

## *Supplementary Material*

**Table S1: List of primer sequences used for RT-qPCR**

Gene	NCBI Ref Seq ID	Primer Sequences (5' -> 3')		Primer size (bp <sup>1</sup> )	Primer location	Product size (bp)
<i>ACO1</i>	NM_001278352.2	FP <sup>2</sup>	AGAAGGGCAGACAGTTTACA	20	587 - 606	123
		RP <sup>3</sup>	TGAGCCAGGGGAATAATC	19	709 - 691	
<i>BCAS1</i>	NM_003657.4	FP	TGCACAAGGAAGCAAAGTGC	20	20 - 39	137
		RP	AGCCCCTGTGGGAGTATCTT	20	156 - 137	
<i>BCAT1</i>	NM_001178094.2	FP	GCAAGATGGGAGGGAATTACG	21	916 - 936	178
		RP	GGAGGAGTTGCCAGTTCTTC	20	1093 - 1074	
<i>BNIP3L</i>	NM_001330491.2	FP	TGGCTTTGGGGCTAGGCAT	19	601 - 619	118
		RP	GACAATACACCACTTCACAGG	21	718 - 698	
<i>CLDN10</i>	NM_182848.4	FP	CAACAAAACACCCAGATACA	20	631 - 650	167
		RP	ATAACAAACTCAAGAGGCAG	20	797 - 778	
<i>DMBX1</i>	NM_001387775.1	FP	CGCCTGGCTGACATCATCTT	20	199 - 218	129
		RP	TGGGTAGTGAGTCTTCTGGA	20	327 - 308	
<i>MME</i>	NM_007287.4	FP	GCAACAGAAAAGTGGGAGCAAAA	23	650 - 672	166
		RP	CAAGTCGAGGTTGGTCAATATGAA	24	815 - 792	
<i>MMP11</i>	NM_005940.5	FP	GATCGACTTCGCCAGGTAAT	20	490 - 509	102
		RP	TCCCCTTCTCGGTGAGTCTT	20	591 - 572	
<i>ROS1</i>	NM_001378902.1	FP	CCTACCAACTGCTCCCTTTG	20	613 - 632	154
		RP	CGGTCTGGACACAGTCTTAG	20	766 - 747	
<i>SNCA</i>	NM_001375287.1	FP	GTGGCAACAGTGGCTGAGAA	20	667 - 686	184
		RP	GAATTCCTTCCTGTGGGGCT	20	850 - 831	
<i>TFRC</i>	NM_001313965.2	FP	TCATTCTTTGGACATGCTCATCTG	24	755 - 778	174
		RP	ACAGTCTCCTTCCATATTCCCAA	23	928 - 906	

<sup>1</sup>Base pair; <sup>2</sup>Forward primer; <sup>3</sup>Reverse primer

**Table S2: List of antibodies, and dilutions used in this study**

<b>Antibody</b>	<b>Dilutions for WB<sup>1</sup></b>	<b>Company</b>	<b>Catalogue Number</b>
<b>NLRP3<sup>2</sup> (D2P5E), Rabbit mAb<sup>3</sup></b>	1:1000	Cell Signaling Technology	13158S
<b>IL-1<math>\beta</math><sup>4</sup> (D3U3E), Rabbit mAb</b>	1:1000	Cell Signaling Technology	12703
<b><math>\beta</math>-actin (C4), Mouse monoclonal IgG1<sup>5</sup></b>	1:1000	Santa Cruz Biotechnology	SC47778
<b>Goat anti-rabbit IgG, HRP<sup>6</sup>-linked Ab</b>	1:2000	Cell Signaling Technology	7074S
<b>Horse anti-mouse IgG, HRP-linked Ab</b>	1:2000	Cell Signaling Technology	7076S

<sup>1</sup>Western blotting; <sup>2</sup>Nucleotide oligomerization domain-like receptors family pyrin domain containing 3; <sup>3</sup>Monoclonal antibody; <sup>4</sup>Interleukin 1 beta; <sup>5</sup>Immunoglobulin G1; <sup>6</sup>Horse radish peroxidase

