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1	Mitoquinone mesylate targets SARS-CoV-2 and associated lung inflammation through host
2	pathways
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1 Summary:

2 To date, there is no effective oral antiviral against SARS-CoV-2 that is also anti-inflammatory. 3 Herein, we show that the mitochondrial antioxidant mitoguinone/mitoguinol mesylate (Mito-4 MES), a dietary supplement, has potent antiviral activity against SARS-CoV-2 and its variants of 5 concern in vitro and in vivo. Mito-MES had nanomolar in vitro antiviral potency against the Beta 6 and Delta SARS-CoV-2 variants as well as the murine hepatitis virus (MHV-A59). Mito-MES 7 given in SARS-CoV-2 infected K18-hACE2 mice through oral gavage reduced viral titer by 8 nearly 4 log units relative to the vehicle group. We found *in vitro* that the antiviral effect of 9 Mito-MES is attributable to its hydrophobic dTPP+ moiety and its combined effects scavenging 10 reactive oxygen species (ROS), activating Nrf2 and increasing the host defense proteins TOM70 11 and MX1. Mito-MES was efficacious reducing increase in cleaved caspase-3 and inflammation 12 induced by SARS-CoV2 infection both in lung epithelial cells and a transgenic mouse model of 13 COVID-19. Mito-MES reduced production of IL-6 by SARS-CoV-2 infected epithelial cells 14 through its antioxidant properties (Nrf2 agonist, coenzyme Q₁₀ moiety) and the dTPP moiety. 15 Given established safety of Mito-MES in humans, our results suggest that Mito-MES may 16 represent a rapidly applicable therapeutic strategy that can be added in the therapeutic arsenal 17 against COVID-19. Its potential *long-term* use by humans as diet supplement could help control 18 the SARS-CoV-2 pandemic, especially in the setting of rapidly emerging SARS-CoV-2 variants 19 that may compromise vaccine efficacy.

20 **One-Sentence Summary:** Mitoquinone/mitoquinol mesylate has potent antiviral and anti-

21 inflammatory activity in preclinical models of SARS-CoV-2 infection.

22

Keywords: Mitochondrial antioxidants, antiviral, SARS-CoV-2, inflammation, lung damage,
 COVID-19

3 Introduction:

4 The SARS-CoV-2 pandemic emphasizes the urgent need to determine cellular pathways that 5 can be targeted by novel antivirals. Ideal antivirals would be given orally as soon as possible 6 after disease onset and should not only limit replication of rapidly evolving SARS-CoV-2 7 variants but also associated inflammation that drives morbidity in COVID-19(Hu et al., 2021). 8 The current treatments for COVID-19 have limitations. Remdesivir has shown limited 9 therapeutic efficacy(Ansems et al., 2021). Dexamethasone might suppress host antiviral 10 responses. Monoclonal antibodies are not oral, may not work against neutralization-resistant 11 variants and may even increase inflammation(Lee et al., 2020). Current antivirals in 12 development against SARS-CoV-2 such as nirmatrelvir/ritonavir and molnupiravir do not have 13 anti-inflammatory effects. Molnupiravir may interfere with host RNA polymerases and may be 14 mutagenic in cells(Zhou et al., 2021). Nirmatrelvir/ritonavir could cause severe or life-15 threatening interactions with widely used medications, including statins and blood thinners. 16 Thus, there is a continued need for the development of oral safe antivirals for treatment of 17 COVID-19.

18

Increased reactive oxygen species (ROS) contribute to the pathogenesis driven by respiratory syncytial virus (RSV)(Hu et al., 2019) and coronavirus(Shin et al., 2019). Mitochondria are a major source of ROS (mito-ROS). Aging compromises mitochondrial function and leads to increased production of mito-ROS(Braakhuis et al., 2018). Thus, decreasing mito-ROS and improving mitochondrial health may have broad health benefits including COVID-19 patients in

 mitochondrial antioxidant approved for human use which has been reported to support hea aging (Braakhuis et al., 2018). It can safely be delivered orally long-term to humans and it been used in clinical trials for ROS-related diseases (Rossman et al., 2018; Smith and Mur 2010). Mito-MES is coenzyme Q₁₀ (CoQ₁₀) conjugated to a lipophilic cation (TPP)(Smith Murphy, 2010). CoQ₁₀ is the endogenous mitochondrial coenzyme involved in electron tra and protection from lipid peroxidation (Smith and Murphy, 2010). Inside mitochondria, 	t has rphy, 1 and
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6 Murphy, 2010). Co Q_{10} is the endogenous mitochondrial coenzyme involved in electron tra	
	ansfer
and protection from lipid peroxidation (Smith and Murphy, 2010). Inside mitochondria,	
8 mitoquinone is being converted to its reduced active ubiquinol form, mitoquinol(Smith an	ıd
9 Murphy, 2010). Given that Mito-MES is antiviral against RSV(Hu et al., 2019), which has	S
10 similar mechanisms to evade host inflammatory responses to coronaviruses (Torres et al.,	2015),
11 we investigated whether Mito-MES is antiviral against SARS-CoV-2.	
12	
13 Results	
14 Mito-MES decreases SARS-CoV-2 replication <i>in vitro</i>	
15 We determined the effects of Mito-MES on SARS-CoV-2 replication first in Vero-E6	cells.
16 We found that Mito-MES had a higher half maximal inhibitory concentration (IC50) again	nst
17 SARS-CoV-2 (Figure 1A), compared to remdesivir (RDV) (Figure 1B). The antiviral effe	ect of
18 100-750 nM Mito-MES was confirmed by immunofluorescence (IF) detection of SARS-C	CoV-2
19 (Figure S1A) and by qPCR (Figure S1B). Given that intracellular levels of viral proteins i	s a
20 better parameter determining coronavirus infection, we used flow cytometry to quantify the	ne
21 intracellular content of SARS-CoV-2 Spike S and the Nucleocapsid proteins (NP). Flow	
cytometry further confirmed that 1000 nM Mito-MES reduced cellular levels of SARS-Co	oV-2 N
23 (Figure S1C) and S proteins (Figure S1D). There was no cytotoxicity induced by Mito-M	ES

across the effective dose range (10-1000 nM) in non-infected cells, based on XTT assay (Figure
 1A).

3	Given that Vero-E6 cells lack interferon I (IFN-I), which regulates antiviral response against
4	SARS-CoV-2(Hu et al., 2021), we tested Mito-MES in IFN-I competent human lung epithelial
5	Calu-3 (Calu3) cells. Notably, the IC50 of Mito-MES against SARS-CoV-2 measured by
6	TCID50 was 16-fold lower than remdesivir (Figure 1C and 1D). The antiviral efficacy of 10-
7	1000 nM Mito-MES as assessed by IF (Figures 1E and S1E) and qPCR (Figure S1F) was much
8	higher in Calu3 than in Vero-E6 cells. Flow cytometry further confirmed that Mito-MES
9	attenuated the percent of SARS-CoV-2 infected Calu3 cells (Figure S1G and S1H). The anti-
10	SARS-CoV-2 activity of Mito-MES was also confirmed in additional human cells including
11	HEK 293T expressing ACE2 (Figure S1I) and human airway epithelial (HAE) cells in air-liquid
12	interface (ALI) cultures (Figure 1F). We confirmed by flow cytometry the antiviral efficacy of
13	Mito-MES in human FOXJ1 positive ciliated epithelial cells infected with SARS-CoV-2 (Figure
14	S1J), as these ciliated epithelial cells are the main cells infected by SARS-CoV-2 in the lower
15	respiratory tract (Hu et al., 2021). In summary, our results show that Mito-MES has potent
16	antiviral activity against SARS-CoV-2 at the nM level in interferon competent human epithelial
17	cells. Our data are consistent with data from Codo et al that showed that pretreatment with Mito-
18	MES inhibited SARS-CoV-2 replication in monocytes (Codo et al., 2020). However, monocytes
19	have little to no expression of ACE2 and it remains unclear whether monocytes and macrophages
20	contribute to viral spread and COVID-19 disease progression (Hu et al., 2021). Herein, we
21	provide the first evidence that Mito-MES directly attenuates SARS-CoV-2 replication in airway
22	epithelial cells, the main target of SARS-CoV-2.

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1 Mito-MES is antiviral against various coronaviruses

2

3	Given that Mito-MES targets host cellular targets that impact replication of coronaviruses,
4	we hypothesized that Mito-MES has also antiviral activity against SARS-CoV-2 variants of
5	concerns (VOCs) and other coronaviruses. Mito-MES inhibited in vitro SARS-CoV-2 B.1.351
6	(Beta) (IC50=0.034 μ M) (Figure 2A) and B.1.617.2 (Delta) (IC50=0.041 μ M) variants (Figure
7	2B) in Calu3 cells. Mito-MES 1000 nM also inhibited SARS-CoV-2 Delta variants in ALI lung
8	cultures (Figure 2C). Mito-MES inhibited murine hepatitis virus (MHV-A59) in mouse 17Cl-1
9	fibroblasts (IC50=0.310 μ M) (Figure 2D) as well as SARS-CoV-2 Delta variant in mouse lung
10	cells from K18-hACE2 mice (IC50=1.6 μ M) (Figure 2E) and was more potent antiviral than
11	remdesivir (Figure 2F). Our data suggest that Mito-MES can be a useful antiviral therapy for
12	coronaviruses, especially in the setting of rapidly emerging SARS-CoV-2 variants.
13	
	The TPP moiety of Mito-MES is antiviral
13	The TPP moiety of Mito-MES is antiviral
13 14	The TPP moiety of Mito-MES is antiviral To elucidate the mechanism of action through which Mito-MES inhibits SARS-CoV-2, we
13 14 15	
13 14 15 16	To elucidate the mechanism of action through which Mito-MES inhibits SARS-CoV-2, we
13 14 15 16 17	To elucidate the mechanism of action through which Mito-MES inhibits SARS-CoV-2, we compared the antiviral effects of Mito-MES administered before or concurrently with SARS-
 13 14 15 16 17 18 	To elucidate the mechanism of action through which Mito-MES inhibits SARS-CoV-2, we compared the antiviral effects of Mito-MES administered before or concurrently with SARS-CoV-2. We found that 1000 nM Mito-MES inhibited NP expression in Calu3 cells when added
 13 14 15 16 17 18 19 	To elucidate the mechanism of action through which Mito-MES inhibits SARS-CoV-2, we compared the antiviral effects of Mito-MES administered before or concurrently with SARS-CoV-2. We found that 1000 nM Mito-MES inhibited NP expression in Calu3 cells when added before infection (effect on viral entry) but also when added 4 hours post infection (hpi), which
 13 14 15 16 17 18 19 20 	To elucidate the mechanism of action through which Mito-MES inhibits SARS-CoV-2, we compared the antiviral effects of Mito-MES administered before or concurrently with SARS-CoV-2. We found that 1000 nM Mito-MES inhibited NP expression in Calu3 cells when added before infection (effect on viral entry) but also when added 4 hours post infection (hpi), which allows time for viral entry, in both Calu3 (Figure 2G) and hACE2 HEK293T cells (Figure 2H)

1	To gain further insight into the impact of Mito-MES on host cellular factors used by SARS-
2	CoV-2 for entry in epithelial cells(Hu et al., 2021), we used flow cytometry to determine that
3	Mito-MES did not impact the levels of ACE2, TMPRSS2, CD147 and NRP1 proteins in infected
4	and uninfected Calu3 cells (Figure S2). Given that the hydrophobic TPP moiety of Mito-MES
5	facilitates its entry through phospholipid bilayers (James et al., 2007) important for SARS-CoV-
6	2 entry(Hu et al., 2021), we hypothesized that the TPP of Mito-MES per se is antiviral against
7	SARS-CoV-2. We confirmed by viral titer assays in both hACE2 HEK293T cells and ALI HAE
8	cultures that 1000 nM TPP was not cytotoxic but had potent antiviral activity against the Beta
9	and Delta variants (Figure 2I and 2J), respectively. TPP reduced SARS-CoV-2 entry in hACE2
10	HEK293T cells but had less impact on SARS-CoV-2 cytoplasmic replication (Figure 2I).
11	Collectively, these data showed that antiviral activity of Mito-MES in epithelial cells is partially
12	mediated through its TPP moiety.
12	
12	
	Interferon cellular pathways as mediators of the antiviral activity of Mito-MES
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13 14	
13 14 15	Interferon cellular pathways as mediators of the antiviral activity of Mito-MES
13 14 15 16	Interferon cellular pathways as mediators of the antiviral activity of Mito-MES Given that Mito-MES was less antiviral in interferon deficient Vero-E6 cells compared to
13 14 15 16 17	Interferon cellular pathways as mediators of the antiviral activity of Mito-MES Given that Mito-MES was less antiviral in interferon deficient Vero-E6 cells compared to human cells (Figure 1), we hypothesized that its antiviral activity is mediated through interferon
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 13 14 15 16 17 18 19 20 21 	Interferon cellular pathways as mediators of the antiviral activity of Mito-MES Given that Mito-MES was less antiviral in interferon deficient Vero-E6 cells compared to human cells (Figure 1), we hypothesized that its antiviral activity is mediated through interferon pathways. First, we assessed the impact of Mito-MES on key mitochondrial proteins that mediate interferon responses such as the mitochondrial antiviral signaling (MAVS) and the translocase of the outer membrane 70 (TOM70) (Liu et al., 2010; Sena and Chandel, 2012). Using flow cytometry, we found that Mito-MES had no impact on MAVS content (Figures S3A-S3C) but

