

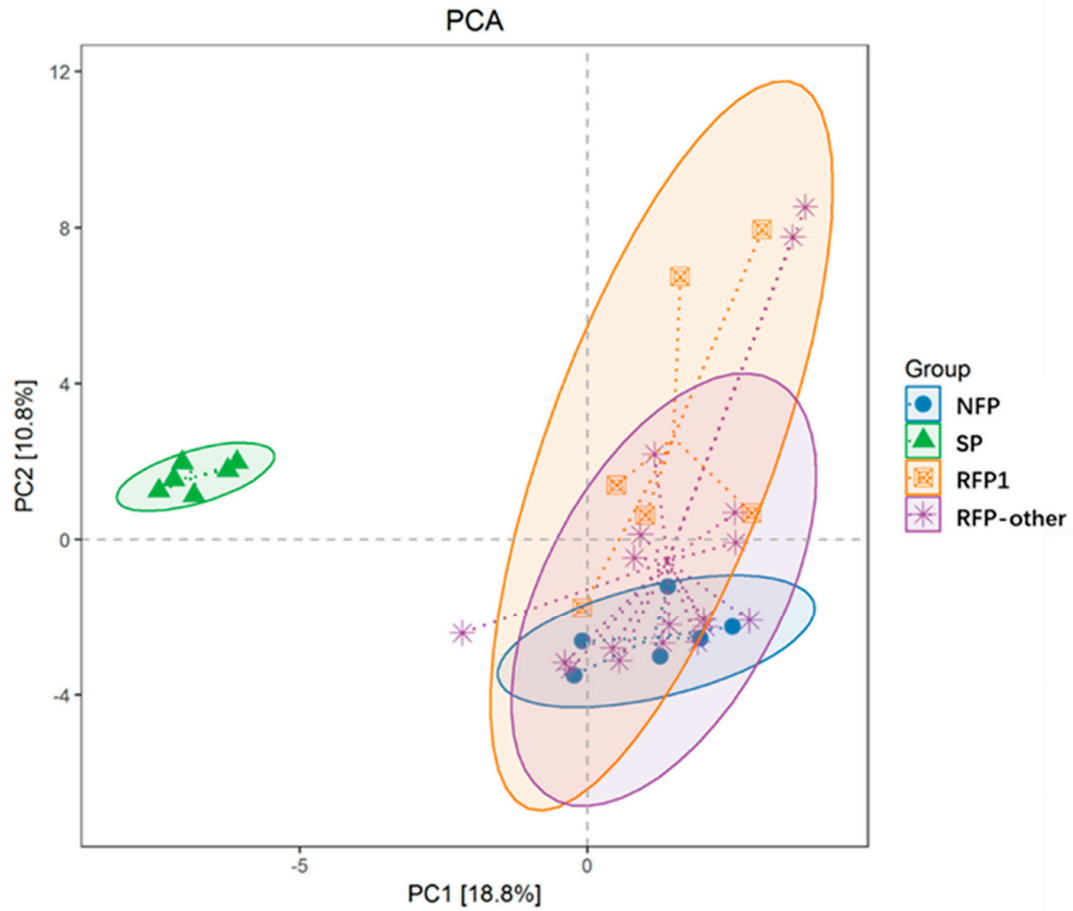


Figure S1. The PCA scores plot of rumen microflora at different periods.

Table S1. Alpha diversity of rumen microflora of yaks through the experimental periods.

Items	Groups						SEM	<i>p</i>
	NFP	SP	RFP1	RFP2	RFP3	RFP4		
Chao I	2072.77 ^b	1956.52 ^c	1991.61 ^c	1831.00 ^d	2199.50 ^a	2192.12 ^a	23.79	0.000
Observed species	1449.5 ^a	1240.33 ^b	1244.33 ^b	1263.00 ^b	1456.67 ^a	1407.00 ^a	21.40	0.000
PD whole tree	95.63 ^a	96.61 ^a	88.93 ^b	88.68 ^b	98.75 ^a	96.24 ^a	0.87	0.000
Shannon-wiener	5.36 ^a	4.37 ^b	4.61 ^b	4.63 ^b	5.18 ^a	5.08 ^a	0.07	0.000

Data with different small letter superscripts within the same row were significantly different ($p < 0.05$). NFP, normal feeding period; SP, starvation period; RFP1, 1st week of refeeding period; RFP2, 2nd week of refeeding period; RFP3, 3rd week of refeeding period; RFP4, 4th week of refeeding period. SEM: standard error of the mean.

Table S2. Effects of starvation and prolonged refeeding on the relative abundances of ruminal bacteria (%) at the genus level in yaks.

