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Virus-induced senescence is driver and therapeutic target in COVID-19

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Derailed cytokine and immune cell networks account for organ damage and clinical severity of COVID-19^{1–4}. Here we show that SARS-CoV-2, like other viruses, evokes cellular senescence as a primary stress response in infected cells. Virus-induced senescence (VIS) is indistinguishable from other forms of cellular senescence and accompanied by a senescence-associated secretory phenotype (SASP), composed of pro-inflammatory cytokines, extracellular matrix-active factors and pro-coagulatory mediators^{5–7}. COVID-19 patients displayed markers of senescence in their airway mucosa in situ and elevated serum levels of SASP factors. Mirroring COVID-19 hallmark features such as macrophage and neutrophil infiltration, endothelial damage and widespread thrombosis in affected lung tissue^{1,8,9}, in vitro assays demonstrated macrophage activation with SASP-reminiscent secretion, complement lysis and SASP-amplifying secondary senescence of endothelial cells, neutrophil extracellular trap (NET) formation as well as activation of platelets and the clotting cascade in response to supernatant of VIS cells, including SARS-CoV-2-induced senescence. Senolytics such as Navitoclax and Dasatinib/Quercetin selectively eliminated VIS cells, mitigated COVID-19-reminiscent lung disease and reduced inflammation in SARS-CoV-2-driven hamster and mouse models. Our findings mark VIS as pathogenic trigger of COVID-19-related cytokine escalation and organ damage, and suggest senolytic targeting of virus-infected cells as a novel treatment option against SARS-CoV-2 and perhaps other viral infections.

The pandemic human pathogenic SARS-CoV-2 coronavirus causes upper respiratory infections and subsequently COVID-19 lung disease that may get further complicated by septic multi-organ failure

and comes with significant mortality^{10,11}. Escalating immune activation with massive cytokine release seems to drive severe COVID-19^{1–3}, possibly more than the virus infection itself. Mechanisms of viral

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entry – primarily *via* interaction of CoV-2 spike protein S with the host cell receptor ACE2 (angiotensin-converting enzyme 2) – and consecutive steps of RNA replication, virus assembly and budding represent therapeutic targets^{12,13}. While anti-inflammatory drugs are clinically being used or currently tested with mixed results^{14,15}, more comprehensive and causal measurements to control the cytokine storm are needed.

Viral entry reflects a major cellular insult, and evokes profound biological changes in infected host cells – potentially leading to cellular senescence as a virus-triggered state switch^{16,17}, with controversial impact on virus propagation^{18,19}. Senescence is also acutely stress-induced by activated oncogenes (OIS) or DNA-damaging cancer therapy, and physiologically occurs in embryonic development, wound healing and ageing⁶. Little is known about systemic ramifications of cellular senescence as an anti-viral host defense. We hypothesize here that cellular senescence with its massive SASP, largely composed of pro-inflammatory cytokines, matrix-degrading proteases and pro-coagulatory factors^{5–7}, underlies the cytokine storm, macrophage activation, NET formation, endothelialitis and widespread pulmonary thrombosis frequently observed in COVID-19 patients^{1,8,9}.

Properties of virus-induced senescence

We first tested signs of senescence in human diploid fibroblast (HDF) models exposed to high-titer retrovirus. At day 5 post infection (p.i.), most of the cells presented with a senescence-typical flattened, enlarged morphology, stained positive in the senescence-associated β -galactosidase (SA- β -gal) assay²⁰, exhibited DAPI (4',6'-diamidin-2-phenylindol)-dense chromatin reminiscent of senescence-associated heterochromatin foci (SAHF)²¹, and overexpressed p16^{INK4a}, an inhibitor of cyclin-dependent kinases (CDK) 4 and 6, in the nucleus (Fig. 1a, Extended Data Fig. 1a). Gene set enrichment analyses (GSEA) of HDF RNA sequencing (RNA-seq) datasets found senescence- and SASP-related gene ontology (GO) terms skewed towards the VIS state, and to overlap with the OIS state of the very same cells in Ras-induced senescence (Fig. 1b). Further underlining the context-overarching role of a senescent stress response, GSEA retrieved host responses to viral infection in OIS (Extended Data Fig. 1b). Specific analyses of VIS-associated expression changes by quantitative RT-PCR (qRT-PCR) found senescence-typical transcriptional changes^{21,22} in VIS (Fig. 1c, Extended Data Fig. 1c). Notably, lower virus titers did not evoke a senescent cell-cycle arrest, as aimed for in retro- or lentivirus-assisted gene transfer experiments (Extended Data Fig. 1d). Multiplex protein analysis found VIS cells to secrete a plethora of SASP factors, many of them *bonafide* NF- κ B targets^{23,24} (Fig. 1d). Importantly, these responses depended on senescence-essential gene activities: HDF expressing the H3K9me3-active demethylase JMJD2C or engineered with a small hairpin stably knocking down p53 (*shp53*) to genetically disable OIS^{22,25}, as well as mouse embryo fibroblasts (MEF) without intact *p53* alleles failed to enter VIS, and lacked senescence-typical changes by qRT-PCR and multiplex secretome analyses (Fig. 1e, Extended Data Fig. 1e–g). Upon viral infection, only VIS-capable cells presented with cGAS/STING activation (Extended Data Fig. 1h), a SASP-underlying interferon response-driving cytoplasmic DNA sensor²⁶. Importantly, blocking retroviral replication *via* the reverse transcriptase inhibitor Azidothymidine prevented VIS, and blunted cGAS/STING activation (Extended Data Fig. 1i, j). cGAS/STING-mediated phospho-activation of the interferon regulatory factor IRF3²⁷, the NF- κ B transcription factor p65²⁸, and other nuclear senescence markers such as p21^{CIP1} and heterochromatin-associated H3K9me3 were strongly increased, or, regarding non-G1-phase-hyperphosphorylated retinoblastoma (Rb) protein, markedly decreased in VIS (Fig. 1f). Hence, viral infection evokes a host cell response reminiscent of and genetically dependent on key features of other well-established types of cellular senescence and their associated secretome.