**Table S3: List of top 10 v-miRNAs encoded by SARS-CoV-2 from Calu-3 and Vero E6 cells**

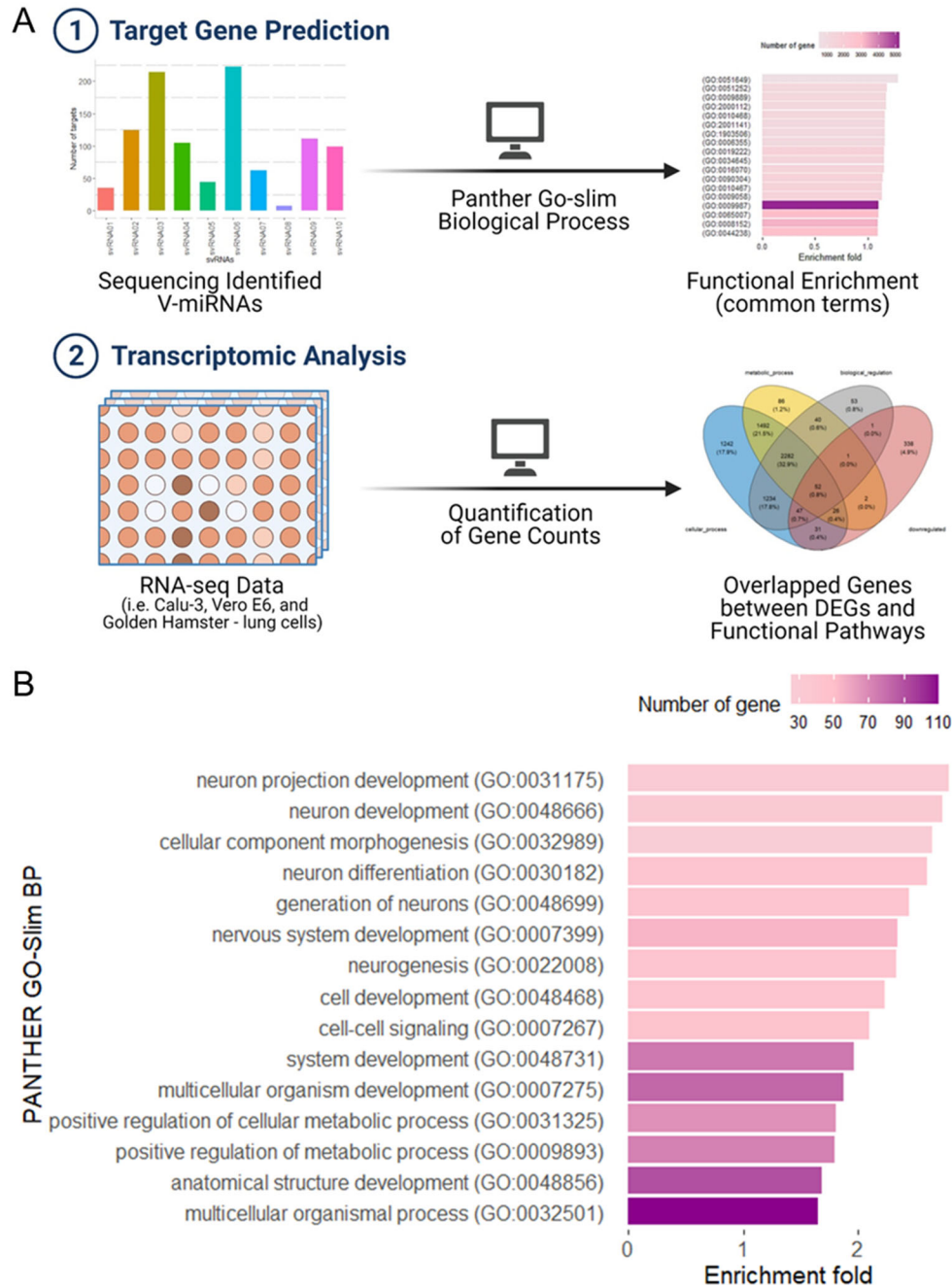
V-miRNA <sup>1</sup>	Genome position	Size (bp <sup>2</sup> )	Sequence 5'→3'	Coding gene	Mean Number of reads (%)
<b>95<sup>3</sup>_Calu-3</b>					
v-miRNA-5'UTR-44	44-63	20	CGATCTCTTGTAGATCTGTT	5'UTR	2.42
v-miRNA-ORF1-2836	2836-2857	22	CTCTGCCTATACAGTTGAACTC	ORF1ab	2.64
v-miRNA-ORF1-13613	13613-13631	19	AAAAGGACGAAGATGACAA	ORF1ab	1.52
v-miRNA-S-22423	22423-22443	21	TGCTGTAGACTGTGCACTTGA	S	1.39
v-miRNA-M-26823	26823-26843	21	AGACTGTTTGC GCGTACGCGT	M	1.56
v-miRNA-ORF7-27409	27409-27428	20	TTCTTGGCACTGATAACACT	ORF7a	2.14
v-miRNA-N-28612	28612-28631	20	AGGAACTGGGCCAGAAGCTG	N	1.49
v-miRNA-N-29094	29094-29112	19	TCGGCAGACGTGGTCCAGA	N	3.80
v-miRNA-N-29443	29443-29463	21	AAGTGTGACTCTTCTCCTGC	N	1.37
v-miRNA-ORF10-29597	29597-29616	20	TATAGTCTACTCTTGTGCAG	ORF10	1.84
<b>405<sup>4</sup>_Calu-3</b>					
v-miRNA-5'UTR-44	44-63	20	CGATCTCTTGTAGATCTGTT	5'UTR	2.57
v-miRNA-ORF1-4581	4581-4599	19	ACGATCTAAATGAAACTCT	ORF1ab	1.36
v-miRNA-ORF1-7458	7458-7479	22	TGCATGTTGTAGACGGTTGTAA	ORF1ab	1.01
v-miRNA-S-22423	22423-22443	21	TGCTGTAGACTGTGCACTTGA	S	3.25
v-miRNA-M-26823	26823-26843	21	AGACTGTTTGC GCGTACGCGT	M	2.36
v-miRNA-ORF7-27409	27409-27428	20	TTCTTGGCACTGATAACACT	ORF7a	1.50
v-miRNA-N-28612	28612-28631	20	AGGAACTGGGCCAGAAGCTG	N	3.14
v-miRNA-N-29094	29094-29112	19	TCGGCAGACGTGGTCCAGA	N	8.01
