

Rarefaction curve

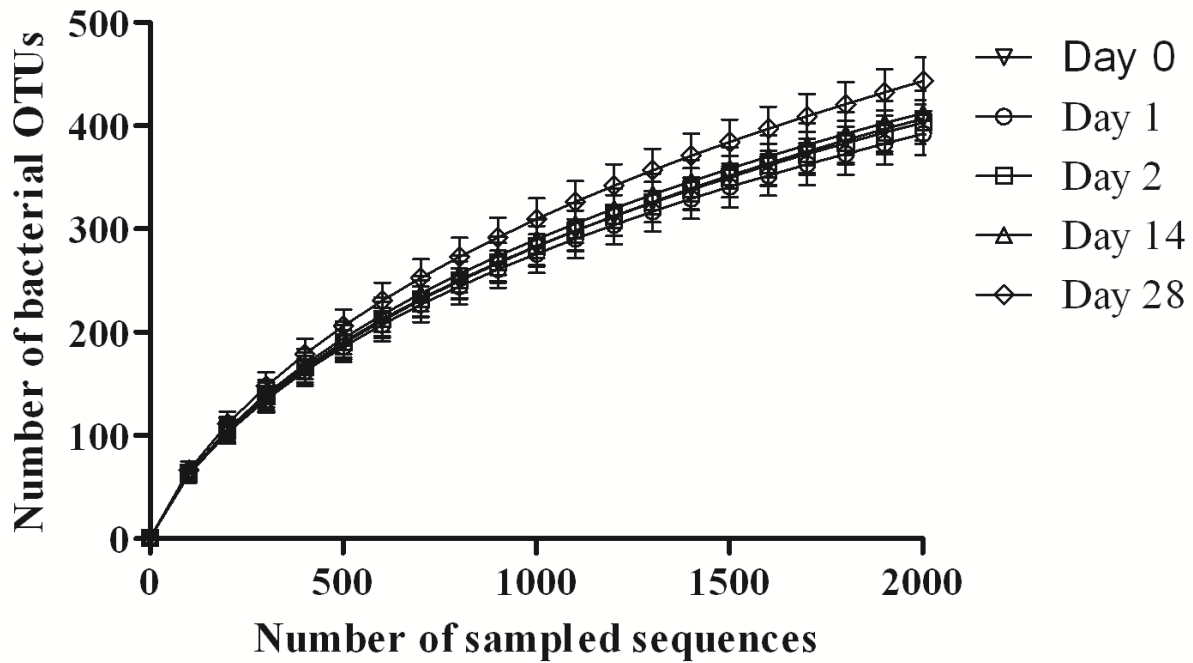


Fig. S1. Rarefaction curves representing the number of observed sequences versus the sequencing depth derived from operational taxonomic units (OTU) tables generated from the mothur pipeline from fecal samples of Angus steers ($n = 12$) grazing either a non-toxic endophyte-infected (Max-Q; $n = 6$) or a toxic endophyte-infected (E+; $n = 6$) tall fescue before (Day 0) and 1, 2, 14, and 28 days post-pasture assignment. Data are presented as means \pm standard deviation.

