Table S2. Summary of the samples and methodologies used for each study.

Study #	Type of data/biological samples	Methodology
1	Lung protein data from the HPRD, Human Proteome Map, Proteomics DB and Human Protein Atlas	SARS-CoV and host protein Interaction: Affinity purification mass spectrometry (AP-MS) Human protein-protein interaction:Human Proteinpedia, BioGRID, HPRD and Intact database. GO/Pathway analysis: KEGG and NCBI Gene Expression Omnibus GEO
2	SARS-CoV-2 (China, Italy, Spain), MERS, SARS, OC43, and 229E genome sequences from NCBI database SARS-CoV-2 sequences from GISAID database (England and Turkey), Vero E6 cells sequence infected with SARS-CoV-2 strain isolated from a Turkish patient	Target prediction: miRTarget and miRbase GO/Pathway analysis: DianaTools miRPath V3, Rosalind, topGO R library, Interpro, NCBI, MSigDB, REACTOME, WikiPathways Mutational analysis of potential miRNA sites: Clustal Omega at EBI
3	SARS-CoV-2 RNA sequences obtained from NCBI (MTO49951.1) Normal lung squamous cells and lung tissue miRNA expression through TCGA-Assembler 2 package (R software)	Virus information: Viral Zone miRNA sequences: miRbase host miRNA and viral genome affinity: RNAhybrid database Selection of efficient miRNAs and transcriptional factors: mirWalk, TransmiR Pathway analysis: KEGG database, Biorender, Cytoscape Modeling analysis: SWISS-MODEL modeling tools Herb phytochemicals: PubChem
4	SARS-CoV-2 sequences from NCBI database Liquid bronchoalveolar lavage fluid samples	Target prediction: miRbase ORF Identification: GeneMark and ORF Finder Homology search: BLAST Pattern/Motif recognition: SMART Epitope analysis: IEDB Protein secondary structure prediction: SPLIT 4.0 3D structure modeling: SWISS-MODEL, I-TASSER Drug prediction: Drugbank and SeeSAR
5	Four SARS and 29 COVID-19 sequences from NCBI and GISAID database	Target prediction: miRDB GO/Pathway analysis: DIANA tools miRPath v 3.0
6	Wuhan-Hu-1 full genome sequences ssRNA spike in glycoprotein (YP_009724390) from Jordanian positive nasopharyngeal specimens (Biolab Diagnostic Laboratories and Andersen Lab at Scripps Research)	Target prediction: miRDB, MirTarget Conversion of miRNA to DNA: http://biomodel.uah.es/en/lab/cybertory/analysis/trans.htm Sequence alignment: ChromosPros Version 2.1.9
7	High confidence mass spectrometry-based SARS-CoV-2 viral protein to human protein interaction network established by Gordon *et al.*, (2020) in HEK293 cells. RNA sequencing data deposited in Gene Expression Omnibus (GEO)	Sequence alignment: FASTX-Toolkit, HISAT, SAMtools, StringTie Differential expression: DE-seq2 Functional enrichment analysis: ClueGO, Cytoscape Alternative splicing events: rMATS RBP motifs: ATtRACT, FIMO miRNA motifs: MEME-suite, FIMO miRNA expression profile: FANTOM5
8	SARS-CoV-2 genome sequences from GISAID from Asia, Europe, Oceania, North America, South America and Africa	Target prediction: RNA22 v2 Sequence Alignment: EMBL-EBI Prediction of human RBP binding: RBPmap Validation of RBP and miRNA expression: The Protein Atlas, RNAseq, CAGE, FANTOM5, GEPIA
9	7 Viral genomes downloaded from the NCBI Virus miRNAseq data from TCGA-LUAD	Target prediction: miRDB v 6.0, TargetScan v 7.2, miRTarBase v.8 Sequence Alignment: MSA GO/Pathway analysis: DIANA miRPath v 3.0

	miRNAseq GSE36971 and GSE90624 for SARS-CoV-2 infected mouse lungs	MiRNA Expression: miRDeep2, DESeq2