Notably, VIS became detectable in response to a broad spectrum of viruses, including lentivirus, adeno-associated virus (AAV), vesicular stomatitis virus (VSV) and the low-pathogenic human alpha-coronavirus NL63 (HCoV-NL63) in human lung carcinoma and non-malignant epithelial cells (Fig. 1g, Extended Data Fig. 2a; see human primary bronchial HBEpC and nasal HNEpC epithelial cells, and multiplicity-of-infection [MOI]/SA- β -gal relationships in Extended Data Fig. 2b–d). To more closely mimic SARS-CoV-2 infection, we exposed ACE2-expressing HNEpC to SARS-CoV spike protein-pseudotyped VSV glycoprotein G-deletion mutants (VSV- Δ G*/CoV-S and VSV- Δ G*/CoV-2-S), which all induced senescence in these cells in a spike protein-dependent manner, since ACE2-negative NIH3T3 cells²⁹ failed to senesce (Fig. 1h, Extended Data Fig. 2e). Retrovirus- as well as VSV-induced senescence exhibited enhanced reactive oxygen species (ROS) and γ -H2AX DNA damage foci (Extended Data Fig. 2f). Conversely, the ROS scavenger N-acetylcysteine (NAC) reduced γ -H2AX foci and abrogated VIS. Similarly affecting γ -H2AX foci, GS-441524, the active metabolite of the viral RNA polymerase inhibitor Remdesivir, blunted cGAS/STING activation in VSV-infected cells (Extended Data Fig. 2g, h).

Importantly, HNEpC infected with the authentic SARS-CoV-2 virus also displayed SASP-positive senescence that was preventable by *shp53*-mediated inability to senesce or by GS-441524 treatment (Fig. 1i, j, Extended Data Fig. 2i, j). Moreover, RNA-seq analysis of SARS-CoV-2-infected alveolar epithelial cells (AEC) as well as publicly available RNA-seq datasets of normal human bronchus epithelial (NHBE) cells and lung cancer cell lines⁴ corroborated robust signs of senescence induction (Fig. 1k, Extended Data Fig. 2k). Thus, virus infection in general and SARS-CoV-2 infection of respiratory epithelial cells in particular evoke full-featured cellular senescence, underscoring our hypothesis that VIS might play a critical pathogenic role in COVID-19 lung disease.

Cellular senescence in COVID-19 patients

Next, we asked whether VIS would be a typical feature detectable in SARS-CoV-2-infected patients and specifically analyzed nasopharyngeal and lung tissue specimens from patients with a fatal course of PCR-proven COVID-19. Strikingly, immunohistochemical analyses (IHA) of the senescence markers lipofuscin, p16^{INK4a}, p21^{CIP1}, H3K9me3 and IL-8 as a SASP representative unveiled robust reactivity in samples from infected individuals with or without remaining SARS-CoV-2 RNA *in situ* but not in non-COVID-19 controls (Fig. 2a, Extended Data Fig. 3a). Single-cell (sc)RNA-seq analyses of upper airway mucosa samples provided further evidence of a senescence switch in COVID-19 patients³⁰, showing induced transcript levels of p16^{INK4a} (CDKN2A) and multiple SASP factors not only in SARS-CoV-2-permissive ciliated respiratory epithelial cells but also in macrophages, implying paracrine senescence spreading to SASP-attracted macrophages as well as to other less virus-susceptible p16^{INK4a}-elevated mucosal epithelial cell types in the nasopharyngeal specimens (Fig. 2b). By gene expression profiling (GEP) of upper and lower airway specimens, we found SASP-reminiscent cytokines in COVID-19 specimens induced at the transcript level (Fig. 2c). scRNA-seq data further underscored that predominantly ciliated epithelial cells and macrophages scored positive for p16^{INK4a}/CDKN2A transcripts (Extended Data Fig. 3b).

