



Relationship between performance phenotypes and rumen microbiome and liver transcriptome data of beef cattle using a systems biology approach

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Introduction

- Feed costs are a major determinant of profitability in beef production
- Identifying and breeding cattle with improved feed efficiency can reduce feed costs
- OBJECTIVE:** examine the relationship between animal performance phenotypes including feed efficiency (residual feed intake; RFI), growth rate (average daily gain; ADG) and dietary intake (dry matter intake; DMI) with both rumen microbiome and liver transcriptome data using a network based systems biology approach

Materials & Methods

- Dietary intake was recorded in Holstein-Friesian and Charolais steers over contrasting dietary phases (70 days)
- RFI, DMI and ADG determined for each steer at the end of each dietary phase and steers with extreme High and Low-RFI values selected for rumen digesta and liver tissue sampling, which were then used for 16s and RNA sequencing, respectively
- An overview of the experimental methodology is provided in Figure 1

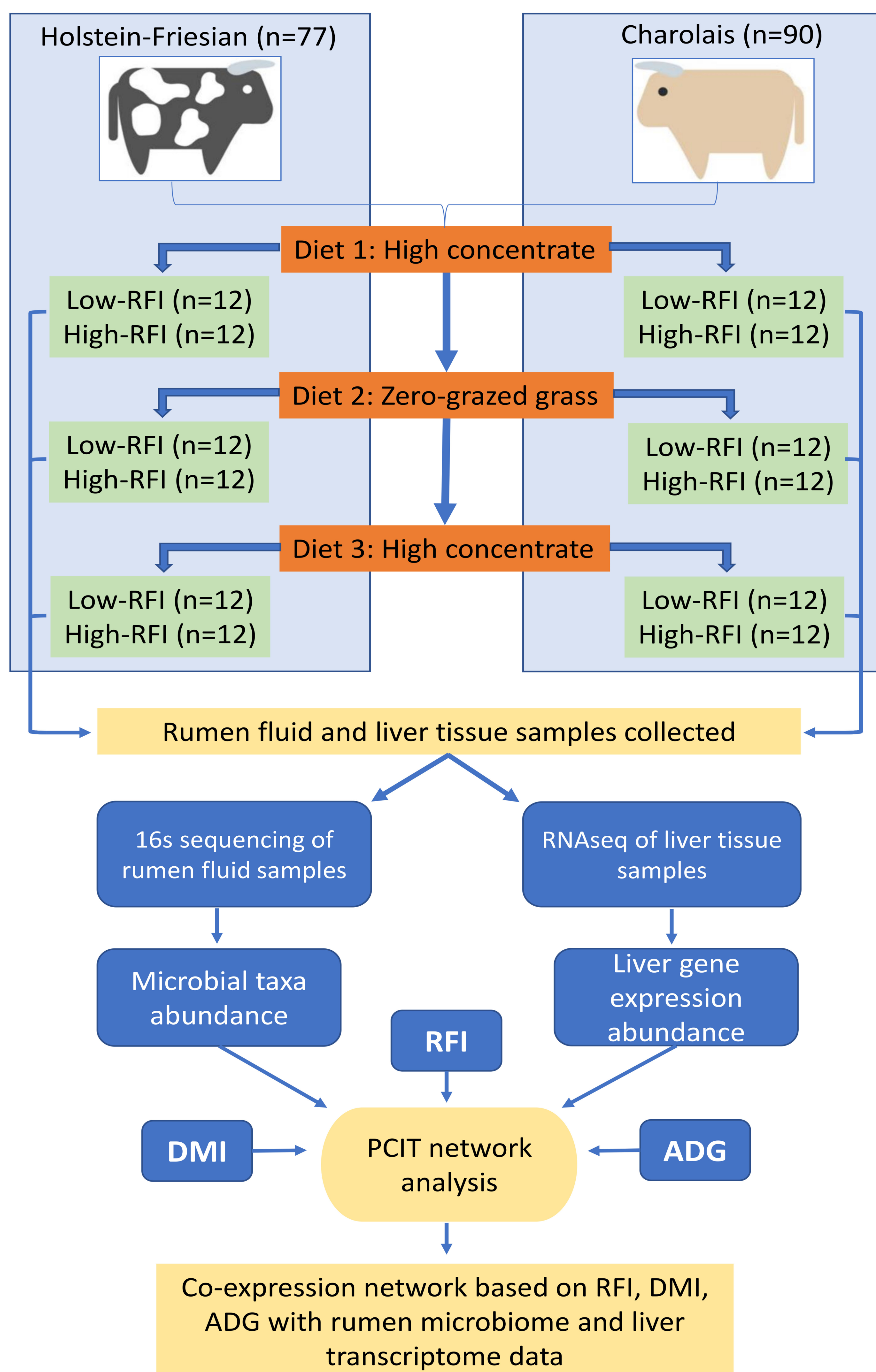


Figure 1. Overview of experimental methodology.

