# Science Translational Medicine

### Supplementary Materials for

## S-217622, a SARS-CoV-2 main protease inhibitor, decreases viral load and ameliorates COVID-19 severity in hamsters

Michihito Sasaki et al.

Corresponding author: Michihito Sasaki, m-sasaki@czc.hokudai.ac.jp; Hirofumi Sawa, h-sawa@czc.hokudai.ac.jp

*Sci. Transl. Med.* **0**, eabq4064 (2022) DOI: 10.1126/scitranslmed.abq4064

#### The PDF file includes:

Materials and Methods Figs. S1 to S7 Table S1

#### Other Supplementary Material for this manuscript includes the following:

Movies S1 to S3 Data file S1 MDAR Reproducibility Checklist

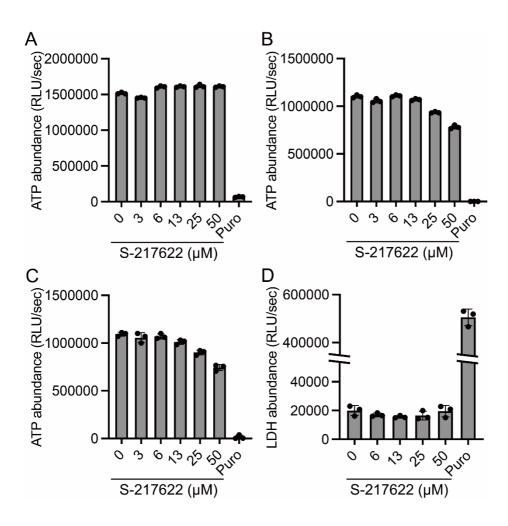
#### **Supplementary Materials and Methods**

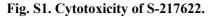
#### Compound cytotoxicity assay

Cells were treated with S-217622 serially diluted in 2-fold increments by culture medium containing 2% fetal bovine serum (FBS). After a 3 day culture, cell toxicity was evaluated by measurement of ATP in live cells with CellTiter-Glo 2.0 reagent (Promega) or lactate dehydrogenase (LDH) released from dead cells in the basal medium with LDH-Glo Cytotoxicity Assay kit (Promega). Luminescence was detected on a luminometer (GloMax-Multi detection system, Promega).

#### Biosensor assay for viral protease activity

The DNA fragments encoding NSP3 or NSP4, NSP5, N-terminal NSP6 (NSP4/5/6N) of SARS-CoV-2 WK-521 strain (lineage A) were cloned into pCMV-derivative pCXSN vector to generate pSARS-CoV-2 papain-like protease (PL<sup>pro</sup>) and pSARS-CoV-2 main protease (M<sup>pro</sup>), respectively. The amino acid sequence AVLQS (for the cleavage by M<sup>pro</sup>) or RLKGG (for the cleavage by PL<sup>pro</sup>) were replaced into pGloSensor-30F vector backbone (CS182101, Promega) to generate firefly luciferase-based biosensor expressing plasmid pGS-AVLQS or pGS-RLKGG, respectively. 293T cells on 96-well plate were co-transfected with a set of pGS-AVLQS and pSARS-CoV-2 M<sup>pro</sup> or a set of pGS-RLKGG and pSARS-CoV-2 PL<sup>pro</sup> using TranIT-LT1 (Mirus Bio) in the presence of serial diluted S-217622. At 24 hours post-transfection, the luminescence signals of biosensors and renilla luciferase (an internal control reporter) from pGS vectors were measured by Dual-Glo Luciferase Assay System (Promega). The ratio (firefly luciferase:renilla luciferase) was calculated to normalize for the influence of transfection efficiency. Non-treated cells were used as a control for 100% biosensor activation.





(A to D) Calu-3 cells (A), Vero-TMPRSS2 cells (B), Vero-TMPRSS2 cells with CP-100356 at 1  $\mu$ M (C), and primary human bronchial epithelial cells (D) were treated with S-217622 for 3 days. Cell toxicity was evaluated by measurement of ATP in live cells (A to C) or LDH released from dead cells in the basal medium (D). Puromycin (puro) was used as a control compound to mediate cell toxicity. The values shown are mean  $\pm$  SD of triplicate samples. RLU, relative light units.

