012	0.116	0.461
Tenericutes	0.508	0.528	0.246	0.482	0.145	0.485	0.398	0.078	0.503	0.324	0.219
Verrucomicrobia	0.003	0.003	0.004	0.002	0.001	0.004	0.002	0.001	0.597	0.057	0.205
Unmapped	43.79	43.44	44.60	47.57	4.895	44.23	45.51	4.32	0.141	0.801	0.454
No-hits	13.82 ^a	10.40 ^b	10.83 ^b	12.95 ^a	0.368	11.65	12.35	0.265	<0.001	0.075	0.451

Means with different superscript (a, b, c, d) between dietary treatments and (a, b) between sampling time differ significantly ($p \leq 0.05$) while, t; trend refers to $p < 0.10$. CON = control concentrate without microalgae; ALG20 = control concentrate with 20 g/Kg *Schizochytrium* sp.; ALG40 = control concentrate with 40 g/ Kg *Schizochytrium* sp.; ALG60 = control concentrate with 60 g/ Kg *Schizochytrium* sp. ‡ Effect: The dietary treatment (T), time (S), and the interaction between dietary treatment x time (TxS) effects were analyzed by ANOVA using a general linear model (GLM) for repeated measures and Post hoc analysis was performed when appropriate using Tukey multiple range test. †SEM: Standard error of the mean.

Table S4. Relative abundance of identified families in the liquid of rumen of the four dietary treatments (CON, ALG20, ALG40, and ALG60) on two sampling points (20th and 40th experimental day).

Family	Treatment (T)					Sampling time (S)			Effect ‡		
	CON	ALG20	ALG40	ALG60	SEM†	20	40	SEM†	T	S	T x S
<i>Prevotellaceae</i>	18.629 ^t	21.737	22.332 ^t	18.756	1.357	19.710	21.017	0.878	0.100	0.270	0.046
<i>Lachnospiraceae</i>	4.157	3.896	3.111	3.386	0.357	3.610	3.665	0.217	0.194	0.847	0.101
<i>Succinivibrionaceae</i>	1.927 ^a	3.704 ^{bc}	4.769 ^c	2.750 ^{ab}	0.648	3.885	2.691	0.423	0.038	0.080	0.029
<i>Ruminococcaceae</i>	3.838 ^a	1.910 ^b	1.513 ^b	2.212 ^b	0.449	2.681 ^a	2.055 ^b	0.261	0.011	0.020	0.080
<i>Spirochaetaceae</i>	1.291	0.777	0.770	0.860	0.184	1.112 ^a	0.736 ^b	0.120	0.185	0.030	0.234
<i>Synergistaceae</i>	1.133 ^a	3.287 ^b	3.288 ^b	2.397 ^{ab}	0.454	2.280	2.772	0.269	0.012	0.116	0.461
<i>Acidaminococcaceae</i>	1.612	2.148	1.860	1.575	0.173	1.907	1.691	0.114	0.112	0.154	0.081
<i>Fibrobacteraceae</i>	1.642	1.792	1.441	1.186	0.269	2.151 ^a	0.789 ^b	0.151	0.439	< 0.001	0.061
<i>Anaeroplasmataceae</i>	0.504	0.526	0.244	0.481	0.145	0.481	0.396	0.075	0.505	0.312	0.251
<i>Selenomonadaceae</i>	1.525	1.747	1.540	1.164	0.300	1.638	1.350	0.201	0.594	0.283	0.731
<i>Hungateiclostridiaceae</i>	0.487 ^t	0.372	0.229 ^t	0.382	0.066	0.473	0.263	0.037	0.089	< 0.001	0.910
<i>Eubacteriaceae</i>	0.514 ^a	0.332 ^b	0.307 ^b	0.333 ^b	0.052	0.376	0.367	0.030	0.046	0.761	0.111
<i>Desulfovibrionaceae</i>	0.210 ^a	0.780 ^b	0.610 ^b	0.610 ^b	0.114	0.574	0.531	0.067	0.018	0.566	0.887
<i>Oscillospiraceae</i>	0.531	0.893	0.795	0.990	0.171	0.682	0.923	0.101	0.296	0.083	0.367
<i>Clostridiales Family XIII. Incertae Sedis</i>	0.278 ^a	0.181 ^b	0.155 ^b	0.165 ^b	0.025	0.165 ^a	0.226 ^b	0.014	0.011	0.001	0.914
<i>Bacteroidaceae</i>	0.168 ^a	0.126 ^b	0.122 ^b	0.130 ^{ab}	0.014	0.136	0.137	0.008	0.050	0.853	0.253
<i>Elusimicrobiaceae</i>	0.201	0.076 ^t	0.190	0.239 ^t	0.044	0.116 ^a	0.237 ^b	0.025	0.090	0.001	0.063
<i>Endomicrobiaceae</i>	0.186 ^a	0.072 ^b	0.081 ^b	0.088 ^b	0.023	0.082	0.131	0.018	0.009	0.128	0.589
<i>Oxalobacteraceae</i>	0.017 ^a	0.075 ^b	0.035 ^{ab}	0.004 ^a	0.016	0.040	0.026	0.009	0.031	0.094	0.739
<i>Clostridiaceae</i>	0.152	0.201	0.105	0.168	0.044	0.154	0.159	0.035	0.502	0.939	0.814
<i>Victivallaceae</i>	0.111	0.151	0.093	0.116	0.046	0.129	0.106	0.024	0.840	0.554	0.661
<i>Methanobacteriaceae</i>	0.104	0.128 ^t	0.046 ^t	0.055 ^t	0.024	0.075	0.091	0.016	0.077	0.455	0.967
<i>Rhodospirillaceae</i>	0.028	0.037	0.031	0.020	0.008	0.025	0.033	0.005	0.602	0.230	0.476
<i>Christensenellaceae</i>	0.229 ^t	0.051 ^t	0.086	0.150	0.048	0.130	0.128	0.028	0.083	0.962	0.758
<i>Anaerolineaceae</i>	0.063 ^a	0.179 ^b	0.141 ^b	0.222 ^b	0.028	0.168	0.134	0.020	0.007	0.297	0.938
<i>Erysipelotrichaceae</i>	0.068 ^a	0.020 ^b	0.015 ^b	0.014 ^b	0.008	0.029	0.030	0.004	< 0.001	0.827	0.651
<i>Fusobacteriaceae</i>	0.024 ^t	0.014	0.012	0.006 ^t	0.005	0.016	0.012	0.003	0.094	0.468	0.919
<i>Oligosphaeraceae</i>	0.052	0.028	0.029	0.057	0.010	0.035	0.047	0.007	0.116	0.201	0.586
<i>Porphyromonadaceae</i>	0.017 ^t	0.009	0.008	0.007	0.003	0.011	0.009	0.002	0.058	0.558	0.647
<i>Atopobiaceae</i>	0.059 ^a	0.019 ^b	0.016 ^b	0.013 ^b	0.006	0.025	0.029	0.004	< 0.001	0.215	0.332
<i>Eggerthellaceae</i>	0.024 ^a	0.014 ^b	0.011 ^b	0.008 ^b	0.002	0.013	0.015	0.001	0.001	0.259	0.463
<i>Moraxellaceae</i>	0.050	0.023	0.012	0.004	0.016	0.024	0.020	0.009	0.240	0.755	0.659
<i>Pasteurellaceae</i>	0.043	0.050	0.022	0.015	0.012	0.026	0.039	0.007	0.158	0.227	0.906
<i>Bifidobacteriaceae</i>	0.028	0.045	0.040	0.022	0.013	0.025 ^a	0.043 ^b	0.007	0.604	0.025	0.344

Means with different superscript (a, b, c, d) between dietary treatments and (A, B) between sampling time differ significantly ($p \leq 0.05$) while, t; trend refers to $p < 0.10$. CON = control concentrate without microalgae; ALG20 = control concentrate with 20 g/Kg *Schizochytrium* sp.; ALG40 = control concentrate with 40 g/Kg *Schizochytrium* sp.; ALG60 = control concentrate with 60 g/Kg *Schizochytrium* sp. ‡ Effect: The dietary treatment (T), time (S), and the interaction between dietary treatment x time (TxS) effects were analyzed by ANOVA using a general linear model (GLM) for repeated measures and Post hoc analysis was performed when appropriate using Tukey multiple range test. †SEM: Standard error of the mean.

Table S5. Relative abundance of most abundant bacteria genera (> 0.06 %) and methanogenic archaea in the liquid of rumen of the four dietary treatments (CON, ALG20, ALG40, and ALG60) on two sampling points (20th and 40th experimental day).

