



## Introduction

- Microbes produce metabolites within the host's microenvironment.
- Metabolites may play significant biological roles in infant development
- This project seeks to understand the metabolite-microbiome associations that exist between mothers and infants

## Time points, samples, & omics

Quality Evaluation

Raw Read Sequences

Data Inspection FASTQC & MULTIQC

Choose appropriate parameter set

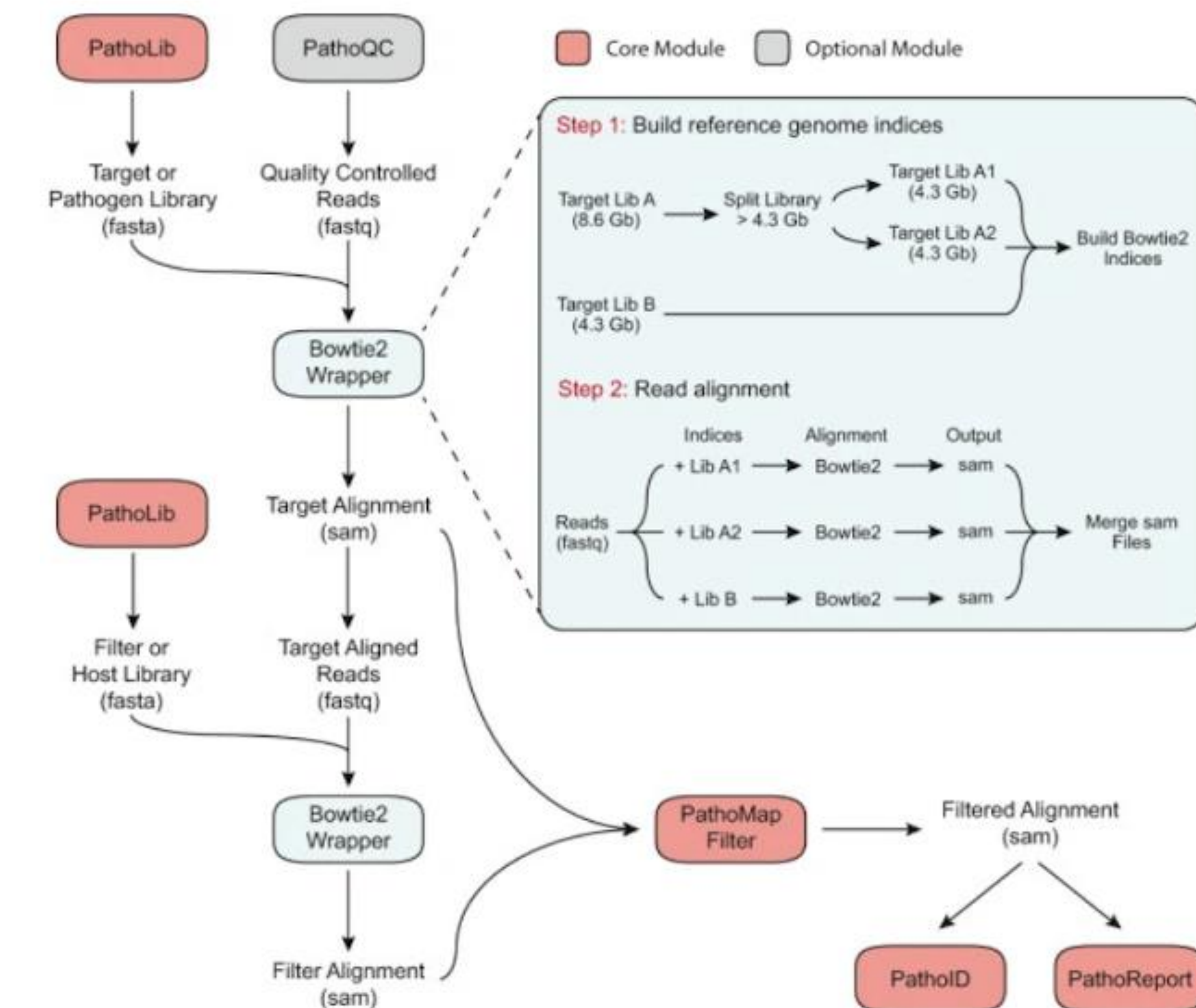
Quality Trimming Trimmomatic

Quality ok?