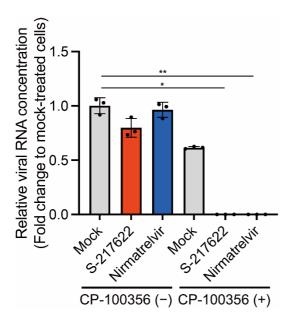
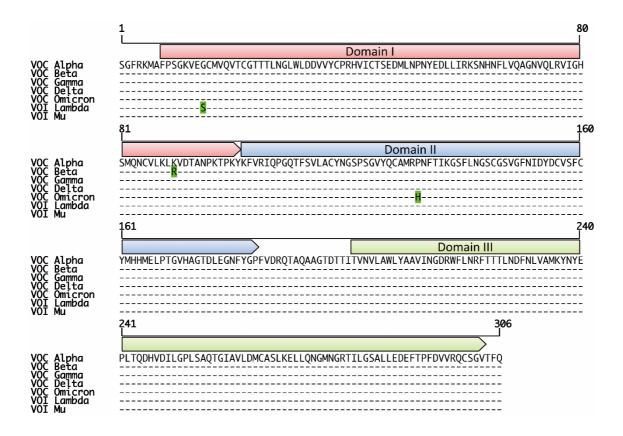


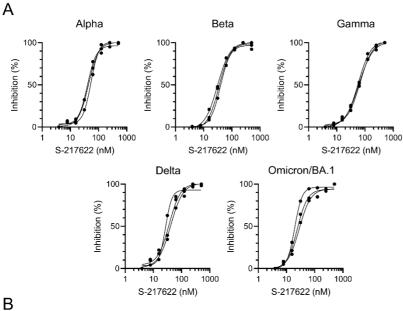
Fig. S2. Antiviral activity of SARS-CoV-2 main protease inhibitors in the presence of a P-glycoprotein (P-gp) inhibitor.

Vero-TMPRSS2 cells were infected with SARS-CoV-2 Delta variant at a multiplicity of infection (MOI) of 0.01 and treated with S-217622 at 100 nM or nirmatrelvir at 300 nM for 24 hours in the absence or presence of the P-gp inhibitor, CP-100356 at 1  $\mu$ M. The inhibitory effect of each treatment was evaluated by measurement of intracellular viral RNA concentration at 24 hours post infection (hpi). The values shown are mean  $\pm$  SD of triplicate samples. \*p<0.05, \*\*p<0.01 by Kruskal-Wallis test with Dunn's test.



## Fig. S3. Multiple amino acid sequence alignments of M<sup>pro</sup> from SARS-CoV-2 variants of concern (VOCs) and variants of interest (VOIs).

Multiple sequence alignment based on the entire length of M<sup>pro</sup> from the VOCs Alpha (lineage B.1.1.7, GISAID: EPI\_ISL\_768526), Beta (lineage B.1.351, GISAID: EPI\_ISL\_1123289), Gamma (lineage P.1, GISAID: EPI\_ISL\_877769), Delta (lineage B.1.617.2, GISAID: EPI\_ISL\_2158617), and Omicron (lineage BA.2.75, GISAID: EPI\_ISL\_14011362), as well as the VOIs Lambda (lineage C.37, GISAID: EPI\_ISL\_4204973), and Mu (lineage B.1.612, GISAID: EPI\_ISL\_4470503). Dashes (-) represent amino acids identical to M<sup>pro</sup> of Alpha. Amino acids different from the consensus are colored in green.



|                   |                | EC <sub>50</sub> |          |          | CC <sub>50</sub> |        |
|-------------------|----------------|------------------|----------|----------|------------------|--------|
|                   | Alpha          | Beta             | Gamma    | Delta    | Omicron<br>/BA.1 |        |
| S-217622 (nM)     | $46.0 \pm 5.5$ | $35.1 \pm 3.5$   | 61.7±3.9 | 34.8±5.9 | 23.9±3.6         | >50000 |
| REGN10933 (ng/ml) | 16.9±2.9       | >1000            | >1000    | 6.3±1.8  | >1000            | >1000  |
| REGN10987 (ng/ml) | 3.7±0.3        | 3.4±0.8          | 8.4±1.8  | 8.6±3.9  | >1000            | >1000  |

#### Fig. S4. Antiviral potency of S-217622 against SARS-CoV-2 VOCs.

Cytopathic effect (CPE) in 293T-hACE2-TMPRSS2 cells induced by SARS-CoV-2 infection was measured at 3 dpi by 3-[4,5-dimethyl-2-thiazolyl]-2,5-diphenyl-2H-tetrazolium bromide (MTT) assay. (A) The inhibitory effect of S-217622 on SARS-CoV-2 VOCs was examined. Uninfected cells were used as a control for 100% inhibition. (B) The 50% effective concentration (EC<sub>50</sub>) and cytotoxic concentration (CC50) of S-217622 and anti-SARS-CoV-2 neutralizing monoclonal antibodies (REGN10933 and REGN10987) are shown.

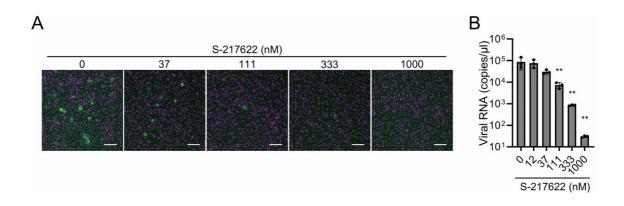
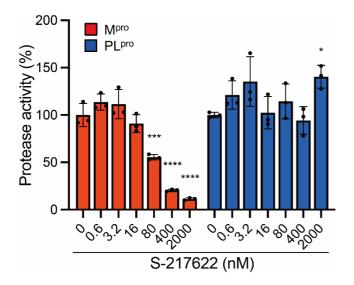


Fig. S5. Susceptibility of the SARS-CoV-2 Omicron variant to treatment with S-217622.

