High Fidelity DNA Polymerase Introduces Bias into 16S rRNA Gene Sequencing Results

Marc A Sze[1] and Patrick D Schloss[1†]

† To whom correspondence should be addressed: pschloss@umich.edu

1 Department of Microbiology and Immunology, University of Michigan, Ann Arbor, MI

Co-author e-mails:

- marcsze@med.umich.edu

Abstract

Background. Using different reagents and kits at different steps of the 16S rRNA gene sequencing workflow can introduce bias by changing the observed microbial community. Although cycle number and high fidelity (HiFi) DNA polymerase are studied less often, they are still important sources of bias in this workflow. Here, we examine how both cycle number and HiFi DNA polymerase can change the bacterial community and introduce bias to the final obtained results.

Methods. DNA from fecal samples (n=4) were extracted 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. Mock communities (technical replicates n=4) consisting of previously isolated whole genomes of 8 different bacteria were also amplified using the same approach. The number of OTUs (Operational Taxonomic Units) were examined for both fecal samples and mock communities. Next, Bray-Curtis index, the error rate, sequence error prevalence, and chimera prevalence were investigated. Finally, the chimera prevalence correlation with number of OTUs was assessed.

Results. When analyzing fecal samples a different number of OTUs was observed between HiFi DNA polymerases at 35 cycles (P-value < 0.0001). These HiFi dependent differences in the number of OTUs were identified as early as 20 cycles in the mock communities (P-value = 0.002). Chimera prevalence varied by HiFi DNA polymerase and this variation was still present after chimera removal using VSEARCH. The chimera prevalence was positively correlated with the number of OTUs and was also not affected by chimera removal with VSEARCH.

Conclusions. HiFi DNA polymerase dependent differences in the number of OTUs and chimera prevalence makes comparison across studies difficult. Care should be exercised

when choosing both HiFi DNA polymerase and cycle number to be used in 16S rRNA gene sequencing studies.

Introduction

This study will specifically address how cycle number and high fidelity (HiFi) DNA polymerases can bias observed bacterial community results derived from 16S rRNA gene sequencing. First, it is important to differentiate between bias, reproducibility, and standardization since often times these three can be confused and used interchangeably with each other. Bias can change the observed results in a way that is reproducible and standardized. For example, if one group uses one brand of DNA extraction kit for their 16S rRNA gene sequencing, their results may be biased versus another group not using the same brand kit but within their group they can still have reproducible results. Therefore, standardization of 16S rRNA gene sequencing methods to increase reproducibility can still be problematic due to bias. Determining how different aspects of a 16S rRNA gene sequencing workflow could bias the observed results is critical for the interpretation of specific studies in the broader context of the overall field.

A typical 16S rRNA gene sequencing workflow can be divided into preservation, extraction, PCR, and sequencing steps. Generally, not using a preservation media and leaving samples at room temperature has been shown to cause overgrowth of low abundance members of the fecal bacterial community (Amir et al., 2017). Similarly, this overgrowth can still occur if the preservation media does not adequately inhibit growth (Song et al., 2016; Luo et al., 2016). Reports have also shown that changes in specific community members might occur due to differing susceptibility to freeze thaw cycles amongst microbes (Gorzelak et al., 2015). Additionally, reagent contamination has been shown to add community members and the contribution of these contaminant members grows larger with lower biomass samples (Salter et al., 2014). Recent studies have shown that the majority of these biases due to either preservation or extraction tend to be smaller than the overall biological signal being measured (Song et al., 2016; Bassis et al., 2017). However, the contribution of PCR bias to this overall workflow is not well characterized since these

studies use the same PCR approach while varying preservation or extraction method.

