

24 **Materials and Methods**

25 **Cells and Viruses**

26 Human hepatoma cell line (Huh7.0 cells), Vero-E6 cells, Vero cells, the human epithelial cell
27 line (Caco-2 cells), and human cervical cancer cell line (HeLa cells) were maintained in
28 Dulbecco's modified Eagle's medium (DMEM; HyClone). HEK293T cells were maintained in
29 Roswell Park Memorial Institute medium (RPMI; HyClone). Medium was supplemented with
30 10% foetal bovine serum (FBS; PAN Biotech) at 37°C in a 5% CO₂ humidified atmosphere.
31 SARS-CoV-2 (strain HB-01) was kindly provided by the National Virus Resource Center,
32 Wuhan Institute of Virology, Chinese Academy of Sciences. The complete genome for this
33 SARS-CoV-2 strain was submitted to GISAID (BetaCoV/Wuhan/IVDC-HB-01/2020|EPI-ISL-
34 402119).

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36 **Antibodies and Reagents**

37 Rabbit anti-LC3B (cat. no. 3868S) polyclonal antibodies (Abs), anti-Ribosomal protein L7a
38 (cat. no. 2415S), anti-PA28 α (cat. no. 2408S) polyclonal antibodies (Abs) were purchased from
39 Cell Signalling Technology. Rabbit anti-p62 (cat. no. PM045) polyclonal Abs and mouse anti-
40 tubulin (cat. no. M175-3) monoclonal Abs were purchased from MBL. Rabbit anti-Calnexin
41 (cat. no. C4731) polyclonal Abs and anti-TUFM polyclonal Abs were purchased from Sigma-
42 Aldrich. Mouse anti-SARS-CoV-2 nucleocapsid antibody was purchased from Sino Biological
43 (cat. no. 40143-MM05). Rabbit anti-TOM20 (cat. no. 11802-1-AP), anti-TIM23 (cat. no.
44 11123-1-AP) polyclonal Abs and mouse anti-GFP tag (cat. no. 66002-1-Ig) monoclonal Abs
45 were purchased from Proteintech. Mouse anti-Flag tag (cat. no. AE005) and anti-HA tag (cat.

46 no. AE008) monoclonal Abs were purchased from ABclonal Technology. Horseradish
47 peroxidase (HRP)-conjugated anti-mouse (cat. no. AS003) and anti-rabbit (cat. no. AS014)
48 secondary Abs were purchased from ABclonal Technology. CoraLite 594-conjugated goat anti-
49 mouse (cat. no. SA00013-3) secondary Abs were purchased from Proteintech.
50 Chloroquine (CQ) (cat. no. HY-17589A), 3-methyladenine (3-MA) (cat. no. HY-19312),
51 Wortmannin (cat. no. HY-10197) and MG132 (cat. no. HY-13259) were purchased from
52 MedChemExpress. Lipofectamine 2000 (cat. no. 11668) were purchased from Invitrogen.

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54 **SDS-PAGE and Western Blotting**

55 For the SDS-PAGE assay, protein samples were prepared by using cell lysis buffer for Western
56 blotting and Immunoprecipitation (IP) (Beyotime) that contained an EDTA-free protease
57 inhibitor cocktail (Bimake). After SDS-PAGE separation, proteins were transferred to
58 nitrocellulose membranes (GE Healthcare). After blocking with 2% bovine serum albumin
59 (BSA, Biofrox) in Phosphate Buffered Saline (PBS), the membranes were incubated with
60 corresponding primary antibodies, followed by horseradish peroxidase-conjugated secondary
61 antibodies.

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63 **Immunofluorescence Analysis**

64 Huh7.0/Vero-E6 cells were transfected with the indicated plasmids with Lipofectamine 2000
65 (Invitrogen) according to the manufacturer's protocol. After transfection for 24 hours, Huh7.0
66 cells were infected with SARS-CoV-2 at a MOI of 1, and Vero-E6 cells were infected with
67 SARS-CoV-2 at a MOI of 0.05 for 24 or 48 hours. For immunofluorescence analysis, the cells

68 to be tested were fixed with 4% paraformaldehyde (PFA) at room temperature for 30 min and
69 treated with 0.1% (vol/vol) Triton X-100 for 10 min. The cells were incubated in 2% (vol/vol)
70 BSA for 1 hour at room temperature. Then, the cells were incubated with the designated primary
71 antibody for 2 hours and then with the appropriate Alexa Fluor-conjugated secondary antibody
72 for 1 hour. Finally, DAPI staining was used to visualize DNA according to the purpose of the
73 experiment. The cells were then observed with a ZEISS confocal microscope under a 60 × oil
74 objective.

