

Final Technical Report
FCEB Project #38

Final Report
August 15, 2024
FCEB # 38

Title: Impact of Brahman genetics on feed efficiency and methane emissions of heifers with implications for the Florida cow-calf producers

Principal investigator:

Nicolas DiLorenzo, Ph.D.
University of Florida - NFREC
3925 Highway 71, Marianna, FL 32446
Tel: (850) 526-1615
Email: ndilorenzo@ufl.edu

Co-Principal investigators:

Raluca G. Mateescu, Ph.D. – UF Department of Animal Sciences, Gainesville, FL
Fernanda Rezende, PhD – UF Department of Animal Sciences, Gainesville, FL

1. Specific aims:

Reviewing the literature, it becomes evident that our understanding of the contribution of *Bos indicus* genetics to feed efficiency and reproductive efficiency is incomplete, demonstrating the need to continue this work. The role played by thermotolerance with respect to feed efficiency was addressed in a previously funded proposal (2019) and it showed a clear connection between selection for thermotolerance and its impact on feed efficiency in Brangus cattle. Now that we are beginning to understand the link between feed efficiency and thermotolerance, we aim at assessing the genetic potential of the replacement heifers that are part of the UF Multibreed project, with the potential of assessing the optimal percentage of Brahman influence needed in order to maximize feed efficiency and profitability, particularly in the current scenario of increasing feed costs.

The rationale for uncovering the relationships underlying the Brahman influence-feed efficiency complex are twofold:

1) in the context of rising feed costs, selection for feed efficiency becomes quite relevant, creating the potential to impact profitability across multiple generations. The in-depth knowledge of feed efficiency genetic architecture generated in this proposal will allow us to develop tools to be used in selection and management programs to select for superior animals with great adaptability to the region.

2) Animal productivity is a key determinant of overall ranch profitability. While greater Brahman influence confers greater adaptability to the environment, particularly as we moved south in the Florida peninsula, often a decrease in growth performance and carcass qualities are observed as the percentage of Brahman influence in the herd increases. Finding the optimum amount of Brahman influence in terms of performance and feed efficiency is imperative in order to select cattle that can ensure the sustainability of Florida's beef production. **At the conclusion of this project, we will provide beef cattle producers with genomic tools for selection for improved**

feed efficiency across various percentage of Brahman influence in the herd. This in turn can lead to a greater tolerance to heat stress while maintaining animal productivity.

2. Significance

The great majority of RFI research has been conducted using feedlot animals and mostly of the *Bos taurus* genus. Both the Brahman project and the Multibreed project of the University of Florida Department of Animal Science have been contributing over the years to the understanding of the importance of the Brahman breed influence on several aspects of Florida beef production systems. This proposal aims at synergizing some of the efforts of these projects while filling important gaps of knowledge. It is our understanding that other proposals are being submitted for funding by the Beef Cattle Enhancement Board to address the selection of superior bulls from the Brahman project in terms of feed efficacy. **There is a distinct lack of research focused on RFI assessment across different proportions of Brahman-influenced Florida cattle, particularly heifers, including the impact of selection for feed efficiency on mature cow productivity and methane emissions. Our project will address this knowledge gap.** Identifying the optimal percentage of Brahman influence needed in order to maximize animal performance and carcass quality, while maintaining the adaptability to the environment, will have a great impact in the future of Florida's beef production.

3. Approach

The Department of Animal Sciences Multibreed herd has been in existence since 1988. For mating purposes, animals in the multibreed herd are assigned to 6 breed groups based on breed composition: 100% Angus = 100% to 80% Angus; 75% Angus = 79% to 60% Angus; Brangus = 62.5% Angus; 50% Angus = 59% to 40% Angus; 25% Angus = 39% to 20% Angus; and 100% Brahman = 19% to 0% Angus.

A total of 137 replacement heifers (60 from the Brahman herd and 77 from the Multibreed herd) were transported to the University of Florida, Feed Efficiency Facility (UF-FEF) on January 2,



2024. The UF-FEF has a total of 24 concrete floored pens (111 m² each) equipped with GrowSafe technology for individual feed intake via radio-frequency identification. At the UF-FEF, the Multibreed herd heifers were gradually adapted over a 21-day period to a growing diet fed ad libitum (0.71 Mcal NEg/kg DM; 12% crude protein, DM basis) formulated to meet nutrient requirements of

Figure 1. The University of Florida Feed Efficiency Facility at NFREC.



Figure 2. Measuring methane using the GreenFeed technology at the NFREC Feed Efficiency Facility at.

growing beef cattle gaining approximately 0.9 kg/d (NASEM, 2016).

Heifers were weighed on two consecutive days at the beginning and at the end of the feed efficiency test, and interim body weight (unshrunk) and hip height were determined every 14 days. Growth rate and feed efficiency (measured both as feed conversion ratio and as residual feed intake) was calculated at the end of the 56-d backgrounding period.

Methane was measured using the GreenFeed system (C-Lock Inc., Rapid City, SD), and cattle were divided in 4 groups to stagger the measurement periods. Each measurement period will consist of 21 days of adaptation to the GreenFeed system and 7 days of methane emissions collection.

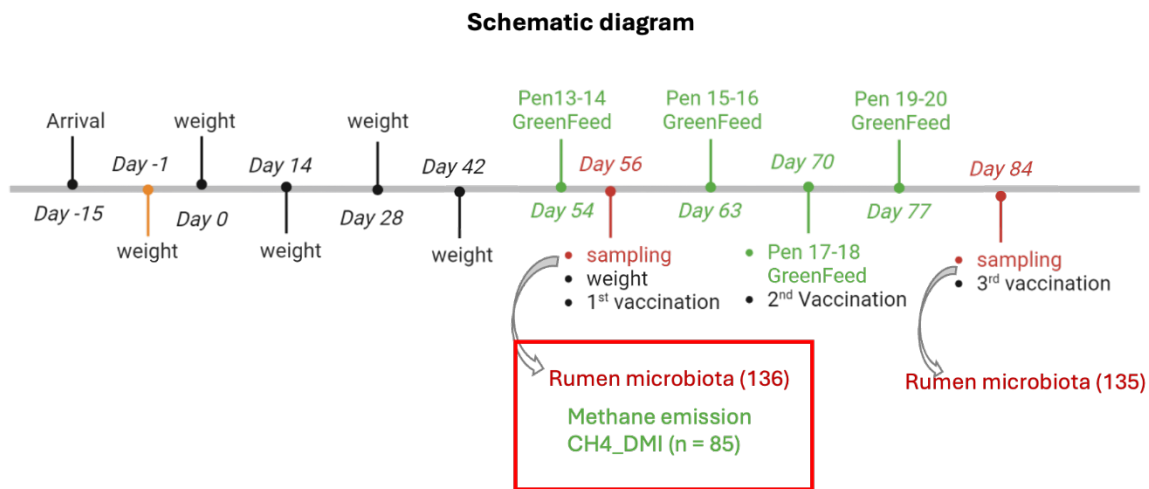


Figure 3. Sample collection schematic.

