



# miRNA target prediction might explain the reduced transmission of SARS-CoV-2 in Jordan, Middle East

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## ABSTRACT

MicroRNAs (miRNAs) are non-coding RNAs that control many functions within the human cells by controlling protein levels through binding to messenger RNA (mRNA) translation process or mRNA abundance. Many pieces of evidence show that miRNAs affect the viral RNA replication and pathogenesis through direct binding to the RNA virus to mediate changes in the host transcriptome. Many previous studies have been studying the interaction between human cells' miRNA and viral RNA to predict many targets along the viral genome. In this work, via the miRDB database, we determined the target scores of predicted human miRNA to bind with the ss-RNA of the severe acute respiratory syndrome coronavirus (SARS-CoV-2) in general and its spike gene in specific. Our predicted miRNA targets of the ss-RNA of SARS-CoV-2 might destabilize the ss-RNA translation of SARS-CoV-2 that has been established by more than 80% of asymptomatic infected cases in Jordan due to host miRNA interactions. In respiratory epithelial cells, the high prediction scoring for miRNAs covers the RNA from 5' to 3' that explains successful antiviral defenses against ss-RNA of SARS-CoV-2 and might lead to new nucleotide deletion mechanisms. The exciting findings here that the nucleotide substitution 1841A > G at the viral genomic RNA level, which is an amino acid substitution D614G at the spike protein level showed a change in the predicted miRNA sequence from hsa-miR-4793-5p to hsa-miR-3620-3p with an increase in the target score from 91 to 92.

## 1. Introduction

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) caused an outbreak in Wuhan city and characterized as a pandemic by the World Health Organization WHO [1]. The first case of SARS-CoV-2 was reported to the Jordanian Ministry of Health on March 2, 2020, for a Jordanian citizen who was in Italy. To the date of this report, there are 1218 confirmed cases, 1131 recovered and 11 deaths of COVID-19 in Jordan, according to the Jordanian Ministry of Health official web site which has been launched as a unified source of information about the preventive measurements and symptoms of corona virus-2019 (<https://corona.moh.gov.jo/en>).

In 2003, severe coronavirus acute breathing syndrome (SARS-CoV) appeared in China. It has spread to over 30 countries, infecting around 8000 people, killing young people with 10%, and aging with 50%. There are no approved coronavirus vaccines or antiviral treatments against, for example, such as the Middle East respiratory CoV (MERS-CoV) yet [2]. The molecular mechanisms of viral pathogenesis provide thoughtful help in the search for effective and secure therapeutic

strategies against new human SARS-CoV-2.

MicroRNAs (miRNAs) are non-coding RNAs that control many functions within a cell by controlling protein levels through binding to mRNA translation process. Many shreds of evidence show that miRNAs affect the RNA viral replication and, consequently, pathogenesis through direct binding to the RNA virus-mediated changes in the host transcriptome. Host miRNAs can bind to a wide range of RNA viruses, straight adapt their pathogenesis through mimicking cellular mRNAs, and tolerating direct binding of the miRNA to the viral RNA. Theoretically, the abovementioned regulation is analogous to that of the host mRNAs [3,4].

Many miRNA sequences that targeted Influenza viral RNA segments were linked with the activity of host miRNA-induced antiviral defense. This link represents potential treatment with a combination of five miRNAs through Antagomirs delivery to suppress the viral replication and effectively improve protection against lethal challenge with PR8 influenza virus strain in mice [5].

Severe acute coronavirus syndrome (SARS-CoV) caused human fatal disease and reaction and extensive pulmonary disease. The significance

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of small non-coding RNAs for SARS-CoV pathologies, lung RNAs sequences of infected mice, and three (18–22 nt) small viral RNAs (svRNAs) were discovered. The three svRNAs originated from the SARS-CoV genomic regions nsp3 (svRNA-nsp3.1 and -nsp3.2), and N (svRNA-N). CoV svRNAs were characterized as independent from cell type and host species RNase III, but the extent of the viral replication machinery was a dependent process. In vivo, lung pathology and pro-inflammatory cytokine release, antagomir-mediated inhibition of svRNA-N significantly decreased. This indicates that svRNAs contribute to the pathogenesis of SARS-CoV and demonstrates the potential for antagomirs of svRNA-N as antivirals [6].

To understand the early steps of COVID-19 infection, we predicted miRNAs sequences targeting the submitted 29903bp of viral ss-RNA of the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2 complete genomic RNA sequence) from the isolate of Wuhan-Hu-1. A predicted miRNAs targeting region at 3822 bp ss-RNA of the spike glycoprotein of SARS-CoV-2 was revealed. Also, we predicted miRNAs targeting a variable region of the ss-RNA spike glycoprotein of SARS-CoV-2 sequences from 20 positive nasopharyngeal specimens from Jordan. These specimens were collected and sequenced by Biolab Diagnostic Laboratories (Jordan) & Andersen lab at Scripps Research (USA), who deposited the sequences in GISAID, a maintained global database based in Germany. The perception in this work might help scientists to understand the molecular mechanisms of viral pathogenesis. Besides, it might support the research for effective, safe therapeutic strategies against known human coronaviruses and new emergent strains with a focus on miRNA-induced antiviral human body defense, which could be a potential treatment developed for SARS-CoV-2.