Yes

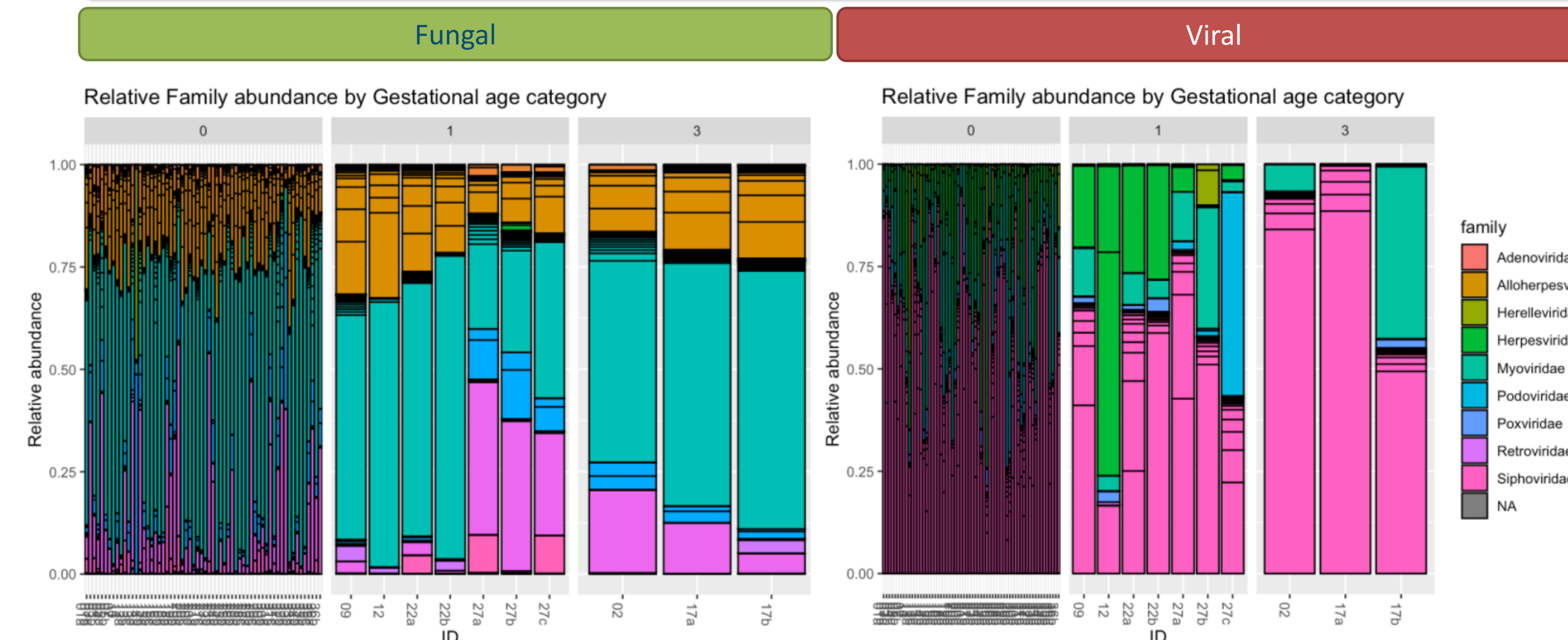
Analysis

## Microbial Strain Identification

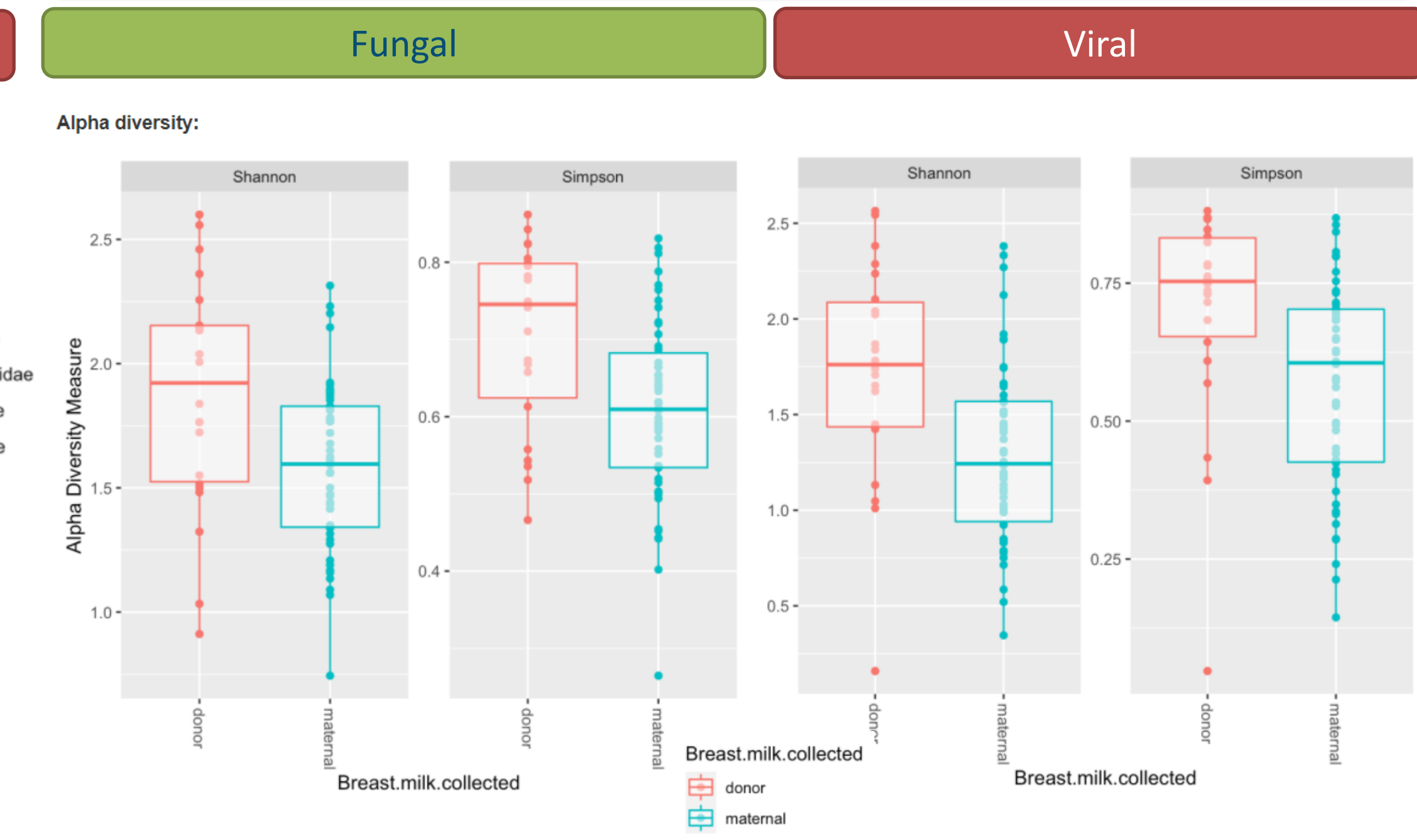


