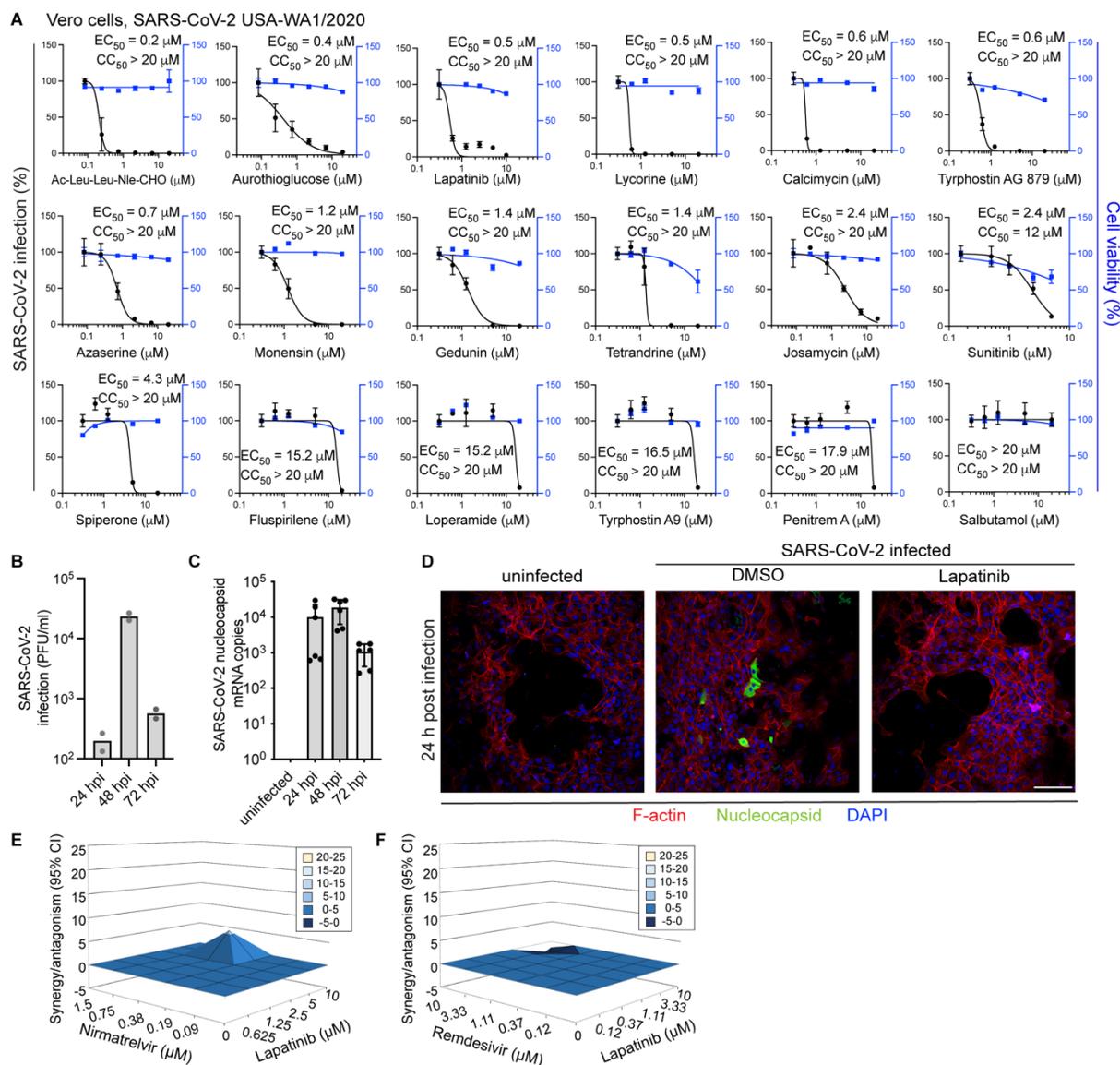


## **Supplemental data**

### **This document includes:**

1. Supplemental figures and figure legends
2. Supplemental texts
3. Supplemental methods
4. Supplemental data references
5. Uncut gels





27

28 **Supplemental Figure 2. Validation of hits emerging from the HTS and characterization**  
 29 **of human ALO-derived monolayers for studying the antiviral effect of emerging hits.**  
 30 **Related to figures 1 and 2.**

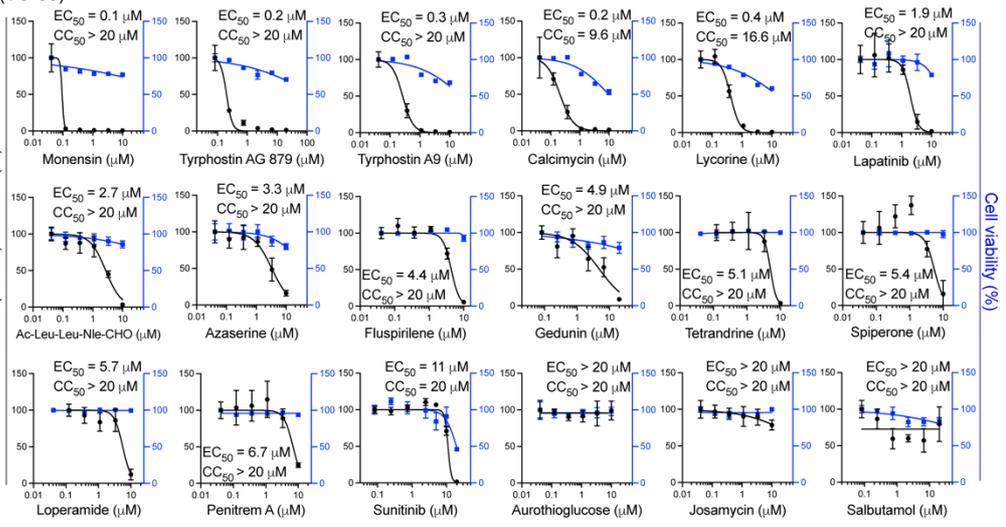
31 **A**, Dose response curves to the indicated hits emerging from the HTS of SARS-CoV-2  
 32 infection (black, USA-WA1/2020 strain, MOI=0.05) and cell viability (blue) in Vero cells  
 33 measured via plaque and alamarBlue assays at 24 hpi, respectively. **B**, **C**, Viral titer by  
 34 plaque assays in culture supernatants (**B**) and viral nucleocapsid (N) copy number analyzed  
 35 by RT-qPCR in lysates (**C**) from human ALO-derived monolayers at 24, 48 and 72 hpi. **D**,  
 36 Confocal IF microscopy images of F-actin (red), SARS-CoV-2 nucleocapsid (green) and  
 37 DAPI (blue) in naive and SARS-CoV-2-infected ALO-derived monolayers pre-treated with  
 38 DMSO or 10 μM lapatinib at 24 hpi. 20x magnification of the images in figure 2J are shown.  
 39 Scale bar is 100 μm. **E**, **F**, Synergy/antagonism of lapatinib and nirmatrelvir (**E**) or remdesivir  
 40 (**F**) combination treatment on cellular viability measured in Calu-3 cells infected with rSARS-  
 41 CoV-2/Nluc (USA-WA1/2020 strain) at 24 hpi via alamarBlue assays. Data represent  
 42 differential surface analysis at the 95% confidence interval (CI), analyzed via the  
 43 MacSynergy II program. Synergy and antagonism are indicated by the peaks above and  
 44 below the theoretical additive plane, respectively. The level of synergy or antagonism is  
 45 depicted by the color code. Data are representative (A, B, D-F) or combination (A, C) of two

46 independent experiments with 2-3 replicates each. Means $\pm$ SD are shown (A, C). Data in A is  
47 relative to DMSO control.  
48

**A U-87 MG cells, VEEV (TC-83)**

VEEV (TC-83)			
	EC <sub>50</sub>	CC <sub>50</sub>	SI
Monensin	0.1	>20	>200
AG 879	0.2	>20	>100
A9	0.3	>20	>67
Calcimycin	0.2	9.6	48
Lycorine	0.4	16.6	42
Lapatinib	1.9	>20	>10
A-L-L-N	2.7	>20	>7.4
Azaserine	3.3	>20	>6.0
Fluspirilene	4.4	>20	>4.5
Gedunin	4.9	>20	>4.0
Tetrandrine	5.1	>20	>3.9
Sipiperone	5.4	>20	>3.7
Loperamide	5.7	>20	>3.5
Penitrem A	6.7	>20	>2.9
Sunitinib	11	20	1.8
Au-thioglucl	>20	>20	>1
Josamycin	>20	>20	>1
Salbutamol	>20	>20	>1

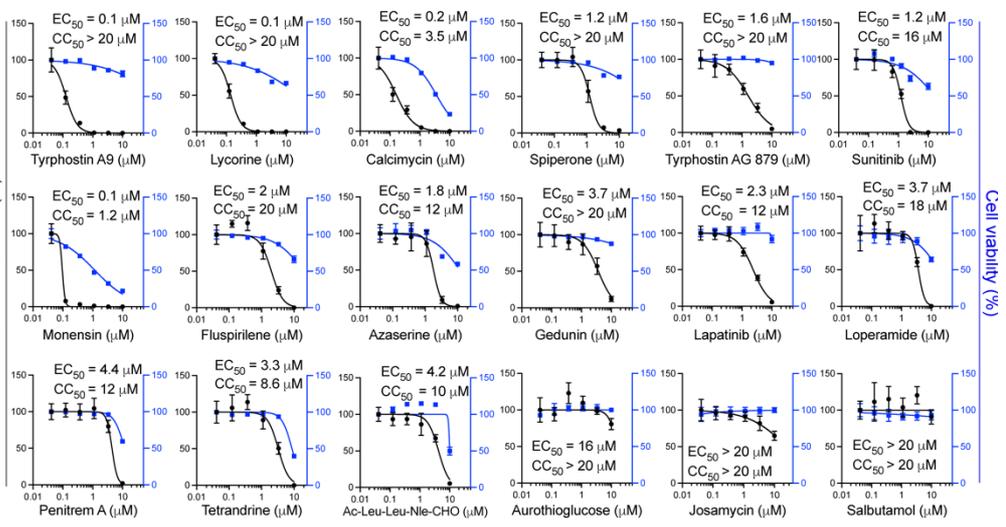
+ EC<sub>50</sub> - + CC<sub>50</sub> -  
■ activity ■ toxicity



**B Huh7 cells, DENV2**

DENV2			
	EC <sub>50</sub>	CC <sub>50</sub>	SI
A9	0.1	>20	>200
Lycorine	0.1	>20	>200
Calcimycin	0.2	3.5	17.5
Sipiperone	1.2	>20	>16
AG 879	1.6	>20	>13
Sunitinib	1.2	16	13
Monensin	0.1	1.2	12
Fluspirilene	2	20	10
Azaserine	1.8	11.7	6.5
Gedunin	3.7	>20	>5.4
Lapatinib	2.3	12	5.2
Loperamide	3.7	17.8	4.8
Penitrem A	4.4	12	2.7
Tetrandrine	3.3	8.6	2.6
A-L-L-N	4.2	10	2.4
Au-thioglucl	15.9	>20	>1.2
Josamycin	>20	>20	>1
Salbutamol	>20	>20	>1

+ EC<sub>50</sub> - + CC<sub>50</sub> -  
■ activity ■ toxicity



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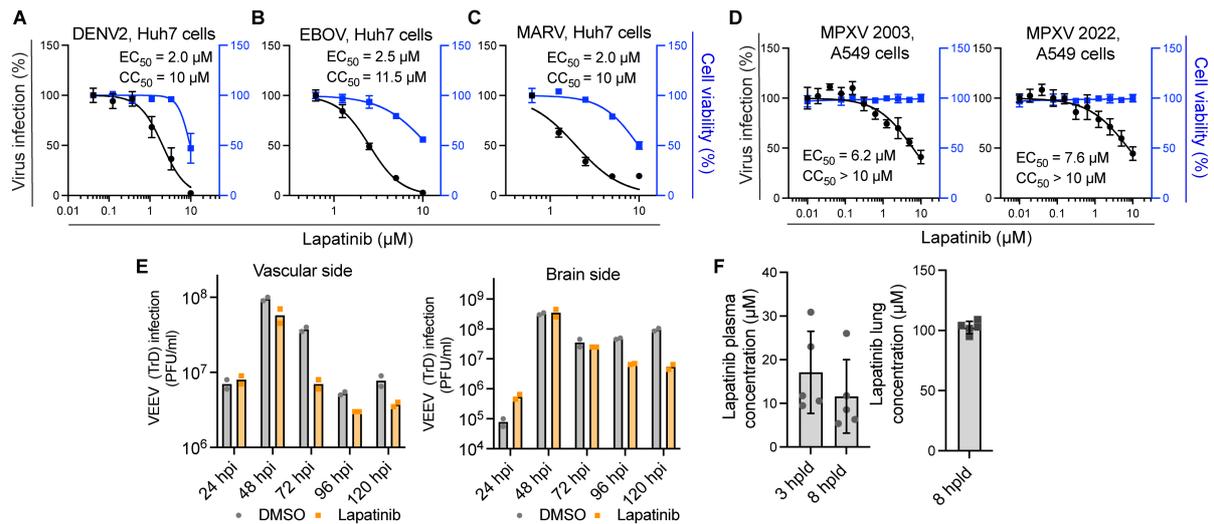
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**Supplemental Figure 3. Broad-spectrum potential of hits. Related to figures 1 and 2.**  
**A, B,** The 18 compounds emerging from the HTS were tested for their effect on VEEV (TC-83) (A) and DENV2 (B) infections in U-87 MG and Huh7 cells, respectively, via luciferase assays, and for their effect on cell viability via alamarBlue assays. Left panels: Heat maps of the EC<sub>50</sub> and CC<sub>50</sub> values of the indicated compounds color-coded based on the antiviral activity (green) and toxicity (orange). Selectivity indices (SI) greater than 5 are depicted in yellow. Right panels: Dose response curves to the indicated compounds of VEEV (TC-83) (MOI=0.1) or DENV2 (MOI=0.05) infections (black) in U-87 MG and Huh7 cells, respectively, measured via luciferase assays and cell viability (blue) measured by alamarBlue assays at 24 hours post-infection. Data are representative of two independent experiments with 4 replicates each. Means±SD are shown. Data are relative to DMSO control.

