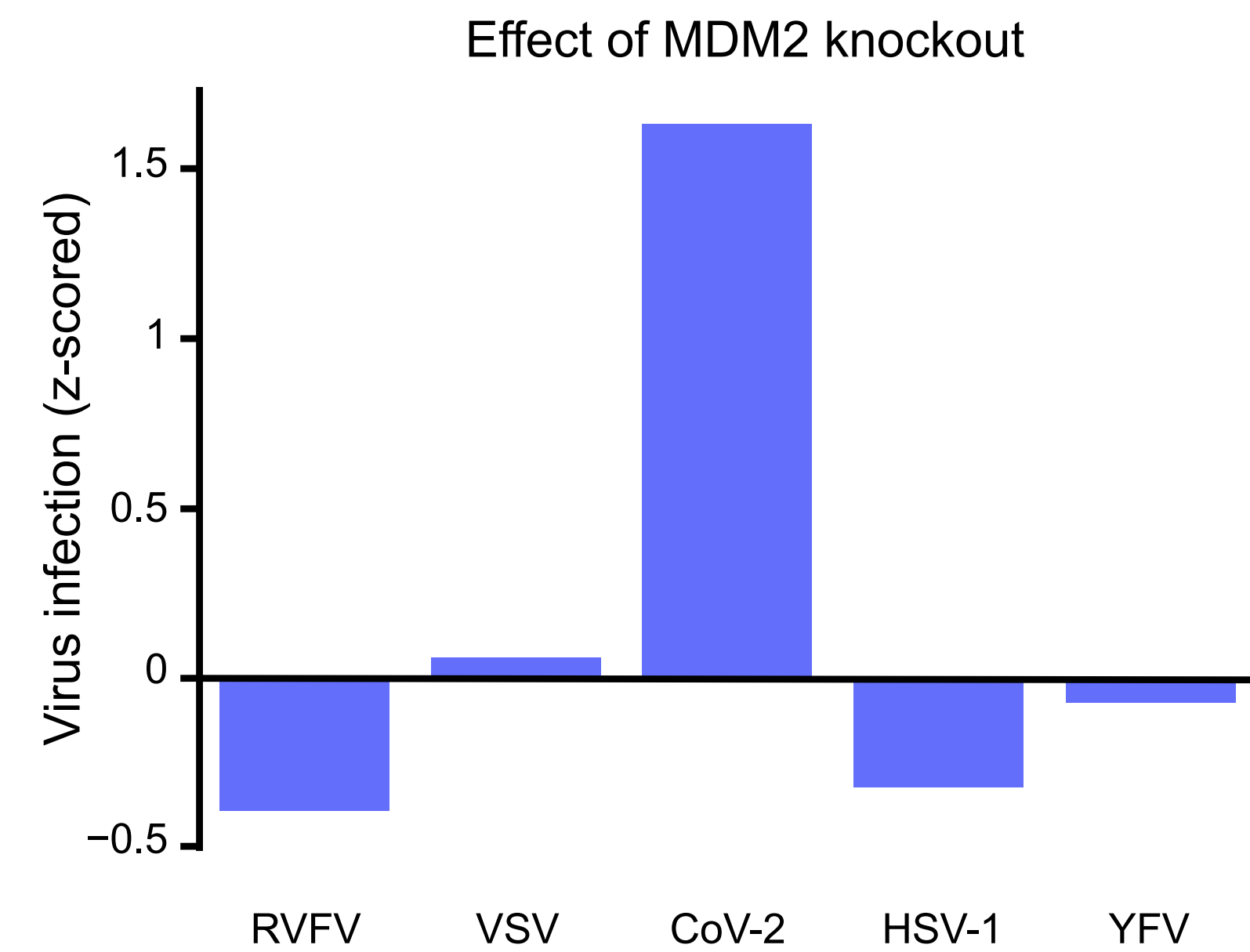
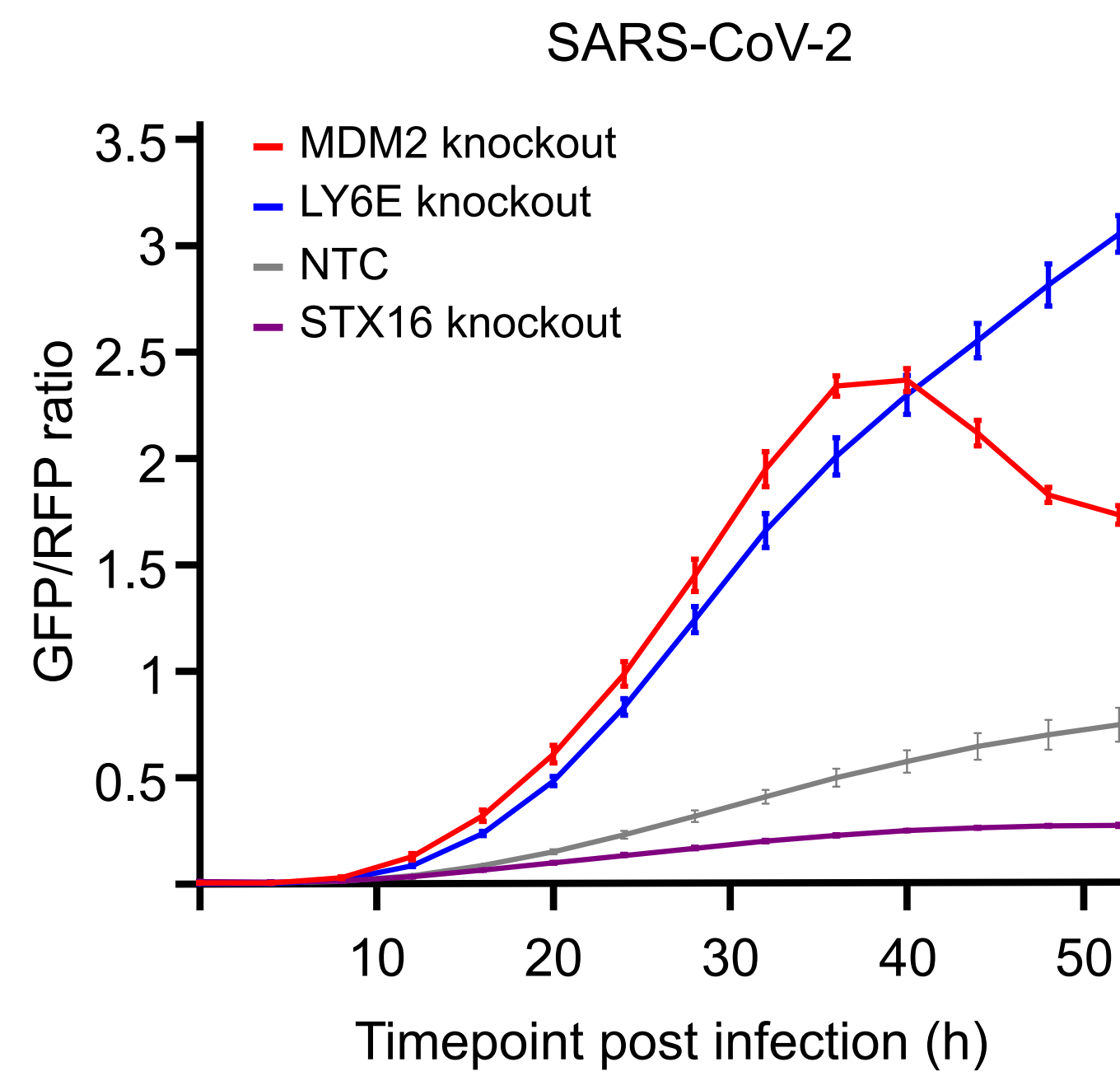


