

# Error Introduced into 16S rRNA Gene Sequencing Results Varies by High Fidelity DNA Polymerase Used

Marc A Sze<sup>1</sup> and Patrick D Schloss<sup>1†</sup>

† To whom correspondence should be addressed: [pschloss@umich.edu](mailto:pschloss@umich.edu)

<sup>1</sup> Department of Microbiology and Immunology, University of Michigan, Ann Arbor, MI

Co-author e-mails:

- [marcsze@med.umich.edu](mailto:marcsze@med.umich.edu)

## Abstract

**Background.** It is challenging to compare 16S rRNA gene sequencing data across studies and one of the reasons for this is due to error. There are many different places throughout the workflow where error can be introduced into the pipeline. Here, we focus on studying how the number of cycles and high fidelity (HiFi) DNA polymerase introduce error by varying cycle number and polymerase used to amplify 16S rRNA genes in human fecal and mock community samples.

**Methods.** We extracted DNA from fecal samples ( $n=4$ ) using a PowerMag DNA extraction kit with a 10 minute bead beating step and amplified at 15, 20, 25, 30, and 35 cycles using Accuprime, Kappa, Phusion, Platinum, or Q5 HiFi DNA polymerase. Amplification of mock communities (technical replicates  $n=4$ ) consisting of previously isolated whole genomes of 8 different bacteria used the same approach. The analysis initially examined the number of Operational Taxonomic Units (OTUs) for fecal samples and mock communities. It also assessed polymerase dependent differences in the Bray-Curtis index, error rate, sequence error prevalence, chimera prevalence, and the correlation between chimera prevalence and number of OTUs.

**Results.** When analyzing fecal samples we observed that the range in the number of OTUs detected was not consistent between HiFi DNA polymerases at 35 cycles (Accuprime = 84 - 106 (min - max) versus Phusion = 84 - 136). Additionally, the median number of OTUs varied by HiFi DNA polymerase used ( $P$ -value  $< 0.0001$ ). When analyzing mock community samples the variation in the number of OTUs detected by the polymerases was observable as early as 20 cycles ( $P$ -value = 0.002). There also was a large range in the number of OTUs amplified by the polymerases at 35 cycles (Accuprime = 15 - 20 versus Phusion = 14 - 73). Chimera prevalence in mock communities varied by polymerase with differences being most notable at 35 cycles (Kappa = 5.71% (median) versus Platinum = 26.62%) and this variation persisted after chimera removal using VSEARCH. We also observed positive correlations between chimera prevalence and the number of OTUs with Platinum having the highest ( $R^2 = 0.974$ ) and Kappa having the worst ( $R^2 = 0.478$ ).

**Conclusions.** Although the variation in the number of OTUs in fecal samples could be due to certain polymerases capturing the biological variability better than others, this is unlikely to be the

28 main reason for our observed differences. In mock community samples, the strong correlation  
29 between chimera prevalence and the number of OTUs suggests that this is the main reason for  
30 differences between the polymerases. Ultimately, this variation makes comparison across studies  
31 difficult and care should be exercised when choosing the polymerase and number of cycles in 16S  
32 rRNA gene sequencing studies.

## Introduction

The bacterial community is reported to vary between case and control for a number of diseases []. However, for diseases like obesity, the taxa identified have varied widely depending on the study []. Some of this variation could be due to error introduced during the 16S rRNA gene sequencing workflow. Yet, standardizing a 16S rRNA gene sequencing workflow will ultimately result in a standardized and reproducible bias due to choices made on the methods used for preservation, extraction, PCR, and sequencing. Within this context, all 16S rRNA gene sequencing methods are biased even when these workflows are standardized to increase reproducibility. In order to interpret specific studies within the broader context of the overall field, assessing error at different parts of the 16S rRNA gene sequencing workflow is critical.

A typical 16S rRNA gene sequencing workflow can be divided into preservation, extraction, PCR, and sequencing steps. The preservation and extraction stages of the 16S rRNA gene sequencing workflow have been the most extensively studied []. For preservation and extraction stages of the workflow, it has been consistently found that there are biases based on the kits used, but that these differences are smaller than the overall biological difference measured between samples with different kits (Song et al., 2016; Bassis et al., 2017). Since these studies use the same PCR approach while varying preservation or extraction method, the contribution of PCR bias to this overall workflow is not well characterized.

