	PNAS
1	
2	
4	Supporting Information for
5	
6 7	
8	Tight junction protein occludin is an internalization factor for SARS-CoV-2
9	infection and mediates virus cell-to-cell transmission
10 11 12 13	Jialin Zhang ^{a,b} , Wenyu Yang ^{a,b} , Sawrab Roy ^{a,b} , Heidi Liu ^{a,b} , R. Michael Roberts ^{c,d} , Liping Wang ^{a,b} , Lei Shi ^{a,b} , Wenjun Ma ^{a,b,*}
14 15	
10	1 o whom correspondence should be addressed: Wenjun Ma
1/ 10	Email: <u>wma@missouri.edu</u>
18 19	
20	This PDF file includes:
$\frac{21}{22}$	Supporting text
23	Figures S1 to S5
24 25	SI References
26	
27	
28	
29	
30	
31	
32	
33	

34 Supplementary Materials and Methods

35 Cell lines

36 Vero-E6 cells (ATCC, CRL-1586), Caco-2 cells (kindly provided by Dr. Feng Li at University of 37 Kentucky), and BSR-T7/5 cells (kindly provided by Dr. Karl-Klaus Conzelmann) were cultured in 38 Dulbecco's modified Eagle's medium (DMEM) supplemented with 10% fetal bovine serum (FBS) 39 and 1% penicillin/streptomycin at 37°C in a 5% CO₂ incubator. 293FT cells expressing human 40 ACE2 and Transmembrane Serine Protease 2 (TMPRSS2) (293FT-hACE2-TMRPSS2) (a kind gift 41 from Dr. Marc Johnson at University of Missouri-Columbia) were maintained in DMEM 42 supplemented with 10% FBS, MEM vitamin, L-glutamine, sodium pyruvate, non-essential amino 43 acids and selected with puromycin (1 µg/mL) and hygromycin (200 µg/mL) (1). A549-hACE2 cell 44 line expressing human ACE2 was maintained in DMEM supplemented with 10% FBS and selected 45 with 0.5 µg/mL of puromycin (InvivoGen, a549-hace2) 46

47 Viruses

48 SARS-CoV-2 reverse genetic system was kindly provided by Dr. Pei-Yong Shi at University of 49 Texas Medical Branch. SARS-CoV-2-mNG virus expressing the mNeonGreen gene was rescued 50 on Vero-E6 cells in a BSL-3 facility according to an appropriate protocol (2). The SARS-CoV-2 51 USA-WA1/2020 strain was acquired from BEI Resources (Manassas, VA, USA) and kindly 52 provided by Drs. Jeff Adamovicz and Jeff Whyte at University of Missouri. Plasmids encoding 53 codon-optimized full-length Spike of the Wuhan-1 strain (VRC7480), Alpha (B.1.1.7), Beta 54 (B.1.351), Gamma (P.1), Delta (B.1.617.2), Kappa (B.1.617.1) and Omicron (BA.2) were kindly 55 provided by Dr. Tongging Zhou at the Vaccine Research Center, NIAID/NIH. Vesicular stomatitis 56 virus (VSV) reverse genetic system was kindly provided by Dr. Sean Whelan at Washington 57 University in St. Louis. rVSV-eGFP-SARS-CoV-2-S virus (rVSV-eGFP-S) was rescued on BSR-58 T7/5 cells and passaged on Vero-E6 cells. Recovery of the rVSV-eGFP-S virus was performed as 59 described previously (3). Briefly, BSR-T7/5 cells in a 6-well plate were infected with the vaccinia 60 virus MVA-T7 (kindly provided by Dr. Bernard Moss at NIH) at 37°C for 1 h and subsequently 61 transfected with 7 µg of mixed plasmids of VSV-eGFP-SARS-CoV-2, N, P, and L with a 5:3:5:1 62 ratio. Forty-eight hours posttransfection, the supernatants were filtered to remove the vaccinia virus 63 and passaged on Vero-E6 cells. SARS-CoV-2-mNG and rVSV-eGFP-S virus stocks were prepared 64 and titrated on Vero-E6 cells and stored at -80°C. The PEDV strain was isolated from pigs by Dr. 65 Ma's laboratory in 2013.

66

67 Hamster study

Nine 6 to 8-weeks-old male and female Syrian hamsters were divided into 2 groups and held in the BSL3 animal facility at the University of Missouri Laboratory for Infectious Disease Research. Six hamsters were intranasally infected with 10⁶ TCID₅₀ of the SARS-CoV-2/USA-WA1/2020 virus per animal and 3 hamsters were mock-infected with PBS as controls. Clinical signs were monitored daily. Three infected and control hamsters were euthanized and necropsied on day 3 postinfection and the remaining 3 infected hamsters were necropsied on day 5 postinfection. During necropsy, the lung was collected from each animal for western blot assay to determine levels of OCLN.

