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**DEPARTMENT OF MICROBIOLOGY AND IMMUNOLOGY**

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Dear Editor,

We are happy to submit our manuscript, **Quantifying the impact of DNA polymerase and number of rounds of amplification in PCR on 16S rRNA gene sequence data**, to *mSphere*. This manuscript describes the impact of the choice of the DNA polymerase and number of rounds of amplification in PCR on the downstream interpretation of sequence data generated from microbial communities. Our lab and others have spent considerable effort on quantifying and remediating errors generated by a DNA sequencer; however, the role of PCR in generating base mis-incorporations, chimeras, bias, and drift has been less well studied. We are optimistic that our story will have a significant impact on shaping the best practices that are used in the exponentially growing field of microbiome research.

A version of this manuscript has been deposited to bioRxiv as a preprint.

Sincerely,



Patrick D. Schloss, PhD

Professor