

Supplementary Table S1. Comparison of similarities in microbiota composition between lambs in the three treatment groups by ANOSIM analysis. Unweighted unifrac distance

	R-value	P-value
Rumen samples		
C30 vs. C50 ¹	0.144	0.096
C30 vs. C70	0.524	0.007
C50 vs. C70	0.260	0.020
Fecal samples		
C30 vs. C50 ¹	0.144	0.051
C30 vs. C70	0.660	0.007
C50 vs. C70	0.268	0.028

¹ C30 = 30:70 concentrate: forage; C50 = 50:50 concentrate: forage; C70 = 70:30 concentrate: forage.

Supplementary Table S2. Relative abundance of top 7 phyla in the ruminal and fecal microbiome of Tibetan sheep fed diets with different concentrate-to-forage ratios.

Index	Dietary Treatment ¹			SEM	P-value	^z P-value
	C30	C50	C70			
Rumen samples						
<i>Bacteroidota</i>	49.38	46.24	47.20	1.62	0.914	0.949
<i>Firmicutes</i>	41.33	45.15	41.78	1.27	0.264	0.640
<i>Spirochaetota</i>	1.45	1.08	4.19	0.72	0.379	0.640
<i>Patescibacteria</i>	1.78	2.11	1.24	0.26	0.691	0.825
<i>Verrucomicrobiota</i>	2.20 ^a	2.09 ^a	0.71 ^b	0.26	0.018	0.499
<i>Actinobacteriota</i>	1.47	0.69	0.59	0.39	0.733	0.825
<i>Fibrobacterota</i>	0.31	0.11	1.85	0.36	0.147	0.640
Fecal samples						
<i>Firmicutes</i>	53.23	41.92	51.22	3.53	0.691	0.801
<i>Bacteroidota</i>	31.43 ^b	18.99 ^b	40.02 ^a	2.85	0.004	0.054
<i>Proteobacteria</i>	2.85 ^b	15.74 ^a	2.21 ^b	2.42	0.048	0.277
<i>Spirochaetota</i>	5.23	4.70	3.93	0.92	0.756	0.812
<i>Actinobacteriota</i>	0.37	4.42	0.62	1.18	0.733	0.812
<i>Verrucomicrobiota</i>	2.32	1.30	0.49	0.31	0.075	0.326
<i>Patescibacteria</i>	0.41	1.37	0.84	0.23	0.145	0.383

^{a-b} Mean values accompanied by different letters within a row indicate significant differences. ¹ C30 = 30:70 concentrate: forage; C50 = 50:50 concentrate: forage; C70 = 70:30 concentrate: forage. ^zP-value is an adjusted BH-FDR correction value.

Supplementary Table S3. Relative abundance of the top 14 genera in the ruminal and fecal microbiome of lambs Tibetan sheep fed diets with different concentrate-to-forage ratios.

Index	Dietary Treatment ¹			SEM	P-value	^z P-value
	C30	C50	C70			
Rumen samples						
<i>Prevotella</i>	10.36	8.62	9.62	0.90	0.827	0.908
<i>Rikenellaceae_RC9_gut_group</i>	8.95	8.07	6.43	0.57	0.357	0.553
<i>Christensenellaceae_R_7_group</i>	5.87	6.26	6.31	0.63	0.932	0.974
<i>Succiniclasticum</i>	4.26	3.46	6.02	0.45	0.090	0.553
<i>NK4A214_group</i>	3.56	4.11	3.88	0.44	0.932	0.974
<i>Prevotellaceae_UCG_003</i>	2.11	2.38	2.97	0.35	0.613	0.731
<i>Treponema</i>	1.39	1.05	4.16	0.71	0.379	0.568
<i>Butyrivibrio</i>	0.78 ^b	3.08 ^a	1.46 ^{ab}	0.38	0.031	0.481
<i>Prevotellaceae_UCG_001</i>	1.78	1.72	1.68	0.24	0.914	0.963
<i>Saccharofermentans</i>	2.12	1.29	1.53	0.16	0.121	0.553
<i>Candidatus_Saccharimonas</i>	1.15	1.83	0.86	0.26	0.512	0.710
<i>Ruminococcus</i>	0.91 ^{ab}	0.71 ^b	1.60 ^a	0.15	0.042	0.510
<i>Veillonellaceae_UCG_001</i>	0.59	1.43	1.01	0.18	0.310	0.553
<i>Bacteroidales_bacterium_Bact_22</i>	1.80	0.38	0.49	0.32	0.196	0.553
Fecal samples						
<i>UCG_005</i>	5.40	5.61	6.35	0.70	0.811	0.848
<i>Rikenellaceae_RC9_gut_group</i>	7.19	3.62	5.08	0.85	0.068	0.448
<i>Alistipes</i>	4.34	2.93	6.04	0.76	0.481	0.566
<i>Treponema</i>	4.65	4.61	3.93	0.90	0.914	0.931
<i>Christensenellaceae_R_7_group</i>	5.83	3.77	3.41	0.53	0.249	0.448
<i>Bacteroides</i>	4.28	2.04	5.05	0.52	0.065	0.448
<i>Succinivibrio</i>	2.32	6.44	0.44	1.71	0.686	0.738
<i>Prevotellaceae_UCG_003</i>	2.90	1.43	2.49	0.80	0.402	0.485
<i>Monoglobus</i>	3.24 ^a	0.77 ^b	2.33 ^{ab}	0.49	0.018	0.361
<i>Lachnoclostridium</i>	1.72	2.16	1.42	0.24	0.330	0.448
<i>Prevotella</i>	0.20 ^b	0.32 ^b	4.00 ^a	0.61	0.013	0.302
<i>28_4</i>	1.10	1.17	2.24	0.31	0.454	0.539
<i>UCG_002</i>	2.57 ^a	1.08 ^b	0.62 ^b	0.28	0.013	0.302
<i>Akkermansia</i>	1.84	0.67	0.44	0.27	0.089	0.448

^{a-b} Mean values accompanied by different letters within a row indicate significant differences. ¹ C30 = 30:70 concentrate: forage; C50 = 50:50 concentrate: forage; C70 = 70:30 concentrate: forage. ^zP-value is an adjusted BH-FDR correction value.