

**Supplementary Table S1:** Auto Plate Content required for nucleic acid isolation when using ABNOVA SpiralPipet and Autostage System.

Column	Buffer Solution	Volume
1/7	Lysis Buffer	600 $\mu$ L
2/8	Wash Buffer I	800 $\mu$ L
3/9	Wash Buffer II	800 $\mu$ L
4/10	Wash Buffer II	800 $\mu$ L
5/11	Magnetic Beads	800 $\mu$ L
6/12	Elution Buffer	100 $\mu$ L

Step	Well	Action	RPM	Time (Second)	CW/CCW (Second)	Temperature	Temperature Control
1	5/11	Collection	0	30	0	60	YES
2	1/7	Mixing	3000	480	0	60	YES
3	1/7	Collection	0	30	0	60	YES
4	2/8	Mixing	3000	60	0	45	YES
5	2/8	Collection	0	30	0	45	YES
6	3/9	Mixing	3000	60	0	45	YES
7	3/9	Collection	0	30	0	45	YES
8	4/10	Mixing	3000	60	0	45	YES
9	4/10	Collection	0	30	0	45	YES
10	4/10	Vapor	0	300	0	45	YES
11	6/12	Mixing	3000	300	0	45	YES
12	6/12	Collection	0	30	0	45	YES
13	5/11	Mixing	3000	60	0	0	NO

**Supplementary Table S2:** ABNOVA SpiralPipet and Autostage System program.

Strain	Lineage	Target	Accession	% Homology Test FP%	% Homology Test RP%	% Homology Test Probe%
hCoV-19/Scotland/CVR837/2020	B.1.5	N gene, RdRP	MT882022.1	100.0%	100.0%	100.0%
hCoV-19/Scotland/CVR2224/2020	B.1.222	N gene, RdRP	FR998185.1	100.0%	100.0%	100.0%
hCoV-19/Denmark/DCGC-3024/2020	B.1.1.298	N gene, RdRP	MT919525.1	100.0%	100.0%	100.0%
hCoV-19/Japan/TY7-503/2021	P.1. (or 20J/501Y.V3)	N gene, RdRP	MZ252337.1	100.0%	100.0%	100.0%
hCoV-19/USA/MD-HP12112/2021	B.1.1.207	N gene, RdRP	MW049023.1	100.0%	100.0%	100.0%
hCoV-19/USA/MD-HP12155/2020	B.1.1.4	N gene, RdRP	FR995320.1	100.0%	100.0%	100.0%
hCoV-19/USA/MD-HP01101/2021	B.1.1.7	N gene, RdRP	MZ259007.1	100.0%	100.0%	100.0%
hCoV-19/USA/MD-HP01542/2021	B.1.351	N gene, RdRP	MW580574.1	100.0%	100.0%	100.0%
hCoV-19/USA/NY-NP-DOH1/2021	B.1.526	N gene, RdRP	MZ259007.1	100.0%	100.0%	100.0%
hCoV-19/USA/CA-Stanford-15_S02/2021	B.1.617.1	N gene, RdRP	MZ571142.1	100.0%	100.0%	100.0%
Severe acute respiratory syndrome coronavirus 2 TKYTK1734_2021 genomic RNA	B.1.617.2	N gene, RdRP	LC633760.1	100.0%	100.0%	100.0%
hCoV-19/USA/NY-MSHSPSP-PV29369/2021	B.1.1.1 (C.7)	N gene, RdRP	FR990203.1	100.0%	100.0%	100.0%
hCoV-19/USA/NY-MSHSPSP-PV28887/2021	R.1	N gene, RdRP,	BS001048.1	100.0%	100.0%	100.0%
BA.1 (omicron)	B.1.1.529	N gene, RdRP	OL869974.1	100.0%	100.0%	100%

**Supplementary Table S3:** Representative results of *In Silico* analysis for inhouse COVID-19 Multiplex rRT-PCR against the reported 2019-nCoV Lineage sequences by February 14, 2022.

Virus	Source/ Sample type	Ct Value (RdRP gene/N Gene)
MERS-coronavirus (18 Samples)	Clinical specimen	Undetected
Influenza A (20 Samples)	Clinical specimen	Undetected
Influenza B (18 Samples)	Clinical specimen	Undetected
Rhinovirus (19 Samples)	Clinical specimen	Undetected