76 Plasmids

77 SARS-CoV-2 S1 subdomain (aa 14-685) was amplified and cloned into pCAGGS vector with a HA 78 tag or a His tag in the C-terminal to generate pCAGGS-S1-HA or pCAGGS-S1-His plasmid. The 79 human OCLN (hOCLN) gene was amplified from RNA of 293T cells and cloned into pCAGGS 80 vector with a Flag tag in the C-terminal or pCold-GST vector (Takara, 3372), resulting in pCAGGS-81 hOCLN-flag and pCold-GST-hOCLN plasmids. The hOCLN gene was cloned into pLenti-CMV/TO-82 eGFP-Puro plasmid by using BamHI/Xbal to generate the lentiviral plasmid pLenti-CMV/TO-83 hOCLN-Puro to overexpress OCLN on Vero-E6 cells or A549-hACE2 cells. Mouse occludin 84 (mOCLN) was amplified from RNA extracted from mouse lung tissue and cloned into pCAGGS 85 vector with a Flag tag in the C-terminal to generate a plasmid, named the pCAGGS-mOCLN-Flag. 86 hOCLN/ΔN (deletion of aa 1-63), hOCLN/ΔC (deletion of aa 267-522), hOCLN/ΔEL1 (deletion of 87 aa 94-128), and hOCLN/ Δ EL2 (deletion of aa 200-238) as described previously (4) were amplified 88 by using overlap-PCR and cloned into pCAGGS vector with a Flag tag in the C-terminal to generate

92 OCLN knockout cell line

93 The guide sequence oligonucleotides including the BsmBI restriction site overhangs (gRNA1: 5'-94 CACCGAGTGTAGGCTACCCTTATGG-3', 5'-AAACCCATAAGGGTAGCCTACACTC-3'; gRNA2: 95 5'-CACCGGATAATAGTGAGCGCTATCC-3', 5'-AAACGGATAGCGCTCACTATTATCC-3') were 96 designed and cloned into the lentiCRISPRv2-blast vector (Addgene, 98293) to generate 97 lentiCRISPRv2-blast-gRNA. 293T cells in 100-mm dishes were transfected with plasmids using 98 Lipofectamine 3000 according to the manufacturer's instructions to prepare lentivirus. Briefly, 10 99 µg of lentiCRISPRv2-blast-gRNA, 8 µg of psPAX2 (Addgene, 12260), and 5 µg of pCMV-VSV-G 100 (Addgene, 8454) were transfected into 293T cells. The medium was changed at 6 h 101 posttransfection and at 48 h the supernatant was collected, filtered through a 0.45 µm PES filter, 102 and concentrated with Amicon Ultra-4 centrifugal filters. Vero-E6 cells in 6-well plates were infected 103 with the concentrated lentivirus at 37°C for 6 h. Then, the virus was removed, and 2 ml of fresh 104 medium was added. After 48 h of incubation, the medium was replaced with the selective medium 105 containing 6 µg/ml of Blasticidin S HCl (ThermoFisher, A1113903). After 7 days of selection, cells 106 were subjected to single-clone selection using serial dilutions in a 96-well plate. After 3 days of 107 incubation, wells containing single cells were marked and knockout cells were identified by the Guide-it Genotype Confirmation Kit (Takara, 632611), and further confirmed by IFA and western 108 109 blot. Positive colonies were transferred into 6-well plates for amplification and further experiments. 110

111 Confocal assay

112 Vero-E6 cells in a 35-mm glass dish were infected with SARS-CoV-2-mNG or rVSV-eGFP-S virus 113 at an MOI of 0.1. The cells were then fixed with 4% paraformaldehyde for 20 mins and 114 permeabilized with 0.25% Triton X-100 for 15 min followed by blocking with 5% non-fat milk for 1 h 115 at room temperature. Rabbit anti-OCLN antibody (1:200, Invitrogen, 71-1500), mouse anti-ZO-1 116 antibody (1:250, Invitrogen, 339100), rabbit anti-claudin antibody (1:1000, Abcam, ab211737) were 117 added and incubated at 4°C overnight, followed by incubating with an Alexa Fluor™ 647-118 conjugated goat anti-rabbit IgG (H+L) cross-adsorbed secondary antibody (A-21244, Invitrogen) or 119 an Alexa Fluor™ 647-conjugated goat anti-mouse IgG (H+L) cross-adsorbed secondary antibody 120 (A-21235, Invitrogen) at 37°C for 1 h, respectively. Nuclei were stained with 4',6-diamidino-2-121 phenylindole (DAPI).

