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**DEPARTMENT OF MICROBIOLOGY AND IMMUNOLOGY**

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Dear Dr. McMahon,

We are happy to resubmit our manuscript, **The impact of DNA polymerase and number of rounds of amplification in PCR on 16S rRNA gene sequence data**, to *mSphere*. We are grateful to the largely positive feedback we received from the reviewers and your conditional acceptance. We hope that through our incorporation to the reviewers’ comments we have improved the manuscript so that it is now ready for publication.

As you may recall, 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