## Metagenomic Analysis R

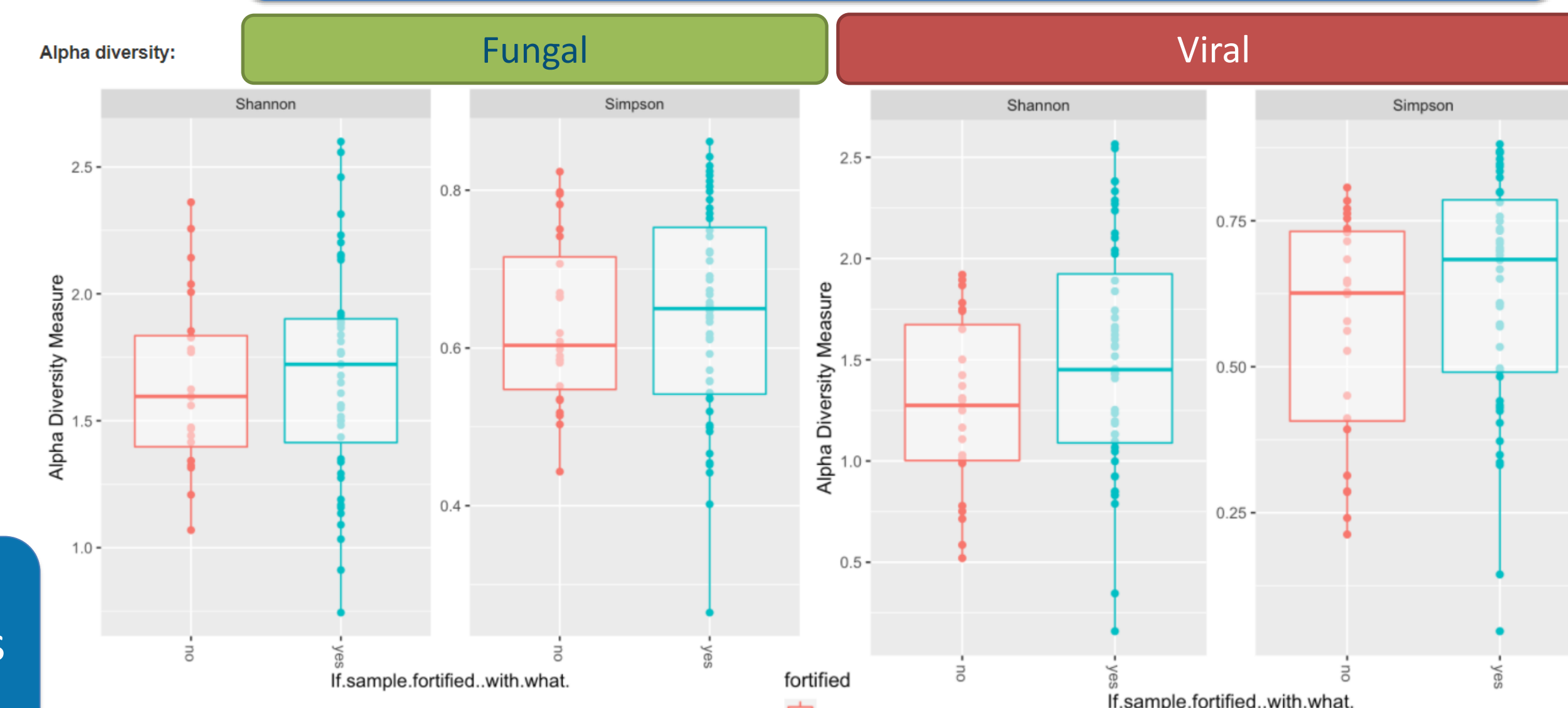
1. How does the breastmilk microbiome vary with prematurity and gestational age?