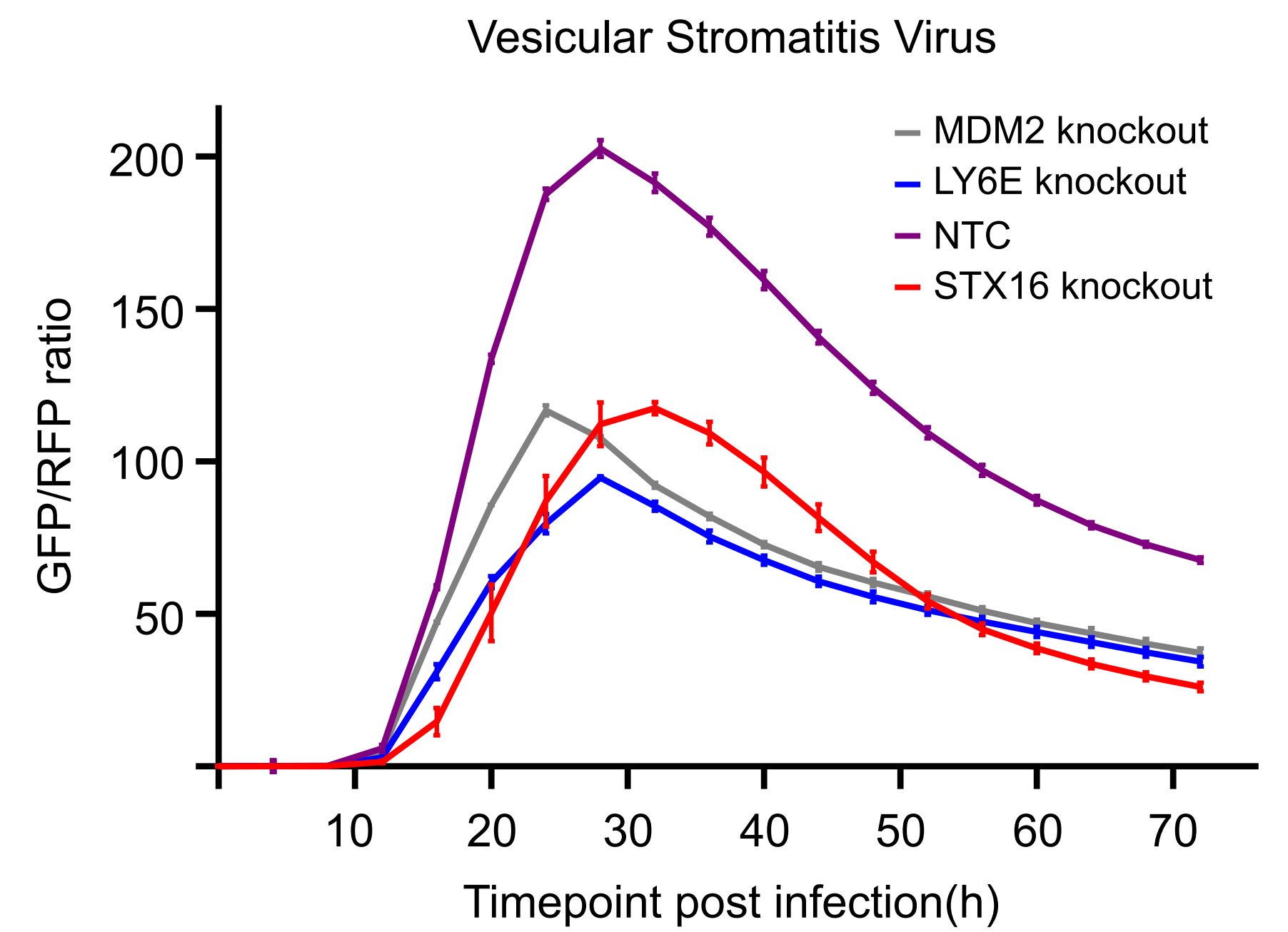
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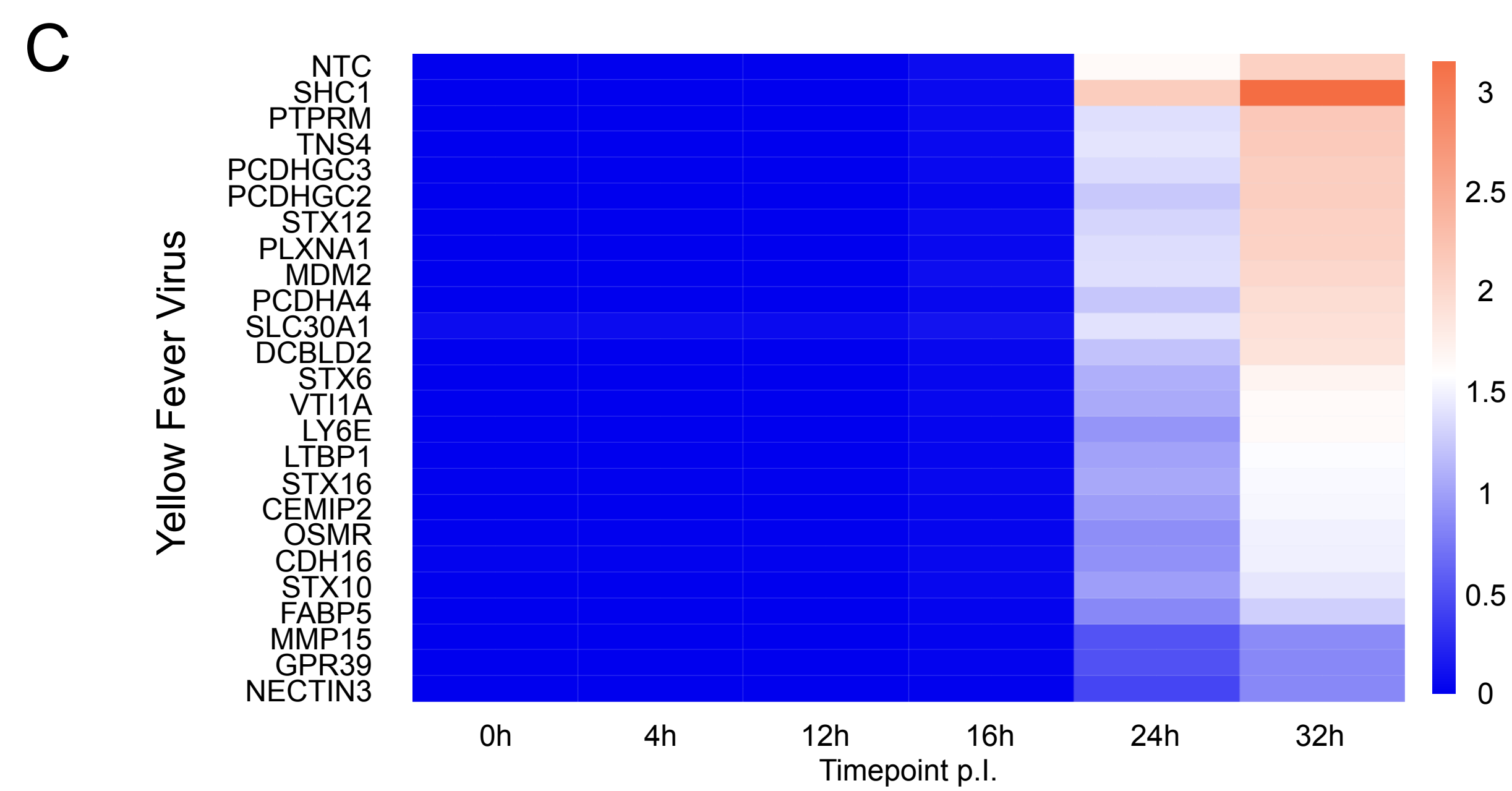
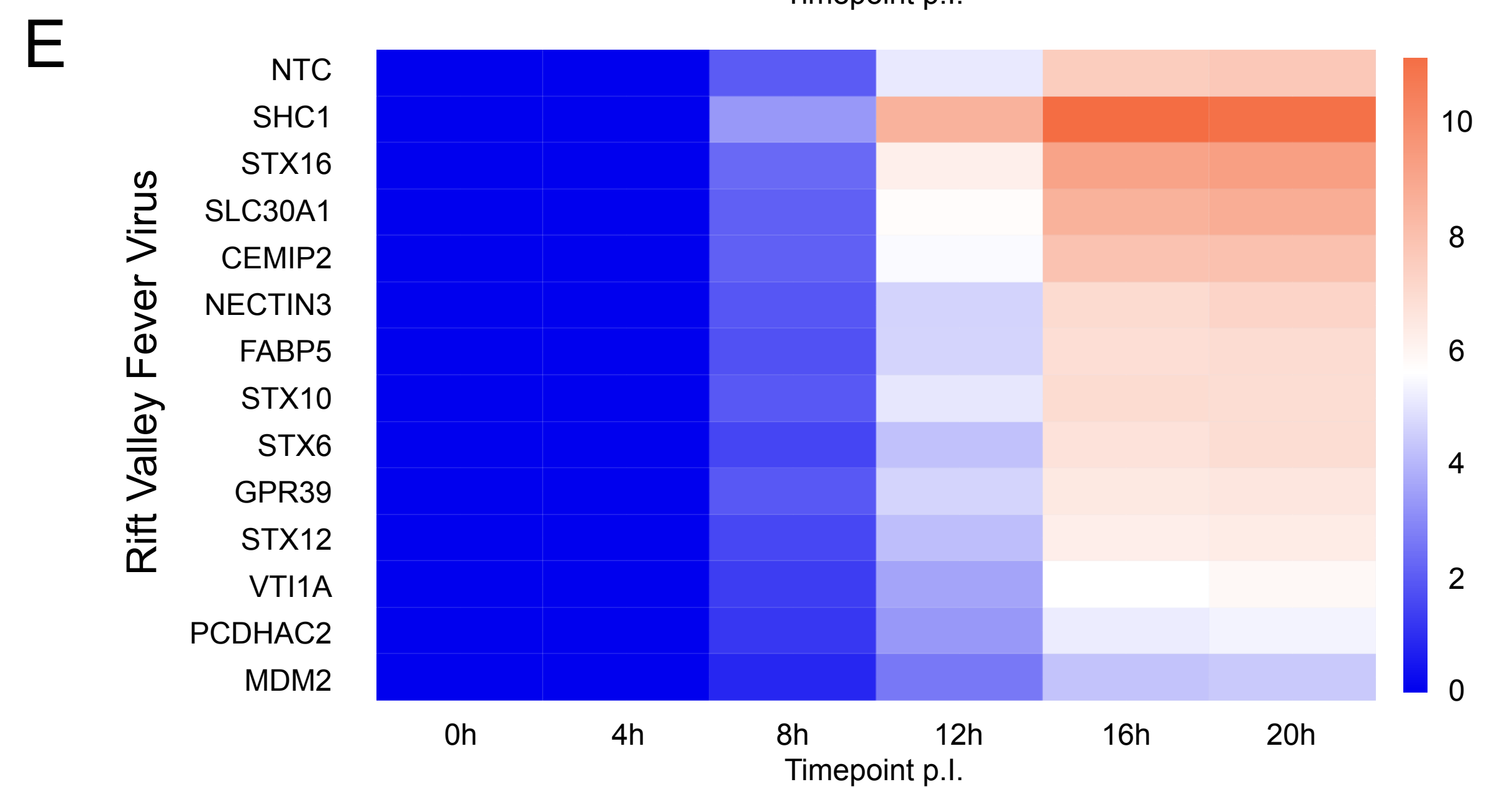
