E-SUPPLEMENT

for

**Rumen bacterial community structure impacts feed efficiency in beef cattle**

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**SUPPLEMENTAL TABLES**

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| **Table S1.** Final taxa-based (family level) linear models constructed using forward-stepwise regression for predicting average daily feed intake (ADFI), average daily gain (ADG), and gain-to-feed ratio (G:F) for the heifer cohort | | | | | | | |
| Trait | Predictor | Coefficient | SEa | t-statistic | P-value | AICb | R2c |
| ADFI | Intercept | 0.1304 | 0.6396 | 0.204 | 0.83880 | -45.63 | 0.0779 |
|  | No Assigned Family | 21.4395 | 12.2998 | 1.743 | 0.08420 |  |  |
|  | Veillonellaceae | -4.2211 | 2.4386 | -1.731 | 0.08640 |  |  |
|  | Coriobacteriaceae | 17.2989 | 12.1602 | 1.423 | 0.15780 |  |  |
| ADG | Intercept | 0.2903 | 0.1167 | 2.487 | 0.014456 | -387.97 | 0.1195 |
|  | Veillonellaceae | -1.7999 | 0.4886 | -3.684 | 0.000363 |  |  |
|  | Coriobacteriaceae | 4.9920 | 2.3940 | 2.085 | 0.039455 |  |  |
| G:F | Intercept | 0.03626 | 0.01310 | 2.768 | 0.00667 | -870.34 | 0.1415 |
|  | Veillonellaceae | -0.17601 | 0.05416 | -3.250 | 0.00155 |  |  |
|  | Coriobacteriaceae | 0.83747 | 0.29105 | 2.877 | 0.00486 |  |  |
|  | No Assigned Family | -0.23374 | 0.12384 | -1.887 | 0.06187 |  |  |

a Standard error.

b Akaike information criteria.

c Adjusted R-squared.

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| **Table S2.** Final taxa-based (family level) linear models constructed using forward-stepwise regression for predicting average daily feed intake (ADFI), average daily gain (ADG), and gain-to-feed ratio (G:F) for the steer cohort | | | | | | | |
| Trait | Predictor | Coefficient | SEa | t-statistic | P-value | AICb | R2c |
| ADFI | Intercept | -1.1341 | 0.4666 | -2.430 | 0.01689 | -11.94 | 0.1183 |
|  | No Assigned Family | -21.6366 | 7.3303 | -2.952 | 0.00395 |  |  |
|  | Paraprevotellaceae | 3.6602 | 1.3543 | 2.703 | 0.00810 |  |  |
|  | Lachnospiraceae | 3.5709 | 1.4587 | 2.448 | 0.01613 |  |  |
|  | Coriobacteriaceae | -15.5451 | 5.0767 | -3.062 | 0.00283 |  |  |
|  | Bifidobacteriaceae | 8.5743 | 4.2298 | 2.027 | 0.04534 |  |  |
|  | Erysipelotrichaceae | 3.2415 | 2.0898 | 1.551 | 0.12408 |  |  |
| ADG | Intercept | -0.21208 | 0.08431 | -2.515 | 0.0135 | -395.36 | 0.06433 |
|  | p-2534-18B5 | 0.42280 | 0.26345 | 1.605 | 0.1117 |  |  |
|  | Lachnospiraceae | 0.57580 | 0.24498 | 2.350 | 0.0207 |  |  |
|  | Coriobacteriaceae | -1.33373 | 0.73841 | -1.806 | 0.0739 |  |  |
|  | Bifidobacteriaceae | 1.12435 | 0.68550 | 1.640 | 0.1041 |  |  |
|  | No Assigned Family | 1.51900 | 1.04199 | 1.458 | 0.1480 |  |  |
| G:F | Intercept | -0.004213 | 0.004517 | -0.933 | 0.3532 | -844.27 | 0.08804 |
|  | No Assigned Family | 0.385488 | 0.142953 | 2.697 | 0.0082 |  |  |
|  | Paraprevotellaceae | -0.045782 | 0.025234 | -1.814 | 0.0726 |  |  |
|  | No Assigned Family | 0.193173 | 0.116797 | 1.654 | 0.1012 |  |  |

a Standard error.

b Akaike information criteria.

c Adjusted R-squared.