Key components of COVID-19 are cytokine storm and macrophage activation syndrome (MAS)³. We reasoned that the SASP of senescent upper airway epithelial cells may attract and activate macrophages through paracrine senescence induction³¹, thereby contributing to MAS escalation, a condition in which macrophages subsequently infiltrate the lungs. Notably, COVID-19 lungs showed infiltration by pro-inflammatory CD86⁺ macrophages and an M1-macrophage polarization profile^{32,33} (Fig. 2d, Extended Data Fig. 3c). In serum samples of COVID-19 patients, we found SASP peptides such as IL-8, PAI-1/Serpin E1, CCL2/MCP-1, MMP1, MMP9, and TIMP-1 among the most strongly

upregulated factors (Fig. 2e). Selective scanning for clotting-relevant factors by ultra-high-throughput mass spectrometry-based proteomics³⁴ also unveiled a massive induction of those factors in COVID-19 serum probes (Fig. 2f), in line with the transcriptional skewing of GO terms “coagulation” and “complement” in SARS-CoV-2-infected NHBE cells, retrovirally senescent and even OIS or irradiation-senescent HDF cells (Extended Data Fig. 1b, 2k)⁷. Further underscoring the pro-thrombogenic propensity in COVID-19 patients, we detected elevated CD62⁺-marked platelet activation in their blood samples (Extended Data Fig. 3d). Accordingly, clinically more severe cases of COVID-19 exhibited a tight association of higher SASP serum levels, clotting-relevant factors and activated coagulation³⁵ (Fig. 2g, Extended Data Fig. 3e, f), and a close correlation between senescence marker transcripts and microthrombosis in COVID-19 lungs *in situ* (Extended Data Fig. 3g, h). Thus, findings in COVID-19 patient material unveiled alterations consistent with VIS and its SASP in the upper airway epithelia, and suggest SASP-mediated effects as critical contributors to the respective lung disease and associated pro-inflammatory, tissue-damaging and pro-thrombogenic features.

Linking COVID-19 features to VIS

Next, we mechanistically interrogated whether supernatant (SN) from VIS cells (SN_{VIS}) might evoke COVID-19-typical functionalities in critical target cell types. Indeed, human THP-1 macrophages turned to a CD86⁺ or CD13⁺ M1-like state³² when incubated with SN_{VIS}, but not SN of non-infected proliferating cells (SN_{prol.}) or genetically senescence-incapable virus-infected HDF (Fig. 3a, Extended Data Fig. 4a). They themselves exhibited a strong SASP-reminiscent secretory profile, indicative of paracrine senescence, since only replication-incompetent viruses were used here (Fig. 3b, Extended Data Fig. 4b). Notably, SN_{VIS}-induced CD86⁺-associated THP-1 transcripts were similarly detected in COVID-19 lungs (Fig. 3c). Indeed, SN_{VIS} exposure enforced paracrine, SA- β -gal-positive senescence in macrophages (Fig. 3d), all in line with their contribution as a VIS-triggered SASP-amplifying cellular messenger to COVID-19 disease. Underscoring the critical role of an altered endothelium as a cytokine-releasing relay³⁶, SN_{VIS} also evoked paracrine senescence in HUVEC human endothelial cells, which, in turn, launched a pro-inflammatory and pro-thrombogenic SASP (Fig. 3e, Extended Data Fig. 4c). Consistent with microangiopathic thrombosis observed in severely affected COVID-19 lungs, transfer of SN_{VIS}, but not SN_{prol.} or SN of virus-infected senescence-incapable HDF, prompted platelet activation³⁷ (Fig. 3f), accelerated clotting time (Fig. 3g), and provoked NET formation *in vitro*⁹ (Fig. 3h). Moreover, mirroring the strongly elevated complement-activating factors in COVID-19 patient samples, we observed enhanced formation of the C5b-C9 membrane attack complex and its ultimate cytotoxic action on HUVEC cells in response to SN_{VIS}-activated human serum (Fig. 3i, j). In essence, the pathogenesis of COVID-19 lung disease appears to be closely linked to senescence-governed immune escalation and pro-thrombotic effects.

Eliminating VIS cells by senolytic drugs

Based on these findings we considered VIS cells a central therapeutic target in SARS-CoV-2 infection whose early elimination might mitigate the course of disease. Previously, we and others presented evidence that senolysis, *i.e.* the selective depletion of senescent cells by drugs such as Bafilomycin, the BCL-2 family inhibitor ABT-263 (a.k.a. Navitoclax) or the multiple kinases-inhibiting flavonoids Fisetin and Quercetin, the latter typically in combination with the tyrosine kinase inhibitor Dasatinib (D/Q), reduced undesirable local and system-wide effects that persistent senescent cells might otherwise exert^{38–42}. We first profiled transcript and protein expression of anti-apoptotic BCL-2 family members in VIS cells, and found BCL-xL (BCL2L1), BCL-w (BCL2L2),

and MCL-1 (BCL2L3) induced (Fig. 4a, Extended Data Fig. 5a; see also Fig. 2a, Extended Data Fig. 3a, b for elevated BCL2L1 and BCL2L2 expression in COVID-19 patients), thereby providing a rationale for Navitoclax to selectively kill VIS cells. We also found the PI3K/AKT/p70S6K axis, p38MAPK and the tyrosine kinase SRC to be deregulated in VIS, and, hence, to serve as potential targets especially for Fisetin and D/Q according to predicted protein-chemical interactions^{43–45} (Fig. 4a, Extended Data Fig. 5b). Indeed, Navitoclax, unlike the BCL-2-specific Venetoclax (a.k.a. ABT-199), as well as Fisetin and D/Q exerted cytotoxic potential selectively against retrovirus- or VSV-driven VIS cells but not equally infected senescence-incapable HDF *in vitro* (Fig. 4b, Extended Data Fig. 5c–e). Considering release of infectious virions as a potential concern, we found no enhanced infectivity upon lysis of VIS cells (Extended Data Fig. 5f, g).