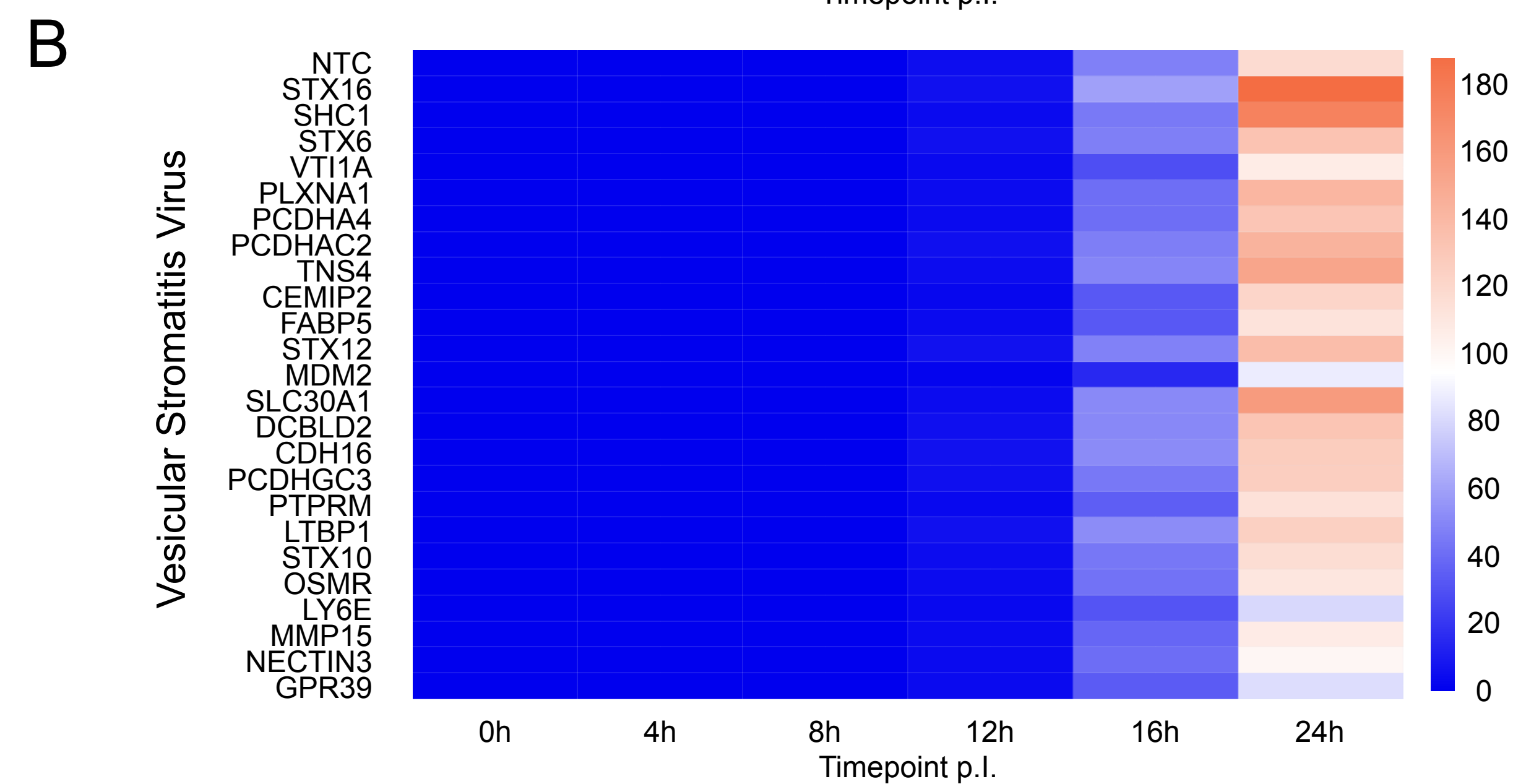
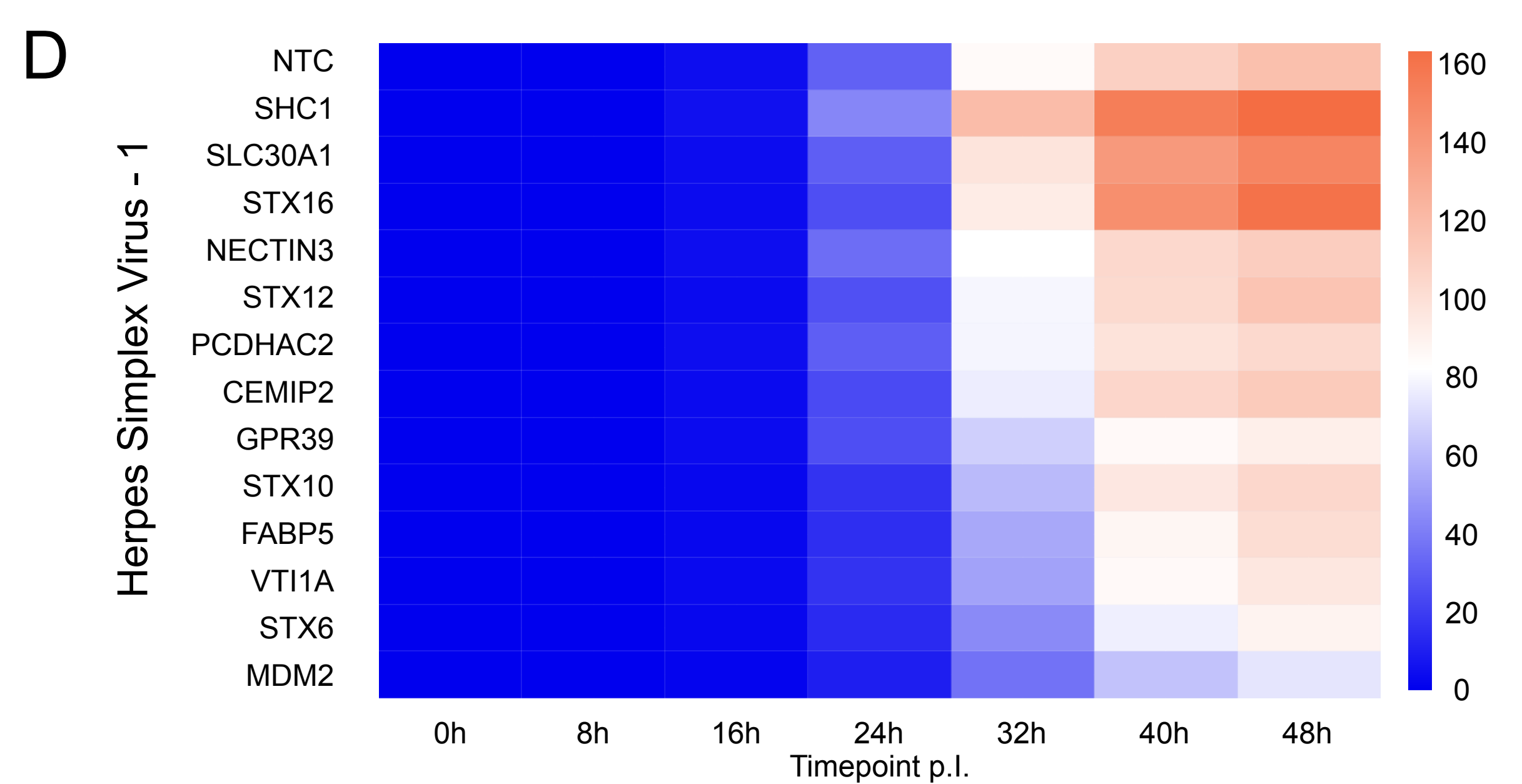
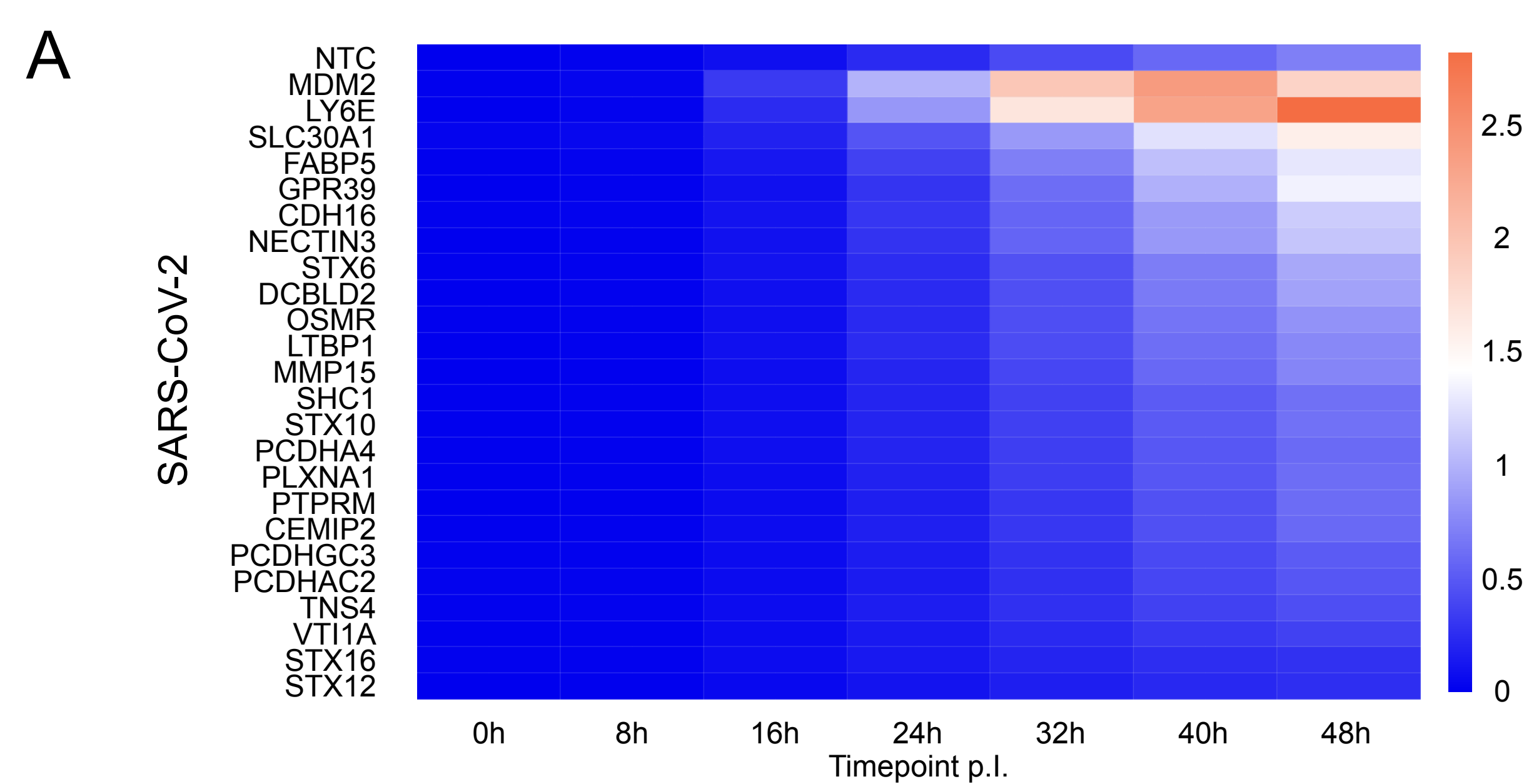
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C