## 2. Methods

The miRDB is an online <http://mirdb.org/custom.html> database for the target and working annotations of miRNA. All targets in miRDB were anticipated by MirTarget, a bioinformatics tool that was developed through the study of thousands of miRNA target interactions from high-performance research [7,8].

We have utilized the tool in the following link: <http://biomodel.uah.es/en/lab/cybertory/analysis/trans.htm> to convert submitted sequences from miRNA to DNA to demonstrate genome sequence alignment using ChromosPros Version 2.1.9. The Wuhan-Hu-1 full genome sequence (accession number: [NC\\_045512.2](https://ncbi.nlm.nih.gov/nuccore/NC_045512.2)) has been used as a reference sequence against miRNAs targeting the area of 3822 bp ss-RNA of the SARS-CoV-2 Spike gene. We predicted miRNA targets against the full length of 29903 bp ss-RNA (SARS-CoV-2 sequence) from the isolate of Wuhan-Hu-1. In addition, variable miRNAs were predicted to target regions on the SARS-CoV-2 sequences against the reference sequence ss-RNA spike glycoprotein (accession number: [YP\\_009724390](https://ncbi.nlm.nih.gov/nuccore/YP_009724390)) from Jordanian positive nasopharyngeal specimens sequenced by Biolab Diagnostic Laboratories (Jordan) & Andersen lab at Scripps Research (USA) who published sequences retrieved from GISAID (<https://corona.moh.gov.jo/en>) (<https://gisaid.org>).

## 3. Results and discussion

We predicted top ten miRNAs targeting score between (98–99) against the submitted 29903 bp ss-RNA SARS-CoV-2 full length genome correspondingly, hsa-miR-4288, hsa-miR-195-5p, hsa-miR-16-5p, hsa-miR-15b-5p, hsa-miR-15a-5p, hsa-miR-6838-5p, hsa-miR-497-5p, hsa-miR-424-5p, hsa-miR-3133, hsa-miR-21-3p, please see [Table 1](#) (Appendix). These miRNAs are presented in miRDB, along with associated function annotations. As a recent update, miRDB displays expressions of hundreds of cell lines, and the user may limit their search for the cell line of interest miRNA targets. miRDB offers an integrative analysis of the target prediction and ontological gene data found in [Tables 2,3,4,5,6,7,8,9,10 and 11](#) (Appendix), to promote the prediction of miRNA functions. Also, we predicted only three miRNAs (hsa-miR-510-

3p, hsa-miR-624-5p, and hsa-miR-497-5p) with targeting scores of (92, 90 and 84) respectively for the submitted 3822 bp of the ss-RNA spike glycoprotein of SARS-CoV-2 sequence of Wuhan-Hu-1 (from the complete genome NCBI reference sequence: [NC\\_045512.2](https://ncbi.nlm.nih.gov/nuccore/NC_045512.2) Region: 21563–25384) as shown in [Table 13](#) (Appendix). These miRNAs, as well as associated functional annotations, presented in miRDB present the expression profiles of hundreds of cell lines. To facilitate the prediction of miRNA functions miRDB offers an integrative analysis of target prediction and Gene Ontology data found in [Tables 14 and 15](#) (Appendix).

Moreover, in our study, we predicted the regions of miRNAs targeting score against many ss-RNA spike glycoprotein of SARS-CoV-2 sequences from Jordanian samples with amino acid substitutions (NCBI reference sequence: [NC\\_045512.2](https://ncbi.nlm.nih.gov/nuccore/NC_045512.2) region: 21563–25384 and nomenclature sequence, Single Amino Acid Variant (SAV) and annotation used the accession number [YP\\_009724390.1](https://ncbi.nlm.nih.gov/nuccore/YP_009724390.1)) showed in [Tables 16–24](#) (Appendix). The original sequence of the del 432TTA, and the del Y144 have the same miRNA with a target score of 91. The original 1841A target miRNA scored (91, 64 and 56) for (hsa-miR-4793-5p, hsa-miR-143-5p and hsa-miR-3133) respectively. The interesting finding here that the 1841A > G, and D614G showed a change in the predicted miRNA and an increase in the target score from 91 to 92 (hsa-miR-4793-5p to hsa-miR-3620-3p). However, the original and 3415G > T D1139Y showed the same sequence of the miRNA (hsa-miR-548g-3p) and an increase in the target score from 80 to 81. The last substitution of 3499 G > A G1167S showed the same miRNA sequence of (hsa-miR-155-5p) and a decrease in the target score from 73 to 72.