Results

- Hepatic genes related to lipid metabolism:
 - Connected to RFI and DMI
- Hepatic genes related to immune response:
 - Connected to DMI

Table 1. Number of microbial and gene connections with ADG, DMI and RFI

Node type	ADG	DMI	RFI
Total connections	37	180	49
Microbe	4 (10.8%)	10 (5.55%)	9 (18.4%)
Gene	31 (83.8%)	164 (91.1%)	39 (79.6%)

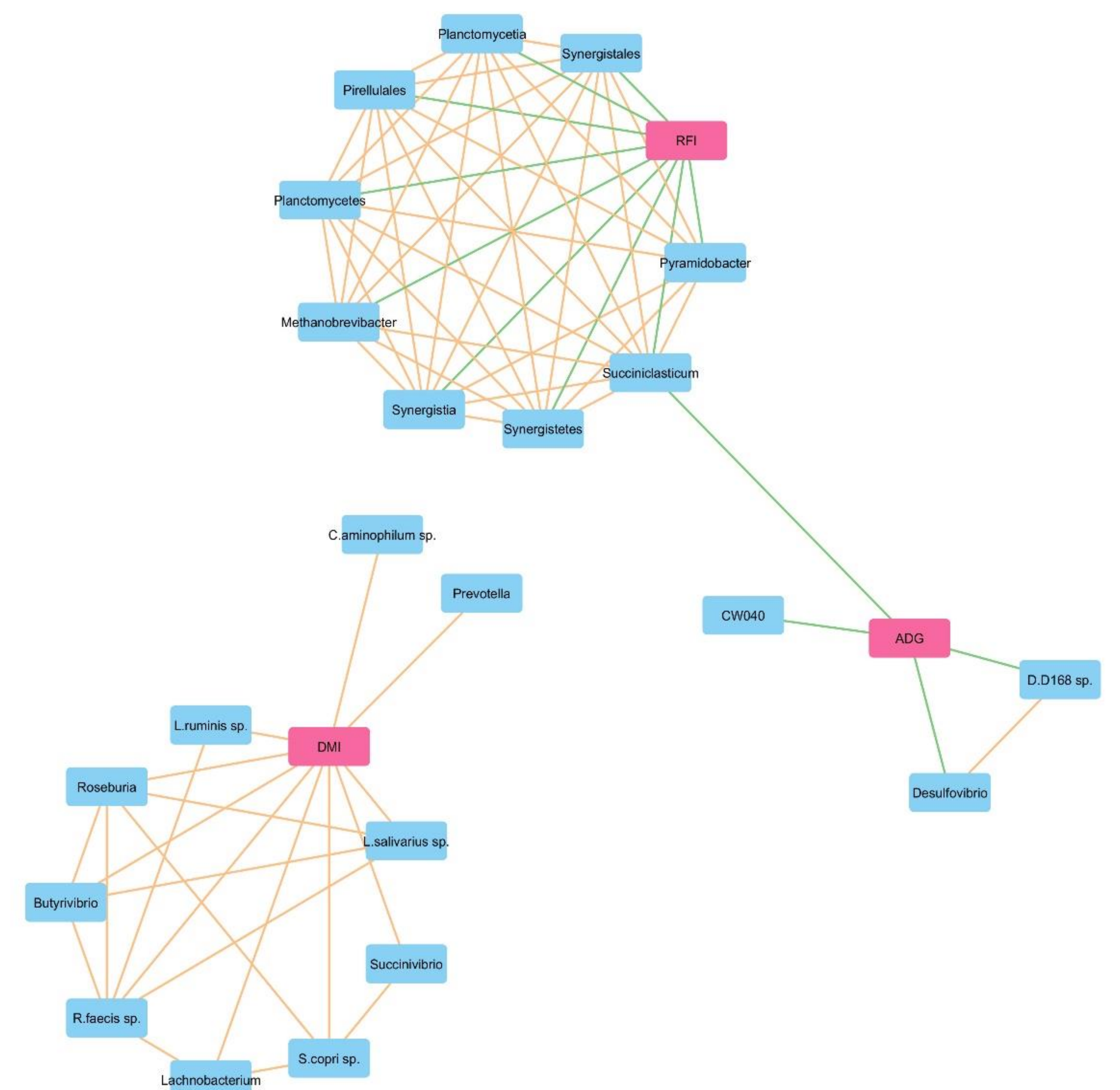


Figure 2. Direct microbial connections with RFI, DMI and ADG. RFI, DMI and ADG nodes are in pink and microbial taxa nodes in blue. Green lines represent negative connections and orange lines positive connections

- No single microbe was directly connected to all three phenotypes (Figure 2)
- Succinoclasticum* genus was negatively connected to both RFI and ADG

Conclusions

Results from this study highlight the complex interplay between rumen microbiome and hepatic transcriptome data with key economically important traits in beef cattle and enhance our understanding of the biology underlying RFI, DMI and ADG

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