For the ACE2 and OCLN colocalization assay, Vero-E6 cells were infected with SARS-CoV-2/WA1 strain at an MOI of 0.1, and then fixed with methanol/acetone (3:2) at -20°C for 30 min. After blocking with 5% non-fat milk, the cells were incubated with a mouse anti-ACE2 antibody (1:200, Invitrogen, MA5-31395) or a rabbit anti-occludin antibody (1:200, Invitrogen, 71-1500) at 4°C overnight, followed by exposure to secondary antibodies as described above. Images were captured with a Leica SP8 spectral confocal microscope.

128

129 Immunofluorescence assay

Vero-E6 cells in 24-well plates were infected with the SARS-CoV-2-mNG virus at an MOI of 0.01 at 37°C for 1 h. Then, the cells were washed three times with PBS and fresh DMEM with 2% FBS was added. After 48 h, the cells were fixed with methanol/acetone (3:2) at -20°C for 30 min and non-specific antibody binding blocked with 2% BSA for 2 h at room temperature. The cells were stained with an OCLN monoclonal antibody diluted 1:250 in 0.1% BSA (Invitrogen, 33-1500) at 4°C overnight, and then stained with the Alexa Fluor 594-conjugated goat anti-mouse IgG (H+L) at a dilution of 1:500 (Jackson ImmunoResearch Laboratories, 115-585-003) at 37°C for 2 h.

For the siRNA assays, the cells were stained with ZO-1 (1:250, Invitrogen, 339100) or Claudin-1 (1:1000, Abcam, ab211737) antibody after fixation and blocking at 4°C overnight, followed by incubating with an Alexa Fluor 594-conjugated goat anti-mouse IgG (H+L) (Jackson ImmunoResearch Laboratories, 115-585-003) and Alexa Fluor Plus 594 labeled goat anti-rabbit IgG (H+L) antibody at 37°C for 2 h, respectively. Nuclei were stained with DAPI. Images were acquired with the EVOS™ M5000 imaging system.

143

144 Western blot assay

145 Vero-E6 cells were infected with SARS-CoV-2 at an MOI of 0.01. Cells were harvested at indicated 146 time points (24 h and 48 h) and lysed with RIPA on ice for 30 min. Lungs were collected from three 147 mock-infected hamsters at day 3 postinfection and three hamsters infected with the SARS-CoV-148 2/WA1 virus at day 3 and 5 postinfection, respectively, for the western blot assay. Lung tissues 149 (100 mg) from each animal were mixed with 1 ml CelLytic[™] M buffer (C2978, Sigma-Aldrich) 150 containing protease inhibitors and homogenized. The supernatant was collected after 151 centrifugation at 12,000 x g for 30 min. The supernatants were mixed with 4 X loading buffer and 152 boiled for 20 mins to prepare samples for electrophoresis on a 10% SDS-PAGE gel. After 153 transferring protein to the PVDF membrane, the membrane was blocked with 5% non-fat milk in 154 PBS for 1 h at room temperature. Then, the membrane was incubated with an OCLN monoclonal 155 antibody (1:1,000, Invitrogen, 33-1500), an anti-SARS-CoV-2-nucleocapsid (N) rabbit monoclonal 156 antibody (1:2,000, Genuin Biotech LLC, VYN7), and an anti-GAPDH mouse monoclonal antibody 157 (1:1,000, Santa Cruz, sc-166545) at 4°C overnight, followed by incubation of the HRP-conjugated 158 goat anti-rabbit IgG (H+L) (1:10.000. Invitrogen, A16096) or HRP-conjugated goat anti-mouse IgG 159 (H+L) (1:10,000, Invitrogen, A16066) for 1 h at room temperature. Chemiluminescent detection 160 was performed by using Pierce™ ECL Western blot Substrate (Thermo Scientific, 32106).

