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.

This is very simple research, but the authors found 8 miRNAs that may target the 25 top nodes from 149 COVID-19-relevant genes. I got some comments, especilly comment 5, below that may help the authers to improve the manuscripts.

1. Page 5: For "The 25 top nodes were detected in the protein-protein interaction network (Figure 1 and Table S1) based on the combined output of the twelve algorithms in cytoHubba". Could the authers explian how the results of twelve algorithms in cytoHubba were combined.

2. Page 6: I believe the Figure 2 showed the functional enrichment results. It is important show the p-value of each enriched pathways, so that readers can understand which enriched pathways are more important than others.

3. Page 8: p-value should be showed on the boxplots in Figure 4. There are three out of 25 genes were upregulated. Why were these 9 genes showed in Figure 4?

4. Please check the order of Figure 3 and 4. How was the networks in Figure 3 developed?

5. Dose the COVID19db include the expression information of the eight miRNAs? If yes, it would be great to show them align their target genes as Figure 4.