

Title: Development and evaluation of a Duo SARS-CoV-2 RT-qPCR assay combining two assays approved by the World Health Organization targeting the envelope and the RNA-dependant RNA polymerase (RdRp) coding regions

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Supplementary data

Suppl. Dataset#1. Sequences of the two IVT RNA used in the study.

Highlighted in blue: primers

Highlighted in green: probe

Bold underlined, T7 promoter sequence

Italicized, T7 termination sequence

>IVT_E gene

TAATACGACTCACTATAGGGAGAACATGAGGATCACCCATGT**ACAGGTACGTTAATAGTTAATAGCGT**ACTTCTTTTCTTATTATAGCGGCCGCTTATTAAGTT**ACACTA**
GCCATCCTTACTGCGCTTCGATT**TGTGTGCGTACTGCTGCAATAT**ACATGAGGATCACCCATGT*gcaataactagcataacccttggggcctctaaacgggtcttgaggggttttttgctga*

>IVT_RdRp-IP4

TAATACGACTCACTATAGGGAGAACATGAGGATCACCCATGTCAAGTATTGA**ATTATAGCGGCCGCTTATTA**CGAAATGCTGGTATTGTTGGTGTACTGACATTAG
ATAATCAAGATCTCAAT**GGTAACTGGTATGATTTCG**GTGATT**TCATACAAACCACGCCAGG**TAGTGGAGTTCCTGTTGTAGATTCTTATTATTCATTGTTAATG**CC**
TATATTAACCTTGACCAGGGCTTACATGAGGATCACCCATGT*gcaataactagcataacccttggggcctctaaacgggtcttgaggggttttttgctga*

Suppl. Figure 1. Flowchart of molecular testing on clinical samples using E-Sarbeco, RdRp-IP4 and Duo SARS-CoV-2 assays.