1	assessed the impact of Mito-MES on extramitochondrial proteins that mediate interferon
2	responses. The stimulator of interferon genes (STING)(Liu et al., 2010) together with mito-ROS
3	participate in retinoic acid-inducible gene I (RIG-I)-like receptors signaling to regulate IFNs
4	(Sena and Chandel, 2012). Mito-MES did not impact STING in SARS-CoV-2 infected Calu3
5	cells (Figures S4A-S4C). In Mito-MES treated compared to vehicle treated uninfected Calu3
6	cells, flow cytometry also demonstrated that Mito-MES increased levels of MX1 (Figures S4D-
7	S4F), a key antiviral effector in COVID-19 patients(Bizzotto et al., 2020) that interacts with
8	mitochondria(Cao et al., 2020). Lastly, using ELISA we found that at 48 hpi, Mito-MES did not
9	impact increase in secreted IFN- β and IFN- λ in cell culture supernatants of SARS-CoV-2
10	infected Calu3 cells (Figures S4G and S4I). Mito-MES also did not impact cellular content of
11	IFN- β and IFN- λ of SARS-CoV-2 infected Calu3 cells (Figure S4H and S4J). Overall, our data
12	demonstrate that Mito-MES does not upregulate IFN- β , IFN- λ , MAVS and STING protein
13	content in SARS-CoV-2 infected Calu3 cells, while it selectively induces mediators of IFN-I
14	(TOM70 and MX1) which can explain better antiviral activity in interferon competent cells.
15	
16	The antioxidant activity of Mito-MES partially mediates its antiviral activity
17	
18	SARS-CoV2 infection increases mito-ROS(Codo et al., 2020). Given that antiviral activity of
19	Mito-MES is still present in interferon deficient cells and that the antiviral activity of Mito-MES
20	against RSV is mainly achieved by decreasing mito-ROS (Hu et al., 2019), we hypothesized that
21	the antioxidant activity of Mito-MES is a major contributor to its anti-SARS-CoV-2 activity. In
22	SARS-CoV-2 infected Calu3 cells, flow cytometry showed that Mito-MES reduced fluorescence
23	of the mitochondrial superoxide reporter MitoSOX Red (Figure S5A-S5D). Consistent with the

1	importance of the TPP bringing Coenzyme Q10 (CoQ10), inside mitochondria to scavenge ROS
2	more efficiently, only higher concentrations (1000-2000 nM) of CoQ ₁₀ , had antiviral activity
3	against both the Beta and the Delta strain in hACE2 HEK293T (Figure 2I) and HAE cells
4	(Figure 2K). Both Mito-TEMPO, an independent mitochondrial antioxidant (Zielonka et al.,
5	2017), and Mito-MES had potent and similar antiviral activity against SARS-CoV-2 in Calu3
6	cells (Figure 2L and 2M) and Vero-E6 cells (Figure S5E) at 1000 nM and as low as 25 nM.
7	Notably, consistent with prior evidence that very high concentrations of Mito-MES can have
8	in vitro prooxidant effect that does not appear in vivo (Rodriguez-Cuenca et al., 2010), treatment
9	with 1000 nM Mito-MES increased ROS levels in Calu3 cells, while preserving potent antiviral
10	activity (Figure 2M). Consistent with prior data that excessive ROS scavenging decreases
11	mitochondrial function, Mito-MES treatment at concentrations 50-1000 nM that displayed anti-
12	SARS-CoV2 activity reduced mitochondrial oxygen consumption in vitro regardless of SARS-
13	CoV-2 infection status (Figure S5F-S5I)(Fink et al., 2012). Consequently, mitochondrial
14	respirometry further supported that mitochondrial scavenging of ROS or changes in
15	mitochondrial respiration are not the main mediators of the anti-SARS-CoV-2 activity of Mito-
16	MES in Calu3 cells.
17	
18	Mito-MES is antiviral through the Nrf2 antioxidant pathway
19	
20	In view of our data that the anti-SARS-CoV-2 activity of Mito-MES may be mediated
21	through non-mitochondrial antioxidant pathways (Figure 2) and since Mito-MES induces the
22	antiviral antioxidant Nrf2 pathway in epithelial cells(Zhang et al., 2020), we hypothesized that
23	the antiviral activity of Mito-MES against SARS-CoV-2 in lung cells is mediated through the

1	Nrf2 pathway. To confirm our hypothesis, we pretreated Calu3 cells with the Nrf2 agonist
2	Dimethyl fumarate (DMF) that is cytoprotective at lower concentrations (<25 μ M)(Saidu et al.,
3	2017). Pretreatment of Calu3 with 10 μ M DMF for 24 hours increased anti–SARS-CoV-2
4	activity of 10-1000 nM Mito-MES as measured by flow cytometry (Figure 3A). The additive
5	anti–SARS-CoV-2 activity of Mito-MES was decreased under a higher (100 μ M) concentration
6	of DMF known to be less cytoprotective (Figure 3A)(Saidu et al., 2017). Use of TCID50 assay
7	confirmed these data (Figure 3B). The combination of Mito-MES with DMF also reduced the
8	IC50 of Mito-MES by 3-fold (Figure 3C). Flow cytometry also showed that pretreatment with
9	Mito-MES and DMF did not impact protein levels of Nrf2 (Figure S6) but reduced protein levels
10	of the endogenous Nrf2 inhibitor, Keap1(Saha et al., 2020) (Figure S7) in infected and
11	uninfected Calu3 cells. Pretreatment of Calu3 cells with 10 μ M but not with 100 μ M DMF, 100-
12	1000 nM Mito-MES or the combination of Mito-MES with DMF, increased protein levels of
13	heme oxygenase-1 (HO-1) (Figure S8), a key antiviral protein of the Nrf2 pathway(Saha et al.,
14	2020). 100 μ M DMF, but not 0.25 μ M brusatol and 10 μ M DMF, were cytotoxic in similarly
15	treated uninfected cultures (Figure 3D).
16	Pretreatment of Calu3 for 24 hours with the Nrf2 small-molecule inhibitor brusatol (0.25
17	μ M)(Saidu et al., 2017) significantly increased SARS-CoV2 replication as assessed by
18	TCID50(Figure 3E) and flow cytometry (Figure 3F) and inhibited the antiviral effect of Mito-
19	MES. Pretreatment with brusatol reduced protein levels of Nrf2 (Figure S6) and increased
20	protein levels of Keap (Figure S7) in infected and uninfected Calu3 cells. Pretreatment of Calu3
21	with 0.25 μ M brusatol did not have an impact on the effect of Mito-MES on HO-1 protein levels
22	(Figure S8). Collectively, our data suggest that the antiviral activity of Mito-MES against SARS-

1	CoV-2 is partially mediated through the Nrf2 pathway which may not be reflected by the total
2	cellular protein levels of Nrf2 and Keap and is not mediated by the HO-1 protein.
3	Nrf2 pathway also regulates apoptosis of lung cells (Saha et al., 2020) which is associated
4	with viral replication, lung injury and severe COVID-19(Hu et al., 2021). Thus, we assessed the
5	impact of Mito-MES on cellular apoptosis associated with SARS-CoV-2 infection.
6	Immunostaining showed that Mito-MES reduced SARS-CoV-2-induced increase in cleaved
7	caspase 3, a key regulator of apoptosis in both Vero-E6 (Figures S9A-S9E) and Calu3 cells
8	(Figure S9F).
9	Our data are in agreement with Olagnier et al who showed that the Nrf2 agonist DMF had
10	anti-SARS-CoV2 activity which is not mediated through HO-1(Olagnier et al., 2020). Of note a
11	much higher cytotoxic (Saidu et al., 2017) concentration of DMF (200 μ M) was used in their
12	study.
13	
	Mito-MES shows anti-SARS-CoV-2 efficacy in mice <i>in vivo</i>
13	Mito-MES shows anti-SARS-CoV-2 efficacy in mice <i>in vivo</i>
13 14	Mito-MES shows anti-SARS-CoV-2 efficacy in mice <i>in vivo</i> The anti-SARS-CoV-2 activity of Mito-MES at the nM level can be achieved therapeutically
13 14 15	
13 14 15 16	The anti-SARS-CoV-2 activity of Mito-MES at the nM level can be achieved therapeutically
13 14 15 16 17	The anti-SARS-CoV-2 activity of Mito-MES at the nM level can be achieved therapeutically <i>in vivo</i> with oral Mito-MES that has good bioavailability at the respiratory mucosa(Smith and
13 14 15 16 17 18	The anti-SARS-CoV-2 activity of Mito-MES at the nM level can be achieved therapeutically <i>in vivo</i> with oral Mito-MES that has good bioavailability at the respiratory mucosa(Smith and Murphy, 2010). Accordingly, doses of Mito-MES in mice of 4 mg/kg/day achieve good lung
13 14 15 16 17 18 19	The anti-SARS-CoV-2 activity of Mito-MES at the nM level can be achieved therapeutically <i>in vivo</i> with oral Mito-MES that has good bioavailability at the respiratory mucosa(Smith and Murphy, 2010). Accordingly, doses of Mito-MES in mice of 4 mg/kg/day achieve good lung tissue penetration and have been translated to oral doses in humans(Smith and Murphy, 2010).
13 14 15 16 17 18 19 20	The anti-SARS-CoV-2 activity of Mito-MES at the nM level can be achieved therapeutically <i>in vivo</i> with oral Mito-MES that has good bioavailability at the respiratory mucosa(Smith and Murphy, 2010). Accordingly, doses of Mito-MES in mice of 4 mg/kg/day achieve good lung tissue penetration and have been translated to oral doses in humans(Smith and Murphy, 2010). Therefore, we tested the <i>in vivo</i> efficacy of Mito-MES to reduce viral replication in the lung of

1 intraperitoneally (i.p) 24 hours before SARS-CoV-2 infection that was continued daily for 3 days 2 following infection (Figure 4A). There was a reduction of nearly 3 log units in SARS-CoV-2 3 viral titers in the lungs of the Mito-MES group relative to the vehicle control group (Figures 4B 4 and 4C), which is higher than the anti-SARS-CoV-2 effect of remdesivir in K18-hACE2 mice 5 (White et al., 2021). The anti-SARS-CoV-2 activity of Mito-MES was also seen in mice that 6 were treated with 4 mg/kg Mito-MES 8 hpi (Figures 4B and 4C). We then assessed whether oral 7 Mito-MES derived from the formulation given to humans as a dietary supplement capsule is 8 antiviral against the Delta variant in vivo (Figure 4D). Mito-MES treatment in SARS-CoV-2 9 infected K18-hACE2 mice through oral gavage at concentration 20 mg/kg/day reduced viral titer 10 by nearly 4 log units relative to the vehicle group (Figure 4E). The anti-SARS-CoV-2 activity of 11 Mito-MES was confirmed by ELISA that showed that SARS-CoV-2 NP levels were reduced in 12 lungs of infected K18-hACE2 mice that were treated with Mito-MES versus vehicle (Figure 4F). 13 Given that Mito-MES acts in both epithelial and endothelial cells(Smith and Murphy, 2010) and 14 to fully characterize the anti–SARS-CoV-2 activity at the single cell level, we determined by 15 flow cytometry levels of SARS-CoV-2 NP among lung cell subtypes in murine lung (see gating 16 strategy in Figure S10) after 3 days post infection (dpi), when viral replication is the highest 17 (Winkler et al., 2020). We confirmed that Mito-MES had anti-SARS-CoV-2 activity among lung 18 epithelial cells (Figures 4G-4I, S11A and S11B) that was high in ciliated lung epithelial cells 19 (Figures 4 J-L; Figures S11C and S11D). Mito-MES had antiviral activity in alveolar type 1 20 (AT1) (Figure S12A-S12D), AT2 (Figure S12E-S12H) cells, endothelial cells (Figure S12I-21 S12L). Taken together, these experiments show that Mito-MES treatment can reduce the 22 replication of SARS-CoV-2 by at least 3 orders of magnitude in mouse model of SARS-CoV-2 23 infection. Given that Mito-MES works through host mechanisms and has higher antiviral activity

1	against coronaviruses in human compared to mouse cells (Figure 2), Mito-MES has compelling
2	potential for clinical efficacy for the treatment of COVID-19.
3	
4	Mito-MES is anti-inflammatory in SARS-CoV-2 infection
5	
6	Increased release of IL-1 β and IL-6 by SARS-CoV-2 infected epithelial cells is associated
7	with lung injury and severe COVID-19(Hu et al., 2021). Given previously described anti-
8	inflammatory effects of Mito-MES(Smith and Murphy, 2010), we also assessed the impact of
9	Mito-MES on SARS-CoV-2-associated inflammatory responses. Using ELISA and Luminex
10	immunoassays, we found that Mito-MES attenuated SARS-CoV-2-induced increase in secretion
11	of IL-6 by Calu3 (Figures 5A and 5B) cells and of IL-6 and IL-1 β in upper (Figure 5C) and
12	lower (Figure 5D) airway respiratory epithelium ALI cultures. Our data is consistent with prior
13	evidence that Mito-MES attenuates ROS, activation of inflammasome, NF κ B signaling that
14	collectively drive a cytokine storm, release of IL-1 β , IL-6 (Zhang et al., 2020) and ultimately
15	lung damage in viral infections (Hu et al., 2019). In conclusion, our results show that Mito-MES
16	not only has antiviral activity against SARS-CoV-2 but also attenuates inflammatory responses
17	of the infected epithelial cells that drive severe lung injury in COVID-19.
18	
19	Mito-MES is anti-inflammatory in SARS-CoV-2 infection through its antioxidant
20	properties and the TPP moiety.
21	
22	Since Mito-MES is anti-inflammatory(Smith and Murphy, 2010) and an agonist of Nrf2 that
23	has a major role in regulation of inflammation and reduces production of IL-1β and IL-6 (Saha et