4. Results.

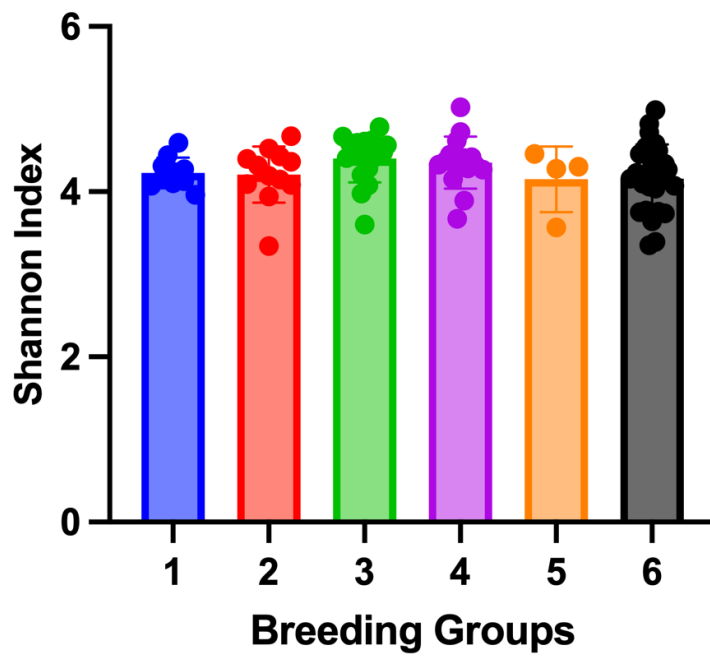
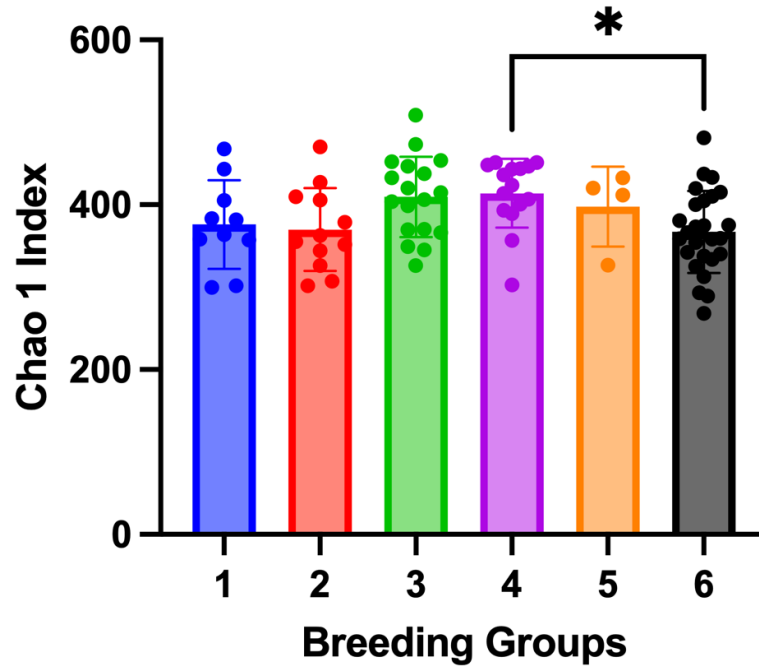
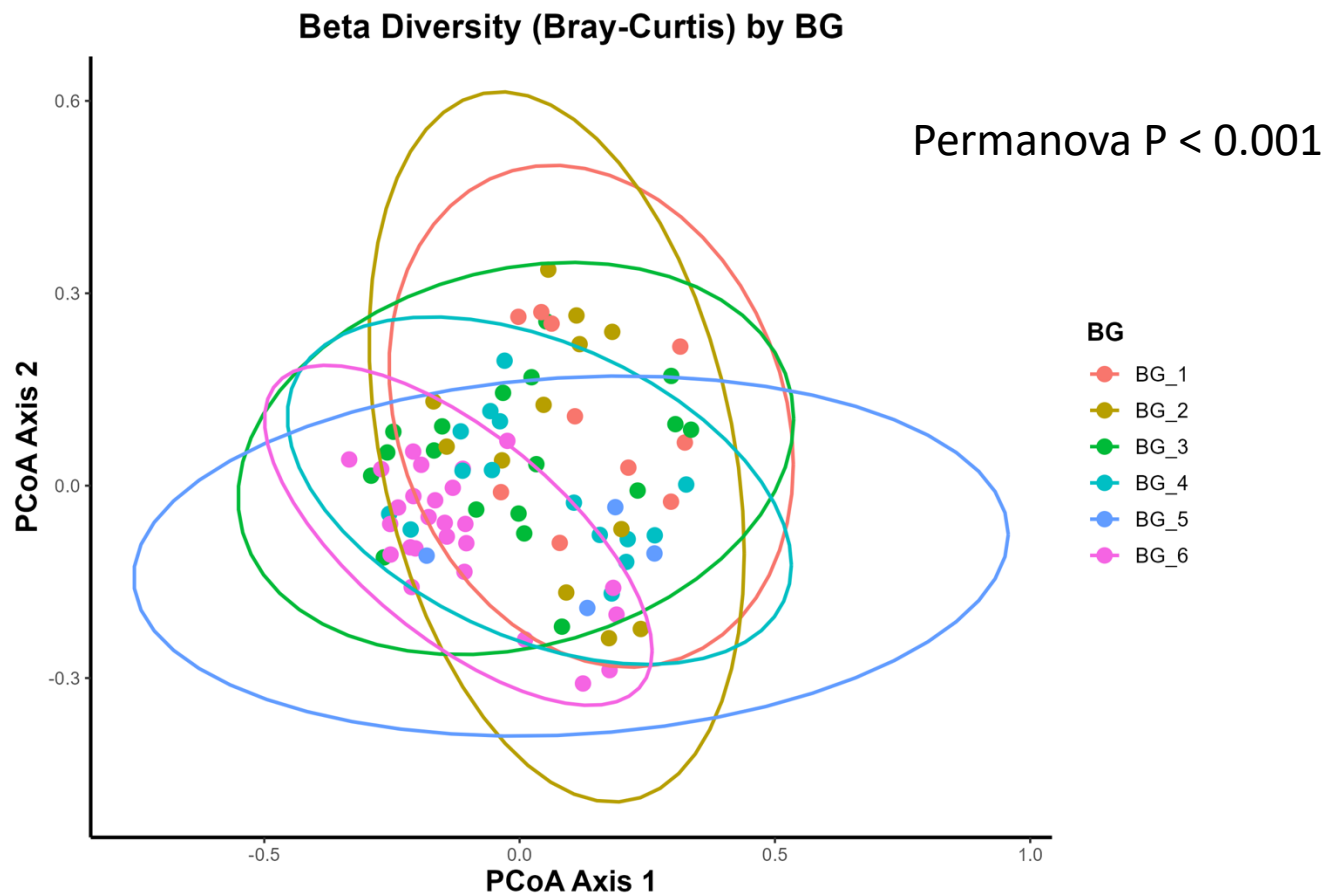


Figure 4. Alpha-diversity in the microbiome across breeding groups.