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76 **In Vivo Coimmunoprecipitation**

77 Huh7.0 cells were transfected with the appropriate plasmids with Lipofectamine 2000
78 according to the manufacturer's protocol, and 36 hours later, cells were harvested and lysed
79 with lysis buffer (50 mM Tris-HCl [pH 7.4], 150 mM NaCl, 1% [wt/vol] Triton X-100, 1 mM
80 EDTA [pH 8.0], 0.1% [vol/vol] sodium dodecyl sulfate [SDS], and protease inhibitor cocktail)
81 for 30 min at 4°C. The supernatants were collected by centrifugation at 13,000 rpm for 30 min
82 at 4°C and precleared by incubation with protein G Sepharose 4 Fast Flow beads for 1 hour at
83 4°C with rotation. The supernatants were collected via centrifugation at 3,000 rpm for 2 min at
84 4°C, and specific primary antibodies were added and incubated overnight at 4°C with rotation.
85 The beads were collected via centrifugation at 3,000 rpm for 2 min at 4°C and washed three
86 times with 1 mL lysis buffer. Then, the collected beads were boiled at 100°C for 5 min in 50 µL
87 2 × SDS protein-loading buffer and analysed via Western blot.

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89 **Transmission Electron Microscopy**

90 Vero-E6 cells were infected with SARS-CoV-2 for 24 hours at a MOI of 0.05 or treated with
91 CQ (50 mM) for 6 hours. Then, the cells were fixed with 2.5% glutaraldehyde for 2 hours at
92 room temperature. The cells were harvested and fixed with 2.5% glutaraldehyde on ice for 2
93 hours followed by fixation in 2% osmium tetroxide, and then, the cells were dehydrated with
94 sequential washes in 50%, 70%, 90%, 95%, and 100% ethanol. Areas containing cells were
95 block-mounted and thinly sliced.

96

97 **Autophagy Analysis**

98 For analyses involving CQ (50 mM), Huh7.0/Vero-E6 cells were treated for 6 hours before
99 further experiments. For analyses involving 3-MA (5 mM) and Wortmannin (10 μ M), Huh7.0
100 cells were treated for 4 hours and treated again after absorption of SARS-CoV-2 until the
101 samples were harvested. For analyses involving only 3-MA (1 mM), Vero-E6 cells were treated
102 for 4 hours and treated again after absorption of SARS-CoV-2 until the samples were harvested.

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104 **Virus Plaque Assay**

105 Huh7.0 cells or Caco-2 cells pretreated with 3-MA, Wortmannin were infected by SARS-CoV-
106 2 for 1 hour at a MOI of 1, and then, the medium was replaced with the same medium as that
107 was used for the pretreatment. Additionally, Vero-E6 cells pretreated with 3-MA or Wortmannin
108 were infected with SARS-CoV-2 for 1 hour at a MOI of 0.05, and then, the medium was
109 replaced with the same medium as that used for the pretreatment. The supernatants were
110 obtained at 24 hours after infection for the virus plaque assay. Briefly, the sample to be tested
111 was diluted in basal DMEM, and confluent Vero cells in 12-well plates were inoculated with

112 the samples and incubated at 37°C for 1 hour. The cells were washed twice with PBS (HyClone)
113 to remove unbound virus. Subsequently, the cells were covered with 1 mL of 4% sodium
114 carboxymethyl cellulose (containing 3% FBS) per well. After culturing for 72 hours, when the
115 cells showed lesions or plaques, each well was filled with 10% neutral formaldehyde and fixed
116 for more than 4 hours. Finally, plaques were stained with 0.1% crystal violet and counted.

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118 **Subcellular Fractionation**

119 Subcellular fractionation assays were performed as previously described ¹. Briefly, Huh7.0 cells
120 were transfected with the indicated plasmids, and 36 hours later, cells were harvested and
121 resuspended in 300 mL mitochondria isolation buffer (10 mM Tris-HCl [pH 7.4], 2 mM MgCl₂,
122 10 mM KCl, and 250 mM sucrose) and homogenized with a Dounce tissue grinder for 20 min
123 at 4°C. The supernatants were collected after centrifugation at 500 g for 10 min at 4°C and then
124 centrifuged for another 5,000 g for 10 min to yield the cytosolic fraction. Precipitates were
125 resuspended in 1 mL mitochondria extraction buffer and collected after centrifugation at 5,000
126 g for 10 min at 4°C to yield the mitochondrial fraction. Equivalent amounts of protein from
127 each fraction were analysed by Western blot with the indicated antibodies.

