

Loss of detection of sgN precedes viral abridged replication in COVID19-affected patients – a target for SARS-CoV-2 propagation

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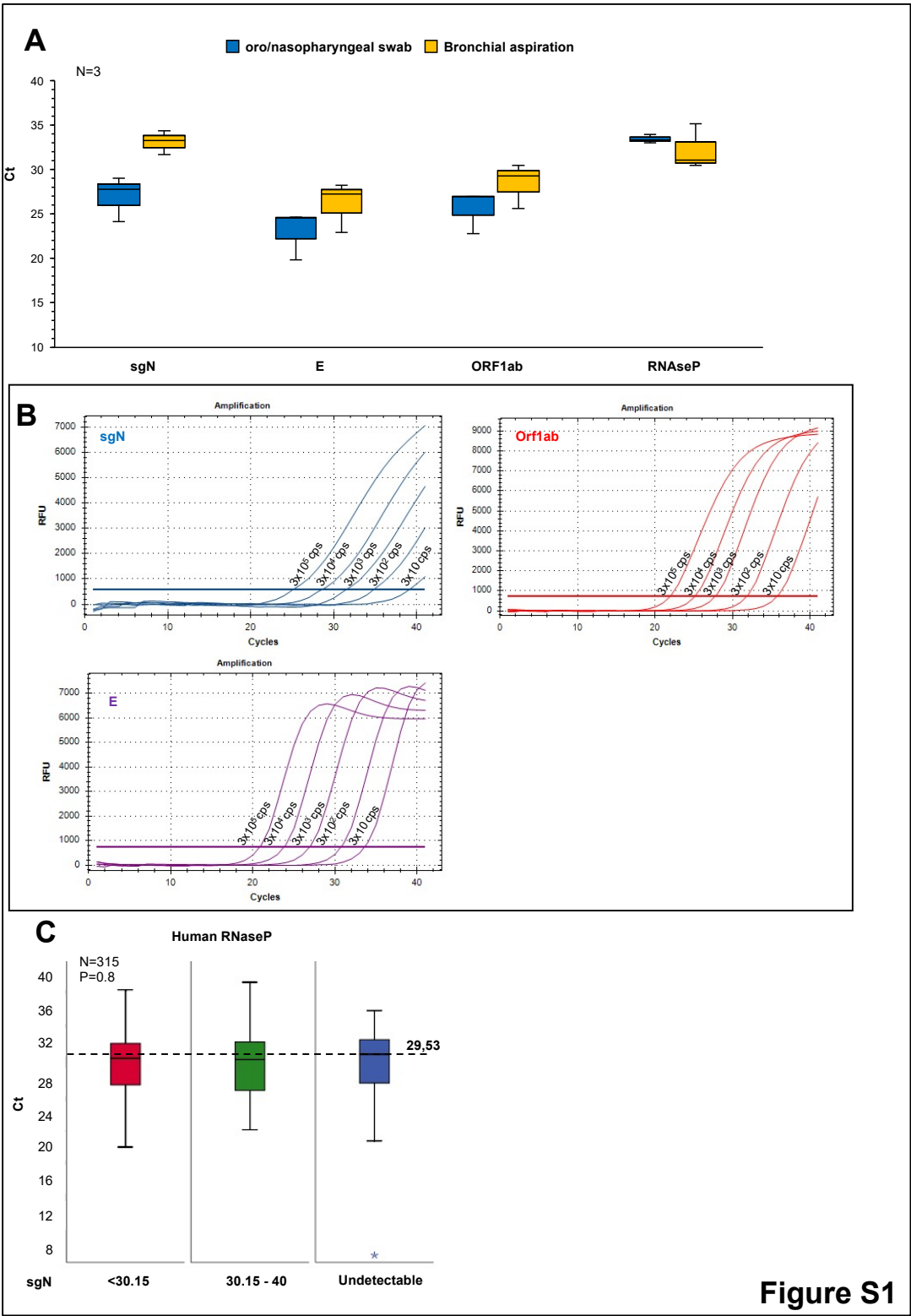
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Supplementary Figures

