Table S1. Methodological approaches used in the studies dedicated to miRNAs potentially able to bind with the SARS-CoV-2 and other coronaviruses genomes

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **N** | **Number of SARS-CoV-2 genomes analyzed** | **Genomes of other coronaviruses** | **Number of miRNAs analyzed** | **Databases and tools for miRNA analysis** | **Identified number of miRNAs**  **able to bind with SARS-CoV-2 genome** | **References** |
| 1 | 1 (MN908947) | MERS-CoV (NC\_019843), SARS-CoV (NC\_004718) | 2565 | miRBase v2.21; miRTarget | 3 | [1] |
| 2 | 24 from NCBI and GISAID | 4 SARS-CoV, including NC\_004718.3 | *--* | miRDB | 873, including 315 unique for SARS-CoV-2 | [2] |
| 3 | 60 | *No* | 2654 | miRBase | 34 miRNAs for the *plus* strand of viral RNA, 45 – miRNAs for the *minus* strand | [3] |
| 4 | 1 (MN908947.3.) | *No* | 2654 | miRBase v2.21; izMiR | 479 | [4] |
| 5 | 65 from NCBI and GISAID | *No* | *--* | *Not specified* | 10 | [5] |
| 6 | 1 (NC\_045512.2) | 1 SARS-CoV (NC\_004718.3), 1 MERS-CoV (NC\_019843.3), 4 nonpathogenic coronaviruses | 896 | miRBbase v2.21; RNA22 v2 | 28 unique for SARS-CoV-2 | [6] |
| 7 | 67 | 1 SARS-CoV (NC\_004718.3) | *--* | miRBase | 79 unique for SARS-CoV-2 | [7] |
| 8 | 1 reference genome (NC\_045512.2); 8595 genomes from GISAID | *No* | *--* | miRBase v2.21; RNA22 v2 | 12 miRNAs able to bind with 3’-UTR in SARS-CoV-2 genome | [8] |
| 9 | 1 (MTO49951.1) | *No* | 1872 | miRbase; RNAhybrid | 42 | [9] |
| 10 | 1 (NC\_045512.2) | *No* | *--* | miRDB; MirTarget, | 10 miRNAs with the top target scores to bind with SARS-CoV-2 RNA are specified | [10] |
| 11 | 7 | 1 SARS-CoV (NC\_004718.3);  1 MERS-CoV (KC164505.2) | *--* | VIRmiRNA; miRanda v3.3a | 9 | [11] |
| 12 | 1 (NC\_045512.2) | 1 SARS-CoV (NC\_004718.3);  1 MERS-CoV (NC\_019843.3) | 2605 | TargetScan v7.2; RNA22 v2 | 128 miRNAs, 6 of them are unique for SARS-CoV-2 | [12] |
| 13 | 1 (NC\_045512.2) | *No* | *--* | miRBase v2.21; miRanda, PITA, Targetscan and ComiR | 5 | [13] |
| 14 | 820 | *No* | 1019 | miRDB; RNAhybrid | 1019 | [14] |
| 15 | 1 reference genome (NC\_045512.2); 34 217 genomes from GISAID | 693 beta-coronaviruses genomes, including SARS-CoV | *--* | miRBase v2.21; TargetScan, psRNATarget, IntaRNA, RNA22, RNAhybrid | 8 miRNAs able to bind with 3’-UTR and 7 miRNAs — with 5’-UTR in SARS-CoV-2 genome | [15] |
| 16 | 10 | *No* | 2654 | miRBase database v22.1; miRanda tool v3.3a | 160 miRNAs, including 15 with more than 3 binding sites and 12 — with a significant free energy binding value | [16] |

Footnote. NCBI – National Center for Biotechnology Information; GISAID – source that provides open-access to genomic data of influenza viruses and the SARS-CoV-2; «--» no information is given.

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