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129 **Reporter Assays**

130 HEK293T cells cultured in 12-well plates were transfected with a control plasmid or plasmids
131 expressing RIG-I-N, MAVS, TBK1, IKK ϵ , or IRF3-5D, along with IFN- β luciferase reporter
132 plasmids or plasmids expressing viral proteins. After 24 hours of transfection, cells were
133 harvested, and cell lysates were used to measure luciferase levels using a Dual Luciferase

134 Reporter Assay System (Promega). In addition, Sendai virus was used as a positive stimulus.

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136 **Flow Cytometric Analyses**

137 Mitochondria-associated ROS levels were measured by staining cells with MitoSOX
138 (Invitrogen) at 2.5 μ M for 30 min at 37 °C. Mitochondria membrane potential was measured
139 using the kit from Invitrogen and performed according to the manufacturer's instructions. Cells
140 were then washed with PBS solution and re-suspended in cold PBS solution for FACS analysis.

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142 **Statistical Analysis**

143 Data are expressed as the means \pm standard errors of the means (SEMs). Statistical analysis was
144 performed by Student's t test using GraphPad Prism software (version 5.0). A P value equal to
145 or lower than 0.05 was considered significant.

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147 **Abbreviation**

148 SARS-CoV-2: Severe Acute Respiratory Syndrome Coronavirus 2; CQ: chloroquine; 3-MA: 3-
149 methyladenine; ATG: autophagy related; p62: sequestosome 1; LC3: microtubule-associated
150 proteins light chain 3; TIM23: mitochondrial import inner membrane translocase subunit;
151 TOM20: mitochondrial 20 kDa outer membrane protein; PA28: proteasome activator 28 subunit;
152 L7a: 60S ribosomal protein L7a. RFP-LC3: LC3 fused to red fluorescent protein (gene); GFP-
153 LC3: LC3 fused to green fluorescent protein (gene); BID: BH3-interacting domain death
154 agonist; WT: wild type; SeV: sendai virus; IFN: interferon; RIG-I: antiviral innate immune
155 response receptor; MAVS: mitochondrial antiviral-signaling protein; TBK1: serine/threonine-

156 protein kinase; IKK ϵ : inhibitor- κ b kinase ϵ ; IRF3-5D: interferon regulatory factor 3 mutant;
157 TUFM: Tu translation elongation factor mitochondrial; MOI: multiplicity of infection; hpi:
158 hours post-infection; hpt: hours post-transfection.

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160 **References**

161 1 Ding, B. *et al.* The Matrix Protein of Human Parainfluenza Virus Type 3 Induces Mitophagy that
162 Suppresses Interferon Responses. *Cell Host Microbe* **21**, 538-547 e534, doi:10.1016/j.chom.2017.03.004
163 (2017).