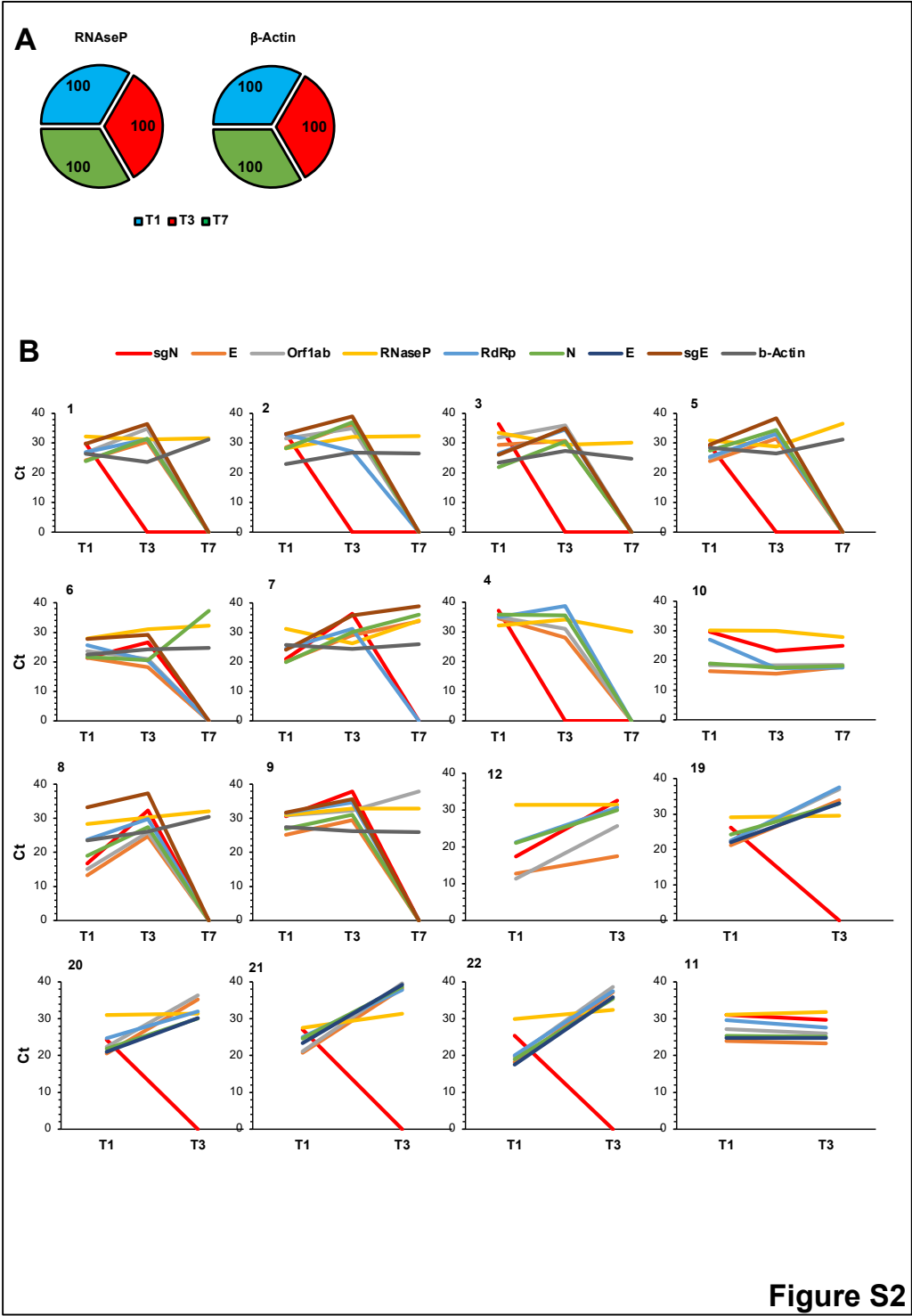
Supplementary Figure S1



Supplementary Figure S1. SARS-CoV-2 Viral3 kit to detect sgN. Related to Figures 1. (A)

