



Effects of exogenous fibrolytic enzymes on beef cattle fed growing diets: Ruminal microbiome

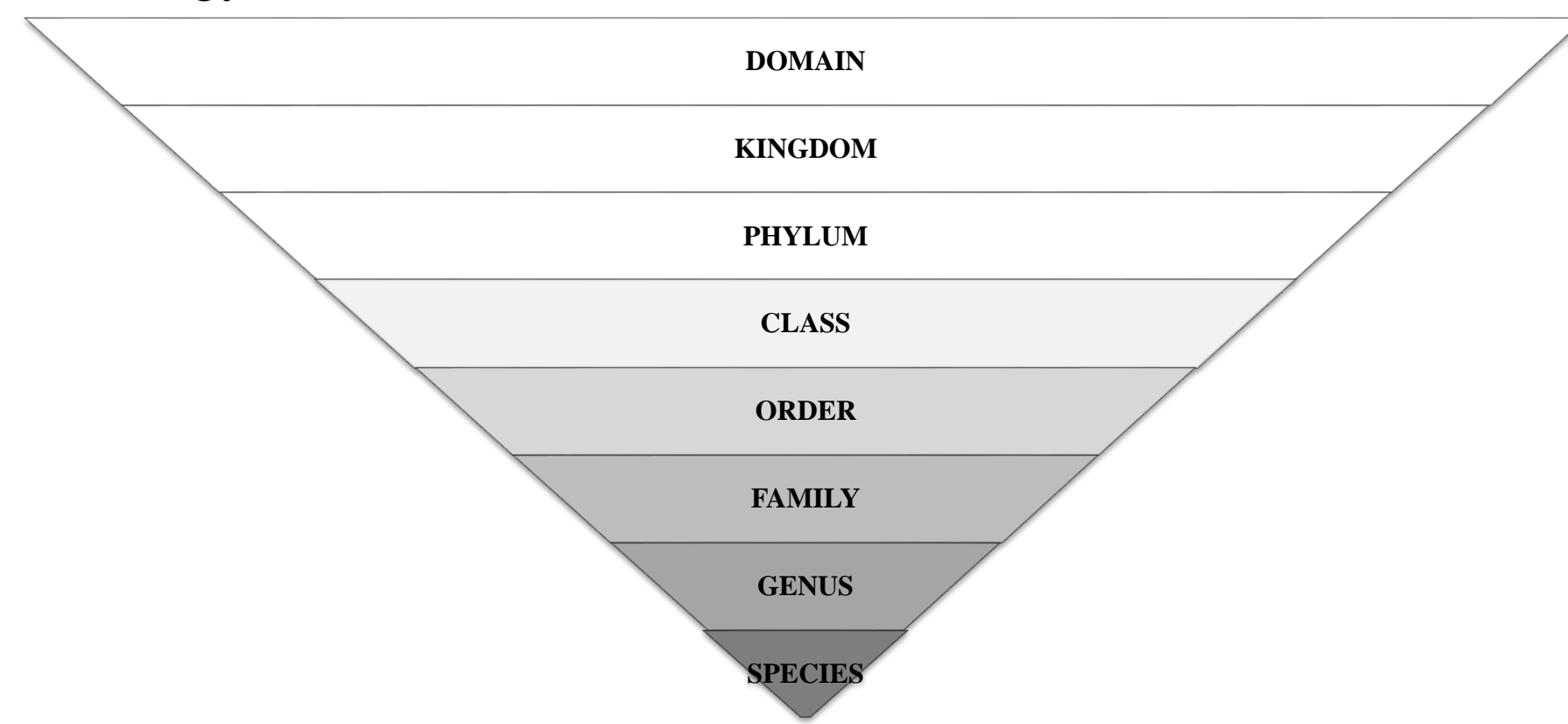


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Introduction:

- Fiber is an important fraction of ruminant diets. Digestibility may limit diet utilization due to the difficulty of the ruminal microbes ability to completely digest fiber fractions. However, exogenous enzymes extraction procedures have been developed, and so there is potential to improve fiber digestibility (Beauchemin, 2003).
- Including fibrolytic enzymes in ruminant diets maybe an option to aid fiber degradation by ruminal microbes (Chung et al., 2012), and therefore changes in ruminal microbiome relative abundances might be eluded by such strategy.



