# What the Taq? The Influence of Different Hi-Fidelity Taq Polymerase on 16S rRNA Sequencing

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# Abstract

**Background.**

**Methods.**

**Results.**

**Conclusions.**

# Introduction

## Materials & Methods

***Human and Mock Samples:*** A single fecal sample was obtained from 4 individuals who were part of the Enterics Research Investigational Network (ERIN) and the processing and storage of these samples have been published previously (Seekatz et al., 2016). Clinical data and other types of meta data were not utilized or accessed for this study. All samples were extracted using the MOBIO™ PowerMag Microbiome RNA/DNA extraction kit (now Qiagen, MD, USA). The ZymoBIOMICS™ Microbial Community DNA Standard (Zymo, CA, USA) was used in this study and is made up of *Pseudomonas aeruginosa*, *Escherichia coli*, *Salmonella enterica*, *Lactobacillus fermentum*, *Enterococcus faecalis*, *Staphylococcus aureus*, *Listeria monocytogenes*, and *Bacillus subtilis* at equal genomic DNA abundance (http://www.zymoresearch.com/microbiomics/microbial-standards/zymobiomics-microbial-community-standards).

***PCR Protocol:*** The five different high fidelity Taq DNA polymerase that were tested were AccuPrime™ (ThermoFisher, MA, USA), KAPA HIFI (Roche, IN, USA).

***Reproducible Methods:*** The code and analysis can be found here https://github.com/SchlossLab/Sze_PCRSeqEffects_XXXX_2017.

# Results

## *Insert Sub title here*

# Discussion

# Conclusion

## Acknowledgements

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# References

Seekatz AM., Rao K., Santhosh K., Young VB. 2016. Dynamics of the fecal microbiome in patients with recurrent and nonrecurrent clostridium difficile infection. *Genome Medicine* 8. DOI: 10.1186/s13073-016-0298-8.

**Table 1:**

**Table 2:**

**Figure 1: .**

**Figure 2: .**

**Figure 3: .**

**Figure 4: .**

**Figure 5: .**

**Figure 6: .**

**Figure 7: .**

**Figure S1: .**

**Figure S2: .**

**Figure S3: .**

**Figure S4: .**

**Figure S5: .**

**Figure S6: .**

**Figure S7: .**