Importantly, infection by the authentic SARS-CoV-2 virus rendered HNEpC susceptible to Navitoclax, Fisetin or D/Q (Fig. 4c). Moreover, as seen before with other viruses, SN transfer from SARS-CoV-2-infected cells expanded CD86⁺ THP-1 macrophages, and led to paracrine senescence or complement-mediated lysis of HUVEC cells, if not carried out in *shp53*- or GS-441524-pretreated epithelial cells or under exposure to any of the three senolytic treatment options (Fig. 4d–f, Extended Data Fig. 5h, and i–l regarding VIS, SASP and senolytic susceptibility in the context of the spike protein-affecting SARS-CoV-2 mutations alpha and beta).

Senolytic targeting of COVID-19 *in vivo*

To determine the impact of senolytic treatment on clinical severity of COVID-19-like lung disease, we first tested early intervention with Navitoclax in the well-established SARS-CoV-2-driven Syrian golden hamster model^{46,47}. After intranasal infection with SARS-CoV-2 virus, animals developed COVID-19-like pneumonia within the first three to five days. scRNA-seq profiling of SARS-CoV-2-infected *vs.* mock-infected hamster lungs unveiled upregulated p16^{INK4a}/CDKN2A, core senescence and SASP factor as well as SRC transcript expression in alveolar epithelial cells, macrophages and neutrophils due to primary virus infection or paracrine senescence induction during days 3 to 5 p.i. (Extended Data Fig. 6a). This analysis also demonstrated induction of *BCL-w* transcripts in these cell types at day 5 p.i. (Extended Data Fig. 6b), in support of Navitoclax as a suitable senolytic. Animals on the Navitoclax protocol exhibited moderate adverse effects (Extended Data Fig. 6c, d), presented with profoundly reduced senescent cells and improvement of some histopathological features when compared to a solvent-only-treated but equally SARS-CoV-2-infected cohort on day 7 p.i. (Fig. 5a, Extended Data Fig. 6e–g, Extended Data Table 1). Strikingly, we detected much lower concentrations of key pro-inflammatory SASP factors in the serum of Navitoclax-exposed hamsters on day 7 p.i., virtually indistinguishable from uninfected controls (Extended Data Fig. 6h).

To evaluate the potential of senolytic intervention in model systems with a more severe COVID-19-like clinical course, we next considered the Roborovski dwarf hamster model⁴⁸. On day 4 p.i. and treatment with either Navitoclax, D/Q or solvent-only, animals with senolytic intervention presented with a substantial reduction of H3K9me3- or lipofuscin-marked senescent cells in their respiratory epithelium, and a profound reduction in lung disease features, especially in the D/Q arm (Fig. 5b–d). Both senolytic regimens also produced in this model a dramatic reduction in SASP-reminiscent serum cytokines on day 4 p.i., close to healthy controls (Fig. 5e). Effects in the D/Q-treated group were particularly meaningful; 5/5 animals survived, displayed no apparent signs of disease and no or only moderate weight loss (Extended Data Fig. 7a). By contrast, 4/5 animals in the Navitoclax- and 3/5 animals in the placebo-treated group had to be terminated due to weight loss and clinical impairment by day 4 p.i. Lastly, we investigated the *K18-hACE2*-transgenic mouse model, which also supports a more severe and typically lethal SARS-CoV-2 infection^{49,50}. Mice were treated comparably to the dwarf hamster model

with oral administrations of Navitoclax, D/Q and here also Fisetin, and scheduled for lung analysis on day 6 p.i.. While 2/5 solvent-only-treated and 1/5 Navitoclax-treated mice died on or before day 6, and another Navitoclax-treated mouse just slipped underneath the acceptable weight limit on day 6, all D/Q- and Fisetin-treated mice were alive, had limited weight loss and presented clinically well on day 6 (Extended Data Fig. 7a, b). Although overall histopathological analyses could not unveil overt differences regarding COVID-19-like parameters (Extended Data Fig. 7c, and d regarding virus loads in this and the hamster models), markers of senescent cells were found to significantly lesser extents in the lungs of senolytics-treated mice across all regimens applied (Extended Data Fig. 7e). Moreover, Quercetin was recently tested as an oral formulation with sunflower lecithin against standard care (SC) in two randomized clinical trials (NCT04578158 and NCT04861298) for patients with confirmed SARS-CoV-2 infection and mild COVID-19-associated symptoms. Both trials, based on 152 and 42 patients, respectively, demonstrated clinical improvement by the senolytic intervention^{51,52}. Agglomerative hierarchical clustering of the second trial across numerous parameters separated the baseline-indistinguishable patient population by Quercetin *vs.* SC at day 7 (Fig. 5f, Extended Data Table 2). Moreover, collective analysis of all 194 patients concluded significant risk reductions regarding the needs of hospitalization and oxygen therapy for the Quercetin group, which was also superior to SC in terms of length of hospitalization, referral to the intensive care unit and number of deaths (Extended Data Fig. 8a, b). Taken together, early senolytic intervention during SARS-CoV-2 infection significantly attenuates COVID-19-like lung disease and systemic inflammation.