Objective:

To evaluate the effects of dietary pre-treatment with fibrolytic enzyme-based cocktail on high- and low-quality growing diets fed to beef steers on ruminal microbiome relative abundance.

Materials & Methods:

- Ruminally cannulated crossbred beef steers ($n = 5$; BW = 520 ± 30 kg).
- Steers were individually fed ad libitum through four 21 days periods consisting of 14 days of adaptation and 7 days of collections.
- 5 × 4 unbalanced Latin square design.
- 2 × 2 factorial arrangement of treatments.
- Diet quality:
 - High quality (HQ) 0.00 mL/kg of diet DM (Control)
 - Low quality (LQ) 0.75 mL/kg of diet DM (Enzyme)
- Enzyme inclusion [cellulose/xylanase (*Trichoderma reesei*)]:
 - High quality (HQ) 0.00 mL/kg of diet DM (Control)
 - Low quality (LQ) 0.75 mL/kg of diet DM (Enzyme)
- Data were sequenced by Illumina® NovaSeq™ (16S rRNA).
- Ruminal fluid samples (100mL) were collected 6 hours after-feeding on day 5 of each period for ruminal microbiome analysis.
- A QIAamp PowerFecal Pro DNA Kit was used to extract DNA from each ruminal sample.
- Data were analyzed using the GLIMMIX procedures of SAS.
- Bioinformatics was completed by LC Biosciences, and the taxonomy relative abundance (RA) reported.