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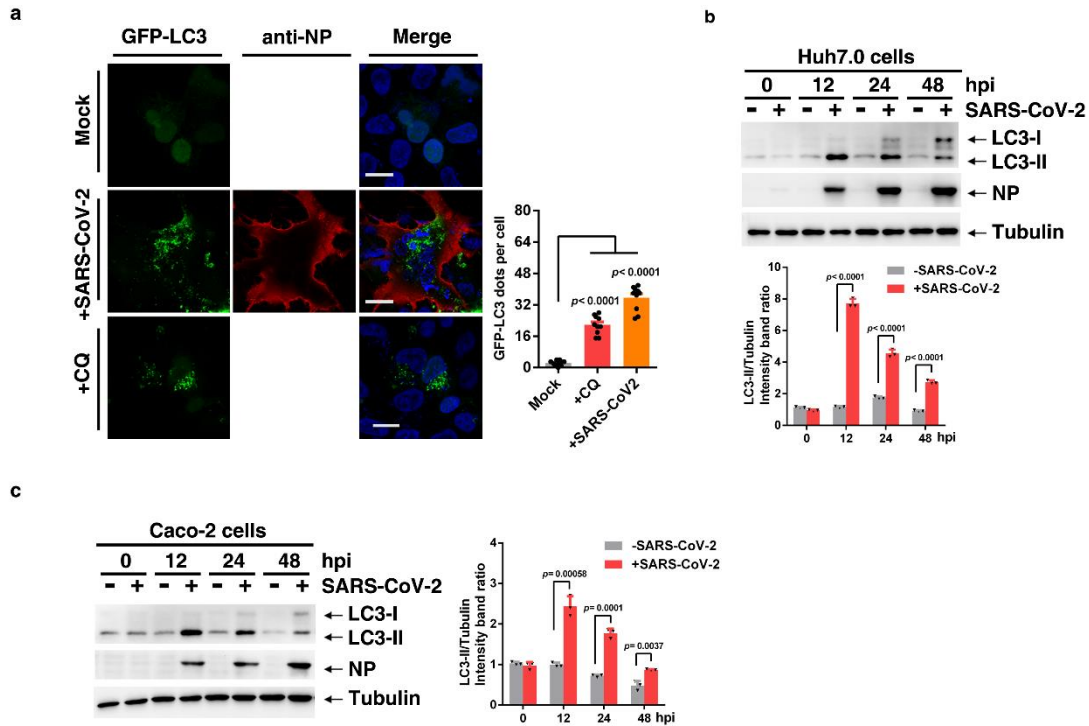
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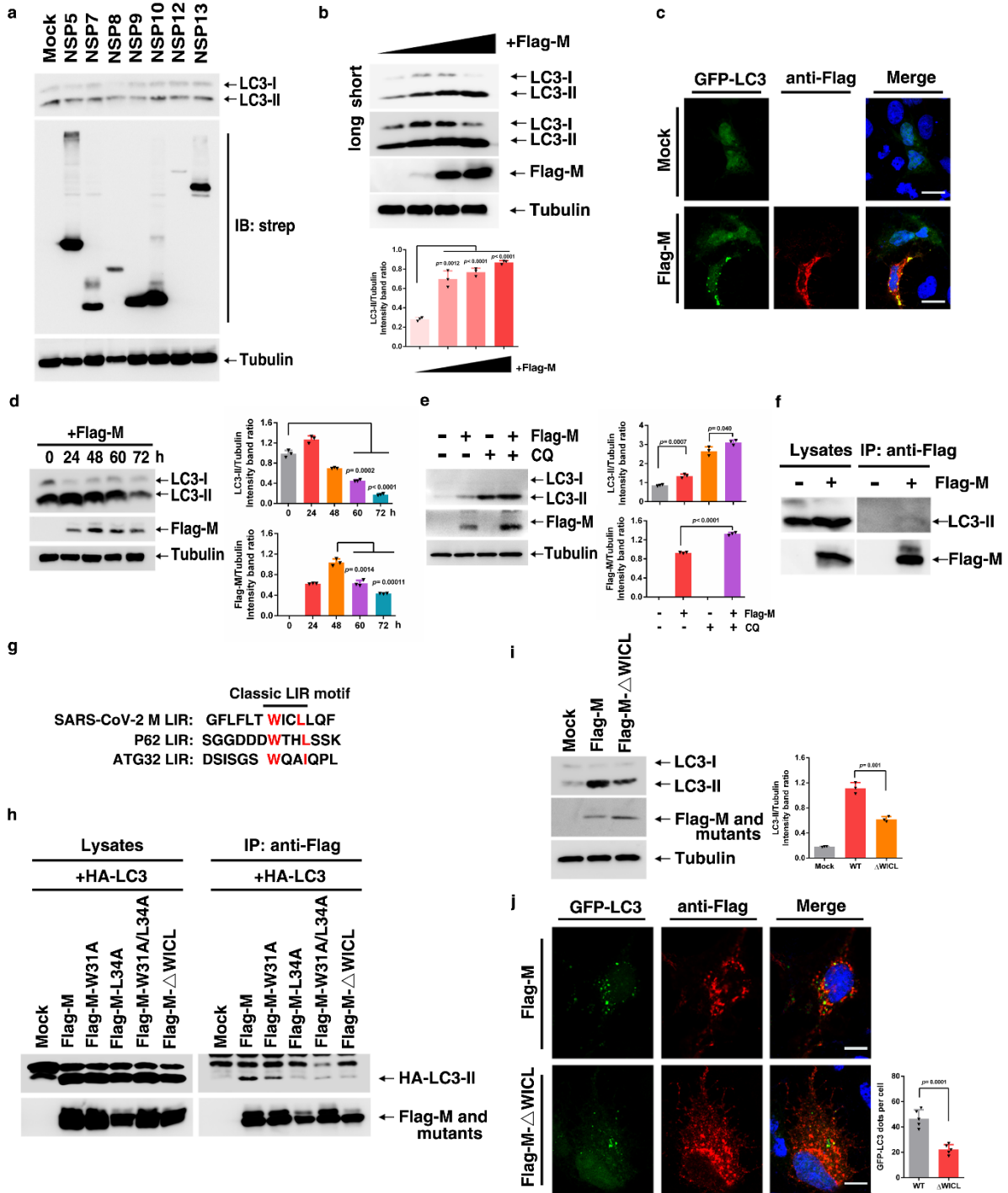
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180 **Supplementary Figures**



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 182 **Fig. S1** SARS-CoV-2 infection triggers autophagy in vitro. **a** GFP-LC3 dot formation in
 183 Huh7.0 cells transiently transfected with GFP-LC3 and either left uninfected (Mock) or infected
 184 with SARS-CoV-2 (MOI of 1) for 48 hours or treated with CQ for 4 hours. Scale bar, 10 μ m. **b**
 185 Huh7.0 cells were uninfected (-) or infected (+) with SARS-CoV-2. Lysates were evaluated by
 186 Western blotting (WB). **c** Caco-2 cells were uninfected (-) or infected (+) with SARS-CoV-2.
 187 Lysates were evaluated by Western blotting (WB). Three independent experiments with three
 188 technical repetitions were performed. Data are expressed as mean \pm SEM (error bars). Statistical
 189 analyses used Student's t test. $P < 0.05$ was considered statistically significant.