**Supplementary Table S4:** Cross-Reactivity of inhouse COVID-19 Multiplex rRT-PCR.

Pathogen (Taxonomy ID)	Strain	Target	GenBank Acc#	% Homology Test FP	% Homology Test RP	% Homology Test Probe
Human coronavirus 229E (11137)	camel/Abu Dhabi/B38	N gene	MF593473.1	76.20%	62.50%	54.80%
Human coronavirus 229E (11137)	camel/Abu Dhabi/B38	RdRP gene	MF593473.1	81.00%	62.50%	72.00%
Human coronavirus OC43 (31631)	HCoV_OC43/Seattle/USA/SC9 428/2018	N gene	MN310476.1	86.40%	67.94%	83.30%
Human coronavirus OC43 (31631)	HCoV_OC43/Seattle/USA/SC9 428/2018	RdRP gene	MN310476.1	86.40%	76.90%	45.80%
Human coronavirus HKU1 (290028)	HKU1 SC2628	N gene	KY983584.1	70.00%	45.50%	70.80%
Human coronavirus HKU1 (290028)	HKU1 SC2628	RdRP gene	KY983584.1	90.90%	80.80%	43.20%
Human coronavirus NL63 (277944)	HCoV_NL63/Seattle/USA/SC0 179/2018	N gene	MN306018.1	70.00%	43.20%	70.80%
Human coronavirus NL63 (277944)	HCoV_NL63/Seattle/USA/SC0 179/2018	RdRP gene	MN306018.1	82.60%	88.00%	72.00%
MERS-CoV (1335626)	BtVs-BetaCoV/SC2013	N gene	KJ473821.1	75.00	58.30%	55.90%
MERS-CoV (1335626)	BtVs-BetaCoV/SC2013	RdRP gene	KJ473821.1	66.70%	92.00%	57.60%
Adenoviridae (10508)	53/FS161/Fukui/2004	N gene	AB568098.1	70.00%	65.40%	50.00%
Adenoviridae (10508)	53/FS161/Fukui/2004	RdRP gene	AB568098.1	82.60%	65.60%	73.10%
Adenoviridae (10508)	ITA/2018/251170-16	N gene	MK625182.1	84.20%	54.50%	52.60%
Adenoviridae (10508)	ITA/2018/251170-16	RdRP gene	MK625182.1	59.30%	42.30%	60.60%
Human metapneumovirus (162145)	bj0154	N gene	MN745086.1	70.00%	45.80%	68.00%
Human metapneumovirus (162145)	bj0154	RdRP gene	MN745086.1	37.20%	56.20%	50.00%
Human metapneumovirus (162145)	C-85473	N gene	KM408077.1	60.90%	Not Sig	43.60%
Human metapneumovirus (162145)	C-85473	RdRP gene	KM408077.1	60.70%	Not Sig	60.00%
Paramyxoviridae (11158)	MVs/Venezia.ITA/22.17/3[D8]	N gene	MK513627.1	77.80%	69.60%	61.30%
Paramyxoviridae (11158)	HPIV3/MEX/2822/2006	RdRP gene	KF687324.1	71.40%	65.40%	54.30%
Orthomyxoviridae (11308)	A/Homo sapien/China/LS314/2019	N gene	MT106847.1	76.20%	67.90%	63.00%
Influenza A virus (11320)	A/sanderling/New Jersey/756/1986	RdRP gene	CY117434.1	56.70%	57.70%	37.70%
Orthomyxoviridae (11308)	A/sanderling/New Jersey/756/1986	N gene	CY117434.1	77.30%	64.00%	54.80%
Influenza B virus (11520)	B/New York/20/2018	N gene	MK999210.1	43.80%	66.70%	66.70%
Influenza B virus (11520)	B/Alabama/12/2019	RdRP gene	MT029398.1	51.90%	61.50%	50.00%
Enterovirus (12059)	Donovan	N gene	AY421766.1	65.00%	60.70%	48.60%
Rhinovirus (12059)	Donovan	RdRP gene	AY421766.1	70.00%	66.70%	64.50%
Enterovirus (12059)	PS87/Belfast; ATCC VR-774	RdRP gene	DQ092794.1	72.70%	66.70%	52.90%
Respiratory syncytial virus (12814)	B/WI/629-Q0306/10	N gene	JN032121.2	68.20%	68.20%	59.30%
Respiratory syncytial virus (12814)	99-901	RdRP gene	MK947359.1	43.20%	47.20%	40.00%
Rhinovirus (12059)	PS-87	RdRP gene	X79368.1	58.10%	66.70%	65.40%
SARSr-CoV (694009)	SARS coronavirus Frankfurt 1	N gene	AB257344.1	69.60%	91.70%	95.70%
SARSr-CoV (694009)	SARS coronavirus Frankfurt 1	RdRP gene	AB257344.1	95.50%	96.20%	88.00%
hCoV-19/pangolin/Guangxi/P4L/ 2017	-	N gene	EPI_ISL_410 538	61.10%	46.70%	45.70%
hCoV- 19/pangolin/Guangxi/P4L/2017	-	RdRP gene	EPI_ISL_410 538	45.50%	69.20%	65.20%
Bat coronavirus		N gene	NC_048212.1	62.50%	76.90%	56.20%
Bat coronavirus		RdRP gene	NC_048212.1	72.70%	84.60%	82.60%

**Supplementary Table S5:** The *In Silico* Specificity Analysis of Primer and Probe Sets for Other Respiratory Pathogens.