There is a large body of literature that shows there are different biases within each of the steps in the PCR stage of 16S rRNA gene sequencing. One source of error is from primers chosen for the 16S rRNA gene sequencing. There are variable region dependent binding affinities for different bacteria, and depending on the primer pair used they do not detect specific bacteria (e.g. V1-V3 does not detect *Haemophilus influenzae* and V3-V5 does not detect *Propionibacterium acnes*) (Sze et al., 2015 (Table S4); Meisel et al., 2016). Another source of error is the selective amplification of AT-rich over GC-rich sequences which exaggerate the difference between 16S rRNA genes higher in AT versus those higher in GC content (Polz & Cavanaugh, 1998). Many of these sources of biases are made worse as the number of cycles increases (Wang & Wang, 1996; Haas et al., 2011; Kebschull & Zador, 2015). For example, both amplification error and non-specific amplification

(e.g. incorrect amplicon size products) also can increase as the number of cycles increases. This will increase the number of Operational Taxonomic Units (OTUs) observed and drastically change the values obtained from commonly used diversity measures (Acinas et al., 2005; Santos et al., 2016). Additionally, as the number of cycles increases more chimeras can form from an aborted extension step that causes a priming error and subsequent secondary extension (Haas et al., 2011). These chimeras will artificially increase community diversity by increasing the number of OTUs that are observed (Haas et al., 2011). In addition to these sources of errors, there also are multiple families of DNA polymerases that have their own error rate and proof reading capacity (Ishino & Ishino, 2014). Interestingly, the influence that these different DNA polymerases can have on the observed 16S rRNA gene sequencing results have not been well studied like some of the other sources of PCR-based bias.

A recent study found differences in the number of OTUS and chimeras between normal and high fidelity DNA polymerases (Gohl et al., 2016). The authors could reduce the difference between the two polymerases by optimizing the annealing and extension steps within the PCR protocol (Gohl et al., 2016). Yet, within this study there was no comparison made between different high fidelity DNA polymerases. Due to this gap, it is natural to extend this line of inquiry and test if biases in the number of OTUs and chimeras also are dependent on the type of high fidelity DNA polymerase. This study will investigate how high fidelity DNA polymerases can bias observed bacterial community results derived from 16S rRNA gene sequencing. We will accomplish this by examining the number of OTUs, error rate, number of sequences with an error, and chimera prevalence at varying number of cycles in five different high fidelity DNA polymerases

## 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). The processing and storage of these samples were previously published (Seekatz et al., 2016). Other than confirmation that none of these individuals had a *Clostridium difficile* infection, 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 for mock communities and was 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/zymbiomics-microbial-community-standards>).

**PCR Protocol:** The five different high fidelity DNA polymerases (hereto referred to as polymerases) that were tested included AccuPrime™ (ThermoFisher, MA, USA), KAPA HIFI (Roche, IN, USA), Phusion (ThermoFisher, MA, USA), Platinum (ThermoFisher, MA, USA), and Q5 (New England Biolabs, MA, USA). The PCR cycle conditions for Platinum and Accuprime followed a previously published protocol (Kozich et al., 2013) ([https://github.com/SchlossLab/MiSeq\\_WetLab\\_SOP/blob/master/MiSeq\\_WetLab\\_SOP\\_v4.md](https://github.com/SchlossLab/MiSeq_WetLab_SOP/blob/master/MiSeq_WetLab_SOP_v4.md)). The polymerases activation time was 2 minutes, unless a different activation was specified. For Kappa and Q5, a previously published protocol was used (Gohl et al., 2016). For Phusion, the company defined conditions were used except for extension time, where the Accuprime and Platinum settings were used.

The cycle conditions for both fecal and mock samples started at 15 and increased by 5 up to 35 cycles with amplicons used at each 5-step increase for sequencing. The PCR of fecal DNA samples consisted of all 4 samples at 15, 20, 25, 30, and 35 cycles for each polymerase (total sample n=100). The mock communities had 4 replicates at 15, 20, 25, and 35 cycles and 10 replicates for 30 cycles for all polymerases (total samples n=130). No mock community sample had enough PCR product at 15 cycles for adequate 16S rRNA gene sequencing.

