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## How Microbial Communities Differ in Ruminants on a Glycerin vs Common Diet

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# How Microbial Communities Differ in Ruminants on a Glycerin vs Common Diet

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## Abstract

- Glycerin is a by-product of ethanol production and can be used as a feed additive to keep production cost low
- Effects of glycerin supplementation on rumen microbial community composition is undocumented
- We use culture independent high throughput sequencing methods to characterize the rumen microbial community to better understand the effect of glycerin on the rumen microbial community
- **Problem** – The microbial community composition when glycerin is supplemented in the diet is unknown. Additionally, if level of glycerin supplementation would effect rumen microbial population structure is unknown.
- **Goal** of this research project was to characterize the rumen microbial population during glycerol supplementation and also to evaluate the microbial community composition under different levels of glycerin supplementation.

## Introduction

- Glycerin has been shown to increase performance
- Glycerin is a glycolytic substrate
- Decreases in the acetate to propionate ratio
- May have positive impacts on F:G.
- The impacts of crude glycerin on fiber digestion are unclear and changes in ruminal microbial populations may help understand this relationship
- However, changes in microbial community composition during glycerin supplementation are undocumented.

## Hypothesis

- Glycerin supplementation and level of supplementation will change microbial community composition

## Objective

- Evaluate rumen microbial community composition during glycerin supplementation



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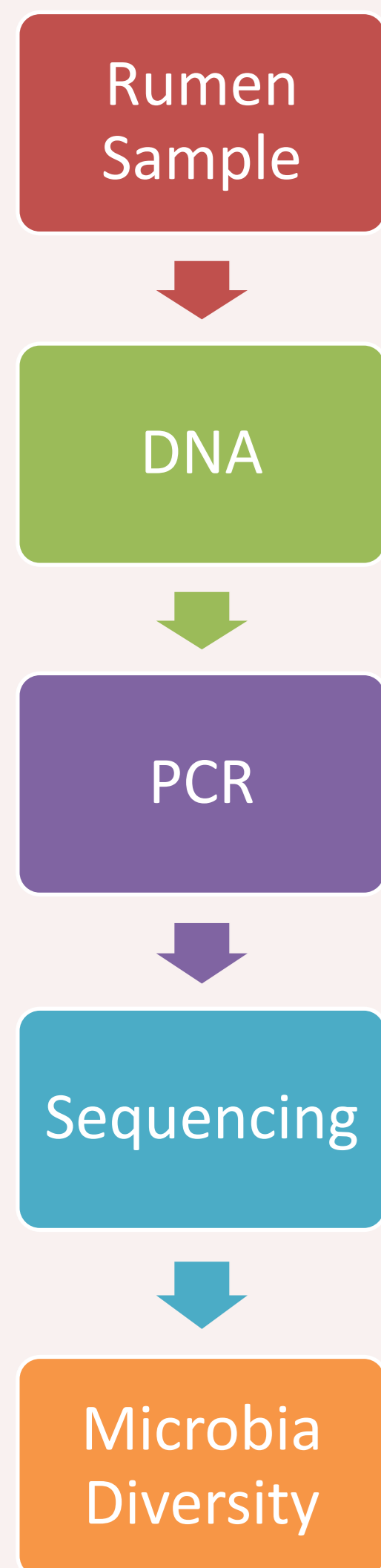
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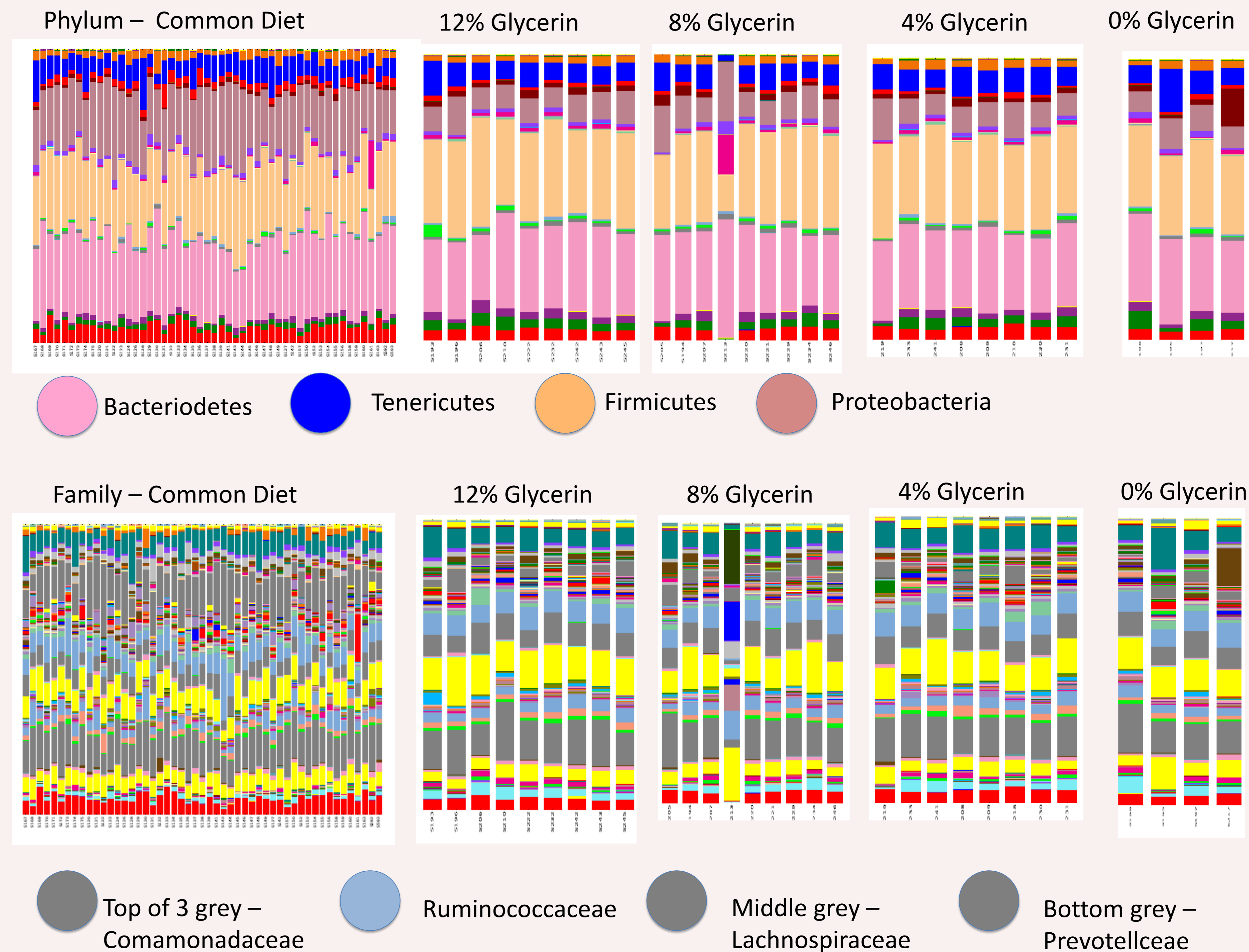
## Material and Methods

- The experiment was conducted using 60 beef steers
- Maintained on a common diet for 21 days
- Transition to 4 treatment diets (0% Glycerin, 4% Glycerin, 8% Glycerin and 12% Glycerin) for 150 days
- Rumen samples were collected using esophageal tubing
- High throughput sequencing
- Bioinformatics analyses