One of the record genomic changes observed in the severe acute respiratory syndrome coronavirus (SARS-CoV-1) isolated from humans after human to human transmission was the acquisition of a specific 29-nucleotide deletion occurred in open reading frame 8 (ORF8). Three top target scores of miRNAs prediction (hsa-miR-497-5p, hsa-miR-195-5p and hsa-miR-21-3p) showed in [Table 12, 16 and 24](#) (Appendix). They had an expression in the respiratory epithelial cells, and effective antiviral defenses against the ss-RNA of SARS-CoV-2 might lead to a new mechanism of interaction binding miRNA to cause nucleotide deletion in SARS-CoV-2 in reflection to previous reports [5,6,9].

## 4. Conclusion

Over the past few years, some articles reported the target prediction of miRNA and viral RNA interaction. In our forecasts, more than asymptomatic 80% of the COVID-19 diseased persons raised due to the host miRNA interactions, which have identified the target where the genome replication of the ss-RNA of SARS-CoV-2 has changed to probably inhibit the translation of the ss-RNA and hence possible preventing viral replication and stabilization by subsequent generations. The top target scores of miRNAs prediction cover from 5' to 3' in the human respiratory epithelial cells that might be the reason for an effective antiviral defense against the ss-RNA of SARS-CoV-2 and lead to a new mechanism of nucleotide deletion in the coding region of a protein. The miRNAs found in all tissues have targeted gene functions, which lead to an identification of novel cellular pathways to block viral RNA replication or even host cell-specific targeting the regulation for the ss-RNA of SARS-CoV-2.

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## CRedit authorship contribution statement

**Hazem Haddad:** Conceptualization, Methodology, Software, Data curation, Writing - original draft, Visualization, Investigation, Supervision, Software, Validation, Writing - review & editing. **Walid Al-Zyoud:** Conceptualization, Methodology, Software, Data curation,

Writing - original draft, Visualization, Investigation, Supervision, Software, Validation, Writing - review & editing.

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## Declaration of competing interest

All authors declare no conflict of interest.

## Appendix

Table 1

Predicted miRNAs targeting the submitted 29903 bp ss-RNA SARS-COV-2 genome, accession number [NC\\_045512.2](#).

Target Rank	Target Score	miRNA Name
1	99	<a href="#">hsa-miR-4288</a>
2	99	<a href="#">hsa-miR-195-5p</a>
3	99	<a href="#">hsa-miR-16-5p</a>
4	99	<a href="#">hsa-miR-15b-5p</a>
5	99	<a href="#">hsa-miR-15a-5p</a>
6	99	<a href="#">hsa-miR-6838-5p</a>
7	98	<a href="#">hsa-miR-497-5p</a>
8	98	<a href="#">hsa-miR-424-5p</a>
9	98	<a href="#">hsa-miR-3133</a>
10	98	<a href="#">hsa-miR-21-3p</a>

Table 2

Predicted targets function for hsa-miR-4288 on 29903 bp ss-RNA SARS-COV-2 genome.

Target Rank	Target Score	miRNA Name	Gene Symbol	Gene Description
1	97	<a href="#">hsa-miR-4288</a>	<a href="#">UIMC1</a>	ubiquitin interaction motif containing 1
2	97	<a href="#">hsa-miR-4288</a>	<a href="#">CC2D1A</a>	coiled-coil and C2 domain containing 1A
3	96	<a href="#">hsa-miR-4288</a>	<a href="#">ING3</a>	inhibitor of growth family member 3
4	96	<a href="#">hsa-miR-4288</a>	<a href="#">KCMF1</a>	potassium channel modulatory factor 1
5	96	<a href="#">hsa-miR-4288</a>	<a href="#">CAPZB</a>	capping actin protein of muscle Z-line subunit beta
6	96	<a href="#">hsa-miR-4288</a>	<a href="#">BCL11A</a>	BCL11A, BAF complex component
7	96	<a href="#">hsa-miR-4288</a>	<a href="#">AMELX</a>	amelogenin X-linked
8	96	<a href="#">hsa-miR-4288</a>	<a href="#">NTM</a>	Neurotrimin
9	95	<a href="#">hsa-miR-4288</a>	<a href="#">LRRC4C</a>	leucine rich repeat containing 4C
10	95	<a href="#">hsa-miR-4288</a>	<a href="#">PSIP1</a>	PC4 and SFRS1 interacting protein 1

Table 3

Predicted targets function for hsa-miR-195-5p on 29903 bp ss-RNA SARS-COV-2 genome.