v-miRNA-N-29443	29443-29463	21	AAGTGTGACTCTTCTCCTGC	N	1.82
v-miRNA-ORF10-29597	29597-29616	20	TATAGTCTACTCTTGTGCAG	ORF10	1.96
<b>95_Vero E6</b>					
v-miRNA-ORF1-3109	3109-3127	19	GTATGGTACTGAAGATGAT	ORF1ab	1.34
v-miRNA-ORF1-3237	3237-3255	19	AAGACGGCAGTGAGGACAA	ORF1ab	0.91
v-miRNA-ORF1-7459	7459-7479	21	GCAATGTTGTAGACGGTTGTAA	ORF1ab	1.07
v-miRNA-S-22423	22423-22443	21	TGCTGTAGACTGTGCACTTGA	S	2.34
v-miRNA-M-26823	26823-26843	21	AGACTGTTTGC GCGTACGCGT	M	1.50
v-miRNA-M-26990	26990-27011	22	AGGACGCTGTGACATCAAGGAC	M	1.17
v-miRNA-N-28386	28386-28405	20	AACAACGTCGGCCCCAAGGT	N	1.07
v-miRNA-N-28612	28612-28631	20	AGGAACTGGGCCAGAAGCTG	N	0.74
v-miRNA-N-29094	29094-29112	16	TCGGCAGACGTGGTCCAGA	N	1.48
v-miRNA-ORF10-29597	29597-29616	20	TATAGTCTACTCTTGTGCAG	ORF10	1.15
<b>405_Vero E6</b>					
v-miRNA-ORF1-3109	3109-3127	19	GTATGGTACTGAAGATGAT	ORF1ab	1.65
v-miRNA-ORF1-3237	3237-3255	19	AAGACGGCAGTGAGGACAA	ORF1ab	1.74
v-miRNA-ORF1-7459	7459-7479	21	GCAATGTTGTAGACGGTTGTAA	ORF1ab	1.37
v-miRNA-S-22423	22423-22443	21	TGCTGTAGACTGTGCACTTGA	S	13.5
v-miRNA-ORF3-25528	25528-25547	20	CTTATTGTTGGCGTTGCACT	ORF3a	1.60
v-miRNA-M-26820	26820-26841	22	TTCAGACTGTTTGC GCGTACGC	M	2.74
v-miRNA-M-26990	26990-27011	22	AGGACGCTGTGACATCAAGGAC	M	2.55
v-miRNA-N-28612	28612-28631	20	AGGAACTGGGCCAGAAGCTG	N	0.34
v-miRNA-N-29136	29136-29156	21	ACCAGGAATAATCAGACAAG	N	1.03
v-miRNA-3'UTR-29688	29688-29708	21	GTGTGTAACATTAGGGAGGAC	3'UTR	2.16