Our investigation marks VIS as a central pathogenic principle and valid therapeutic target in SARS-CoV-2 infection to prevent severe COVID-19 lung disease. The primary virus/host cell encounter evokes a senescence response associated with massive pro-inflammatory cytokine secretion that complements virus spreading to the lower airway tract. Our data pinpoint macrophages as pivotal cellular messengers in this process. Attracted to and primed by upper airway VIS cells, macrophages undergo a secondary, SASP-amplifying senescent state switch. Subsequently deployed in the lungs, they further induce senescence, particularly in endothelial cells. System-wide and locally active pro-coagulatory and complement-activating SASP factors contribute to hallmark histopathological features and clinical severity of COVID-19. Hence, early senolytic intervention is an appealing strategy to interrupt such escalating immune cascade at its beginnings. The D/Q-, Fisetin-, and Navitoclax-mediated effects we observed here are encouraging, but optimized dose-scheduling to maximize their clinical potential and limit potential toxicities is needed. Due to their excellent safety profiles, compounds such as the flavonoids Quercetin and Fisetin are particularly attractive candidates as VIS-targeting senolytics. As already demonstrated for Quercetin^{51,52}, Fisetin is currently being investigated in COVID-19 trials. Robbins and colleagues recently reported enhanced SASP production of pre-existing senescent cells in old mice by pathogen-associated molecular pattern factors such as lipopolysaccharide or the SARS-CoV-2 spike protein⁵³. In turn, pharmacological removal of senescent cells by Fisetin or D/Q in mouse β -coronavirus-infected animals was clinically effective – thereby adding to the rationale of senolytic VIS cell elimination as proposed here for SARS-CoV-2-evoked senescence. Moreover, it will be interesting to explore whether early senolytic intervention may also mitigate chronic post-COVID-19 impairment known as long COVID⁵⁴. Finally, we like to highlight that effective and worldwide available vaccinations hopefully make COVID-19 history soon, while our approach remains conceptually valid in the context of other viral epidemics/pandemics in the future.

Online content

Any methods, additional references, Nature Research reporting summaries, source data, extended data, supplementary information,

acknowledgements, peer review information; details of author contributions and competing interests; and statements of data and code availability are available at <https://doi.org/10.1038/s41586-021-03995-1>.

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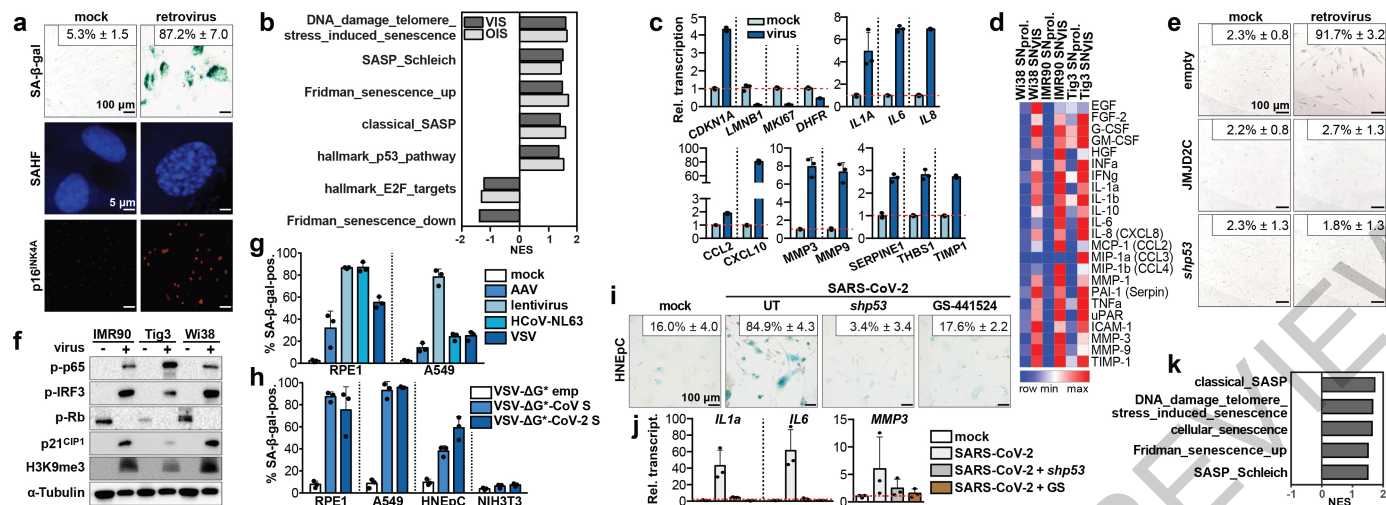


