Dear PLOS One Editorial Team,

I am pleased to submit my latest research article, titled “Re-analysis of Covid-19-related RNASeq count data reveals a robust list of genes that exhibit significant Covid-19-dependent differential expression,” for your consideration. This study represents a valuable contribution to the study of Covid-19 and holds broader significance as an instructional aid for researchers interested in conducting large-scale analyses of biological count data with R. I believe its merits align well with the scope and mission of PLOS One, particularly its commitment to *accelerating progress in science and medicine through transformative research communication*.

This manuscript was originally submitted to PLoS Computational Biology, where it underwent initial review. Based on the feedback received from the editors, it was determined that PLOS One would be a better fit for publication. I appreciate the opportunity to submit it to your prestigious journal.

Building upon my prior work, including the study titled "Meta-analysis of Drosophila circadian microarray studies identifies a novel set of rhythmically expressed genes" published in PLoS Computational Biology in 2007, the current research follows a similar approach of re-analyzing large-scale data to identify robust gene sets. While my previous study focused on circadian genes in Drosophila microarray data, the present study delves into the timely and relevant topic of Covid-19-related gene expression in humans based on recent RNASeq studies—a subject that is timely and relevant to the current global context. Despite numerous published studies utilizing RNASeq to investigate Covid-19, my study is unique in its use of multiple datasets to derive a common set of Covid-19-related genes.

Through an analysis of multiple large-scale studies, I have identified a novel set of Covid-19-related genes with potential significance for both the scientific and medical communities. The inclusion of R code used in the analysis, provided as supplemental information with the manuscript and available on GitHub, ensures transparency and facilitates reproducibility of the results.

I hope that the gene list I have identified will be useful to the scientific and medical communities. Given the prescient nature of Covid-19, I anticipate that it will generate considerable interest. Likewise, the inclusivity of the included R code, particularly its presence on GitHub to facilitate dynamic interaction with interested readers, coupled with its detailed commentary, will enable anyone to reproduce and improve upon my analyses and results, thereby contributing to the reproducibility and openness of scientific research.

In selecting appropriate Academic Editors for the manuscript, I would like to suggest Danillo G. Augusto at the University of North Carolina at Charlotte and Nafees Ahmad at the University of Arizona College of Medicine. Their expertise in genetics, gene expression, and infectious diseases aligns well with the multidisciplinary nature of the study.

Thank you for considering my submission. I am excited about the possibility of sharing this research with the PLOS One community and contributing to the advancement of scientific knowledge.

Sincerely,

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