

Dear *Frontiers in Genetics* Editors,

I am pleased to submit our manuscript titled, "Re-analysis of COVID-19 Related RNA-Seq Count Data Reveals a Robust List of Genes Exhibiting Significant COVID-19 Dependent Differential Expression," for consideration in *Frontiers in Genetics* (Bioinformatics and Computational Biology Section). This work explores the integration of RNA-Seq datasets with robust bioinformatics workflows to identify and validate genes significantly associated with COVID-19 disease states. By leveraging public datasets and employing reproducible analytical techniques, this study offers a valuable resource for further research in understanding the molecular underpinnings of COVID-19.

The key findings of my study include:

- The identification of 61 genes, 60 of which are annotated, exhibiting significant differential expression in COVID-19 cases across three large public RNA-Seq datasets.
- A novel approach for harmonizing and analyzing diverse datasets using R programming, enabling reproducibility and transparency.
- Preliminary pathway analyses highlighting potential biological processes impacted by COVID-19, providing insights for future therapeutic exploration.

The manuscript aligns with the scope of *Frontiers in Genetics* by addressing critical questions at the intersection of computational biology and genetic research. Our work demonstrates the power of bioinformatics in elucidating complex biological phenomena, fostering interdisciplinary collaboration, and promoting open science—values that resonate with the mission of this journal.

We believe this manuscript will be of interest to researchers in the fields of genomics, bioinformatics, and infectious diseases. Furthermore, the reproducible R workflows included in the study serve as a practical template for other scientists working with large-scale genomic datasets.

I confirm that this manuscript has not been published elsewhere and is not under consideration by any other publication. As sole author I approve the manuscript and agree with its submission to *Frontiers in Genetics*. There are no conflicts of interest to disclose, and this research received no specific funding.

Thank you for considering our work. I look forward to the possibility of contributing to *Frontiers in Genetics*. Please do not hesitate to contact me should you require any further information or documentation.

Sincerely,

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