1	al., 2020), we hypothesized that not only the antiviral but also the anti-inflammatory activity of
2	Mito-MES in SARS-CoV-2 infection is mediated through the Nrf2 pathway. Pretreatment of
3	Calu3 cultures with 10 μ M of the Nrf2 agonist DMF for 24 hours resulted in reduction in
4	subsequent release of IL-6 to the cell supernatant from infected cells at 48 hpi as measured by
5	immunoassays (Figure 5E). Compared to treatment of Calu3 with 1000 nM Mito-MES alone,
6	treatment of Calu3 with 10 or 100 μ M DMF in combination with Mito-MES for 72 hours
7	resulted in an additive reduction in release of IL-6 to the cell supernatant from SARS-CoV-2
8	infected cells (Figure 5E). Pretreatment of Calu3 with 0.25 μ M of the Nrf2 inhibitor brusatol
9	(Saidu et al., 2017) significantly increased subsequent release of IL-6 by infected cells (Figure
10	5F) and inhibited the anti-inflammatory effect of Mito-MES (Figure 5F). Notably, the dTPP
11	moiety and the mitochondrial antioxidant CoQ10 also reduced subsequent release of IL-6 to the
12	cell supernatant from SARS-CoV-2 infected ALI cultures (Figure 5G). Collectively, these data
13	suggest that Mito-MES reduces production of IL-6 by SARS-CoV-2 infected epithelial cells
14	through its antioxidant properties (Nrf2 agonist, CoQ10 moiety, antioxidant against mito-ROS)
15	and the dTPP moiety.
16	
17	Mito-MES shows in vivo anti-inflammatory efficacy in mouse model of SARS-CoV-2
18	infection
19	
20	We then tested the <i>in vivo</i> anti-inflammatory efficacy of 4 mg/kg intraperitoneal daily dosage
21	of Mito-MES in K18-hACE2 mice infected with the SARS-CoV-2 wild type (WT)(cohort A) as

- 22 early as 3 dpi and in K18-hACE2 mice infected with Beta variant (cohort B), after 5-7 dpi, when
- 23 lung inflammation is the highest (Winkler et al., 2020)(Figure 6A). Using Luminex

1	immunoassays we showed that there was a reduction of at least 2 orders of magnitude in IL-1 β
2	(Figure 6B) and IL-6 (Figure 6C) in the lungs of the Mito-MES treated SARS-CoV-2 infected
3	relative to the vehicle treated group as early as 3 dpi. The Mito-MES-induced reduction in IL-1 β
4	and IL-6 in the lung after 5-7 dpi was confirmed in mice from cohort B infected with the SARS-
5	CoV-2 Beta variant (Figures 6D and 6E). Mito-MES did not change protein levels of IL-18
6	(Figures S13A and S13C) and did not consistently reduce levels of TNF- α in SARS-CoV-2
7	infected K18-hACE2 mice (Figure S13B and S13D). To fully characterize the anti-inflammatory
8	activity of Mito-MES at the cell level, we determined the infiltration of different immune cell
9	subtypes into murine lungs by flow cytometry (see gating strategy in Figure S14). Mito-MES
10	reduced frequency of CD45+ immune as early as 3 dpi in mice infected with WT SARS-CoV-2
11	(Figures 6F and 6G) but not at 5 dpi in mice infected with the Beta variant SARS-CoV-2 (Figure
12	S13E). Mito-MES also reduced frequency of NK cells in murine lungs of mice infected with
13	both the WT and the Beta variant SARS-CoV-2 (Figures S15M-S15O). Mito-MES did not alter
14	frequency of neutrophils (Figure S15A-S15C), macrophages (Figure S15D-S15F), myeloid
15	dendritic cells (DCs) (Figure S15G-S15I), lymphoid DCs (Figure S15J-S15L), T cells (Figure
16	S15P-S15R) and B cells (Figures S15S and S15T). Immunofluorescence analysis showed that
17	Mito-MES inhibited SARS-CoV-2-associated increase in cleaved caspase 3, a marker of tissue
18	apoptosis and damage, in K18-hACE2 mice infected with Beta variant (Figure S13F).
19	Histopathology analysis also showed a reduction of lung inflammation and tissue damage in
20	Mito-MES treated mice over vehicle-treated mice at day 5-7 after infection (Figures 6H to 6J).
21	Taken together, these experiments show that Mito-MES treatment has an anti-inflammatory
22	effect that is seen at both early and late stages of SARS-CoV-2 infection and has good
23	therapeutic efficacy against COVID-19 in vivo.

Discussion

4	The SARS-CoV-2 pandemic necessitates the development of antiviral and anti-inflammatory
5	therapeutics that can be rapidly moved into the clinic. Herein, we demonstrate that Mito-MES
6	has in vitro and in vivo antiviral, antiapoptotic and anti-inflammatory effects on SARS-CoV-2
7	infected epithelial cells. Unlike vaccines, attenuation of detrimental host responses that
8	propagate viral replication may be efficacious even in the setting of mutant strains of SARS-
9	CoV-2 to which viral-targeted therapeutics and vaccines may be less effective. Mito-MES had
10	nanomolar antiviral potency against the Beta and Delta SARS-CoV-2 variants as well as MHV.
11	Thus, Mito-MES is expected to have antiviral activity against rapidly emerging SARS-CoV-2
12	variants such as the B.1.1.159 (omicron) variant.
13	We show that the antiviral effect of Mito-MES against SARS-CoV-2 in epithelial cells is
14	mediated partially through its antioxidant properties (reduces mito-ROS and induces the Nrf2
15	pathway) and through the hydrophobic dTPP cation that integrates into cellular membranes that
16	are important for SARS-CoV-2 replication(Hu et al., 2021). Mito-MES had more potent antiviral
17	activity in interferon competent epithelial cells compared to interferon deficient Vero-E6 cells
18	and it induced mitochondrial mediators of IFN-I responses (TOM70 and MX1) that have an
19	important role in host cellular responses against SARS-CoV-2 (Bizzotto et al., 2020). The anti-
20	inflammatory effect of Mito-MES was mostly seen against IL-6 and NK cell infiltration in
21	SARS-CoV-2 infected mouse lungs. Importantly, Mito-MES at nanomolar concentrations had
22	additive antiviral and anti-inflammatory activity together with DMF which is currently used as
23	an anti-inflammatory drug in relapsing-remitting multiple sclerosis(Blair, 2019). Thus, the

1 combination of an FDA-approved drug (DMF) with Mito-MES could easily be repurposed and 2 tested in clinical trials to establish a potent novel combined antiviral and anti-inflammatory 3 therapeutic strategy in COVID-19 patients. Our data suggest that Mito-MES may have multiple 4 favorable therapeutic effects in COVID-19 (Figure S16). 5 Although host-targeted antivirals may be toxic, the safety profile of Mito-MES is well 6 established in humans. Mito-MES is currently available as a dietary supplement (10 mg orally 7 daily) and its safety for up to one year in doses as high as 80 mg orally daily has been validated 8 in independent clinical trials for oxidative damage-related diseases such as Parkinson's, hepatitis 9 C, as well as vascular dysfunction (Rossman et al., 2018; Smith and Murphy, 2010). Thus, Mito-10 MES could easily be repurposed and tested in clinical trials as a small molecule inhibitor of 11 SARS-CoV-2 replication and inflammation-induced pathology for outpatient treatment of mild 12 to moderate acute COVID-19 and for post-exposure prophylaxis against SARS-CoV-2 in high-13 risk exposures. 14 To date, there is no safe, efficacious oral antiviral that is effective against SARS-CoV-2 15 variants, has anti-inflammatory activity and can also be given long term in humans. Both Mito-16 MES and CoQ_{10} are nutraceuticals that can be very useful as preexposure prophylaxis in high 17 risk (un)vaccinated or immunocompromised patients where the SARS-CoV-2 vaccines may have 18 low efficacy. The favorable antiviral, antioxidant and anti-inflammatory properties of Mito-19 MES, its use for treatment of neurodegenerative and heart diseases and its excellent safety 20 profile in humans(Rossman et al., 2018; Smith and Murphy, 2010), can establish Mito-MES as a 21 novel therapeutic strategy for Post-acute COVID-19 syndrome (PACS) where residual low-grade 22 SARS-CoV-2 replication in combination with aberrant proinflammatory mechanisms have been

23 observed (Nalbandian et al., 2021). Finally, Mito-MES can have a favorable effect on

- 1 comorbidities associated with morbidity in COVID-19 such as vascular dysfunction and
- 2 aging(Rossman et al., 2018; Smith and Murphy, 2010). To date, an oral therapy for COVID-19
- 3 and PACS that has anti-inflammatory, antiviral, antiapoptotic properties and favorable impact on
- 4 comorbidities such as vascular dysfunction, does not exist. Mito-MES may represent a rapidly
- 5 applicable therapeutic strategy that can be added in the therapeutic arsenal against COVID-19.

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Declaration of interest

- 3 Competing interests: This manuscript is related to patents PCT/US2021/040869,
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1 FIGURE LEGENDS

2 Figure 1. Mitoquinone mesylate strongly inhibits SARS-CoV-2 replication in multiple types 3 of epithelial cells. (A-D) Vero-E6 cells [(A) and (B)], Calu3 cells [(C), (D)] were treated with 4 indicated doses of remdesivir (RDV) [(B)(D)] or mitoquinone mesylate (Mito-MES) [(A), (C)]. 5 IC50, 50% cytotoxic concentration (CC50) values are indicated. Viral replication at 48 hours 6 post infection (hpi) by TCID50-assay. Cell cytotoxicity was assessed in uninfected cells at 48 7 hours by the XTT assay. (E) Immunofluorescent analysis (48 hpi) of infected Calu3 cells treated 8 with Mito-MES (10 nM). Scale bar=50µm. (F) Viral replication by flow cytometry in human 9 airway epithelial cells. For all experiments cells were infected with SARS-CoV-2 at an MOI of 10 0.1 and were treated with drugs for at least 2 hours before infection and throughout the 11 experiment unless stated otherwise. For "Entry" treatment, the drugs were added to the cells for 12 2 h before infection and at 2 hpi and the virus-drug supernatant was then replaced with culture 13 medium. In all panels, data are means \pm SEM of at least three independent experiments with at 14 least 3 replicates in each experiment.

15

Figure 2. Mitoquinone mesylate (Mito-MES) has antiviral activity against coronaviruses that partially depends on its lipophilic and antioxidant components. (A-F) Calu3, human airway epithelial (HAE) cells, 17CL-1 cells and lung cells isolated from K18-hACE2 mice were infected with SARS-CoV-2 Beta or Delta variant or mouse hepatitis virus (MHV) and treated with vehicle control (Ctrl) or Mito-MES versus remdesivir (RDV) as shown. Viral replication by TCID50-assay and XTT assay at 48 hpi. IC50, 50% cytotoxic concentration (CC50) values are indicated. (G to I) Time-of-addition experiment of RDV, Mito-MES, dTPP and coenzyme Q10

1	(CoQ10) in Calu3 cells, hACE2 HEK293T cells [at entry, post-viral entry and throughout 24 hpi
2	(full time)]. Levels of intracellular SARS-CoV-2 Nucleocapsid protein were determined by
3	ELISA. [(J)(K)] Viral replication at 48 hpi by TCID50-assay in HAE cells treated with dTPP or
4	CoQ_{10} as shown. [(L)(M)] Calu3 cells were treated as shown with Ctrl, Mito-TEMPO (MT) or
5	Mito-MES and were infected with green fluorescent icSARS-CoV-2-mNG (MOI 0.3). Oxidative
6	stress by dihydroethidum (DHE) fluorescence and viral replication at 48 hpi by SARS-CoV-2-
7	mNG fluorescence and TCID50-assay (L) in Calu3 cells. For all experiments cells were infected
8	with SARS-CoV-2 and treated as in Figure 1. In all panels, data are representative or mean \pm
9	SEM of at least two experiments in 3 replicates. Unless otherwise stated, statistical comparison
10	was done between the Ctrl and each shown experimental group by using two-tailed Mann-
11	Whitney (*** <i>p</i> < 0.001).