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199 **Fig. S2** SARS-CoV-2 M induces autophagy and interact with LC3. **a** Huh7.0 cells were
 200 transfected with the indicated plasmids. Lysates were analysed by immunoblotting. **b** Huh7.0
 201 cells were transfected with the indicated plasmids and analysed for the colocalization of Flag-
 202 M and GFP-LC3. **c** Huh7.0 cells were transfected with different concentrations of Flag-M
 203 plasmid (0 μ g, 0.3 μ g, 1 μ g and 2 μ g). Lysates were analysed by immunoblotting. **d** HEK293T

204 cells were transfected with Flag-M plasmid and collected at different times. Lysates were
205 analysed by immunoblotting. **e** Huh7.0 cells were transfected with Flag-M and treated with CQ.
206 Lysates were analysed by immunoblotting. **f** Interaction between Flag-M and endogenous LC3
207 in Huh7.0 cells. **g** Typical LIR sequences in SARS-CoV-2-M. **h** Interaction between HA-LC3
208 and wild-type M and mutants. **i** Huh7.0 cells were transfected with the indicated plasmids and
209 analysed by immunoblotting. **j** Huh7.0 cells were transfected with Flag-M plasmid and mutant
210 plasmids and analysed for GFP-LC3 dots. Scale bar, 10 μ m. Three independent experiments
211 with three technical repetitions were performed. Data are expressed as mean \pm SEM (error bars).
212 Statistical analyses used Student's t test. $P < 0.05$ was considered statistically significant.

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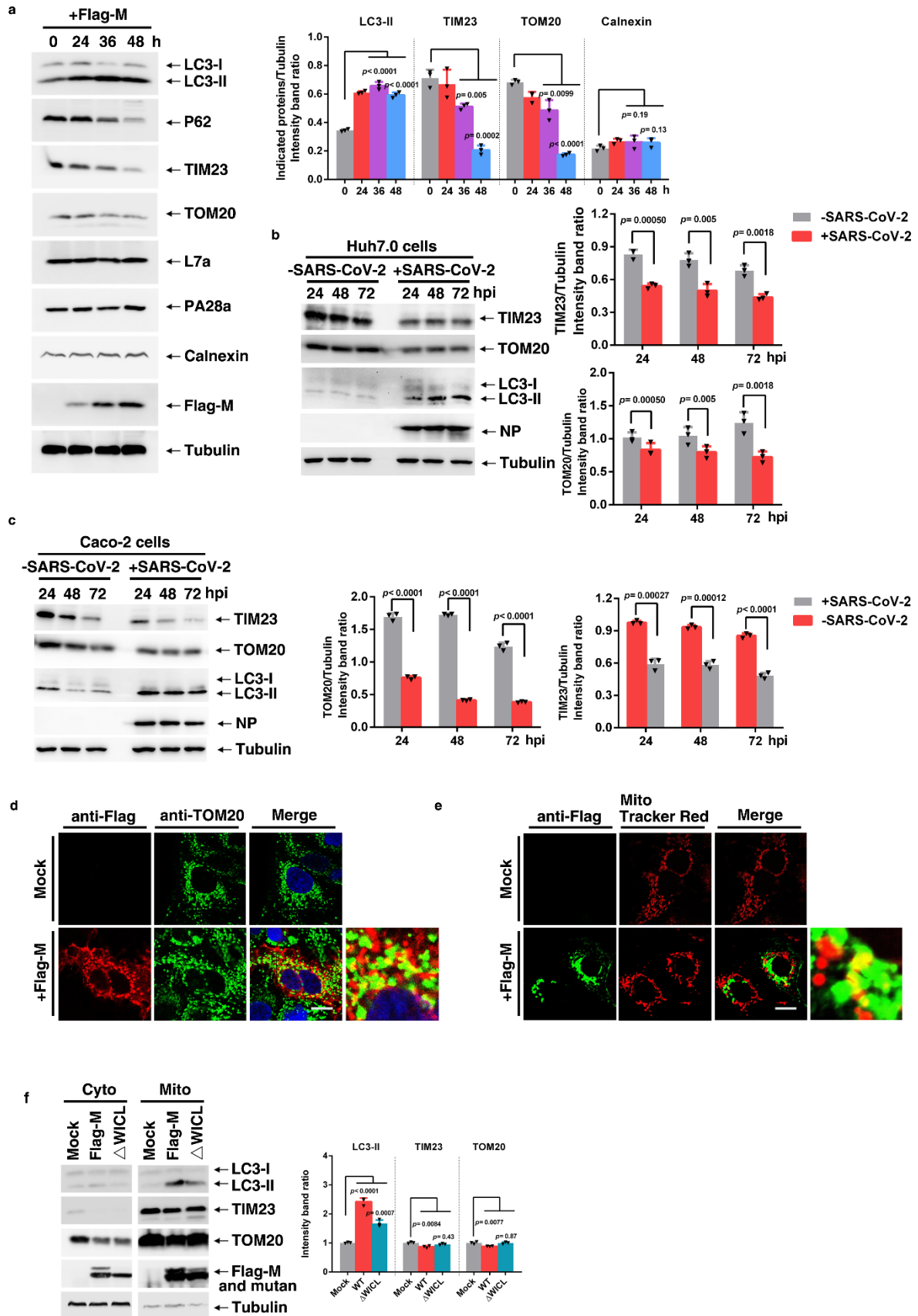
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234 **Fig. S3** SARS-CoV-2 and M induces selective mitochondrial autophagy. **a** Huh7.0 cells were