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| **Table S3.** Evaluation of taxa-based (family level) model accuracy to predict average daily feed intake (ADFI), average daily gain (ADG), and gain-to-feed ratio (G:F) for the heifer and steer cohorts | | |
| Traita | P-value | R2b |
| ADFI |  |  |
| Heifer | 0.78 | <0.01 |
| Steer | 0.63 | <0.01 |
| ADG |  |  |
| Heifer | 0.66 | <0.01 |
| Steer | 0.10 | 0.04 |
| G:F |  |  |
| Heifer | 0.50 | <0.01 |
| Steer | 0.05 | 0.05 |

a Heifer data was used to assess the steer model and steer data was used to assess the heifer model.

b Adjusted R-squared.

**SUPPLEMENTAL FIGURES**



**Figure S1.** Principal coordinates analysis (PCoA) using the weighted Unifrac distance matrix displaying significant structuring of bacterial communities by beef cattle cohort.

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**Figure S2.** Boxplots of linear model residuals from average daily feed intake and average daily gain from (a) heifer (*n*=125) and (b) steer (*n*=122) cohorts to evaluate outlier observations.

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**Figure S3.** Rarefaction curves at even sample depth for (a) heifer (9,081 reads) and (b) steer (12,430 reads) cohorts. Feed efficiency quadrants: high ADG and high ADFI (ADGH-ADFIH), high ADG and low ADFI (ADGH-ADFIL), low ADG and high ADFI (ADGL-ADFIH), and low ADG and low ADFI (ADGL-ADFIL).



**Figure S4.** Alpha diversity measures (observed operational taxonomic units (OTUs), Shannon-Weiner index (logarithm base 2), and dominance (1-Simpson index)) for (**a**) heifer and (**b**) steer cohorts. Circles represent sample values and diamonds represent means. Feed efficiency quadrants: high ADG and high ADFI (ADGH-ADFIH), high ADG and low ADFI (ADGH-ADFIL), low ADG and high ADFI (ADGL-ADFIH), and low ADG and low ADFI (ADGL-ADFIL).



**Figure S5.** Phylum level classification of the bacterial community composition across feed efficiency quadrants from the heifer discovery population. Feed efficiency quadrants: high ADG and high ADFI (ADGH-ADFIH), high ADG and low ADFI (ADGH-ADFIL), low ADG and high ADFI (ADGL-ADFIH), and low ADG and low ADFI (ADGL-ADFIL).



**Figure S6.** Phylum level classification of the bacterial community composition across feed efficiency quadrants from the steer discovery population. Feed efficiency quadrants: high ADG and high ADFI (ADGH-ADFIH), high ADG and low ADFI (ADGH-ADFIL), low ADG and high ADFI (ADGL-ADFIH), and low ADG and low ADFI (ADGL-ADFIL).



**Figure S7.** Bipartite network showing distinctive clustering of differentially abundant OTUs (black circles) by heifer (red edges) and steer (blue edges) cohort. Differentially abundant OTUs were identified through pairwise comparisons across feed efficiency quadrants using the linear discriminatory analysis (LDA) effect size (LefSe) method within cohort. Feed efficiency quadrants: high ADG and high ADFI (magenta squares), high ADG and low ADFI (red squares), low ADG and high ADFI (blue squares), and low ADG and low ADFI (green squares)

 **Figure S8.** Percent transporters from the selected bacterial features across feed efficiency models for both heifer and steer cohorts. Transporters functional categories were determined using the phylogenetic investigation of communities by reconstruction of unobserved states (PICRUSt) approach. Percent of ABC transporters and percent of others transporters in bacterial features with a negative coefficient were similar (t-test, *P*=0.55) to those with a positive coefficient.