<sup>1</sup>Viral microRNA; <sup>2</sup>Base pair; <sup>3</sup>SARS-CoV-2, clone Hong Kong-95; <sup>4</sup>SARS-CoV-2, clone Hong Kong-405

**Table S4: List of differentially expressed metabolic genes and their respective log<sub>2</sub> fold changes**

Target gene	Log <sub>2</sub> FC <sup>1</sup>	P value	Key functions in the metabolic pathways
<i>ACO1</i>	-1.6	3.93E <sup>-20</sup>	Involved in TCA cycle and interacts with mRNA to control the levels of iron inside cells, and carbon metabolism
<i>BCAS1</i>	-2	2.47E <sup>-3</sup>	Plays a role in myelinating oligodendrocytes related to multiple sclerosis lesions
<i>BCAT1</i>	-1.9	8.94E <sup>-9</sup>	Controls metabolic reprogramming, and promotes cell proliferation through amino acid catabolism
<i>BNIP3L</i>	-1.4	5.05E <sup>-21</sup>	Apoptosis modulation; signaling and gene expression
<i>CLDN10</i>	-1.3	2.87E <sup>-7</sup>	Regulates blood-brain barrier, and immune cell transmigration
<i>DMBX1</i>	-2.3	4.33E <sup>-5</sup>	Plays a role in brain and sensory organ development, and in normal regulation of energy homeostasis and behavior
<i>KIF12</i>	-1.2	1.44E <sup>-6</sup>	Antioxidant activity; intracellular transport; cell division
<i>MME</i>	-1.5	1.56E <sup>-7</sup>	A neutral endopeptidase that cleaves and inactivates peptides, including hormones
<i>MMP11</i>	-2.4	2.14E <sup>-19</sup>	Plays a role in controlling energy metabolism; extracellular matrix (ECM) remodeling/degradations; metabolic reprogramming
<i>PBX1</i>	-1.2	3.43E <sup>-3</sup>	Promotes cell proliferation and plays oncogenic activity; regulate osteogenesis; enhances cellular metabolism
<i>ROS1</i>	-2.2	6.38E <sup>-5</sup>	Involved in cell differentiation and has oncogenic role
<i>SNCA</i>	-2.8	8.04E <sup>-15</sup>	Enhances glucose uptake and utilization; integrate presynaptic signaling, and membrane trafficking
<i>SYT12</i>	-1.3	2.57E <sup>-3</sup>	Mediate calcium-dependent regulation of membrane trafficking in synaptic transmission
<i>TFRC</i>	-1.1	1.22E <sup>-151</sup>	Required for erythropoiesis and neurologic development; iron transport
<i>UPK1B</i>	-1.2	2.52E <sup>-16</sup>	Mediate signal transduction events that play a role in the regulation of cell development, activation, growth and motility

<sup>1</sup>Log<sub>2</sub> Fold Change



**Figure S1.** SARS-CoV-2-encoded v-miRNAs target host genes that are involved in metabolic pathways. **(A)** GO analysis indicates the main enrichment terms targeted by SARS-CoV-2-encoded v-miRNAs. (1) Shows the target gene prediction and selected common terms; (2) Shows transcriptomic analysis, and genes overlapping between DEGs and functional pathways. **(B)** Enriched common GO pathways for v-miRNA potential targets predicted by using the overlap of miRDB and Diana. The most significant 15 GO terms are selected for the presentation. The color represents the number of predicted genes in each GO term.