Genera	Treatment (T)					Sampling time (S)			Effect ‡		
	CON	ALG20	ALG40	ALG60	SEM†	20	40	SEM†	T	S	T x S
<i>Prevotella</i>	18.485 ^t	21.607	22.245 ^t	18.666	1.370	19.601	20.901	0.897	0.099	0.271	0.859
<i>Treponema</i>	1.289	0.774	0.769	0.857	0.184	1.110 ^a	0.735 ^b	0.121	0.186	0.030	0.224
<i>Ruminococcus</i>	2.816 ^a	1.443 ^b	1.059 ^b	1.609 ^b	0.377	2.061 ^a	1.403 ^b	0.214	0.026	0.008	0.357
<i>Fretibacterium</i>	1.044 ^a	3.179 ^b	3.189 ^b	2.304 ^{ab}	0.451	2.196	2.663	0.262	0.012	0.133	0.019
<i>Anaerocolumna</i>	0.226	0.058	0.058	0.104	0.081	0.173	0.050	0.032	0.433	0.117	0.854
<i>Ruminobacter</i>	0.837 ^a	1.144 ^{ab}	2.061 ^b	0.677 ^a	0.344	1.292	1.067	0.231	0.049	0.498	0.181
<i>Succiniclasticum</i>	1.611	2.145	1.857	1.573	0.173	1.905	1.688	0.114	0.113	0.152	0.466
<i>Succinivibrio</i>	0.984	2.355	2.499	1.920	0.547	2.341	1.539	0.354	0.237	0.151	0.947
<i>Fibrobacter</i>	1.642	1.792	1.441	1.186	0.269	2.151 ^a	0.879 ^b	0.150	0.439	< 0.001	0.061
<i>Anaeroplasma</i>	0.485	0.492	0.210	0.453	0.144	0.462	0.358	0.072	0.476	0.208	0.219
<i>Butyrivibrio</i>	0.821	0.936 ^t	0.459 ^t	0.802	0.134	0.695	0.813	0.076	0.100	0.121	0.907
<i>Flintibacter</i>	0.908 ^a	0.137 ^b	0.130 ^b	0.152 ^b	0.115	0.373	0.290	0.065	< 0.001	0.188	0.067
<i>Intestinimonas</i>	1.143 ^a	0.348 ^b	0.129 ^b	0.240 ^b	0.090	0.472	0.458	0.068	< 0.001	0.873	0.785
<i>Selenomonas</i>	1.074	0.944	0.920	0.855	0.208	1.036	0.860	0.129	0.898	0.399	0.616
<i>Eubacterium</i>	0.512 ^a	0.332 ^b	0.307 ^b	0.331 ^b	0.052	0.375	0.365	0.030	0.046	0.742	0.112
<i>Lachnoclostridium</i>	0.499 ^{ab}	0.562 ^a	0.349 ^b	0.407 ^b	0.052	0.427	0.481	0.035	0.048	0.263	0.852
<i>Acetatifactor</i>	0.072	0.060	0.052	0.061	0.021	0.071	0.051	0.012	0.920	0.331	0.844
<i>Saccharofermentans</i>	0.326	0.295	0.175	0.286	0.055	0.372 ^a	0.169 ^b	0.032	0.272	< 0.001	0.736
<i>Sporobacter</i>	0.506 ^a	0.197 ^b	0.106 ^b	0.116 ^b	0.069	0.238	0.224	0.040	0.003	0.771	0.640
<i>Desulfovibrio</i>	0.199 ^a	0.772 ^b	0.600 ^b	0.595 ^b	0.115	0.559	0.524	0.069	0.019	0.634	0.857
<i>Kineothrix</i>	0.239	0.315	0.370	0.389	0.071	0.356	0.301	0.051	0.468	0.520	0.723
<i>Pseudobutyrvibrio</i>	0.370	0.361	0.248	0.269	0.050	0.284	0.340	0.029	0.241	0.087	0.521
<i>Succinimonas</i>	0.106	0.195	0.206	0.151	0.080	0.246 ^a	0.083 ^b	0.050	0.808	0.048	0.764
<i>Ethanoligenens</i>	0.126	0.081	0.136	0.112	0.050	0.142	0.085	0.027	0.872	0.106	0.344
<i>Oscillibacter</i>	0.531	0.893	0.795	0.990	0.171	0.682	0.923	0.104	0.293	0.083	0.367
<i>Paraprevotella</i>	0.099	0.027	0.028	0.049	0.029	0.046	0.056	0.017	0.299	0.607	0.595
<i>Neglecta</i>	0.064 ^a	0.007 ^b	0.004 ^b	0.004 ^b	0.012	0.031 ^a	0.008 ^b	0.007	0.007	0.034	0.064
<i>Blautia</i>	0.302 ^a	0.214 ^b	0.156 ^b	0.169 ^b	0.027	0.191	0.230	0.018	0.007	0.108	0.674
<i>Anaerovibrio</i>	0.343 ^a	0.703 ^b	0.517 ^{ab}	0.233 ^a	0.114	0.491	0.408	0.062	0.049	0.269	0.968
<i>Oribacterium</i>	0.182	0.225	0.129	0.165	0.037	0.158	0.192	0.030	0.357	0.489	0.379
<i>Ruminococcaceae;null</i>	0.194	0.122	0.143	0.268	0.051	0.115 ^a	0.248 ^b	0.031	0.225	0.020	0.278
<i>Elusimicrobium</i>	0.201	0.076 ^t	0.190	0.239 ^t	0.044	0.113 ^a	0.237 ^b	0.025	0.090	0.001	0.063
<i>Bacteroides</i>	0.133	0.112	0.118	0.125	0.012	0.124	0.120	0.007	0.651	0.609	0.354
<i>Anaerosporebacter</i>	0.061	0.061	0.076	0.052	0.016	0.081	0.044	0.012	0.779	0.069	0.649
<i>Endomicrobium</i>	0.186 ^a	0.072 ^b	0.081 ^b	0.088 ^b	0.023	0.082	0.131	0.018	0.009	0.128	0.111
<i>Aminipila</i>	0.142	0.099	0.093	0.096	0.018	0.089 ^a	0.126 ^b	0.010	0.219	0.015	0.857
<i>Herbinix</i>	0.117	0.087	0.349	0.068	0.077	0.162	0.148	0.052	0.069	0.854	0.547
<i>Stomatobaculum</i>	0.211 ^a	0.147 ^b	0.131 ^b	0.069 ^c	0.021	0.124	0.155	0.016	0.002	0.215	0.679
<i>Hungateiclostridium</i>	0.093 ^a	0.033 ^b	0.033 ^b	0.065 ^{ab}	0.014	0.062	0.050	0.009	0.018	0.358	0.438
<i>Victivallis</i>	0.111	0.151	0.093	0.116	0.046	0.129	0.106	0.023	0.840	0.554	0.542
<i>Methanobrevibacter</i>	0.102 ^t	0.126 ^t	0.045 ^t	0.054	0.024	0.074	0.089	0.016	0.083	0.472	0.973
<i>Tyzzerella</i>	0.097	0.139	0.108	0.165	0.024	0.143	0.111	0.019	0.225	0.271	0.841
<i>Fusicatenibacter</i>	0.060	0.087	0.060	0.049	0.015	0.064	0.065	0.012	0.352	0.512	0.966
<i>Methanosphaera</i>	0.002	0.002	0.001	0.001	< 0.001	0.001	0.002	< 0.001	0.635	0.416	0.875
<i>Methanomicrobium</i>	0.002 ^t	0.002 ^t	0.06	0.021 ^t	0.005	0.011	0.004	0.003	0.074	0.214	0.323
<i>Methanimicrococcus</i>	nd	nd	0.001	0.002	< 0.001	0.001	0.001	< 0.001	0.016	0.366	0.232
<i>Methanomassiliicoccus</i>	0.001	nd	0.001	nd	< 0.001	0.001	0.001	< 0.001	0.805	0.725	0.343

Means with different superscript (a, b, c, d) between dietary treatments and (A, B) between sampling time differ significantly ($p \leq 0.05$) while, t; trend refers to $p < 0.10$. CON = control concentrate without microalgae; ALG20 = control concentrate with 20 g/Kg *Schizochytrium* sp.; ALG40 = control concentrate with 40 g/Kg *Schizochytrium* sp.; ALG60 = control concentrate with 60 g/Kg *Schizochytrium* sp. ‡ Effect: The dietary treatment (T), time (S), and the interaction between dietary treatment x time (TxS) effects were

analyzed by ANOVA using a general linear model (GLM) for repeated measures and Post hoc analysis was performed when appropriate using Tukey multiple range test. †SEM: Standard error of the mean. Denote the yellow highlighted genera were used in discriminant analyses (Figure 1).