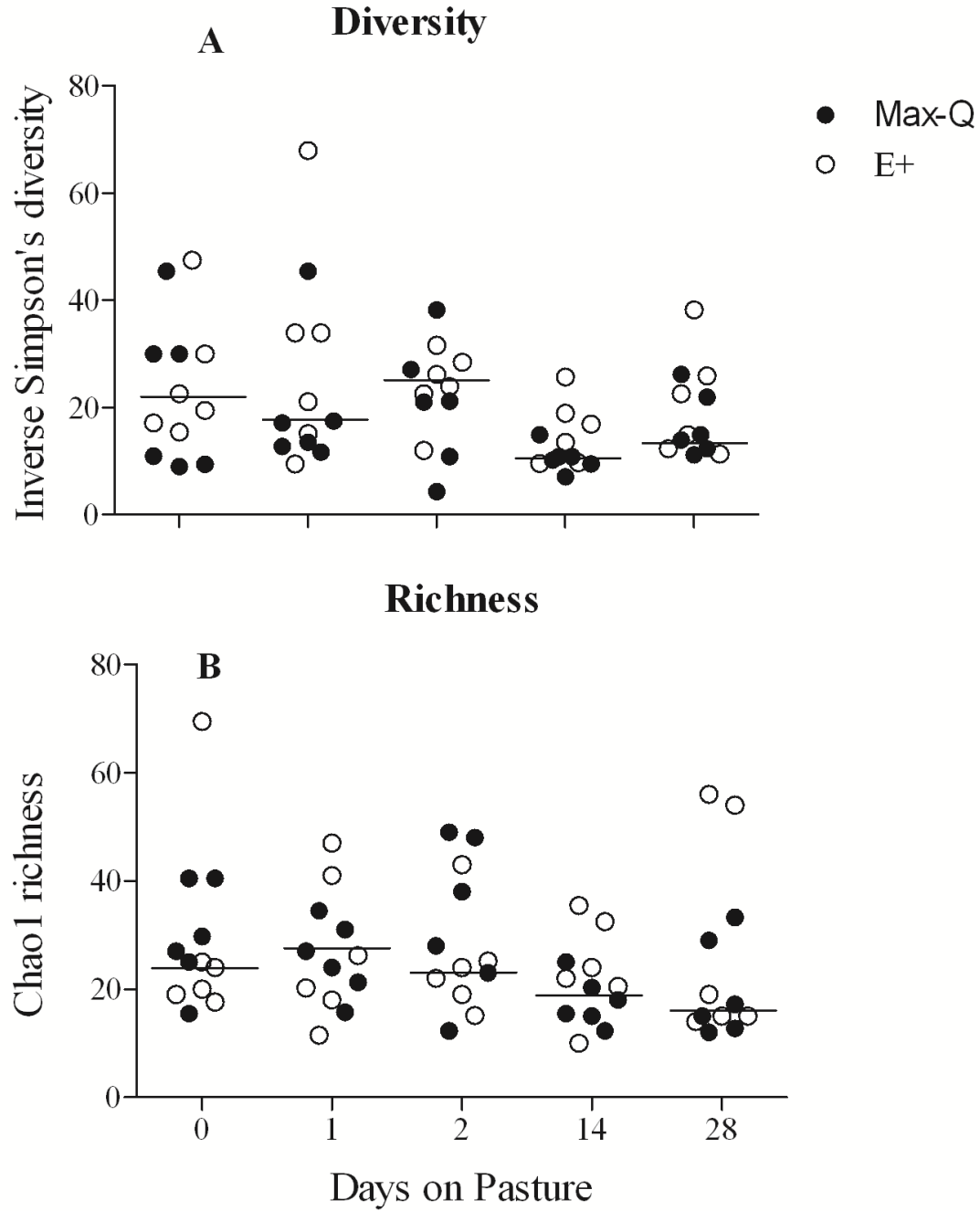


Fig. S2. Changes in (A) diversity (inverse of Simpson's diversity index) and (B) richness (Chao1 richness) metrics in Angus steers grazing either a non-toxic endophyte-infected (Max-Q; n= 6) or a toxic endophyte-infected (E+; n= 6) tall fescue before placement on pastures (Day 0) and for 1, 2, 14, and 28 days. Diversity and richness means are presented as a line for each sampling date.