Identifying the biases in the PCR stage of 16S rRNA gene sequencing is important because a large body of literature shows that there are a variety of steps during PCR that can change the observed results (Eckert & Kunkel, 1991; Burkardt, 2000). Many of these sources of biases are made worse as cycle number increases (Wang & Wang, 1996; Haas et al., 2011; Kebschull & Zador, 2015). For example, the selective amplification of AT-rich over GC-rich sequences can exaggerate the difference between 16S rRNA genes higher in AT versus those higher in GC (Polz & Cavanaugh, 1998). Both amplification error and non-specific amplification (e.g. incorrect amplicon size products) can also increase as cycle number increases which can drastically change commonly used diversity measures (Acinas et al., 2005; Santos et al., 2016). Additionally, chimeras can form from an aborted extension step followed by a subsequent priming error and secondary extension and will also artificially increase community diversity (Haas et al., 2011).

There are also intrinsic properties to primers and DNA polymerases chosen that can introduce bias. Primers have variable region dependent binding affinities for different bacteria and depending on the primer pair 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). Additionally, there 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 previously mentioned sources of PCR-based bias.

A recent study found clear differences between normal and high fidelity (HiFi) DNA polymerase and that optimization of the PCR protocol could reduce error and chimera generation (Gohl et al., 2016). This study also found that regardless of DNA polymerase, the number of Operational Taxonomic Units (OTUs) or taxa generated were not easily

reduced using the authors chosen bioinformatic pipeline (Gohl et al., 2016). It is natural to extend this line of inquiry and ask if biases in the number of OTUs and chimeras are also dependent on the type of HiFi DNA polymerase. There is some reason to think that this may be the case since many of these HiFi DNA polymerases come from different families (e.g. *Taq* belongs to the family A polymerases) and may intrinsically have different error rates that cannot be completely removed with modifications (Ishino & Ishino, 2014). In this study, we examine if any of five different types of HiFi DNA polymerases introduce significant biases into 16S rRNA gene surveys, if this is a cycle dependent phenomenon, and whether they can be removed using a standard bioinformatic pipeline.

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 difficle* 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/zymobiomics-microbial-community-standards).

PCR Protocol: The five different HiFi DNA 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). The HiFi DNA polymerase 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 HiFi DNA 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 HiFi DNA 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). 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 before the 'pre.cluster' command, before chimera removal, and after chimera removal (Schloss et al., 2009; Cole et al., 2013; Rognes et al., 2016).

Analysis Workflow: The total number of OTUs was analyzed after sub-sampling 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, etc.). These community based measures for fecal samples were analyzed at 4 different sub-sampling sequence depths (1000, 5000, 10000, and 15000) while the mock community samples were analysed at 3 levels (1000, 5000, 10000). Based on these observations we analyzed potential reasons for these differences. Analysis of the mock community of each HiFi DNA polymerase for general sequence error rate, number of sequences with an error, base substitution, and numbers of chimeras were assessed before the 'pre.cluster' command, before chimera removal, and after chimera removal. Additionally, the correlation between the number of chimeras and the number of OTUs was also assessed before the 'pre.cluster' command,

before chimera removal, and after chimera removal.

Statistical Analysis: All analysis was done with the R (v 3.4.3) 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. The raw sequences can be found in the SRA at the following accession number SRP132931.

Results

The Number of OTUs are Dependent on HiFi DNA Polymerase: A consistent difference in the number of OTUs, that was dependent on the HiFi DNA polymerase used was observed regardless of sub-sampling depth for fecal samples [Figure 1]. Additionally, there was a trend for lower cycle numbers (15-20) to result in less differences in the number of OTUs versus higher cycle numbers (25, 30, and 35) between HiFi DNA polymerases [Figure 1]. For fecal samples, all sub-sampling levels had significant differences between HiFi DNA polymerases at 35 cycles (P-value < 0.0001) [Table S1]. Most of the differences observed at 35 cycles were between Platinum and other HiFi DNA polymerases, based on a Tukey post-hoc test (P-value < 0.05) [Table S2]. Differences in the number of OTUs between HiFi DNA polymerases were identifiable at earlier cycles (25 and 30) but the sub-sampling depth had to be 5000 sequences or higher (P-value < 0.05) [Table S1].

