

Figure S1. Effects of cholesterol-depleting agent MBCD on the content of intracellular cholesterol. Huh7 and Vero E6 cells were grown in DMEM containing 10% FBS until confluency, and then treated with increasing concentrations of MBCD for 1h to deplete cholesterol from cells (**Panel A**, N=3). In subsequent experiments, Huh7 (**Panel B**, N=2) and Vero E6 cells (**Panel C**, N=2) were treated with either BMCD alone (10 mM) or MBCD-cholesterol complexes (10 mM- 0.125 mM) for 5min-60 min. After the treatment, total cholesterol was extracted from the cells and measured by colorimetric cholesterol assay.

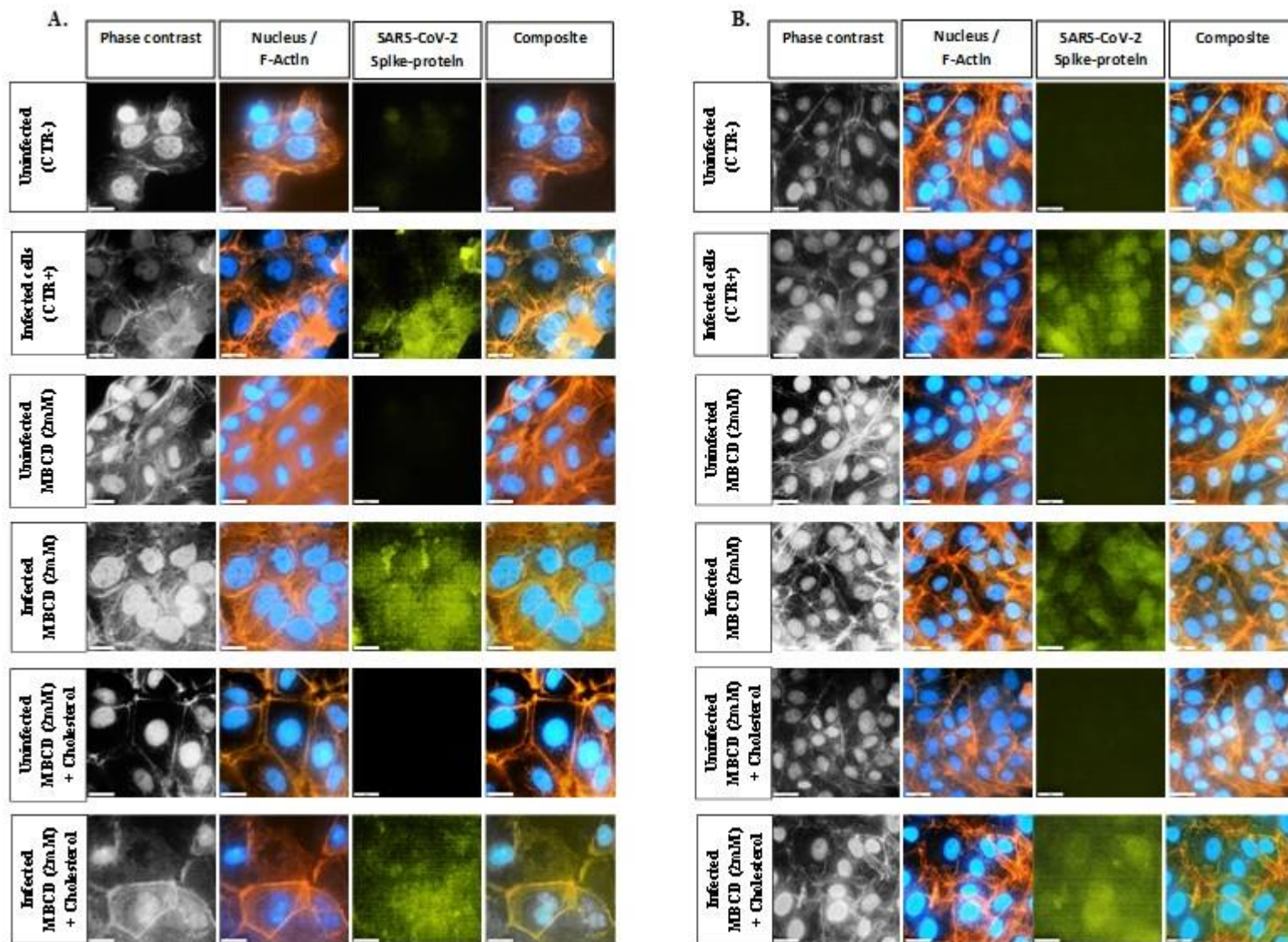


Figure S2. M β CD treatment did not disturb the cell morphology in wild-type SARS-CoV-2 infected cells. Huh7 and Vero E6 cells were treated with M β CD (2mM) or MB β CD + cholesterol for 1h prior infection with wild-type SARS-CoV-2pp (MOI=0.1). At 48h p.i., Huh7 (**Panel A**) and Vero E6 cells (**Panel B**) were fixed and analyzed by immunofluorescence staining using DAPI for cell nuclei (blue), anti-actin antibody (orange), SARS-CoV-2 anti-spike proteins (green) and merged double stained (composite). M β CD-treated cells were compared to controls: untreated-uninfected (CTR-) and untreated-infected (CTR+) cells. Images were taken and analyzed with resolution of fluorescence microscopy up to 20 μ m.