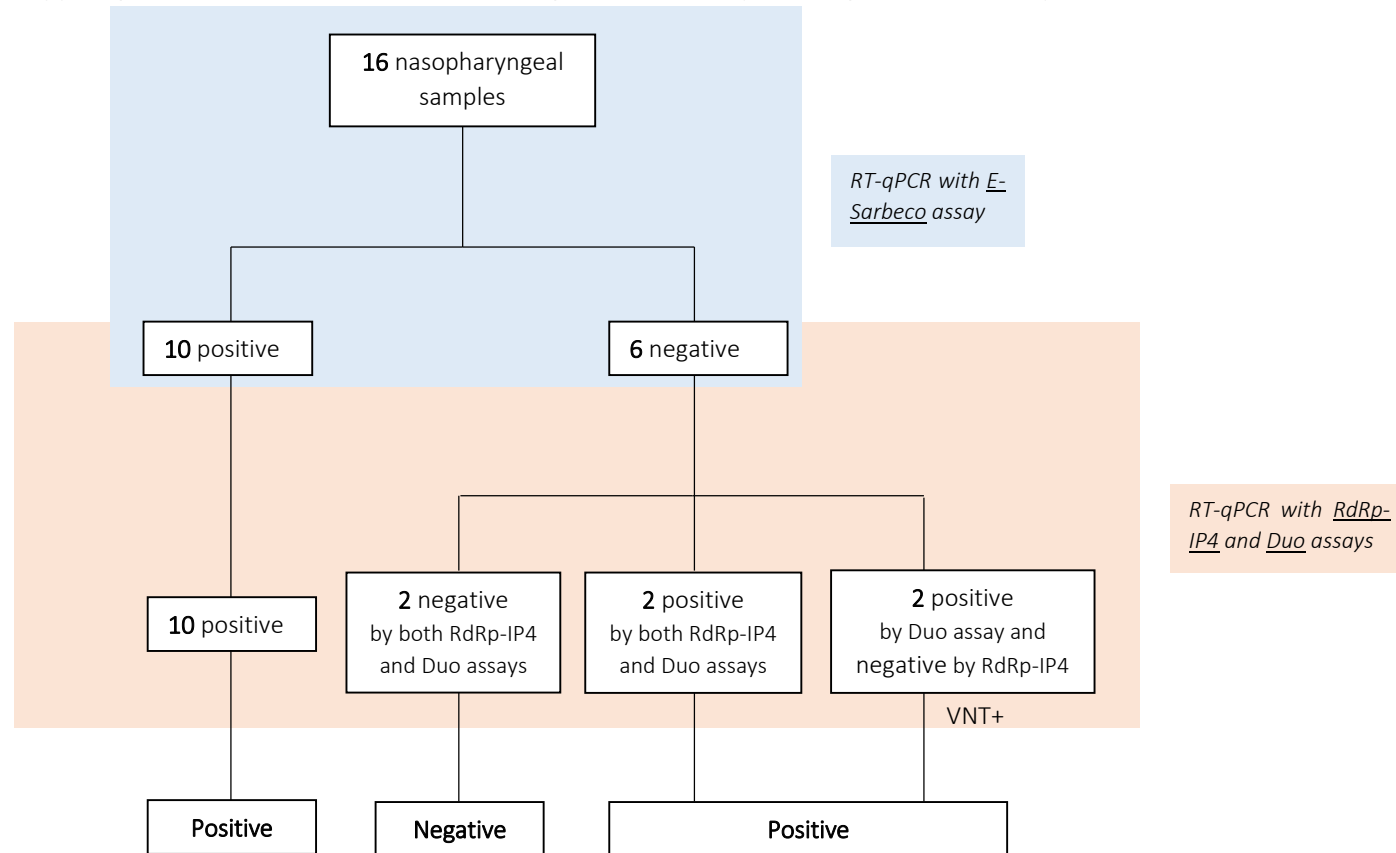
