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

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Title: Authors mentioned about miRNA-COVID19 associated signatures, but probably it should extend to in which condition actually signature happened, because in general there always be a modulation of miRNA genes

Introduction: Authors mentioned miRNA related to differential expression of miRNA but did not elaborate in which condition. It is important to highlight the type of experiment or samples because the expression will always modulated time by time and depend on specific condition.

Methods: In PPI section, authors mentioned many algorithms used in this study, but did not discussed in details. So, what is the power of different algorithms in order to support the findings. In functional enrichment section, authors mentioned affinity propagation as filtering parameter to reach representative categories. However, the expected categories not yet described. In pairwise miRNA association, there is weighting score for miRNA interaction, but authors did not describe how to weight between 2 different software. In Independent validation, authors only use DB from whole blood. Probably this is also should mentioned or reflected in the abstract or title.

Results and Discussion: Authors should put side by side the experiment that involved in other studies to create strong evidence based on the bioinformatics pipeline developed in this study. Especially also to see how miRNA regulated in healthy and infected patient of covid19. The result focusing on the expression of genes, but the miRNA data coming from the experiment should be added also.

Overall: The manuscript is well-written but need to be improved in content