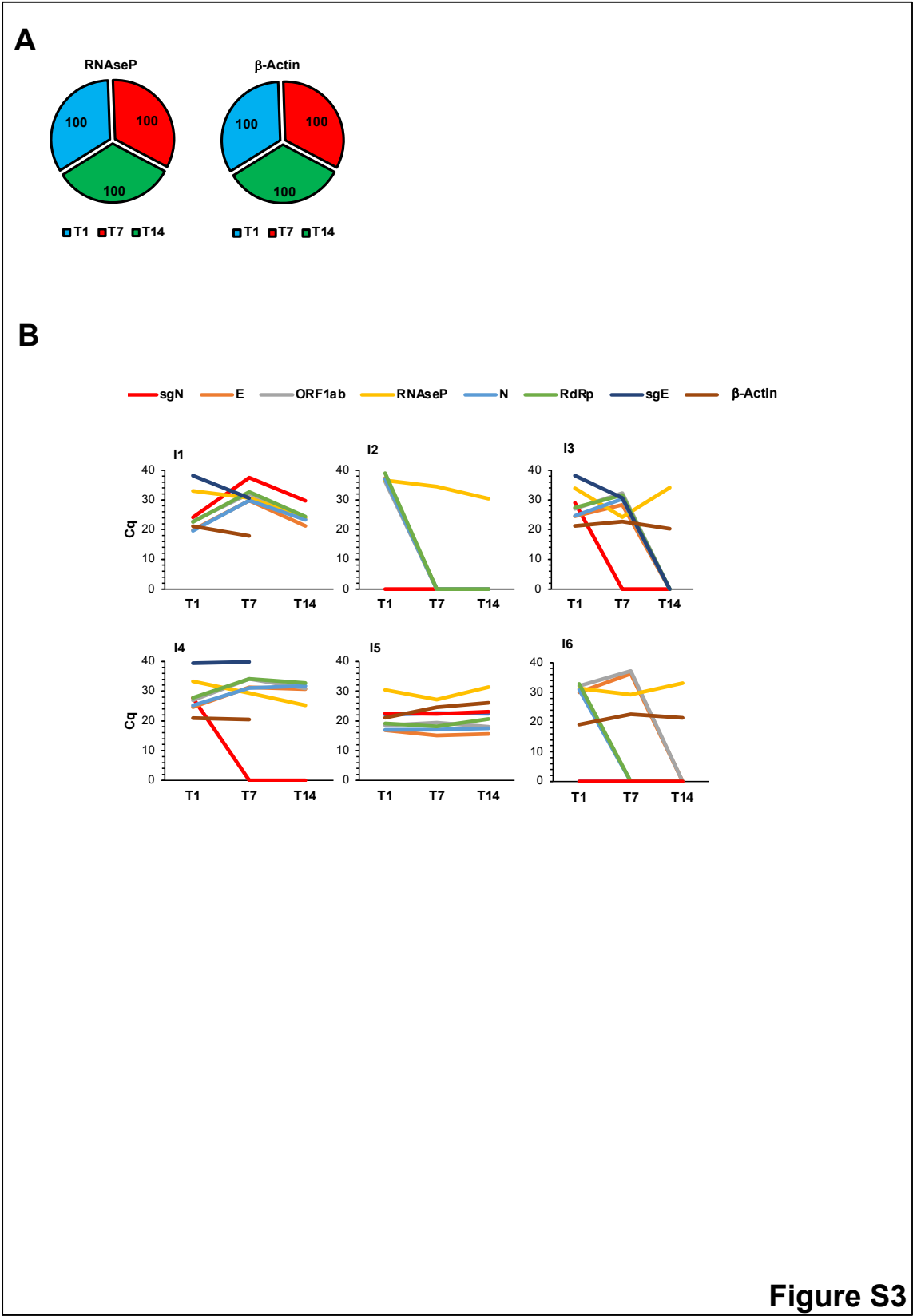
Detection of viral sgN, gene E, gene ORF1ab and human RNase P gene using the SARS-CoV-2 Viral3 kit for oro/nasopharyngeal swabs (orange) and bronchial aspirate samples (orange) in 3 hospitalized COVID19-positive patients. Mean Cq values are shown. **(B)** qPCR assays for the sensitivity of the SARS-CoV-2 Viral3 kit. Human 2019-nCoV strain 2019-nCoV/Italy INMI1 RNA was used as reference to test the sensitivity. Serial dilutions (from 3×10^5 to 3×10) of Human 2019-nCoV strain 2019-nCoV/Italy INMI1 RNA) were used. cps, standard copy particles. **(C)** Samples obtained from oro/nasopharyngeal swabs from COVID19-positive patients (N = 315) were stratified into three groups according to the median Cq values of sgN (sgN Cq median = 33.51). The first group consisted of those samples where Cq values for sgN were below the median value (i.e., Cq <30.51; 99 samples, in red). The second group of samples were characterized by Cq values of sgN ranged from the Cq median value (30.51) to 40 (96 samples, in green). Third group comprised samples in which sgN was not detectable (i.e., Cq >40; 120 samples, in blue). One-way analysis of variance (ANOVA) was used through IBM SPSS Statistics to determine the cut-off for sgN detection. SgN was detected in these samples independent of human RNaseP detection (P <0.8).