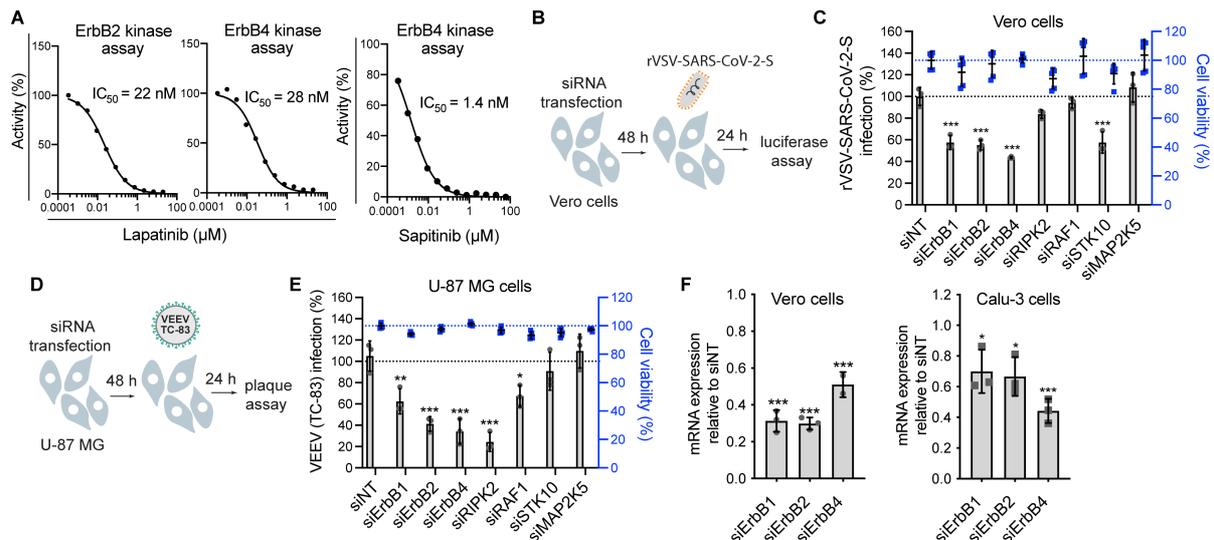


62

63 **Supplemental Figure 4: Lapatinib is a potent broad-spectrum antiviral. Related to**  
 64 **figure 3.**

65 **A**, Dose response of DENV2 infection (black) and cellular viability (blue) to lapatinib  
 66 measured in Huh7 cells via plaque and alamarBlue assays at 24 hpi (MOI=0.1), respectively.  
 67 **B, C**, Dose response of EBOV (Kikwit isolate, MOI=1) (**B**) and MARV (Ci67 strain, MOI=2)  
 68 (**C**) infections (black) and cellular viability (blue) to lapatinib measured in Huh7 cells 48 hpi  
 69 via microneutralization assay and CellTiter-Glo luminescent cell viability assay, respectively.  
 70 **D**, Dose response of MPOXV 2003 and 2022 infection (black) and cellular viability (blue) to  
 71 lapatinib measured in A549 cells via Focus forming reduction assay (FFRA) and MTT  
 72 assays at 24 hpi (MOI=0.005), respectively. **E**, Viral load in longitudinal samples collected  
 73 from the vascular and brain sides of the gNVU following infection with VEEV (TrD) and  
 74 treatment with lapatinib or DMSO. **F**, lapatinib's plasma and lung concentrations after 8 days  
 75 of twice daily treatment with 200 mg/kg in C57BL/6 mice measured 3 and 8 hours post last  
 76 dose (hpld). Data are combination (A) or representative (B, C, D, E) of two independent  
 77 experiments with 2-5 replicates each. Means±SD are shown (A-D, F). Data in A-D are  
 78 relative to DMSO control.

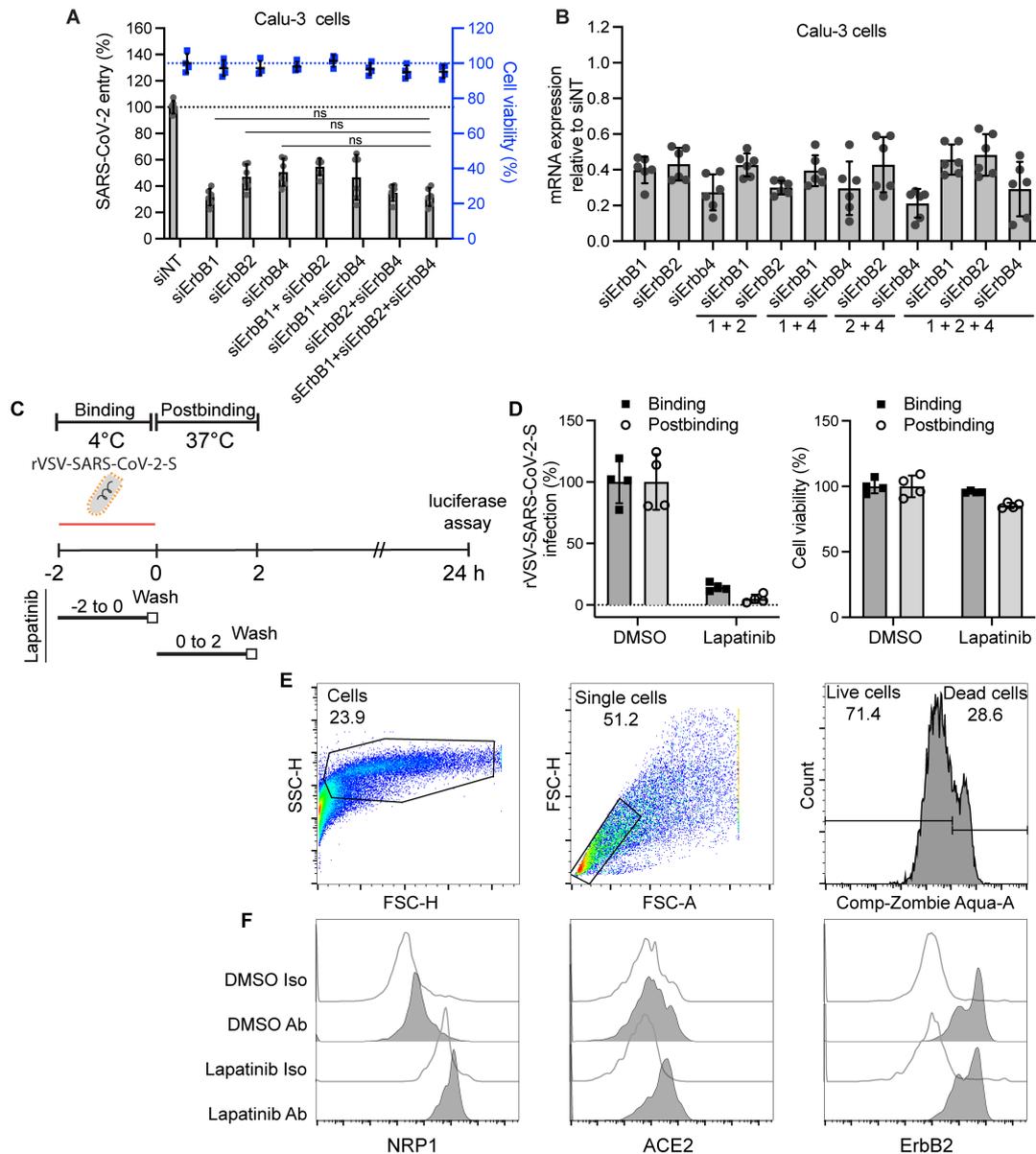
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81 **Supplemental Figure 5: Validation of ErbBs as an antiviral target. Related to figure 4.**

82 **A**, Dose response to lapatinib and sapatitinib of ErbB2 and/or ErbB4 kinase activity in vitro  
 83 (Nanosyn). **B**, Schematic of the experiment shown in panel C. **C**, Percentage of infection by  
 84 luciferase assays (grey) and cell viability by alamarBlue assays (blue) measured at 24 hpi of  
 85 Vero cells transfected with the indicated siRNA pools with rVSV-SARS-CoV-2-S  
 86 pseudovirus. **D**, Schematic of the experiment shown in panel E. **E**, Percentage of infection  
 87 by plaque assays (grey) and cell viability by alamarBlue assays (blue) measured at 24 hpi of  
 88 U-87 MG cells transfected with the indicated siRNA pools with VEEV (TC-83). **F**,  
 89 Confirmation of siRNA-mediated gene expression knockdown by RT-qPCR in Vero and  
 90 Calu-3 cells. Shown is gene expression normalized to GAPDH and expressed relative to the  
 91 respective gene level in the siNT control at 48 hours post-transfection. Data are  
 92 representative (C, E, F) of two independent experiments with 3-5 replicates each.  
 93 Means±SD are shown (C, E, F). Data are relative to DMSO (A) or siNT (C, E, F) controls.  
 94 \**P* < 0.05, \*\*\**P* < 0.001 relative to siNT by one-way ANOVA followed by Dunnett's multiple  
 95 comparisons test.