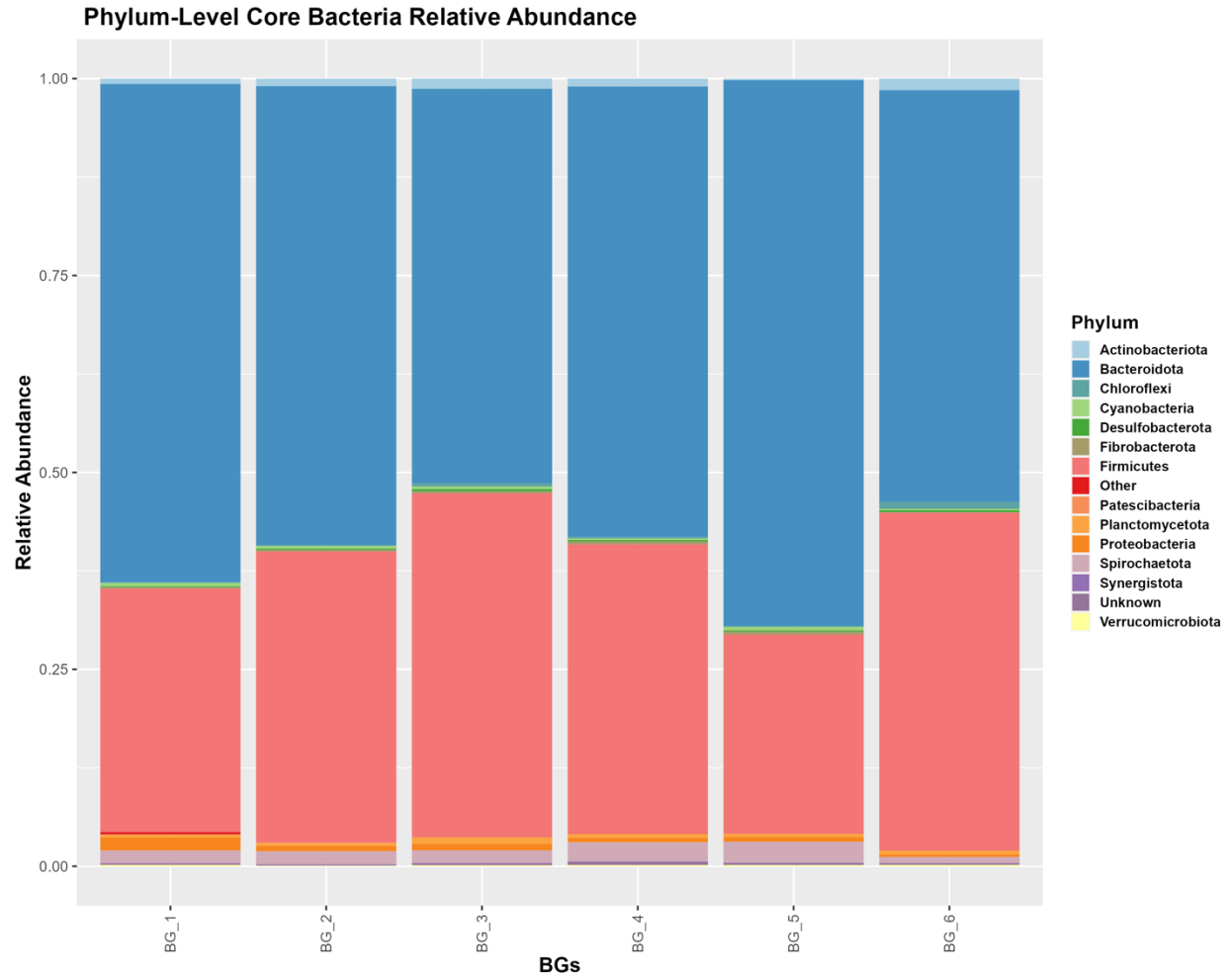
- No significant difference of microbiome alpha diversity (Shannon) were identified between breeding groups.
- Significant difference was identified in Chao1 index between BG4 and BG6

Beta-diversity (bray-curtis) across breeding groups



- **Significant difference of microbiome communities (compositions) was identified between breeding groups.**

Bacterial relative abundance (Phylum)

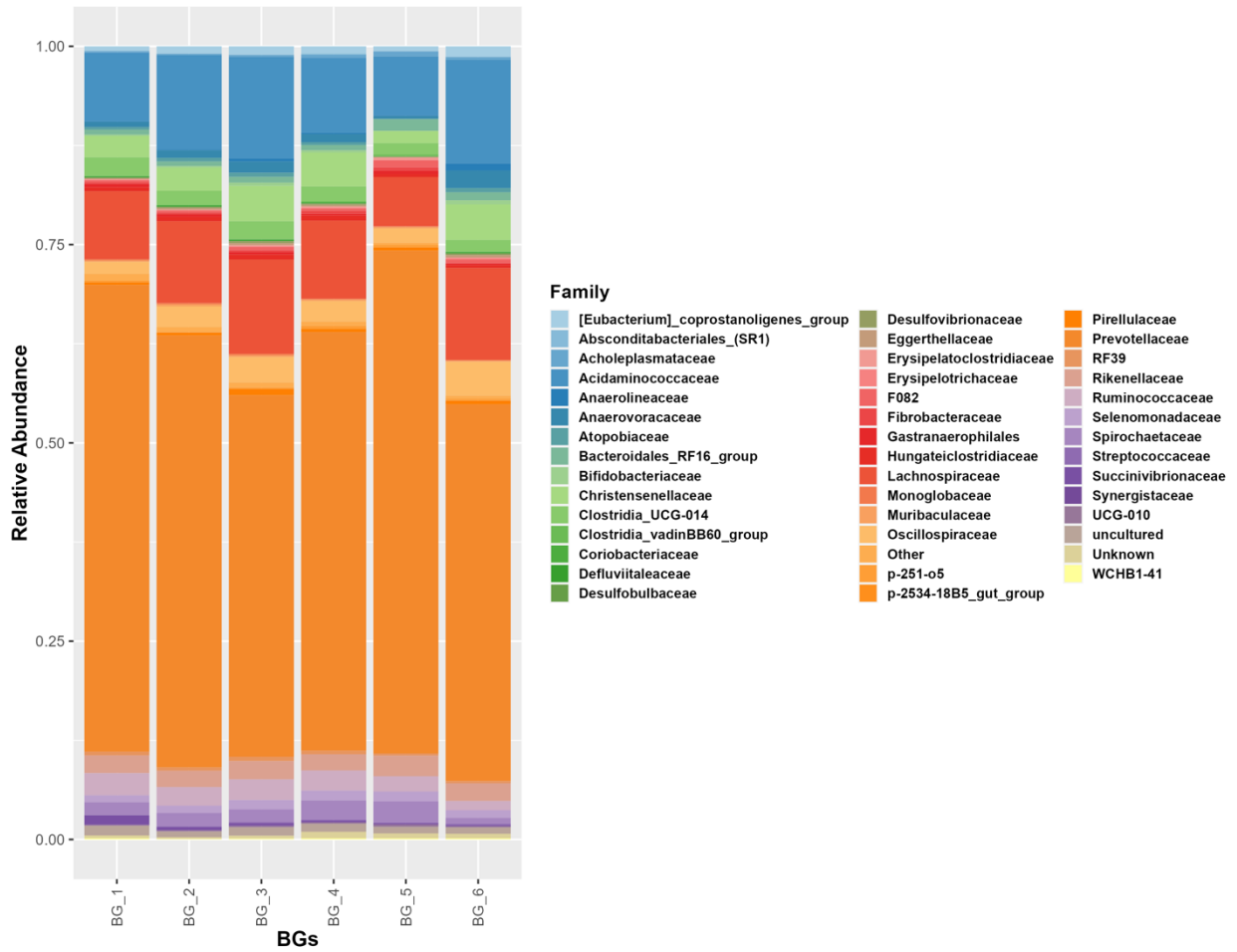


Parameter:

- Detected in more than 50% of the samples,
- Relative abundance > 1%

Bacterial relative abundance (Family)

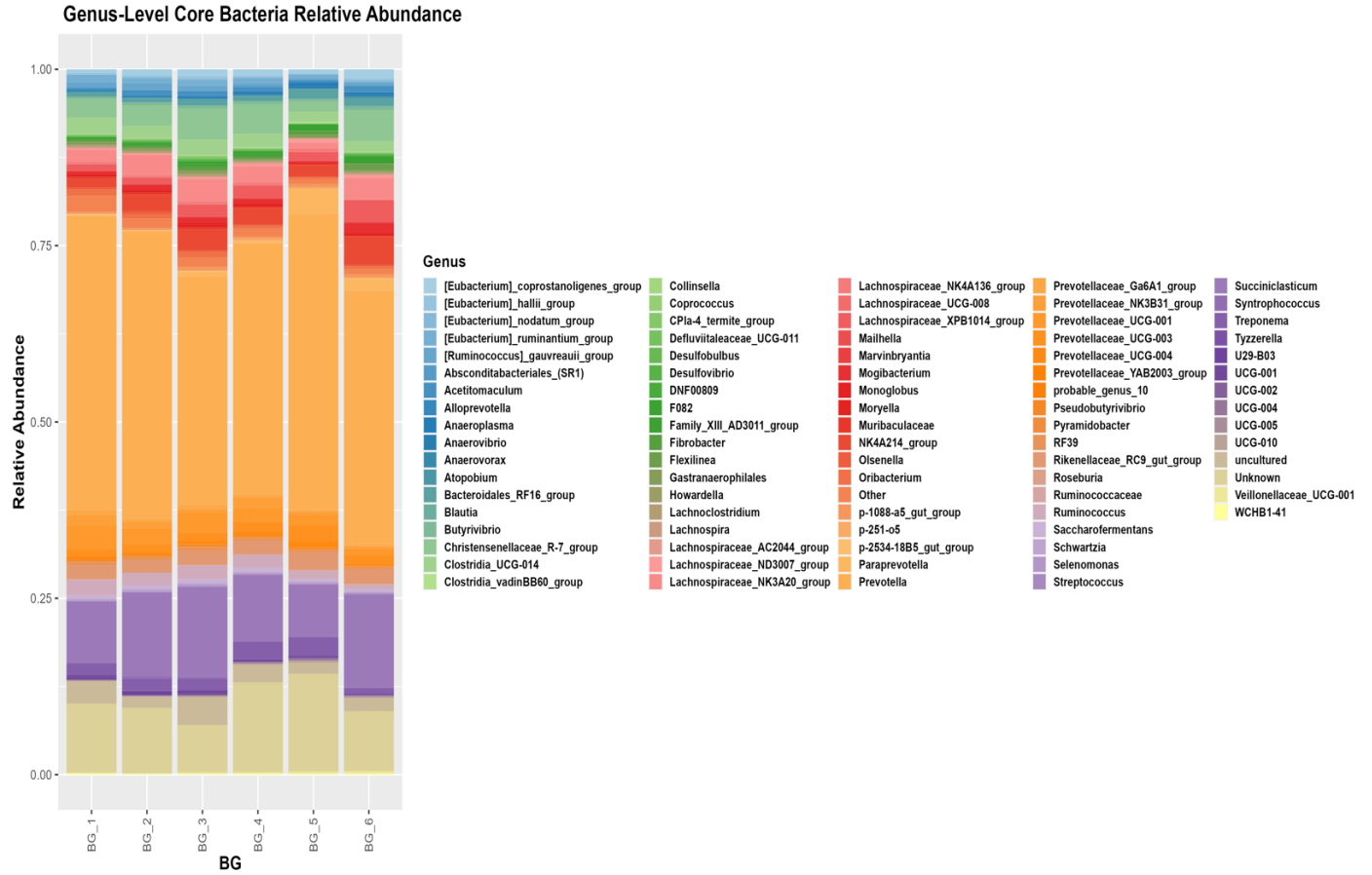
Family-Level Core Bacteria Relative Abundance



Parameter:

- Detected in more than 50% of the samples,
- Relative abundance > 1%

Bacterial relative abundance (Genus)



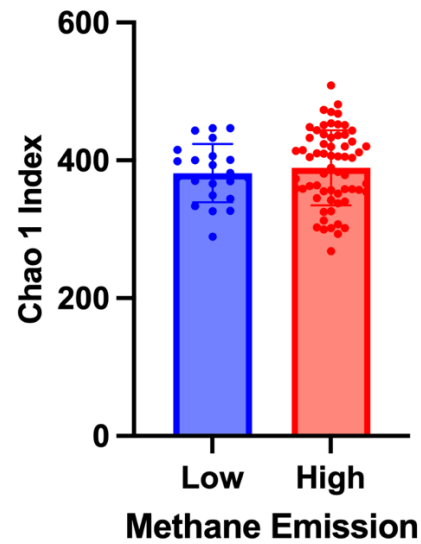
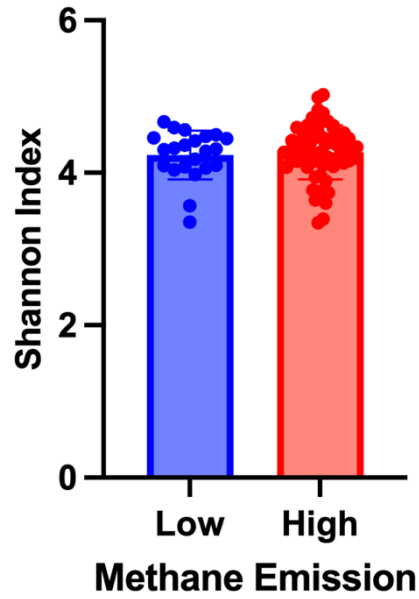
Parameter:

- Detected in more than 50% of the samples,
- Relative abundance > 1%

Methane yield (g CH₄/ kg DM) – Microbiome

Set 2 categories based on CH₄_DMI value: High (>= 11); Low (<11)