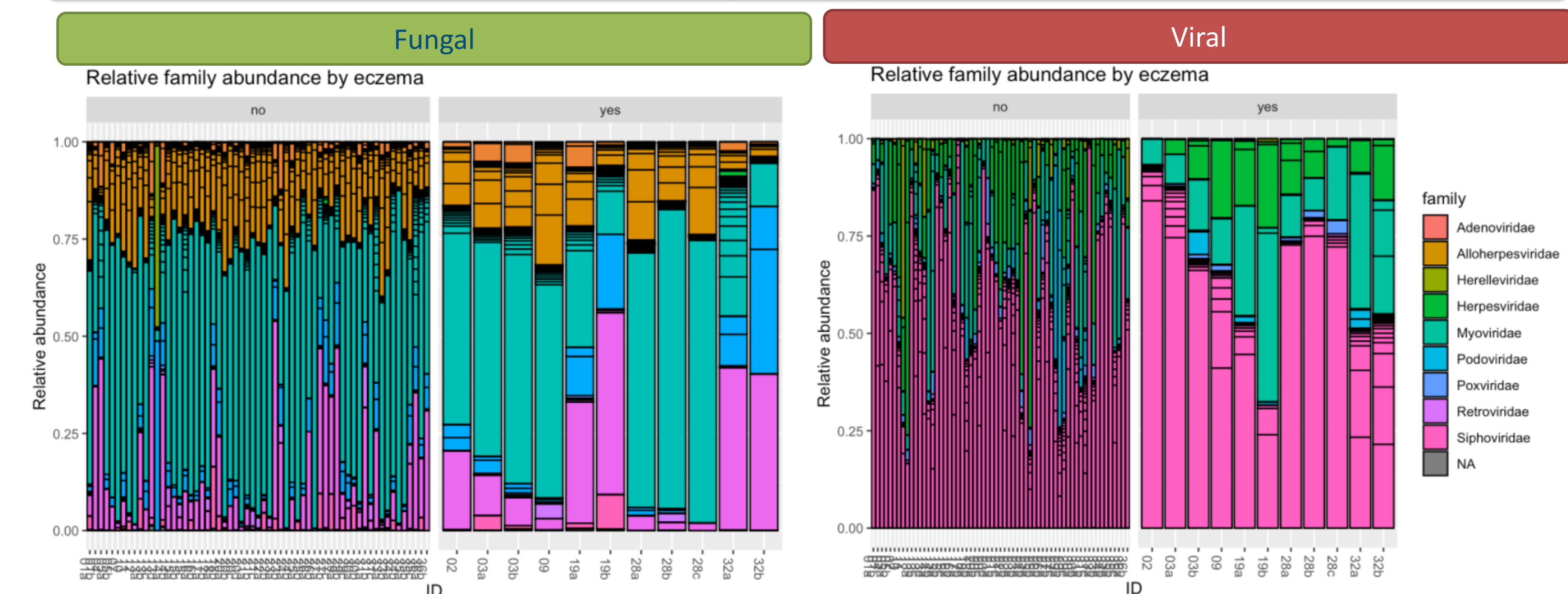
2. How does the breastmilk microbiome vary between maternal and donor milk?