Supplementary Figure S2.



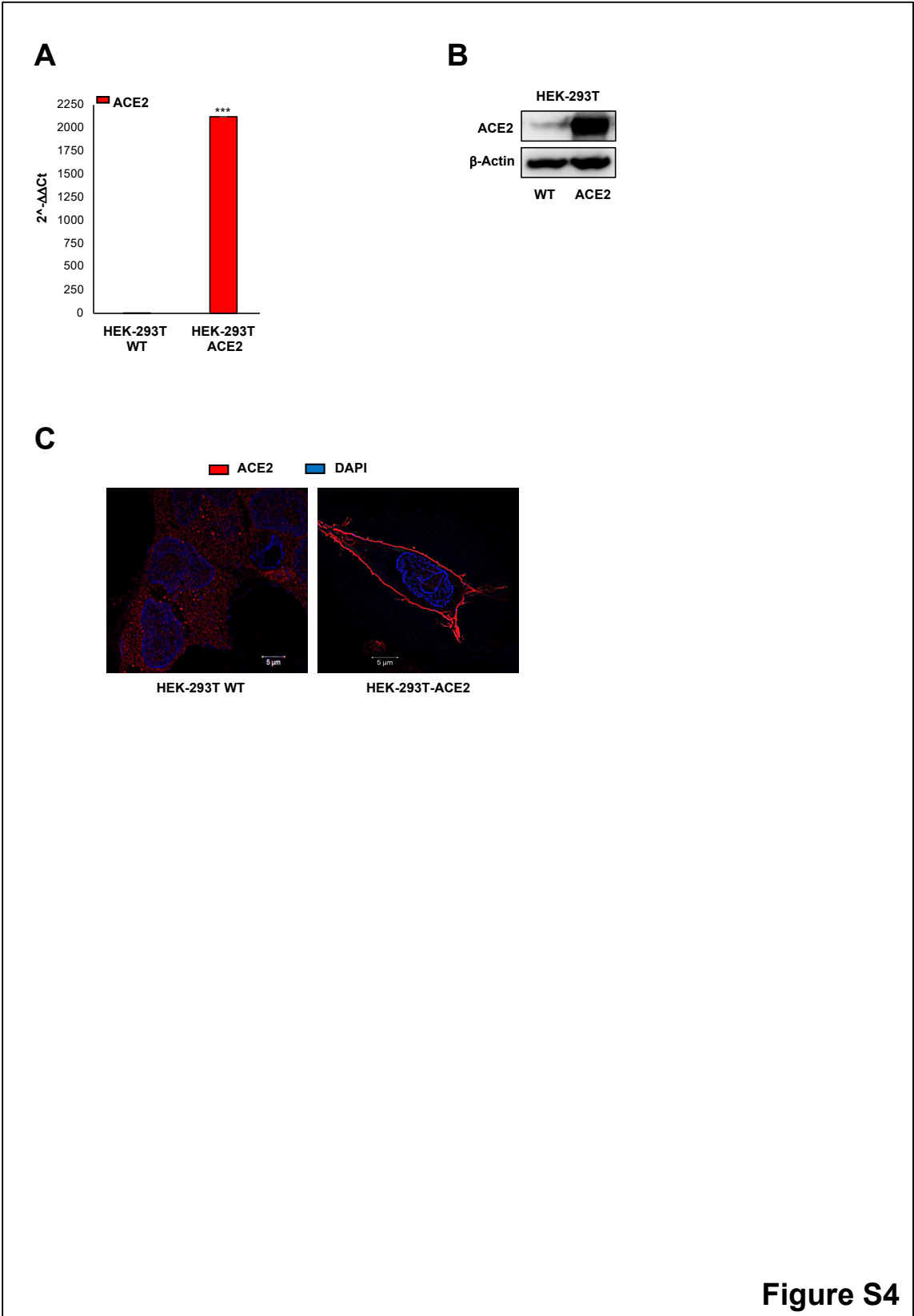
Supplementary Figure S2. Loss of detection of sgN precedes SARS-CoV-2 replication failure in home-isolated COVID19-affected patients. Related to Figures 2A-B. (A) Pie charts showing the proportions (%) of positivity of the oro/nasopharyngeal samples from home-isolated patients to human RNase P and β -actin genes at the different times (blue, first swab [n = 16]; red, second swab collected after 3 days [n = 16]; green, third swab collected after 7 days [n = 10]). (B) Line graphs showing changes over time of the Cq values related to viral sgN (red), sgE (brown), gene N (green), gene E (orange), gene ORF1ab (light gray), RdRp (light blue), and human RNase P (yellow) and β -actin (dark gray) genes in the oro/nasopharyngeal samples from 16 home-isolated patients.

Supplementary Figure S3.



Supplementary Figure S3. Loss of detection of sgN precedes SARS-CoV-2 replication failure in home-isolated COVID19-affected patients. Related to Figures 2C-D. (A) Pie chart showing the proportions (%) of positivity of the oro/nasopharyngeal samples from 6 hospitalized COVID19-positive patients to human RNase P gene at the different times (blue, first swab; red, second swab collected after 7 days; green, third swab collected after 14 days). (B) Line