235 transfected with Flag-M plasmid and collected at different times. Lysates were analysed by
236 immunoblotting. **b** Huh7.0 cells were uninfected (-) or infected (+) SARS-CoV-2. Lysates were
237 collected at different times and analysed by immunoblotting. **c** Caco-2 cells were uninfected (-)
238 or infected (+) SARS-CoV-2. Lysates were collected at different times and analysed by
239 immunoblotting. **d** Huh7.0 cells were transfected with Flag-M plasmid plasmids and analysed
240 for the colocalization of Flag-M and TOM20 (mitochondrial 20 kDa outer membrane protein).
241 Scale bar, 10 μ m. **e** Huh7.0 cells were transfected with Flag-M plasmid plasmids and analysed
242 for the colocalization of Flag-M and mitochondria labeled with probes. Scale bar, 10 μ m. **f**
243 Huh7.0 cells were transfected with the indicated plasmids, and mitochondrial fractions were
244 isolated via ultracentrifugation. Cytoplasm (Cyto) and mitochondria (Mito) were analysed by
245 immunoblotting. Three independent experiments with three technical repetitions were
246 performed. Data are expressed as mean \pm SEM (error bars). Statistical analyses used
247 Student's t test. $P < 0.05$ was considered statistically significant.

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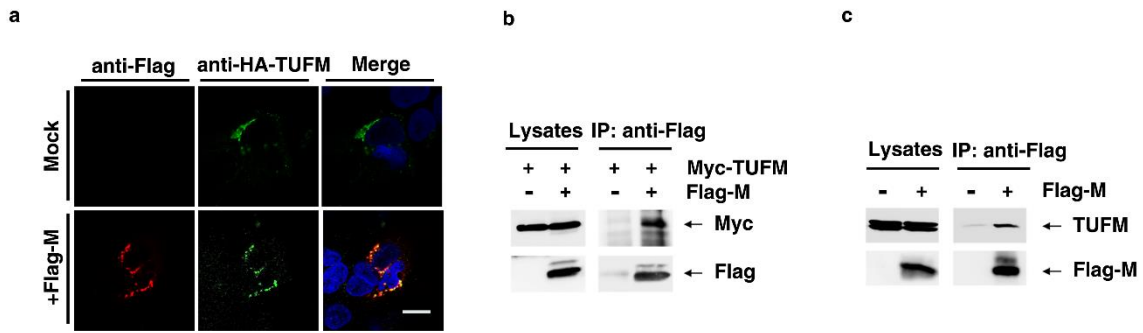
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265 **Fig. S4** SARS-CoV-2 M interact with TUFM (Tu translation elongation factor mitochondrial).

266 **a** Huh7.0 cells were transfected with Flag-M plasmid plasmids and HA-TUFM plasmid,

267 analysed for the colocalization of Flag-M and HA-TUFM. Scale bar, 10 μ m. **b** Interaction

268 between Flag-M and Myc-TUFM. **c** Interaction between Flag-M and endogenous TUFM in