Table S1. Primers and probes used to detect SARS-CoV-2

Gene	Primer/Probe	Sequence (5'–3')
RdRp-gene	RdRP_SARSr-F2 RdRP_SARSr-R1 RdRP_SARSr-P2 RdRP_SARSr-P1	GTGARATGGTCATGTGTGGCGG CARATGTTAAASACACTATTAGCATA FAM CAGGTGGAACCTCATCAGGAGATGC-BBQ FAM-CCAGGTGWACRTCATCMGGTGATGC-BBQ
E-gene	E_Sarbeco_F1 E_Sarbeco_R2 E_Sarbeco_P1	ACAGGTACGTTAATAGTTAATAGCGT ATATTGCAGCAGTACGCACACA FAM-ACACTAGCCATCCTTACTGCGCTTCG-BBQ
N-gene	N_Sarbeco_F1 N_Sarbeco_R1 N_Sarbeco_P1	CACATTGGCACCCGCAATC GAGGAACGAGAAGAGGCTTG FAM-ACTTCCTCAAGGAACAACATTGCCA-BBQ

R, A/G; W, A/T; FAM, 6-fluorescein amidite; BBQ, blackberry quencher

Table S2. List of primers used for qRT-PCR

Target Gene (Human)	Primer Sequences (5'-3')
CH25H	F: CTTTCCGTGGAGGACCACTC R: GTGAGAGTGATGCAGGTCGT
SREBF1	F: CAGCAGCTACTGACAGTCACA R: CTTGATGAAGTGGGGCTGC
SCAP	F: TGCACTGAACCTGGACTTGG R: CCCAAAGTGCCTGACAGATG
LDLR	F: CGTGCTCCTCGTCTTCCTTT R: TCTGTCTCGAGGGGTAGCTG
ACAT1	F: GTTCTGGTCCAAAAACCGCC R: CGCCGAGACCTTGAAGTAG
HMGCR	F: CTCTTATTGGTCGAAGGCTCG R: CCACAAAGAGGCCATGCATTC
HMGCS1	F: GGGCGTTGAGGTCTAGGTATTCT R: TTTCCTCCTTCGGGCACTCTA
APOA1	F: CTGTTTGCCCACTCTATTTGCC R: CCTGTTGCTGCTCACTGGTC
APOB	F: ACTGCTAAAGGCATGGCACT R: TGCCGTGATCTCAAATGGCT
SREBP2	F: TCTGGAGACCATGGAGACCC R: GTCAGGGAACTCTCCCACTTG
NPC1L1	F: TGAGCTGCATGGCTGACTAC R: AGGGCCTCTGCCTCAGAATA
PPARA	F: GCGAACGATTCGACTCAAGC R: CCAGGACGATCGTTGTGTGA
PPARG	F: CCAGAAGCCTGCATTTCTGC R: CACGGAGCTGATCCCCAAAGT
PPARD	F: CCGGGACAGTGTGTACAGT R: AGGTCTCGTTGGTGCATCTG
FDFT1	F: GCATGAGCGACTTTTGCGTG R: GCCTGGATAACAGCTGCGAA
NR1H2	F: TGTCTCTCCTACCACGAGT R: TTCAGAAAGGACGCCCCAGT
NR1H3	F: AGCCAAGGTACAGGTAACGA R: GGTTCCAGCTTGTTTGCTGC
MBTPS1	F: GGACCAAGTGTGCTTCTCCA R: CTGCTTCATACTGGCGGGAT
MBTPS2	F: TGTCGTCTACCTGACCGACT R: TCCGTGTGTTTCCAGCCAGT
ACAT2	F: GACTTCGTCTCCTTCGTGCC R: CCCCAAATCCGAAGGACTGG
ACE2	F: GGGATCAGAGATCGGAAGAAGAAA R: AGGAGGTCTGAACATCATCAGTG
ABCA1	F: GGGTGGTGTCTTCCTCATTACTG R: CCGCCTCACATCTTCATCTTCATC
ACTIN	F: ATCGTGCGTGACATTAAGGAGAAG R: AGGAAGGAAGGCTGGAAGAGTG

F, forward; R, reverse