10	For miRNA target prediction: Reference genomes for SARS-CoV (NC_004718.3), MERS-CoV (NC_019843.3), and SARS-CoV-2 (NC_045512.2) from GenBank For miRNA expression: 46 matched “normal” lung tissue miRNA-Seq expression dataset from the TCGA-LUAD project, and Calu3cells post-infection miRNA-sequencing data (SARS-Cov-2 and mock infection) from GSE148729	Target prediction: TargetScan v 7.2, RNA22 v 2 Differential expression: edgeR
11	SARS-CoV2 genome sequences from GISAID database SARS-CoV and MERS genome sequences from NCBI database	Target prediction: miRanda v 3.3 Gene annotation and protein sequences: ViPR Mutation analysis: Genome Detective Coronavirus Subtyping Tool, I-MUTANT, MuPro Host antiviral miRs identification: miRBase, VIRmiRNA Post-tranlational modifications prediction: NetOglyc 4.0, NetNfly 1.0, Net-Corona 1.0, CSS-Palm 2.0 Antiviral peptides prediction: AVPpred Host gene expression analysis: NCBI GEO database
12	67 whole-genome sequences of SARS-CoV-2 isolates covering 24 different countries from NCBI database	Target prediction of hosts miRNAs: Funrich, miRTarBase miRNA sequences: miRbase Human 3’UTR sequences: Ensembl-Biomart Prediction of viral pre-miRNA: miRNAFold, RNAfold, FOMmiR. iMiRNA-SSF Prediction of Mature miRNA: MatureBayes RNA-RNA Interaction: IntaRNA 2.0, microRNA.org, psRNATarget GO/Pathway analysis*:* EnsEMBL, KEGG, Gitools Enrichment analysis: EnrichR, DAVID 6.8, WebGestalt 2019, FunRich 3.1.3 Microarray expression analysis: RNA-seq
13	Wuhan-Hu-1 isolate from NCBI database (MN908947.3)	Target prediction: psRNATarget miRNA sequences: miRBase Pre-miRNA prediction: izMiR GO analysis: PANTHER
14	SARS-CoV-2 genome sequences from NCBI and GenBank	Sequence alignment: BLAST
15	SARS-CoV-2 genome sequences from NCBI	Target prediction: miRDB Identification of SARS-CoV-2 pre-miRNA: Vmir v 2.3, ViralMir Identification of mature miRNAs: Mature Bayes GO analysis: PANTHER, Enrichr
16	SARS-CoV-2 genome sequences from NCBI (China, India, USA, Italy, Jamaica)	Prediction of viral pre-miR:VMir Prediction of human miRNA from precursor miRNA hairpin: SSEARCH, miRbase, RNA hybrid Hybridization between viral pre-miRNA and human miRNA: RNA hybrid Identification of mature miRNAs from pre-miRs: Mature Bayes Prediction of the secondary structure of pre-miR: RNAfold GO analysis: PANTHER
17	Peripheral blood samples from ten patients with COVID-19 one week after treatment with antiviral reagents and medical support and four healthy donors.	MiRNA prediction: miRanda RNA expression: High-throughput sequencing (Illumina HiseqX Ten PE75) GO analysis: geneontology.org
18	RING database (integration of more than 30 publicly available data repositories)	Network analysis: Graph Tools (RING database: TRUUST, SIGNOR, MIRIAD, DGIdB, DRUGBANK)

		Enrichment analysis: R pipeline, clusterProfiler package, GO, KEGG, Wikipathways
19	RNASeq datasets from GEO database: GSE147507: SARS-CoV-2 infection in lung epithelium and lung alveolar cells of humans GSE35145: eight samples including Idiopathic Pulmonary Fibrosis cells and normal tissue of the lung	Differential expression.: limma package, DESeq2, GEO2R GO/Pathway analysis: WikiPathays, Reactome, BioCarta, Enrichr Protein-protein interaction analysis: STRING, Cytoscape, cytoHubba, MCODE TF-gene interactions: NetworkAnalyst, ENCODE TF-miRNA coregulatory network: NetworkAnalyst Identification of candidate drugs: DSigDB, Enrichr