13 Figure 3. The antiviral activity of Mito-MES against SARS-CoV-2 in epithelial cells is 14 mediated through the Nrf2 pathway. (A-F) Calu3 cells infected with SARS-CoV-2 (48 h) 15 (MOI 0.1) and treated with Mito-MES (10-1000 nM, 72 h) and/or the Nrf2 agonist Dimethyl 16 fumarate (DMF) (10, 100 μ M, 16-24 hrs) and/or the Nrf2 inhibitor brusatol (0.25 μ M, 16-24 hrs) 17 or DMSO vehicle control (Ctrl). (A to C) Viral replication by flow cytometry (A) or TCID50-18 assay at 48 hrs post infection (hpi) [(B), (C)] in Calu3 cells treated as shown. IC50 values for 19 Mito-MES \pm DMF 10 μ M are shown (C). (D) Cell cytotoxicity (XTT assay) in uninfected Calu3 20 cells treated as shown for 24 hrs. [(E), (F)] Viral replication by TCID50-assay (E) or flow 21 cytometry (F) at 48 hpi in Calu3 cells treated as shown. [(G)(H)] Protein levels of cleaved 22 caspase-3 in Calu3 cells as assessed by immunofluorescence (G) or flow cytometry (H). 23 Summary (means \pm SEM) or representative data of at least three experiments in duplicates and

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1	triplicates are shown. Each data-point represents one biological sample. Unless otherwise stated,
2	statistical comparison was done between the Ctrl and each shown experimental group by using
3	two-tailed Mann–Whitney (* $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$).
4	
5	Figure 4. Mitoquinone mesylate (Mito-MES) inhibits SARS-CoV-2 replication in mouse
6	model of SARS-CoV-2 infection. (A-L) hACE2 K18 mice were infected intranasally with
7	SARS-CoV-2 (10,000 PFU/mouse) and lung tissue was harvested 72 hours post infection (hpi).
8	Supernatants from lung homogenates were used for viral titer [based on cytopathic effect; CPE
9	or measurement of intracellular SARS-CoV-2 nucleocapsid protein (NP) by ELISA] in Vero-E6
10	cells [(B), (C), (E)]. (A) Study design for cohort A. Mice were infected with wild type (WT)
11	SARS-CoV-2 and treated with vehicle control (saline 10% DMSO; Ctrl) (n=5) or Mito-MES 4
12	mg/kg/day (n=10) given intraperitoneally 24 hours before the infection (hbi) (n=5) or 8 hpi
13	(n=5). (D) Study design for cohort B. Mice were infected with SARS-CoV-2 Delta variant and
14	treated through gavage with Ctrl (n=10) or Mito-MES 20 mg/kg/day (n=10) 24 hbi. (F)
15	Measurement of SARS-CoV-2 NP by ELISA in lung homogenates. (G to L) Assessment of
16	SARS-CoV-2 NP in EPCAM (+) lung cells (G to I) and FOXJ1(+) ciliated cells (J to L) by flow
17	cytometry. Representative or summary (mean \pm SEM) data from experiments in triplicates. Each
18	data-point represents one biological sample. Unless otherwise stated, statistical comparison was
19	done between the Ctrl and each shown experimental group by using two-tailed Mann-Whitney
20	***p<0.001, **p<0.01, *p<0.05.
21	
22	Figure 5. Mitoquinone mesylate (Mito-MES) has anti-inflammatory activity in SARS-CoV-

23 2 infected epithelial cells. [(A), (B)] Calu3 cells treated with vehicle control (Ctrl) or Mito-MES

1	(100 or 1000 nM, 72 hrs) and infected with wild type (WT) SARS-CoV-2 (48 hrs)(MOI 0.1). IL-
2	6 was measured by ELISA (A) and other cytokines by Luminex immunoassay (B) in cell culture
3	supernatants collected 48 hours post infection (hpi). (C) Large airway epithelial cells cultured in
4	air-liquid interface (ALI) were treated with Ctrl or Mito-MES (1000 nM) and were infected with
5	SARS-CoV-2 Delta variant (MOI 1). Cytokines were measured by Luminex immunoassay at 48
6	hpi. (D) As in (C) but a small distal airway epithelial ALI culture system was used. [(E), (F)]
7	Calu3 cells treated with Mito-MES (10-1000 nM, 72 hrs) and/or the Nrf2 agonist Dimethyl
8	fumarate (DMF)(10, 100 μ M, 16-24 hrs) (E) and/or the Nrf2 inhibitor brusatol (0.25 μ M, 16-24
9	hrs)(F) and infected with WT SARS-CoV-2 (48 h)(MOI 0.1). Cytokines were measured by
10	Luminex immunoassay at 48 hpi. (G) As in (D) but cells were treated with Mito-MES, dTPP and
11	CoQ_{10} as shown. Data are pooled data (mean \pm SEM) from three experiments in triplicates. Each
12	data-point represents one biological sample. Unless otherwise stated, statistical comparison was
13	done between the Ctrl and each shown experimental group by using two-tailed Mann-Whitney
14	(*p < 0.05, **p < 0.01).
15	

16 Figure 6. Mitoquinone mesylate (Mito-MES) inhibits SARS-CoV-2 associated

17 inflammation and lung damage in mouse model of SARS-CoV-2 infection. hACE2 K18 mice

18 were infected intranasally with SARS-CoV-2 wild type (WT) or Beta variant (10,000

19 PFU/mouse), treated with Mito-MES 4 mg/kg/day or vehicle control (Ctrl) and lung was

20 harvested on day 3 (cohort A see Figure 4) or 5-7 (cohort B) post infection. (A) Study design of

- 21 cohort B. (B to E) Supernatants from lung homogenates of mice from cohort A [(B), (C)] or B
- 22 [(D), (E)] were used for measurement of cytokines using Luminex immunoassay. [(F), (G)]
- 23 Flow cytometry assessed frequency of CD45+ immune cells in lungs from mice in cohort A.

1	Representative (F) and summary data (G). (H-J) Harvested lungs from mice in cohort B were
2	paraffin-embedded and 5-µm sections were stained for hematoxylin and eosin. Histopathology
3	score was determined according to Methods. Representative images of lung sections. Regions of
4	the lung where inflammation was assessed are highlighted by red boxes and arrows. Normal
5	regions of the lung are highlighted by yellow boxes. Representative or summary (mean \pm SEM)
6	data from experiments in triplicates. Each data-point represents one biological sample. Unless
7	otherwise stated, statistical comparison was done between the Ctrl and each shown experimental
8	group by using two-tailed Mann–Whitney ***p<0.001, **p<0.01, *p<0.05.
9	

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1 SUPPLEMENTAL FIGURE TITLES AND LEGENDS

2

3 Figure S1 (related to Figure 1). Mitoquinone mesylate (Mito-MES) inhibits SARS-CoV-2 4 replication in independent epithelial cell types. (A to J) Vero E6 [(A), (B), (C), (D)], Calu3 5 [(E), (F), (G), (H)] HEK293T-hACE2 (I) and human airway ciliated (positive for FOXJ1 6 protein) epithelial (J) cells were treated with 10 μ M of remdesivir (RDV) [(B), (F)] or indicated 7 doses of Mito-MES or DMSO vehicle control (Ctrl). Viral replication at 48 hrs post infection 8 (hpi) by immunofluorescence [(A), (E)], qPCR [(B), (F)] or flow cytometry [(C), (D), (G), (H),9 (I), (J)]. Viral replication at the protein level was measured by assessing SARS-CoV-2 Spike (S) 10 protein [(A), (D), (E), (H)] and nucleocapsid (N) protein [(C), (G), (I), (J)]. For all experiments 11 cells were infected with SARS-CoV-2 at an MOI of 0.1 and they were treated with drugs for 2 12 hrs before infection and throughout the experiment until 48 hpi. In all panels summary data are 13 presented as mean \pm SEM or representative images of three or more experiments (with at least 2 14 replicates). Each data-point represents one biological sample. Unless otherwise stated, statistical 15 comparison was done between the Ctrl and each shown experimental group by using two-tailed 16 Mann–Whitney (*p < 0.05, **p < 0.01, ***p < 0.001).

- 17
- 18

Figure S2 (related to Figure 2). Impact of Mito-MES on host membrane proteins important
for SARS-CoV-2 entry. (A to L) Assessment of levels of membrane proteins important for
SARS-CoV-2 entry by flow cytometry in SARS-CoV-2 (un)infected Calu3 cells treated with
Mito-MES (1000 nM, blue line) or vehicle control (Ctrl, red line) (72 h) and infected with
SARS-CoV-2 (48 h). The negative stain control (fluorescence minus one; FMO) is shown in

1	light grey. (A) Median fluorescence intensity (MFI) of ACE2 in total Calu3 cells. (B) MFI of
2	ACE2 in SARS-CoV-2 infected Calu3 cells. (C) % of total Calu3 cells positive for ACE2. (D)
3	MFI of TMPRSS2 in total Calu3 cells. (E) MFI of TMPRSS2 in SARS-CoV-2 infected Calu3
4	cells. (F) % of total Calu3 cells positive for TMPRSS2. (G) MFI of Neuropilin 1 (NRP-1) in
5	total Calu3 cells. (H) MFI of NRP-1 in SARS-CoV-2 infected Calu3 cells. (I) % of total Calu3
6	cells positive for NRP-1. (J) MFI of CD147 in total Calu3 cells. (K) MFI of CD147 in SARS-
7	CoV-2 infected Calu3 cells. (L) % of total Calu3 cells positive for CD147. Representative data
8	from at least three independent experiments with at least 2 replicates are shown.
9	
10	Figure S3 (related to Figure 2). Impact of Mito-MES on mitochondrial proteins that
11	mediate interferon host immune responses in SARS-CoV-2 infected epithelial cells. (A to C)
12	Assessment of protein levels (fluorescence intensity and % of cells positive for the target protein)
13	of MAVS by flow cytometry in total [(A), (C)] and SARS-CoV-2 infected (B) (48 hrs) Calu3
14	cells treated with Mito-MES (1000 nM, blue line) or vehicle control (Ctrl, red line) (72 hrs).
15	$[(\mathbf{D}), (\mathbf{E}), (\mathbf{F})]$ Assessment of protein levels of TOM70 by flow cytometry in total $[(\mathbf{D}), (\mathbf{F})]$ and
16	SARS-CoV-2 infected (E) Calu3 cells [(G), (H)] Immunofluorescence shows levels of TOM70
17	in Calu3 cells at 48 hrs post-infection. (G) Representative panels show immunostaining for
18	SARS-CoV-2 spike protein (green) and TOM70 (red) in uninfected cells, infected cells treated
19	with Ctrl or Mito-MES (100 nM). DAPI stained cell nuclei. Scale bar= 100 μ m. (H) Summary
20	analysis of immunofluorescence experiments for TOM70 protein [median fluorescence intensity
21	(MFI), arbitrary units]. Data in (A to G) are representative for three or more experiments with at
22	least 2 replicates. Pooled data from at least three experiments in (H). Bars indicate mean \pm SEM.

1 Statistical comparison was done between the Ctrl and each shown experimental group by using 2 two-tailed Mann–Whitney (*p < 0.05, **p < 0.01, ***p < 0.001).

3

4	Figure S4 (related to Figure 2). Impact of Mito-MES on interferon host immune responses
5	in SARS-CoV-2 infected epithelial cells. (A to C) Protein levels (fluorescence intensity and %
6	of cells positive for the target protein) of STING were assessed by flow cytometry in total [(A),
7	(C)] and SARS-CoV-2 infected (B) Calu3 cells. (D to F) Similarly, protein levels of MX1 were
8	assessed by flow cytometry in total [(D), (F)] and SARS-CoV-2 infected (E) Calu3 cells. (G to
9	J) ELISA was done to assess protein levels of secreted $[(G), (I)]$ and cellular $[(H), (J)]$
10	interferons [beta: IFN- β (G), (H), lambda: IFN- λ (I), (J)] in Calu3 cells treated with Mito-MES
11	(100-1000 nM) or vehicle control (Ctrl) (72 h) and infected with SARS-CoV-2 (48 h). Data in (A
12	to \mathbf{F}) show representative data from at least three independent experiments. Data in (\mathbf{G} to \mathbf{J}) are
13	pooled from three or more independent experiments with at least 2 replicates. Bars indicate
14	mean \pm SEM. Each datapoint represents one biological sample. Unless otherwise stated,
15	statistical comparison was done between the Ctrl and each shown experimental group by using
16	two-tailed Mann–Whitney.

17

Figure S5 (related to Figure 2). The antiviral activity of Mito-MES against SARS-CoV-2 in epithelial cells depends partially on its antioxidant activity. (A to D) Assessment of fluorescence [fluorescence intensity (MFI) (A), (B) and percent of positive cells (C), (D)] of MitoSOX Red in Calu3 cells infected with SARS-CoV-2 (48 hrs) and treated with Mito-MES (100 nM) or DMSO vehicle control (Ctrl). (E) Vero-E6 cells were treated with Ctrl, Mito-

1	TEMPO (MT) or Mito-MES and were infected with fluorescent SARS-CoV-2 (MOI 0.3)
2	(48 hrs). Immunofluorescent analysis of viral replication and cellular oxidative stress
3	[fluorescence of dihydroethidium (DHE)] at 48 hpi. (F to H) Seahorse XF Analyzer determined
4	cellular bioenergetics [oxygen consumption rate (OCR) (F) and extracellular acidification rate
5	(ECAR) (G to I) in live (un)infected Calu3 cells treated with Mito-MES or Ctrl and infected with
6	SARS-CoV-2. For all experiments cells were infected with SARS-CoV-2 at an MOI of 0.1 and
7	were treated with drugs 25-1000 nM for at least 2 hrs before infection and for 48 hpi. In all
8	panels, data are representative or mean \pm SEM of at least three experiments with at least 2
9	replicates. Statistical comparison was done between the Ctrl and each shown experimental group
10	by using two-tailed Mann–Whitney (*p < 0.05, **p < 0.01, ***p < 0.001).
11	

12 Figure S6 (related to Figure 3). Impact of Mito-MES on protein levels of Nrf2 in SARS-13 CoV-2 infected and uninfected epithelial cells. (A to D) Calu3 cells infected with SARS-CoV-14 2 (48 hrs) (MOI 0.1) and treated with Mito-MES (10-1000 nM, 72 hrs) and/or the Nrf2 agonist 15 Dimethyl fumarate (DMF) (10, 100 µM, 16-24 hrs) and/or the Nrf2 inhibitor brusatol (0.25 µM, 16 16-24 hrs) or DMSO vehicle control (Ctrl). [(A), (B)] Protein levels (fluorescence intensity) of 17 Nrf2 were determined by flow cytometry in total (infected and uninfected) (A) and SARS-CoV-2 18 infected (B) Calu3 cells. [(C), (D)] Viral replication (% of cells positive for the Nucleocapsid N 19 SARS-CoV-2 protein) and Nrf2 protein levels (% of cells positive for the target protein) by flow 20 cytometry at 48 hrs post infection in Calu3 cells treated with DMF and/or Mito-MES (C) or with 21 brusatol and/or Mito-MES (D). Data in all panels are representative data from at least three 22 independent experiments with at least 2 experimental replicates.