This HiFi DNA polymerase dependent difference in the number of OTUs was also observed in the mock community samples [Figure 2]. Regardless if fecal or mock communities were used, the same HiFi DNA polymerases had high (Platinum) and low (Accuprime) number of OTUs and this was consistent across cycle number and sub-sampling depth [Figure 1-2 & Table S1-S4]. In contrast to the results obtained with fecal samples, differences between HiFi DNA polymerases were observed as early as 20 cycles and at as low of a sub-sampling depth as 1000 sequences in the mock community samples (P-value = 0.002) [Table S3]. For both cycle numbers and sub-sampling depths, the majority of differences in the number of OTUs were between Platinum and the other HiFi DNA polymerases [Table S4]. Based on these observations in fecal and mock communities, it is clear that different HiFi DNA polymerases result in a different total number of OTUs observed within a sample.

Minimal Bray-Curtis Differences are Detected and are Dependent on both Cycle Number and Sub-Sampling Depth: A few small differences based on sub-sampling and

cycle number were detected in overall bacterial community composition. Within the same fecal sample and independent of HiFi DNA polymerases, there were differences in the community composition between 20 and 25 cycles that was dependent on sub-sampling depth (sub-sampled to 1000 = 0.51 (0.4 - 0.79) (median (IQR)), sub-sampled to 5000 = 0.43 (0.33 - 0.63), sub-sampled to 10000 = 0.4 (0.24 - 0.43)) [Figure 3A]. Further, when data was available for the mock communities, there were larger observed differences between 20 and 25 cycles (sub-sampled to 1000 = 0.88 (0.42 - 0.91)) [Figure 3B]. Additionally, these stated community differences disappear when comparing 25 to 30 cycles and do not persist past 25 cycles [Figure 3]. Although these trends are clearly noticeable, we found that there was 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 cycle number within HiFi DNA polymerases, only Phusion had cycle dependent differences at 1000 and 5000 sub-sampling depths (P-value = 0.03 and 0.01). For fecal samples, Phusion was one of two HiFi DNA polymerases that had enough sequences to reach a sub-sampling depth of 1000 at 15 cycles. Overall, these data suggest that there are small HiFi DNA polymerase differences in Bray-Curtis index that are dependent on both sub-sampling depth and cycle number.

Sequence Error is Dependent on both HiFi DNA Polymerase and Cycle Number: Differences in the median average per base error varied by HiFi DNA polymerase without a clear pattern across sub-sampling depth [Table S5]. The highest median average per base error rates were for the Kappa HiFi DNA polymerase [Figure 4]. This error rate was minimally affected by both the 'pre.cluster' step and chimera removal by VSEARCH [Figure 4]. The differences in the median average per base error rate between the different HiFi DNA polymerases was cycle dependent with Platinum having the largest changes versus other HiFi DNA polymerases [Figure 4B-C and Table S6]. The total sequences with at least one error was also cycle number dependent and differences between HiFi DNA

polymerases could be drastically reduced by the use of the 'pre.cluster' step [Figure S1]. These differences in sequences with at least one error were mostly due to differences in Accuprime™ and Platinum versus the other HiFi DNA polymerases [Figure S1 & Table S7 & S8]. Finally, we did not observe a HiFi DNA polymerase dependent difference on base substitution rate [Figure S2]. Although sequence error is dependent on HiFi DNA polymerase some of these error dependent differences can be corrected using existing bioinformatic approaches.