**Sequence Processing:** The mothur software program was used for all sequence processing steps (Schloss et al., 2009). The protocol has been previously published (Kozich et al., 2013) ([https://www.mothur.org/wiki/MiSeq\\_SOP](https://www.mothur.org/wiki/MiSeq_SOP)). Two major differences from the published protocol were the use of VSEARCH instead of UCHIME for chimera detection and the use of the OptiClust algorithm instead of average neighbor for OTU generation at 97% similarity (Edgar et al., 2011; Rognes et al., 2016; Westcott & Schloss, 2017). Sequence error was determined using the 'seq.error' command on mock samples (Schloss et al., 2009; Cole et al., 2013; Rognes et al., 2016).

**Analysis Workflow:** All samples were rarefied to 1000 sequence. The total number of OTUs was analyzed for both the fecal and mock community samples. For fecal samples, cycle dependent affects on Bray-Curtis indices were assessed for cycle group and within individual differences from the previous cycle (e.g. 20 versus 25, 25 versus 30). Based on these observations we analyzed potential reasons for these differences. Analysis of the mock community of each polymerase for sequence error rate, number of sequences with an error, base substitution, and numbers of chimeras before and after chimera removal with VSEARCH was assessed. Additionally, the correlation between the number of chimeras and the number of OTUs was also assessed.

**Statistical Analysis:** All analysis was done with the R (v 3.4.4) software package (R Core Team, 2017). Data transformation and graphing was completed using the tidyverse package (v 1.2.1) and colors selected using the viridis package (v 0.4.1) (Garnier, 2017; Wickham, 2017). Differences in the total number of OTUs were analyzed using an ANOVA with a tukey post-hoc test. For the fecal samples the data was normalized to each individual by cycle number to account for the biological variation between people. Bray-Curtis distance matrices were generated using mothur after 100 sub-samplings at 1000, 5000, 10000, and 15000 sequence depth. The distance matrix data was analyzed using PERMANOVA with the vegan package (v 2.4.5) (Oksanen et al., 2017) and Kruskal-Wallis tests within R. For both error and chimera analysis, samples were tested using Kruskal-Wallis with a Dunns post-hoc test. Where applicable correction for multiple comparison utilized the Benjamini-Hochberg method (Benjamini & Hochberg, 1995).

**Reproducible Methods:** The code and analysis can be found here [https://github.com/SchlossLab/Sze\\_PCRSeqEffects\\_XXXX\\_2017](https://github.com/SchlossLab/Sze_PCRSeqEffects_XXXX_2017). The raw sequences can be found in the SRA at the following

137 accession number SRP132931.



## Results

***The Number of OTUs are Dependent on Polymerase:*** Differences in the range of the number of OTUs detected for fecal samples is dependent on the polymerase used [Figure 1]. Additionally, there is a trend for lower number of cycles (15-20) to result in a reduced range in the number of OTUs versus higher number of cycles (25, 30, and 35) for all polymerases [Figure 1]. There is an overall difference in the number of OTUs detected within fecal samples between polymerases at 35 cycles (F-stat > 16.35, P-value = 9.7e-05) [Table S1]. No differences between the polymerases was found based on a Tukey post-hoc test (P-value > 0.05) [Table S2]. The polymerase dependent difference in the range of the number of OTUs also was observed in the mock community samples [Figure 2]. Regardless if fecal or mock communities were used, the same polymerases had high (Platinum) and low (Accuprime) number of OTUs and this was consistent across the number of cycles used [Figure 1-2 & Table S1-S4]. In contrast to the results obtained with fecal samples, differences between polymerases were observed as early as 20 cycles in the mock community (F-stat = 15.82, P-value = 0.002) [Table S1]. The majority of differences for the number of OTUs detected in the Mock community is largely due to Kappa and Platinum differences to the other polymerases across the different number of cycles [Table S2]. Based on these observations in fecal and mock communities, it is clear that different polymerases result in a different total number of OTUs within a sample.