Table S6. Relative abundance of most abundant bacteria species and methanogenic archaea in the liquid of rumen of the four dietary treatments (CON, ALG20, ALG40, and ALG60) on two sampling points (20th and 40th experimental day).

Species	Treatment (T)					Sampling time (S)			Effect ‡		
	CON	ALG20	ALG40	ALG60	SEM†	20	40	SEM†	T	S	T x S
<i>Prevotella ruminicola</i>	9.789	11.299	11.560	9.244	1.162	10.366	10.580	0.700	0.440	0.802	0.801
<i>Fretibacterium fastidiosum</i>	1.044 ^a	3.179 ^b	3.189 ^b	2.304 ^b	0.451	2.196	2.663	0.268	0.012	0.133	0.019
<i>Prevotella brevis</i>	1.339 ^t	1.526 ^t	2.216	2.589 ^t	0.374	2.006	1.829	0.202	0.097	0.575	0.343
<i>Prevotella oralis</i>	0.959	1.799	1.643	1.517	0.258	1.422	1.536	0.166	0.153	0.614	0.548
<i>Ruminobacter amylophilus</i>	0.837 ^a	1.144 ^{ab}	2.061 ^b	0.677 ^a	0.344	1.292	1.067	0.231	0.050	0.498	0.908
<i>Succinoclasticum ruminis</i>	1.611 ^t	2.145 ^t	1.857	1.573 ^t	0.173	1.905	1.688	0.113	0.098	0.152	0.710
<i>Succinivibrio dextrinosolvens</i>	0.984 ^a	2.355 ^b	2.499 ^b	1.920 ^{ab}	0.547	2.341	1.539	0.358	0.042	0.151	0.947
<i>Fibrobacter succinogenes</i>	1.620	1.692	1.432	1.186	0.270	2.096 ^a	0.869 ^b	0.150	0.566	< 0.001	0.126
<i>Treponema bryantii</i>	0.551 ^a	0.279 ^b	0.187 ^b	0.292 ^b	0.045	0.368 ^a	0.283 ^s	0.025	< 0.001	0.047	0.075
<i>Ruminococcus bromii</i>	1.837 ^a	0.787 ^b	0.574 ^b	0.734 ^b	0.304	1.240 ^a	0.726 ^b	0.172	0.037	0.020	0.751
<i>Prevotella corporis</i>	0.516	0.367	0.437	0.502	0.266	0.607	0.303	0.155	0.977	0.186	0.433
<i>Treponema saccharophilum</i>	0.312	0.293	0.360	0.249	0.115	0.400	0.207	0.078	0.921	0.077	0.403
<i>Anaeroplasmia abactoclasticum</i>	0.199	0.329	0.119	0.384	0.112	0.315	0.200	0.058	0.356	0.120	0.337
<i>Butyrivibrio proteoclasticus</i>	0.474	0.505	0.212	0.498	0.142	0.365	0.483	0.078	0.446	0.103	0.722
<i>Prevotella copri</i>	1.861	1.307	1.779	1.657	0.403	1.468	1.834	0.241	0.778	0.163	0.729
<i>Flintibacter butyricus</i>	0.908 ^a	0.137 ^b	0.130 ^b	0.152 ^b	0.115	0.373	0.290	0.065	< 0.001	0.188	0.067
<i>Intestinimonas butyriciproducens</i>	1.143 ^a	0.348 ^b	0.129 ^b	0.240 ^b	0.090	0.472	0.458	0.066	< 0.001	0.873	0.785
<i>Prevotella shahii</i>	0.805 ^{ab}	1.573 ^a	0.464 ^b	0.220 ^b	0.297	0.873	0.658	0.167	0.028	0.269	0.069
<i>Acetatifactor muris</i>	0.072	0.060	0.052	0.061	0.021	0.071	0.051	0.012	0.920	0.331	0.844
<i>Saccharofermentans acetigenes</i>	0.326	0.295	0.175	0.286	0.055	0.372 ^a	0.169 ^b	0.033	0.275	< 0.001	0.736
<i>Sporobacter termitidis</i>	0.506 ^a	0.197 ^b	0.106 ^b	0.116 ^b	0.069	0.238	0.224	0.041	0.003	0.771	0.640
<i>Kineothrix alysoides</i>	0.239	0.315	0.370	0.389	0.071	0.356	0.301	0.050	0.468	0.520	0.723
<i>Pseudobutyrvibrio ruminis</i>	0.368	0.360	0.247	0.268	0.050	0.283	0.339	0.033	0.240	0.087	0.516
<i>Succinimonas amylolytica</i>	0.106	0.195	0.206	0.151	0.080	0.246 ^a	0.083 ^b	0.050	0.808	0.048	0.764
<i>Ethanoligenens harbinense</i>	0.126	0.081	0.136	0.112	0.050	0.142	0.085	0.027	0.872	0.106	0.344
<i>Paraprevotella clara</i>	0.099	0.026	0.028	0.049	0.029	0.045	0.055	0.018	0.296	0.590	0.597
<i>Treponema ruminis</i>	0.321	0.165	0.180	0.260	0.074	0.284	0.181	0.049	0.420	0.150	0.675
<i>Desulfovibrio desulfuricans</i>	0.085 ^a	0.543 ^b	0.452 ^b	0.324 ^{ab}	0.111	0.379	0.323	0.063	0.049	0.407	0.606
<i>Eubacterium coprostanoligenes</i>	0.260 ^a	0.162 ^a	0.161 ^a	0.146 ^a	0.032	0.188	0.177	0.020	0.078	0.624	0.190
<i>Ruminococcus flavefaciens</i>	0.271 ^a	0.158 ^{ab}	0.097 ^b	0.268 ^a	0.040	0.190	0.208	0.023	0.016	0.494	0.463
<i>Anaerovibrio lipolyticus</i>	0.343 ^a	0.703 ^b	0.517 ^{ab}	0.233 ^a	0.114	0.491	0.408	0.062	0.049	0.269	0.968
<i>Ruminococcus gauvreauii</i>	0.179 ^t	0.105	0.069 ^t	0.110	0.027	0.151 ^a	0.080 ^b	0.019	0.070	0.017	0.162
<i>Oribacterium asaccharolyticum</i>	0.146	0.164	0.108	0.149	0.036	0.127	0.157	0.030	0.729	0.531	0.288
<i>Oscillibacter valericigenes</i>	0.154	0.483	0.500	0.699	0.158	0.437	0.482	0.090	0.178	0.683	0.536
<i>Elusimicrobium minutum</i>	0.201	0.076 ^t	0.190	0.239 ^t	0.044	0.116 ^a	0.237 ^b	0.026	0.090	0.001	0.063
<i>Selenomonas ruminantium</i>	0.586	0.292	0.251	0.204	0.146	0.413	0.283	0.091	0.283	0.302	0.827
<i>Prevotella micans</i>	0.278	0.467	0.267	0.069	0.131	0.227	0.314	0.101	0.241	0.589	0.851
<i>Ruminococcus albus</i>	0.243 ^t	0.171	0.131 ^t	0.195	0.037	0.204 ^a	0.167 ^b	0.020	0.099	0.036	0.600
<i>Anaerosporeobacter mobilis</i>	0.061	0.061	0.076	0.052	0.016	0.081	0.044	0.012	0.779	0.069	0.614
<i>Prevotella marshii</i>	0.043 ^t	0.133 ^t	0.081	0.072	0.026	0.104	0.061	0.020	0.100	0.206	0.908
<i>Eubacterium siraeum</i>	0.119	0.073	0.086	0.213	0.047	0.070 ^a	0.176 ^b	0.026	0.187	0.039	0.310
<i>Clostridium clostridioforme</i>	0.093	0.157	0.113	0.058	0.030	0.078	0.138	0.022	0.183	0.109	0.238
<i>Endomicrobium proavitum</i>	0.186 ^a	0.072 ^b	0.081 ^b	0.088 ^b	0.023	0.082	0.131	0.017	0.009	0.128	0.111
<i>Prevotella amnii</i>	0.032	0.177	0.096	0.404	0.119	0.199	0.155	0.087	0.176	0.772	0.578
<i>Aminipila butyrica</i>	0.142	0.099	0.093	0.096	0.018	0.089 ^a	0.126 ^b	0.009	0.213	0.015	0.857
<i>Prevotella oulorum</i>	0.216	0.163	0.530	0.210	0.213	0.211	0.349	0.120	0.608	0.125	0.572