Fig. 1 | Senescence is a universal host cell response to viral stress. **a**, SA- β -gal, SAHF formation by DAPI, and p16^{INK4a} staining of IMR90 five days after retroviral infection or mock control. **b**, GSEA probing senescence-associated genes in WI38 HDF in VIS and OIS. Positive Normalized Enrichment Scores (NES) indicate enrichment compared to proliferating counterparts. Presented NES are statistically significant (FDR q -value < 0.05 , Supplementary Information for individual values). **c**, Relative expression of core senescence and SASP transcripts in cells as in **a** by qRT-PCR compared to mock control. **d**, Multiplex bead-based protein analysis in the SN of HDF IMR90 (as in **a**), WI38 and Tig3. **e**, SA- β -gal staining of IMR90 cells expressing JMJD2C, *shp53*, or control vector. **f**, Immunoblot analysis of nuclear senescence markers in samples as in **d**. α -Tubulin as a loading control. **g**, Quantification of SA- β -gal positivity in human cell lines (RPE1, A549) infected with AAV, lentivirus, HCoV-NL63, and VSV. **h**, Quantification of SA- β -gal positivity in human cell lines

and primary HNEPC infected with VSV- ΔG^* -CoV-S, VSV- ΔG^* -CoV-2-S, or VSV- ΔG^* /empty vector (VSV- ΔG^* -emp). NIH3T3 as ACE2-negative, infection-resistant control. **i**, SA- β -gal staining of stably hACE2-engineered primary nasal epithelial cells (HNEPC-hACE2) infected with SARS-CoV-2 and treated as indicated at 48 hours p.i. **j**, Relative expression of the indicated transcripts by qRT-PCR of cells as in **i**. **k**, GSEA of RNA-seq-based GEP from AEC infected with SARS-CoV-2 *vs.* uninfected controls ($n = 4$). Preselected senescence-associated terms with FDR q -value ≤ 0.01 are shown (see Supplementary Information for individual values). All scale bars in this figure represent 100 μ m, except 5 μ m for SAHF in **a**. All quantifications in this figure refer to mean $\pm$ s.d. of $n = 3$ independent experiments (except **k**) with individual values as dots in bar plots or representative photomicrographs shown.

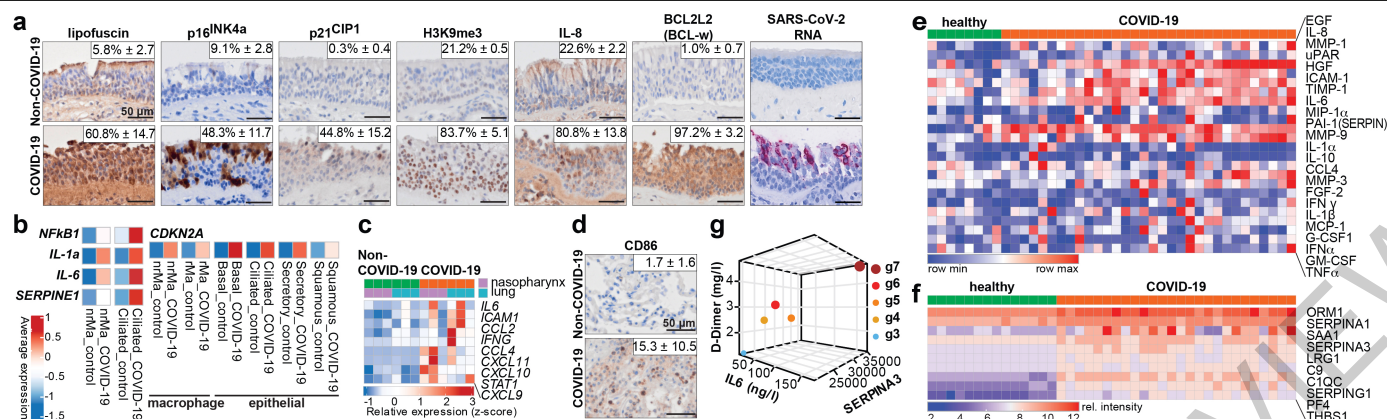


Fig. 2 | COVID-19 patients exhibit features of VIS. a, Immunohistochemical analysis (IHA) of senescence markers, BCL-w, and *in situ* hybridization of SARS-CoV-2 RNA in the respiratory mucosa of nasopharyngeal specimens from COVID-19 patients ($n = 6$ for p16^{INK4a} and IL-8, otherwise $n = 5$) *vs.* non-COVID-19 individuals ($n = 2$). Quantification of affected areas as mean percentages of positive cells $\pm$ s.d. or mean percentage of positive area $\pm$ s.d (lipofuscin only). **b**, scRNA-seq-based GEP of upper airway tissue from COVID-19 patients ($n = 19$) and normal controls ($n = 5$). Color-coded average-scaled (z-scores) expression levels of the respective transcripts and cell types. (n)rMa = (non-)residential macrophage. **c**, GEP of SASP-reminiscent cytokines in upper (nasopharynx) and lower airway (lung) tissue samples from COVID-19 *vs.* non-COVID-19 autopsies ($n = 3$ each) by oligonucleotide-based transcript hybridization.