***Minimal Bray-Curtis Differences are Detected and are Dependent on Cycle Number:*** A few small differences based on the number of cycles were detected in overall bacterial community composition. Within the same fecal sample and independent of polymerases, there are large differences in the community composition between 20 and 25 cycles [Figure 3A]. Additionally, when data was available for the mock communities, there are also large observed differences between 20 and 25 cycles [Figure 3B]. These community differences within a sample disappear when comparing 25 to 30 cycles and do not persist past 25 cycles [Figure 3]. Although these trends are clearly noticeable, there is no detectable difference in Bray-Curtis index when comparing to the previous 5-cycle increment for both fecal and mock communities after multiple comparison correction (P-value > 0.05). Using PERMANOVA to test for community differences based on the

number of cycles within polymerases, only Phusion had cycle dependent differences (P-value = 0.03. For fecal samples, Phusion was one of two polymerases that had enough sequences to be rarefied to 1000 at 15 cycles. Overall, these data suggest that there are small polymerase differences in Bray-Curtis index that are dependent on the number of cycles.

**Sequence Error is Dependent on both Polymerase and Cycle Number:** Differences in the median error rate varied by polymerase, with Kappa being the highest [Figure 4 & Table S3]. The differences in the median error rate between the polymerases also is dependent on the number of cycles, with Platinum and Kappa having the most differences versus other polymerases [Figure 4 and Table S4]. The total sequences with at least one error also is dependent on the number of cycles [Table S3 & S4]. These differences in sequences with at least one error is mostly due to differences in Accuprime™ and Kappa versus the other polymerases [Table S3 & S4]. The differences in error rates were not due to polymerase dependent differences in base substitution rate [Figure S1]. These results suggest that sequence error is dependent on polymerase and the number of cycles, but is not attributable to a specific type. Based on these results, we examined whether chimeras also were dependent on polymerase and whether this also could affect the number of OTUs.

**Prevalence of Chimeric Sequences are Polymerase Dependent and Correlate with the Number of OTUs:** There is significant differences in the chimera prevalence based on polymerase at all the number of cycles used (P-value < 0.05) [Table S3]. Differences in chimera prevalence between Platinum and all other polymerases accounted for the majority of these differences [Table S4]. Accuprime™ had the lowest chimera prevalence of all polymerases regardless of whether chimera removal with VSEARCH was used [Figure 5A & 5B]. Additionally, there was a plateau in the total percent of chimeras that were removed that was similar for all polymerases [Figure 5C]. A positive correlation was observed between chimeric sequences and the number of OTUs for all polymerases [Figure 6]. This positive correlation was strongest for Accuprime™, Platinum, and Phusion [Figure 6]. This data suggests that chimera prevalence depends on polymerase used and confirms that the number of OTUs is dependent on the prevalence of these chimeric sequences.

## Discussion

In this study we show that the number of OTUs, error rate, and chimera prevalence depends on polymerase used [Figure 1-5]. These differences are important because many diversity metrics rely on the number of OTUs or other measures dependent on error rate and chimera prevalence as part of their metric calculations (e.g. richness). Additionally, the earlier detection of differences in total number of OTUs between polymerases in the mock versus fecal samples might indicate that high biomass samples may underestimate the biases present within low biomass samples. We observed that undetected chimeras that were not identified and removed using standard bioinformatic approaches cause many of these differences. This suggests that some of the specific diversity differences between studies can be attributed to differences in polymerase used. Based on these observations, metrics that measure within sample diversity like richness depend on polymerase but this may not be the case for metrics that assess between sample diversity.

There were few differences that depend on polymerase for between sample diversity, as measured by the Bray-Curtis index. Our observations generally found no differences in the overall bacterial community composition for the number of cycles used. One possible reason for this outcome is that our study did not have enough power to detect differences due to low sample number in each group. Another reason is that many of the OTUs are likely not highly abundant, allowing the Bray-Curtis index to be able to successfully down-weight chimeric OTUs (Minchin, 1987). The choice of downstream diversity metric could be an important consideration in helping to mitigate these observed polymerase dependent differences in chimera prevalence. Metrics that solely use presence/absence of OTUs (e.g. Jaccard (Real & Vargas, 1996)) may be less robust to chimera prevalence and by extension total number of OTU differences in polymerases. When choosing a distance metric, careful consideration of the biases introduced from the PCR step of the 16S rRNA gene sequencing workflow need to be taken into account. With differences in the number of OTUs and chimera prevalence depending on polymerase used, it might be easier to avoid specific DNA polymerase families altogether.