<i>Ruminococcus champanellensis</i>	0.210	0.173	0.135	0.257	0.048	0.217	0.171	0.026	0.356	0.054	0.501
<i>Prevotella buccalis</i>	0.200	0.249	0.150	0.188	0.053	0.176	0.218	0.036	0.636	0.353	0.606
<i>Herbinix luporum</i>	0.117 ^t	0.086	0.343 ^t	0.067 ^t	0.077	0.162	0.147	0.052	0.068	0.854	0.543
<i>Oscillibacter ruminantium</i>	0.376	0.410	0.295	0.291	0.123	0.245 ^a	0.441 ^b	0.074	0.871	0.009	0.688
<i>Prevotella oris</i>	0.267	0.800	0.410	0.161	0.226	0.243	0.575	0.120	0.246	0.122	0.252
<i>Stomatobaculum longum</i>	0.211 ^a	0.147 ^b	0.131 ^b	0.069 ^c	0.021	0.124	0.155	0.016	0.002	0.215	0.679
<i>Victivallis vadensis</i>	0.111	0.151	0.093	0.116	0.046	0.129	0.106	0.022	0.840	0.554	0.661
<i>Desulfovibrio intestinalis</i>	0.041 ^a	0.153 ^b	0.099 ^{ab}	0.215 ^b	0.039	0.120	0.134	0.026	0.036	0.683	0.840
<i>Prevotella paludivovensis</i>	0.086	0.074	0.092	0.048	0.017	0.063	0.087	0.010	0.306	0.064	0.030
<i>Prevotella stercorea</i>	0.169	0.293	0.390	0.433	0.126	0.437	0.206	0.075	0.480	0.109	0.340
<i>Selenomonas lacticifex</i>	0.015	0.028	0.028	0.038	0.010	0.032	0.023	0.005	0.440	0.196	0.608
<i>Blautia luti</i>	0.121 ^a	0.059 ^b	0.087 ^{ab}	0.052 ^b	0.016	0.079	0.078	0.012	0.034	0.963	0.089
<i>Clostridium asparagiforme</i>	0.104	0.156	0.046	0.076	0.033	0.095	0.096	0.020	0.144	0.973	0.714
<i>Euscatenibacter saccharivorans</i>	0.060	0.087	0.060	0.049	0.015	0.064	0.065	0.013	0.352	0.966	0.512
<i>Butyrivibrio hungatei</i>	0.294	0.375	0.222	0.289	0.056	0.309	0.281	0.047	0.322	0.719	0.718
<i>Selenomonas flueggei</i>	0.097	0.176	0.148	0.132	0.056	0.179	0.098	0.037	0.788	0.092	0.541
<i>Anaerotaenia torta</i>	0.080	0.051	0.035	0.058	0.017	0.070 ^a	0.042 ^b	0.009	0.356	0.046	0.294
<i>Murimonas intestini</i>	0.078	0.056	0.044	0.053	0.010	0.054	0.061	0.007	0.123	0.454	0.069
<i>Prevotella colorans</i>	0.133	0.071	0.084	0.066	0.042	0.096	0.081	0.024	0.676	0.622	0.809
<i>Methanobrevibacter thaueri</i>	0.027	0.042	0.012	0.016	0.013	0.012	0.037	0.008	0.377	0.078	0.079
<i>Butyrivibrio fibrisolvens</i>	0.048	0.055	0.018	0.014	0.015	0.021	0.047	0.009	0.161	0.065	0.869
<i>Faecalicatena orotica</i>	0.077	0.020	0.012	0.009	0.007	0.028	0.031	0.005	< 0.001	0.759	0.953
<i>Hungateiclostridium alkalicellulosi</i>	0.048 ^a	0.004 ^b	0.009 ^b	0.021 ^b	0.009	0.019	0.022	0.006	0.016	0.784	0.981
<i>Prevotella dentalis</i>	0.123	0.073	0.437	0.074	0.152	0.096	0.257	0.075	0.310	0.315	0.180
<i>Ruminococcus faecis</i>	0.031	0.026	0.023	0.021	0.005	0.033 ^a	0.018 ^b	0.003	0.569	0.003	0.878
<i>Anaerocolumna cellulolytica</i>	0.067	0.049	0.050	0.056	0.015	0.070	0.041	0.008	0.812	0.066	0.955
<i>Ihubacter massiliensis</i>	0.060 ^a	0.041 ^b	0.030 ^b	0.032 ^b	0.007	0.034 ^a	0.048 ^b	0.004	0.018	0.025	0.757
<i>Eubacterium ruminantium</i>	0.075	0.094	0.088	0.103	0.025	0.088	0.092	0.015	0.887	0.797	0.078
<i>Prevotella melaninogenica</i>	0.235	0.337	0.498	0.236	0.201	0.316	0.337	0.121	0.769	0.907	0.061
<i>Coprococcus eutactus</i>	0.055	0.034	0.031	0.042	0.009	0.044	0.037	0.006	0.288	0.463	0.249
<i>Prevotella bryantii</i>	0.157	0.046	0.028	0.033	0.027	0.049	0.083	0.017	0.010	0.273	0.249
<i>Ruminococcus lactaris</i>	0.032 ^a	0.010 ^b	0.006 ^b	0.006 ^b	0.003	0.013	0.014	0.003	< 0.001	0.770	0.981
<i>Prevotella loeschei</i>	0.331	0.034	0.186	0.140	0.114	0.102	0.243	0.080	0.355	0.317	0.883
<i>Tyzzerella nexilis</i>	0.081	0.078	0.035	0.090	0.017	0.069	0.073	0.012	0.141	0.845	0.885
<i>Eubacterium hallii</i>	0.055	0.044	0.029	0.040	0.011	0.042	0.042	0.006	0.462	0.965	0.365
<i>Eubacterium oxidoreducens</i>	0.062 ^a	0.008 ^b	0.007 ^b	0.012 ^b	0.012	0.027	0.017	0.007	0.013	0.183	0.275
<i>Selenomonas diana</i>	0.046	0.079	0.089	0.092	0.016	0.070	0.082	0.012	0.183	0.544	0.043
<i>Selenomonas noxia</i>	0.181	0.080	0.123	0.175	0.058	0.162	0.118	0.040	0.580	0.495	0.736
<i>Clostridium colinum</i>	0.016	0.062	0.072	0.076	0.016	0.074	0.039	0.011	0.062	0.051	0.381
<i>Clostridium methylpentosum</i>	0.050	0.034	0.040	0.013	0.017	0.020	0.049	0.011	0.505	0.118	0.777
<i>Lachnoclostridium pacaense</i>	0.032	0.041	0.041	0.065	0.009	0.050	0.039	0.007	0.113	0.353	0.458
<i>Hungateiclostridium straminisolvans</i>	0.015	0.010	0.004	0.007	0.004	0.010	0.008	0.002	0.296	0.179	0.379
<i>Selenomonas sputigena</i>	0.097 ^t	0.247 ^t	0.247 ^t	0.152	0.046	0.131 ^a	0.241 ^b	0.034	0.092	0.045	0.541
<i>Abyssivirga alkaniphila</i>	0.048 ^a	0.024 ^b	0.015 ^b	0.012 ^b	0.004	0.026	0.023	0.003	< 0.001	0.585	0.581
<i>Clostridium scindens</i>	0.042 ^a	0.017 ^b	0.009 ^b	0.010 ^b	0.005	0.020	0.019	0.003	0.001	0.588	0.688
<i>Bacteroides stercoris</i>	0.017	0.014	0.015	0.012	0.002	0.015	0.014	0.001	0.473	0.322	0.378
<i>Bacteroides vulgatus</i>	0.014	0.011	0.016	0.015	0.003	0.013	0.015	0.002	0.602	0.401	0.486
<i>Pseudoflavonifractor phocaensis</i>	0.024	0.006	0.009	0.032	0.009	0.014	0.021	0.005	0.192	0.426	0.557
<i>Prevotella denticola</i>	0.124	0.006	0.012	0.008	0.055	0.036	0.039	0.027	0.376	0.109	0.244
<i>Prevotella saccharolytica</i>	0.019	0.060	0.048	0.027	0.017	0.037	0.040	0.009	0.321	0.863	0.597
<i>Selenomonas bovis</i>	0.042	0.031	0.025	0.028	0.013	0.034	0.030	0.009	0.774	0.769	0.571
<i>Solobacterium moorei</i>	0.037 ^a	0.010 ^b	0.006 ^b	0.006 ^b	0.006	0.016	0.013	0.004	0.004	0.766	0.507
<i>Faecalibacterium prausnitzii</i>	0.025	0.014	0.019	0.016	0.004	0.020	0.017	0.003	0.279	0.326	0.100
<i>Prevotella dentasini</i>	0.023	0.005	0.012	0.005	0.006	0.014	0.008	0.003	0.178	0.339	0.737
<i>Clostridium lavalense</i>	0.018	0.022	0.016	0.054	0.014	0.028	0.026	0.007	0.204	0.828	0.740