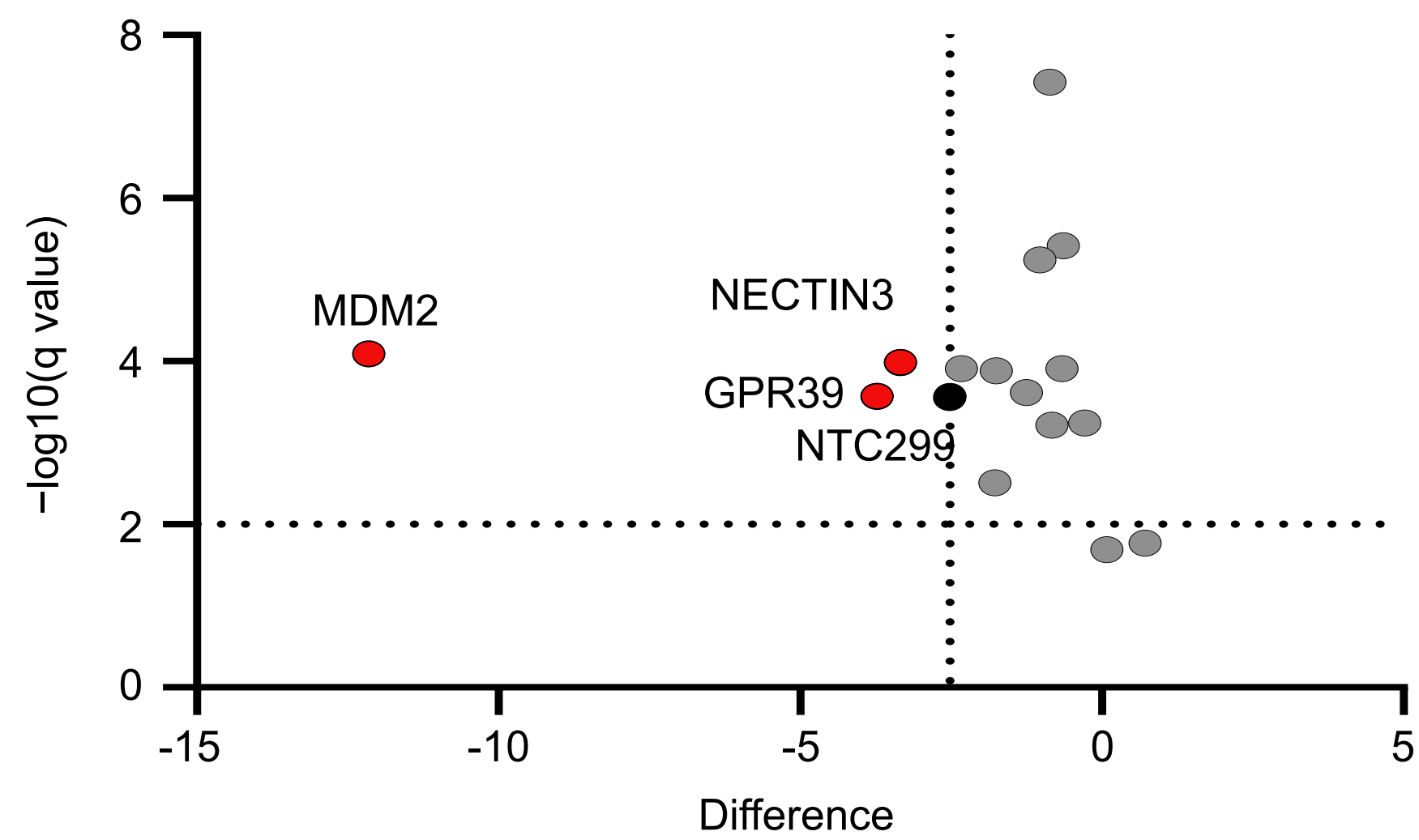


Supplementary Figure S1. Comparison of MDM2 knockout phenotype. (A) Related to Figure 1 - graph shows the z-score of the mean of the maximal infection value (integrated intensity GFP/mRFP ratio) for SARS-CoV-2, VSV, YFV, HSV-1, and RVFV of MDM2 knockout cells. (B-C) The indicated knockout cells or controls (NTC) were infected with SARS-CoV-2-GFP or VSV-GFP reporter viruses, and infection kinetics were measured. The virus signal (GFP integrated intensity) was normalized to the cell signal (mRFP integrated intensity) (mean +/- SD, n = 3).

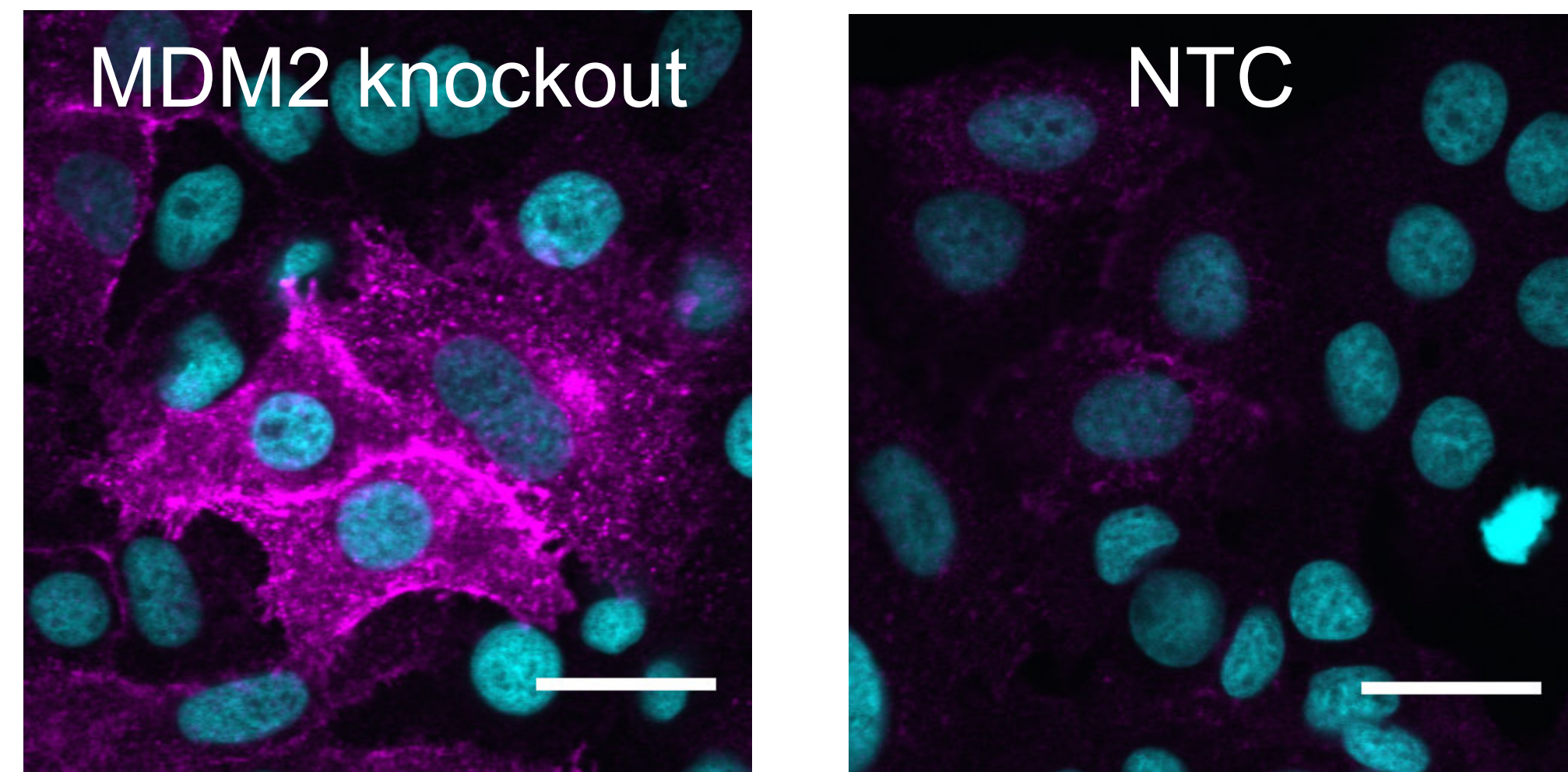


Supplementary Figure S2. Comparative virus growth in candidate knockout cell lines. Related to Figure 1 - The indicated A549-H2B-mRFP-ACE2 knockout cells were infected with (A) SARS-CoV-2-GFP (MOI 3), (B) Vesicular Stomatitis Virus (MOI 0.01), (C) Yellow Fever Virus (MOI 0.1), (D) Herpes Simplex Virus 1 (MOI 0.1), (E) Rift Valley Fever Virus (MOI 0.1). Heatmaps show the average signal (GFP/RFP) in relation to time post-infection.