graphs showing the changes over time of the Cq values related to viral sgN (red), gene N (light blue), gene E (orange), gene ORF1ab (light gray), and RdRp (green), human RNase P gene (yellow), sgE (dark blue and orange) and β -Actin (brown) in the oro/nasopharyngeal samples from 6 hospitalized patients.

Supplementary Figure S4.



Supplementary Figure S4. HEK-293T overexpressing ACE2 cellular model. Related to Figures 3C-E, 4A-B. (A) Quantification of mRNA abundance relative to that of HEK-293T cells ($2^{-\Delta\Delta Ct}$) for the ACE2 gene. RT-PCR analysis with SYBR Green of RNA extracted from HEK-293T wild-type (WT) and HEK-293T-overexpressing ACE2 cells. Data are means \pm SD. ***P <0.001 (unpaired two-tailed Student's t test; n = 3 independent experiments per group). (B) Representative immunoblotting (using antibodies against the indicated proteins) of human HEK-293T cells and HEK-293T stable clones overexpressing ACE2. B-Actin was used as the loading control. (C) Immunofluorescence staining with an antibody against the human ACE2 (red) protein in human HEK-293T cells and HEK-293T stable clones overexpressing ACE2. DAPI was used for nuclei. The SIM image was acquired with Elyra 7 and processed with the Zeiss ZEN software (blue edition). Magnification, $\times 63$. Scale bars: 5 μ m.