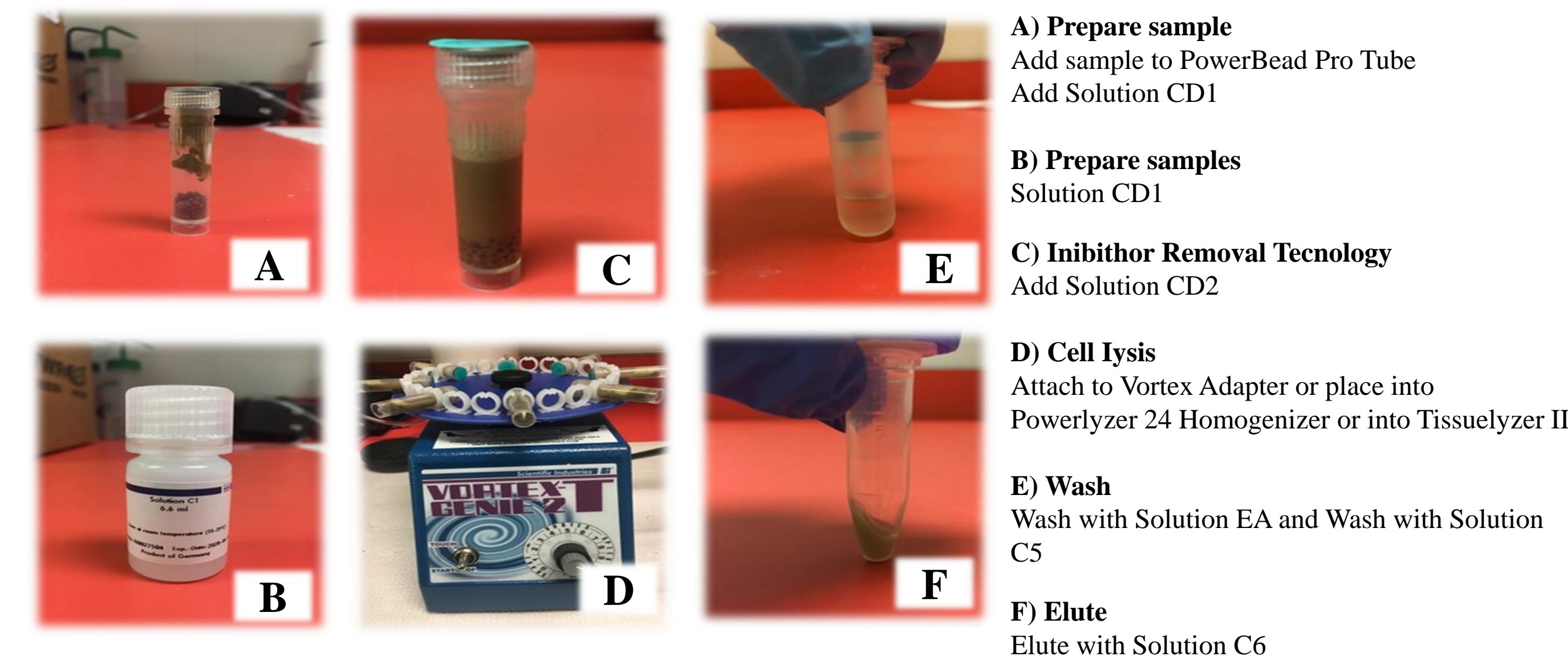


Figure 1: Process of extraction of Ruminal DNA utilizing QIAamp PowerFecal Pro DNA Extraction Kit In Lab Procedure

Results:

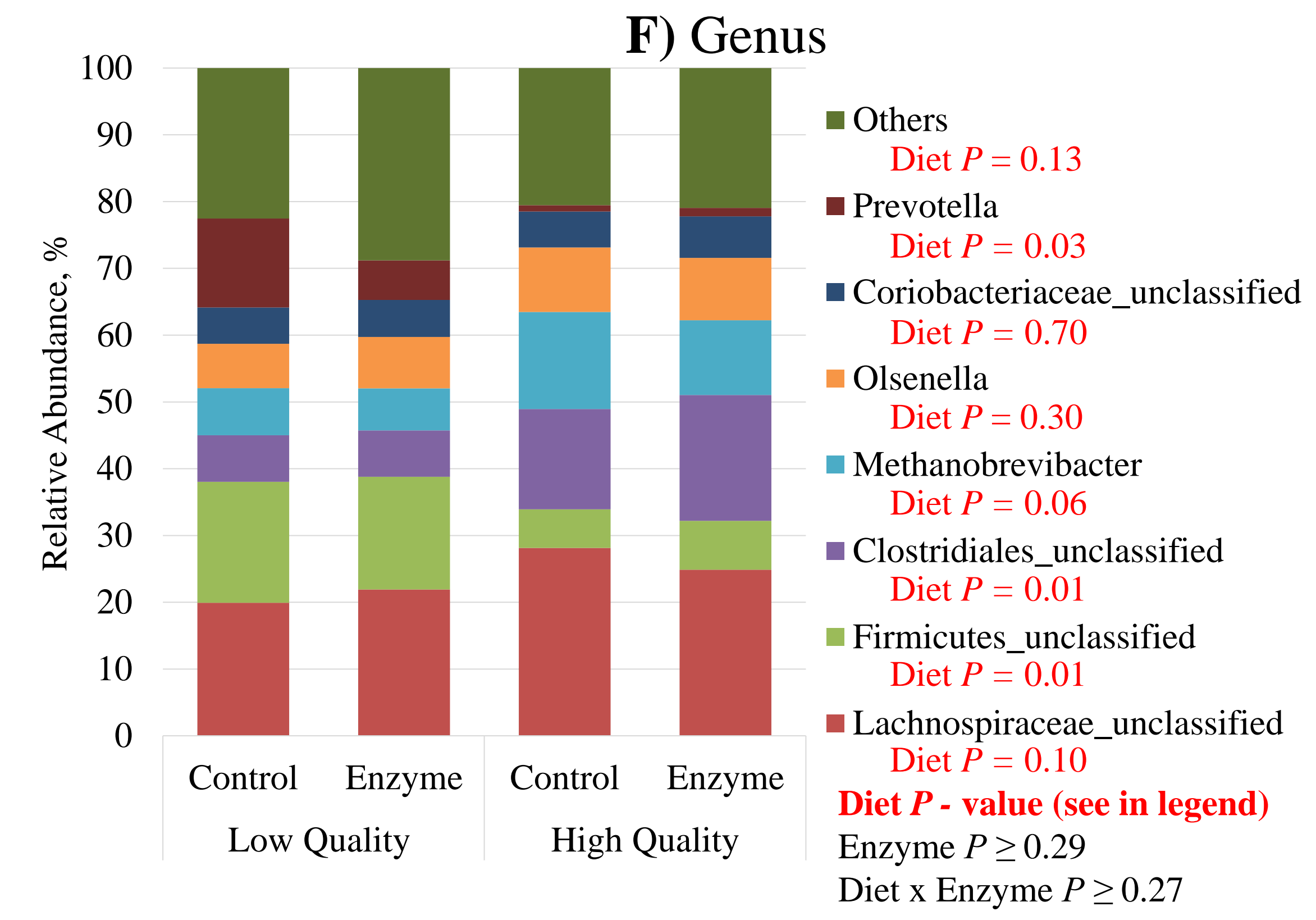