2	Figure S7 (related to Figure 3). Impact of Mito-MES on protein levels of Keap1 in SARS-
3	CoV-2 infected and uninfected epithelial cells. (A to D) Calu3 cells infected with SARS-CoV-
4	2 (48 hrs) (MOI 0.1) and treated with Mito-MES (10-1000 nM, 72 hrs) and/or the Nrf2 agonist
5	Dimethyl fumarate (DMF) (10, 100 μ M, 16-24 hrs) and/or the Nrf2 inhibitor brusatol (0.25 μ M,
6	16-24 hrs) or DMSO vehicle control (Ctrl). (A) Viral replication (% of cells positive for the
7	SARS-CoV-2 N protein) and Keap1 protein levels (% of cells positive for the target protein) by
8	flow cytometry at 48 hrs post infection (hpi) in Calu3 cells treated with DMF and/or Mito-MES.
9	(B) Keap1 fluorescence intensity was measured by flow cytometry in total (infected and
10	uninfected) Calu3 cells treated with Mito-MES and/or DMF. (C) Viral replication and Keap1
11	protein levels by flow cytometry at 48 hpi in Calu3 cells treated with brusatol and/or Mito-MES.
12	(D) Keap1 fluorescence intensity was measured by flow cytometry in total (infected and
13	uninfected) Calu3 cells treated with Mito-MES and/or brusatol. Data in all panels are
14	representative data from three or more independent experiments with at least 2 replicates.
15	
16	
17	Figure S8 (related to Figure 3). Impact of Mito-MES on protein levels of Heme oxygenase-1
18	(HO-1) in SARS-CoV-2 infected and uninfected epithelial cells. (A to D) Calu3 cells infected
19	with SARS-CoV-2 (48 hrs) (MOI 0.1) and treated with Mito-MES (10-1000 nM, 72 hrs) and/or
20	the Nrf2 agonist Dimethyl fumarate (DMF) (10, 100 μ M, 16-24 hrs) and/or the Nrf2 inhibitor
21	brusatol (0.25 μ M, 16-24 hrs) or DMSO vehicle control (Ctrl). (A) Viral replication (% of cells
22	positive for the Nucleocapsid N SARS-CoV-2 protein) and HO-1 protein levels (% of cells
23	positive for the target protein) by flow cytometry at 48 hrs post infection (hpi) in Calu3 cells

1	treated with DMF and/or Mito-MES. (B) HO-1 protein level (fluorescence intensity) was

- 2 quantified by flow cytometry in total (infected and uninfected) Calu3 cells treated with Mito-
- 3 MES and/or DMF. (C) Viral replication and HO-1 protein levels by flow cytometry at 48 hpi in
- 4 Calu3 cells treated with brusatol and/or Mito-MES. (D) HO-1 protein level (fluorescence
- 5 intensity) was quantified by flow cytometry in total (infected and uninfected) Calu3 cells treated
- 6 with Mito-MES and/or brusatol. Data panels are representative from three or more independent
- 7 experiments with at least 2 replicates.
- 8

1 Figure S9 (related to Figure 3). Mitoquinone mesylate restricts SARS-CoV-2 associated 2 apoptosis in epithelial cells. (A to F) Vero-E6 (A to E) and Calu3 (F) cells were treated with 3 indicated doses of Mito-MES versus DMSO vehicle control (Ctrl) and infected with SARS-CoV-4 2 for 48 hrs (MOI of 0.1). (A) Panels show immunostaining for SARS-CoV-2 spike protein (red) 5 and apoptosis marker cleaved caspase-3 (green) at 48 hrs post-infection (hpi) in cells treated with 6 Ctrl or Mito-MES (250 nM). DAPI stained cell nuclei. Scale bar=100 µm. [(B), (C)] Summary 7 of data for protein levels [% of cells positive for protein (**B**) and median fluorescence intensity 8 (MFI)(C)] of cleaved caspase-3 in Vero-E6 were assessed by immunofluorescence. [(D), (E)] 9 Protein levels [% of positive cells (D) and MFI (E)] of cleaved caspase-3 in Vero-E6 were 10 assessed by flow cytometry. (F) Protein levels (% of positive cells) of cleaved caspase-3 in Vero-11 E6 were assessed by flow cytometry. In all panels, data are shown as summary data (mean \pm 12 SEM) or representative images of three or more independent experiments with at least 2 13 replicates. Unless otherwise stated, statistical comparison was done between the Ctrl and each 14 shown experimental group by using two-tailed Mann–Whitney (*p < 0.05, **p < 0.01, 15 ***p<0.001).

16

Figure S10 (related to Figure 4). Gating strategy for flow panel A (assessment of SARS-CoV-2 Nucleocapsid protein among lung cell types). Representative data of gates: 1) Single cells based on forward scatter (FSC); \rightarrow 2) Single cells based on side scatter (SSC). Cells were gated on the (1) gate; \rightarrow 3) Viable non-red blood cells (non-RBCs) were gated as negative stain for the Violet Ghost dye (viability dye) and the BV421-Ter119 (mouse RBC marker). Cells were gated on the (2) gate; \rightarrow 4) Cells (FSC/SSC) were gated to exclude debris; \rightarrow 5) Non-immune lung cells were gated as CD45(-) on gate 4 \rightarrow 6) Endothelial cells were gated as CD31(+) CD45(-

1) cells on gate 5. 7) Lung epithelial cells were gated as CD326 [(epithelial cell adhesion molecule
2	(EpCAM)] positive cells that were negative for CD31 and CD45 on gate 6; \rightarrow 8) Alveolar type 2
3	(AT2) lung cells were gated as cells positive for the AT2 marker major histocompatibility
4	complex class II (MHCII)) on lung epithelial cells in gate 7. 9) Alveolar type 1 (AT1) lung cells
5	positive for the AT1 marker podoplanin but negative for MHCII on gate 8. 10) Ciliated lung
6	cells positive for FOXJ1 but negative for podoplanin on gate 9.

- 7
- 8

9 Figure S11 (related to Figure 4). Mitoquinone mesylate inhibits SARS-CoV-2 replication in 10 lung cells in mouse model of SARS-CoV-2 infection. hACE2 K18 mice (n=15) were infected 11 with SARS-CoV-2 and treated intraperitoneally with Mito-MES (n=10) or vehicle control (Ctrl) 12 (n=5) as in Fig. 4. Lung tissue was harvested on day 3 post infection. (A to D) Assessment of 13 SARS-CoV-2 N protein by flow cytometry in EPCAM (+) lung epithelial cells [(A), (B)] and 14 FOXJ1(+) EPCAM (+) ciliated cells [(C), (D)]. (A) Representative data for MFI of SARS-CoV-15 2 N protein in EPCAM (+) lung cells. (B) Summary data for (A). (C) Representative data for 16 MFI of SARS-CoV-2 N protein in FOXJ1(+) EPCAM (+) ciliated cells. (D) Summary data for 17 (C). Summary (means \pm SEM) or representative data of at least three experiments in duplicates 18 and triplicates are shown. Each datapoint represent a single sample. Unless otherwise shown, 19 statistical comparison was done between the Ctrl and each shown experimental group by using 20 two-tailed Mann–Whitney (*p < 0.05, **p < 0.01). 21

1 Figure S12 (related to Figure 4). Anti-SARS-COV-2 activity of Mito-MES in distal airway

2 lung cells in hACE2 K18 mice. Mice were infected with SARS-CoV-2 and treated with Mito-

3 MES (n=10) or vehicle control (Ctrl) (n=5) as in Fig. 4. Assessment of SARS-CoV-2

4 Nucleocapsid (N) protein by flow cytometry on day 3 post infection in alveolar type 1 (AT1)

5 cells (A to D) AT2 lung cells (E to H) and CD31(+) CD45(-) endothelial cells (ECs) (I to L).

6 [(A), (B)] Representative and summary data for % of infected AT1 cells. [(C), (D)]

7 Representative and summary data for MFI of SARS-CoV-2 NP in AT1 cells. [(E), (F)]

8 Representative and summary data for % of infected AT2 cells. [(G), (H)] Representative and

9 summary data for MFI of SARS-CoV-2 NP in AT2 cells. [(I), (J)] Representative and summary

10 data for % of infected endothelial cells. [(K), (L)] Representative and summary data for MFI of

11 SARS-CoV-2 NP in endothelial cells. Summary (mean \pm SEM) or representative data of at least

12 three experiments in duplicates and triplicates are shown. Each datapoint represents one sample.

13 Unless otherwise shown, statistical comparison was done between the Ctrl and each shown

14 experimental group by using two-tailed Mann–Whitney (*p < 0.05, **p < 0.01).

15

16 Figure S13 (related to Figure 6). Mitoquinone mesylate inhibits SARS-CoV-2 associated 17 inflammation and lung cell apoptosis in mouse model of SARS-CoV-2 infection. hACE2 18 K18 mice were infected intranasally with SARS-CoV-2 wild type (WT) or Beta variant (10,000 19 PFU/mouse), treated with Mito-MES 4 mg/kg/day or vehicle control (Ctrl). The lung tissue was 20 harvested on day 3 (cohort A) or day 5-7 (cohort B) post infection, as shown in Fig. 6. (A to D) 21 Supernatants from lung homogenates of mice from cohort A [(A), (B)] and B [(C), (D)] were 22 used for measurement of cytokines using Luminex immunoassay. (E) Flow cytometry was used 23 to assess frequency of CD45+ immune cells in lung cell suspension from mice infected with

	SARS-CoV-2 Beta variant. (F) Assessment of SARS-CoV-2 nucleocapsid (N) protein and
2	cleaved caspase 3 in lung tissues of mice from cohort B treated as shown. The sections were
3	stained with anti-SARS-CoV-2 N (green), anti-cleaved caspase 3 (red) antibodies and DAPI
4	(blue). White arrows show the SARS-CoV-2 N and caspase 3. Scale bars, 100 μ m.
5	Representative (F) or summary (A to E) data (mean \pm SEM) from experiments in triplicates.
6	Each datapoint represents one biological sample. Unless otherwise stated, statistical comparison
7	was done between the Ctrl and each shown experimental group by using two-tailed Mann-
8	Whitney (*p < 0.05, **p < 0.01).
9	
10	
11	Figure S14 (related to Figure 6). Gating strategy for flow panel B (assessment of frequency
12	of immune cell types among lung cells isolated from mice infected with SARS-CoV-2).
12 13	of immune cell types among lung cells isolated from mice infected with SARS-CoV-2). Representative data of gates: 1, 2) Single cells based on forward (FSC) and side scatter (SSC) \rightarrow
13	Representative data of gates: 1, 2) Single cells based on forward (FSC) and side scatter (SSC) \rightarrow
13 14	Representative data of gates: 1, 2) Single cells based on forward (FSC) and side scatter (SSC) → 3) Viable non-red blood cells (non-RBCs) were gated as negative stain for Violet Ghost dye
13 14 15	Representative data of gates: 1, 2) Single cells based on forward (FSC) and side scatter (SSC) \rightarrow 3) Viable non-red blood cells (non-RBCs) were gated as negative stain for Violet Ghost dye (viability dye) and the BV421-Ter119 (mouse RBC marker). Cells were gated on the (2) gate; \rightarrow
13 14 15 16	Representative data of gates: 1, 2) Single cells based on forward (FSC) and side scatter (SSC) \rightarrow 3) Viable non-red blood cells (non-RBCs) were gated as negative stain for Violet Ghost dye (viability dye) and the BV421-Ter119 (mouse RBC marker). Cells were gated on the (2) gate; \rightarrow 4) Cells (FSC/SSC) were gated to exclude debris; \rightarrow 5) Immune cells were gated as CD45(+) on
13 14 15 16 17	Representative data of gates: 1, 2) Single cells based on forward (FSC) and side scatter (SSC) \rightarrow 3) Viable non-red blood cells (non-RBCs) were gated as negative stain for Violet Ghost dye (viability dye) and the BV421-Ter119 (mouse RBC marker). Cells were gated on the (2) gate; \rightarrow 4) Cells (FSC/SSC) were gated to exclude debris; \rightarrow 5) Immune cells were gated as CD45(+) on gate 4 \rightarrow 8) Natural killer (NK) cells were gated as CD335 (NKp46) (+) cells on gate 7 major
13 14 15 16 17 18	Representative data of gates: 1, 2) Single cells based on forward (FSC) and side scatter (SSC) \rightarrow 3) Viable non-red blood cells (non-RBCs) were gated as negative stain for Violet Ghost dye (viability dye) and the BV421-Ter119 (mouse RBC marker). Cells were gated on the (2) gate; \rightarrow 4) Cells (FSC/SSC) were gated to exclude debris; \rightarrow 5) Immune cells were gated as CD45(+) on gate 4 \rightarrow 8) Natural killer (NK) cells were gated as CD335 (NKp46) (+) cells on gate 7 major histocompatibility complex class II (MHCII) (CD11b (+) CD45(+) cells. 9) Neutrophils were
13 14 15 16 17 18 19	Representative data of gates: 1, 2) Single cells based on forward (FSC) and side scatter (SSC) \rightarrow 3) Viable non-red blood cells (non-RBCs) were gated as negative stain for Violet Ghost dye (viability dye) and the BV421-Ter119 (mouse RBC marker). Cells were gated on the (2) gate; \rightarrow 4) Cells (FSC/SSC) were gated to exclude debris; \rightarrow 5) Immune cells were gated as CD45(+) on gate 4 \rightarrow 8) Natural killer (NK) cells were gated as CD335 (NKp46) (+) cells on gate 7 major histocompatibility complex class II (MHCII) (CD11b (+) CD45(+) cells. 9) Neutrophils were gated as Ly-6G/Ly-6C(Gr-1) (+) cells on negative gate 7 [MHCII (-) CD11b (+) CD45(+)]. 10)

1	(DC) were gated as CD11c (+) cells on negative gate 6. 14) T cells were gated as CD3(+) cells
2	on negative gate 6. 15) B cells were gated as CD19(+) cells on negative gate 14.
3	

5	Figure S15 (related to Figure 6). Anti-inflammatory activity of Mito-MES in distal airway
6	lung cells in hACE2 K18 mice. In cohort A mice were infected with wild type (WT) SARS-
7	CoV-2 and treated with either vehicle control (saline 10% DMSO; Ctrl) (n=5) or mitoquinone
8	mesylate (Mito-MES) 4 mg/kg/day (n=10) intraperitoneally either 24 hrs before the infection
9	(hbi) (n=5) or 8 hrs post infection (hpi) (n=5) until day 3 post infection. In cohort B mice were
10	infected with SARS-CoV-2 Beta variant and treated with Ctrl (n=10) or Mito-MES 4 mg/kg/day
11	(n=10) intraperitoneally 24 hbi (n=10) until 5-7 days post infection. Lung tissue was harvested
12	on day 3 (cohort A) or day 5-7 (cohort B) post infection. Assessment of frequency of immune
13	cell subtypes in murine lung tissue by flow cytometry. Representative and summary data from
14	mice in cohorts A and B treated with Mito-MES or Ctrl are shown for neutrophils (A to C),
15	macrophages (D to F), myeloid dendritic cells (DCs) (G to I), lymphoid DCs (J to L), natural
16	killer (NK) cells (M to O), T cells (P to R) and B cells [(S), (T)]. Statistical comparison was
17	done between the Ctrl and each shown experimental group by using two-tailed Mann-Whitney
18	(**p<0.01).