Target Rank	Target Score	miRNA Name	Gene Symbol	Gene Description
1	100	<a href="#">hsa-miR-195-5p</a>	<a href="#">PAPPA</a>	pappalysin 1
2	100	<a href="#">hsa-miR-195-5p</a>	<a href="#">FASN</a>	fatty acid synthase
3	100	<a href="#">hsa-miR-195-5p</a>	<a href="#">UNC80</a>	unc-80 homolog, NALCN channel complex subunit
4	100	<a href="#">hsa-miR-195-5p</a>	<a href="#">FGF2</a>	fibroblast growth factor 2
5	100	<a href="#">hsa-miR-195-5p</a>	<a href="#">TNRC6B</a>	trinucleotide repeat containing 6B
6	100	<a href="#">hsa-miR-195-5p</a>	<a href="#">PTPN4</a>	protein tyrosine phosphatase, non-receptor type 4
7	100	<a href="#">hsa-miR-195-5p</a>	<a href="#">PHF19</a>	PHD finger protein 19
8	100	<a href="#">hsa-miR-195-5p</a>	<a href="#">DESI1</a>	desumoylating isopeptidase 1
9	99	<a href="#">hsa-miR-195-5p</a>	<a href="#">UBE2Q1</a>	ubiquitin conjugating enzyme E2 Q1
10	99	<a href="#">hsa-miR-195-5p</a>	<a href="#">LSM11</a>	LSM11, U7 small nuclear RNA associated

Table 4

Predicted targets function for hsa-miR-16-5p on 29903 bp ss-RNA SARS-COV-2 genome.

Target Rank	Target Score	miRNA Name	Gene Symbol	Gene Description
1	100	<a href="#">hsa-miR-16-5p</a>	<a href="#">PAPPA</a>	pappalysin 1
2	100	<a href="#">hsa-miR-16-5p</a>	<a href="#">FASN</a>	fatty acid synthase
3	100	<a href="#">hsa-miR-16-5p</a>	<a href="#">UNC80</a>	unc-80 homolog, NALCN channel complex subunit
4	100	<a href="#">hsa-miR-16-5p</a>	<a href="#">FGF2</a>	fibroblast growth factor 2
5	100	<a href="#">hsa-miR-16-5p</a>	<a href="#">TNRC6B</a>	trinucleotide repeat containing 6B
6	100	<a href="#">hsa-miR-16-5p</a>	<a href="#">PTPN4</a>	protein tyrosine phosphatase, non-receptor type 4
7	100	<a href="#">hsa-miR-16-5p</a>	<a href="#">PHF19</a>	PHD finger protein 19

(continued on next page)

Table 4 (continued)

Target Rank	Target Score	miRNA Name	Gene Symbol	Gene Description
8	100	hsa-miR-16-5p	DESI1	desumoylating isopeptidase 1
9	99	hsa-miR-16-5p	UBE2Q1	ubiquitin conjugating enzyme E2 Q1
10	99	hsa-miR-16-5p	LSM11	LSM11, U7 small nuclear RNA associated

Table 5

Predicted targets function for hsa-miR-15b-5p on 29903 bp ss-RNA SARS-COV-2 genome.

Target Rank	Target Score	miRNA Name	Gene Symbol	Gene Description
1	100	hsa-miR-15b-5p	PAPPA	pappalysin 1
2	100	hsa-miR-15b-5p	FASN	fatty acid synthase
3	100	hsa-miR-15b-5p	UNC80	unc-80 homolog, NALCN channel complex subunit
4	100	hsa-miR-15b-5p	FGF2	fibroblast growth factor 2
5	100	hsa-miR-15b-5p	TNRC6B	trinucleotide repeat containing 6B
6	100	hsa-miR-15b-5p	PTPN4	protein tyrosine phosphatase, non-receptor type 4
7	100	hsa-miR-15b-5p	PHF19	PHD finger protein 19
8	100	hsa-miR-15b-5p	DESI1	desumoylating isopeptidase 1
9	99	hsa-miR-15b-5p	UBE2Q1	ubiquitin conjugating enzyme E2 Q1
10	99	hsa-miR-15b-5p	LSM11	LSM11, U7 small nuclear RNA associated

Table 6

Predicted targets function for hsa-miR-15a-5p on 29903 bp ss-RNA SARS-COV-2 genome.

Target Rank	Target Score	miRNA Name	Gene Symbol	Gene Description
1	100	hsa-miR-15a-5p	PAPPA	pappalysin 1
2	100	hsa-miR-15a-5p	FASN	fatty acid synthase
3	100	hsa-miR-15a-5p	UNC80	unc-80 homolog, NALCN channel complex subunit
4	100	hsa-miR-15a-5p	FGF2	fibroblast growth factor 2
5	100	hsa-miR-15a-5p	TNRC6B	trinucleotide repeat containing 6B
6	100	hsa-miR-15a-5p	PTPN4	protein tyrosine phosphatase, non-receptor type 4
7	100	hsa-miR-15a-5p	PHF19	PHD finger protein 19
8	100	hsa-miR-15a-5p	DESI1	desumoylating isopeptidase 1
9	99	hsa-miR-15a-5p	UBE2Q1	ubiquitin conjugating enzyme E2 Q1
10	99	hsa-miR-15a-5p	LSM11	LSM11, U7 small nuclear RNA associated

Table 7

Predicted targets function for hsa-miR-6838-5p on 29903 bp ss-RNA SARS-COV-2 genome.