Supplementary Figure S5.

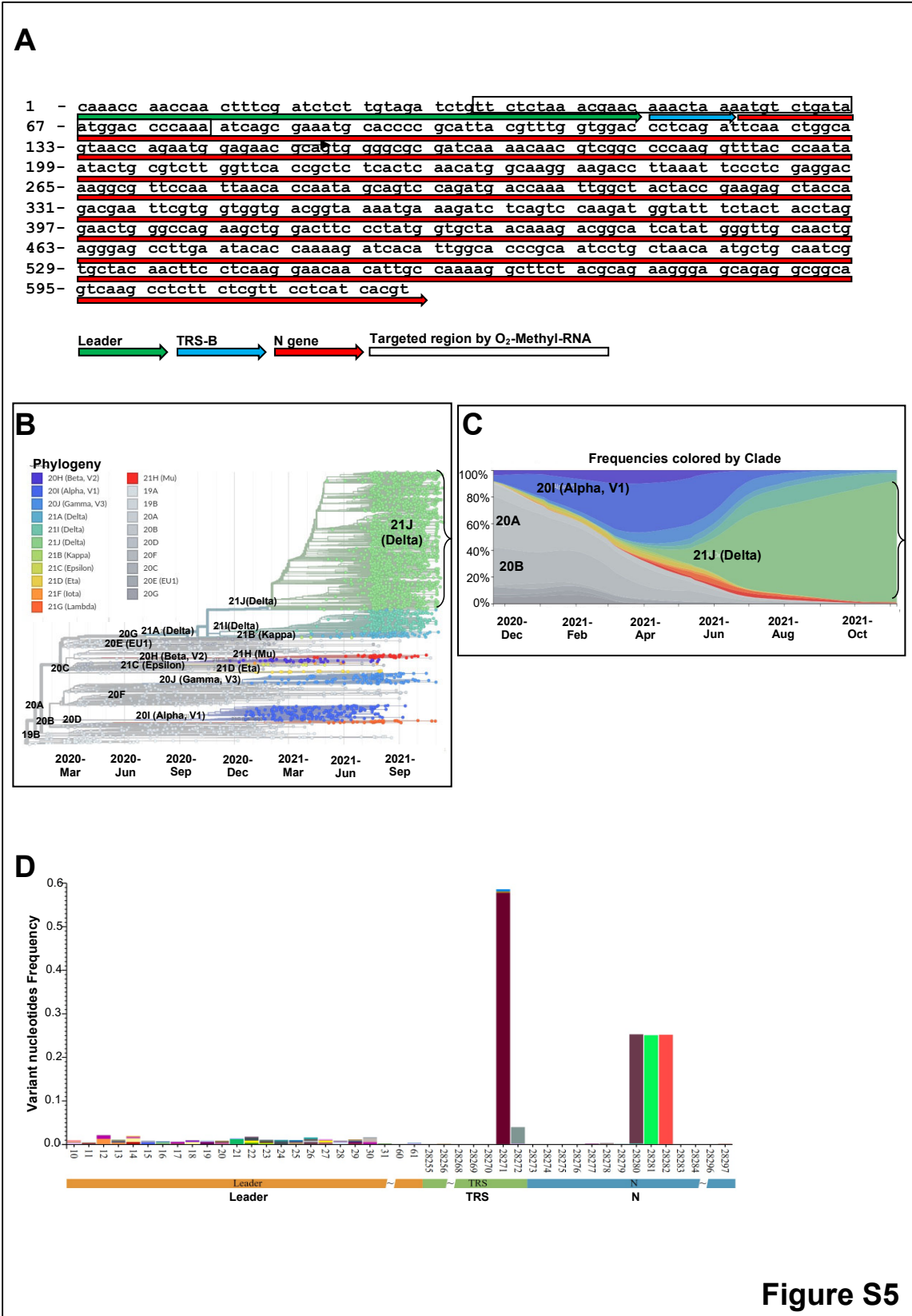


Figure S5

Supplementary Figure S5. 2'-*O*-methyl RNA against sgN sequence. Related to Figure 3A-B. (A) Sanger sequencing of the sgN region of SARS-CoV-2. Green arrow indicates the leader sequence, blue arrow indicates the TRS upstream gene N, and red arrow indicates gene N. The region recognized by 2'-*O*-methyl antisense RNA is highlighted in yellow. (B, C) Clade 21J is now the predominant form of Delta, with an estimated ~90% global frequency. (D) Frequencies of variant nucleotides calculated on a collection of about 350,000 sequences. Dataset downloaded from Global Initiative on Sharing Avian Influenza Data (GISAID) on November 15, 2021.

S61	19.59	26.54	19.72	33.18	19.43	19.54	21.25
S67	21.28	27.30	21.02	34.16	19.69	19.86	21.39
S73	26.40	27.75	26.50	35.30	24.31	24.95	23.14
S84	24.14	29.04	24.19	32.04	23.95	24.12	25.81
S120	28.05	31.87	28.04	36.70	28.22	28.68	26.32
S106	25.72	31.05	25.38	32.90	25.08	26.34	26.45
S163	30.14	35.75	29.64	36.23	28.30	27.76	26.56