161 162 **RT-qPCR**

163 The OCLN mRNA level was determined after SARS-CoV-2 infection. The cellular RNA was 164 prepared and extracted with 1 mL TRIzol (Invitrogen, 15596026) according to the manufacturer's 165 instructions. RT-qPCR was performed by using Invitrogen™ SuperScript™ III Platinum™ SYBR™ 166 Green One-Step RT-qPCR Kit (Invitrogen, 11-736-051) according to the manufacturer's 167 instructions under the following conditions: reverse transcription (50°C for 5 min; 95°C for 2 min) 168 for one cycle; PCR (95°C for 3 s; 60°C for 30 s) for 40 cycles with a CFX96 Touch Real-Time PCR System (Bio-Rad). Primers targeting green monkey OCLN gene and human OCLN gene were 169 170 OCLN-F: GACTTCAGGCAGCCTCGTTAC; OCLN-R: monkev monkev 171 GCCAGTTGTGTGTGTCTGTTTCA; and human OCLN-F: ACTTCAGGCAGCCTCGTTAC; human 172 OCLN-R: GCCAGTTGTGTAGTCTGTCTCA. Primers for monkey β -actin, human ACE2 and 173 human 28S rRNA genes were used as described previously (5). Primers targeting green monkey 174 ACE2 gene were monkey ACE2-F: TGGGACTCTGCCATTTACTTAC; and monkey ACE2-R: 175 CCCAACTATCTCTCGCTTCATC. Primers (2019-nCoV_N2-F/2019-nCoV_N2-R) and probe 176 (2019-nCoV N2-P) targeting SARS-CoV-2 N were used as CDC recommended to detect viral RNA 177 (https://www.cdc.gov/coronavirus/2019-ncov/lab/rt-pcr-panel-primer-probes.html). RT-gPCR was 178 performed by using gScript® XLT One-Step RT-gPCR ToughMix® (Quantabio, 95132-02K) 179 according to the manufacturer's instructions under the following conditions with some 180 modifications: reverse transcription (50°C for 10 min; 95°C for 3 min) for one cycle; PCR (95°C for 181 3 s; 55°C for 30 s) for 45 cycles with a CFX96 Touch Real-Time PCR System (Bio-Rad). Relative 182 quantification was performed by the cycle threshold ($\Delta\Delta$ Ct) method.

183184 Co-immunoprecipitation

185 293T cells were co-transfected with pCAGGS-SARS-CoV-2-S1-HA, pCAGGS-hACE2-HA, and 186 pCAGGS-OCLN-flag, or pCAGGS empty vector using lipofectamine 3000 (Invitrogen, L3000075) 187 according to the manufacturer's instructions. Seventy-two hours posttransfection, the cells were 188 washed three times with cold PBS and lysed with Pierce™ IP Lysis Buffer (Thermo Scientific, 189 87787) on ice for 30 min. The supernatant was collected and mixed with 25 µl of pre-washed 190 Pierce[™] Protein G Magnetic Beads (Thermo Scientific, 88848) for 4 h at 4°C on a tube revolver 191 rotator (Thermo Scientific, 11676341). The beads were removed with a magnetic stand and an anti-192 HA antibody (Abcam, ab9110) was added to the supernatant and incubated overnight at 4°C. Pre-193 washed Protein G Magnetic Beads (25 µl) were added to the sample and incubated at 4°C for 4-6 194 h. After five times washing with cold TBST, the magnetic beads were mixed with the loading buffer 195 and boiled for 15 min to prepare the sample for SDS-PAGE.

196

197 GST pull-down assay

293T cells were transfected with the pCAGGS-S1-His plasmid. At 60 h post-transfection, cells and
supernatant were collected, and S1 protein was purified with a His tag by using ProBond
Purification System (ThermoFisher, K850-01). pCold-GST-hOCLN and pCold-GST empty plasmids

201 were transformed into E. coli BL21 (DE3) competent cells and induced with IPTG, respectively. 202 GST and GST-tagged hOCLN were purified by glutathione agarose according to the manufacturer's 203 instructions. In brief, IPTG-induced bacteria cultures were harvested and resuspended with cold 204 PBS, followed by mild sonication on ice. The supernatant containing soluble proteins were collected 205 after centrifugation at 12.000 x q for 30 min, then mixed with the resin and incubated for 4 h at 4°C 206 with purified SARS-CoV-2 S1 protein. The resin was washed five times with cold PBS and 207 incubated at 4°C for 4 h with the lysates of the HEK293T cells transfected with pCAGGS-S1-His. 208 After five times washing with cold PBS, the bound proteins were detected by western blot by using 209 a mouse anti-His tag monoclonal antibody (1:1,000) and a GST Tag monoclonal antibody (1:1,000).

