Supplementary Table 1. miRNAs selection criteria

miRNAs	Justification for validation	Reference
miR-16	Involved in regulation of inflammation and programmed cell death, acute lung injury, sepsis, phenotypic changes on T cells survival, differentiation, and proliferation. Targeting genes responsible for host-SARS-CoV-2 interaction. Influence viral entry receptor (ACE2) related networks	[19,35,44,57,77–80] [57,80,81]
miR-155	Involved in inflammation. T cell differentiation and innate immunity. Regulates pathways related with IFN superfamily, NF-kB and MAP Kinase pathways. Cardiac, lung and kidney damage.	[11,43–45,82] [23,83–85]
miR-34a	Thrombotic events and Ras signaling Can bind to multiple sites on noncoding SARS-CoV-2 RNA, which can affect the host immune response	[19,86] [87]
miR-146a	Regulation of cytokine-responsive gene expression, and the pro-inflammatory cytokines like IL-6, TNF-a, IL-1 and IL-8. Regulation of NF-kB, MAP kinase, and STAT 3 pathways. Thrombo-inflammatory processes. Cytokine storm.	[8,13,60,70–72,88,89]
miR-221	Regulation of inflammation and vascular remodeling. Lung injury, coagulopathy, thrombosis. Regulation of innate immune response and promoting viral infection.	[19,56,90] [44,57–59]

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