Prevalence of Chimeric Sequences are HiFi DNA Polymerase Dependent and Correlate with the Number of OTUs: There were significant differences in the chimera prevalence based on HiFi DNA polymerase used at all levels of sub-sampling and cycle numbers (P-value < 0.05) [Table S9]. Differences in chimera prevalence between Platinum and all other HiFi DNA polymerases accounted for the majority of these differences [Table S10]. Accuprime™ had the lowest chimera prevalence of all HiFi DNA polymerases regardless of whether 'pre.cluster' or chimera removal with VSEARCH was used [Figure 5]. A positive correlation was observed between chimeric sequences and the number of OTUs for all HiFi DNA polymerases [Figure 6]. This positive correlation was strongest for Accuprime™, Platinum, and Phusion HiFi DNA Polymerases [Figure 6]. The R^2 value between the number of OTUs and chimeric sequences did not change with the use of 'pre.cluster' or with the removal of chimeras using VSEARCH [Figure 6]. This data suggests that chimera prevalence depends on HiFi DNA 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 are HiFi DNA polymerase dependent [Figure 1-2 & 4-5]. 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). Importantly, many of these differences are due to undetected chimeras that cannot be fully removed using standard bioinformatic approaches. This suggests that some of the diversity differences between studies can be attributed to differences in HiFi DNA polyermase used. Interestingly, the earlier detection of differences in total number of OTUs between HiFi DNA polymerases in the mock versus fecal samples might indicate that high biomass samples may underestimate the biases present within low biomass samples.

Although the variation in error rate and chimera prevalence may be due to the DNA polymerase family, the highest and lowest chimera rates both belonged to a family A polymerase (Platinum and Accuprime^{TM} respectively) (Ishino & Ishino, 2014). Additionally, based on the material safety data sheet (MSDS) the differences between the two HiFi DNA polymerases are not immediately apparent. Both HiFi DNA 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 HiFi DNA polymerases.

There were few differences in bacterial community composition based on HiFi DNA polymerase. The data also suggests that there were no differences in the overall bacterial community composition for sub-sampling depth or cycle number used. One possible reason for this outcome was that our study did not have enough power to detect differences due to low sample number in each group. Another reason was 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 HiFi DNA polymerase dependent differences in chimera prevalence. Metrics that simply look at 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 HiFi DNA 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.

Similar to using different preservation methods or different DNA extraction kits, the type of HiFi DNA polymerase can add bias to the observed bacterial community. The sequence error introduced by the HiFi DNA polymerase is 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). However, the chimarea prevalence for some HiFi DNA polymerases (e.g. Platinum) are relatively large and might be greater than the oberseved biological variation within a specific study. Within the larger context of the different 16S rRNA gene sequencing steps, the choice of HiFi DNA polymerase can be as important a consideration as either preservation or DNA extraction method used.

Heavy standardization has been commonly suggested as a reasonable answer to finding the most reproducible approach. However, bias can be easily reproduced and can be found in every step of the 16S rRNA gene sequencing workflow. This study shows that specific diversity metrics used to measure the microbial community consistently vary based on HiFi DNA polymerase. Standardizing multiple workflows to one specific HiFi DNA polymerase could be detrimental since the PCR step not only misses entire species based on primer chosen (Meisel et al., 2016) but also can artifically increase the number of OTUs observed. 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 more difficult it will help to avoid systematic biases from occuring due to widespread standardization of approaches.

Conclusion

The number of OTUs are dependent on both HiFi DNA polymerase and cycle number chosen. Care should be taken when choosing a HiFi DNA 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.

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 Sze came from the Canadian Institute of Health Research and the Michigan Institute for Clinical and Health Research Postdoctoral Translational Scholar Program.

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.

Burkardt H-J. 2000. Standardization and quality control of PCR analyses. *Clinical Chemistry and Laboratory Medicine* 38. DOI: 10.1515/cclm.2000.014.

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.

Eckert KA., Kunkel TA. 1991. DNA polymerase fidelity and the polymerase chain reaction. *Genome Research* 1:17–24. DOI: 10.1101/gr.1.1.17.

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.

Gorzelak MA., Gill SK., Tasnim N., Ahmadi-Vand Z., Jay M., Gibson DL. 2015. Methods for improving human gut microbiome data by reducing variability through sample processing and storage of stool. *PLOS ONE* 10:e0134802. DOI: 10.1371/journal.pone.0134802.

Haas BJ., Gevers D., Earl AM., Feldgarden M., Ward DV., Giannoukos G., Ciulla D., Tabbaa D., Highlander SK., Sodergren E., Methe B., DeSantis TZ., Petrosino JF., Knight R., and BWB. 2011. Chimeric 16S rRNA sequence formation and detection in sanger and 454-pyrosequenced PCR amplicons. *Genome Research* 21:494–504. DOI: 10.1101/gr.112730.110.