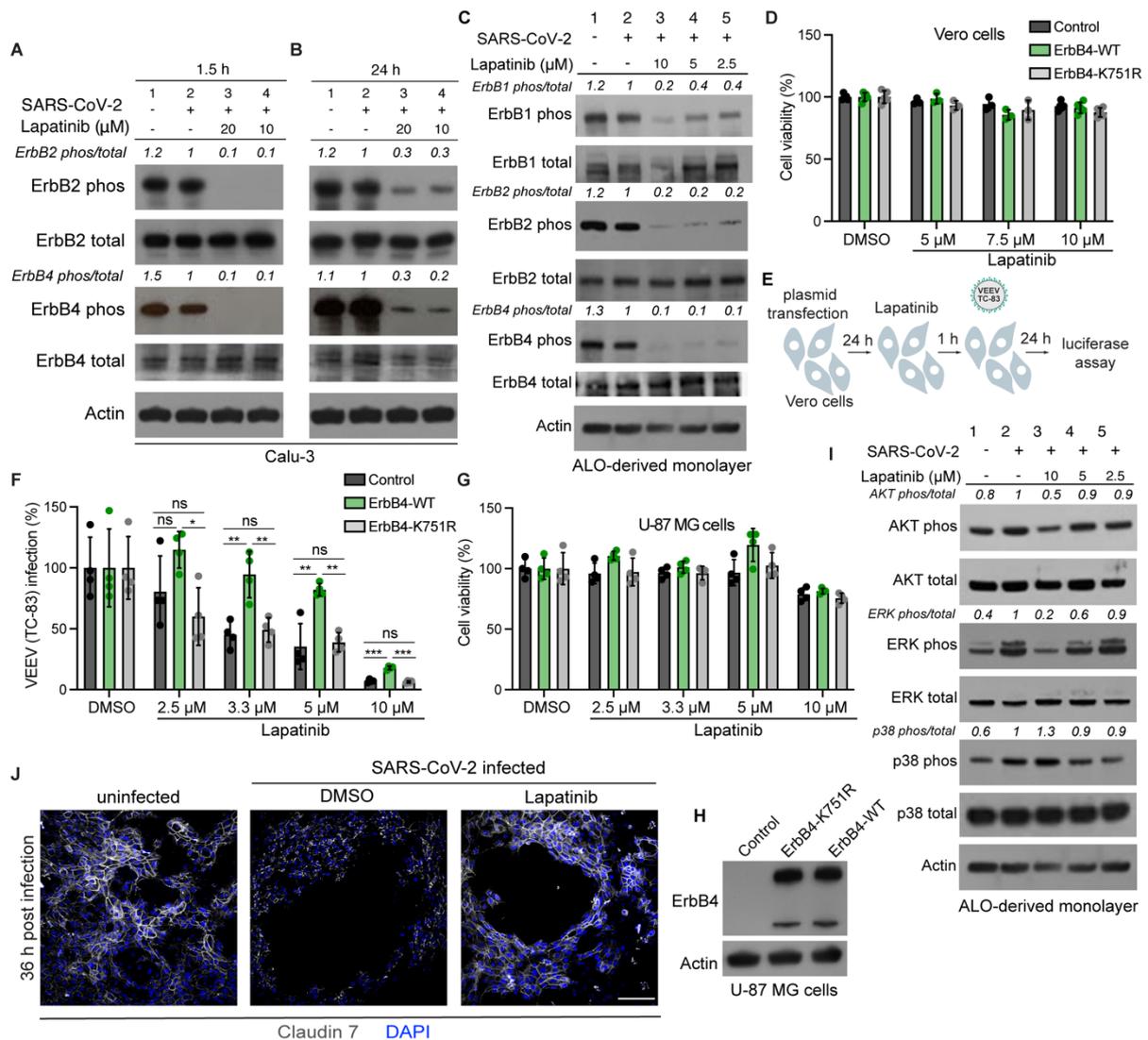


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97 **Supplemental Figure 6: Lapatinib treatment suppresses viral entry at a postbinding**  
 98 **stage. Related to figure 5.**

99 **A**, WT SARS-CoV-2 entry at 2 hpi of Calu-3 cells (MOI=1) depleted of the indicated ErbBs  
 100 individually or in double and triple combinations measured by RT-qPCR. **B**, Confirmation of  
 101 siRNA-mediated gene expression knockdown by RT-qPCR in Calu-3 cells transfected with  
 102 the indicated siRNAs. Shown is gene expression normalized to GAPDH and expressed  
 103 relative to the respective gene level in the siNT control at 48 hours post-transfection. 1+2,  
 104 1+4, 2+4 refer to ErbB combinations in double knockdown. 1+2+4 depicts simultaneous  
 105 knockdown of ErbB1, ErbB2 and Erbb4. **C**, Schematic of the temperature-shift experiments  
 106 shown in panel D. **D**, Vero cells were infected with VSV-SARS-CoV-2-S for 2 hours at 4°C in  
 107 the presence or absence of 10 μM lapatinib or DMSO before the temperature was shifted to  
 108 37°C to initiate infection. 24 hpi virus infection was measured via luciferase assay and cell  
 109 viability by alamarBlue assay. **E**, Representative dot plots showing gating strategy. Cell  
 110 debris were excluded by size, and dead cells were excluded using Zombie Aqua live/dead  
 111 staining. **F**, Representative histograms depicting surface expression of NRP1, ACE2 and  
 112 ErbB2 in SARS-CoV-2-infected and DMSO- or lapatinib-treated cells. Antibody isotype

113 control histograms are also shown. Data are combination (A, B) or representative (D) of two  
114 independent experiments with 2-4 replicates each. Means $\pm$ SD are shown (A, B, D). Data are  
115 relative to siNT (A, B) or DMSO (D) controls.  
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**Supplemental Figure 7: Lapatinib treatment modulates ErbBs and suppresses activation of downstream tissue injury signals. Related to figure 6.**

**A, B**, ErbB2 and ErbB4 phosphorylation in Calu-3 cells that are uninfected (lane 1), infected and treated with DMSO (lane 2) or infected and treated with lapatinib (lanes 3 and 4) measured by Western blotting 1.5 (**A**) and 24 (**B**) hpi with SARS-CoV-2 (USA-WA1/2020 strain, MOI=1). **C**, Dose-dependent effect of lapatinib treatment on ErbB1, 2 and 4 phosphorylation in ALO-derived monolayers that are uninfected (lane 1), SARS-CoV-2-infected and treated with DMSO (lane 2) or infected and treated with lapatinib (lanes 3-5) measured by Western blotting 48 hpi. Shown are representative membranes blotted for phospho- and total ErbB2, ErbB4, and actin and quantitative phospho- to total ErbB ratio data relative to infected cells treated with DMSO (lane 2). **D**, Vero cell viability measured by alamarBlue assays 48 hours post-transfection of the indicated plasmids. **E**, Schematic of the experiments shown in F-H. **F**, Rescue of VEEV (TC-83) infection in the presence of lapatinib upon ectopic expression of the indicated plasmids measured by luciferase assays 24 hpi in U-87 MG cells. **G**, U-87 MG cell viability measured by alamarBlue assays 48 hours post-transfection of the indicated plasmids. **H**, Level of ErbB4 and actin expression measured via Western blot following transfection of U-87 MG cells with control or ErbB4-expressing plasmids. **I**, Dose-dependent effect of lapatinib treatment on AKT, ERK and p38 MAPK

137 phosphorylation in ALO-derived monolayers that are uninfected (lane 1), SARS-CoV-2-  
138 infected and treated with DMSO (lane 2) or infected and treated with lapatinib (lanes 3-5)  
139 measured by Western blotting 48 hpi. Membranes shown in C and I were cut from the same  
140 membrane prior to blotting with the indicated antibodies based on the molecular weight  
141 marker and size of proteins of interest. Therefore, the actin membrane is the same for both  
142 insets. **J**, Confocal IF microscopy images of Claudin 7 (grey) and DAPI (blue) in naïve or  
143 SARS-CoV-2- infected ALO-derived monolayers treated at 4 hpi either with DMSO or 10  $\mu$ M  
144 lapatinib and imaged at 36 hpi. 20x magnification of the images in figure 6I are shown. Scale  
145 bar is 100  $\mu$ m. Data are combination (D) or representative (F, G) of two independent  
146 experiments with 2-4 replicates each. Means $\pm$ SD are shown (D, F, G). \* $P < 0.05$ , \*\* $P <$   
147  $0.005$ , \*\*\* $P < 0.001$  relative to DMSO control by one-way ANOVA followed by Tukey's  
148 multiple comparisons test at each lapatinib concentration.  
149

150 **Supplemental text 1. The HTS of compound libraries for SARS-CoV-2 inhibitors is**  
151 **robust and specific.**

152 The libraries were screened in two independent experiments. Data were normalized to the  
153 median of each plate. The average percent fluorescent area for control wells included in  
154 each plate was  $102.9 \pm 5\%$  for uninfected cells (cell control),  $0.1 \pm 0.2\%$  for infected untreated  
155 cells (virus control), and  $0.0 \pm 0.164\%$  for infected cells treated with DMSO (Figure 1C). The  
156 Z-score was calculated on the basis of the  $\log_2(\text{fold change})$  ( $\log_2\text{FC}$ ) with the average and  
157 standard deviation of each plate. The Z' and RZ' values of each of the 29 screen plates,  
158 calculated based on the virus control and cell control wells, were greater than 0.78 and the  
159 signal-to-background (S/B) value, representing the ratio of the median value of the raw data  
160 between the virus control and the cell control, was greater than 120 (Supplemental Figure  
161 1B). The two replicate screens demonstrated good correlation ( $r = 0.76$ ) (Supplemental  
162 Figure 1C). Remdesivir and its major metabolite, GS-441524, used as positive controls,  
163 demonstrated dose-dependent anti-SARS-CoV-2 activity in this assay (Supplemental Figure  
164 1D). Overall, these data indicate that this antiviral assay is robust for HTS and is specific. 40  
165 compounds from the screen were selected according to the cutoff of fluorescence % area  
166 greater than 15 in at least one of the two screens, which is 15 times greater than the values  
167 obtained with untreated or DMSO treated cells.

168

169 **Supplemental text 2. Broad-spectrum antiviral activity of hits.**

170 The effect of the 18 emerging hit compounds on replication of two unrelated RNA viruses,  
171 TC-83, the vaccine strain of the alphavirus VEEV, and the flavivirus, dengue (DENV2) was  
172 measured in human astrocytes (U-87 MG) and human hepatoma (Huh7) cells, respectively,  
173 both via luciferase assays. Lycorine, calcimycin, monensin, azaserine, gedunin, and the  
174 kinase inhibitors lapatinib and AG 879 dose-dependently inhibited replication of TC-83 and  
175 DENV2 in addition to SARS-CoV-2 (Supplemental Figure 3A, B). Several compounds, such  
176 as tyrphostin A9, an investigational inhibitor of PDGFR (platelet-derived growth factor  
177 receptor), and fluspirilene, a neuroleptic agent, demonstrated more potent anti-TC-83 and  
178 DENV2 activity than anti-SARS-CoV-2 activity, and others showed variable activity against  
179 one or two of these viruses. Salbutamol demonstrated minimal to no activity against all three  
180 viruses (Supplemental Figure 3A, B).

181

182 **Supplemental text 3. Safety considerations and drug-drug interactions of lapatinib.**  
183 **Related to discussion.**

184 Although toxicity is a concern when targeting host functions, lapatinib has a favorable safety  
185 profile, particularly when used as a monotherapy and for short durations, as those required  
186 to treat acute infections.

187 Notably, lapatinib's safety profile in the package insert was based on data from over 12,000  
188 patients with advanced cancer who received lapatinib in combination with capecitabine or  
189 trastuzumab plus an aromatase inhibitor and for long durations (1-3). As monotherapy,  
190 lapatinib was tested in several open-label studies with a median duration of 7-28 weeks in  
191 patients with advanced cancer (4-11). The most common adverse events attributed to  
192 lapatinib were diarrhea, rash, nausea, pruritus, and fatigue, with diarrhea being the most  
193 common adverse event resulting in drug discontinuation. The most common laboratory  
194 abnormalities with combination therapy were increased liver function tests, which were  
195 infrequently severe (1-3, 12). More severe adverse events including transient, reversible  
196 decreases in left ventricular ejection fraction, prolongation of QT interval, and hepatotoxicity,  
197 were also documented, yet infrequently, and with the exception of cardiac toxicity, primarily  
198 in patients receiving lapatinib in combination treatment (1, 10, 13, 14).

199 Notably, unlike erlotinib and gefitinib, lapatinib monotherapy has not been associated with  
200 pneumonitis, interstitial lung disease or lung fibrosis (4-11). The estimated incidence of 0.2%  
201 for these adverse effects is based on patients receiving lapatinib in combination with other  
202 drugs (15-20) known to cause pneumonitis and/or lung fibrosis (21-23), and sometimes also  
203 with radiation, for a median duration of 24-45 weeks. We predict that lapatinib's distinct off-  
204 target profile accounts for this difference in the occurrence of these adverse events. Indeed,  
205 cyclin G-associated kinase (GAK), an off-target of erlotinib ( $K_D=3.1$  nM,  $IC_{50}=0.88$   $\mu$ M) and  
206 gefitinib ( $K_D=6.5$  nM,  $IC_{50}=0.41$   $\mu$ M), but not of lapatinib ( $K_D=980$  nM,  $IC_{50}>5$   $\mu$ M)(24), has  
207 been implicated in pulmonary alveolar function and stem cell regeneration, and its inhibition  
208 is thought to be the mechanism underlying gefitinib- and erlotinib- induced lung toxicity(25,  
209 26).

210 An important consideration with lapatinib is, however, its potential for drug-drug interactions.  
211 Since metabolized by CYP3A4, concurrent use of suppressors of CYP3A4 should be  
212 avoided to reduce risk of QT prolongation. Concurrent treatment with CYP3A4 inducers  
213 should also be avoided, as this can reduce lapatinib's levels to sub-therapeutic. Of particular  
214 relevance is the CYP3A4 inducer dexamethasone used as standard of care for moderate  
215 COVID-19 patients. Since other steroids do not induce CYP3A4, lapatinib could be studied  
216 in combination with hydrocortisone or prednisone, which have been shown to comparably  
217 protect COVID-19 patients (27-29).

218

#### 219 **Supplemental text 4. Broad-spectrum potential of other hits emerging in the screen.** 220 **Related to discussion.**

221 Another approved anticancer drug that emerged in the HTS was sunitinib, a multi-kinase  
222 inhibitor that we have shown to protect mice from DENV and EBOV challenges when given  
223 in combination with erlotinib by inhibiting NAK-mediated intracellular viral trafficking(30-32).