<i>Eubacterium rectale</i>	0,015	0,012	0,016	0,020	0,005	0,009 ^a	0,022b	0,002	0,672	0,006	0.637
<i>Lachnoanaerobaculum orale</i>	0,006 ^a	0,014	0,024	0,064b	0,014	0,035	0,019	0,010	0,051	0,326	0.890
<i>Mitsuokella multacida</i>	0,066	0,078	0,073	0,060	0,014	0,081	0,058	0,008	0,846	0,132	0,876
<i>Clostridium aminophilum</i>	0,048	0,066	0,043	0,060	0,009	0,044 ^a	0,065b	0,006	0,312	0,007	0.936
<i>Ruminococcus callidus</i>	0,014	0,011	0,021	0,018	0,008	0,013	0,019	0,004	0,811	0,165	0,933
<i>Prevotella maculosa</i>	0,058	0,166	0,326	0,140	0,152	0,082	0,263	0,081	0,657	0,236	0,458
<i>Ruminiclostridium cellulolyticum</i>	0,021	0,016	0,007	0,009	0,005	0,012	0,015	0,004	0,176	0,727	0,894
<i>Clostridium leptum</i>	0,018	0,005	0,006	0,028	0,012	0,012	0,017	0,006	0,453	0,495	0,304
<i>Clostridium saudiense</i>	0,003	0,003	0,003	0,003	0,001	0,004 ^a	0,001b	0,001	0,976	0,001	0.721
<i>Collinsella aerofaciens</i>	0,006	0,002	0,003	0,004	0,001	0,005	0,003	0,001	0,167	0,407	0,040
<i>Clostridium populeti</i>	0,021	0,025	0,014	0,013	0,007	0,018	0,018	0,004	0,566	0,959	0,326
<i>Clostridium xylanolyticum</i>	0,027	0,026	0,007	0,022	0,008	0,030 ^a	0,011b	0,004	0,330	0,001	0.104
<i>Methanobrevibacter olleyae</i>	0,006 ^a	0,001b	0,000b	0,000b	<0,001	0,002	0,002	<0,001	<0,001	0,295	0.084
<i>Methanobrevibacter millerae</i>	0,066	0,075	0,027	0,033	0,021	0,056	0,044	0,013	0,336	0,481	0,053
<i>Methanomicrobium mobile</i>	0,002 ^a	0,002 ^a	0,006 ^a b	0,021b	0,005	0,011	0,004	0,003	0,074	0,214	0,323
<i>Ruminococcus gnavus</i>	0,005	0,007	0,004	0,011	0,002	0,008	0,006	0,001	0,160	0,377	0,175
<i>Ruminococcus torques</i>	0,003	0,002	0,002	0,001	0,001	0,002	0,002	0,001	0,666	0,703	0,215
<i>Streptococcus pharyngis</i>	0,003	0,001	0,001	<0,001	0,001	0,002	0,001	<0,001	0,127	0,297	0,288
<i>Methanobrevibacter boviskoreani</i>	0,003	0,004	0,004	0,003	0,002	0,002	0,005	0,001	0,957	0,216	0,890
<i>Methanimicrococcus blatticola</i>	<0,001 ^a	<0,001 ^a	0,001 ^a b	0,002b	<0,001	0,001	0,001	<0,001	0,016	0,366	0,232
<i>Methanobrevibacter ruminantium</i>	-	-	-	-	-	-	-	-	-	-	-
<i>Methanobrevibacter smithii</i>	-	-	-	-	-	-	-	-	-	-	-
<i>Methanomassiliicoccus luminyensis</i>	0,001	0,000	0,001	0,000	<0,001	0,000	0,001	<0,001	0,805	0,725	0,343
<i>Methanobrevibacter boviskoreani</i>	0,003	0,004	0,004	0,003	0,002	0,002	0,005	0,001	0,957	0,216	0,890
<i>Methanospaera stadtmannae</i>	0,002	0,002	0,001	0,001	0,001	0,001	0,002	<0,001	0,635	0,416	0,762

Means with different superscript (a, b, c, d) between dietary treatments and (A, B) between sampling time differ significantly ($p \leq 0.05$) while, t; trend refers to $p < 0.10$. CON = control concentrate without microalgae; ALG20 = control concentrate with 20 g/Kg *Schizochytrium* sp.; ALG40 = control concentrate with 40 g/Kg *Schizochytrium* sp.; ALG60 = control concentrate with 60 g/Kg *Schizochytrium* sp. ‡ Effect: The dietary treatment (T), time (S), and the interaction between dietary treatment x time (TxS) effects were analyzed by ANOVA using a general linear model (GLM) for repeated measures and Post hoc analysis was performed when appropriate using Tukey multiple range test. †SEM: Standard error of the mean Yellow highlighted; species used as proteolytic (Figure 4A,B). Blue highlighted; species used as amylolytic (Figure 5A,B). Green highlighted; species used as cellulolytic (Figure 6A,B). Grey highlighted; species used as other important bacteria (Figure 7). Purple highlighted; species used as methanogenic (Figure 8).

Table S7. Ingredients of concentrate (g/Kg), average feed consumption (g/goat/day), intake of nutrients and fatty acids (g/goat) of the four diets.

Ingredients (g/Kg)	Concentrate			
Maize grain	367			
Barley grain	200			
Wheat middlings	210			
Sunflower meal	80			
Soybean meal	100			
Calcium phosphate	15			
Calcium carbonate	5			
Salt	3			
Mineral and vitamin	20			
Daily feed consumption (g/goat)	CON	ALG20	ALG40	ALG60
Alfalfa hay	1000	1000	1000	1000
Concentrate	1000	1000	1000	670*
Daily intake of nutrients (g/goat)				
Dry matter	1849	1854	1854	1547
Crude protein	260	261	261	219
Ether extract	56	70	76	66
Crude fiber	369	371	371	357
NDF	660	655	652	621

ADF	442	437	438	424
<i>Fatty acids intake (g/goat/day)</i>				
C _{14:0}	0.34	1.10	2.06	3.08
C _{16:0}	10.26	12.77	15.88	14.01
C _{18:0}	2.43	2.58	2.46	2.08
^{Cis-9} C _{18:1}	17.03	18.49	16.75	13.05
C _{18:2 n-6}	21.58	24.23	23.03	18.57
C _{18:3 n-3}	2.78	3.47	3.38	2.90
C _{22:5 n-6}	-	1.65	3.34	3.28
C _{22:6 n-3}	-	4.16	8.44	8.20

*denotes that concentrate were decreased in ALG60 by 33%. CON = control concentrate without microalgae (*Schizochytrium sp.*); ALG20 = CON with 20 g/Kg *Schizochytrium sp.*; ALG40 = CON with 40 g/Kg.; ALG60 = CON with 60 g/Kg *Schizochytrium sp.*; NDF = Neutral detergent fiber; ADF = Acid detergent fiber.

Table S8. Effect of supplementing microalgae *Schizochytrium* sp on pH, ammonia concentration, α -amylase, protease, cellulase, and xylanase activity in the liquid of rumen of the four dietary treatments (CON, ALG20, ALG40, and ALG60) on two sampling points (20th and 40th experimental day).