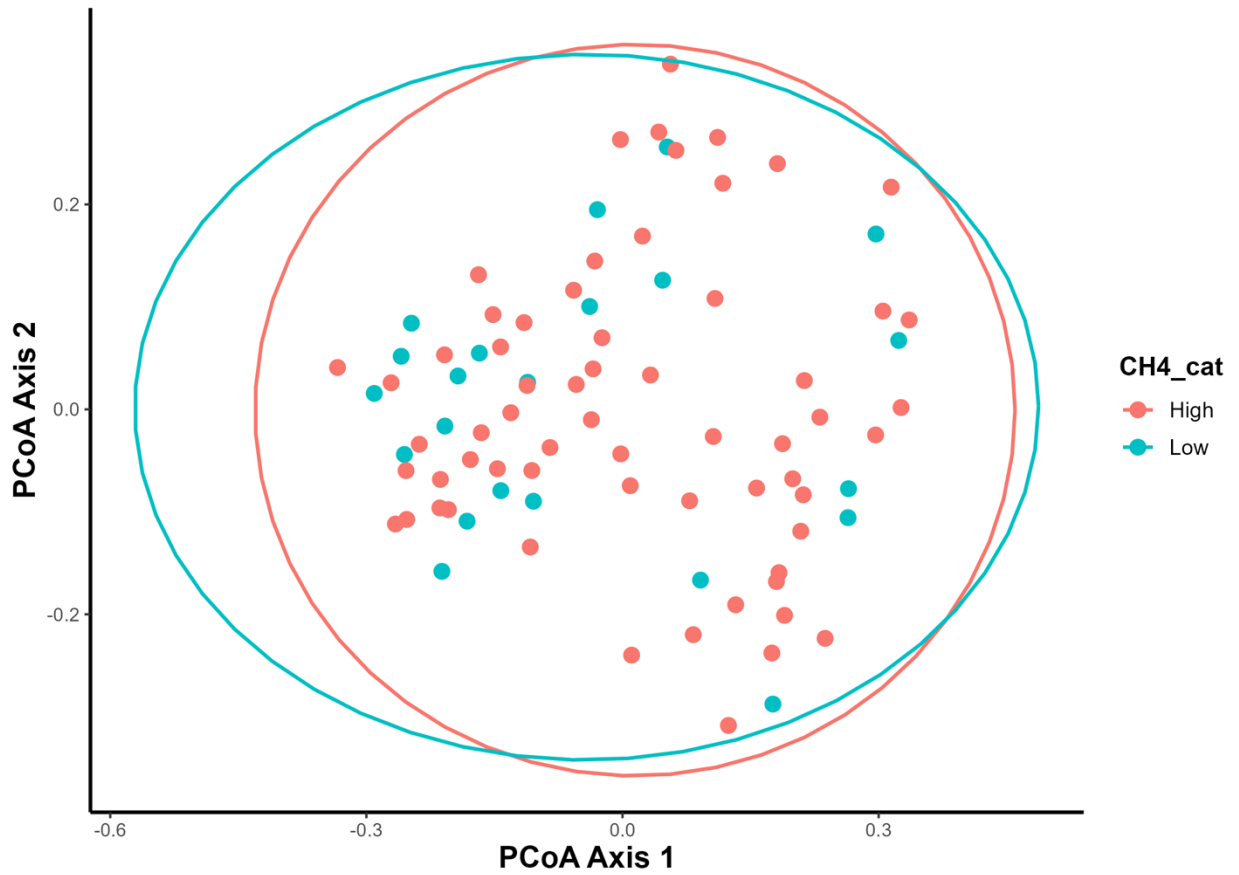
Alpha-diversity and Methane Emission



- No significant difference of microbiome richness and evenness were identified between methane emission groups

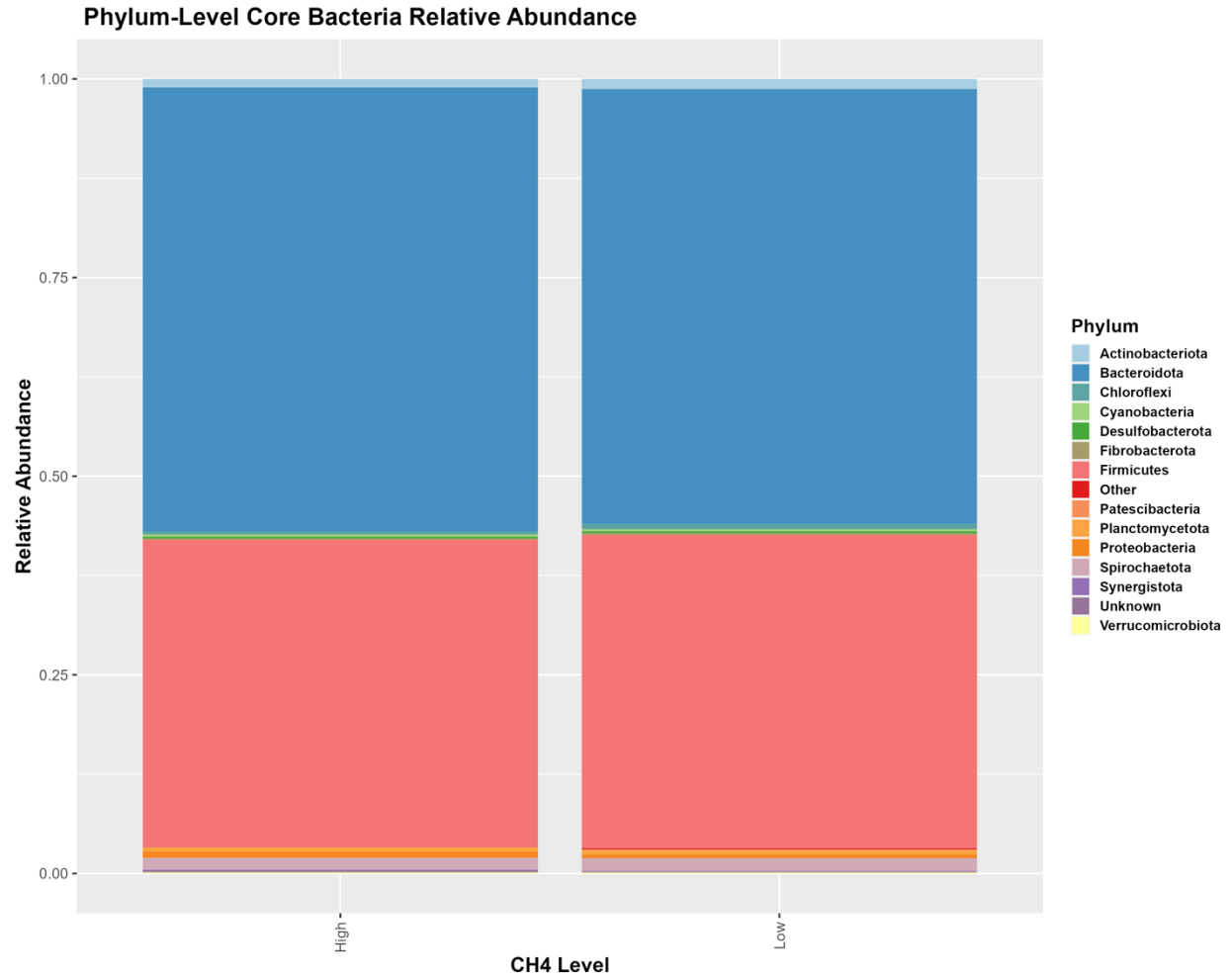
Beta-diversity and Methane Emission

Beta Diversity (Bray-Curtis) by CH4_cat



- Permanova: $P = 0.387$
- No significant difference of microbiome compositions were identified between CH4 emission groups