File S1. Interactive fecal bacterial community composition analyses using Krona Tools 2.7 of the microbiota of Angus steers either prior to pasture placement or after 1, 2, 14, or 28 days of grazing either toxic- (E+; n = 6) or a non-toxic (Max-Q; n = 6) tall fescue. The number of sequences classified within a taxonomic level are expressed as percentages of the total sequence number. To access, follow the link, download the .html file, and open it in a web browser. Then, the interactive Krona plots would appear in the web browser. The link to the .html file is below:

<https://drive.google.com/open?id=1AL67gnXwpPvc1SgP6WdOJWEMYTiTj6M7>

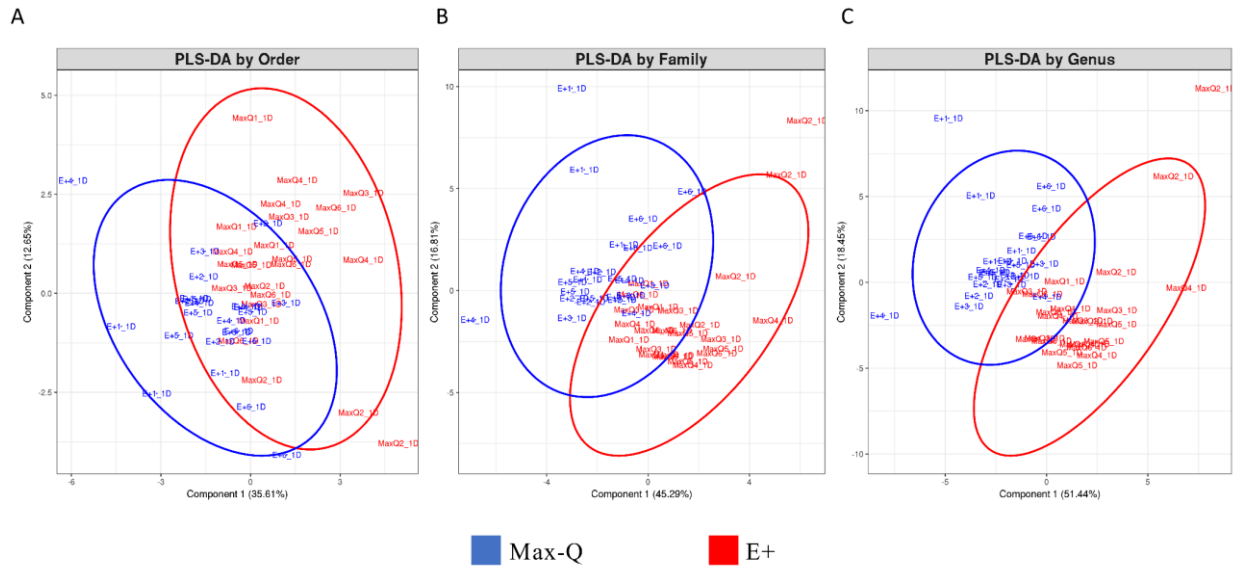


Fig. S3. Partial least square discriminant analysis (PLS-DA) plots analyzing the fecal microbiota at the (A) order (B) family and (C) genus level of Angus steers grazing either a non-toxic endophyte-infected (Max-Q; n = 6) or a toxic endophyte-infected (E+; n = 6) tall fescue over the course of a 28-day grazing trial.