Although the variation in error rate and chimera prevalence may be due to the DNA polymerase family, this is unlikely to be the only contributor. For example, the highest and lowest chimera

rates both belonged to a family A polymerase (Platinum and Accuprime™ respectively) (Ishino & Ishino, 2014). Additionally, based on the material safety data sheet the differences between the two polymerases are not immediately apparent. Both polymerases contain a recombinant *Taq* DNA polymerase, a *Pyrococcus* spp GB-D polymerase and a platinum *Taq* antibody. With everything else being equal, it is possible that differences in how the recombinant *Taq* was generated could be a contributing factor for the differences observed between the polymerases. We are unlikely to avoid adding polymerase dependent bias to 16S rRNA gene sequencing results, however, these differences may not be large enough to mask the actual biological signal.

The majority of polymerases we studied add small increases in the number of OTUs and chimera prevalence and may be masked by biological differences. The sequence error introduced by the polymerase is also small and likely to be smaller than the biological variation within a specific study, which would be consistent with previous findings for preservation and DNA extraction methods (Salter et al., 2014; Song et al., 2016; Luo et al., 2016). The choice of polymerase should be an important consideration in the creation of a 16S rRNA gene sequencing workflow because using different polymerases can add error and bias to the downstream observations. Although standardization of the workflow may partially solve this problem by introducing a consistent bias to all samples, it does come at a cost.

Methods can be standardized but they commonly contain bias that is reproducible and may miss important associations. Bias can be easily reproduced and can be found in every step of the 16S rRNA gene sequencing workflow (Salter et al., 2014; Gohl et al., 2016; Luo et al., 2016; Amir et al., 2017). This study shows that specific diversity metrics used to measure the microbial community consistently vary based on polymerase. Standardizing multiple workflows to one specific polymerase could be detrimental since some polymerases may work better in certain situations over others. Arguably, the degree of workflow standardization across studies and research group needs to be approached on a study by study basis and not every project needs to use the exact same approach. All aspects of the 16S rRNA gene sequencing workflow need to be customized for the specific microbial community that will be sampled. Although a diversity of approaches may make reproducibility and replicability more difficult it will help to avoid systematic biases from occurring due to widespread standardization of approaches.

## Conclusion

Our observations fill a gap in knowledge on the bias introduced to 16S rRNA gene sequencing results due to differences in polymerases. We found that the number of OTUs and the chimera prevalence is dependent on both polymerase and cycle number chosen. Care should be taken when choosing a polymerase for 16S rRNA gene surveys because their intrinsic differences can change the number of OTUs observed and influence diversity based metrics that do not down-weight rare observations. Knowing the inherent bias associated with different polymerases allows for better interpretation of the relationship between an individual study to their respective field of research.

## Acknowledgements

The authors would like to thank all the study participants in ERIN whose samples were utilized. We would also like to thank Judy Opp and April Cockburn for their effort in sequencing the samples as part of the Microbiome Core Facility at the University of Michigan. Salary support for Marc A. Sze came from the Canadian Institute of Health Research and NIH grant UL1TR002240. Salary support for Patrick D. Schloss came from NIH grants P30DK034933 and 1R01CA215574.

## References

- Acinas SG., Sarma-Rupavtarm R., Klepac-Ceraj V., Polz MF. 2005. PCR-induced sequence artifacts and bias: Insights from comparison of two 16S rRNA clone libraries constructed from the same sample. *Applied and Environmental Microbiology* 71:8966–8969. DOI: 10.1128/aem.71.12.8966-8969.2005.
- Amir A., McDonald D., Navas-Molina JA., Debelius J., Morton JT., Hyde E., Robbins-Pianka A., Knight R. 2017. Correcting for microbial blooms in fecal samples during room-temperature shipping. *mSystems* 2:e00199–16. DOI: 10.1128/msystems.00199-16.
- Bassis CM., Nicholas M. Moore., Lolans K., Seekatz AM., Weinstein RA., Young VB., Hayden MK. 2017. Comparison of stool versus rectal swab samples and storage conditions on bacterial community profiles. *BMC Microbiology* 17. DOI: 10.1186/s12866-017-0983-9.
- Benjamini Y., Hochberg Y. 1995. Controlling the false discovery rate: A practical and powerful approach to multiple testing. *Journal of the Royal Statistical Society. Series B (Methodological)* 57:289–300.
- Cole JR., Wang Q., Fish JA., Chai B., McGarrell DM., Sun Y., Brown CT., Porras-Alfaro A., Kuske CR., Tiedje JM. 2013. Ribosomal database project: Data and tools for high throughput rRNA analysis. *Nucleic Acids Research* 42:D633–D642. DOI: 10.1093/nar/gkt1244.
- Edgar RC., Haas BJ., Clemente JC., Quince C., Knight R. 2011. UCHIME improves sensitivity and speed of chimera detection. *Bioinformatics* 27:2194–2200. DOI: 10.1093/bioinformatics/btr381.
- Garnier S. 2017. *Viridis: Default color maps from 'matplotlib'*.
- Gohl DM., Vangay P., Garbe J., MacLean A., Hauge A., Becker A., Gould TJ., Clayton JB., Johnson TJ., Hunter R., Knights D., Beckman KB. 2016. Systematic improvement of amplicon marker gene methods for increased accuracy in microbiome studies. *Nature Biotechnology* 34:942–949. DOI: 10.1038/nbt.3601.
- Haas BJ., Gevers D., Earl AM., Feldgarden M., Ward DV., Giannoukos G., Ciulla D., Tabbaa D.,