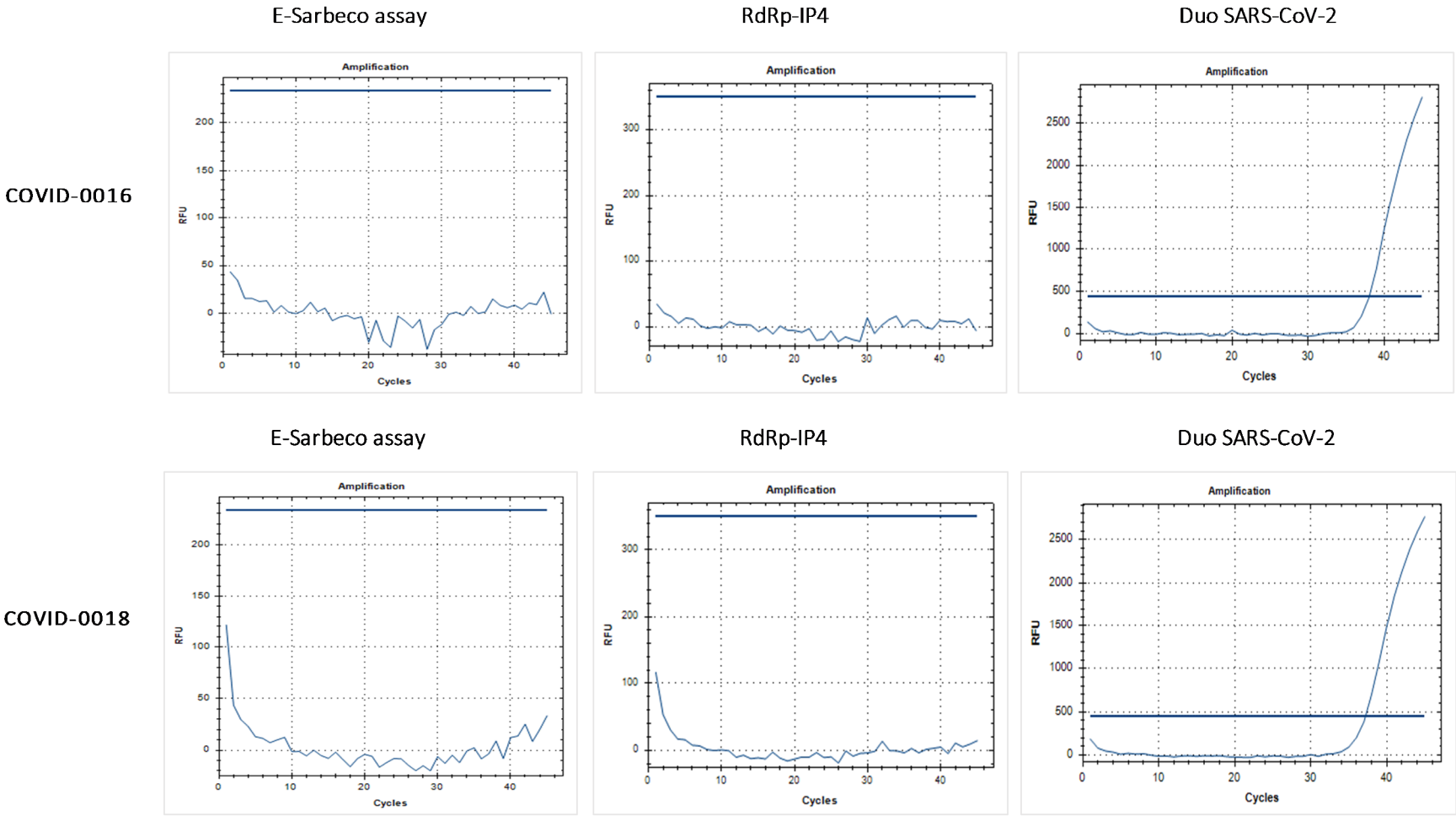