Target Rank	Target Score	miRNA Name	Gene Symbol	Gene Description
1	100	hsa-miR-6838-5p	PAPPA	pappalysin 1
2	100	hsa-miR-6838-5p	FASN	fatty acid synthase
3	100	hsa-miR-6838-5p	UNC80	unc-80 homolog, NALCN channel complex subunit
4	100	hsa-miR-6838-5p	FGF2	fibroblast growth factor 2
5	100	hsa-miR-6838-5p	TNRC6B	trinucleotide repeat containing 6B
6	100	hsa-miR-6838-5p	PTPN4	protein tyrosine phosphatase, non-receptor type 4
7	100	hsa-miR-6838-5p	PHF19	PHD finger protein 19
8	99	hsa-miR-6838-5p	UBE2Q1	ubiquitin-conjugating enzyme E2 Q1
9	99	hsa-miR-6838-5p	LSM11	LSM11, U7 small nuclear RNA associated
10	99	hsa-miR-6838-5p	ANKUB1	ankyrin repeat and ubiquitin domain containing 1

**Table 8**  
Predicted targets function for hsa-miR-497-5p on 29903 bp ss-RNA SARS-COV-2 genome.

Target Rank	Target Score	miRNA Name	Gene Symbol	Gene Description
1	100	hsa-miR-497-5p	PAPPA	pappalysin 1
2	100	hsa-miR-497-5p	FASN	fatty acid synthase
3	100	hsa-miR-497-5p	UNC80	unc-80 homolog, NALCN channel complex subunit
4	100	hsa-miR-497-5p	FGF2	fibroblast growth factor 2
5	100	hsa-miR-497-5p	TNRC6B	trinucleotide repeat containing 6B
6	100	hsa-miR-497-5p	PTPN4	protein tyrosine phosphatase, non-receptor type 4
7	100	hsa-miR-497-5p	PHF19	PHD finger protein 19
8	99	hsa-miR-497-5p	UBE2Q1	ubiquitin conjugating enzyme E2 Q1
9	99	hsa-miR-497-5p	LSM11	LSM11, U7 small nuclear RNA associated
10	99	hsa-miR-497-5p	ANKUB1	ankyrin repeat and ubiquitin domain containing 1

**Table 9**  
Predicted targets function for hsa-miR-424-5p on 29903 bp ss-RNA SARS-COV-2 genome.

Target Rank	Target Score	miRNA Name	Gene Symbol	Gene Description
1	100	hsa-miR-424-5p	PAPPA	pappalysin 1
2	100	hsa-miR-424-5p	FASN	fatty acid synthase
3	100	hsa-miR-424-5p	UNC80	unc-80 homolog, NALCN channel complex subunit
4	100	hsa-miR-424-5p	FGF2	fibroblast growth factor 2
5	100	hsa-miR-424-5p	TNRC6B	trinucleotide repeat containing 6B
6	100	hsa-miR-424-5p	PTPN4	protein tyrosine phosphatase, non-receptor type 4
7	100	hsa-miR-424-5p	PHF19	PHD finger protein 19
8	99	hsa-miR-424-5p	UBE2Q1	ubiquitin-conjugating enzyme E2 Q1
9	99	hsa-miR-424-5p	LSM11	LSM11, U7 small nuclear RNA associated
10	99	hsa-miR-424-5p	ANKUB1	ankyrin repeat and ubiquitin domain containing 1

**Table 10**  
Predicted targets function for hsa-miR-3133 on 29903 bp ss-RNA SARS-COV-2 genome.

Target Rank	Target Score	miRNA Name	Gene Symbol	Gene Description
1	100	hsa-miR-3133	HOOK3	hook microtubule tethering protein 3
2	100	hsa-miR-3133	RIMS2	regulating synaptic membrane exocytosis 2
3	100	hsa-miR-3133	TGFBRAP1	transforming growth factor-beta receptor-associated protein 1
4	99	hsa-miR-3133	RPRD1A	regulation of nuclear pre-mRNA domain-containing 1A
5	99	hsa-miR-3133	TFAP2B	transcription factor AP-2 beta
6	99	hsa-miR-3133	PTPRK	protein tyrosine phosphatase, receptor type K
7	99	hsa-miR-3133	MAP2	microtubule-associated protein 2
8	99	hsa-miR-3133	NRF1	nuclear respiratory factor 1
9	99	hsa-miR-3133	KAT6A	lysine acetyltransferase 6A
10	99	hsa-miR-3133	URI1	URI1, prefoldin like chaperone