3. How does caloric fortification change the breastmilk microbiome?

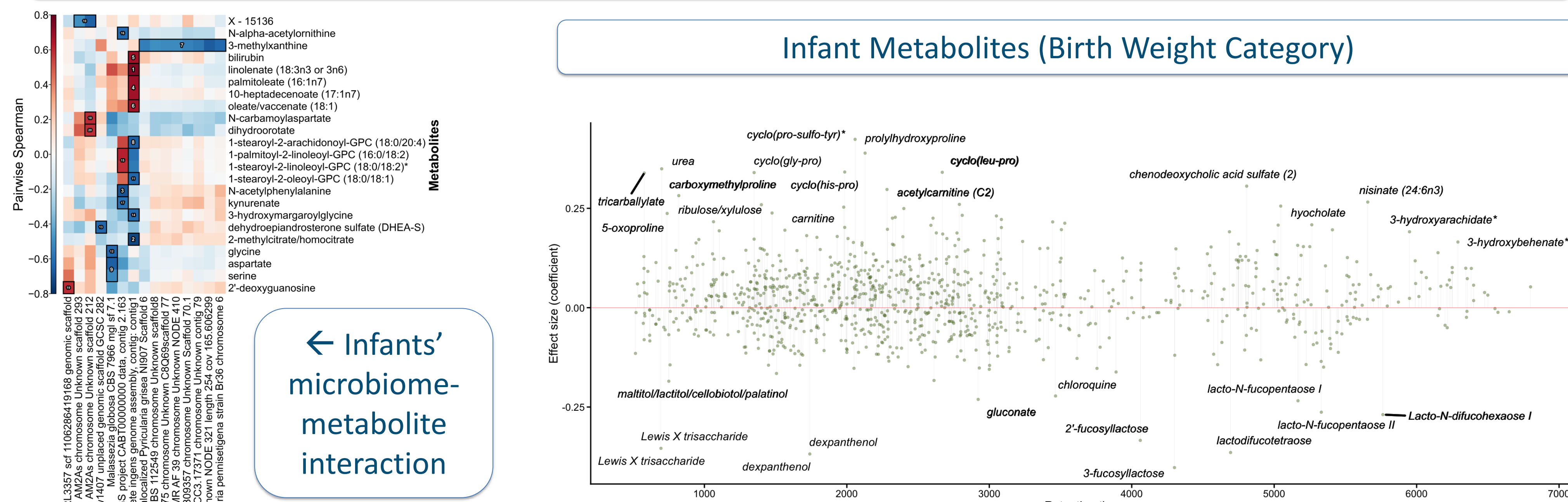


4. How is the breastmilk microbiome associated with early childhood health outcomes (eczema)?



## Metabolomic Analysis

### Infant Metabolites (Birth Weight Category)



← Infants' microbiome-metabolite interaction

## Discussion / Conclusion

- Small differences between origin and content of breastmilk may have significant effects on infant development
- Future analyses will be conducted on bacterial data
- Future analyses will reveal the correlation between the breastmilk microbiome and the infant gut microbiome

## References

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Hong, C., Manimaran, S., Shen, Y. et al. PathoScope 2.0: a complete computational framework for strain identification in environmental or clinical sequencing samples. *Microbiome* 2, 33 (2014). <https://doi.org/10.1186/2049-2618-2-33>

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