	Treatment (T)					Sampling time (S)			Effect†		
	CON	ALG20	ALG40	ALG60	SEM†	20	40	SEM†	T	S	T * S
Protease activity (U/mL) ^a	0.106	0.142	0.144	0.137	0.019	0.114	0.150	0.015	0.456	0.234	0.991
α -Amylase activity (U/mL) ^b	2.738 ^a	2.784 ^a	3.483 ^b	2.822 ^a	0.207	2.837	3.077	0.148	0.048	0.313	0.641
Cellulose activity (U/mL/h) ^c	11.29 ^a	11.07 ^{ab}	10.28 ^b	9.76 ^b	0.450	9.95 ^a	11.25 ^b	0.287	0.050	0.008	0.248
Xylanase (U/mL/h) ^d	8.09	8.32	8.75	7.72	0.400	8.13	8.31	0.247	0.356	0.555	0.599
NH ₃ -N mg/L	123.7 ^a	124.1 ^a	93.3 ^b	114.0 ^a	6.137	105.1A	122.5B	4.201	0.008	0.008	0.018
pH	7.30	7.36	7.12	7.24	0.057	7.24	7.27	0.044	0.120	0.703	0.868

Means with different superscript (a, b, c, d) between dietary treatments and (A, B) between sampling time differ significantly ($p \leq 0.05$). CON = control concentrate without microalgae; ALG20 = control concentrate with 20 g/Kg *Schizochytrium* sp.; ALG40 = control concentrate with 40 g/Kg *Schizochytrium* sp.; ALG60 = control concentrate with 60 g/Kg *Schizochytrium* sp. † Effect: The dietary treatment (T), time (S), and the interaction between dietary treatment x time (TxS) effects were analyzed by ANOVA using a general linear model (GLM) for repeated measures and Post hoc analysis was performed when appropriate using Tukey multiple range test. †SEM: Standard error of the mean a Units/mL = $[(\mu\text{mol of protein equivalent to ABS}) \times (\text{total volume of reaction in mL}) \times (\text{dilution factor})] / [(\text{incubation time in minutes}) \times (\text{volume of colorimetric determination in mL}) \times (\text{volume of rumen sample in mL})]$. b One unit of α -amylase activity will liberate 1.0 mg of maltose from starch in 10 min at pH 6.9 at 39 °C. c One unit of cellulase activity based on endo-cellulase (*A. niger*) clearance activity in 24h incubation at 50 °C. d One unit of xylanase activity based on endo-1-4-beta-Xylanase M1 (*T. viride*) clearance activity in 24h incubation at 37 °C.

Table S9. The mean individual fatty acids (FA) (% of total FA) of goats' rumen fluid of the four dietary treatments (CON, ALG20, ALG40, and ALG60) on two sampling points (20th and 40th experimental day).

	Treatment (T)					Sampling time (S)			Effect †		
	CON	ALG20	ALG40	ALG60	SEM†	20	40	SEM†	T	S	TxS
C _{14:0}	1.61 ^a	2.86 ^b	3.74 ^c	4.37 ^d	0.142	3.16	3.13	0.101	<0.001	0.857	0.367
C _{14:1}	1.06	1.51	1.11	1.24	0.117	1.21	1.24	0.087	0.056	0.732	0.002
C _{15:0}	1.06	1.36	0.92	0.96	0.100	0.99	1.16	0.060	0.022	0.093	0.019
C _{16:0}	26.64 ^a	29.36 ^b	25.27 ^a	25.22 ^a	0.545	25.26 ^A	27.98 ^B	0.345	<0.001	<0.001	0.008
C _{16:1}	0.209	0.512	0.324	0.612	0.113	0.305 ^A	0.524 ^B	0.069	0.082	0.021	0.398
C _{18:0}	44.27 ^a	6.62 ^b	3.67 ^b	3.39 ^b	1.483	14.75	14.23	0.821	<0.001	0.509	0.113
trans C _{18:1}	1.48 ^a	3.06 ^b	2.08 ^a	1.85 ^a	0.283	2.25	1.94	0.159	0.005	0.295	0.159
trans-11 C _{18:1}	4.80 ^a	27.47 ^b	25.84 ^b	23.14 ^b	1.212	21.96 ^A	18.66 ^B	0.702	<0.001	<0.001	<0.001
trans-10 C _{18:1}	0.00 ^a	2.18 ^b	1.64 ^b	1.59 ^b	0.138	1.50 ^A	1.21 ^B	0.098	<0.001	<0.001	0.241
cis-9 C _{18:1}	9.86 ^a	12.32 ^b	9.65 ^a	8.34 ^a	0.552	9.19 ^A	10.91 ^B	0.345	0.001	<0.001	0.241
C _{18:2 n-6 cis}	6.23 ^a	4.53 ^{ab}	3.77 ^b	3.18 ^b	0.509	4.07	4.79	0.321	0.003	0.104	0.262
C _{18:3 n-3}	1.27	1.01	0.98	1.04	0.268	0.816	1.34	0.191	0.866	0.058	0.305
C _{18:2 conjugated}	1.07	1.43	1.36	1.25	0.181	0.969 ^A	1.59 ^B	0.102	0.521	0.001	0.278
C _{22:5 n-6}	0.00 ^a	2.32 ^b	6.81 ^c	8.33 ^d	0.248	4.64 ^A	4.09 ^B	0.191	<0.001	0.034	0.010
C _{22:6 n-3}	0.00 ^a	3.08 ^b	12.72 ^c	15.32 ^d	0.547	8.70 ^A	6.86 ^B	0.359	<0.001	0.003	0.030

Means with different superscript (a, b, c, d) between dietary treatments and (A, B) between sampling time differ significantly ($p \leq 0.05$). CON = control concentrate without microalgae; ALG20 = control concentrate with 20 g/Kg *Schizochytrium* sp.; ALG40 = control concentrate with 40 g/Kg *Schizochytrium* sp.; ALG60 = control concentrate with 60 g/Kg *Schizochytrium* sp. † Effect: The dietary treatment (T), time (S), and the interaction between dietary treatment x time (TxS) effects were analyzed by ANOVA using a general linear model (GLM) for repeated measures and Post hoc analysis was performed when appropriate using Tukey multiple range test. †SEM: Standard error of the mean.

Table S10. The mean individual fatty acids (FA) (% of total FA), FA groups, SFA/UFA and $\omega 6/\omega 3$ ratios and Δ -9 desaturase indexes of milk from goats fed diets with different levels (g/kg concentrate) of microalgae *Schizochytrium* sp. (CON, ALG20, ALG40 and ALG60) on two sampling points (20th and 40th experimental day).