Principal Component Analysis

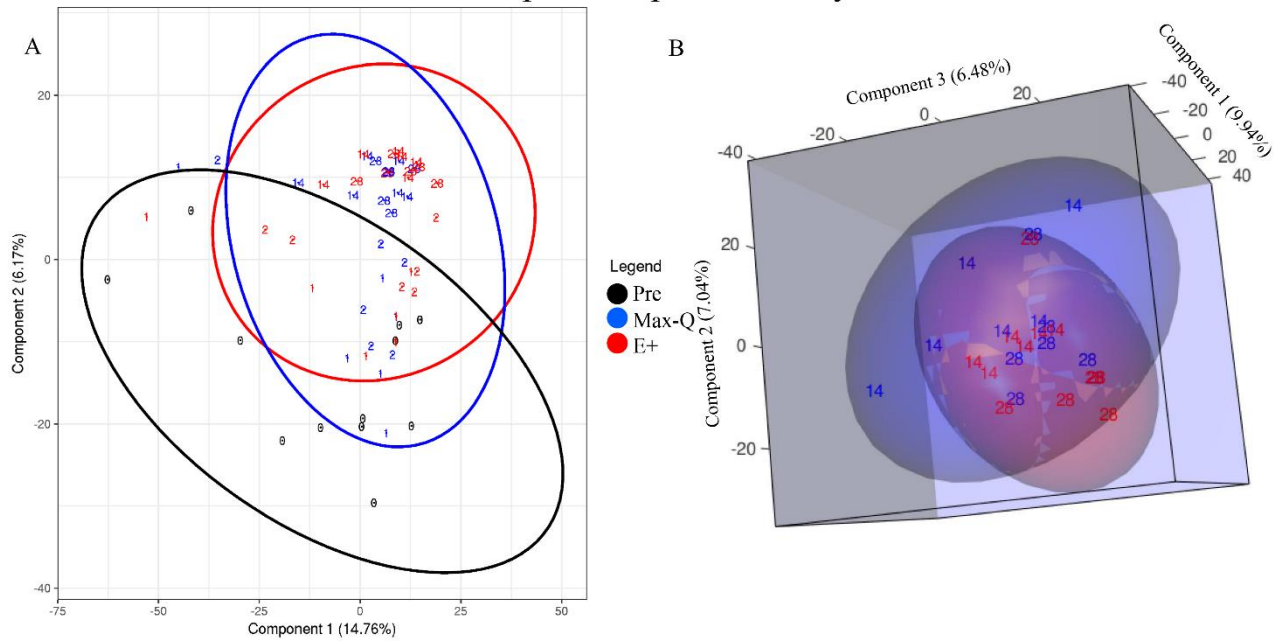
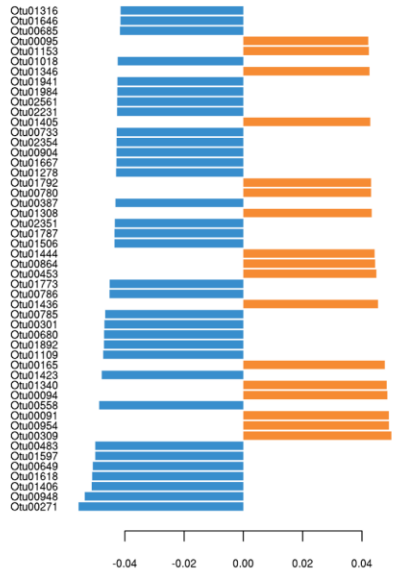
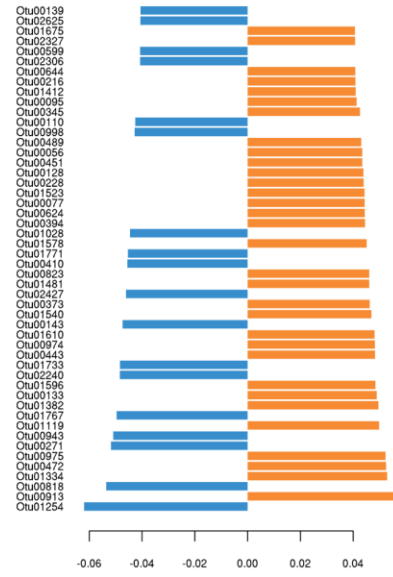


Fig. S4. Principal component plots analyzing the fecal microbiota of Angus steers grazing either a non-toxic endophyte-infected (Max-Q; n = 6) or a toxic endophyte-infected (E+; n = 6) tall fescue (**A**) throughout the 28-day grazing trial and (**B**) only at 14 and 28 days of the grazing trial.