224 Sunitinib was recently shown by others to suppress pan-corona pseudotyped viral infections  
225 (33) and by us to suppress WT SARS-CoV-2 infection (34). AG 879, another kinase inhibitor  
226 demonstrating anti-SARS-CoV-2 activity, was reported to suppress replication of multiple  
227 viruses including a mouse hepatitis virus (Coronaviridae) in cultured cells and to protect mice  
228 from influenza A virus (IAV) challenge (35-37). Nevertheless, since we could not confirm its  
229 anti-ErbB activity, the precise target(s) mediating the antiviral effect remain to be elucidated.

230

231 Ion transport across cell membranes is another function that emerged in our HTS as a  
232 candidate target for anti-SARS-CoV-2 approaches. Among the hits was tetrandrine, a  
233 calcium channel blocker with anti-inflammatory and anti-fibrogenic properties used as a  
234 medicinal herb for the treatment of lung silicosis, liver cirrhosis, and rheumatoid arthritis (38).  
235 Tetrandrine was previously shown to inhibit EBOV entry in cultured cells and protect EBOV-  
236 infected mice by inhibiting endosomal calcium channels (39). Monensin, an antiprotozoal  
237 agent, and calcimycin, shown to inhibit VSV and IAV infections (40, 41), are both ionophores  
238 that facilitate the transport of sodium/potassium and calcium across the membrane,  
239 respectively. Spiperone, an activator of chloride channels licensed in Japan for the treatment  
240 of schizophrenia, was another hit.

241

242 The emergence of gedunin, a natural product that inhibits HSP90 and has anti-inflammatory  
243 properties, suggests a potential role for HSP90 in SARS-CoV-2 infection, as in other viral  
244 infections (42, 43). Lycorine, a protein synthesis inhibitor (44) was also shown to suppress  
245 replication of multiple viruses including SARS-CoV in cultured cells (45-48) and mortality of  
246 mice infected with human enterovirus 71 (49). The underlying mechanism of action in  
247 influenza was thought to be inhibition of export of viral ribonucleoprotein complexes from the  
248 nucleus (45), yet lycorine also exhibits anti-inflammatory effects (50). Azaserine is a natural  
249 serine derivative that irreversibly inhibits  $\gamma$ -glutamyltransferase in the metabolic hexosamine  
250 pathway. Independently of this target, it was shown to protect from endothelial cell  
251 inflammation and injury (51).

252

253 Aurothioglucose has been used for the treatment of rheumatoid arthritis and is thought to  
254 inhibit the activity of adenylyl cyclase in inflammatory pathways (52). Ac-Leu-Leu-Nle-CHO is  
255 used as a research tool to inhibit calpain 1 and 2 (CAPN1 and 2) (53), cysteine proteases  
256 required for SARS-CoV (54), echovirus 1 (55) and herpes simplex virus (56) infections.  
257 Targeting calpain proteases was shown to inhibit SARS-CoV-2 (57), SARS-CoV (58) and  
258 IAV replication (59) and to exert anti-inflammatory and tissue protective effects (60, 61)  
259 including in a reovirus-induced myocarditis mouse model (62). Beyond their host-targeted  
260 effects, Ac-Leu-Leu-Nle-CHO and aurothioglucose may have direct antiviral effects against

261 the SARS-CoV-2 M<sup>pro</sup> or 3C-like proteases, respectively (57, 63). Lastly, josamycin is  
262 a natural macrolide antibiotic with an anti-inflammatory activity used in humans in Europe  
263 and Japan. Other macrolides have shown anti-IAV and anti-inflammatory activities (64).  
264 These findings reveal candidate targets for anti-SARS-CoV-2 approaches. Moreover, they  
265 underscore the potential utility of natural products as broad-spectrum antivirals, yet limited  
266 scalability typically challenges the use of these products.

267 **Supplemental methods:**

268

269 **Compounds.** The Microsource Spectrum, two Biomol and LOPAC libraries were available at  
270 the Stanford High-Throughput Bioscience Center. Small molecule inhibitors were purchased  
271 from MedchemExpress or Cayman Chemical. Dinaciclib and ribociclib were a gift from Dr.  
272 Mardo Koivomagi (Department of Biology, Stanford University, Stanford).

273

274 **Plasmids.** Plasmids used for production of SARS-CoV-2 pseudovirus were a gift from Jing  
275 Lin (Vitalant, San Francisco). The rSARS-CoV-2/WT and rSARS-CoV-2/Nluc (rSARS-CoV-2  
276 expressing Nluc-reporter gene) plasmids were generated as previously described (65, 66).  
277 Flag-tagged SARS-CoV-2 (2019-nCoV) Spike S1 expression plasmid was purchased from  
278 Sino Biological (#VG40591-CF). Plasmid encoding VEEV TC-83 with a nanoluciferase  
279 reporter (VEEV TC-83-Cap-nLuc-Tav) was a gift from Dr. William B. Klimstra (Department of  
280 Immunology, University of Pittsburgh, Pittsburgh) (67). DENV2 (New Guinea C strain)  
281 TSV01 Renilla reporter plasmid (pACYC NGC FL) was a gift from Pei-Yong Shi (Institute for  
282 Drug Discovery, University of Texas Medical Branch, Galveston) (68). pDONR223-EGFR,  
283 pDONR223-ERBB2, pDONR223-ERBB4 were a gift from William Hahn & David Root  
284 (Addgene plasmid #23935, #23888, # 23875) (Broad Institute of Harvard and Massachusetts  
285 Institute of Technology, Cambridge) (69). ORFs were recombined into a gateway-compatible  
286 pGluc destination vector using Gateway technology (Invitrogen). Mutations were introduced  
287 by site-directed mutagenesis using the QuikChange Lightning Site-Directed Mutagenesis Kit  
288 (Agilent).

289 **Cells.** The African green monkey kidney cell line (Vero E6) constitutively expressing  
290 enhanced green fluorescent protein (eGFP) was provided by Dr. Marnix Van Loock (Janssen  
291 Pharmaceutica, Beerse, Belgium) (70). Cells were maintained in Dulbecco's modified  
292 Eagle's medium (DMEM, Gibco) supplemented with 10% v/v fetal calf serum (Biowest),  
293 0.075% sodium bicarbonate and 1x Pen-strep (Gibco). Vero E6, Vero, Calu-3, HEK-293T, U-  
294 87 MG, A549 and BHK-21 cells (ATCC, CRL-1586, CCL-81, HTB-55, CRL-3216, HTB-14,  
295 CCL-185, CCL-10) were maintained in DMEM (Corning) supplemented with 10% fetal  
296 bovine serum (FBS, Omega Scientific, Inc), 1% L-glutamine 200mM, 1% penicillin-  
297 streptomycin, 1% nonessential amino acids, 1% HEPES (Gibco), 1% Sodium pyruvate  
298 (Thermofisher scientific). A549-NRP1<sup>KO</sup> cells (abcam, ab269507) were grown in  
299 DMEM:Hams F12 (Cytiva) supplemented with 5% FBS. TMPRSS2-expressing Vero E6 cells  
300 (XenoTech, JCRB1819) were maintained in DMEM supplemented with 10% FBS and G418  
301 (1 mg/mL) (Thermofisher, Gibco). All cells were maintained in a humidified incubator with 5%  
302 CO<sub>2</sub> at 37°C and tested negative for mycoplasma by MycoAlert (Lonza, Morristown, NJ).

303 **Viral stocks preparation and sequencing.** Belgium-GHB-03021 SARS-CoV-2 strain was  
304 recovered from a nasopharyngeal swab taken from a patient returning from China early  
305 February 2020 (54) and passaged 6 times on Huh7 and Vero E6 cells. 2019-nCoV/USA-  
306 WA1/2020 SARS-CoV-2 isolate (NR-52281) (BEI Resources) was passaged 3-6 times in  
307 Vero E6-TMPRSS2 cells. The rSARS-CoV-2/WT and rSARS-CoV-2/Nluc (rSARS-CoV-2  
308 expressing Nluc-reporter gene) viral stocks were generated as previously described  
309 (55). USA-WA1/2020 from passage 3 used for the majority of the experiments was subject to  
310 SARS-CoV-2 whole-genome amplicon-based sequencing on a MiSeq platform (Illumina) by  
311 adapting an existing pipeline as described in (56), showing no deletion or point mutations in  
312 the multi-basic cleavage (MBC) domain. Belgium/GHB-03021/2020 SARS-CoV-2 from  
313 passage 6 was sequenced following a metagenomics pipeline (57) showing 100% deletion  
314 of the MBC domain. VEEV-TC-83-nLuc RNA was transcribed in vitro from cDNA plasmid  
315 templates linearized with MluI via MEGAscript SP6 kit (Invitrogen #AM1330) and  
316 electroporated into BHK-21 cells. DENV RNA was transcribed in vitro from pACYC-DENV2-  
317 NGC plasmid by mMessage/mMachine (Ambion) kits and electroporated into BHK-21 cells.  
318 WT Trinidad Donkey (TrD) VEEV strain, EBOV (Kikwit isolate) and MARV (Ci67 strain) (BEI  
319 Resources) were grown in Vero E6 cells. Supernatants were collected, clarified and stored  
320 at -80 °C. Viral titers were determined via plaque assays on BHK-21 (DENV, VEEV) or Vero  
321 E6 cells (SARS-CoV-2, EBOV, MARV). MPOXV 2003 (clade II) (NR-2500) and MPOXV  
322 2022 (Lineage B.1, Clade IIb) (NR-58622) were obtained from BEI Resources.

323

324 For rVSV-SARS-CoV-2-S production, HEK-293T cells were transfected with spike  
325 expression plasmid followed by infection with VSV-G pseudotyped  $\Delta$ G-luciferase VSV virus  
326 and harvesting of culture supernatant, as described (56).

327

328 **Antibodies.** *Antibodies targeting the phosphorylated and total protein forms:* anti-ErbB4  
329 (Santa Cruz, sc-8050), ErbB1, ErbB2, AKT, ERK, p38 (Cell Signaling, #4267, #2242, #4691,  
330 #4695, #8690), P-ErbB1 (Tyr1173), P-ErbB2 (Tyr1248), P-ErbB4 (Tyr1284), P-AKT  
331 (Ser473), P-ERK (Thr202/Tyr204), P-p38 (Thr180/Tyr182) (Cell Signaling, #4407, #2247,  
332 #4757, #4060, #4370, #4511), and  $\beta$ -actin (Sigma-Aldrich, catalog A3854) antibodies.

333 *Co-immunoprecipitation:* anti-ErbB1, ErbB2, ErbB4 (Cell Signaling, #4267, #2165, #4795).  
334  $\beta$ -actin (Sigma-Aldrich, catalog A3854), mouse monoclonal anti-Flag® M2-Peroxidase  
335 (HRP) (Sigma-Aldrich, A8592)

336 *Flow cytometry:* mouse anti-human NRP1-BV421 (Biolegend, 354513), goat anti-human  
337 ACE2-APC (R&D systems, FAB933A) and mouse-anti human ErbB2-Alexa Fluor 488 (R&D  
338 systems, FAB9589G),

339 *Infection assays and pharmacological inhibition:* anti-VACV A33R antibody (BEI Resources,  
340 NR-628)

341 *Immunofluorescence:* mouse mAb SARS-CoV-2 nucleocapsid antibody (SinoBiological,  
342 #40143-MM05), DAPI (ThermoFisher, D3571) and Alexa Fluor™ 594 Phalloidin  
343 (ThermoFisher, #A12381) Claudin 7 polyclonal antibody (ThermoFisher, #34-9100)  
344 Rab7 (Origene, #AB0033-200)

345

346 **siRNAs.** ON-TARGETPlus siRNA SMARTpools against 7 genes and non-targeting siRNA  
347 (siNT) were purchased from Dharmacon/Horizon Discovery with gene IDs as follows: EGFR  
348 (1956), ErbB2 (2064), ErbB4 (2066), RIPK2 (8767), RAF1 (5894), STK10 (6793), MAP2K5  
349 (5607).

350

351 **In vitro kinase assays.** These assays were performed on the LabChip platform (Nanosyn)  
352 or radiometric HotSpot™ platform (Reaction Biology).

353

354 **Sequences of primers used for RT-qPCR.**

355 GAPDH (F- GTCTCCTCTGACTTCAACAGCG; R- ACCACCCTGTTGCTGTAGCCAA),  
356 ErbB1 (F- AACACCCTGGTCTGGAAGTACG; R- TCGTTGGACAGCCTTCAAGACC), ErbB2  
357 (F- GGAAGTACACGATGCGGAGACT; R- TACCTTCCTCAGCTCCGTCTCTT), ErbB4 (F-  
358 GGAGTATGTCCACGAGCACAAG; R- CGAGTCGTCTTTCTTCCAGGTAC), SARS-CoV2-N  
359 (F- AAGCTGGACTTCCCTATGGTG; R- CGATTGCAGCATTGTTAGCAGG).