210

211 Pharmacological inhibitors

212 Vero-E6 cells were infected with rVSV-eGFP-S virus at an MOI of 0.01 for 1 h at 37°C. Then, the 213 cells were washed three times with PBS, and the medium for the plaque assay containing 50 nM 214 Bafilomycin (Baf-A1, Abcam, ab120497) or 5 µM Cathepsin L inhibitor III (Sigma, 219427-5mg) 215 was overlaid onto the cells, respectively. After 48 h of incubation, the GFP signal was observed, 216 and images were acquired with the EVOS™ M5000 imaging system. For virus entry assay, Vero-217 E6 cells were pre-treated with EIPA or rottlerin at 50 μ M and 10 μ M, respectively at 37°C for 1 h, 218 then infected with SARS-CoV-2 at an MOI of 1 at 4°C for 1 h. The infected cells were washed three 219 times with cold PBS to remove unbound viruses. The plate was transferred to 37°C for 1 h to allow 220 virus entry. The bound viruses were then removed by washing three times with acidic buffer (50 221 mM glycine, 100 mM NaCl, pH 3.0), and trypsinized to remove SARS-CoV-2. Viral RNA was 222 detected by RT-qPCR targeting the N gene after RNA was extracted with 1 ml TRIzol. 223

224 Statistical analysis

Data were analyzed by using a Student's t test, and values are indicated with mean \pm SD. All data are representative of at least three independent experiments. Data analysis was performed with the GraphPad PRISM 9 software (ns, p > 0.05; ****p < 0.0001; ***p < 0.001; **p < 0.01; *p < 0.05).

228

229

231 Supplemental Figures



232

Fig. S1. OCLN knockdown has no effect on ACE2 expression. (*A*) Vero-E6 cells were transfected with two OCLN-specific siRNAs for 72 h, and IFA was performed to detect OCLN, ZO-1 and Claudin-1 expression (scale bars, 150 µm). (*B*) RT-qPCR was used to determine OCLN and ACE2 mRNA level after siRNAs treatment for 72 h. The results were representative of three independent experiments. (*C*) Western blot was used to determine OCLN and ACE2 expression after siRNAs treatment for 72 h.







Fig. S2. ACE2 knockdown by ACE2-specific siRNA. (*A*) RT-qPCR was used to determine ACE2 knockdown after siRNA transfection in Vero-E6 cells and A549-hACE2 cells for 72 h. The results were representative of three independent experiments. (*B*) ACE2 knockdown in A549-hACE2 cells was determined by western blot.

245



Fig. S3. Generation of Vero-E6 OCLN KO cell line. (*A*) OCLN expression was detected by IFA and (*B*) OCLN KO cells were confirmed by western blot by using an OCLN antibody. Wild type Vero-E6 was used as a positive control (scale bars, 150 µm). (*C*) Wild-type Vero-E6, wild-type Vero-E6 cells transfected with OCLN siRNA#1, and OCLN KO Vero-E6 cells were infected with SARS-CoV-2-mNG virus at an MOI of 0.01. At 24 h postinfection, imagines were captured (scale bars, 150 µm) and (*D*) Ten different fields for each group were captured and GFP-positive cells were analyzed with ImageJ software.

255



Fig. S4. OCLN polyclonal antibody blocking assay. Vero-E6 cells were incubated with BSA or an OCLN polyclonal antibody at indicated concentrations at 37°C for 1 h. Then, cells were infected with SARS-CoV-2 at an MOI of 0.001, and plaque assays were performed. Plaque number and plaque size were determined 72 h postinfection. The results were representative of three 260 261 262 independent experiments.



273

274

Fig. S5. Expression of mOCLN in Vero-E6 OCLN KO cells increases SARS-CoV-2 cell-to-cell 266 transmission and internalization. (A) mOCLN was transfected to Vero-E6 OCLN KO cells and 267 its expression production was detected by IFA with an anti-Flag antibody (scale bars, 150 µm). (B) 268 Plaque assays were used to determine the effect of mOLCN expression on virus spread by 269 measuring (C) plaque size and plaque number. (D) Virus internalization and virus binding were 270 determined by RT-qPCR after mOCLN expression. The results were representative of three 271 independent experiments. 272

Supplementary References

- 275 M. C. Johnson et al., Optimized Pseudotyping Conditions for the SARS-COV-2 Spike 1. 276 Glycoprotein. J Virol 94 (2020).
- 277 X. Xie et al., An infectious cDNA clone of SARS-CoV-2. Cell host & microbe 27, 841-848. 2. 278 e843 (2020).
- 279 3. J. B. Case et al., Neutralizing antibody and soluble ACE2 inhibition of a replication-280 competent VSV-SARS-CoV-2 and a clinical isolate of SARS-CoV-2. Cell host & microbe 281 28, 475-485. e475 (2020).
- 282 S. Liu et al., The second extracellular loop dictates Occludin-mediated HCV entry. 4. 283 Virology 407, 160-170 (2010).
- 284 5. J. Wang et al., SARS-CoV-2 uses metabotropic glutamate receptor subtype 2 as an 285 internalization factor to infect cells. Cell discovery 7, 1-16 (2021).
- 286