A

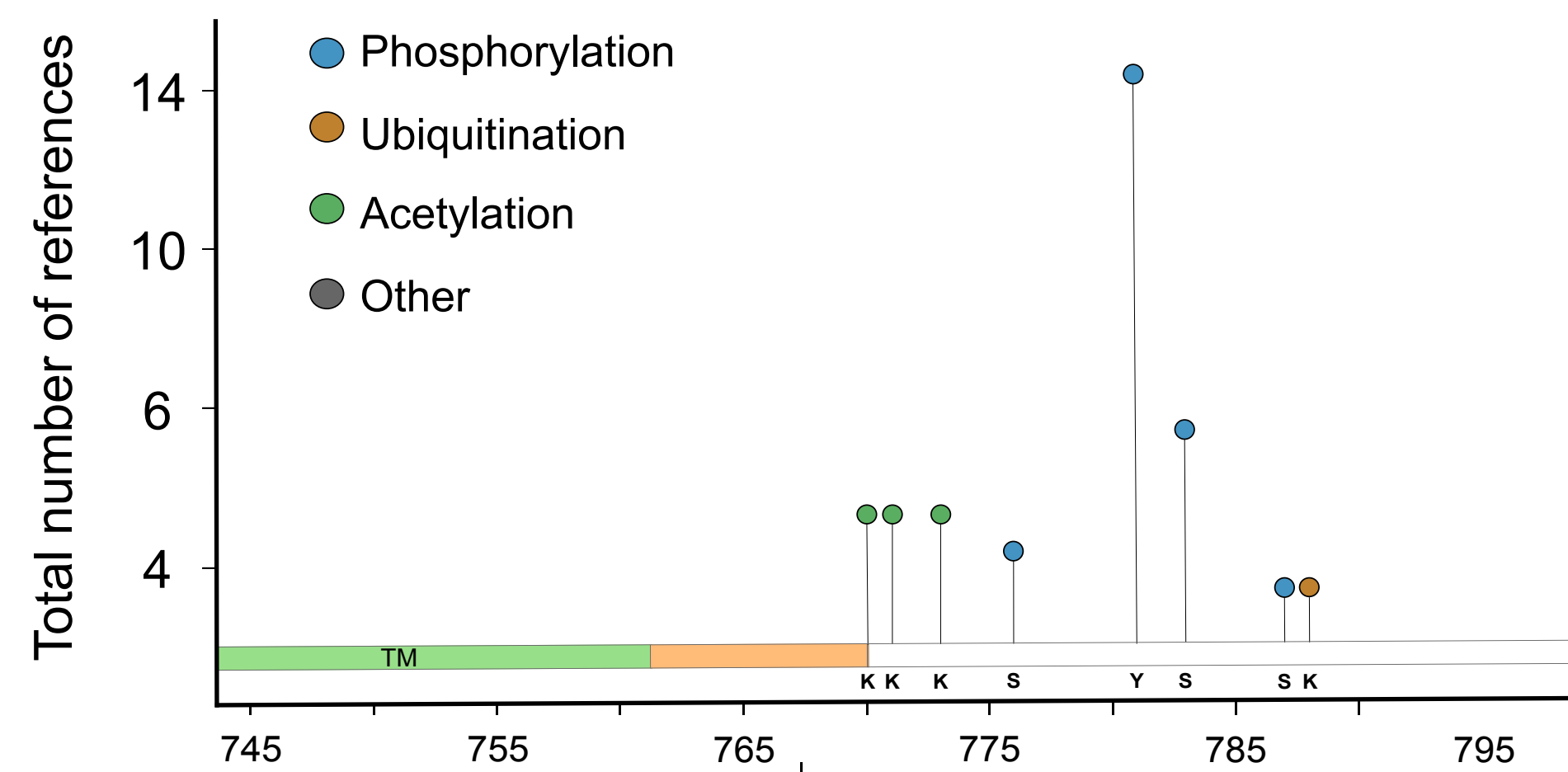


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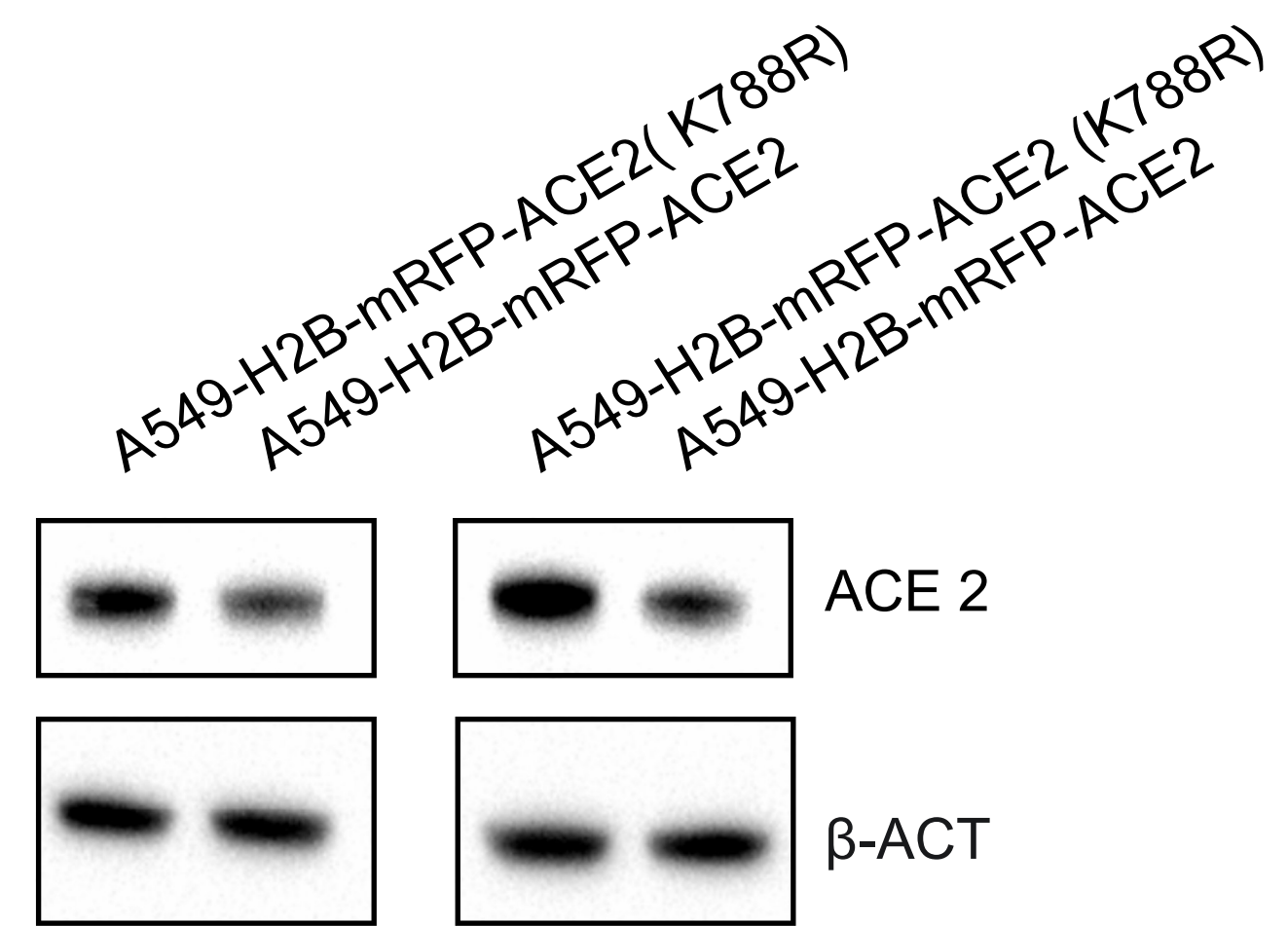


Supplementary Figure S3. MDM2 knockout increases SARS-CoV-2 RNA abundance in selected knockout cells and ACE2 protein levels (A) Difference in $-\Delta\Delta C_t$ SARS-CoV-2 N RNA levels between 12 h to 24 h and corresponding q-value. The knockout cells that allowed a higher increase in transcript level as compared to the NTC are depicted in red (mean \pm SD, $n = 3$). (B) Representative confocal images of A549-H2B-mRFP-ACE2 MDM2 knockout (MDM2 KO) or control cells (NTC). ACE2 (magenta), nuclei (cyan). Scale bar equals 25 μm .