360

361

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Figure 4E

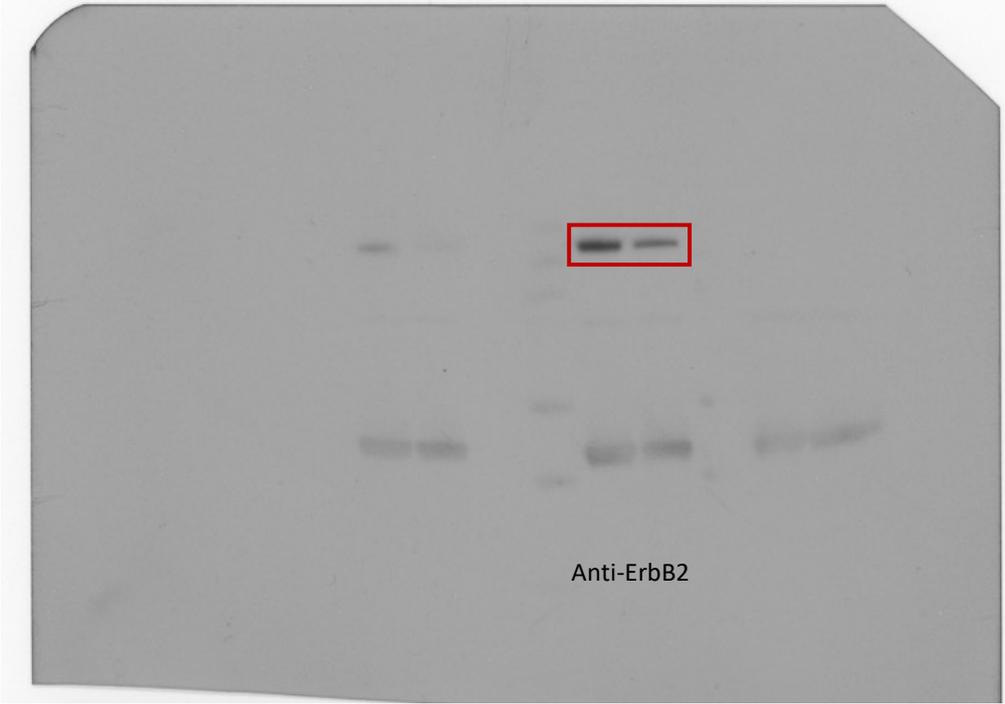
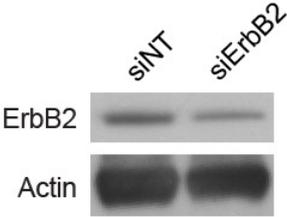
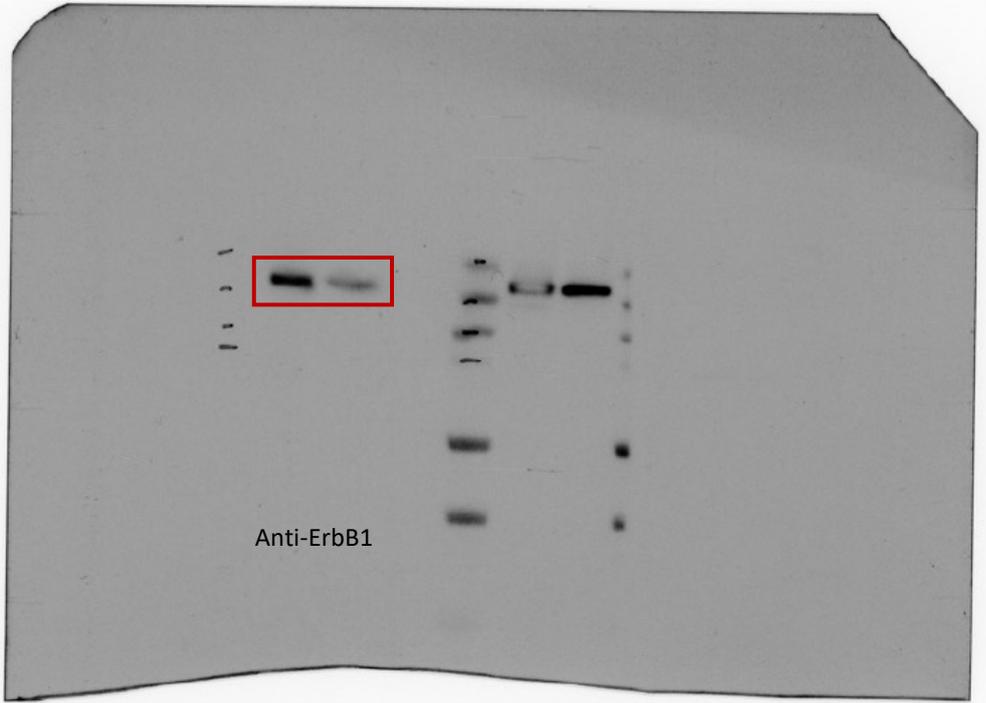
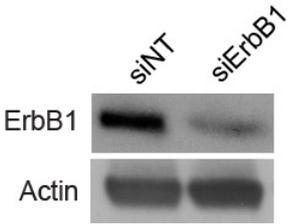
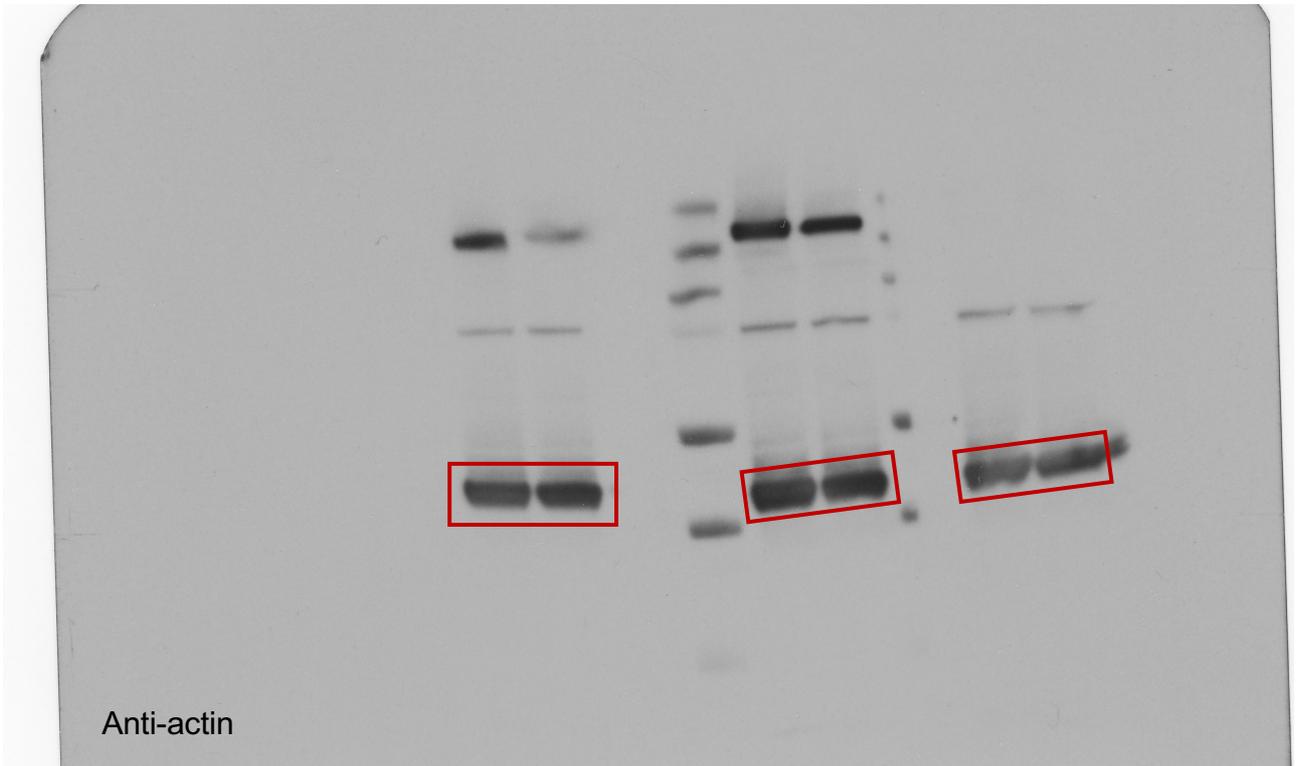
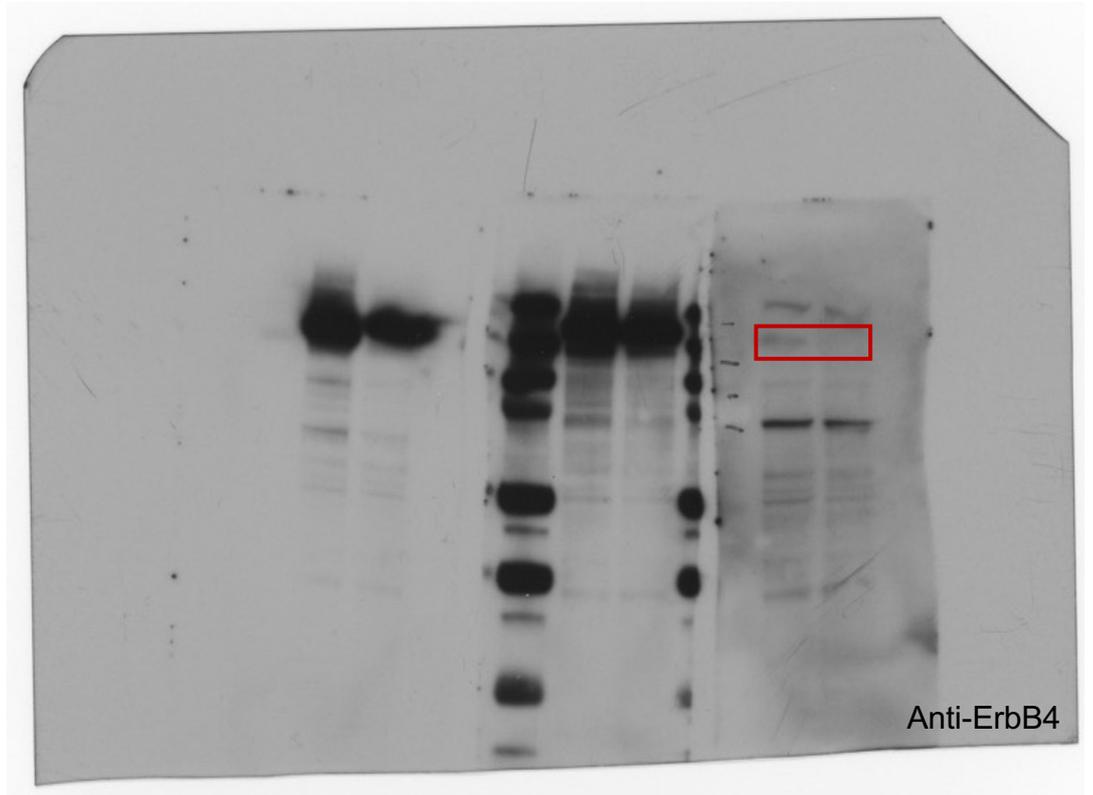
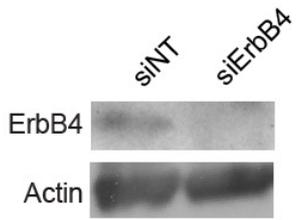
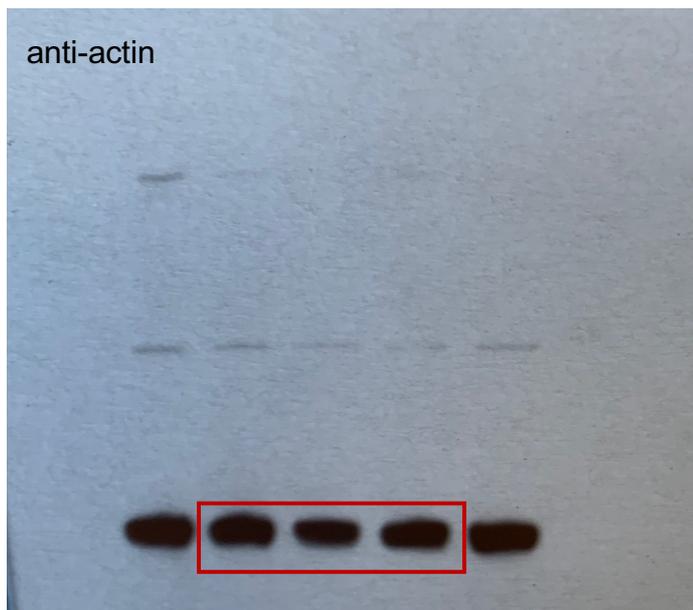
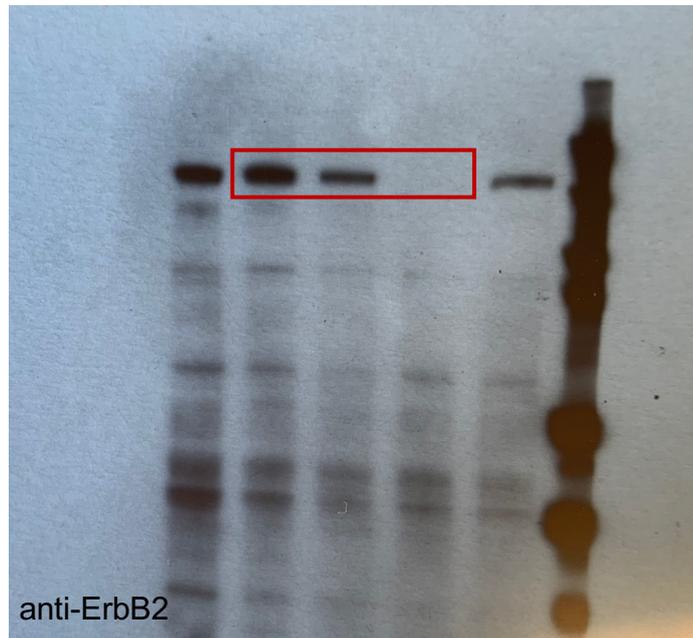
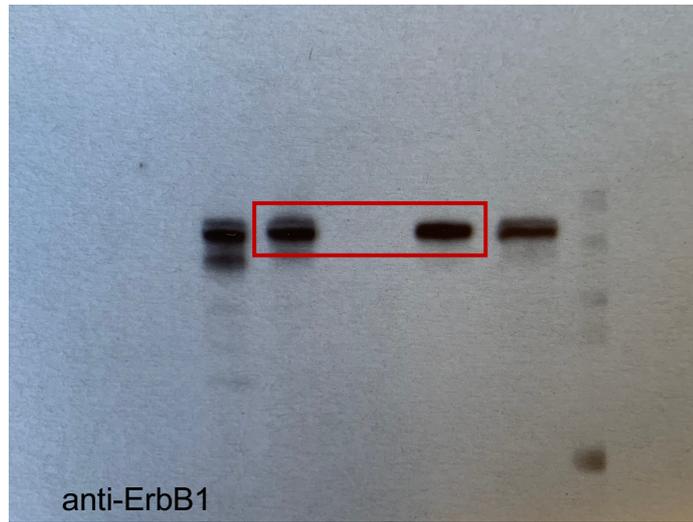
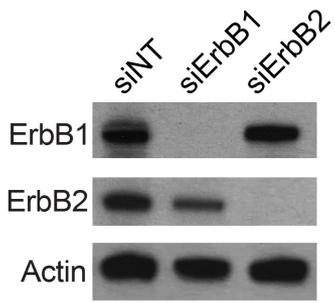


