Dear BMC Bioinformatics 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 BMC Bioinformatics.

Building upon my prior work, including a 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.

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

Sincerely,

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