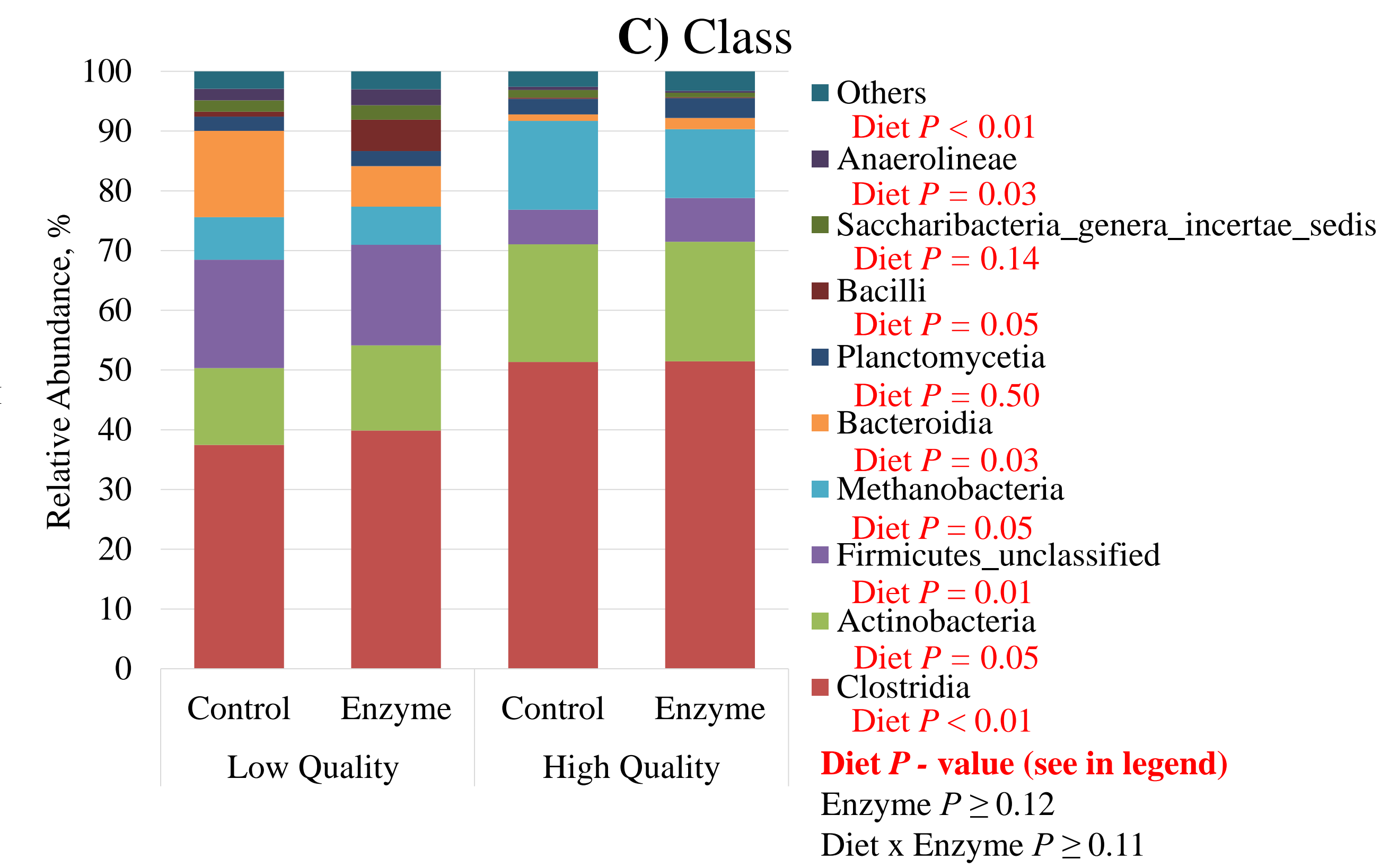