A Day 1 Contributions



B Day 2 Contributions



C Day 14 Contributions



D Day 28 Contributions

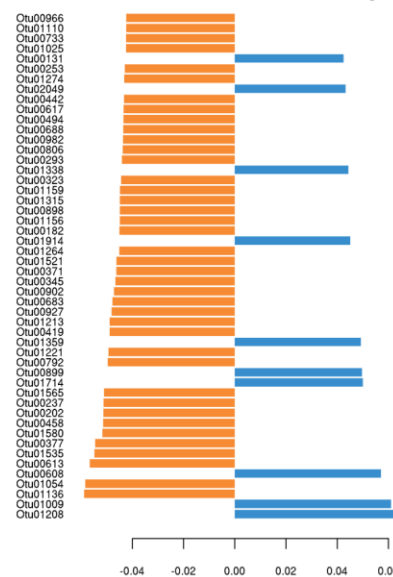


Fig. S5. Partial least square discriminant analysis (PLS-DA) loadings plots representing the top 50 operational taxonomic units (OTUs) that contributed to separation between Angus steers grazing a non-toxic endophyte-infected (Max-Q; n = 6) and a toxic endophyte-infected (E+; n = 6) tall fescue for the PLS-DA analysis performed on the fecal microbiota at: **(A)** 1, **(B)** 2, **(C)** 14, and **(D)** 28 days. Colors are indicative of: Max-Q = blue, E+ = orange. Bars represent the fescue treatment in which the OTUs had higher abundances and the x-axis is the respective loading weight for each OTU.