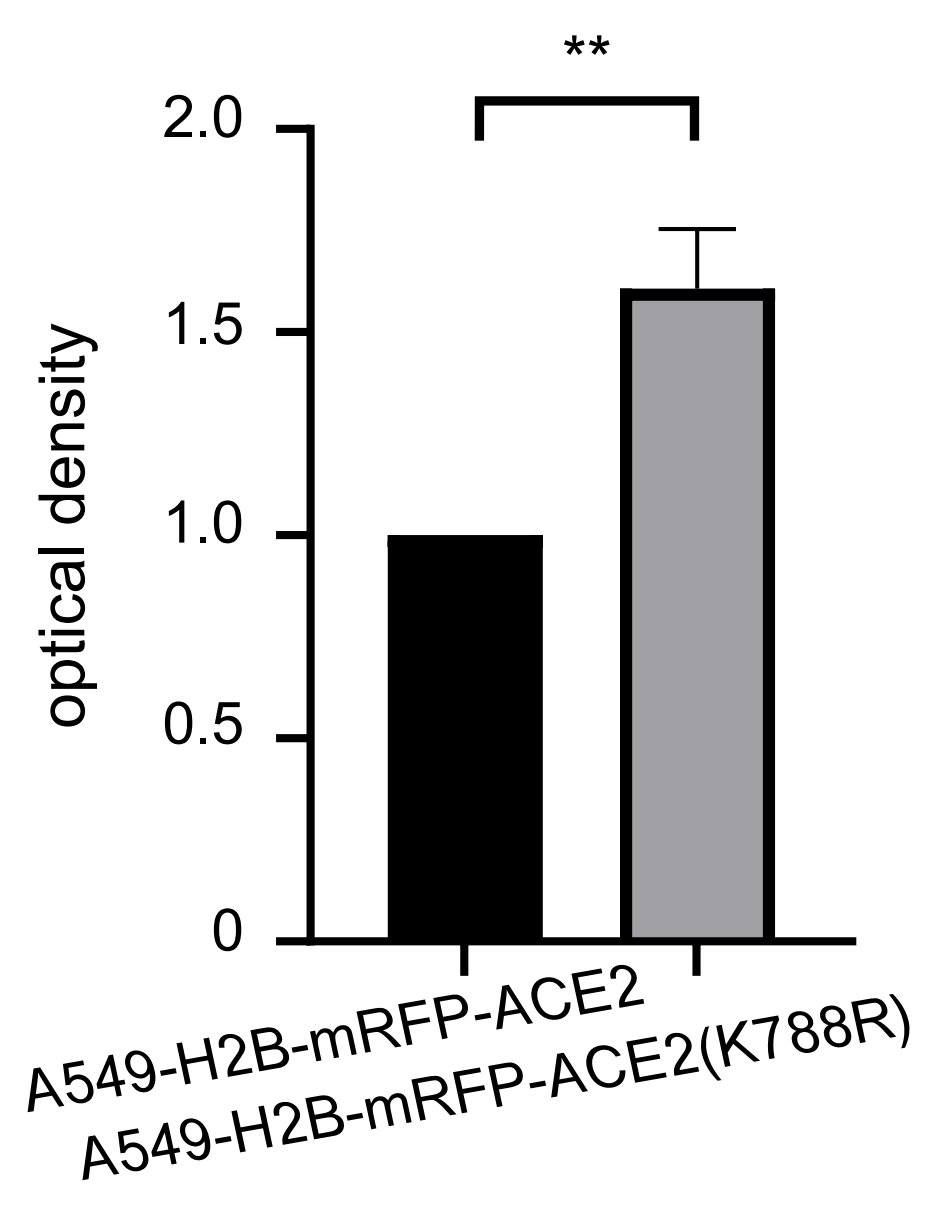
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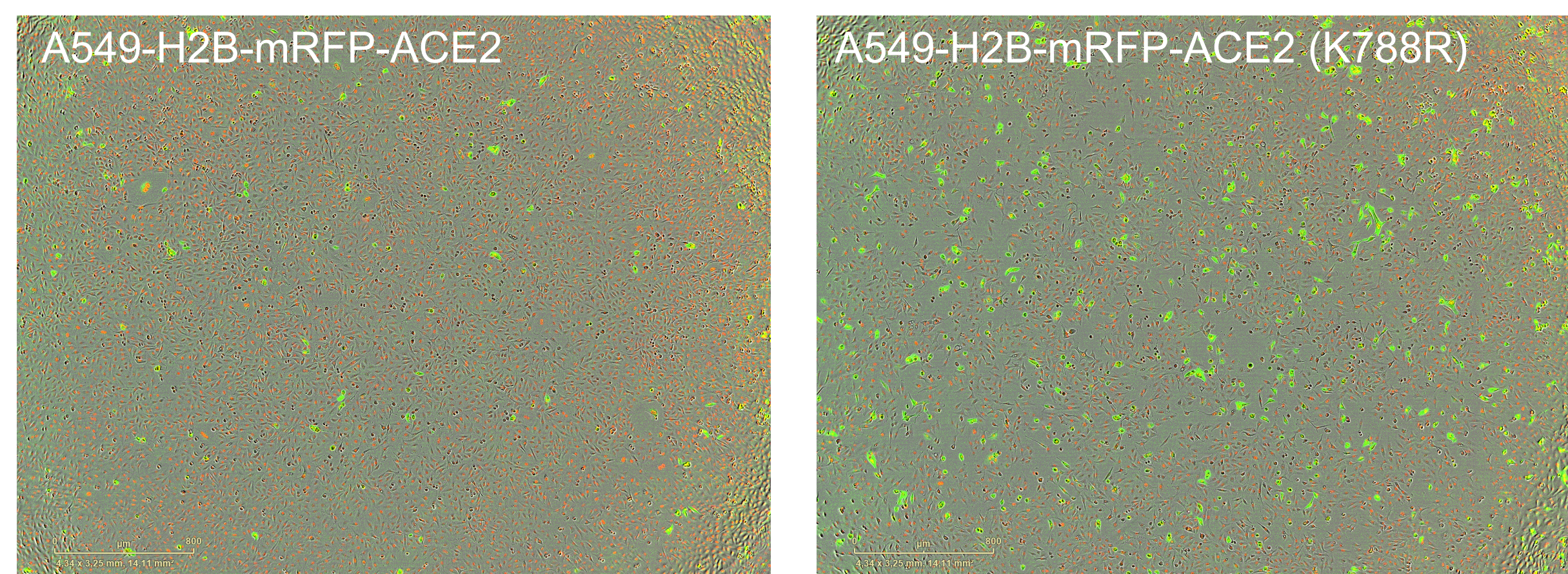
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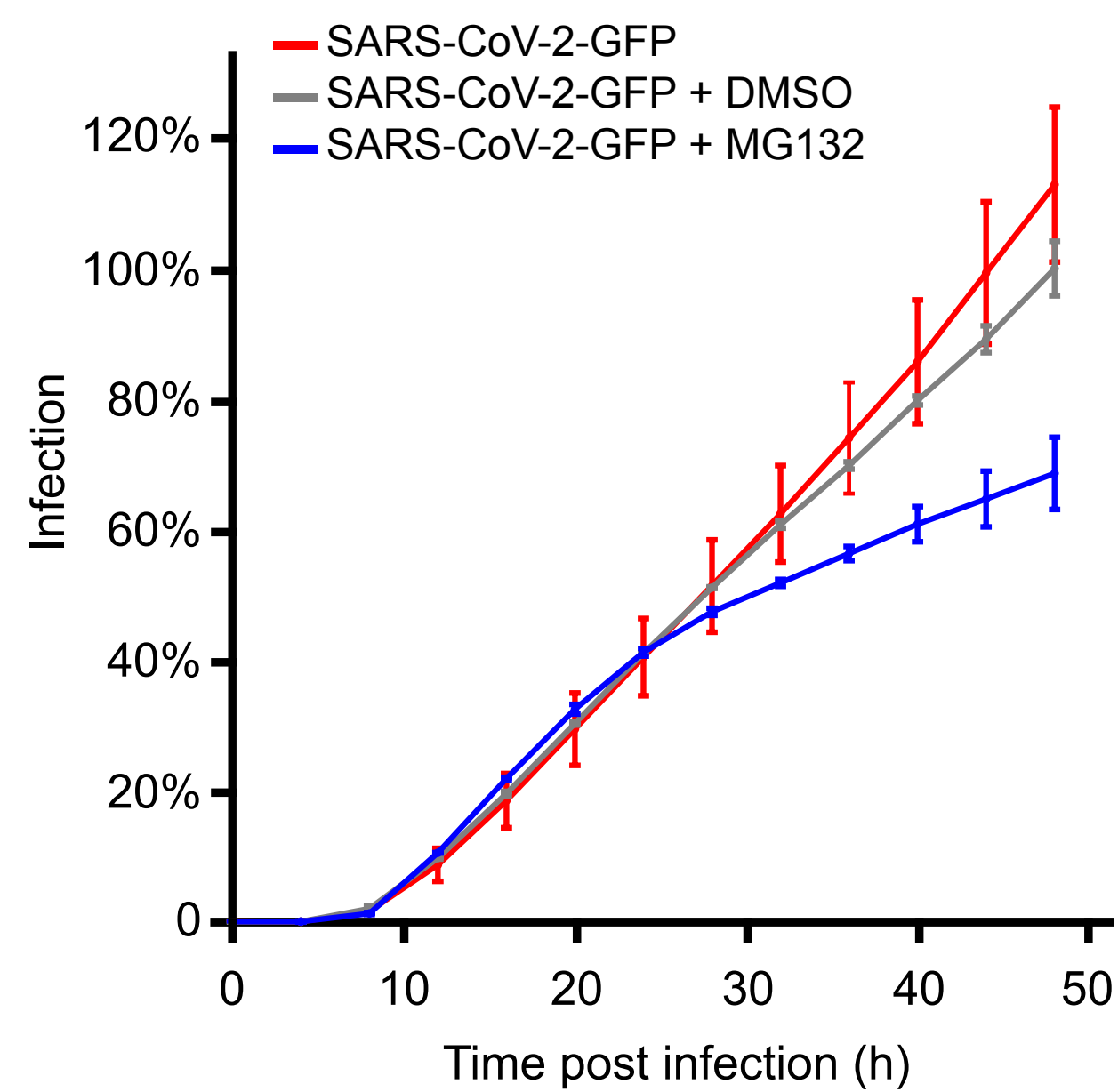