d, CD86-IHA of macrophages in lung specimens from COVID-19 ($n = 13$) *vs.* non-COVID-19 patients ($n = 6$). Mean number of positive non-epithelial cells in $0.1 \text{ mm}^2 \pm$ s.d., $p = 0.0005$. **e**, Multiplex bead-based protein analysis of serum samples from COVID-19 patients ($n = 32$) and healthy donors ($n = 8$). **f**, Mass spectrometry-based proteome analysis of serum from COVID-19 patients ($n = 26$) and healthy donors (serum $n = 3$ and plasma $n = 11$). Heatmaps in **e** and **f** present scaled (z-scores) protein intensities. **g**, 3D-plot showing serum levels of D-Dimer (clotting activity), SERPINA3 (coagulation-related SASP factor), and IL6 (pro-inflammatory SASP factor) correlated to WHO-graded clinical COVID-19 severity. $n = 133$ patients; size of the sphere is proportional to the population size. All photomicrographs are representative and scale bars mark $50 \mu\text{m}$ in this figure.

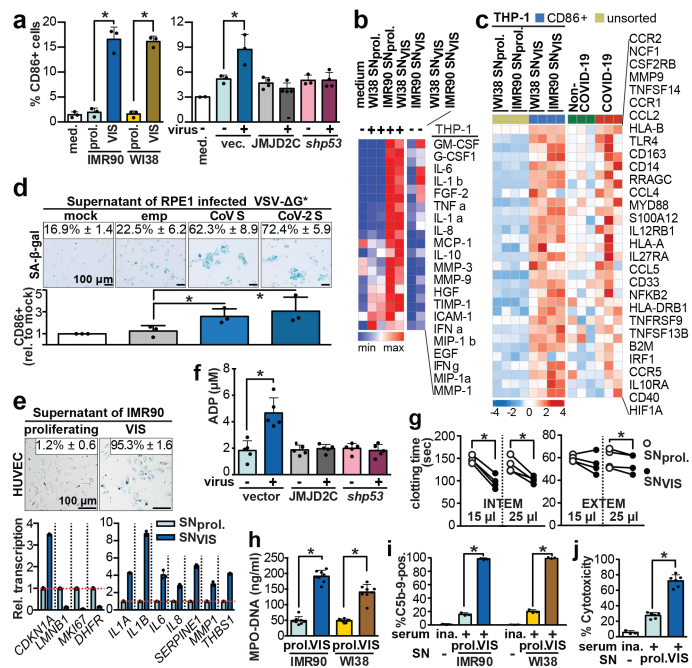


Fig. 3 | The VIS-associated secretome drives key immune-thrombotic components of COVID-19. **a**, Percentage of CD86⁺ cells in the THP-1 macrophage population exposed to SN from retroviral VIS *vs.* proliferating (left) or senescence-incapable (right) IMR90 cells. **b**, Multiplex bead-based protein analysis of the SN of THP-1 exposed to SN as in *a* (SN_{prol.} = SN of proliferating cells, SN_{vis} = SN of VIS cells, SN_{vis} without THP-1 cells shown on the right). **c**, GEP of M1-macrophage polarization-related transcripts by RNA-seq of THP-1 cells exposed to SN_{prol.} or SN_{vis} and sorted for CD86-positivity (*n* = 2 each, left) and by oligonucleotide-based transcript hybridization of lung tissue from COVID-19 *vs.* non-COVID-19 autopsies (*n* = 3 each, right). **d**, SA-β-gal and the CD86⁺ fraction of THP-1 exposed to SN as indicated. **e**, SA-β-gal and transcript expression by qRT-PCR of HUVEC endothelial cells incubated with the SN as indicated. **f**, Platelet activation measured by ADP release from healthy donor platelets incubated with the SN of IMR90 as in *a*. *n* = 5 donors. **g**, Clotting time in whole blood samples (*n* = 4 healthy donors) mixed with indicated SN volumes (WI38, as in *b*). **h**, NET formation after exposing neutrophils to SN from HDF as in *b*. *n* = 4 healthy donors, two measurements each. **i**, Quantification of the cytolytic complement complex C5b-9 on HUVEC incubated with human serum and SN as indicated. **j**, Cytotoxicity assay of HUVEC as in *i*. All quantifications (mean ± s.d. with individual values as dots) and representative photomicrographs are from *n* = 3 independent experiments except otherwise noted. “*” indicates *p* < 0.05 by unpaired-t-test (two-tailed; *a, f, h, i, j*), unpaired-t-test (one-tailed; *d*), paired-t-test (two-tailed; *g*). All scale bars in this figure represent 100 μm.

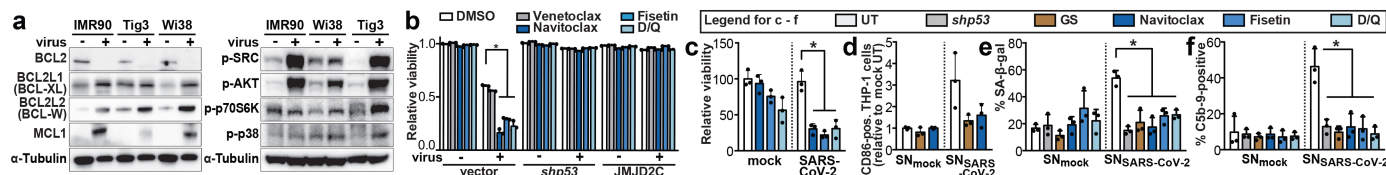


Fig. 4 | VIS cells are sensitive to senolytic targeting. **a**, Immunoblot of BCL2 family members (left) and kinases (right) in HDF lysates as indicated. α -Tubulin as a loading control. **b**, Relative viability of IMR90 cells as in Fig. 1e, 48 hours after treatment with senolytics as indicated or solvent-only (DMSO). **c**, Viability of HNEpC-hACE2 infected with SARS-CoV-2 or mock, and treated with senolytics as indicated for c-f. **d**, Relative change of the CD86⁺ fraction in the THP-1 cell population after receiving SN of HNEpC-hACE2 as in c. Of note, SN transfer experiments were carried out in the presence of SARS-CoV-2