269 Huh7.0 cells. Three independent experiments with three technical repetitions were performed.

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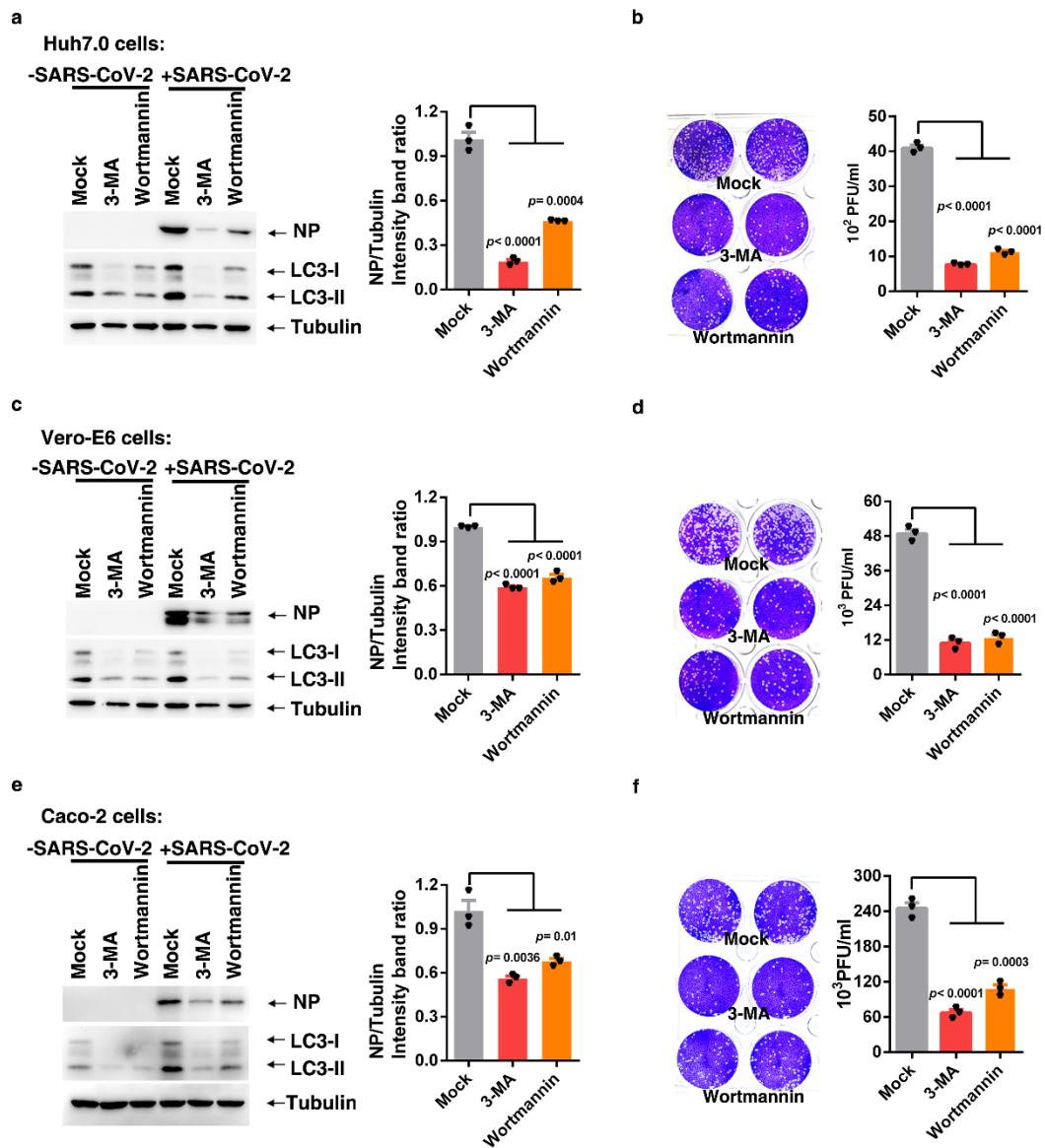
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289 **Fig. S5** Blocking autophagy with two pharmaceutical inhibitors (3-MA and Wortmannin)
 290 significantly suppresses SARS-CoV-2 infection. **a** Huh7.0 cells were untreated (Mock) or
 291 treated with 3-MA/Wortmannin and then uninfected (-) or infected (+) with SARS-CoV-2
 292 (MOI of 1) for 24 hours. Lysates were evaluated by WB. **b** Huh7.0 cells were untreated (Mock)
 293 or treated with 3-MA/Wortmannin and then uninfected (-) or infected (+) with SARS-CoV-2
 294 (MOI of 1) for 24 hours. Extracellular viral yields were evaluated by virus plaque assay. **c** Vero-
 295 E6 cells were untreated (Mock) or treated with 3-MA/Wortmannin and then uninfected (-) or
 296 infected (+) with SARS-CoV-2 (MOI of 0.05) for 24 hours. Lysates were evaluated by WB. **d**
 297 Vero-E6 cells were untreated (Mock) or treated with 3-MA/Wortmannin and then uninfected

298 (-) or infected (+) with SARS-CoV-2 (MOI of 0.05) for 24 hours. Extracellular viral yields were
299 evaluated by virus plaque assay. **e** Caco-2 cells were untreated (Mock) or treated with 3-
300 MA/Wortmannin and then uninfected (-) or infected (+) with SARS-CoV-2 (MOI of 1) for 24
301 hours. Lysates were evaluated by WB. **f** Caco-2 cells were untreated (Mock) or treated with 3-
302 MA/Wortmannin and then uninfected (-) or infected (+) with SARS-CoV-2 (MOI of 1) for 24
303 hours. Extracellular viral yields were evaluated by virus plaque assay. Three independent
304 experiments with three technical repetitions were performed. Data are expressed as
305 mean \pm SEM (error bars). Statistical analyses used Student's t test. $P < 0.05$ was considered
306 statistically significant.