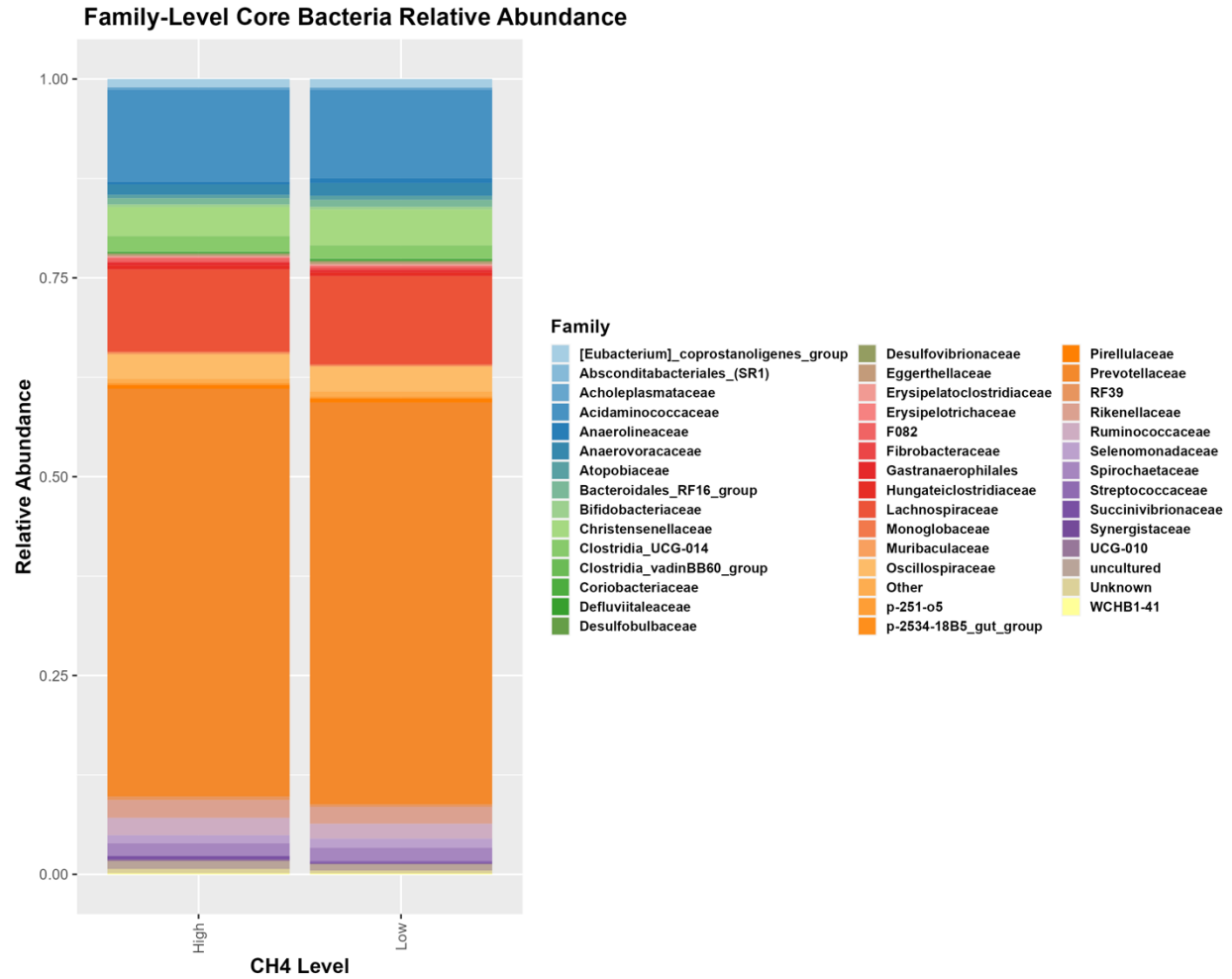
Bacterial relative abundance (Phylum)



Parameter:

- Detected in more than 50% of the samples,
- Relative abundance > 1%

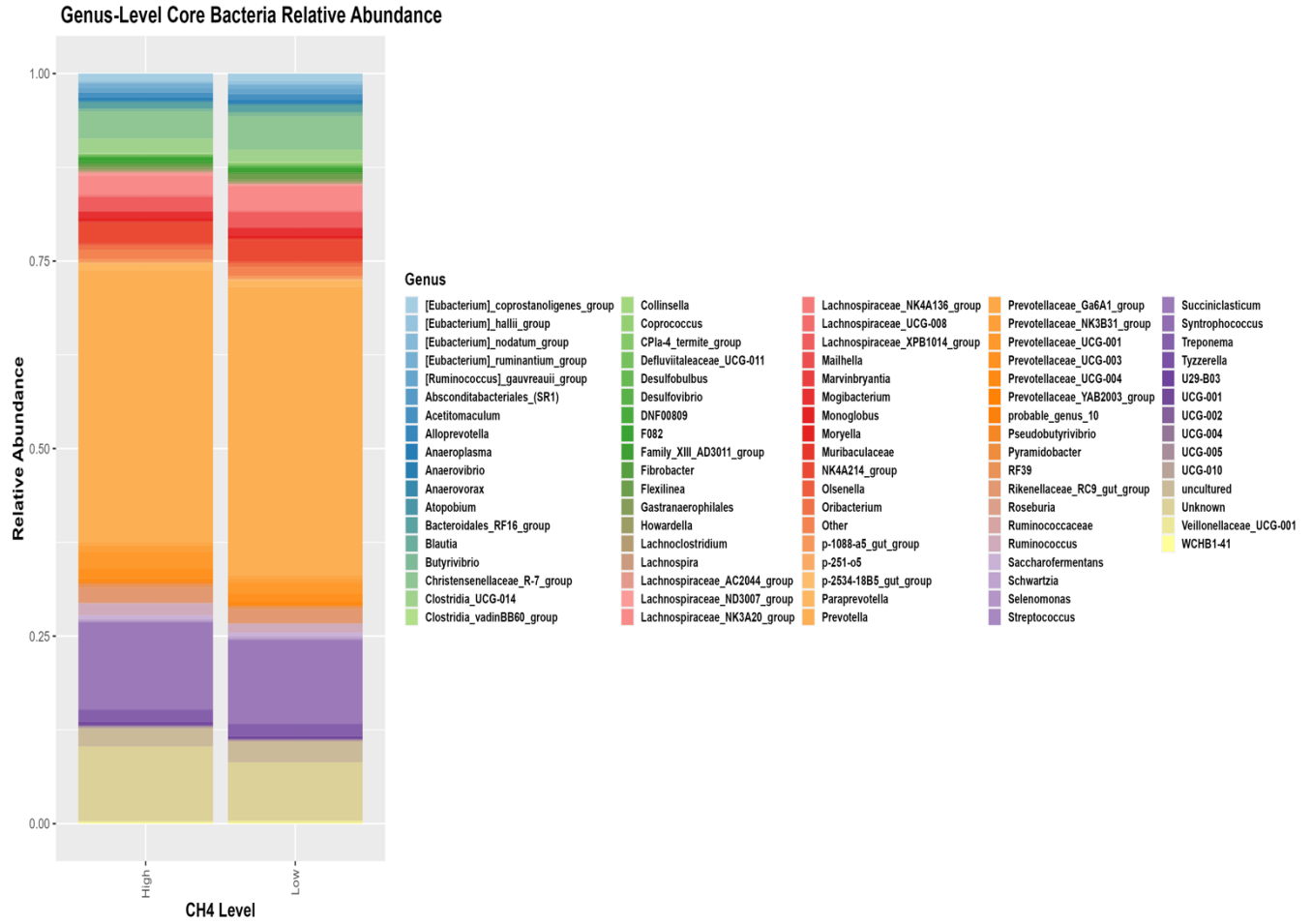
Bacterial relative abundance (Family)



