Review of: "In Silico Investigation of Potential COVID-19-Associated MicroRNA Signatures"

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Potential competing interests: No potential competing interests to declare.

The authors investigated potential COVID-19 associated microRNA signatures. To identify microRNAs that potentially regulate COVID-19 related genes, the authors utilized four tools, including microT_CDS, TargetScan, PITA, and miRDB, to search for COVID-19 related microRNAs. microRNA-gene interactions predicted by more than 3 tools were prioritized for further investigation. However, the study lacks of experimental validation, with only indirect evidences based on differential gene expression analysis of blood tissues between COVID-19 patients and healthy controls. Other issues for the study are listed as follows:

1. In the abstract, it is necessary to mention the tissue source of gene expression data used in the current study of microRNA signatures, as different tissues may display variable microRNA signatures. The rationale for selecting RNAseq data of specific tissue needs to be justified and aligned with the biology of SARS-CoV2 infection or COVID-19 severity.

2. The quality of figures, particular for figure 2, should be improved according to the publication standard. Figure 4 was generated by COVID19db and was used by the authors directly without modification in the current study, of which no statistical test or statistical significance annotation provided in the figure legend.

3. There are eight microRNA potentially targeting COVID-19 genes proposed by the authors. However, it is necessary to show details of how these miRNA regulate these COVID-19 genes. For example, the authors may display the miRNA targeted mRNA sequences for these genes. It is highly recommended to have experimental data from the authors or other researchers to support findings discovered in the current study.