Items	Groups						SEM	<i>p</i>
	NFP	SP	RFP1	RFP2	RFP3	RFP4		
<i>Prevotella 1</i>	55.03 ^a	7.96 ^b	48.58 ^a	56.40 ^a	46.49 ^a	48.97 ^a	3.607	0.009
<i>Prevotellaceae UCG-001</i>	2.72 ^b	24.33 ^a	1.31 ^b	1.85 ^b	2.27 ^b	2.35 ^b	1.848	0.001
<i>Succinivibrionaceae UCG-002</i>	0.63 ^b	0.53 ^b	8.40 ^a	4.83 ^{ab}	3.56 ^{ab}	3.10 ^{ab}	0.913	0.030
<i>Prevotellaceae UCG-003</i>	1.77 ^{ab}	0.57 ^b	1.57 ^{ab}	2.43 ^a	2.41 ^a	1.33 ^{ab}	0.213	0.016
<i>Thauera</i>	0.03 ^b	9.13 ^a	0.06 ^b	0.04 ^b	0.04 ^b	0.05 ^b	0.892	0.003
<i>Ruminobacter</i>	0.12 ^b	0.45 ^b	4.62 ^a	0.35 ^b	0.23 ^b	0.18 ^b	0.686	0.010
<i>Christensenellaceae R-7 group</i>	0.25 ^b	2.28 ^a	0.20 ^b	0.26 ^b	0.29 ^b	0.17 ^b	0.109	0.004
<i>Prevotellaceae UCG-004</i>	0.94 ^a	0.23 ^b	0.23 ^b	0.33 ^{ab}	0.52 ^{ab}	0.37 ^{ab}	0.016	0.046
<i>Prevotellaceae NK3B31 group</i>	0.72 ^a	0.22 ^b	0.31 ^b	0.32 ^b	0.37 ^b	0.36 ^b	0.042	0.005
<i>Succinilasticum</i>	0.66 ^a	0.11 ^c	0.19 ^{bc}	0.45 ^{ab}	0.35 ^{bc}	0.31 ^{bc}	0.046	0.004
<i>Burkholderia</i>	0.07 ^b	0.73 ^a	0.13 ^b	0.12 ^b	0.10 ^b	0.11 ^b	0.056	0.007
<i>Arcobacter</i>	0.00 ^b	0.70 ^a	0.01 ^b	0.01 ^b	0.00 ^b	0.00 ^b	0.109	0.026

The significantly changed predominant genera populations (abundance > 0.5% in at least one of the groups) were shown. Data with different small letter superscripts within the same row were significantly different ($p < 0.05$). NFP, normal feeding period; SP, starvation period; RFP1, 1st week of refeeding period; RFP2, 2nd week of refeeding period; RFP3, 3rd week of refeeding period; RFP4, 4th week of refeeding period. SEM: standard error of the mean.

Table S3. Effects of starvation and prolonged refeeding on the relative abundances of predominant microbial metabolic pathways (%).

Items	Groups						SEM	<i>p</i>
	NFP	SP	RFP1	RFP2	RFP3	RFP4		
DNA repair and recombination proteins	3.72 ^a	3.40 ^b	3.69 ^a	3.75 ^a	3.70 ^a	3.71 ^a	0.030	0.046
Peptidases	2.46 ^a	2.28 ^b	2.34 ^{ab}	2.45 ^a	2.44 ^a	2.45 ^a	0.020	0.049
Amino acid related enzymes	1.91 ^a	1.77 ^b	1.87 ^{ab}	1.91 ^a	1.89 ^{ab}	1.90 ^{ab}	0.013	0.032
Ribosome Biogenesis	1.75 ^b	1.69 ^b	1.83 ^a	1.78 ^{ab}	1.77 ^{ab}	1.77 ^{ab}	0.012	0.008
Arginine and proline metabolism	1.55 ^a	1.44 ^b	1.46 ^{ab}	1.54 ^{ab}	1.52 ^{ab}	1.53 ^{ab}	0.010	0.015
Starch and sucrose metabolism	1.28 ^a	1.01 ^b	1.18 ^a	1.24 ^a	1.22 ^a	1.24 ^a	0.020	0.012
Homologous recombination	1.27 ^a	1.15 ^b	1.27 ^a	1.28 ^a	1.27 ^a	1.27 ^a	0.012	0.050
Glycolysis / Gluconeogenesis	1.23 ^a	1.19 ^b	1.18 ^b	1.20 ^{ab}	1.22 ^a	1.22 ^a	0.006	0.004
Two-component system	1.21 ^b	1.81 ^a	1.38 ^{ab}	1.23 ^b	1.25 ^b	1.22 ^b	0.053	0.049
Secretion system	1.21 ^b	1.58 ^a	1.42 ^{ab}	1.26 ^{ab}	1.25 ^{ab}	1.25 ^{ab}	0.034	0.008
Glycine, serine and threonine metabolism	1.19 ^a	1.03 ^b	1.19 ^{ab}	1.22 ^a	1.18 ^{ab}	1.20 ^a	0.013	0.010
Phenylalanine tyrosine and tryptophan biosynthesis	1.17 ^a	0.97 ^b	1.13 ^{ab}	1.17 ^a	1.15 ^{ab}	1.16 ^a	0.015	0.006

The significantly changed predominant functional pathways (abundance > 0.5% in at least one of the groups) were shown. Data with different small letter superscripts within the same row were significantly different ($p < 0.05$). NFP, normal feeding period; SP, starvation period; RFP1, 1st week of refeeding period; RFP2, 2nd week of refeeding period; RFP3, 3rd week of refeeding period; RFP4, 4th week of refeeding period. SEM: standard error of the mean.