S121	31.98	31.90	30.87	38.98	28.59	27.68	26.91
S156	29.34	35.06	29.15	35.59	28.79	28.89	27.15
S119	27.28	31.84	27.44	34.63	25.27	25.79	27.16
S96	28.64	30.49	28.91	27.29	26.11	25.69	28.21
S161	30.29	35.39	30.30	33.30	27.03	27.30	28.22

Supplementary Table S2. Related to Figure 1. Cq values obtained for 12 oro/nasopharyngeal swabs from negative COVID19-tested people according to the SARS-CoV-2 Viral3 kit and the Allplex 2019-nCoV assay.

Code	Cq values						
	SARS-CoV-2 Viral3 kit				Allplex 2019-nCoV assay		
	E gene	sgN transcript	ORF1ab gene	RNAse P gene	E gene	N gene	RdRP/S gene
N1	N.A.	N.A.	N.A.	38.26	N.A.	N.A.	N.A.
N2	N.A.	N.A.	N.A.	34.59	N.A.	N.A.	N.A.
N3	N.A.	N.A.	N.A.	34.82	N.A.	N.A.	N.A.
N4	N.A.	N.A.	N.A.	31.12	N.A.	N.A.	N.A.
N6	N.A.	N.A.	N.A.	37.75	N.A.	N.A.	N.A.
N7	N.A.	N.A.	N.A.	25.58	N.A.	N.A.	N.A.
N8	N.A.	N.A.	N.A.	28.54	N.A.	N.A.	N.A.
N9	N.A.	N.A.	N.A.	23.17	N.A.	N.A.	N.A.
N10	N.A.	N.A.	N.A.	26.42	N.A.	N.A.	N.A.
N11	N.A.	N.A.	N.A.	30.46	N.A.	N.A.	N.A.
N12	N.A.	N.A.	N.A.	26.49	N.A.	N.A.	N.A.

N.A., not amplified (i.e., Cq value >40).

