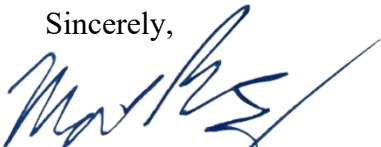


Dear Leah,

I am writing to express my enthusiasm for your F31 proposal entitled, “Interplay between bacterial colonization, RSV infection, and human nasal epithelium”. I am excited to continue my collaboration with you and your Sponsor, Dr. Lemon to characterize the transcriptional response of bacteria when colonizing human nasal epithelial organoids (HNOs) during RSV infection. It has been great to learn about the goals of your project during our meetings thus far, and I am excited to learn how bacterial transcription is affected by RSV infection of HNOs. I affirm that my lab will assist you in analyzing your RNA sequencing data by teaching you our pipeline and being available for help during your analysis.

Using our analysis pipeline, RNA sequencing reads are aligned and mapped using bowtie2 and HTseq. Differentially expressed transcripts are analyzed using DESeq2 and R using custom Unix shell and R scripts. Following identification of significantly differentially expressed genes (DEGs), KEGG annotations are obtained for each of the genomes using BlastKOALA. Pathway analysis for the DEGs is then carried out by mapping to KEGG orthology. This pipeline was recently published in my groups 2021 ISME paper (cited in biosketch) and began its initial development when I was a postdoctoral fellow in the Lemon lab. I look forward to your continued success with this work.

Sincerely,



Matthew Ramsey
University of Rhode Island
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