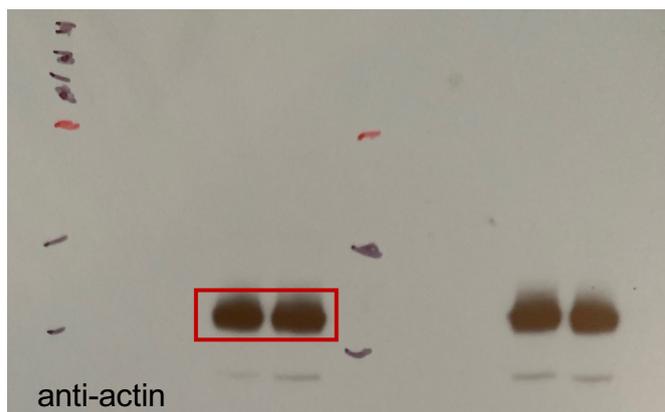
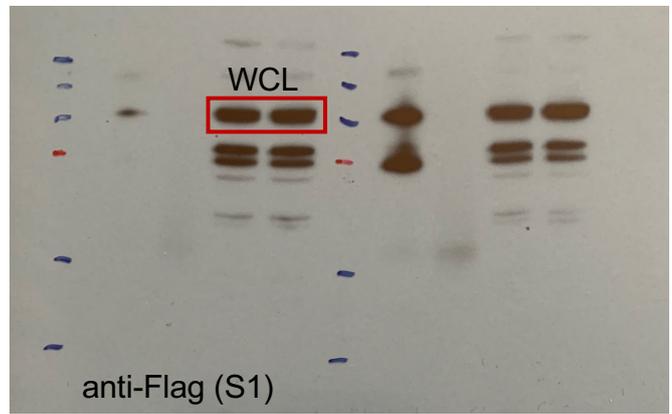
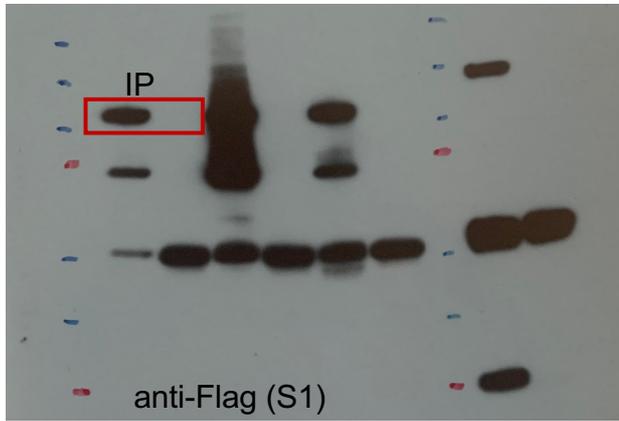
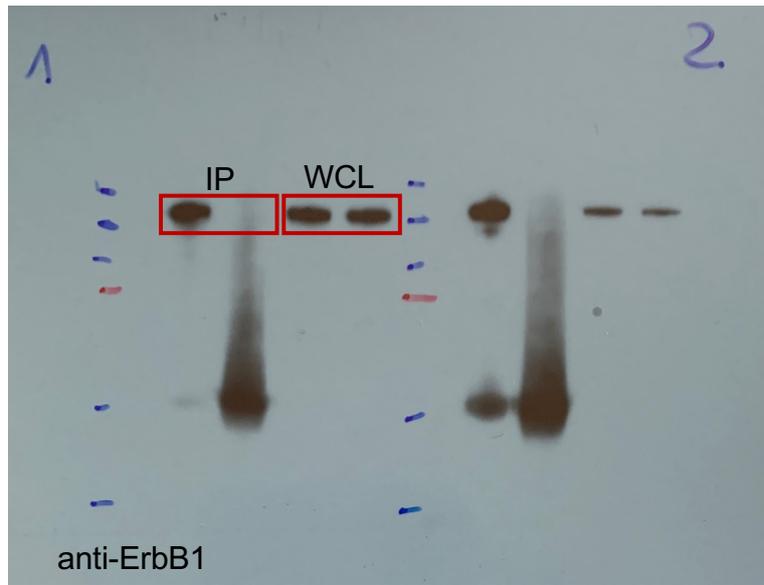
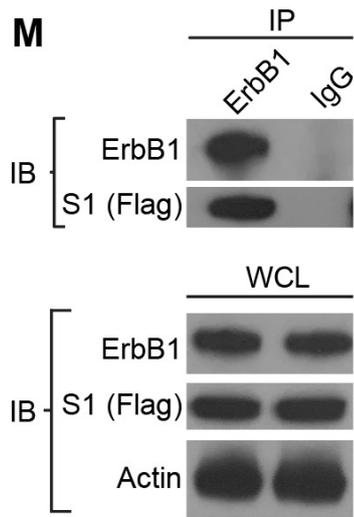
Figure 4E



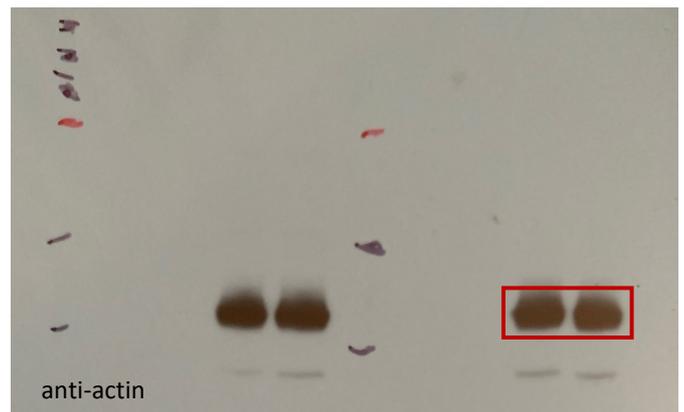
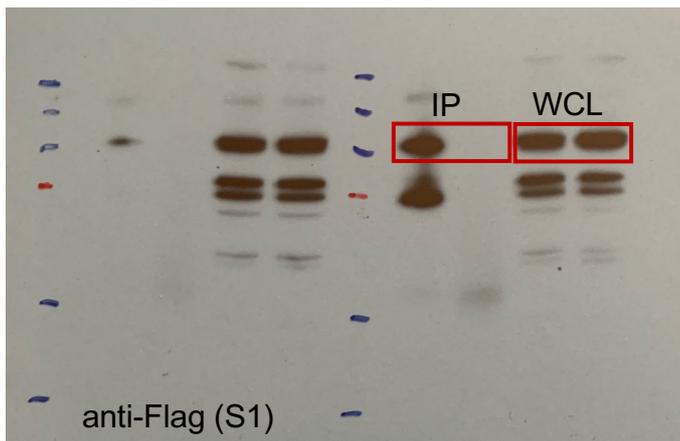
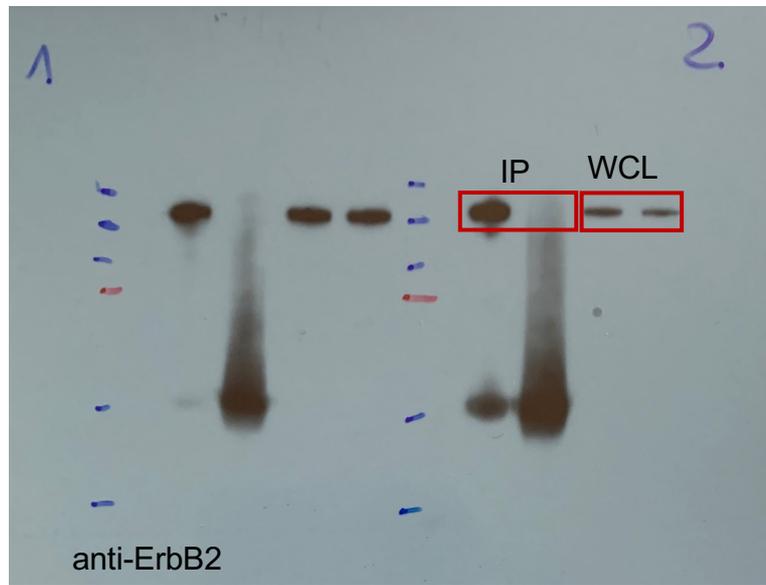
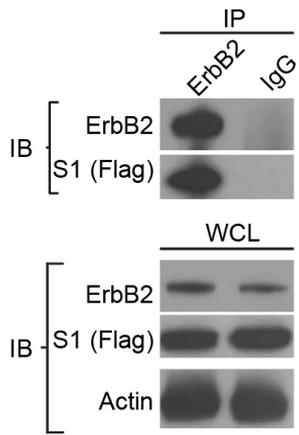
**Figure 4F**