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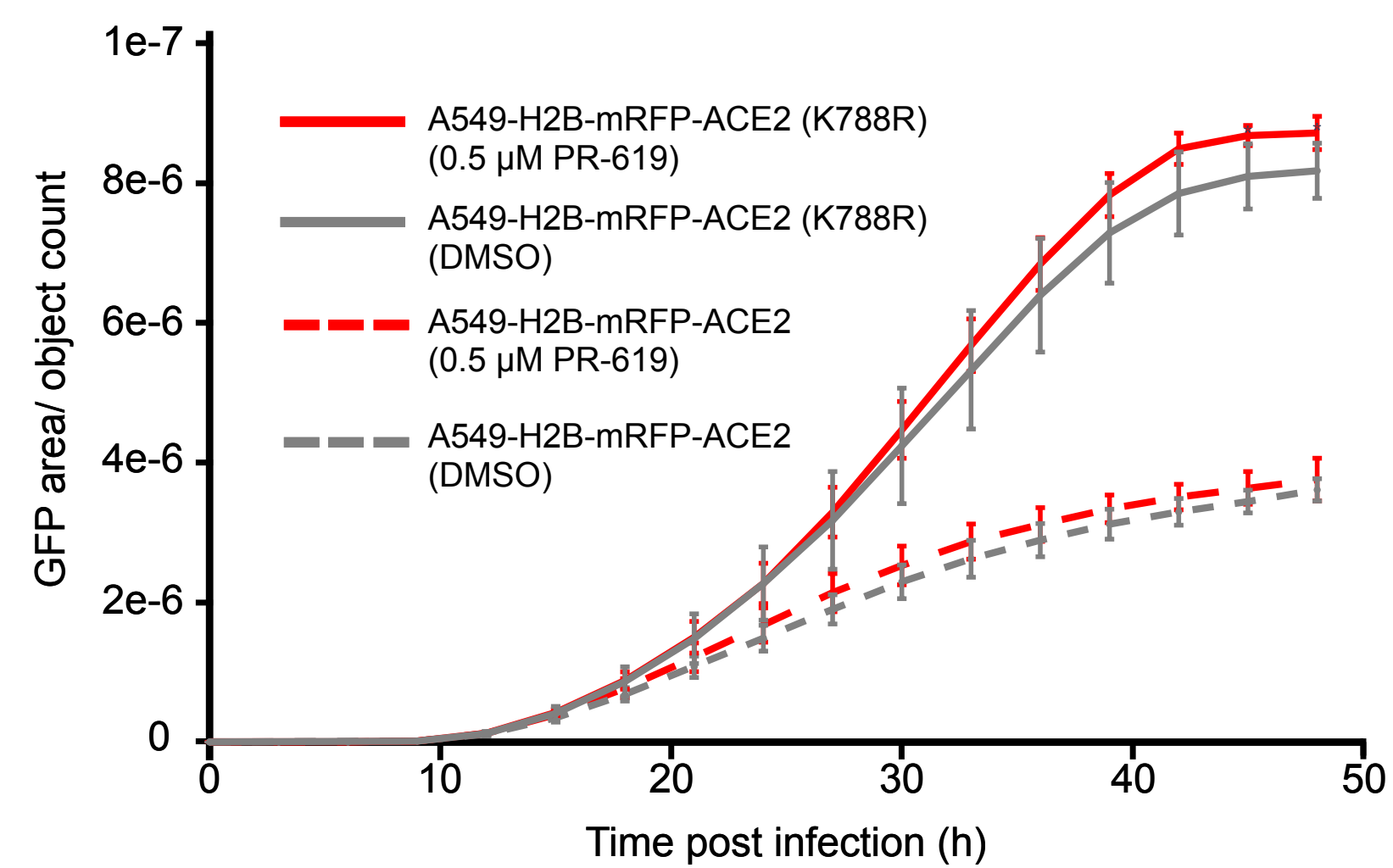
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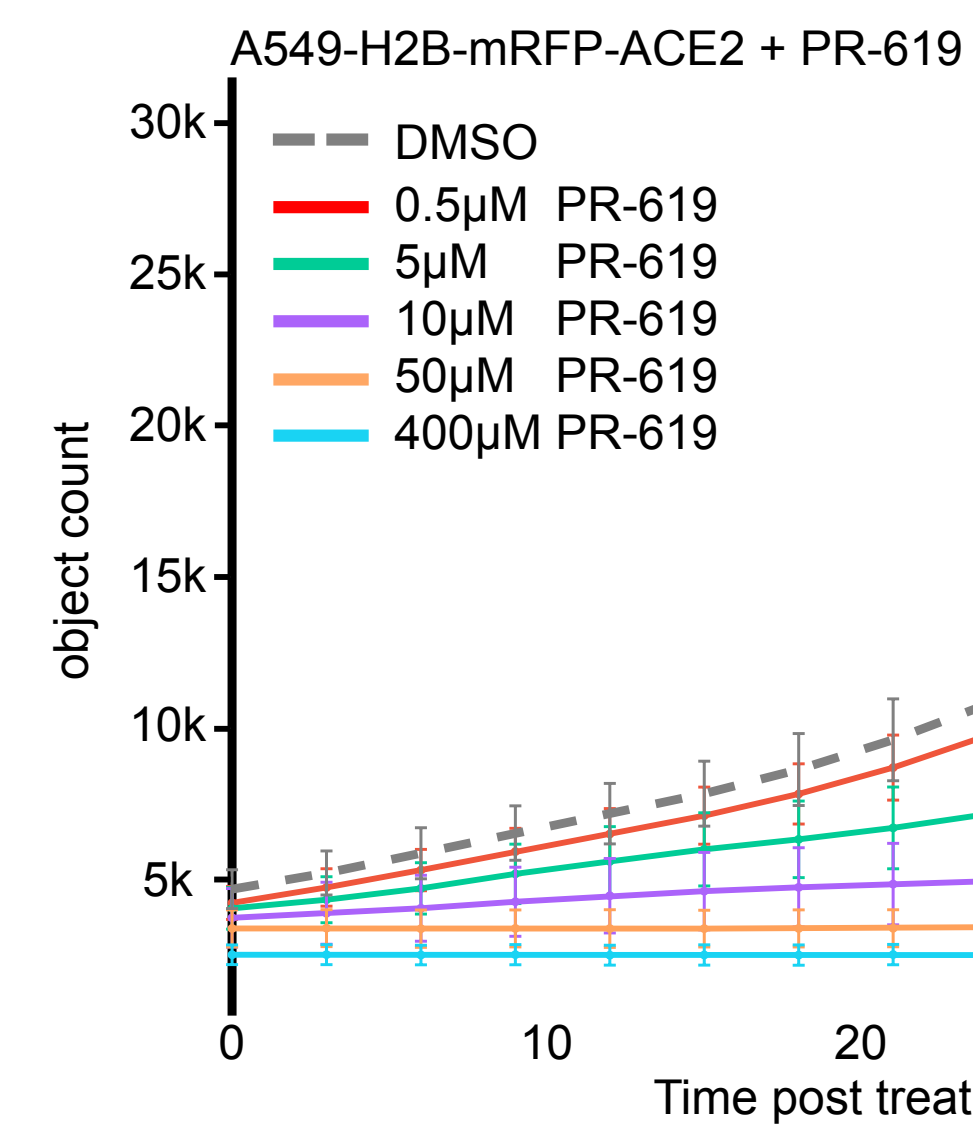
E