(A) Immunofluorescence staining is shown of Vero-TMPRSS2 cells infected with the SARS-CoV-2 Omicron variant BA.1. Cells were inoculated with the SARS-CoV-2 Omicron variant at an MOI of 0.1 and then cultured in the presence of S-217622 for 24 hours. Cells were stained with anti-SARS-CoV-2 nucleocapsid antibody (green) and Hoechst 33342 (magenta). Scale bars, 100  $\mu$ m. (B) Viral RNA concentrations were measured in the culture supernatant of Vero-TMPRSS2 at 24 hpi with the SARS-CoV-2 Omicron variant at an MOI of 0.01. The values shown are mean  $\pm$  SD of triplicate samples. \*\*p<0.01 by one-way ANOVA with Dunnet's test.





293T cells were co-transfected with expression plasmids of SARS-CoV-2 M<sup>pro</sup> and a biosensor for SARS-CoV-2 M<sup>pro</sup> and maintained in the presence of S-217622. The luminescence signal from the biosensor was measured as the protease activity at 24 hours post transfection. 293T cells expressing SARS-CoV-2 PL<sup>pro</sup> and another biosensor for PL<sup>pro</sup> were used as a control for the target specificity of S-217622. The values shown are mean  $\pm$  SD of triplicate samples. \*p<0.05, \*\*\*p<0.001, \*\*\*\*p<0.0001 by one-way ANOVA with Dunnett's test.

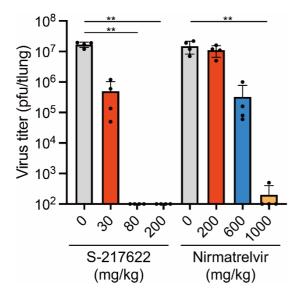


Fig. S7. In vivo antiviral efficacy of SARS-CoV-2 main protease inhibitors.

Hamsters were intranasally inoculated with 5,000 plaque-forming units (pfu) of the SARS-CoV-2 Delta variant. The hamsters were treated with oral administration of S-217622 or nirmatrelvir twice daily (b.i.d.) from the time of infection (0 hpi) for prophylactic treatment (n=4 for each treatment). Virus titers in lungs from hamsters at 4 dpi were determined by plaque assay. The values shown are mean  $\pm$  SD. \*\*p<0.01 by Kruskal-Wallis test with Dunn's test.

|                                     | S-217622 in plasma |                 |                 |  |
|-------------------------------------|--------------------|-----------------|-----------------|--|
|                                     | 10 mg/kg           | 30 mg/kg        | 100 mg/kg       |  |
| C <sub>max</sub> (μM)               | 12.7±2.2           | $61.6 \pm 18.7$ | $254 \pm 24$    |  |
| T <sub>max</sub> (h)                | $0.5 \pm 0.0$      | $1.17 \pm 0.76$ | $2.67 \pm 1.15$ |  |
| t <sub>1/2,z</sub> (h) <sup>a</sup> | $4.46 \pm 1.03$    | $3.96 \pm 0.74$ | $3.43 \pm 0.13$ |  |
| AUC₀₋₂ଃհ (µM⋅h)                     | 78.3±11.0          | 415±52          | $2480 \pm 350$  |  |
| AUC₀ <sub>-inf</sub> (µM⋅h)         | $79.3 \pm 10.5$    | 417±51          | $2500 \pm 350$  |  |

Table S1. Pharmacokinetic parameters of S-217622 in plasma after a single oral administrationof S-217622 in hamsters.

a: t<sub>1/2, 8-28hr</sub>

 $C_{max}$ , maximum concentration;  $T_{max}$ , time to peak drug concentration;  $t_{1/2}$ , half-life; AUC, area under the curve.

**Movie S1. Reconstructed 3D image of viral antigen distribution in the lung of a vehicle-treated hamster at 4 dpi**. The hamster was inoculated with SARS-CoV-2 Delta variant and treated with 0.5% methyl cellulose solution (vehicle for S-217622) from 1 dpi to 3 dpi. Related to Fig. 5E.

Movie S2. Reconstructed 3D image of viral antigen distribution in the lung of a S-217622-treated hamster at 4 dpi. The hamster was inoculated with SARS-CoV-2 Delta variant and treated with S-217622 (200 mg/kg) from 1 dpi to 3 dpi. Related to Fig. 5F.

**Movie S3. Reconstructed 3D image of viral antigen distribution in the lung of a MPV-treated hamster at 4 dpi.** The hamster was inoculated with SARS-CoV-2 Delta variant and treated with MPV (200 mg/kg) from 1 dpi to 3 dpi. Related to Fig. 5G.

Data file S1. Raw, individual-level data for all experiments.