Table 1. Results of RT-qPCR on clinical samples with E-Sarbeco, RdRp-IP4 and Duo SARS-CoV-2 assays. Highlighted in grey, samples with discrepant results obtained with the three assays.

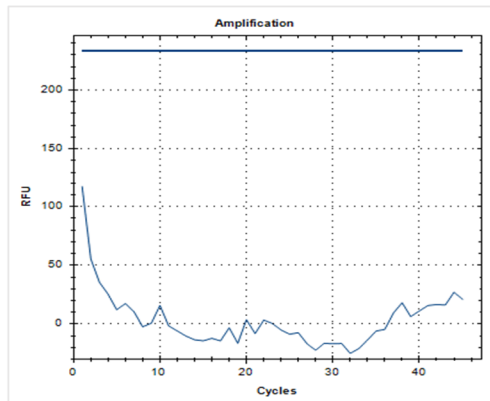
Sample nb	Sample name	Days between onset of symptoms and sampling (sera and nasopharyngeal swabs)	E-Sarbeco assay		RdRp-IP4 assay		Duo SARS-CoV-2		VNT	Titre VNT
1	COVID-0002	16	Positive	35,2	Positive	34,9	Positive	35,2	Positive	80
2	COVID-0004	9	Positive	31,4	Positive	31,2	Positive	31,2	Positive	>160
3	COVID-0006	11	Negative	>40	Negative	>40	Negative	>40	Negative	-
4	COVID-0008	13	Negative	>40	Negative	>40	Negative	>40	Positive	80
5	COVID-0010	13	Positive	31	Positive	30,4	Positive	30,8	Positive	80
6	COVID-0012	9	Positive	31	Positive	30,8	Positive	31	Positive	80
7	COVID-0016	17	Negative	>40	Negative	>40	Positive	38,1	Positive	>160
8	COVID-0018	15	Negative	>40	Negative	>40	Positive	37,2	Positive	>160
9	COVID-0020	12	Positive	35,4	Positive	37,4	Positive	35,8	Positive	>160
10	COVID-0022	16	Positive	32,8	Positive	34,2	Positive	33,1	Positive	40
11	COVID-0024	13	Positive	34	Positive	35,8	Positive	34,4	Positive	40
12	COVID-0026	15	Positive	37,1	Positive	36,4	Positive	35,9	Positive	40
13	COVID-0029	13	Positive	21,5	Positive	22,5	Positive	21,9	Positive	>160
14	COVID-0031	14	Positive	36,2	Positive	34,7	Positive	34,8	Negative	-
15	COVID-0033	7	Negative	>40	Positive	35,2	Positive	36,8	Positive	>160
16	COVID-0035	9	Negative	>40	Positive	36,6	Positive	38,9	Positive	80

Suppl Figure 2. Detection curves of samples with discrepant results obtained with the three RT-qPCR assays.