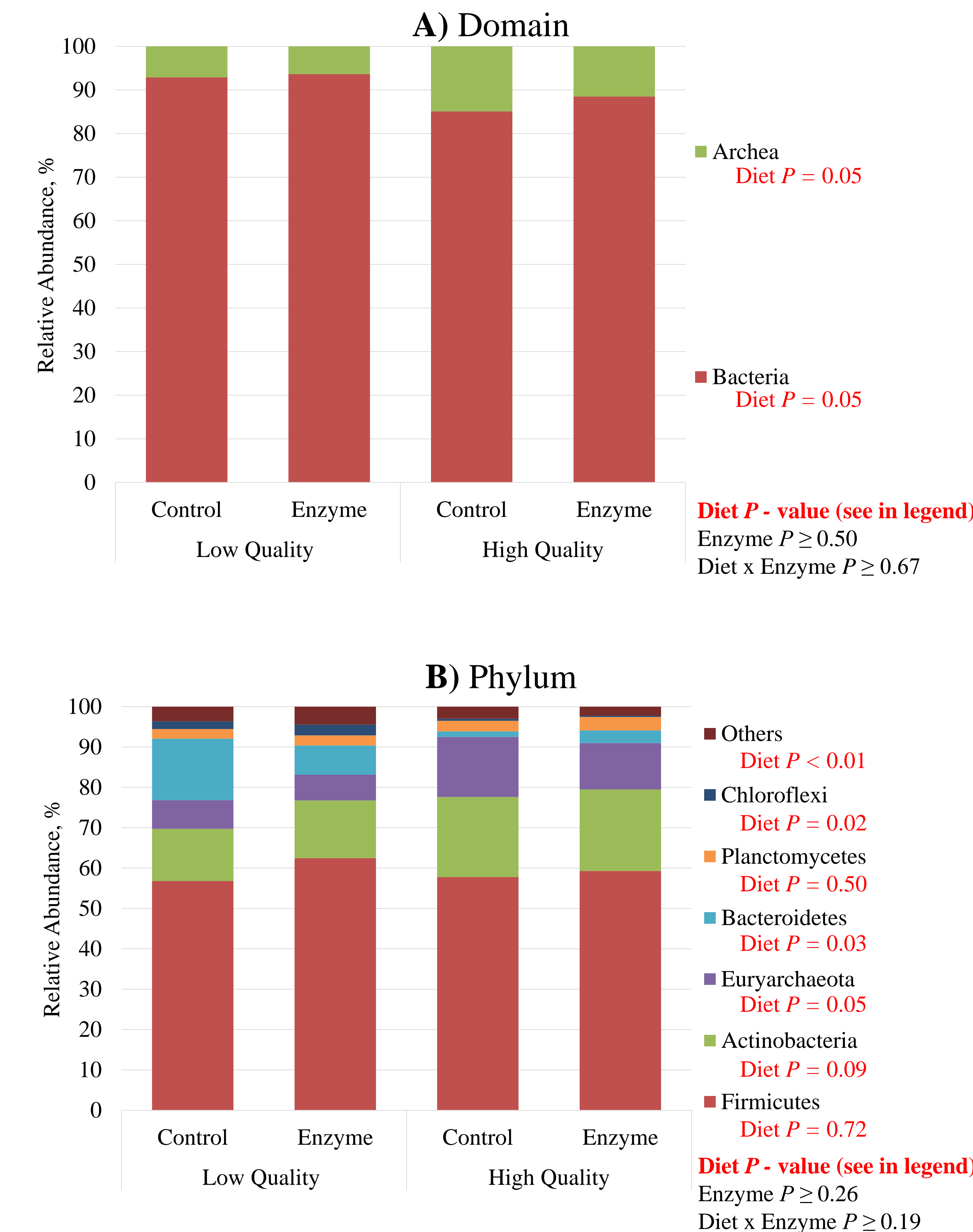