	Treatment (T)					Sampling time (S)			Effect ‡		
	CON	ALG20	ALG40	ALG60	SEM†	20	40	SEM†	T	S	TxS
C _{4:0}	2.26	2.43	2.44	2.15	0.131	2.09 ^A	2.54 ^B	0.072	0.401	0.001	0.008
C _{6:0}	2.73	2.77	2.89	2.80	0.120	2.66 ^A	2.93 ^B	0.073	0.807	0.005	0.374
C _{8:0}	3.31	3.28	3.61	3.72	0.180	3.40	3.57	0.112	0.273	0.232	0.344
C _{10:0}	10.77	10.54	11.43	12.19	0.700	10.73	11.73	0.419	0.39	0.061	0.371
C _{12:0}	4.49	4.16	4.75	5.07	0.400	4.35	4.88	0.244	0.452	0.071	0.572
C _{14:0}	9.92 ^a	9.99 ^a	12.79 ^b	11.28 ^{ab}	0.583	10.61	11.38	0.400	0.011	0.211	0.257
C _{14:1}	0.30 ^a	0.28 ^{ab}	0.24 ^b	0.30 ^{ab}	0.025	0.32 ^A	0.24 ^B	0.012	0.265	0.001	0.001
C _{15:0}	0.90 ^{ab}	0.97 ^a	0.78 ^b	0.86 ^{ab}	0.043	0.92 ^A	0.83 ^B	0.026	0.046	0.008	0.139
C _{15:1}	0.20 ^a	0.20 ^{ab}	0.17 ^b	0.19 ^{ab}	0.015	0.22 ^A	0.16 ^B	0.011	0.503	0.001	0.591
C _{16:0}	24.13 ^a	27.55 ^b	27.67 ^b	28.12 ^b	1.164	26.10 ^A	27.64 ^B	0.664	0.071	0.044	0.511
C _{16:1}	0.96 ^a	0.77 ^{ab}	0.71 ^b	0.66 ^b	0.081	0.68 ^A	0.87 ^B	0.046	0.077	0.003	0.314
C _{17:0}	0.61 ^a	0.37 ^b	0.28 ^b	0.28 ^b	0.066	0.39 ^A	0.39 ^A	0.040	0.006	0.973	0.723
C _{18:0}	9.66 ^a	2.97 ^b	1.85 ^b	1.85 ^b	0.660	4.33	3.84	0.350	< 0.001	0.170	0.653
trans C _{18:1} ††	0.71 ^a	1.25 ^b	1.01 ^{ab}	0.95 ^{ab}	0.103	1.09 ^B	0.87 ^A	0.062	0.009	0.050	0.627
trans-10 C _{18:1}	0.61 ^a	0.96 ^b	0.82 ^b	0.82 ^b	0.064	0.83	0.77	0.038	0.005	0.191	0.227
trans-11 C _{18:1}	1.59 ^a	10.36 ^b	9.25 ^b	9.80 ^b	0.700	9.01 ^A	6.49 ^B	0.436	< 0.001	< 0.001	0.009
cis-9 C _{18:1}	21.86 ^a	11.57 ^b	8.93 ^b	8.11 ^b	1.280	12.65	12.58	0.734	< 0.001	0.942	0.437
C _{18:2} n-6 t	0.29	0.37	0.34	0.28	0.031	0.29 ^A	0.35 ^B	0.019	0.171	0.017	0.389
C _{18:2} n-6 c	2.84 ^a	2.79 ^a	1.93 ^b	1.60 ^b	0.165	2.21	2.37	0.095	< 0.001	0.124	0.170
C _{18:3} n-3	0.24	0.26	0.25	0.26	0.033	0.21 ^A	0.30 ^B	0.017	0.919	< 0.001	0.220
cis-9, trans-11 C _{18:2}	0.96 ^a	3.87 ^b	4.36 ^b	4.21 ^b	0.360	3.82 ^A	2.87 ^B	0.188	< 0.001	< 0.001	0.009
trans-10, cis-12 C _{18:2}	0.03 ^a	0.17 ^b	0.18 ^b	0.18 ^b	0.022	0.13	0.15	0.015	< 0.001	0.527	0.045
C _{20:3} n-3	0.23 ^a	0.33 ^b	0.52 ^c	0.55 ^c	0.030	0.41 ^A	0.40 ^A	0.017	< 0.001	0.338	0.490
C _{22:5} n-6	0.00 ^a	0.25 ^b	0.53 ^c	0.74 ^d	0.034	0.44 ^A	0.32 ^B	0.020	< 0.001	< 0.001	0.001
C _{22:6} n-3	0.00 ^a	0.70 ^b	1.26 ^c	1.55 ^d	0.075	0.96 ^A	0.80 ^B	0.043	< 0.001	0.003	0.001
SCFA	19.10	19.09	20.37	20.90	0.900	18.93 ^A	20.80 ^B	0.565	0.410	0.020	0.407
MCFA	39.46 ^a	42.69 ^{ab}	45.98 ^b	45.35 ^b	1.705	42.01 ^A	44.74 ^B	0.994	0.054	0.018	0.184
LCFA	10.39 ^a	3.70 ^b	2.60 ^b	2.75 ^b	0.705	5.20	4.52	0.380	< 0.001	0.116	0.729
MUFA	26.46 ^a	25.75 ^{ab}	21.64 ^b	21.58 ^b	1.445	25.33 ^A	22.38 ^B	0.926	0.050	0.031	0.292
PUFA	4.59 ^a	8.77 ^b	9.41 ^b	9.42 ^b	0.420	8.54 ^A	7.56 ^B	0.225	< 0.001	< 0.001	0.001
SFA	68.95	65.48	68.95	69.00	1.600	66.13 ^A	70.06 ^B	1.009	0.287	0.009	0.119
UFA	31.05	34.52	31.05	31.00	1.600	33.87 ^A	29.94 ^B	1.009	0.287	0.009	0.119
SFA/UFA	2.25	1.97	2.27	2.35	0.155	2.03 ^A	2.40 ^B	0.100	0.308	0.009	0.036
$\omega 6$	3.15 ^{ab}	3.44 ^a	2.84 ^b	2.70 ^b	0.175	3.02	3.04	0.105	0.035	0.852	0.072
$\omega 3$	0.46 ^a	1.29 ^b	2.03 ^c	2.41 ^d	0.090	1.60 ^A	1.50 ^B	0.053	< 0.001	0.044	0.000
$\omega 6/\omega 3$	7.3 ^a	2.72 ^b	1.42 ^{bc}	1.13 ^c	0.500	3.04	3.24	0.308	< 0.001	0.690	0.966
AI	2.24	2.18	2.74	2.68	0.190	2.23 ^A	2.68 ^B	0.124	0.111	0.011	0.029
TI	2.77	2.38	2.21	2.20	0.153	2.22 ^A	2.49 ^B	0.093	0.052	0.031	0.011
HPI	0.44	0.42	0.33	0.34	0.036	0.43	0.35	0.029	0.486	0.648	0.978
Δ-9 desaturase index											
C _{14:1} / C _{14:0}	0.031	0.030	0.019	0.029	0.003	0.032 ^A	0.022 ^B	0.002	0.100	0.001	0.036
C _{16:1} / C _{16:0}	0.040 ^a	0.029 ^b	0.026 ^b	0.023 ^b	0.003	0.027 ^A	0.032 ^B	0.002	0.008	0.047	0.534
cis-9 C _{18:1} / C _{18:0}	2.28 ^a	4.58 ^b	4.91 ^b	4.55 ^b	0.325	3.77 ^A	4.39 ^B	0.178	< 0.001	0.001	0.042
cis-9, trans-11 C _{18:2} / trans-11 C _{18:1}	0.61 ^a	0.38 ^b	0.44 ^{ab}	0.46 ^b	0.044	0.48	0.48	0.026	0.006	0.968	0.055

Means with different superscript (a, b, c, d) between dietary treatments and (A, B) between sampling time differ significantly ($p \leq 0.05$). CON = control concentrate without microalgae; ALG20 = control concentrate with 20 g/Kg *Schizochytrium* sp.; ALG40 = control concentrate with 40 g/Kg *Schizochytrium* sp.; ALG60 = control concentrate with 60 g/Kg *Schizochytrium* sp. ‡ Effect: The dietary treatment (T), time (S), and the interaction between dietary treatment x time (TxS) effects were analyzed by ANOVA using a general linear model (GLM) for repeated measures and Post hoc analysis was performed when appropriate using Tukey multiple range test.

†SEM: Standard error of the mean †† trans C18:1 proportion are not including the trans-11 C18:1 and trans-10 C18:1 content Short-Chain Saturated Fatty Acids (SCFA) = C6:0 + C8:0 + C10:0 + C11:0, Medium-Chain Saturated Fatty Acids (MCFA) = C12:0 + C13:0 + C14:0 + C15:0 + C16:0, Long-Chain Saturated Fatty Acids (LCFA) = C17:0 + C18:0 + C20:0, Mono-Unsaturated Fatty Acids (MUFA) = C14:1 + C15:1 + C16:1 + C17:1 + cis-9 C18:1 + trans-11 C18:1 + trans C18:1, Poly-Unsaturated Fatty Acids (PUFA) = cis-9, trans-11 C18:2 + C18:2n-6c + C18:2n-6t + C18:3n-3 + C18:3n-6 + C20:3n-3, Saturated Fatty Acids (SFA) = SCFA + MCFA + LCFA, Unsaturated Fatty Acids (UFA) = PUFA + MUFA, Saturated/Unsaturated (S/U) = (SCFA + MCFA + LCFA)/(PUFA + MUFA), Atherogenic index (AI) = (C12:0 + 4 × C14:0 + C16:0)/(PUFA + MUFA), Thrombogenic index (TI) = (C14:0 + C16:0 + C18:0)/(0.5 × MUFA) + (0.5 × n-6 PUFA) + (3 × ω3 PUFA) + (ω3 PUFA/ω6 PUFA), Health promoting index (HPI) = (ω6 PUFA + ω3 PUFA + MUF/(C12:0 + 4 × C14:0 + C16:0)).

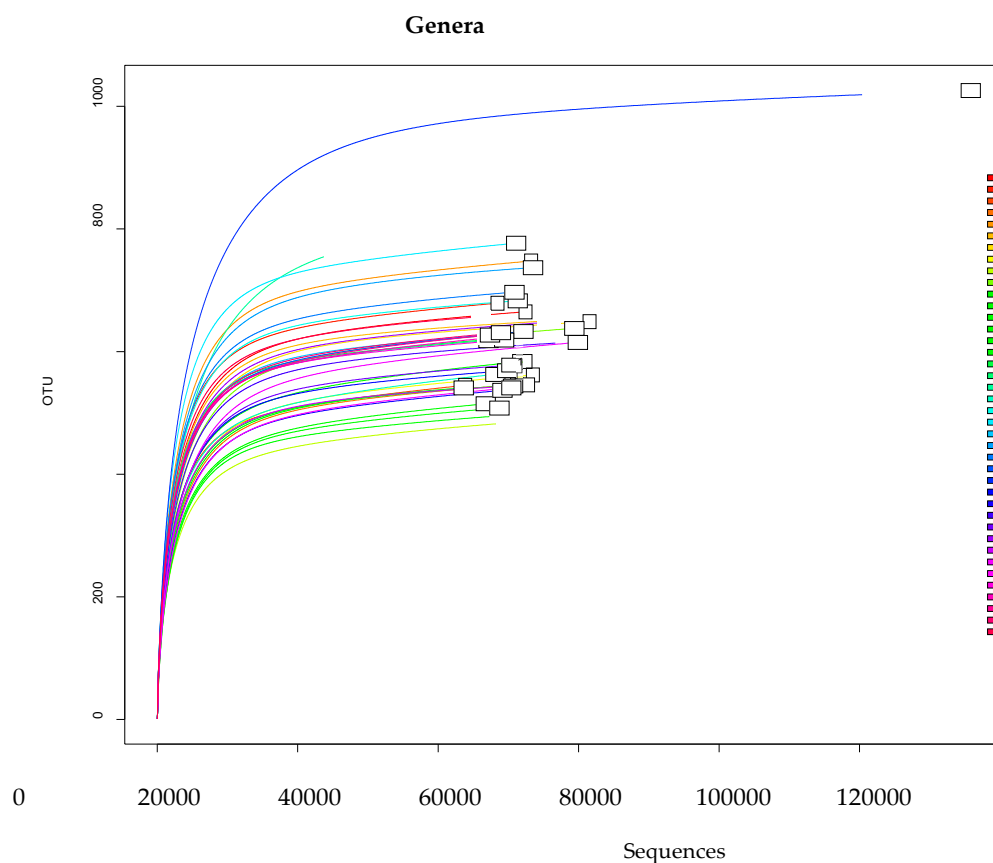


Figure S1. Rarefaction curves of bacterial population at genera taxonomic level for the 16S.