289 Highlander SK., Sodergren E., Methe B., DeSantis TZ., Petrosino JF., Knight R., and BWB. 2011.  
 290 Chimeric 16S rRNA sequence formation and detection in sanger and 454-pyrosequenced PCR  
 291 amplicons. *Genome Research* 21:494–504. DOI: 10.1101/gr.112730.110.

292 Ishino S., Ishino Y. 2014. DNA polymerases as useful reagents for biotechnology â the history of  
 293 developmental research in the field. *Frontiers in Microbiology* 5. DOI: 10.3389/fmicb.2014.00465.

294 Kobschull JM., Zador AM. 2015. Sources of PCR-induced distortions in high-throughput sequencing  
 295 data sets. *Nucleic Acids Research*:gkv717. DOI: 10.1093/nar/gkv717.

296 Kozich JJ., Westcott SL., Baxter NT., Highlander SK., Schloss PD. 2013. Development of a  
 297 dual-index sequencing strategy and curation pipeline for analyzing amplicon sequence data on the  
 298 MiSeq illumina sequencing platform. *Applied and Environmental Microbiology* 79:5112–5120. DOI:  
 299 10.1128/aem.01043-13.

300 Luo T., Srinivasan U., Ramadugu K., Shedden KA., Neiswanger K., Trumble E., Li JJ., McNeil  
 301 DW., Crout RJ., Weyant RJ., Marazita ML., Foxman B. 2016. Effects of specimen collection  
 302 methodologies and storage conditions on the short-term stability of oral microbiome taxonomy.  
 303 *Applied and Environmental Microbiology* 82:5519–5529. DOI: 10.1128/aem.01132-16.

304 Meisel JS., Hannigan GD., Tyldsley AS., SanMiguel AJ., Hodgkinson BP., Zheng Q., Grice EA. 2016.  
 305 Skin microbiome surveys are strongly influenced by experimental design. *Journal of Investigative*  
 306 *Dermatology* 136:947–956. DOI: 10.1016/j.jid.2016.01.016.

307 Minchin PR. 1987. An evaluation of the relative robustness of techniques for ecological ordination.  
 308 *Vegetatio* 69:89–107. DOI: 10.1007/bf00038690.

309 Oksanen J., Blanchet FG., Friendly M., Kindt R., Legendre P., McGlinn D., Minchin PR., O’Hara  
 310 RB., Simpson GL., Solymos P., Stevens MHH., Szoecs E., Wagner H. 2017. *Vegan: Community*  
 311 *ecology package*.

312 Polz MF., Cavanaugh CM. 1998. Bias in template-to-product ratios in multitemplate PCR. *Applied*



and *Environmental Microbiology* 64:3724–3730.

R Core Team. 2017. *R: A language and environment for statistical computing*. Vienna, Austria: R Foundation for Statistical Computing.

Real R., Vargas JM. 1996. The probabilistic basis of jaccards index of similarity. *Systematic Biology* 45:380–385. DOI: 10.1093/sysbio/45.3.380.

Rognes T., Flouri T., Nichols B., Quince C., Mahé F. 2016. VSEARCH: A versatile open source tool for metagenomics. *PeerJ* 4:e2584. DOI: 10.7717/peerj.2584.