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

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

Kozich JJ., Westcott SL., Baxter NT., Highlander SK., Schloss PD. 2013. Development of a dual-index sequencing strategy and curation pipeline for analyzing amplicon sequence data on the MiSeq illumina sequencing platform. *Applied and Environmental Microbiology*

79:5112–5120. DOI: 10.1128/aem.01043-13.

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

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

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

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

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.,

366 Parkhill J., Loman NJ., Walker AW. 2014. Reagent and laboratory contamination
367 can critically impact sequence-based microbiome analyses. *BMC Biology* 12. DOI:
368 10.1186/s12915-014-0087-z.

369 Santos QMB-d los., Schroeder JL., Blakemore O., Moses J., Haffey M., Sloan W., Pinto AJ.
370 2016. The impact of sampling, PCR, and sequencing replication on discerning changes in
371 drinking water bacterial community over diurnal time-scales. *Water Research* 90:216–224.
372 DOI: 10.1016/j.watres.2015.12.010.

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

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

381 Song SJ., Amir A., Metcalf JL., Amato KR., Xu ZZ., Humphrey G., Knight R. 2016.
382 Preservation methods differ in fecal microbiome stability, affecting suitability for field
383 studies. *mSystems* 1:e00021–16. DOI: 10.1128/msystems.00021-16.

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

389 Wang GCY., Wang Y. 1996. The frequency of chimeric molecules as a consequence of

390 PCR co-amplification of 16S rRNA genes from different bacterial species. *Microbiology*
391 142:1107–1114. DOI: 10.1099/13500872-142-5-1107.

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

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

Figure 1: Normalized Fecal Number of OTUs. The x-axis represents the different sub-sampling depths used and the y-axis is the normalized within individual number of OTUs. The red line represents the overall mean Z-score normalized number of OTUs for each respective HiFi DNA polymerase. The dashed black line represents the overall Z-score normalized mean number of OTUs.

Figure 2: Mock Sample Variability in Number of OTUs based on HiFi DNA Polymerase. A) Sub-sampled to 1000 reads. B) Sub-sampled to 5000 reads. C) Sub-sampled to 10000 reads. The dotted line represents the number of OTUs generated when the mock reference sequences are run through the pipeline.

Figure 3: Community Differences by Five-Cycle Intervals and Sub-sampling Depth. A) Fecal samples within person difference based on the next 5-cycle PCR interval. B) Mock samples within replicate difference based on the next 5-cycle PCR interval.

Figure 4: HiFi DNA Polymerase Per Base Error Rate in Mock Samples. A) Error rate before the merger of sequences with pre.cluster and the removal of chimeras with VSEARCH. B) Error rate before the removal of chimeras with VSEARCH. C) Full pipeline. The error bars represent the 75% interquartile range of the median.

Figure 5: HiFi DNA Polymerase Chimera Prevalence in Mock Samples. A) Chimera sequence percentage before the merger of sequences with pre.cluster and the removal of chimeras with VSEARCH. B) Chimera sequence percentage before the removal of chimeras with VSEARCH. C) Full pipeline. The error bars represent the 75% interquartile range of the median.

Figure 6: The Correlation between Number of OTUs and Chimeras. A) Correlation before the merger of sequences with pre.cluster and the removal of chimeras with VSEARCH. B) Correlation before the removal of chimeras with VSEARCH. C) Correlation with full pipeline.

Figure S1: HiFi DNA Polymerase Sequence Error Prevalence in Mock Samples. A) Sequence error prevalence before the merger of sequences with pre.cluster and the removal of chimeras with VSEARCH. B) Sequence error prevalence before the removal of chimeras with VSEARCH. C) Full pipeline. The error bars represent the 75% interquartile range of the median.

Figure S2: HiFi DNA Polymerase Nucleotide Subsitutions in Mock Samples.