**Table 11**  
Predicted targets function for hsa-miR-21-3p on 29903 bp ss-RNA SARS-COV-2 genome.

Target Rank	Target Score	miRNA Name	Gene Symbol	Gene Description
1	99	hsa-miR-21-3p	STK38L	serine/threonine kinase 38 like
2	98	hsa-miR-21-3p	PCDH19	protocadherin 19
3	96	hsa-miR-21-3p	LAMP1	lysosomal associated membrane protein 1
4	96	hsa-miR-21-3p	GRIA2	glutamate ionotropic receptor AMPA type subunit 2
5	96	hsa-miR-21-3p	TOGARAM1	TOG array regulator of axonemal microtubules 1
6	96	hsa-miR-21-3p	ATP1B1	ATPase Na <sup>+</sup> /K <sup>+</sup> transporting subunit beta 1
7	96	hsa-miR-21-3p	TSC22D2	TSC22 domain family member 2
8	96	hsa-miR-21-3p	NAP1L5	Nucleosome assembly protein 1 like 5
9	95	hsa-miR-21-3p	UBE4B	ubiquitination factor E4B
10	95	hsa-miR-21-3p	ZNF326	zinc finger protein 326



Table 12 (continued)

Severe acute respiratory syndrome coronavirus 2 (SARS-COV-2 sequence) isolate Wuhan-Hu-1, complete genome NCBI Reference Sequence: NC_045512.2		miRNAs targeting the submitted 29903 nt SARS-COV-2 complete genome
	Previous Name miRNA Sequence	hsa-miR-21* 5' - caacaccagucgaugggcugu - 3' (length = 21)

Table 13

Predicted miRNAs targeting the submitted 3822 bp ss-RNA spike glycoprotein of SARS-COV-2 sequence, accession number NC\_045512.2 REGION: 21563–25384.

Target Rank	Target Score	miRNA Name
1	92	<a href="#">hsa-miR-510-3p</a>
2	90	<a href="#">hsa-miR-624-5p</a>
14	84	<a href="#">hsa-miR-497-5p</a>

Table 14

Predicted targets function for hsa-miR-510-3p on 3822 bp ss-RNA spike glycoprotein of SARS-COV-2 sequence, accession number NC\_045512.2 REGION: 21563–25384.

Target Rank	Target Score	miRNA Name	Gene Symbol	Gene Description
1	100	hsa-miR-510-3p	<a href="#">CNOT6</a>	CCR4-NOT transcription complex subunit 6
2	99	hsa-miR-510-3p	<a href="#">NEXMIF</a>	neurite extension and migration factor
3	99	hsa-miR-510-3p	<a href="#">RBMS3</a>	RNA binding motif single stranded interacting protein 3
4	99	hsa-miR-510-3p	<a href="#">DENND6A</a>	DENN domain containing 6A
5	99	hsa-miR-510-3p	<a href="#">SNAP91</a>	Synaptosome associated protein 91
6	99	hsa-miR-510-3p	<a href="#">BCLAF1</a>	BCL2 associated transcription factor 1
7	99	hsa-miR-510-3p	<a href="#">LATS2</a>	large tumor suppressor kinase 2
8	99	hsa-miR-510-3p	<a href="#">ELOVL7</a>	ELOVL fatty acid elongase 7
9	98	hsa-miR-510-3p	<a href="#">ZFX3</a>	zinc finger homeobox 3
10	98	hsa-miR-510-3p	<a href="#">FMR1</a>	fragile X mental retardation 1

Table 15

Predicted targets function for hsa-miR-624-5p on 3822 bp ss-RNA spike glycoprotein of SARS-COV-2 sequence, accession number NC\_045512.2 REGION: 21563–25384.

Target Rank	Target Score	miRNA Name	Gene Symbol	Gene Description
1	96	hsa-miR-624-5p	<a href="#">ARL4A</a>	ADP ribosylation factor like GTPase 4A
2	96	hsa-miR-624-5p	<a href="#">SOWAHC</a>	soosondowah ankyrin repeat domain family member C
3	95	hsa-miR-624-5p	<a href="#">SYT1</a>	synaptotagmin 1
4	95	hsa-miR-624-5p	<a href="#">CLOCK</a>	clock circadian regulator
5	95	hsa-miR-624-5p	<a href="#">STK38</a>	serine/threonine kinase 38
6	95	hsa-miR-624-5p	<a href="#">LCP1</a>	lymphocyte cytosolic protein 1
7	95	hsa-miR-624-5p	<a href="#">ZNF800</a>	zinc finger protein 800
8	95	hsa-miR-624-5p	<a href="#">DOCK11</a>	dedicator of cytokinesis 11
9	94	hsa-miR-624-5p	<a href="#">UAP1</a>	UDP-N-acetylglucosamine pyrophosphorylase 1
10	94	hsa-miR-624-5p	<a href="#">NFKBIA</a>	NFKB inhibitor alpha

Table 16

Predicted miRNAs targeting region on 3822 bp ss-RNA spike glycoprotein of SARS-COV-2 sequence.