Parameter:

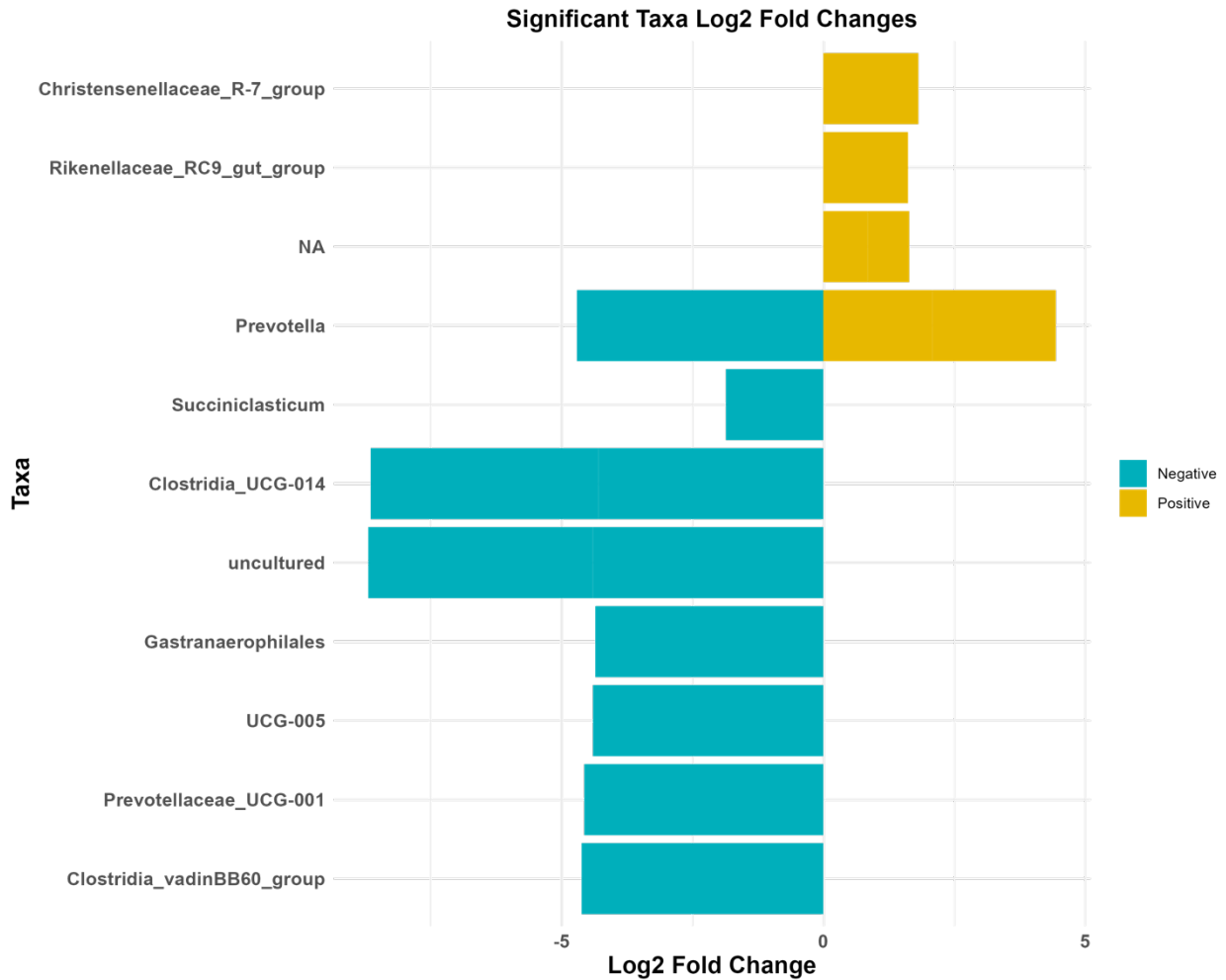
- Detected in more than 50% of the samples,
- Relative abundance > 1%

Bacterial relative abundance (Genus)



Parameter:

- Detected in more than 50% of the samples,
- Relative abundance > 1%



We compared microbiome richness, evenness, and composition across different breeding groups (BGs) to understand the genetic effects on the microbiome. No significant differences were found in bacterial richness and evenness, except for the Chao1 index, which was significantly higher in BG4 than in BG6. A significant difference in beta diversity was observed using the PERMANOVA test, indicating that their genetic background significantly influenced the microbiome composition of cattle.

To determine whether methane emission is associated with the microbiome of the calves, we compared the microbiomes between low and high methane emission groups, defined by the CH₄_DMI value. Cattle with a CH₄_DMI of 11 or more were classified as high-emission, while those with less were low-

emission. No significant differences in microbiome richness, evenness, or composition were observed between these groups.

To identify specific bacteria associated with methane emission, the CH₄_DMI values and bacterial relative abundances (at the genus level) for individual animals were used as input for the DESeq2 test in R. Taxa that were significantly associated (adjusted p-value < 0.05) with methane emission (CH₄_DMI) were extracted. *Christensenella* *R-7_group* and *Rikenellaceae* *RC9_gut_group* showed a positive association with methane emission (CH₄_DMI). *Succiniclasticum*, *Clostridia* *ICG-014*, *Gastranaerophilales*, *UCG-005*, *Prevotellaceae* *UCG-001*, and *Clostridia* *yadomBB60_group* showed a negative association with methane emission. The taxa are negatively associated with methane emissions, which can be potential targets for developing strategies to mitigate methane emissions.