Figure S16 (related to Figures 1-6). Overall hypothesis and impact of Mito-MES on SARSCoV-2 replication and associated inflammation and tissue damage. Mito-MES has antiviral,
antiapoptotic and anti-inflammatory effect in epithelial cells infected with SARS-CoV-2. MitoMES has pleiotropic cellular effects that collectively inhibit SARS-CoV-2 replication: 1) blocks

1	SARS-CoV-2 viral entry through its hydrophobic dTPP moiety; 2) inhibits cytoplasmic viral
2	replication through a) its hydrophobic dTPP moiety, b) upregulation of antiviral host pathways
3	(Nrf2 pathway, MX1, TOM70), c) downregulation of mitochondrial reactive oxygen species
4	(mito-ROS) that induce proviral host factors for replication of coronaviruses such as the
5	coatomer coat protein complex(de Wilde et al., 2015), the mitochondrial permeability transition
6	pore (mPTP)(Halestrap et al., 2004), MEK (Zhang et al., 2016), MNK1(Wang and Zhang, 1999)
7	and MAPK signaling pathways (Emerling et al., 2005; Kulisz et al., 2002; Trempolec et al.,
8	2017) that propagate viral protein synthesis and replication (Jamaluddin et al., 2009;
9	Kefaloyianni et al., 2006; Mizutani et al., 2004). Mito-ROS also alter interferon host
10	responses(Agod et al., 2017), induce aberrant endoplasmic reticulum (ER) stress, lipid
11	peroxidation, alterations of membranes and proteins and activation of cytosolic phospholipases
12	(Adibhatla and Hatcher, 2008; Moon et al., 2012; Sun et al., 2012); 3) blocks SARS-CoV-2-
13	associated cellular apoptosis and subsequent release of SARS-CoV-2 virions to infect other cells.
14	Mito-MES has also anti-inflammatory properties (reduces release of IL-1 β , IL-6, TNF- α) that are
15	mediated partially through the Nrf2 pathway and its dTPP moiety. Collectively, the antiviral,
16	antiapoptotic and anti-inflammatory effects of Mito-MES in epithelial cells infected with SARS-
17	CoV-2 reduce tissue damage and morbidity from COVID-19. Created with Biorender.com and
18	Avogadro.cc.
19	

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1 STAR METHODS

3 RESOURCE AVAILABILITY

4 Lead Contact

- 5 Further information and requests for resources and reagents should be directed to and will be
- 6 fulfilled by the Lead Contact, Theodoros Kelesidis (tkelesidis@mednet.ucla.edu).

7

8 Materials availability

9 This study did not generate new unique reagents.

10

11 Data and code availability:

12 All data are available in the main text or the supplementary materials.

13

14

15 EXPERIMENTAL MODEL AND SUBJECT DETAILS

16

17 <u>Cell cultures</u>

- 18 Calu3, Vero-E6, HEK293-ACE2, Murine 17Cl-1 cells were maintained at 37 °C and 5% CO₂ in
- 19 DMEM or MEM supplemented with 10% (v/v) FBS, penicillin (100 units/ml), and streptomycin
- 20 (100 µg/ml) (1X P/S). HEK293-ACE2 cells were maintained at 37 °C and 5% CO₂ in MEM
- 21 supplemented with 10% (v/v) FBS and hygromycin. Primary mouse lung cells that express

1	human ACE2 were isolated from uninfected K18-hACE2 mice and were maintained at 37 °C and
2	5% CO ₂ in DMEM supplemented with 10% (v/v) FBS and 1X P/S.
3	
4	Human Tissue Procurement
5	Large airways and bronchial tissues were acquired from de-identified normal human donors after
6	lung transplantations at the Ronald Reagan University of California, Los Angeles (UCLA)
7	Medical Center. Tissues were procured under Institutional Review Board-approved protocols at
8	the David Geffen School of Medicine at UCLA. Human airway basal stem cells (ABSCs) from
9	one biological replicate were used for two experiments. The biological replicates were from
10	ABSCs isolated from lung transplant donors. No demographic data was available for the normal
11	lung donor samples.
12	
13	ABSC Isolation
14	Human airway basal stem cells (ABSCs) were isolated following a previously published method
15	by our group(Purkayastha et al., 2020). Briefly, airways were dissected, cleaned, and incubated
16	in 16 units/ml dispase for 30 minutes (min) at room temperature. Tissues were then incubated in
17	0.5 mg/ml DNase for another 30 min at room temperature. Epithelium was stripped and
18	incubated in 0.1% (v/v) Trypsin- EDTA for 30 min shaking at 37 °C to generate a single cell
19	suspension. Isolated cells were passed through a 40 μ m strainer and plated for Air-Liquid
20	Interface cultures.
0.1	

22 <u>ABSC Air-Liquid Interface Cultures (Upper airway ALI cultures)</u>

1	24-well 6.5 mm transwells with 0.4 μ m pore polyester membrane inserts were coated with
2	collagen type I dissolved in cell culture grade water at a ratio of 1:10. 100 μ l was added to each
3	transwell and allowed to air dry. ABSCs were seeded at 100,000 cells per well directly onto
4	collagen-coated transwells and allowed to grow in the submerged phase of culture for 4-5 days
5	with 500 μ l media in the basal chamber and 200 μ l media in the apical chamber. ALI cultures
6	were then established and cultured with only 500 μ l media in the basal chamber, and cultures
7	were infected with SARS-COV-2 as indicated. Media was changed every other day and cultures
8	were maintained at 37 °C and 5% CO ₂ .
9	
10	Human Primary Small Airway Epithelial Cells (HSAECs) Lower Respiratory Epithelium Airway
11	ALI cultures
12	
13	HSAECs were seeded onto collagen coated transwells and grown in the submerged phase of
14	culture for 4–5 days in PneumaCult Ex Plus media with 500 μ l media in the basal chamber and
15	200μ l media in the apical chamber. ALI cultures were then maintained for 21 days with only
16	500μ l PneumaCult ALI media in the basal chamber, and media changed every 2 days. Cultures
17	were maintained at 37 °C and 5% CO ₂ .
18	
19	SARS-CoV-2 infection
20	All studies involving live virus were conducted at the UCLA Biosafety Level 3 (BSL3) high-
21	containment facility with appropriate institutional biosafety approvals. SARS-CoV-2 was
22	passaged once in Vero-E6 cells and viral stocks were aliquoted and stored at -80 °C. Virus titer
23	was measured in Vero-E6 cells by median tissue culture infectious dose (TCID ₅₀) assay. Cell

1	cultures in 96 well plates and ALI cultures were infected with SARS-CoV-2 viral inoculum
2	[Multiplicity of infection (MOI) of 0.1 or at least 1 for ALI; 100 μ l/well] prepared in media. For
3	infection of Calu3 cells in 96 well plates with the fluorescent reporter a stable mNeonGreen
4	SARS-CoV-2 virus (icSARS-CoV-2-mNG), an MOI of 0.3 and 100 μl /well was used. For mock
5	infection, conditioned media (100 µl/well) alone was added.
6	
7	Assessment of SARS-CoV-2 infection among different cell culture systems
8	SARS-CoV-2 infection was assessed by independent experiments that determined either the
9	single cell content of SARS-CoV-2 or the total amount of secreted, intracellular or total (secreted
10	and intracellular) SARS-CoV-2. The intracellular content of the SARS-CoV-2 nucleocapsid
11	protein (NP) or the Spike (S) protein was assessed using ELISA, flow cytometry and
12	immunofluorescence as described in Methods. Protein extract concentration was quantified using
13	the Pierce BCA Protein Assay, according to manufacturer instructions (Thermo Fisher Scientific,
14	Waltham, MA). SARS-CoV-2 NP or S protein content was expressed as either the percentage of
15	cells that were positive for the SARS-CoV-2 viral protein (immunofluorescence or flow
16	cytometry) or the median fluorescence intensity (MFI) of the SARS-CoV-2 viral protein per cell
17	(immunofluorescence or flow cytometry). In ELISA experiments the intracellular SARS-CoV-2
18	NP or S protein content (pg) was normalized by the total cellular amount of protein within each
19	experimental well (pg of viral protein per μ g of total protein). The intracellular genomic
20	expression of SARS-CoV-2 was assessed using primers specific for SARS-CoV-2 and real time
21	PCR as described in Methods. The secreted amount of SARS-CoV-2 in cell culture supernatant
22	of infected cell cultures was assessed using SARS-CoV-2 NP ELISA. The secreted amount of
23	live SARS-CoV-2 in cell culture supernatant of infected cell cultures was assessed using viral

1	titer as described in Methods. Percent infection was quantified as ((Infected cells/Total cells) -
2	Background) *100 and the vehicle control was then set to 100% infection for analysis. The half
3	maximal inhibitory concentration (IC50) for each experiment were determined using the Prism
4	(GraphPad Holdings, San Diego, CA) software.
5	
6	<u>Viral titers</u>
7	Infectious titers were quantified by limiting dilution titration using Vero-E6 cells. Briefly, Vero-
8	E6 cells were seeded in 96-well plates at 5,000 or 10,000 cells/well. The next day, SARS-CoV-
9	2-containing supernatant was applied at serial 10-fold dilutions ranging from 10 ⁻¹ to 10 ⁻⁸ and,
10	after 3-5 days, viral cytopathic effect (CPE) was assessed by microscopy or by determination of
11	the intracellular SARS-CoV-2 NP using ELISA. TCID ₅₀ /ml was calculated using the Reed-
12	Muench method.
13	
14	In-cell SARS-CoV-2 ELISA
15	To independently establish detection of SARS-CoV-2 infection using a more quantitative
16	method to assess viral titer (not based on microscopy), we utilized in-cell SARS-CoV-2 ELISA
17	based on intracellular detection of the SARS-CoV-2 S or NP protein. 5,000 or 10,000 Vero-E6
18	cells were seeded in 96 well plates in 100 μ l. The next day, the cells were inoculated with 10 μ l
19	of a 10-fold titration series of SARS-CoV-2. Two to three days later, SARS-CoV-2 S or NP
20	protein staining was assessed using an anti-SARS-CoV-2 S or NP protein antibody. Cells were
21	fixed by adding 100 μl 8% (v/v) PFA to 100 μl of medium (final 4% solution) and 30 min of
22	room temperature incubation. Medium was then discarded and the cells permeabilized for 5 min
23	at room temperature by adding 100 μ l of Intracellular Staining Permeabilization Wash Buffer

1	(BioLegend). Cells were then washed with PBS and stained with 1:5,000 (anti-Spike S antibody
2	clone 1A9) or 1:10,000 (anti-NP antibody clone ARC2372) in permeabilization buffer at 37 °C.
3	After 1 hour, the cells were washed three times with washing buffer before a secondary anti-
4	mouse or anti-rabbit antibody conjugated with HRP was added (1:20,000) and incubated for 1
5	hour at 37 °C. Following three times of washing, the 3,3',5,5'-tetramethylbenzidine (TMB)
6	peroxidase substrate was added. After 5 min light-protected incubation at room temperature,
7	reaction was stopped using 0.5 M H2SO4. The optical density (OD) was recorded at 450 nm and
8	baseline corrected for 620 nm using the Biotek microplate reader (Agilent Technologies, Santa
9	Clara, CA).