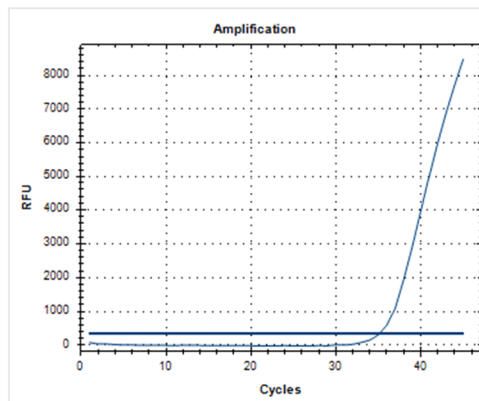


COVID-0033

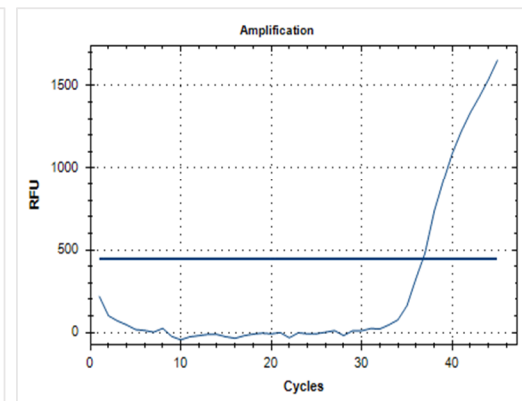
E-Sarbeco assay



RdRp-IP4

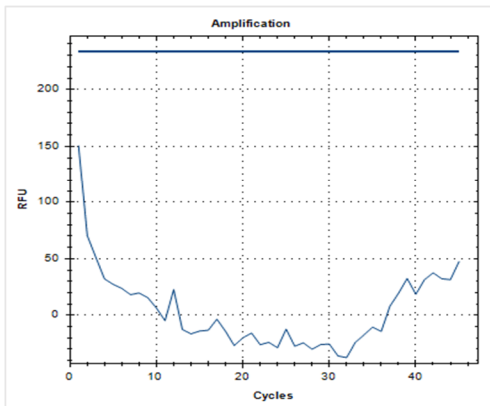


Duo SARS-CoV-2

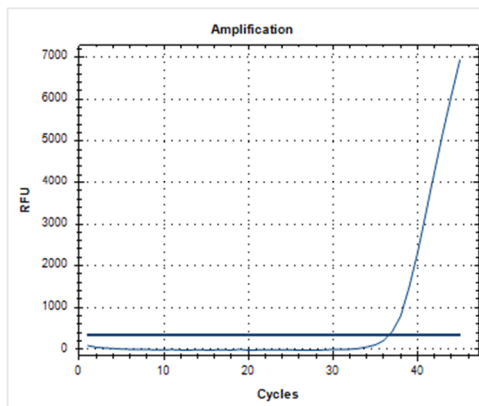


COVID-0035

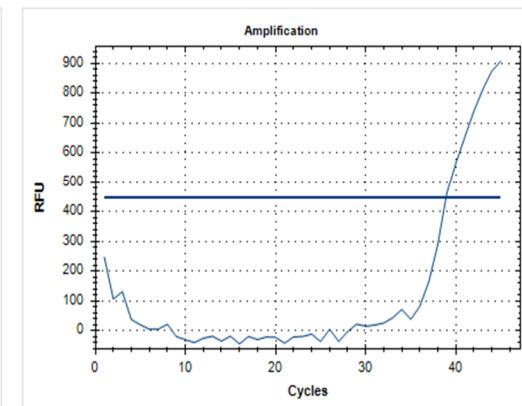
E-Sarbeco assay



RdRp-IP4



Duo SARS-CoV-2



Suppl. Dataset#2. *In silico* analysis of the genetic heterogeneity in the target regions of the assay included in the Duo SARS-CoV-2 assay