Table 1. Effect of breed group on animal performance and methane emission

| Item | Breed group | | | | | | SEM | <i>P</i> |
|--------------------------------|--------------------|---------------------|---------------------|---------------------|---------------------|--------------------|-------|----------|
| | 1 | 2 | 3 | 4 | 5 | 6 | | |
| ADG (kg/d) | 1.6 ^a | 1.4 ^{ab} | 1.4 ^{ab} | 1.3 ^b | 1.2 ^b | 0.9 ^c | 0.05 | < 0.01 |
| Final BW (kg) | 407.1 ^a | 387.4 ^{ab} | 377.5 ^{ab} | 356.2 ^c | 332.0 ^{cd} | 295.5 ^d | 8.08 | < 0.01 |
| DMI (kg/d) | 13.2 ^a | 12.6 ^{ab} | 12.1 ^{ab} | 11.5 ^{bc} | 10.0 ^c | 8.4 ^d | 0.32 | < 0.01 |
| DMI (% of BW) | 3.6 ^a | 3.6 ^a | 3.6 ^a | 3.6 ^a | 3.4 ^{ab} | 3.1 ^b | 0.07 | < 0.01 |
| F:G ratio (kg DM/Kg BW) | 8.2 | 8.7 | 8.3 | 8.4 | 8.0 | 8.7 | 1.42 | 0.81 |
| G:F (kg BW/kg DM) | 0.12 | 0.11 | 0.11 | 0.12 | 0.1 | 0.13 | 0.006 | 0.46 |
| RFI (kg of DM) | -0.08 | 0.65 | 0.11 | 0.76 | -0.41 | -0.42 | 0.432 | 0.08 |
| Methane total (g/d) | 188.3 ^a | 163.1 ^a | 148.7 ^{ab} | 150.7 ^{ab} | 158.8 ^{ab} | 111.2 ^b | 10.56 | < 0.01 |
| Methane yield (g/Kg of DM) | 17.0 | 17.2 | 15.9 | 15.6 | 13.4 | 17.8 | 1.70 | 0.68 |
| Methane intensity (g/Kg of BW) | 115.2 | 116.6 | 113.8 | 111.4 | 153.1 | 107.9 | 7.89 | 0.93 |

Table 2. Effect of breed group on carcass characteristics

| Item | Breed group | | | | | | SEM | P |
|-------------------|--------------------|---------------------|---------------------|---------------------|---------------------|--------------------|-------|--------|
| | 1 | 2 | 3 | 4 | 5 | 6 | | |
| Final BW (kg) | 407.1 ^a | 387.4 ^{ba} | 377.5 ^{ba} | 356.2 ^{bc} | 332.0 ^{dc} | 295.5 ^d | 8.08 | < 0.01 |
| Ribeye area | 10.93 ^a | 10.22 ^{ab} | 10.24 ^{ab} | 9.90 ^{ab} | 9.42 ^{bc} | 8.96 ^c | 0.299 | < 0.01 |
| Ribeye area/CWT | 1.22 ^b | 1.19 ^b | 1.23 ^b | 1.27 ^b | 1.28 ^{ab} | 1.38 ^a | 0.031 | < 0.01 |
| Ratio | 0.47 | 0.49 | 0.48 | 0.49 | 0.48 | 0.47 | 0.011 | 0.628 |
| Intramuscular fat | 5.98 ^a | 4.57 ^b | 3.84 ^{bc} | 4.07 ^b | 3.97 ^{bc} | 3.28 ^c | 0.254 | <0.01 |
| Ft | 0.33 ^a | 0.32 ^a | 0.29 ^a | 0.27 ^{ab} | 0.31 ^a | 0.22 ^b | 0.023 | <0.01 |
| Rump fat | 0.41 ^{ab} | 0.43 ^a | 0.42 ^a | 0.44 ^a | 0.40 ^{ab} | 0.35 ^b | 0.024 | < 0.01 |

6. Conclusions

Cattle with greater % of *Bos indicus* had decreased dry matter intake (DMI) and this was reflected in the decreased rate of weight gain when compared with heifers with greater proportion of Angus. Regarding total methane emissions, because of the decreased DMI in heifers with more Brahman influence, those had lesser daily emission rates (g/d). However, when methane emissions were expressed per lb or kg of DMI, which is referred to as methane yield, no differences were observed among breed groups. Average daily gain and intake were decreased for groups 4, 5 and 6, in agreement with reports of lesser feed intake as the percentage of *B. indicus* blood increases. However, the feed:gain ratio was maintained similar across all breed groups, and only with the purebred Brahman group (Breed group 6), the intake as % of body weight decreased compared to the rest of the groups except 5.

Breeding group 1 (80-100% Angus) had the greatest marbling scores, however ribeye area only decreased in groups 5 and 6, with greater percentage of Brahman. Fat thickness was least in the purebred Brahman group (BG 6)

Considering the ruminal microbiome data, along with the carcass and methane emission phenotypes, it is evident that there is sufficient variation among breed groups to potentially select for cattle with superior carcass quality, but that are also feed efficient, and perhaps even lower emitters of methane. The amount of data in this proposal continues to be explored and the information would be greatly strengthened with a second year of data collection to further enhance selection capabilities.

PLEASE REMIT TO:

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Invoice Date: 08/14/2024
 Invoice Period: 03/01/2024 - 07/31/2024
 Principal Investigator: DiLorenzo, Nicolas
 Award Begin Date: 10/30/2023
 Award End Date: 07/31/2024

SPONSOR:

FL CATTLE ENHANCEMENT BOARD
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| | |
|-------------------------|-------------|
| Invoice # | I000130468 |
| UF Award # | AWD15774 |
| Primary Project # | P0324504 |
| Primary Department: | 60770000 |
| Current Invoice Amount: | \$34,518.70 |

Award Amount: \$126,519.00

| Description | Current | Cumulative |
|-------------------------------------|--------------------|---------------------|
| Personnel - Salary | \$16,050.04 | \$34,477.88 |
| Personnel - Fringe Benefits | \$2,921.98 | \$6,607.77 |
| Materials and Supplies | \$7,347.96 | \$8,576.76 |
| Contractual Services | \$0.00 | \$0.00 |
| Animal | \$3,765.00 | \$54,165.10 |
| Other Expenses | \$138.35 | \$138.35 |
| Domestic Travel | \$597.00 | \$660.19 |
| Direct Cost | \$30,820.33 | \$104,626.05 |
| Facilities and Administrative Costs | \$3,698.37 | \$12,555.01 |
| Total | \$34,518.70 | \$117,181.06 |

For billing questions, please call 352.392.1235
 Peterson, Nathan Kyle npeterson82@ufl.edu
 Please reference the UF Award Number and Invoice Number in all correspondence

By signing this report, I certify to the best of my knowledge and belief that the report is true, complete, and accurate, and the expenditures, disbursements and cash receipts are for the purposes and objectives set forth in the terms and conditions of the federal award. I am aware that any false, fictitious, or fraudulent information, or the omission of any material fact, may subject me to criminal, civil, or administrative penalties for fraud, false statements, false claims or otherwise. (U.S Code Title 18, Section 1001 and Title 31, Sections 3729-3730 and 3801-3812).

Nathan Peterson

 Certifying Official

| Payment History | |
|---|--------------|
| Cumulative Invoices: | \$117,181.06 |
| Payments Received: | \$82,662.36 |
| Outstanding Balance: | \$34,518.70 |
| Note: Outstanding balance includes current invoice amount | |

| FOR UF USE ONLY | | | Additional Projects: N | |
|-----------------|----------|-----------------|------------------------|--------------|
| Project ID | Deptid | Department Name | Current | Cumulative |
| P0324504 | 60770000 | AG-NFREC-QUINCY | \$34,518.70 | \$117,181.06 |