11 Drug treatments

12 A concentration of Mito-MES between 10-1000 nM has been shown to be physiologically 13 relevant, efficacious and non-cytotoxic in human mammalian cells. The antiviral activity of 14 Mito-MES was evaluated in Calu3, Vero-E6, HEK293T and HSAECs ALI cell cultures. All 15 SARS-CoV-2 studies were performed in biological triplicate. Cultured cells were incubated 16 separately with Mito-MES or decyl triphenyl phosphonium cation (DTPP) (0, 10, 100, 250, 500 17 or 1000 nM) — a non-antioxidant mitochondria-targeted control compound which allowed for 18 the effects of the TPP component of Mito-MES to be examined. The concentration of DMSO 19 vehicle control was maintained constant at 0.01% v/v for all treatments. Drug effects were 20 measured relative to vehicle controls in vitro. Unless stated, as proof-of concept experiments and 21 to ensure that adequate time was allowed for Mito-MES to alter host cellular responses in 22 mitochondria enriched epithelial cells, Calu3, Vero-E6, HEK293-ACE2, and ALI cultures were 23 pretreated for 16-24 hours (hrs) with the indicated treatments (Mito-MES, DMF, Brusatol, Mito-

1	TEMPO) or vehicle control. The cells were then washed, infected with SARS-CoV-2 for 2 hrs,
2	the virus was removed, and the treatments (Mito-MES, mito-TEMPO, remdesivir) were added
3	back. Remdesivir (5 μ M), a well characterized direct acting antiviral agent was used as an
4	antiviral control.
5	
6	Assessment of cell cytotoxicity
7	To measure cell viability to determine if there was any treatment-induced cytotoxicity,
8	uninfected cells were plated and treated with the same compound dilutions used for the in vitro
9	efficacy studies. As above, 0.01% DMSO-treated cells served as the 0% cytotoxicity control.
10	After 24-48 hrs, cell viability was measured on a Synergy 2 Biotek microplate reader (Agilent
11	Technologies, Santa Clara, CA) via the XTT Cell Proliferation Assay Kit according to the
12	manufacturer's protocol (ATCC, Manassas, VA). Similar data were obtained in three
13	independent experiments. Flow cytometry was used to independently assess cell viability and
14	levels of target proteins in single viable cells.
15	
16	Imaging and immunofluorescence
17	After 24-48 hrs of SARS-CoV-2 infection (or mock), live cell images were obtained by wide
18	field fluorescence microscopy using a 10x air objective (Leica DM IRB, Wetzlar, Germany). For
19	immunofluorescence, separate wells of cells were fixed with 4% paraformaldehyde in phosphate-
20	buffered saline (PBS) for 20 min. The fixed samples were then permeabilized and blocked for 1
21	hour in a "blocking solution" containing PBS with 2% bovine serum albumin, 5% donkey serum,
22	5% goat serum, and 0.3% Triton X-100. Primary antibodies were diluted in the blocking solution

23 and added to samples overnight at 4 °C. The following antibodies and dilutions were used:

1	polyclonal rabbit anti-Tom70 (1:100), rabbit anti-SARS-CoV-2 Spike S1 (clone #007) (1:100),
2	polyclonal rabbit anti-cleaved caspase-3 (1:200), polyclonal rabbit anti-SARS-CoV-2 NP
3	(1:1000). Samples were then rinsed 5 times for 2 min each with PBS containing 0.3% (v/v)
4	Triton X-100, followed by incubation with fluorescent-conjugated secondary antibodies diluted
5	1:1,000 in blocking buffer for 2 hrs at room temperature. Secondary antibodies were goat anti-
6	rabbit Alexa Fluor 488 IgG, goat anti-mouse Alexa Fluor 546, goat anti-rabbit DyLight 650.
7	Samples were then rinsed 5 times for 2 min each with PBS containing 0.3% Triton X-100,
8	followed by DAPI diluted in PBS at 1:5000 for 10 min. Immunofluorescence (IF) images were
9	obtained using an LSM880 Zeiss confocal microscope (Carl Zeiss GmbH, Jena, Germany) with
10	Airyscan using a 20X air objective or a 63X Apochromat oil-immersion objective.
11	Immunofluorescence images were quantified using CellProfiler 2.0(Kamentsky et al., 2011)
12	(Broad Institute, Cambridge, MA). DAPI was used to count total cell numbers in order to obtain
13	a percentage of cells positive for spike protein, cleaved caspase-3, or TOM70. Alternatively, 96-
14	well plates were imaged using the Operetta (PerkinElmer, Waltham, MA) system.
15	
16	High-throughput imaging
17	Cells plated in Greiner μ Clear 96-well plates were stained with antibodies for
18	immunofluorescence as above and were imaged on Operetta high-content wide-field
19	fluorescence imaging system using a 10X air objective. Fifteen fields were imaged per well with
20	a similar field distribution across all wells. CellProfiler 2.0 was used to quantify cell counts and
21	infection ratios(Kamentsky et al., 2011).
22	
23	Cellular reactive oxygen species analysis

1	Vero-E6 or Calu3 cells were treated and infected with icSARS-CoV-2-mNG reporter virus as
2	indicated for 24-48 hrs. Subsequently, cells were washed once with hanks buffered salt solution
3	(HBSS) with calcium and magnesium, without phenol-red and stained for 10 min with 1 μ g/ml
4	Hoechst 33342 and 5 μ M dihydroethidum (DHE) in HBSS. Following two washes with HBSS,
5	cells were returned to an imaging medium without phenol red (low glucose DMEM,
6	supplemented with 10% (v/v) FBS, 2 mM glutamine and 1 mM sodium pyruvate and 1X P/S and
7	imaged with a Leica DM IRB wide field fluorescence microscope as described above using
8	DAPI, GFP, and RFP filters. CellProfiler 2.0 was used to quantify cell counts, infection ratios
9	per well, and DHE fluorescence intensity per cell(Kamentsky et al., 2011).
10	
11	Flow cytometry
12	Within the UCLA BSL3 high-containment facility, SARS-CoV-2 infected and uninfected cells
13	were resuspended in PBS and single cell suspensions were incubated with viability dye at 1:500
14	(Fixable Ghost Dye Red 780 or Ghost Dye Violet 450) for 20 min in the dark at room
15	temperature. Cells were washed and appropriate antibodies were added to each tube and
16	incubated in the dark for 20 min on ice. Cells were then washed and fixed with $4\% (v/v)$
17	paraformaldehyde or methanol for 30 min at 4 °C. Cells were then washed and were transferred
18	in polypropylene Eppendorf tubes (E-tubes) to BSL2 containment facility for further processing.
19	Appropriate antibodies were added to each tube and incubated in the dark for 20 min on ice.
20	
21	The following antibodies were used for staining in flow cytometry: PE/Cy7 anti-mouse CD3
22	(clone 17A2, 1:25), BV 605 anti-mouse CD8a (clone 53-6.7, 1:10), Alexa Fluor 647 anti-
23	mouse/human CD11b (clone M1/70, 1:50), BV421 anti-mouse CD11c (clone N418, 1:10),

1 PerCP/Cy5.5 anti-mouse CD19 (clone 1D3/CD19, 1:10), PE/Cy7 anti-mouse CD31 (clo

- 2 1:100), BV785 anti-mouse CD45 (clone 30-F11, 1:40), PE/Cy7 anti-human CD147 (clone
- 3 HIM6, 1:10), BV421 anti-human CD304 (Neuropilin-1, clone 12C2, 1:20), BV605 anti-mouse
- 4 CD326 (Ep-CAM, clone G8.8, 1:8)), PE anti-mouse CD335 (NKp46, clone 29A1.4, 1:10),
- 5 BV711 MHC II anti-mouse I-A/I-E (clone M5/114.15.2, 1:25), APC/Cy7 anti-mouse Podoplanin
- 6 (clone 8.1.1, 1:50), BV421 anti-mouse TER-119/Erythroid Cells (clone TER-119, 1:33),
- 7 APC/Cy7 anti-mouse Ly-6G/Ly-6C (Gr-1, clone RB6-8C5, 1:25), rabbit anti-SARS-CoV-2 NP
- 8 (clone ARC2372. 1:50), rabbit anti-SARS-CoV-2 Spike (clone 007, 1:50), mouse anti-SARS-
- 9 CoV-2 Spike (clone 1A9, 1:50), anti-ACE-2 (polyclonal, 1:10), rabbit anti-human TMPRSS2
- 10 (polyclonal, 1:10), Alexa Fluor 647 anti-human Furin (clone 222722, 1:10), rabbit anti-human
- 11 MAVS (clone D5A9E, 1:10), rabbit anti-human TOM70 (polyclonal,1:5), rabbit anti-
- 12 human/mouse Alexa Fluor 647 cleaved caspase-3 (clone D3E9, 1:25), mouse anti-human, HO-1
- 13 (clone HO-1-2, 1:20), anti-MX1 (polyclonal, 1:10), Alexa Fluor 647 anti-human STING (clone
- 14 723505, 1:10). Rabbit anti-NRF2 (polyclonal, 1:50) anti-FOXJ1-CF647 (polyclonal, 1:10). Non-
- 15 fluorescent unconjugated primary antibodies were conjugated with Mix-n-Stain CF488 or CF647

16 Antibody Labeling Kits from MilliporeSigma (Burlington, MA).

- 17
- 18

The cells were washed twice with PBS and were transferred to tubes for fluorescence activated cell sorting (FACS) analysis. Samples were acquired using an LSRFortessa[™] flow cytometer and FACSDiva[™] software (Becton Dickinson, Franklin Lakes, NJ). Data were analyzed using FlowJo[™] software (Becton Dickinson, Franklin Lakes, NJ). At least 10,000 cells were acquired for each analysis and only live and singlet cells were chosen for analysis and gating (i.e., dead

1	cells and aggregates were excluded). Each representative flow plot was repeated at least 3 times.
2	Single stain and also fluorescence minus one (FMO) controls were used in the presence of a
3	given concentration of the antibody staining cocktail.
4	
5	The flow cytometry experiments in single-cell suspensions obtained from enzymatically digested
6	murine lungs were performed using similar methodology like the cell suspensions from cell
7	cultures with the following specifications.
8	
9	To determine SARS-CoV-2 NP expression at the single cell level among different cell subtypes
10	in murine lung [lung EPCAM (+) epithelial cells, ciliated FOXJ-1(+) lung EPCAM epithelial
11	cells, alveolar type 1 (AT1), alveolar type 2 (AT2), CD31(+) CD45(-) endothelial cells, CD45(+)
12	immune cells], one aliquot of cells was stained with a mastermix of antibodies for surface
13	(CD326, MHCII, CD45, CD31, podoplanin, red blood cell marker Ter119) and intracellular
14	antigens (SARS-CoV-2 NP, FOXJ-1). Lung epithelial cells were gated based on the lung
15	epithelial marker EPCAM (CD326) (Hasegawa et al., 2017). Ciliated lung epithelial cells were
16	gated based on the intracellular marker f-box factor FOXJ-1(You et al., 2004). AT1 cells were
17	gated based on the AT1 marker podoplanin(Nakano et al., 2018). To gate AT2 cells we utilized a
18	previously validated methodology that established that the MHCII marker is an AT2 membrane
19	marker, similarly to the pro-surfactant protein C (proSP-C)(Hasegawa et al., 2017). Murine
20	immune lung cells were gated as mouse (m)-CD45(+) cells. Murine endothelial cells were gated
21	as m-CD45(-)/m-CD31(+) cells. Lung epithelial cells were gated as m-CD45(-)/m-CD31(-)/m-
22	EPCAM (+) cells. Lung ciliated epithelial cells were gated as m-CD45(-)/m-CD31(-)/m-EPCAM
23	(+) FOXJ-1(+) cells. AT1 cells were gated as m-CD45(-)/m-CD31(-)/m-EPCAM (+)/m-

1	podoplanin (+) (AT1 marker)/ MHCII (-) (AT2 marker) cells. AT2 cells were gated as m-CD45(-
2)/m-CD31(-)/m-EPCAM (+)/m-podoplanin (-)/MHCII (+) (AT2 marker) cells.

4 To determine lung inflammation at the single cell level and cellular infiltration of murine lung 5 with different immune cell subtypes [neutrophils, monocytes, macrophages, myeloid dendritic 6 cells (mDCs), lymphoid dendritic cells (lymphoid DCs), natural killer cells (NK cells), T 7 lymphocytes and B lymphocytes), one aliquot of lung cells was stained with a mastermix of 8 antibodies for surface markers [CD11b, CD11c, CD8, CD3, CD19, CD45, NKp46, MHCII, Ly-9 6G/Ly-6C (Gr-1), red blood cell marker Ter119)]. To reliably gate immune cells, we utilized a 10 previously validated methodology that established that the Ly6G/Ly6C markers are superior to 11 Gr-1 for identifying murine neutrophils and that F4/80 is unreliable marker to identify certain 12 immune cell subtypes (Rose et al., 2012). Murine immune lung cells were gated as mouse (m)-13 CD45(+) cells. T lymphocytes were gated as m-CD3(+)/m-CD45(+) cells. B lymphocytes were 14 gated as m-CD3(-)/m-CD19(+)/m-CD45(+) cells. NK cells were gated as m-CD11b(+)/m-15 MHCII(+)/m-NKp46(+)/m-CD45(+) cells. NKp46 is expressed by all natural killer (NK) cells 16 but not by lymphocytes, granulocytes or myeloid cells(Westgaard et al., 2004). Non-activated 17 neutrophils do not express MHCII(Hansch and Wagner, 2003) and are positive for Ly6G/Ly6C 18 markers (Rose et al., 2012). Non-activated neutrophils were gated as m-CD11b (+)/m-MHCII (-19)/m-Ly6G/Ly6C (+)/m-CD45(+) cells.