Salter SJ., Cox MJ., Turek EM., Calus ST., Cookson WO., Moffatt MF., Turner P., Parkhill J., Loman NJ., Walker AW. 2014. Reagent and laboratory contamination can critically impact sequence-based microbiome analyses. *BMC Biology* 12. DOI: 10.1186/s12915-014-0087-z.

Santos QMB-d los., Schroeder JL., Blakemore O., Moses J., Haffey M., Sloan W., Pinto AJ. 2016. The impact of sampling, PCR, and sequencing replication on discerning changes in drinking water bacterial community over diurnal time-scales. *Water Research* 90:216–224. DOI: 10.1016/j.watres.2015.12.010.

Schloss PD., Westcott SL., Ryabin T., Hall JR., Hartmann M., Hollister EB., Lesniewski RA., Oakley BB., Parks DH., Robinson CJ., Sahl JW., Stres B., Thallinger GG., Horn DJV., Weber CF. 2009. Introducing mothur: Open-source, platform-independent, community-supported software for describing and comparing microbial communities. *Applied and Environmental Microbiology* 75:7537–7541. DOI: 10.1128/aem.01541-09.

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.

Song SJ., Amir A., Metcalf JL., Amato KR., Xu ZZ., Humphrey G., Knight R. 2016. Preservation methods differ in fecal microbiome stability, affecting suitability for field studies. *mSystems*

337 1:e00021–16. DOI: 10.1128/msystems.00021-16.

338 Sze MA., Dimitriu PA., Suzuki M., McDonough JE., Campbell JD., Brothers JF., Erb-Downward  
339 JR., Huffnagle GB., Hayashi S., Elliott WM., Cooper J., Sin DD., Lenburg ME., Spira A., Mohn  
340 WW., Hogg JC. 2015. Host response to the lung microbiome in chronic obstructive pulmonary  
341 disease. *American Journal of Respiratory and Critical Care Medicine* 192:438–445. DOI:  
342 10.1164/rccm.201502-0223oc.

343 Wang GCY., Wang Y. 1996. The frequency of chimeric molecules as a consequence of PCR  
344 co-amplification of 16S rRNA genes from different bacterial species. *Microbiology* 142:1107–1114.  
345 DOI: 10.1099/13500872-142-5-1107.

346 Westcott SL., Schloss PD. 2017. OptiClust, an improved method for assigning amplicon-based  
347 sequence data to operational taxonomic units. *mSphere* 2:e00073–17. DOI: 10.1128/mspheredirect.00073-17.

348 Wickham H. 2017. *Tidyverse: Easily install and load 'tidyverse' packages*.

**Figure 1: Total Number of OTUs in Fecal Samples by Number of Cycles.** The x-axis represents the different number of cycles used and the y-axis is the number of OTUs. The legend represents the color code for the 5 different HiFi DNA polymerases used. The range in the number of OTUs detected in the different fecal samples increased as cycle number increased. This range was also larger for specific HiFi DNA polymerases.

**Figure 2: Total Number of OTUs in Mock Samples by Number of Cycles.** The x-axis represents the different number of cycles used and the y-axis is the number of OTUs. The legend represents the color code for the 5 different HiFi DNA polymerases used. The dotted black line represents the number of OTUs detected when only the references sequences are clustered. The range in the number of OTUs detected in the Mock samples increased as cycle number increased. This range was also larger for specific HiFi DNA polymerases.

**Figure 3: Bray-Curtis Community Differences by Five-Cycle Intervals.** A) within person differences based on the next 5-cycle PCR interval in fecal samples. B) Within replicate difference based on the next 5-cycle PCR interval in Mock samples.

**Figure 4: HiFi DNA Polymerase Error Rate in Mock Samples.** The error bars represent the 75% interquartile range of the median error rate.

**Figure 5: HiFi DNA Polymerase Chimera Prevalence in Mock Samples.** A) Percentage of chimeric sequences without the removal of chimeras with VSEARCH. C) Percentage of chimeric sequences with the removal of chimeras with VSEARCH. C) The total percent of chimeric sequences removed with VSEARCH by cycle number. The error bars represent the 75% interquartile range of the median.

**Figure 6: The Correlation between Number of OTUs and Chimeras in Mock Samples.**

371 **Figure S1: HiFi DNA Polymerase Nucleotide Substitutions in Mock Samples.**