Fig 2. Experimental design



## Results





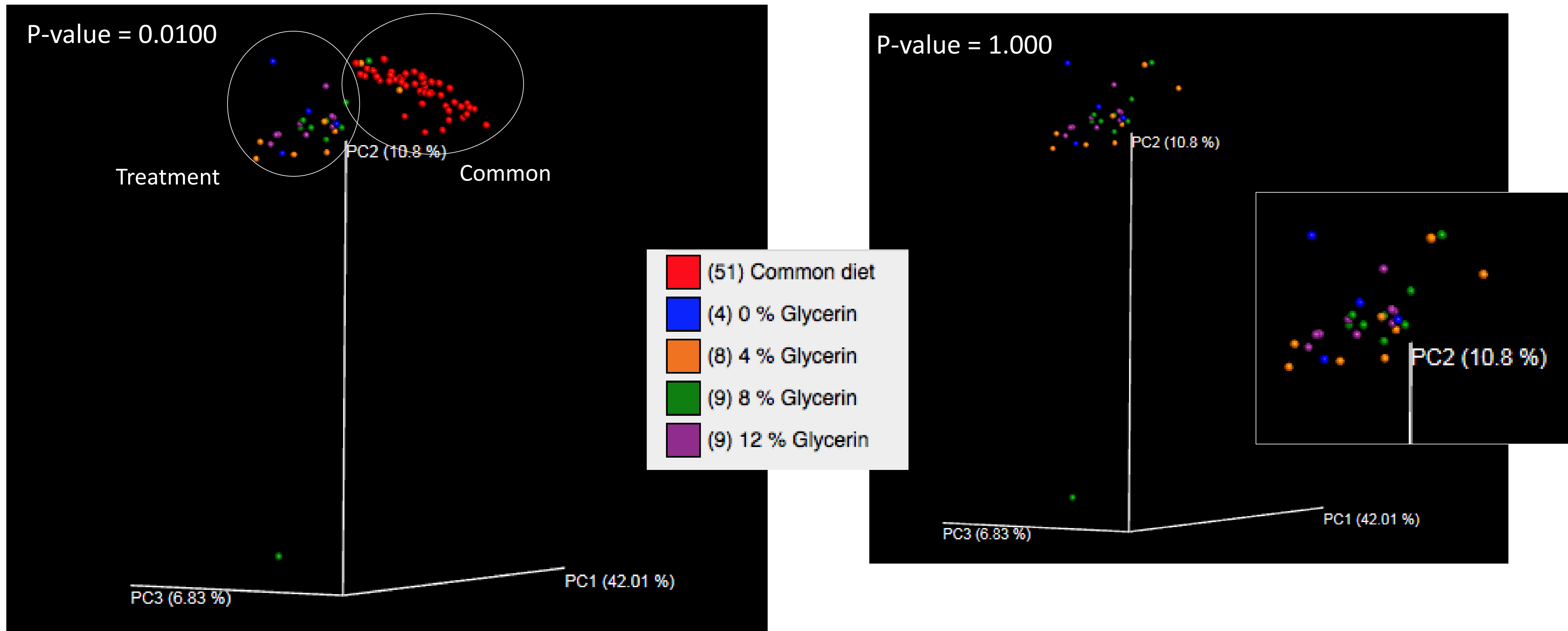
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## Results

Figure 3.



Diet	P-value
1vs2	0.0100
1vs3	0.0100
1vs4	0.0100
1vs5	0.0100
2vs3	1.0000
2vs4	1.0000
2vs5	1.0000
3vs4	1.0000
3vs5	1.0000
4vs5	1.0000

1	Common Diet
2	0% Glycerin
3	4% Glycerin
4	8% Glycerin
5	12% Glycerin

## Conclusions

- Microbial community changed when animals were transitioned to glycerin supplemented diet from the common diet
- Under the different levels of glycerin supplementation the global microbial community composition did not change
- In the common diet and in glycerin diets, phyla Firmicutes, Bacteroidetes, Proteobacteria and Tenericutes predominated

## Future Studies

- OTU level correlation analysis to identify microbial OTUs that respond to glycerin
- Identify differential OTUS that are present in common diet and each of the treatment diets
- Identify a core microbiota that responds to glycerin