3822 bp ss-RNA spike glycoprotein of SARS-COV-2 sequence isolate Wuhan-Hu-1, complete genome NCBI Reference Sequence: NC_045512.2		miRNAs targeting the submitted 3822 bp ss-RNA spike glycoprotein of SARS-COV-2 sequence
1	atgtttgttt tcttgtttt attgccacta gtctctagtc agtgtgttaa tcttacaacc	
		miRNA Name Previous Name miRNA Sequence
		hsa-miR-624-5p hsa-miR-624; hsa-miR-624* 5' - uaguaccaguuaccuuguguuca - 3' (length = 22)
2821	acagcaagtg cacttgaaa acttcaagat gttgtcaacc aaaatgcaca agctttaac	
		miRNA Name miRNA Sequence
		hsa-miR-510-3p 5' - auugaaacucuaagagugga - 3' (length = 21)

(continued on next page)

Table 16 (continued)

3822 bp ss-RNA spike glycoprotein of SARS-COV-2 sequence isolate Wuhan-Hu-1, complete genome NCBI Reference Sequence: NC_045512.2	miRNAs targeting the submitted 3822 bp ss-RNA spike glycoprotein of SARS-COV-2 sequence						
3241 attgtcatg atgaaaaage acacttcct cgtgaagggtg tctttgttc aatggcaca 3301 cactggttg taacacaaag gaattttat gaaccacaaa tcattactac agacaacaca	<table border="1"> <tr> <td>miRNA Name</td> <td>hsa-miR-497-5p</td> </tr> <tr> <td>Previous Name</td> <td>hsa-miR-497</td> </tr> <tr> <td>miRNA Sequence</td> <td>5' - cagcagcacacuguguuugu - 3' (length = 21)</td> </tr> </table>	miRNA Name	hsa-miR-497-5p	Previous Name	hsa-miR-497	miRNA Sequence	5' - cagcagcacacuguguuugu - 3' (length = 21)
miRNA Name	hsa-miR-497-5p						
Previous Name	hsa-miR-497						
miRNA Sequence	5' - cagcagcacacuguguuugu - 3' (length = 21)						
3661 atagctgctg tgattgcat agtaatggtg acaattatgc tttgctgtat gaccagtgc 3721 tgtagttgct tcaaggcgtg ttgttctgt ggatcctgct gcaaatgtga tgaagcagac	<table border="1"> <tr> <td>miRNA Name</td> <td>hsa-miR-624-5p</td> </tr> <tr> <td>Previous Name</td> <td>hsa-miR-624; hsa-miR-624*</td> </tr> <tr> <td>miRNA Sequence</td> <td>5' - uaguaccaguaccuuguguuca - 3' (length = 22)</td> </tr> </table>	miRNA Name	hsa-miR-624-5p	Previous Name	hsa-miR-624; hsa-miR-624*	miRNA Sequence	5' - uaguaccaguaccuuguguuca - 3' (length = 22)
miRNA Name	hsa-miR-624-5p						
Previous Name	hsa-miR-624; hsa-miR-624*						
miRNA Sequence	5' - uaguaccaguaccuuguguuca - 3' (length = 22)						

Table 17

Original and del 432 TTA (del.Y144) have the same miRNA and target score.

Target Rank	Target Score	miRNA Name
1	91	<a href="#">hsa-miR-196a-1-3p</a>

Table 18

Original 1841 A target miRNA score.

Target Rank	Target Score	miRNA Name
1	91	<a href="#">hsa-miR-4793-5p</a>
2	64	<a href="#">hsa-miR-143-5p</a>
3	56	<a href="#">hsa-miR-3133</a>

Table 19

1841A > G D614G showed a change in the sequence of the miRNA and increased in the target score from 90 to 91 on variable ss-RNA spike glycoprotein of SARS-COV-2 sequence from Jordanian samples.

Target Rank	Target Score	miRNA Name
1	92	<a href="#">hsa-miR-3620-3p</a>
2	55	<a href="#">hsa-miR-3133</a>
3	54	<a href="#">hsa-miR-21-3p</a>

Table 20

Original 3415G target miRNA score.

Target Rank	Target Score	miRNA Name
1	80	<a href="#">hsa-miR-548g-3p</a>
2	72	<a href="#">hsa-miR-627-5p</a>
3	61	<a href="#">hsa-miR-506-5p</a>

Table 21

3415G > T D1139Y showed the same the miRNA and increased the target score from 80 to 81 on variable ss-RNA spike glycoprotein of SARS-COV-2 sequence from Jordanian samples.

Target Rank	Target Score	miRNA Name
1	81	<a href="#">hsa-miR-548g-3p</a>
2	72	<a href="#">hsa-miR-627-5p</a>
3	61	<a href="#">hsa-miR-506-5p</a>



Table 22  
Original 3499 G target miRNA score.