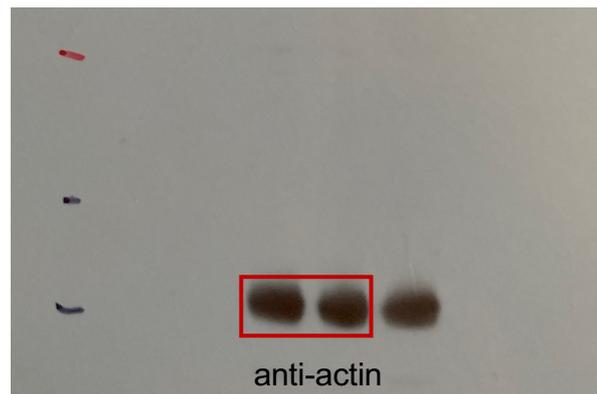
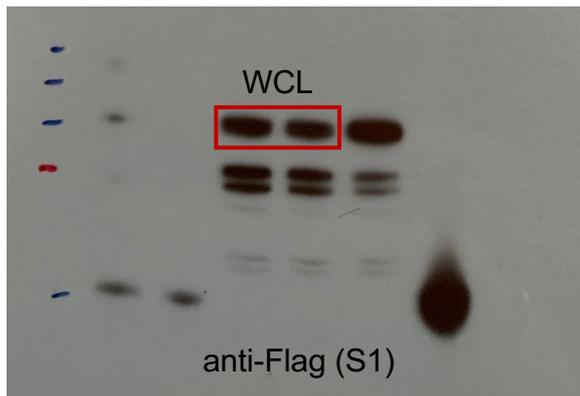
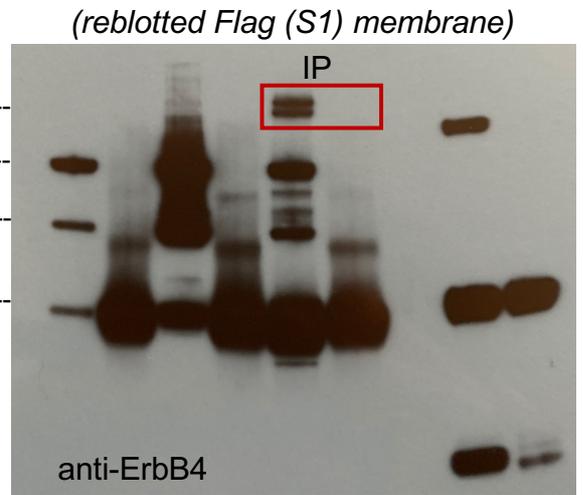
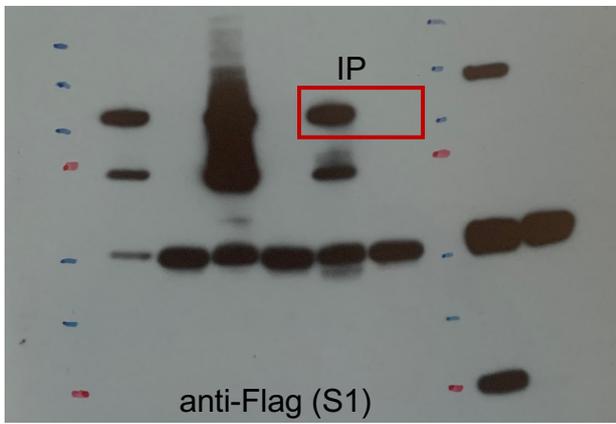
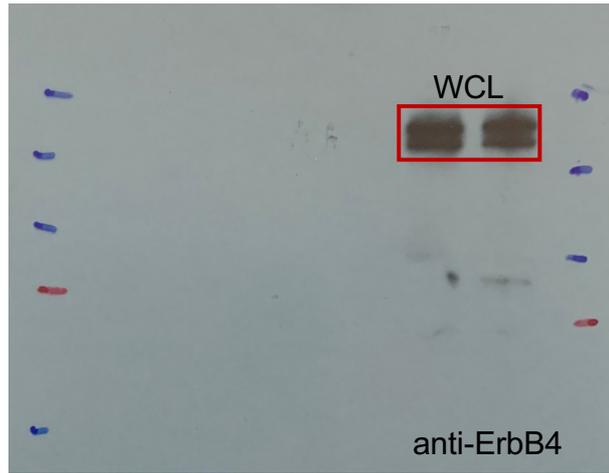
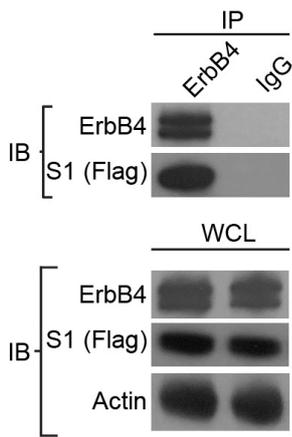
**Figure 5M**



**Figure 5M**



**Figure 5M**



All membranes were cropped prior to blotting to facilitate staining with multiple antibodies. Numbers indicate parts originating from the same membrane. The membranes were blotted first for phosphoproteins (or nucleocapsid), stripped and then blotted for the corresponding total protein. Same volume of sample was loaded for all four membranes. A representative actin is shown. The quantification was done using actin corresponding to each membrane.

**Figure 6A**

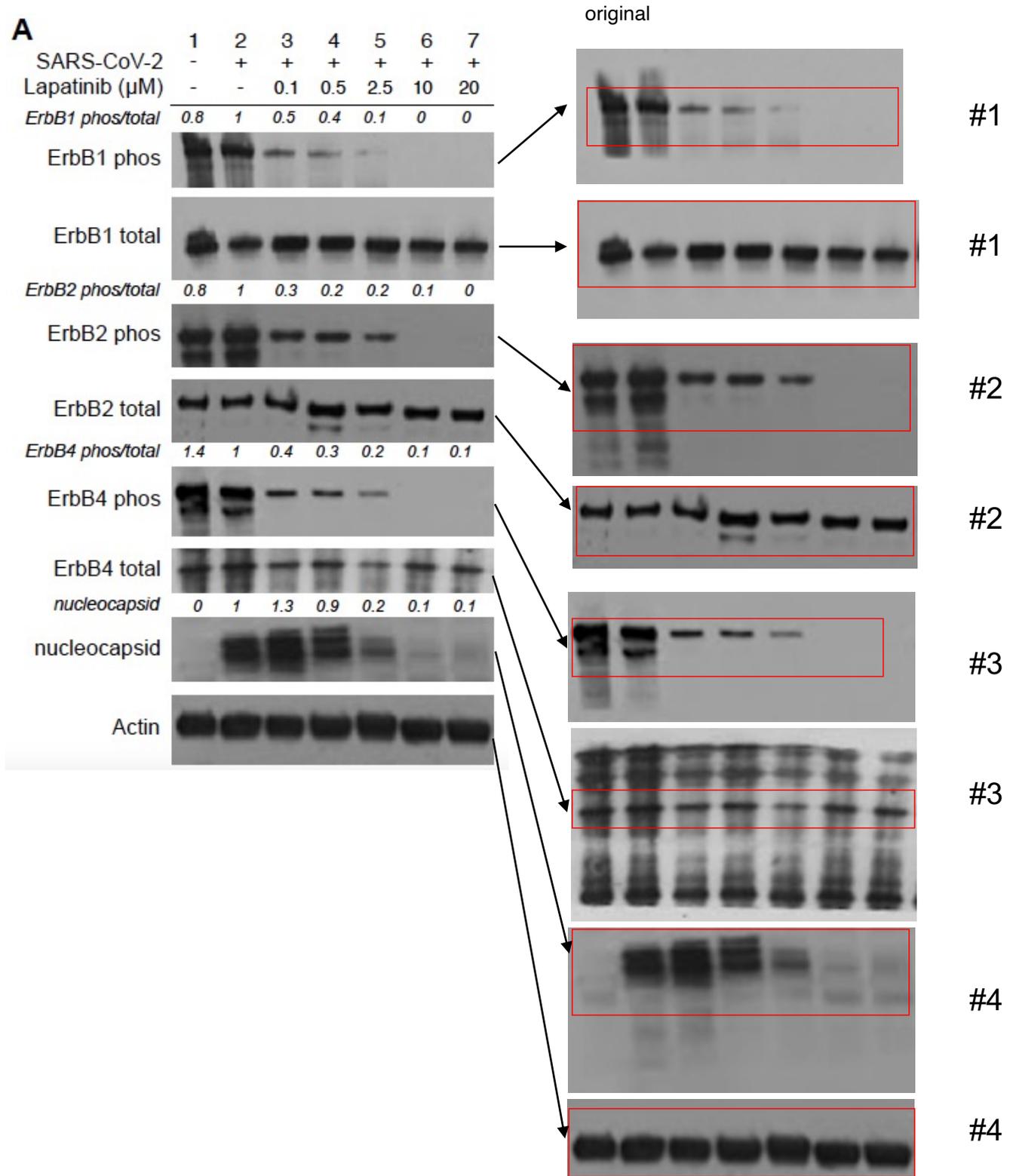
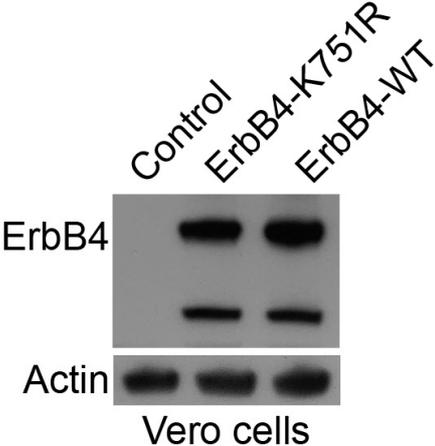
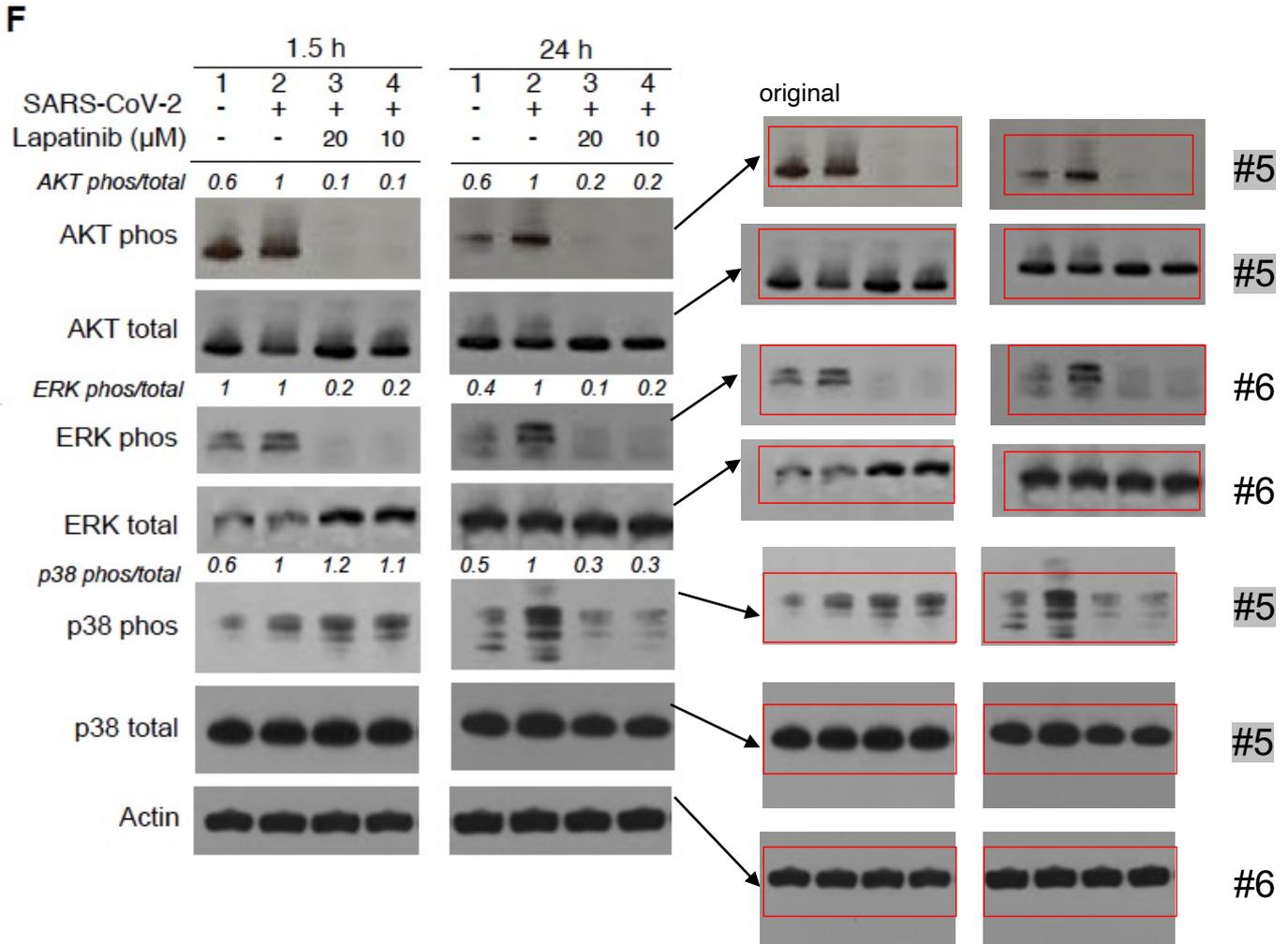


