

Table S1. The bacterial phyla and genera (> 1% abundance) as determined by 16S rRNA gene sequencing in the rumen content of beef cattle fed corn stover silage after fresh-corn harvested (CF) or corn stover silage after ripe-corn harvested (CR) diet (n = 7).

Items ¹	Diets		SEM	p-value
	CF	CR		
p_Bacteroidetes	56.7	58.1	1.15	0.06
g_Prevotella_1	14.5	15.8	1.13	0.48
g_Rikenellaceae_RC9_gut_group	12.7	11.0	0.808	0.22
g_Prevotellaceae_UCG-003	2.48	2.69	0.268	0.22
g_Prevotellaceae_UCG-001	2.63	2.48	0.220	0.95
p_Firmicutes	35.3	32.8	1.15	0.06
g_Succiniclacticum	4.75	4.71	0.396	0.65
g_Ruminococcaceae_UCG-011	2.49	2.09	0.179	0.41
g_Ruminococcaceae_NK4A214_group	2.34	1.76	0.154	0.04
g_Ruminococcaceae_UCG-014	1.93	1.91	0.140	0.75
g_Saccharofermentans	1.93	1.71	0.106	0.34
g_Ruminococcus_1	1.80	1.42	0.094	0.06
g_Ruminococcaceae_UCG-010	1.46	1.45	0.057	0.85
g_Christensenellaceae_R-7_group	1.38	1.26	0.087	0.65
g_Lachnospiraceae_AC2044_group	1.15	1.13	0.072	0.57
p_Fibrobacteres	1.60	1.67	0.128	0.65
g_Fibrobacter	1.57	1.64	0.128	0.65
p_Patescibacteria	1.61	2.02	0.149	0.18
g_Candidatus_Saccharimonas	1.27	1.64	0.141	0.22
p_Proteobacteria	1.27	1.45	0.122	0.34
p_Kiritimatiellaeota	0.92	1.14	0.082	0.14

¹p = phylum, g = genus.