Target Rank	Target Score	miRNA Name
1	73	hsa-miR-155-5p
2	62	hsa-miR-6765-5p
3	53	hsa-miR-551b-5p

Table 23  
3499 G > A G1167S showed the same the miRNA and decreased the target score from 73 to 72 on the variable ss-RNA spike glycoprotein of SARS-COV-2 sequence from Jordanian samples.

Target Rank	Target Score	miRNA Name
1	72	hsa-miR-155-5p
2	62	hsa-miR-6765-5p
3	51	hsa-miR-668-3p

Table 24  
Predicted miRNAs targeting region on variable ss-RNA spike glycoprotein of SARS-COV-2 sequence from Jordanian samples.

Sample number with accession on GISAIID	Sequence variation ss-RNA spike glycoprotein of SARS-COV-2 sequence	Single Amino Acid Variation	miRNAs targeting the submitted variation ss-RNA spike glycoprotein of SARS-COV-2 sequence
<b>NCBI Reference Sequence: NC_045512.2</b>	AATAACGCTACTAATGTTGTTATTAATC TGTGAATTTCAATTTTGTAAATGATCCATT TTTGGGTGTTTATTACCAAAAAACAACAA AAGTTGGATGGAAAGT	original	miRNA Name hsa-miR-196a-1-3p miRNA Sequence 5' - caacaacauuaaaccccca - 3' (length = 21)
Sample 23: hCoV-19/Jordan/SR-042/2020 EP-I_ISL_430000 2020-03-30	AATAACGCTACTAATGTTGTTATTAATC TGTGAATTTCAATTTTGTAAATGATCCATT TTTGGGTGTTTATTACCAAAAAACAACAA GTTGGATGGAAAGT	del 432 TTA del. Y144	miRNA Name hsa-miR-196a-1-3p miRNA Sequence 5' - caacaacauuaaaccccca - 3' (length = 21)
<b>NCBI Reference Sequence: NC_045512.2</b>	GGAACAAATACTTCTAACCAGGTTGCTGT TCTTTATCAGGATGTTAACTGCACAGAAG TCCCTGTGCTATTTCATGCAGATCAACTT ACTCCTACTTGGCGTGT	Original 1841A	miRNA Name hsa-miR-4793-5p miRNA Sequence 5' - acauccuguccacaggagagg - 3' (length = 24)
Sample 3,5,7,8,9,10,11,12,13,15,18,20 and21 Example: hCoV-19/Jordan/SR-036/2020 EPI_ISL_429996 2020-03-23	GGAACAAATACTTCTAACCAGGTTGCTGT TCTTTATCAGGATGTTAACTGCACAGAAG TCCCTGTGCTATTTCATGCAGATCAACTT ACTCCTACTTGGCGTGT	1841A > G D614G	miRNA Name hsa-miR-3620-3p Previous Name hsa-miR-3620 miRNA Sequence 5' - ucaccug-cauccgccaccag - 3' (length = 22)
<b>NCBI Reference Sequence: NC_045512.2</b>	ACTGTGATGTTGTAATAGGAATTGTCAA CAACACAGTTTATGATCCTTTGCAACCTG AATTAGACTCATTCAAGGAGGAGTTAGA TAAATATTTTAAAGAATCATACA	Original 3415G	miRNA Name hsa-miR-548g-3p Previous Name hsa-miR-548g miRNA Sequence 5' - aaaaac-guaauuacuuuuuag - 3' (length = 22)
Sample 21: hCoV-19/Jordan/SR-033/2020 EP-I_ISL_429993 2020-03-16	ACTGTGATGTTGTAATAGGAATTGTCAA CAACACAGTTTATGATCCTTTGCAACCTG AATTAGACTCATTCAAGGAGGAGTTAGA TAAATATTTTAAAGAATCATACA	3415G > T D1139Y	miRNA Name hsa-miR-548g-3p Previous Name hsa-miR-548g miRNA Sequence 5' - aaaaac-guaauuacuuuuuag - 3' (length = 22)
<b>NCBI Reference Sequence: NC_045512.2</b>	TCACCAGATGTTGATTTAGGTGACATCTC TGGCATTAAATGCTTCAGTTGTAACCAATC AAAAAGAAATGACCGCCTCAATGAGGT TGCCAAGAATTTAAATG	Original 3499 G	miRNA Name hsa-miR-155-5p Previous Name hsa-miR-155 miRNA Sequence 5' - uuaaug-cuaaucgugauaggguu - 3' (length = 24)
Sample 16: hCoV-19/Jordan/SR-039/2020 EP-I_ISL_429998 2020-03-28	TCACCAGATGTTGATTTAGGTGACATCTC TGGCATTAAATGCTTCAGTTGTAACCAATC AAAAAGAAATGACCGCCTCAATGAGGT TGCCAAGAATTTAAATG	3499 G > A G1167S	miRNA Name hsa-miR-155-5p Previous Name hsa-miR-155 miRNA Sequence 5' - uuaaug-cuaaucgugauaggguu - 3' (length = 24)

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