Figure 2: Microbiome relative abundance of ruminal samples collected from steers fed high or low-quality growing diets with or without the pre-treatment with fibrolytic enzyme, for: A) Domain; B) Phylum; C) Class; D) Order; E) Family; and F) Genus.

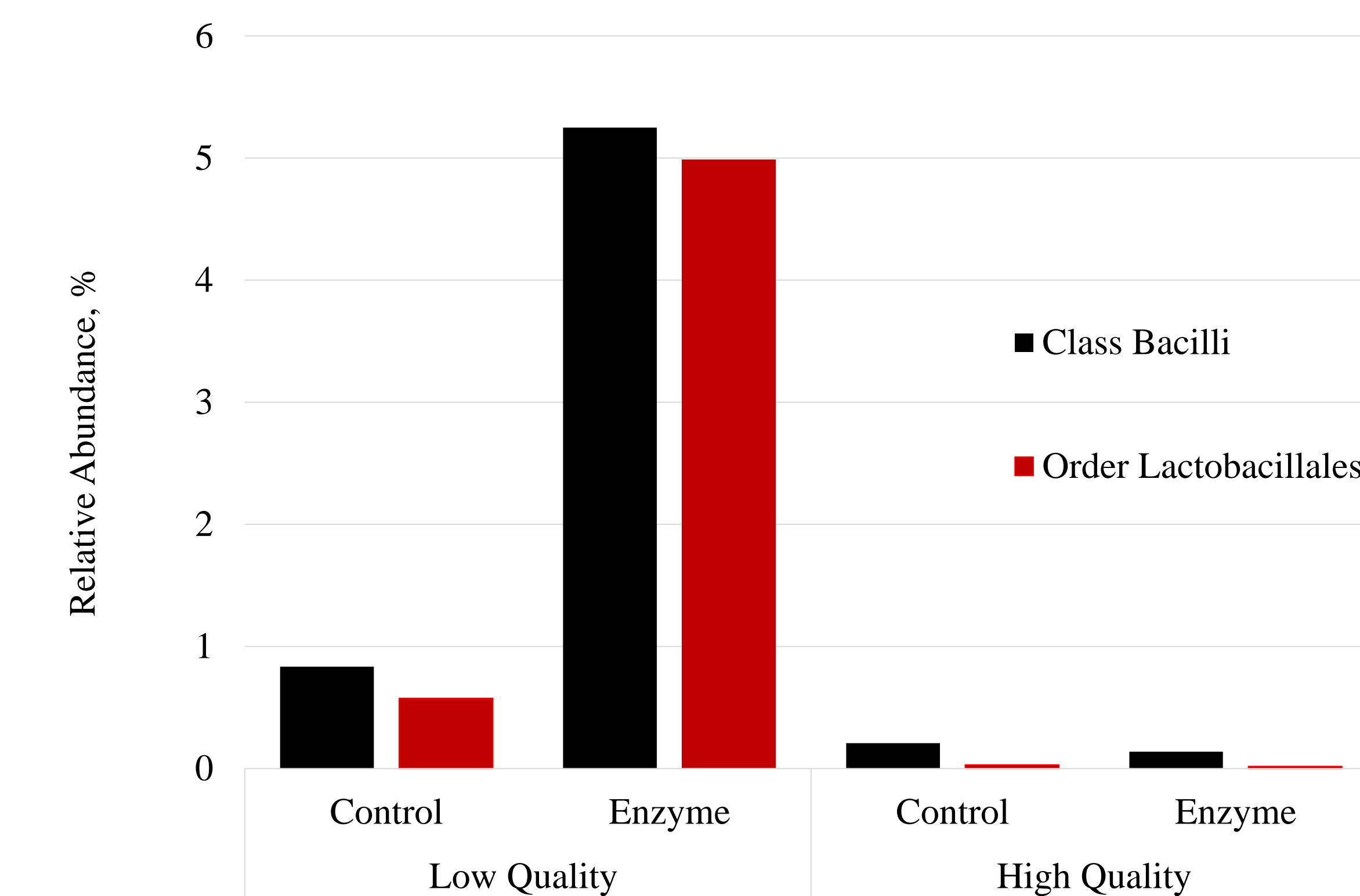


Figure 3: Microbiome relative abundance of ruminal samples collected from steers fed high or low quality growing diets with or without the pre-treatment with fibrolytic enzymes, on behalf of the Diet x Enzyme tendency for interaction on Order Lactobacillales ($P = 0.11$; SEM = 1.3244) and Class Bacilli ($P = 0.11$; SEM = 1.3240).

Conclusion:

While beef cattle growing diet quality greatly influenced ruminal microbiome relative abundance, the pre-treatment of beef cattle low-quality growing diet with fibrolytic enzymes tended to positively affect the relative abundance of ruminal microbiota within Class Bacilli, mainly represented by the Order Lactobacillales.

Acknowledgment:

Current research project received financial support from AB Vista Feed Ingredients, United Kingdom.

Table 1. Dietary feed ingredients and calculated nutrient composition of growing diets (Low or High Quality) fed to beef steers

Ingredient, % DM basis	Nutrient Composition, % DM basis		Low Quality		High Quality		
	Low Quality	High Quality	Low Quality	High Quality	Low Quality	High Quality	
Corn Silage, 35% Grain	-	36	NE Maintenance, Mcal/Kg	1.59	1.81		
Alfalfa Hay, Early Vegetative	-	15	Gain, Mcal/Kg	1.01	1.19		
Gin Trash (Cotton Burrs)	20	-	CP	14.60	14.37		
Sorghum Stalks, hay	25	-	EE	3.02	3.06		
Urea	0.7	-	NDF	28.55	22.42		
Molasses, Cane	5	-	Ca	0.75	0.75		
Corn grain, steam flaked	26.75	26.6	P	0.37	0.45		
Wet Corn Gluten Feed, Cargill	15	15	K	1.41	1.13		
Cottonseed meal	4	4	Mg	0.19	0.29		
Tallow	1	0.4	S	0.18	0.20		
Limestone	0.55	1					
Supplement	2	2					