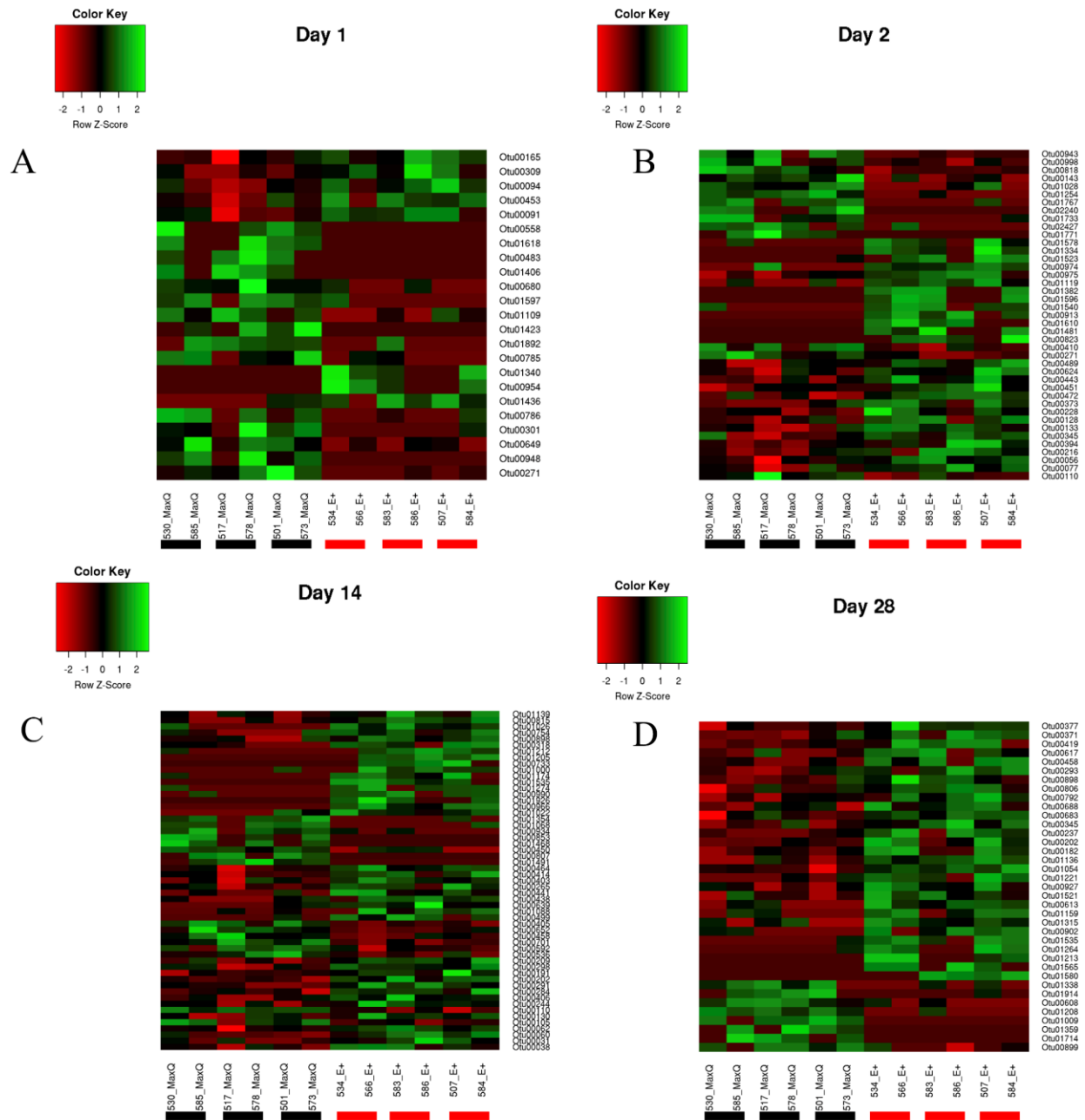


Fig. S6. Heat maps representing operational taxonomic units (OTUs) that were significantly different ($P < 0.05$) between Angus steers grazing either a non-toxic endophyte-infected (Max-Q; $n = 6$) or a toxic (E+; $n = 6$) endophyte-infected tall fescue after (A) 1, (B) 2, (C) 14, and (D) 28 days of grazing. Bars underneath the column labels indicate steers on the same pastures: Black = Max-Q steers; Red = E+ steers.