Figure 6D



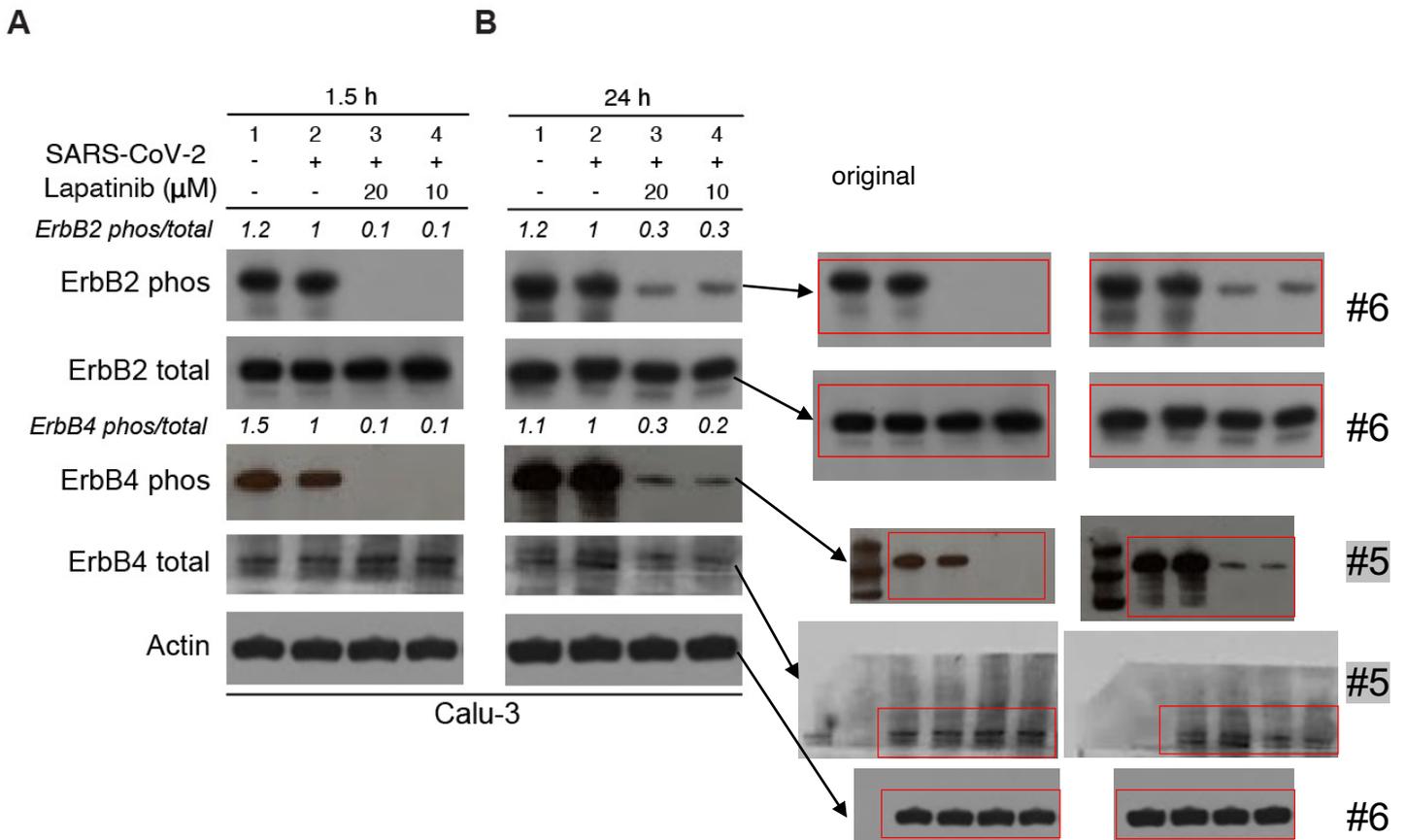
All membranes were cropped prior to blotting to facilitate staining with multiple antibodies. Numbers in Fig. 6F and Fig 7A, B indicate parts originating from the same membrane. The membranes were blotted first for phosphoproteins, stripped and then blotted for the corresponding total protein.

**Figure 6F**



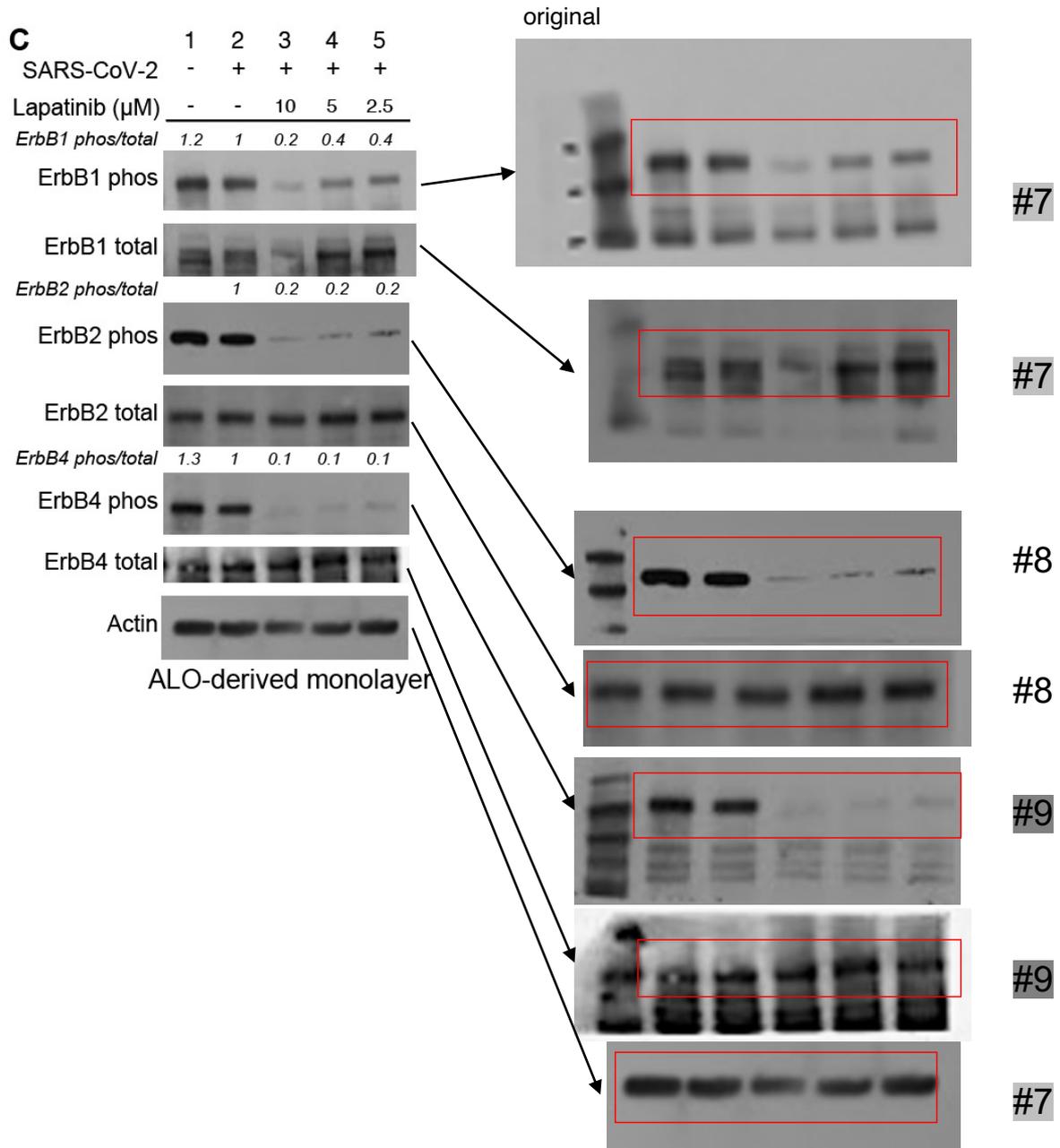
All membranes were cropped prior to blotting to facilitate staining with multiple antibodies. Numbers in Fig. 6F and Fig 7A, B indicate parts originating from the same membrane. The membranes were blotted first for phosphoproteins, stripped and then blotted for the corresponding total protein.

## Supplemental Figure 7A, B



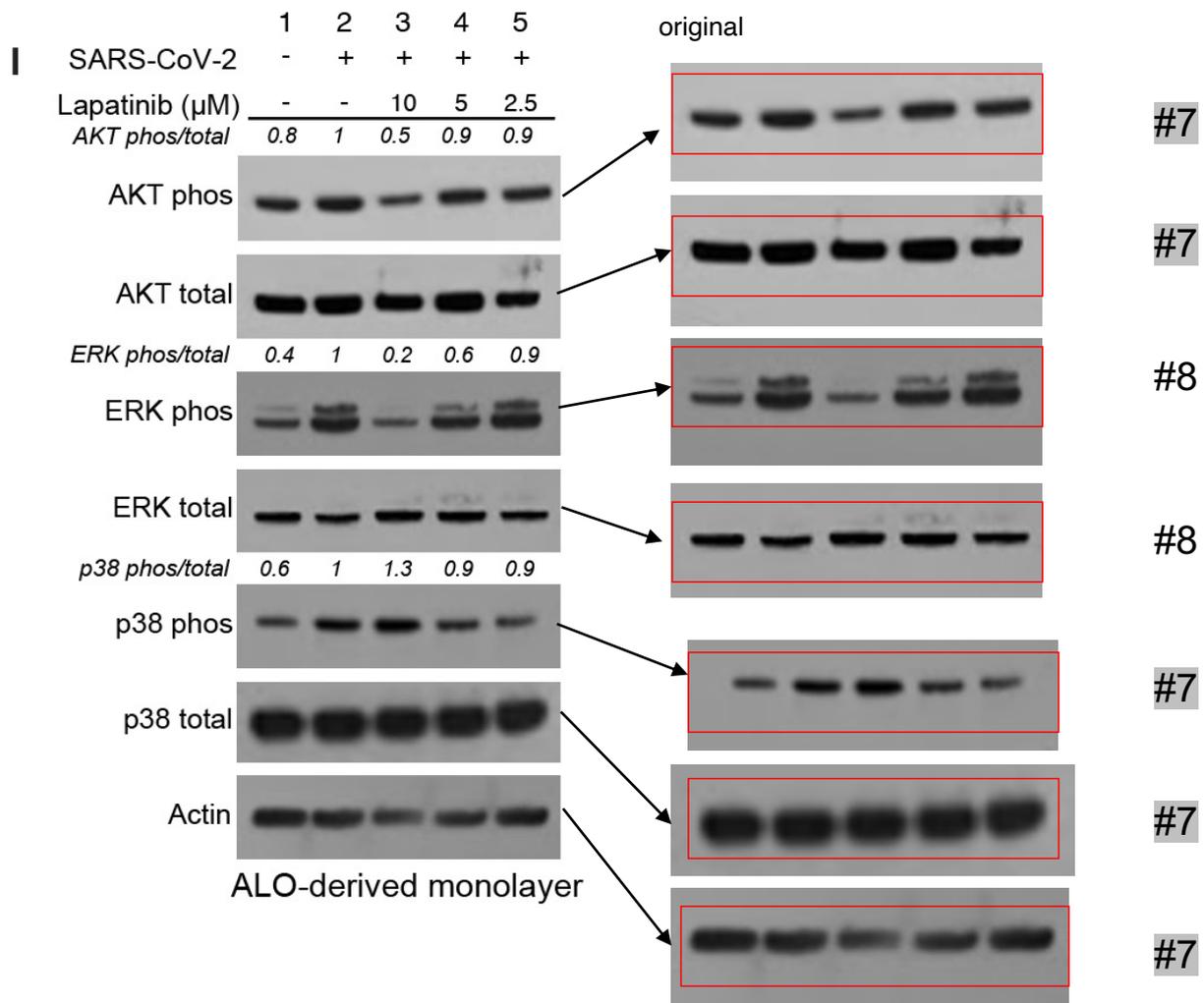
All membranes were cropped prior to blotting to facilitate staining with multiple antibodies. Numbers in Fig. 7C and Fig 7I represent parts originating from the same membrane. The membranes were blotted first for phosphoproteins, stripped and then blotted for the corresponding total protein.

### Supplemental Figure 7C



All membranes were cropped prior to blotting to facilitate staining with multiple antibodies. Numbers in Fig. 7C and Fig 7I indicate parts originating from the same membrane. The membranes were blotted first for phosphoproteins, stripped and then blotted for the corresponding total protein.

## Supplemental Figure 7I



# Supplementary Figure 7H