Analysis #A: Based on 14,277 complete genome sequences of SARS-CoV-2 from COG-UK Consortium (Regions: Scotland, England, Wales, Northern Ireland)

A1. IP4-RdRp

99,16% of sequences (14,156 sequences): no mismatch with IP4-RdRp primers and probe set

0,84% of sequences (121 sequences): 1 or more mismatches with IP4-RdRp primers and probe set

- 8 sequences: 1 or more mismatches with Fw primer
- 37 sequences: 1 or more mismatches with probe
- 76 sequences: 1 or more mismatches with Rev primer

A2. E gene (Charité, Berlin)

99,83% of sequences (14,252 sequences): no mismatch with E gene(Charité) primers and probe set

0,17% of sequences (25 sequences): 1 or more mismatches with E gene(Charité) primers and probe set

- 4 sequences: 1 or more mismatches with Fw primer
- 19 sequences: 1 or more mismatches with probe
- 2 sequences: 1 or more mismatches with Rev primer

Analysis #B: Based on 14,277 complete genome sequences of SARS-CoV-2 from COG-UK Consortium (Regions: Scotland, England, Wales, Northern Ireland)

B1. E-Sarbeco assay regions corresponding to the primers and the probe (73 sequences)

E Sarbeco (Chantre)	57,859	27,884	57,922	57,947	57,950	27,971	Position on the genome according to strain LC528252
	A C A G G T A C G T T A A T A G T T A A T A G C G T		A C A C T A G C C A T C C T T A C T G C G C T T C G		T G T G T G C G T A C T G C T G C A A T A T		
NC_045512 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_Wuhan-Hu-1 complete_genome							
LC529905 Severe_acute_respiratory_syndrome_coronavirus_2_TKY6182_2020_RNA1 complete_genome							
MT371050 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/USA/COV486/2020 complete_genome							
LC542809 Severe_acute_respiratory_syndrome_coronavirus_2_TKY6947_2020_RNA1 complete_genome							
MT135042 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/CHN/213/2020 complete_genome							
MT350282 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/BR/SP002/2020 complete_genome							
MT144412 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/HK/GHKU-9024/2020 complete_genome							
MT192772 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/IRAN/CoV-19-0151/2020 complete_genome							
MT192773 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/VNM/hCoV-19-025/2020 complete_genome							
MT320538 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/IRA/IRA-808/2020 complete_genome							
MT276380 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/USA/PL_5091/2020 complete_genome							
MT304491 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/USA/TX_2967/2020 complete_genome							
MT159722 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_2019-nCoV/USA-CU64-6/2020 complete_genome							
MT451374 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/USA/NY-00000001/2020 complete_genome							
MT422807 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/USA/IL-5/2020 complete_genome							
MT339041 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/USA/AZ-48U2986/2020 complete_genome							
MT326035 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/GRC/13/2020 complete_genome							
MT121215 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/CHN/SH01/2020 complete_genome							
MT058874 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/CHN/SH420/2020 complete_genome							
MT066175 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/NTU01/TWN/human/2020 complete_genome							
MT020781 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_nCoV-FIN-29-Jan-2020 partial_genome							
MT066156 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/ITA/INMI1/2020 complete_genome							
MT281577 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/CHN/Fuyang_FY002/2020 complete_genome							
MT004474 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/KOR/BA-AC1_2604/2020 complete_genome							
MT369241 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/CHN/VN-0056-466/2020 complete_genome							
MT434782 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/USA/NY-CDC-SURV0076NV/2020 complete_genome							
MT106254 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_2019-nCoV/USA-TX1/2020 complete_genome							
MT441156 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/THA/9/2020385-NT/2020 complete_genome							
MT447157 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/THA/9/2020438-NT/2020 complete_genome							
MT192759 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/TWN/GDMH-COV-01/2020 complete_genome							
MT259229 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/CHN/Wuhan_78012602/2020 complete_genome							
MT438718 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/USA/CA-C26-1000/2020 complete_genome							
MT364351 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/CHN/2020-03-09/2020 complete_genome							
MT072688 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/NPL/61-TW/2020 complete_genome							
MT072125 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/ITA/INMI1/2020 complete_genome							
LC528252 Severe_acute_respiratory_syndrome_coronavirus_2 SARS-CoV-2/human/UK/19-003_RNA1 complete_genome							
MT276597 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/ISR/ISR_P0320/2020 complete_genome							
MT020483 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/IND/166/2020 complete_genome							
MT293372 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/ESP/Valencia13/2020 complete_genome							
MT256924 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/COL/79156_Antioquia/2020 complete_genome							
MT255377 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/USA/C28-R025-005/2020 complete_genome							
MT355092 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/HK/GHKU-9048/2020 complete_genome							
MT327745 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/TUR/ERAGEM-001/2020 complete_genome							
MT559696 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/ESP/VN-19015583/2020 complete_genome							
MT559695 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/ESP/VN00001133/2020 complete_genome							
MT385436 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/USA/CA-C28016/2020 complete_genome							
MT435280 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/IND/G88C1/2020 complete_genome							
MT386866 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_EXRS-CoV-2/human/USA/WA-UW-4128/2020 complete_genome							
MT451037 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/AUS/VIC131/2020 complete_genome							
MT300186 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/USA/IL-200179/2020 complete_genome							
MT412331 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/USA/WA-UW-6399/2020 complete_genome							
MT418888 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/USA/VA-DC15-0108/2020 complete_genome							
MT366166 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/mex/IND/1/2020 complete_genome							
MT451038 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/AUS/VIC134/2020 complete_genome							
MT263074 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/PER/Peru-10/2020 complete_genome							
MT446312 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/Guangzhou/CT020/2020 complete_genome							
MT419812 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/USA/PR-CDC-S3/2020 complete_genome							
MT293226 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/CHN/Wuhan_146-1W02/2019 complete_genome							
MT240479 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/PAX/Gilgit/2020 complete_genome							
MT320891 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/IRN/HsRC1-1-IP-8206/2020 complete_genome							
MT093372 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/SRI/E01/2020 complete_genome							
MT098980 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SNU01 complete_genome							
MT007544 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_Australia/VIC01/2020 complete_genome							
MT291836 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/CHN/Wuhan_146-8/07/2020 complete_genome							
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MT447172 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/THA/9/2020529-NT/2020 complete_genome							
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MT428551 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/NAZ/NCB/2020 complete_genome							
MT447171 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/THA/9/2020567-NT/2020 complete_genome							
MT451874 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/IND/G88C1/2020 complete_genome							
MT412330 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/USA/UT-UW-6388/2020 complete_genome							
MT262993 Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/PAX/Mangla/2020 complete_genome							