F

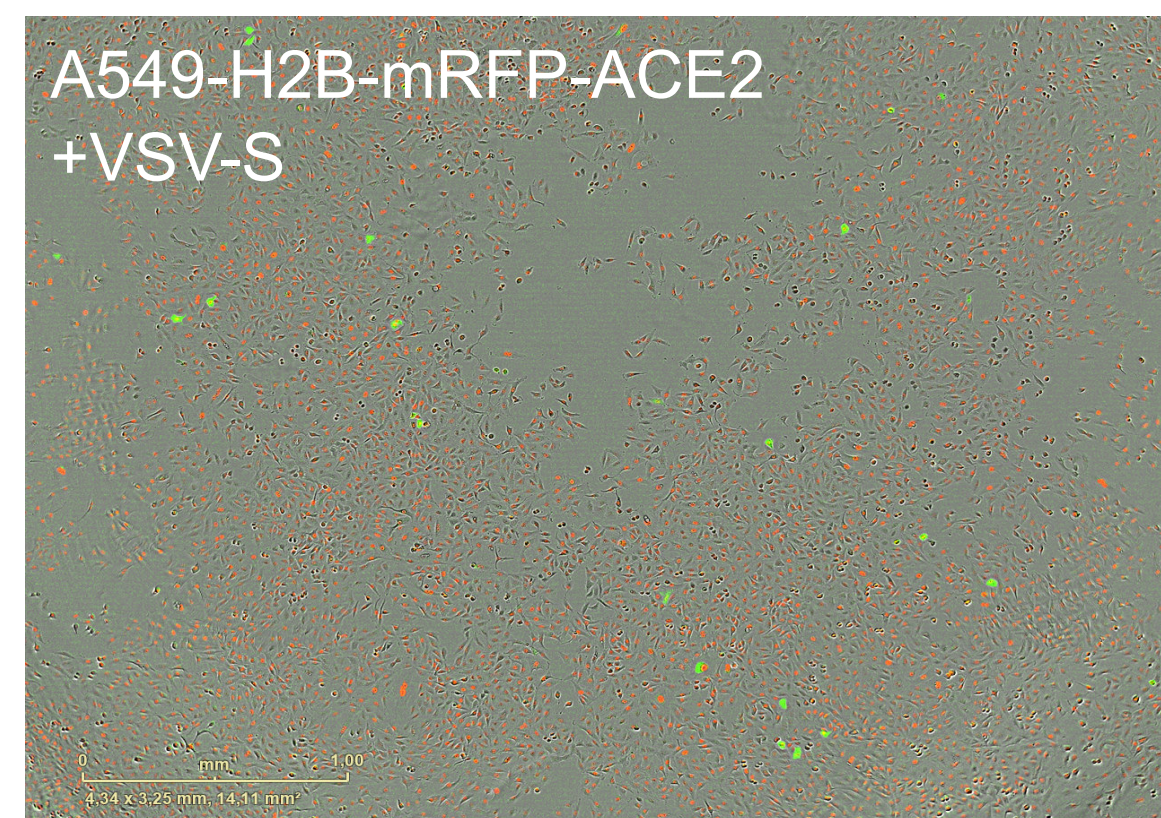


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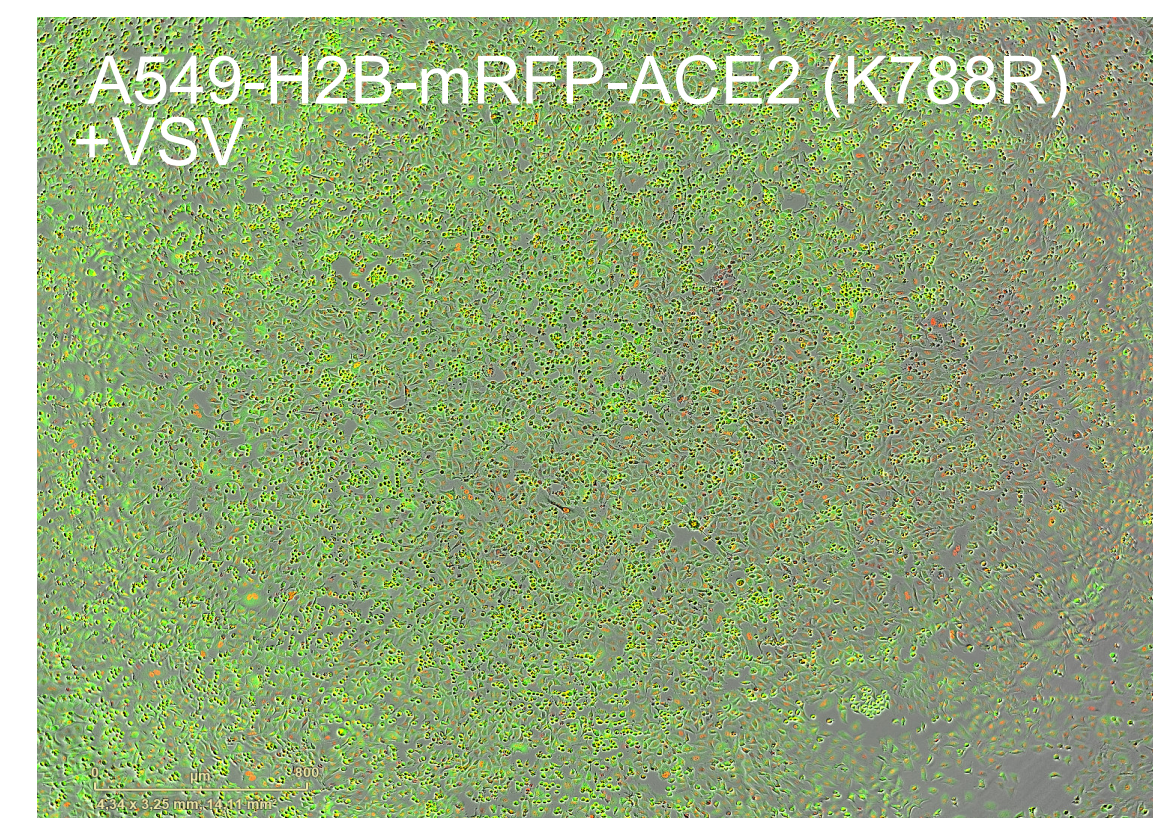
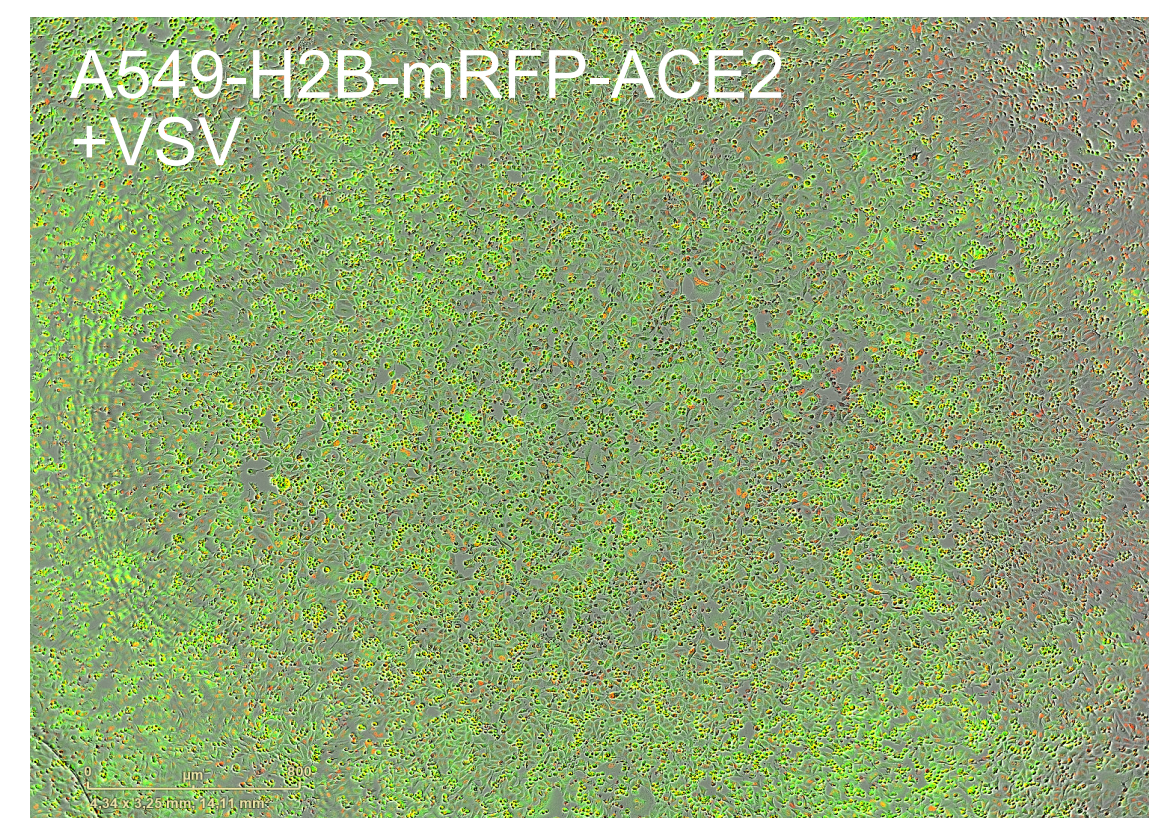
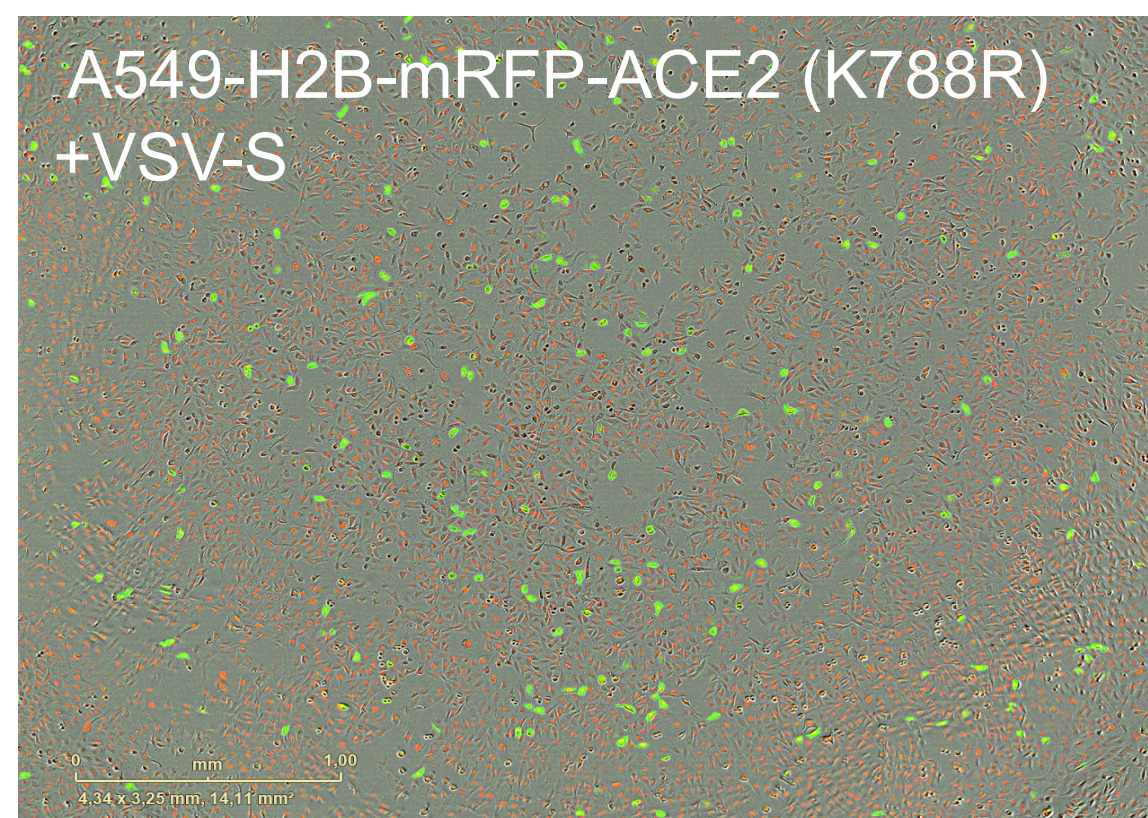


Supplementary Figure 4. SARS-CoV-2 infection of cells expressing ACE2 or ACE2-K788R. (A) ACE2 structure and designated post-translational modifications of the cytosolic domain includes only one ubiquitination site (adapted from PhosPhositePlus, 2022). Lysine (K), Serine (S), Tyrosine (Y), Transmembrane (TM). (B) Western Blot showing ACE2 and β -actin (β -ACT) levels of A549-H2B-mRFP-ACE2 and A549-H2B-mRFP-ACE2(K788R) cells. (C) Western Blot quantification of ACE2 and ACE2(K788R) expressed in A549-H2B-mRFP-ACE2 and A549-H2B-mRFP-ACE2(K788R) cells shown in B and Figure 4A. ACE2 levels were normalized to the corresponding β -actin (β -ACT). The bar graph depicts the ACE2(K788R) levels (relative optical density) normalized to the ACE2. The relative optical density was determined with ImageJ, and the calculation of significance was performed with a two-sample t-test with $p < 0.01$ (**) ($n = 3$, +/- SD). (D) Epifluorescence images of A549-H2B-mRFP-ACE2 and A549-H2B-mRFP-ACE2(K788R) (24 h post-infection) cells infected with SARS-CoV-2-GFP (MOI 3). The images were acquired by a live-cell imaging platform. (E) MG132 inhibits SARS-CoV-2 infection. A549-H2B-mRFP-ACE2 cells were pre-treated with MG132 (1 μ M, 4h), DMSO control or no treatment and infected with SARS-CoV-2-GFP reporter virus (MOI:3). Virus replication was measured for 48 h post infection in a live-cell imaging platform (Incucyte S3) and analyzed by normalizing the virus signal (GFP area) to confluency (phase area). The signal of DMSO control was used to show the effect of the drug on infection (%). (F) A549-H2B-mRFP-ACE2 and A549-H2B-mRFP-ACE2(K788R) cells were pretreated for 6 h with 0.5 μ M PR-619. The cells were infected with SARS-CoV-2-GFP (MOI:3) and virus replication was measured over 48h. Virus signal (GFP) was normalized to cell number (RFP). (G) Cell viability screening of PR-619. A549-H2B-mRFP-ACE2 cells were pretreated 6h with PR-619 at the indicated concentrations. The cell number (RFP counts) was measured in a live-cell imaging platform (Incucyte S3). For statistical analysis a t-test between DMSO control (dashed line) and compound of interest (solid line) was performed at 24h and 48h post infection with $p < 0.01$ (**), 0.001 (***).

A



B



Supplementary Figure S5. ACE2-K788R increases VSV-S but not VSV infection. A549-H2B-mRFP-ACE2 and A549-H2B-mRFP-ACE2(K788R) cells were infected with either (A) VSV-S (MOI 3) or (B) VSV (MOI 0.01). Representative epifluorescence images at 12 h post-infection are shown. The images were acquired by a live-cell imaging platform.