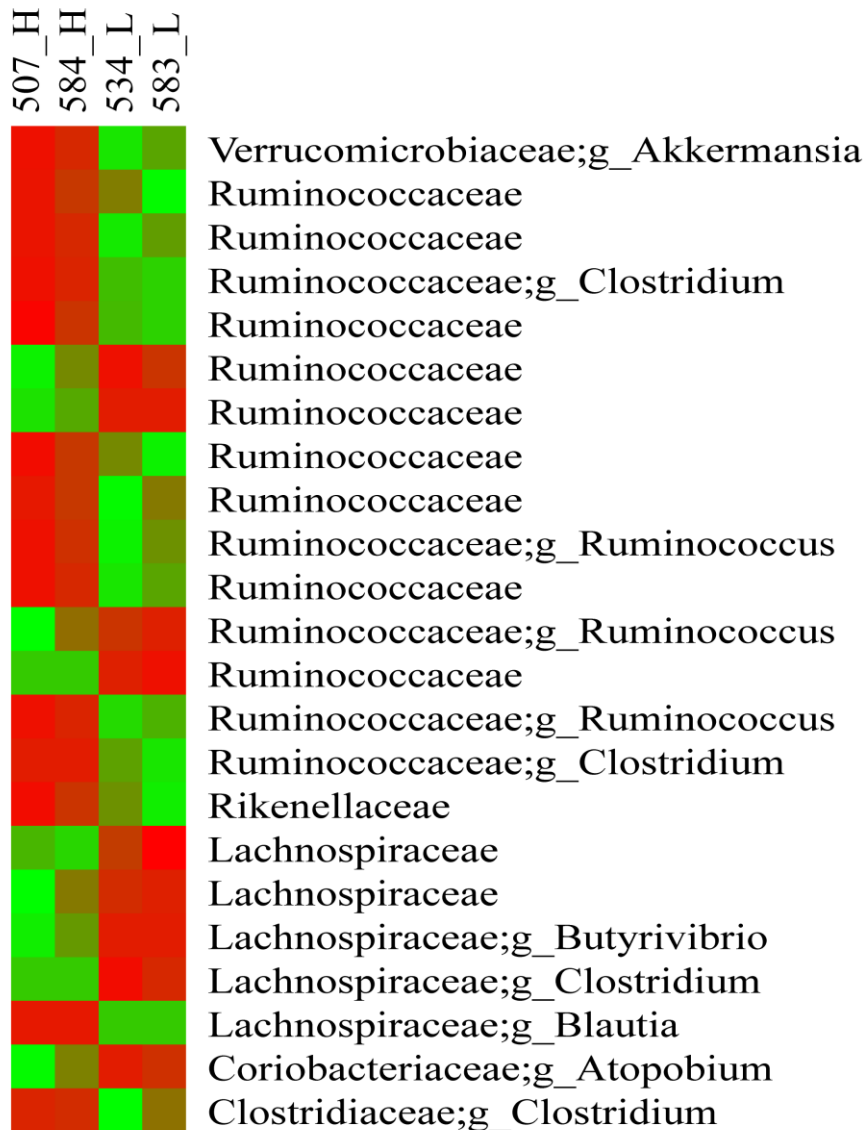


FIG S7. Heat maps representing normalized operational taxonomic unit (OTU) sequence counts for Angus steers that grazed a toxic endophyte-infected tall fescue (E+; n = 4) throughout the 28 day grazing trial stratified by weight gains. “_G” indicates the two steers that gained the most weight and “_NG” indicates the two steers that had not gained weight; red represents sequence counts below the respective OTUs means and green represents sequence counts greater than the respective OTU means.

Table S1. Bacterial families that had operational taxonomic units (OTUs) that were main contributors to the treatment separations seen in partial least squares discriminant analysis (PLS- DA) and the number of days Angus steers spent grazing either a non-toxic endophyte-infected tall fescue (Max-Q; n = 6) or a toxic endophyte-infected tall fescue (E+; n = 6) where the family OTUs resulted from PLS-DA loadings analysis.

Days on pasture	Bacterial families
1	<i>Odoribacteraceae</i>
	<i>Veillonellaceae</i>
	<i>Moraxellaceae</i>
	<i>Mycoplasmataceae</i>
2	<i>Proteobacteria_unclassified</i>
	<i>Rikenellaceae</i>
	<i>Christensenellaceae</i>
14	<i>Mollicutes_unclassified</i>
	<i>ML615J-28_unclassified</i>
28	<i>Anaeroplasmataceae</i>
	<i>Eubacteriaceae</i>
	<i>Dehalobacteriaceae</i>
1 and 2	<i>Paraprevotellaceae</i>
	<i>S24-7</i>
1 and 28	<i>Clostridia_unclassified</i>
14 and 28	<i>Lactobacillaceae</i>
1, 2, and 14	<i>Mogibacteriaceae</i>
	<i>Bacteroidaceae</i>
1, 2, and 28	<i>Erysipelotrichaceae</i>
	<i>Coriobacteriaceae</i>
1, 14, and 28	<i>Prevotellaceae</i>
	<i>Clostridiaceae</i>

Table S2. Top four most frequent classified families, broken down by OTUs classified at the genus level, of bacteria that positively correlated with rectal temperatures (RT) in steers that grazed toxic (E+; n = 6) endophyte-infected tall fescue. The number of OTUs within a family/genus, average Spearman correlation coefficient and P-values are presented.

Rectal Temperatures				
Family	Genus	No. of OTUs	Correlation	P-value
<i>Lachnospiraceae</i>		18	0.46	0.026
	<i>Butyrivibrio</i>	2	0.48	0.018
	<i>Roseburia</i>	1	0.54	0.0065
	<i>Coprococcus</i>	1	0.42	0.040
	<i>Dorea</i>	1	0.42	0.040
<i>Ruminococcaceae</i>		4	0.54	0.0093
<i>Coriobacteriaceae</i>		2	0.44	0.031
	<i>Enterococcus</i>	1	0.45	0.028
<i>Paraprevotellaceae</i>		2	0.42	0.042
	<i>CF231</i>	1	0.43	0.037
	<i>YRC22</i>	1	0.41	0.048