Table S1. Relative abundance ($e^{-\Delta Ct}$) of several microorganisms to the total bacterial 16s rDNA in the rumen solid adherent of goats were fed with the four diets (CON, ALG20, ALG40 and ALG60) at three sampling time (20, 40, 60 experimental days).

	DIET					SAMPLING TIME				EFFECT‡		
	CON	***ALG20***	***ALG40***	***ALG60***	SEM†	**20**	**40**	**60**	**SEM†**	**D**	**T**	**DxT**
Bacteroidetes	0.489^{t}	0.472	0.415	0.399^{t}	0.026	0.401^{a}	0.464^{ab}	0.466^{b}	0.018	0.065	0.049	0.600
Firmicutes	0.315^{a}	0.237^{b}	0.191^{b}	0.217^{b}	0.015	0.214	0.258	0.249	0.014	<0.001	0.143	0.793
Archaea	0.011^{a}	0.008^{b}	0.006^{c}	0.006^{c}	0.001	0.005^{a}	0.009^{b}	0.009^{b}	0.001	<0.001	<0.001	0.043
Methanogens	0.00082^{a}	0.00045^{b}	0.00035^{b}	0.00036^{b}	<0.001	0.00019^{a}	0.00066^{b}	0.00064^{b}	<0.001	0.041	0.000	0.767
Methanomassiliicoccales spp.	0.00043^{a}	0.00023^{b}	0.00022^{b}	0.00015^{b}	<0.001	0.00017^{a}	0.00030^{b}	0.00030^{b}	<0.001	<0.001	<0.001	0.308
Methanobrevibacter spp.	0.00019^{a}	0.00004^{b}	0.00003^{b}	0.00004^{b}	<0.001	0.00005^{a}	0.00008^{b}	0.00009^{b}	<0.001	0.048	0.017	0.048
Methanosphaera stadtmanae	0.00004^{a}	0.00002^{b}	0.00002^{b}	0.00001^{b}	<0.001	0.00003	0.00001	0.00003	<0.001	0.026	0.465	0.678
Methanobacterium formicicum	0.000007^{a}	0.000002^{b}	0.000001^{b}	0.000002^{b}	<0.001	0.000002	0.000004	0.000003	<0.001	0.001	0.051	0.210
Protozoa	0.0017	0.0029	0.0019	0.0020	<0.001	0.0013^{a}	0.0031^{b}	0.0021^{c}	<0.001	0.102	0.007	0.030
Entodinium spp.	0.0010^{t}	0.0023^{t}	0.0014	0.0018	<0.001	0.0013^{b}	0.0022^{a}	0.0013^{b}	<0.001	0.076	0.018	0.167
Total anaerobic fungi	0.0011	0.0006	0.0005	0.0006	<0.001	0.0008^{a}	0.0005^{b}	0.0008^{ab}	<0.001	0.239	<0.001	0.395
Neocallimastigales-specific	0.0004^{a}	0.0003^{b}	0.0002^{b}	0.0002^{b}	<0.001	0.0002^{a}	0.0004^{b}	0.0004^{b}	<0.001	0.016	<0.001	0.788
Eubacterium ruminantium	0.0023	0.0018	0.0016	0.0016	<0.001	0.0018	0.0020	0.0016	<0.001	0.464	0.495	0.156
Butyrivibrio fibrisolvens	0.132^{a}	0.099^{b}	0.084^{b}	0.104^{b}	0.006	0.099	0.108	0.106	0.005	<0.001	0.666	0.471
Butyrivibrio proteoclasticus	0.011	0.010	0.007	0.009	0.001	0.008^{a}	0.010^{b}	0.010^{b}	0.001	0.173	0.046	0.597
Ruminococcus flavefaciens	0.007^{a}	0.002^{b}	0.001^{b}	0.002^{b}	0.001	0.003	0.003	0.003	0.001	0.004	0.888	0.801
Fibrobacter succinogenes	0.012	0.008	0.003	0.012	0.003	0.018^{a}	0.004^{b}	0.004^{b}	0.001	0.127	0.003	0.305
Ruminococcus albus	0.005	0.004	0.005	0.003	0.001	0.002^{a}	0.004^{b}	0.007^{c}	0.000	0.414	0.001	0.125
Ruminobacter amylophilus	0.003	0.007	0.012	0.015	0.004	0.009	0.005	0.014	0.003	0.141	0.087	0.010
Streptococcus bovis	0.000012	0.000008	0.000009	0.000008	<0.001	0.00002^{a}	0.000007^{b}	0.000008^{c}	<0.001	0.819	0.001	0.288
Selenomonas ruminantium	0.0026	0.0026	0.0022	0.0028	<0.001	0.0031	0.0024	0.0024	<0.001	0.389	0.091	0.999
Prevotella spp.	0.249	0.309	0.288	0.255	0.027	0.297	0.261	0.269	0.018	0.363	0.299	0.369
Prevotella brevis	0.0008	0.0005	0.0007	0.0007	<0.001	0.0005	0.0007	0.0008	<0.001	0.724	0.273	0.685
Prevotella ruminicola	0.0030^{a}	0.0036^{a}	0.0018^{b}	0.0017^{b}	<0.001	0.0020	0.0025	0.0030	<0.001	0.009	0.115	0.485

CON= control concentrate without microalgae; ALG20= control concentrate with 20 g/ Kg *Schizochytrium spp.*; ALG40= control concentrate with 40 g/ Kg *Schizochytrium spp.*; ALG60= control concentrate with 60 g/ Kg *Schizochytrium* spp. Means with different superscript (a, b, c) between dietary treatments and (a, b, c) between sampling time differ significantly ($p \leq 0.05$). † SEM: Standard error of the mean. ‡ Effect: The dietary treatment (D), time (T), and the interaction

between dietary treatment x time (DxT) effects were analyzed by ANOVA using a general linear model (GLM) for repeated measures and Post hoc analysis was performed when appropriate using Turkey's multiple range test. t = tendency, P-value < 0.10.