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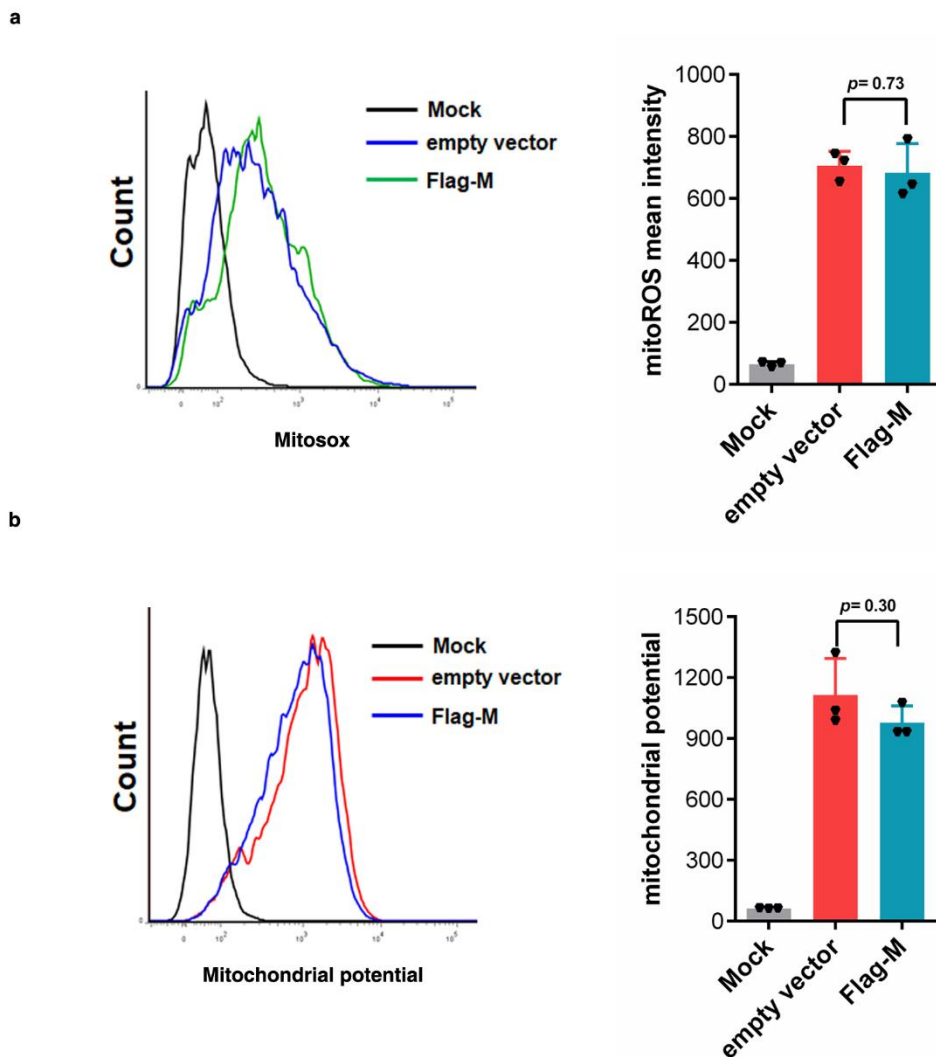
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328 **Fig. S6** Detection of superoxide in live cells using MitoSOX™ Red superoxide indicator and
 329 detection of mitochondrial membrane potential using MitoProbe TMRM. **a** Huh7.0 cells were
 330 transfected with Flag-M plasmid and cells were subsequently stained with MitoProbe TMRM
 331 and analyzed on an Attune NxT Flow Cytometer using a 561 nm laser for excitation and 585
 332 nm/16BP filter for emission. **b** Huh7.0 cells were transfected with Flag-M plasmid and cells
 333 were subsequently stained with MitoSOX™ Red superoxide indicator and analyzed on an
 334 Attune NxT Flow Cytometer using a 561 nm laser for excitation and 585 nm/16BP filter for
 335 emission. Three independent experiments with three technical repetitions were performed. Data
 336 are expressed as mean \pm SEM (error bars). Statistical analyses used Student's *t* test. $P < 0.05$
 337 was considered statistically significant.