20	Microarray data of gene expression profile (E-MTAB-8871) from ArrayExpress: 22 SARS-CoV-2-infected samples and 10 normal control samples	Differential expression: limma package Pathway enrichment analysis: BIOCYC, KEGG. Pathway Interaction Database, REACTOME, GenMAPP, MSigDB C2 BIOCARTA, PantherDB, PathwayOntology, Small Molecule Pathway Database, ToppGene(ToppFun) GO Anakysis:ToppGene (ToppFun) PPI network analysis: STRING, Cytoscape Target gene-miRNA regulatory network: miRNet Target-gene-TF regulatory network: NetworkAnalyst, JASPAR, Cytoscape 3.8.0
21	Nasopharyngeal and oropharyngeal swabs from positive cases of SARS-CoV-2	Viral genome sequencing: MiSeq system (Illumina), CLC Genomics Workbench v20.0.3 Phylogenetic Analysis: IQTREE Structural and function impact of mutations: STArMir, dBDEMC2, TissueAtlas
22	SARS-CoV-2 reference sequences from NCBI (NC_045512.2) and other 65 sequences from NCBI and GISAD databases	Mutation analysis: SNAP v2.1.1, RNAsnp Impact of mutations on RNA secondary structure: RNAfold, RNAalifold, MutaRNA, RNAsnp), Potential miRNA Site Analysis RegRNA2.0, miRDB Potential Splice Site Analysis: RegRNA2.0, HSF, NIPU
23	Human ACE2 gene and peptide sequence was obtained from the NCBI and Uniprot database, respectively	Identification of miRNAs targeting ACE2: miRWalk, miRDB Physiochemical characterization: ProtParam (ExPASy), SignalP-4.1, Protscale server SNP analysis: BioMuta v4.0, dbSNP, SIFT, PolyPhen-2, PROVEAN, PANTHER Subcellular localization: CELLO, TMHMM, HMMTOP, UniProt Methylation sites assessment: MethyCancer Post translational modification assessment: NetCGlyc1.0, NetCorona 1.0, NetOGlyc 1.0, NetGlycate 1.0, NetPhos3.1, NetNGlyc 1.0, ProP 1.0 Functional networks for protein associations: STRING Protein structure building: Swiss Model Tfs of ACE2: NCBI database RNA sequencing data of lung biopsy samples: GEO database, limma, edgeR, gplots, org.Hs.eg.db, TcolorBrewer, Glimma
24	Neonatal rat cardiomyocytes and fibroblasts (data not used in this Review) Human-induced pluripotent stem cell-derived cardiomyocytes, fibroblasts and endothelial cells	Target prediction: TargetScan Modulation of miRNA levels: Transfection, RT-qPCR, Luciferase reporter assay, Western Blot
25	Large airway epithelia (LAE) and Small airway epithelial (SAE) samples of non-smokers and smokers, and Bci-NS1.1 (LAE), and hSABCi-NS1.1 (SAE) cell lines	ACE2 expression: microarray, RNA-seq, single-cell RNA-seq miRNA expression data: Wang *et al*., 2015 (Wang *et al.,2015)*
26	*ACE*2 and *TMPRSS2* gene sequences	Target prediction: miRbase, miRanda, TargetScan and miRWalk

27	Normal colon tissue samples retrieved from the TCGA database (TCGA-COAD)	miRNA and RNA sequencing: NGS sequencing Potential regulatory interactions: Spearman correlation
28	Paired RNA-seq/miRNA-seq data from TCGA-BLCA, TCGA-BRCA, TCGA-COAD, TCGA-ESCA, TCGA-KICH, TCGA-KIRC, TCGA-KIRP, TCGA-LIHC, TCGA-LUAD, TCGA-LUSC, TCGA-PRAD, TCGA-UCEC	Isomir/miRNA analysis: TargetScan Protein-miRNA regulatory interactions: TransmiR v2.0 Single-cell RNA sequencing data
29	*TMPRSS2* sequence obtained from Ensembl TMPRSS2 tissue-specific expression levels: Gtex TMPRSS2 aminoacid sequence: ExPASY2 RNA expression levels: GEPIA, CCLE	Prediction of functional consequences of SNPs: SIFT, POLYPHEN-2, PROVEAN, SNAP2, HSF Prediction of molecular effects of *TMPRSS2* related-SNPS on protein secondary and tertiary structures: Phyre2 Prediction of post-translational modifications: Modpred Functional impact of SNPs on secretory characteristics: Phobius Influence of SNPs on miRNA function: PolymiRTS, miRSNPs