20

21 Lymphoid dendritic cells (labelled as lymphoid DCs) are positive for CD8 marker and negative

for CD11b marker(Shortman and Liu, 2002). Lymphoid DCs were gated as m-MHCII(+)/m-

23 CD8(+)/m-CD11c(+)/m-CD11b(-)/m-CD45(+) cells. Myeloid tissue dendritic cells (labelled as

1	myeloid DCs) are negative for CD8 marker and positive for CD11b marker(Shortman and Liu,
2	2002). Myeloid DCs were gated as m-MHCII(+)/m-CD8(-)/m-CD11c(+)/m-CD11b(+)/m-
3	CD45(+) cells. Monocytes and monocyte derived macrophages (M/M) express CD11b (Misharin
4	et al., 2013) and Ly-6G/Ly-6C(Gr-1)(Rose et al., 2012) but do not express NKp46 (Westgaard et
5	al., 2004) and CD11c (Misharin et al., 2013). Monocytes/macrophages (M/M) were gated as m-
6	Ly-6G/m-Ly-6C(m-Gr-1) (+)/(m-NKp46) (-)/m-CD11c(-)/m-MHCII(+)/m-CD11b(+)/m-
7	CD45(+) cells.
8	
9	Mitochondrial Reactive oxygen species analysis
10	After 24 hrs post infection, cells were collected and stained with 5 μ M MitoSOX Red
11	Mitochondrial reactive oxygen species (mito-ROS) indicator for 30 min at 37 °C. Cells were
12	washed with PBS, fixed with 4% paraformaldehyde for 30 min at 4 °C and transferred to
13	polypropylene FACS tubes. Cells were then analyzed using an LSR Fortessa flow cytometer and
14	FACSDiva software), and data were analyzed using FlowJo software (Becton Dickinson,
15	Franklin Lakes, NJ).
16	
17	Biomarkers of inflammation
18	Protein levels of secreted IL-6 were determined in cell culture supernatants using ELISA kits
19	according to the manufacturer (Bio-Techne, Minneapolis, MN). Luminex immunoassay was
20	used to measure human cytokines [interleukin-1 β (IL-1 β), IL-8, IL-10, TNF- α , Vascular
21	endothelial growth factor (VEGF)] secreted by Calu3 cells and airway lung epithelial cells in cell

22 culture supernatants according to the manufacturer (Bio-Techne, Minneapolis, MN). A 4-Plex

1	ProcartaPlex assay (Thermo Fisher Scientific, Waltham, MA) was used to measure murine
2	cytokines (IL-1 β , IL-6, IL-18, TNF- α) in mouse lung protein lysates.
3	
4	RNA extraction and Real-Time Quantitative Reverse Transcription Polymerase Chain Reaction
5	(<u>RT-qPCR</u>)
6	
7	Total RNA was isolated using the RNeasy Mini Kit or Direct-zol RNA Miniprep kit (Zymo
8	Research) and complementary deoxyribonucleic acid (cDNA) was synthesized using oligo
9	deoxythymine (dT) primers and RevertAid first strand cDNA synthesis kit. Quantitative real-
10	time reverse transcription PCR was performed using SYBR Green Master Mix and primers
11	specific for SARS-CoV-2 as well as glyceraldehyde 3-phosphate dehydrogenase (GAPDH)
12	transcripts. The following primers were used: 2019-nCoV_N1-F:
13	GACCCCAAAATCAGCGAAAT, 2019-nCoV_N1-R: TCTGGTTACTGCCAGTTGAATCTG;
14	h-GAPDH-F: CCACCTTTGACGCTGGG; h-GAPDH-R:
15	CATACCAGGAAATGAGCTTGACA. All qRT-PCR reactions were performed using BIO-
16	RAD CFX96 Touch Real-Time PCR Detection System (Bio-Rad Laboratories, Hercules, CA) on
17	96-well plates. PCR reactions included SYBR Green RT-PCR Master Mix, 10 μ M primers and 5
18	μl of cDNA. Reactions were incubated at 45 °C for 10 min for reverse transcription, 95 °C for 2
19	min, followed by 40 cycles of 95 °C for 15 seconds (sec) and 60 °C for 60 sec. Gene expression
20	fold change was calculated with the Delta-delta-cycle threshold (DDCt) method. Viral RNA
21	levels were normalized to GADPH as an endogenous control and depicted as fold change over
22	mock infected samples.

1 <u>Mitochondrial respirometry analysis</u>

2 Calu3 cells were seeded at a density of 16,000 cells per well into 8-well Seahorse mini plates and 3 allowed to attach for 24 hrs. Treatments were started 24 hrs before infection with SARS-CoV-2 4 (WA1 strain, MOI 0.1-0.5). Cells were infected for 48 hrs and subsequently analyzed by 5 Seahorse respirometry. Briefly, growth media was replaced with Seahorse XF base media 6 (supplemented with 2 mM glutamine and 1 mM sodium pyruvate, pH adjusted to 7.4) twice and 7 respirometry assessed using a Seahorse XF HS Mini Analyzer (Agilent Santa Clara, CA) and the 8 using the Mito Stress Test protocol. After basal respiration, mitochondrial proton leak was 9 assessed after oligomycin injection, maximal respiration was assessed after Carbonylcyanide-4-10 (trifluoromethoxy)-phenylhydrazone (FCCP) injection, and non-mitochondrial respiration after 11 rotenone, and antimycin A injection. Following the assay, cells were fixed in 4% (v/v) 12 paraformaldehyde as described above and SARS-CoV-2 positive cells stained against SARS-13 CoV-2 nucleocapsid protein, and nuclei stained with DAPI. Wells were imaged using an 14 LSM880 Zeiss confocal microscope (Carl Zeiss GmbH, Jena, Germany) with a 10X air objective 15 and cell counts and infection ratios determined using CellProfiler 2.0. Agilent Wave 2.6 software 16 (Agilent Santa Clara, CA) was used to normalize oxygen consumption rates to cell counts. 17

18 Mouse studies of SARS-CoV-2 infection

19 All the antiviral studies were performed in animal biosafety level 3 (BSL3) facility at University

20 of California, Los Angeles. All work was conducted under protocols approved by the

21 Institutional Animal Care and Use Committee (IACUC). We used a model of mice hemizygous

for the expression of hACE2 gene (K18-ACE2) and we performed three studies in these mice to

23 evaluate the *in vivo* efficacy of Mito-MES as antiviral and anti-inflammatory therapeutic agent in

SARS-CoV-2 infection. In total, we utilized 55 male and female 4 to12-week-old specific
pathogen-free hemizygous for Tg(K18-ACE2)2Prlmn (Strain B6.Cg-Tg(K18-ACE2)2Prlmn/J,
the Jackson laboratory strain 034860) mice. Animals were housed in individually ventilated
cages, 5 mice per cage, on a 12-h light-dark cycle at 21–23 °C and 40–60% humidity. Mice were
allowed free access to irradiated standard rodent diet (Tecklad 2914C) and sterilized water.
Littermates of the same sex were randomly assigned to experimental groups and all animal
studies included both male and female mice.

8

9 Cohort A included 15 male K18-hACE2 mice between 4 to 8 weeks of age (16-25 g). Mice were 10 treated intraperitoneally with either vehicle control (normal saline 10% DMSO; Ctrl) (n=10) or 11 Mito-MES 4 mg/kg/day (n=5) for at least 20 hrs before the infection (dose 1). Ten mice were 12 then given a second dose of vehicle or Mito-MES and after 2 hrs were infected intranasally with 13 wild type (WT) SARS-CoV-2 [10,000 plaque-forming unit (PFU)/mouse in <50 µl of PBS, day 14 0]. Mice were anesthetized with a mixture of ketamine/xylazine before each intranasal infection. 15 Five mice were given intraperitoneally Mito-MES (first dose) 8 hrs post infection (hpi)(n=5). 16 Additional doses of Mito-MES (n=10) or vehicle (n=5) were given on day 1 (24 hpi), day 2 (48 17 hpi) and day 3 (72 hpi). The body weight of mice was measured each day. Three days post 18 infection (dpi) animals were humanely euthanized. Whole left lungs were harvested and were 19 processed to create homogenates for viral titration via TCID50, single cell suspension for flow 20 cytometry, or protein lysates for immunoassays. The total (secreted and intracellular) amount of 21 SARS-CoV-2 NP in lung tissue homogenates (protein lysates) from mice infected with SARS-22 CoV-2 was assessed by SARS-CoV-2 NP ELISA. The total (secreted and intracellular) amount

of live SARS-CoV-2 in lung tissue homogenates from mice infected with SARS-CoV-2 was
 assessed by viral titer.

3

4 Cohort B included 20 female K18-hACE2 mice between 4 to 8 weeks of age (16-21 g). Mice 5 were treated intraperitoneally with either vehicle control (normal saline 10% DMSO; Ctrl) 6 (n=10) or Mito-MES 4 mg/kg/day (n=10) for at least 20 hrs before the infection (dose 1). Next 7 day (Day 0), mice were then given a second dose of vehicle or Mito-MES and after 2 hrs were 8 infected intranasally with Beta Variant of SARS-CoV-2 (10,000 PFU/mouse in <50 µl of PBS). 9 Mice were anesthetized with a mixture of ketamine/xylazine before each intranasal infection. 10 Additional doses of Mito-MES (n=10) or vehicle (n=10) were given on each day for up to 5-7 11 dpi. The body weight of mice was measured each day. 5-7 dpi animals were humanely 12 euthanized. Whole left lungs were harvested and were processed for histopathology studies, 13 single cell suspension for flow cytometry or protein lysates for immunoassays. 14 15 Cohort C included 20 male K18-hACE2 mice between 4 to 8 weeks of age (16-25 g). Mice were 16 treated via gavage with either vehicle control (normal saline 10% DMSO; Ctrl) (n=10) or Mito-17 MES 20 mg/kg/day (n=10) for at least 20 hrs before the infection (dose 1). As source of Mito-18 MES the actual diet supplement capsule (5 mg Mito-MES per capsule) that is given in humans 19 was utilized. Each capsule was opened and was dissolved in saline 10% DMSO solution before 20 given via gavage to mice. Next day (Day 0), mice were then given a second dose of vehicle or Mito-MES and after 2 hrs were infected intranasally with Delta Variant of SARS-CoV-2 (10,000 21 22 PFU/mouse in <50 µl of PBS). Mice were anesthetized with a mixture of ketamine/xylazine 23 before each intranasal infection. Additional doses of Mito-MES (n=10) or vehicle (n=10) were

1	given on day 1, day 2 and day 3 post infection. The body weight of mice was measured each day.
2	On 3 dpi animals were humanely euthanized. Whole left lungs were harvested and were
3	processed for single cell suspension for flow cytometry or viral titration via TCID ₅₀ .
4	
5	Mouse tissue processing
6	Tissue samples were collected at necropsy. Less than 20 mg of lung tissue was either embedded
7	in paraffin for hematoxylin and eosin (H&E) staining or was cryoembedded in Tissue-Plus
8	O.C.T Compound for immunofluorescence staining. The right middle lobe was used for cell
9	isolation and flow cytometry analysis. Tissues were weighted and <0.25 gram tissue samples
10	were rinsed with DBPS, cut in 0.5 cm size pieces that were placed in 7 ml
11	screwcap dissociation tubes with ceramic beads (Precellys) filled with 2.5 ml prewarmed (37 °C)
12	digestion medium (2 mg/ml Collagenase, DNAse 0.1 mg/ml, 1% FCS). Tissues
13	were mechanically dissociated at power 3,000 rpm for one 10-second cycle using a Precellys 24
14	homogenizer (Bertin Technologies, Montigny-le-Bretonneux, France), followed by a 30-minute
15	incubation at 37 °C and another 10-second dissociation cycle (3,000 rpm). The homogenate
16	was filtered through a sterile 40 μ m nylon filter and cells were then processed for flow
17	cytometry. The entire left lung was processed immediately for viral titer. Lung tissues were
18	placed in 2 ml screwcap dissociation tubes with 60 X 1.4 mm ceramic beads at power 5,000 rpm
19	using a Precellys 24 homogenizer and were mechanically dissociated in 0.5 ml DPBS for 90 sec.
20	Homogenates were centrifuged at 16,000 g for 10 min and supernatants were then cryopreserved
21	at -80 °C for viral titer in Vero-E6 cells. For tissue lysates that were used for protein
22	measurements, 50-100 mg of lung tissue samples were placed in 2 ml
23	screwcap dissociation tubes with ceramic beads (Precellys) and were mechanically dissociated in

1	T-PER tissue protein extraction Reagent at power 5,000 rpm leaving samples to cool on ice
2	between 1-2 repeated 20-second cycles as previously described(Daskou et al., 2021).
3	
4	Isolation of primary mouse lung cells
5	Following euthanasia, uninfected K18-hACE2 mice of identical age and gender like the mice in
6	cohort C, were perfused with normal saline before removal of the left lung. Lung tissues were
7	then rinsed with DBPS and processed similarly to SARS-CoV-2 infected mice to create cell
8	suspension. Cells were then seeded in T75 flasks with complete medium [DMEM supplemented
9	with 10% (v/v) FBS, 1X P/S] and were allowed to adhere overnight. The next day the medium
10	was exchanged, and cells were maintained in complete medium before seeding in 96 well plates
11	for SARS-CoV-2 infection and treatment with Mito-MES.
12	
13	Mouse lung histological analysis
14	
15	Paraffin-embedded murine lung tissue blocks were cut into 5 μ m sections that were stained with
16	hematoxylin and eosin (H&E) or Trichrome Masson. Light microscopic scans of whole lung
17	were examined by an experienced pathologist using an Olympus BX53 microscope. Perivascular
18	inflammation, airway inflammation, and alveolar inflammation were individually assessed
19	semiquantitatively using a 5-point grading scheme considering the focality and intensity of the
20	inflammatory infiltrate: 0 – absent, 1 – focal mild or patchy minimal, 2 – multifocal mild or focal
21	moderate, 3 – diffuse moderate or focal severe, 4 – diffuse severe or with epithelial

22 injury/necrosis. The overall grade of inflammation was determined using the sum of these three

scores (max 12). Interstitial and airway fibrosis were absent in all cases, confirmed by Masson
 trichrome stain.

3

4 QUANTIFICATION AND STATISTICAL ANALYSIS

5

6 <u>Statistics</u>

7 Unless noted, error bars in all figures represent mean and standard error of means (SEM). In the 8 figures, p-values are presented for comparisons between treatment groups and controls and are 9 denoted by asterisks. To pool cells from different experiments, each measurement was first 10 normalized to the vehicle controls of each experiment. Each experiment contains at least 3 11 biological replicates (number of wells) and each analysis contains at least 2 independent 12 experiments. For flow analysis of cells, at least 10,000 events were acquired for the population of 13 interest. For analysis of data that contains more than 2 groups, the Kruskal-Wallis test was 14 performed to compare samples; if these comparisons had a p value less than 0.05 then Mann-15 Whitney U tests were used to compare statistical difference between 2 groups. P-values less than 16 0.05 by Kruskal-Wallis or Mann-Whitney were considered significant. Consultation on statistical 17 analysis was performed with the UCLA Biostatistics Department. All analyses were performed 18 with GraphPad, version 8.0 (GraphPad Holdings, San Diego, CA).

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