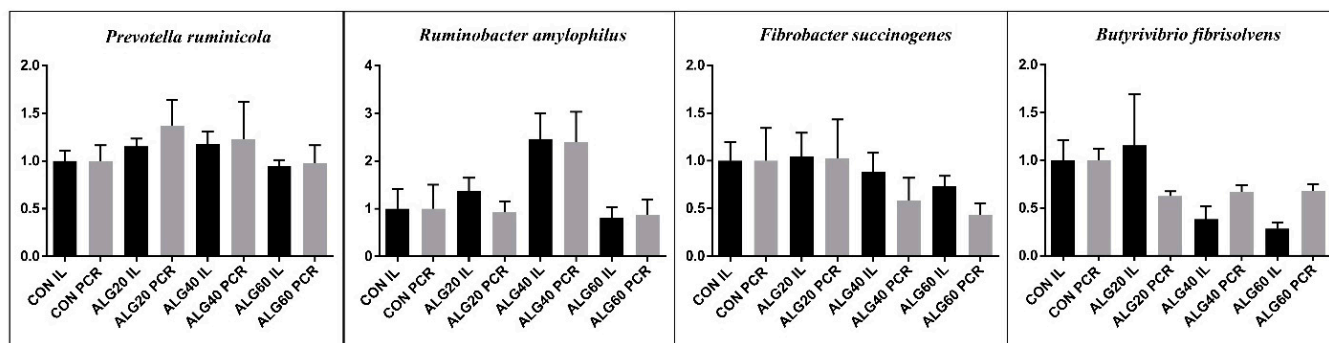


Figure S2. Validation of the 16S

rRNA sequencing (IL) by qPCR (PCR) on the relative abundances of *Prevotella ruminicola*, *Ruminobacter amylophilus*, *Fibrobacter succinogenes*, and *Butyrivibrio fibrisolvens*. The microalgae treated groups (ALG20, ALG40, and ALG60) of each method (IL vs. PCR) have been expressed relatively as fold changes towards to the control (CON) group in order to be similarly visualized. Data are depicted as trends and no statistic has been applied.

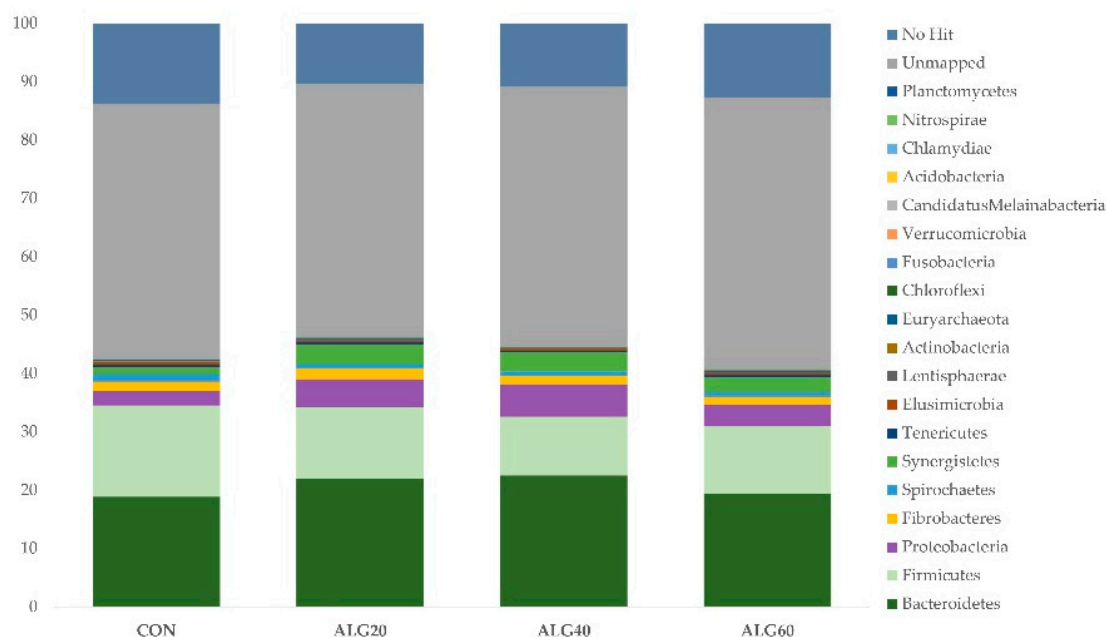


Figure S3. Relative abundance of identified phyla, unidentified clusters, and no-hits sequences in four dietary treatments (CON, ALG20, ALG40, and ALG60) within the two sampling times (20th and 40th) illustrated in cumulative bar graph.

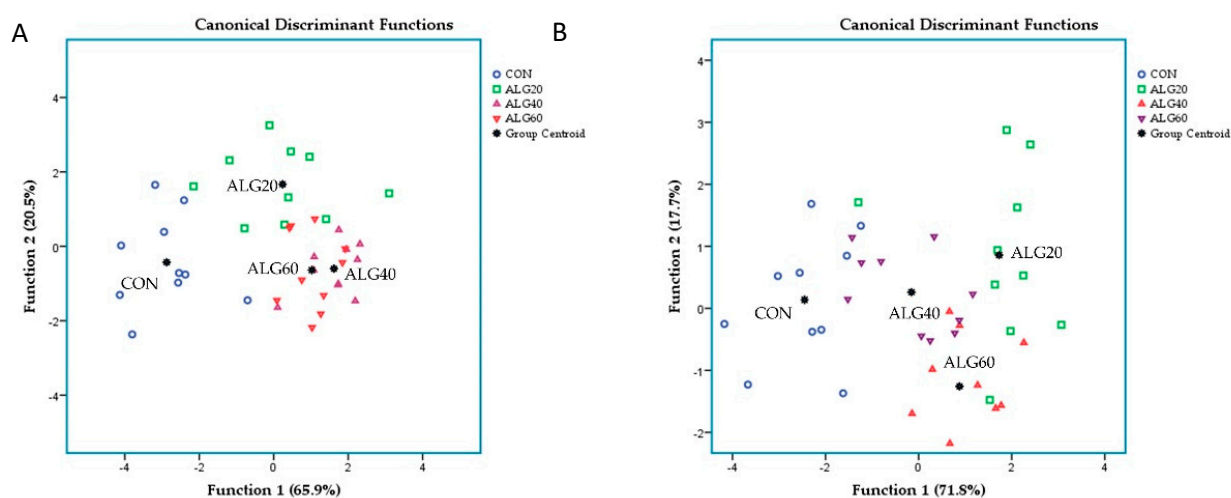


Figure S4. Discriminant plots separating (A) the four dietary treatments (CON; blue \circ , ALG20; green \square , ALG40; purple \triangle , and ALG60; red ∇) according to pooled data of two sampling times (20th and 40th experimental day) that entered independently together on the abundances explained A) the fourteen identified phyla and B) the thirty-four identified families in goats' rumen. In the (A) plot the proportions of the samples that were correctly classified were 80 %, while wilks' λ was observed at 0.067 for Function 1 ($p < 0.001$) and 0.291 for Function 2 ($p = 0.075$). In the (B) plot the proportions of the samples that were correctly classified were 82.5 %, while wilks' λ was observed at 0.115 for Function 1 ($p = 0.013$) and 0.429 for Function 2 ($p = 0.496$). CON = control concentrate without microalgae (*Schizochytrium* spp); ALG20 = CON with 20 g/Kg *Schizochytrium* spp.; ALG40 = CON with 40 g/Kg *Schizochytrium* spp.; ALG60 = CON with 60 g/Kg *Schizochytrium* spp.