S145	20.64	33.71	21.34	24.45	S303	36.39	N.A.	37.25	26.97
S146	23.56	33.72	23.53	30.08	S304	36.71	N.A.	38.21	26.99
S147	20.34	33.77	19.20	23.64	S305	36.74	N.A.	38.25	35.29
S148	20.34	33.77	19.20	23.64	S306	36.98	N.A.	36.69	28.51
S149	24.95	33.92	25.60	33.28	S307	37.13	N.A.	36.05	31.11
S150	27.78	33.96	28.00	31.88	S308	37.19	N.A.	38.09	31.35
S151	27.72	34.07	27.81	30.14	S309	37.61	N.A.	36.69	28.06
S152	28.87	34.18	29.79	33.89	S310	38.07	N.A.	36.32	30.28
S153	22.87	34.24	21.34	21.81	S311	38.30	N.A.	40.20	25.99
S154	22.87	34.24	21.34	21.81	S312	39.79	N.A.	38.81	35.17
S155	22.07	34.58	21.88	31.90	S313	39.79	N.A.	37.27	29.62
S156	29.34	35.06	29.15	35.59	S314	40.23	N.A.	40.40	30.22
S157	19.16	35.14	19.35	26.84	S315	40.26	N.A.	40.08	30.52
S158	19.16	35.14	19.35	26.84					

N.A., not amplified (i.e., Cq >40)

Supplementary Table S6. Related to Figure 2C-D. Cq values obtained from a cohort of 6 oro/nasopharyngeal swabs from hospitalized COVID19-positive patients analyzed according to scheduled times (i.e., 7-day intervals from the first swab) with the SARS-CoV-2 Viral3 kits (sgN, E gene, ORF1ab gene) and the Allplex 2019-nCoV assay (E, N, RdRp/S genes) and by Taqman qPCR (sgE, β -actin genes).

Marker	Days	Cq value					
		I1	I2	I3	I4	I5	I6
SARS-CoV-2 Viral3 kits							
sgN transcript	1	24.13	N.A.	29.01	27.76	22.06	N.A.
	7	37.47	N.A.	N.A.	N.A.	22.62	N.A.
	14	29.63	N.A.	N.A.	N.A.	22.44	N.A.
E gene	1	19.85	37.36	24.56	24.66	16.86	30.04
	7	29.76	N.A.	28.32	31.32	15.09	36.27
	14	21.24	N.A.	N.A.	30.67	15.64	N.A.
ORF1ab gene	1	22.79	36.2	26.95	26.98	18.47	32.16
	7	32.11	N.A.	32.31	34.18	19.37	37.2
	14	23.49	N.A.	N.A.	31.03	18.01	N.A.
RNaseP	1	33.01	36.6	33.93	33.31	30.44	31.34
	7	30.63	34.5	24.21	29.39	27.2	29.24
	14	24.05	30.37	34.12	25.22	31.42	33.14
Allplex 2019-nCoV assay							
E gene	1	20.55	38.46	25.44	25.85	17.26	30.44
	7	30.27	N.A.	29.34	32.1	16.26	37.76
	14	21.96	N.A.	N.A.	30.79	18	N.A.
N gene	1	19.57	37.1	24.61	25.21	17.01	30.92
	7	29.8	N.A.	30.31	31.17	17.11	N.A.
	14	23.25	N.A.	N.A.	31.77	17.52	N.A.
RdRp/S gene	1	22.54	39	27.43	27.8	19.12	32.88
	7	32.69	N.A.	31.64	34.16	18.13	N.A.
	14	24.32	N.A.	N.A.	32.71	20.67	N.A.
Taqman qPCR							
sgE transcript	1	38.15	-	39.13	39.45	22.58	39.55
	7	30.59	-	39.88	39.86	22.34	N.A.
	14	-	-	N.A.	-	23.09	N.A.
β -actin gene	1	21.15	-	21.22	20.93	21.07	19.16
	7	17.87	-	22.68	20.49	24.61	22.64
	14	-	-	20.28	-	26.08	21.41

N.A., not amplified (i.e., Cq values >40)