B2. IP4-RdRp assay regions corresponding to the primers and the probe (73 sequences)

IP4-RdRp	15,150	15,168	15,175	15,198	15,287	15,256	Position on the genome according to strain LC528232
	GGTAACTGGTATGATTTCG		TCAACAAACCACGCCAGG		CTATATTAACTTTGACCA		
NC_045512_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_Wuhan-Hu-1_complete_genome							
LC529905_Severe_acute_respiratory_syndrome_coronavirus_2_TKY6182_2020_RNA1_complete_genome							
MT371050_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/USA/CoV486/2020_complete_genome							
LC542809_Severe_acute_respiratory_syndrome_coronavirus_2_TKY6947_2020_RNA1_complete_genome							
MT135042_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/CHN/231/2020_complete_genome							
MT350282_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/BRA/SP02cc/2020_complete_genome							
MT114412_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/IRG/HKU-904a/2020_complete_genome							
MT192772_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/VNM/nCoV-19-015/2020_complete_genome							
MT192773_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/VNM/nCoV-19-025/2020_complete_genome							
MT320538_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/IRK/RA-RB/2020_complete_genome							
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MT304491_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/USA/TX_2967/2020_complete_genome							
MT159722_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_2019-nCoV/USA/Cruza4/2020_complete_genome							
MT452574_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/USA/N-GDI-00000001/2020_complete_genome							
MT422807_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/USA/UF-6/2020_complete_genome							
MT339041_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/USA/AZ-ASU2936/2020_complete_genome							
MT328035_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/GR/13/2020_complete_genome							
MT121215_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/CHN/SH01/2020_complete_genome							
MT039874_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/CHN/IME-H201/2020_complete_genome							
MT066175_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/NTU01/TWN/human/2020_complete_genome							
MT020781_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_nCoV-FIN-29-Jan-2020_partia_genome							
MT066156_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/ITA/INMI1/2020_complete_genome							
MT281877_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/CHN/Fuyang_FY002/2020_complete_genome							
MT304474_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/KOR/BA-ACH_2604/2020_complete_genome							
MT396241_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/CHN/NV308-464/2020_complete_genome							
MT434782_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/USA/NY-CDC-BU0076W/NC/2020_complete_genome							
MT106054_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_2019-nCoV/USA-TX1/2020_complete_genome							
MT447156_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/THA/9200383-N/2020_complete_genome							
MT447157_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/THA/9200383-N/2020_complete_genome							
MT192759_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/TWN/GMH-CGU-Q1/2020_complete_genome							
MT259225_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/CHN/Wuhan_YB012602/2020_complete_genome							
MT438718_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/USA/CA-CZB-1000/2020_complete_genome							
MT394531_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/USA/CA-CZB-55003/2020_complete_genome							
MT072688_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/NPL/E1-TW/2020_complete_genome							
MT077125_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/ITA/INMI1/2020_complete_genome							
LC528232_Severe_acute_respiratory_syndrome_coronavirus_2_SARS-CoV-2/HuDP/King15-020_RNA1_complete_genome							
MT26597_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/IRG/HKU-904a/2020_complete_genome							
MT050493_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/IND/166/2020_complete_genome							
MT292572_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/ESP/Valencia11/2020_complete_genome							
MT256924_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/COL/79256_Antioquia/2020_complete_genome							
MT258377_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/USA/CZB-R057-005/2020_complete_genome							
MT365032_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/IRG/HKU-904a/2020_complete_genome							
MT327745_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/TUR/ERAGEM-001/2020_complete_genome							
MT358866_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/ESP/138153683/2020_complete_genome							
MT359865_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/ESP/VH000001133/2020_complete_genome							
MT385436_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/USA/CA-CZB016/2020_complete_genome							
MT435080_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/IND/GBRC3/2020_complete_genome							
MT358664_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/USA/WA-UW-4318/2020_complete_genome							
MT451037_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/AUS/VIC131/2020_complete_genome							
MT300186_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/USA/UNC_200173/2020_complete_genome							
MT412331_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/USA/WA-UW-6399/2020_complete_genome							
MT418888_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/USA/VA-DCL54208/2020_complete_genome							
MT396266_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/min/NLD/1/2020_complete_genome							
MT451038_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/AUS/VIC134/2020_complete_genome							
MT263074_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/PER/Peru-10/2020_complete_genome							
MT446312_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/Guangzhou/QTC05/2020_complete_genome							
MT419812_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/PR-CDC-83/2020_complete_genome							
MT291826_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/CHN/Wuhan_IME-WH01/2019_complete_genome							
MT240479_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/PAK/Digit1/2020_complete_genome							
MT320891_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/IRN/HGR-1.1-IP4-8206/2020_complete_genome							
MT093571_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/SWE/01/2020_complete_genome							
MT039890_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SNU01_complete_genome							
MT007544_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_Australia/VIC1/2020_complete_genome							
MT291836_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/CHN/Wuhan_IME-BJ07/2020_complete_genome							
MT418889_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/USA/VA-DCL54209/2020_complete_genome							
MT447172_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/THA/9205523-N/2020_complete_genome							
MT215194_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/IRG/BS_VHX0002868/2020_complete_genome							
MT451882_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/IND/GBRC17b/2020_complete_genome							
MT428551_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/KAZ/NCB-1/2020_complete_genome							
MT447171_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/THA/9205487-N/2020_complete_genome							
MT451874_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/IND/GBRC10/2020_complete_genome							
MT412330_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/USA/CT-UW-6385/2020_complete_genome							
MT262993_Severe_acute_respiratory_syndrome_coronavirus_2_isolate_SARS-CoV-2/human/PAK/Manga1/2020_complete_genome							