neutralizing anti-spike antibodies, preventing transmission of infection (as evidenced by negative target cell SARS-CoV-2 PCR, data not shown). **e**, SA- β -gal staining of HUVEC endothelial cells after receiving SN of HNEpC-hACE2 as in **d**. **f**, Quantification of C5b-9 on HUVEC cells exposed to human serum with SN of HNEpC-hACE2 as in **d**. All bar plots in this figure show mean results $\pm$ s.d. of $n=3$ independent experiments with individual values as dots. All '**' in this figure indicate $p < 0.05$ by unpaired t-test (two-tailed).

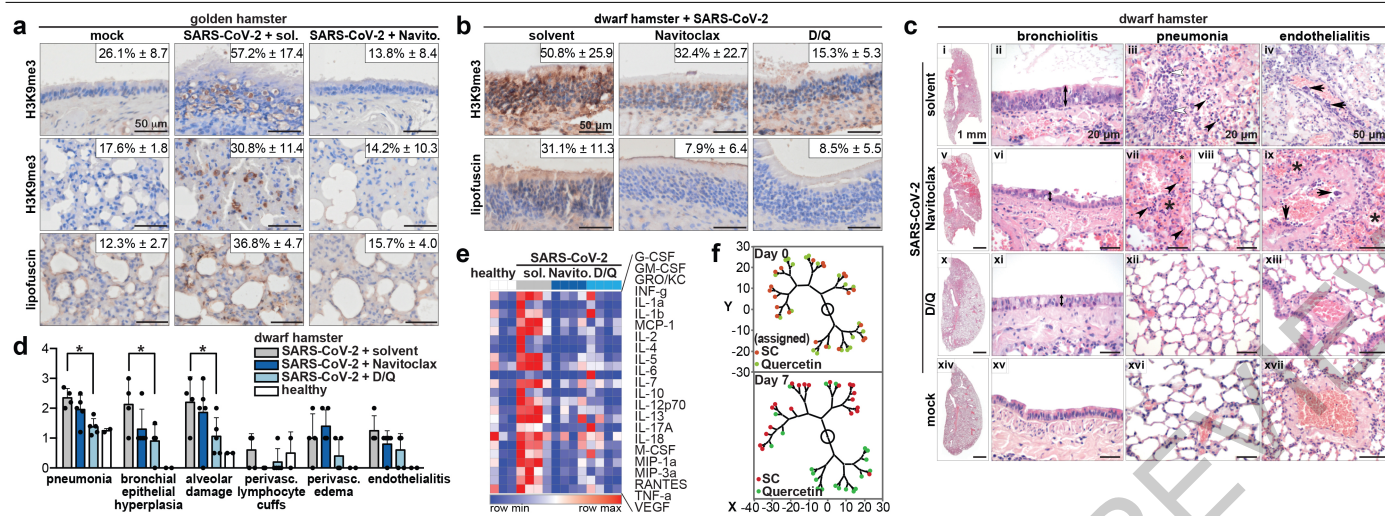


Fig. 5 | Senolytic targeting mitigates disease features of COVID-19 in animal models and patients.

a, H3K9me3 IHA in nasopharyngeal (top) and lung (middle) specimens, as well as lipofuscin-based detection (bottom) of senescent cells in the lung of golden hamsters infected with SARS-CoV-2 and treated with Navitoclax or solvent-only ($n = 5$ animals each), or mock-infected and untreated ($n = 3$ animals) at day 7 p.i.. **b**, H3K9me3 IHA and lipofuscin staining in nasopharyngeal sections of Roborovski dwarf hamsters infected with SARS-CoV-2 or mock, at day 4 p.i. after treatment as indicated. **c** Hematoxylin-eosin (H/E)-stained lung tissue of dwarf hamsters as in **b** on day 4 p.i.; uninfected healthy hamsters (mock) for comparison (xiv–xvii). Lung sections for overview (i, v, x) with signs of COVID-19-like pneumonia and hemorrhage: hyperplasia of bronchial epithelium (double-headed arrow), hemorrhage (asterisks) and necrosis (black arrows) of alveolar epithelial cells

with neutrophil infiltration (white arrows), and endothelialitis (lined black arrows). ** indicates $p < 0.05$ by unpaired-t-test (one-tailed). **d**, Quantification of the findings in **c**. **e**, Multiplex bead-based protein analysis of dwarf hamster serum samples on day 4 p.i. (as in **b–d**). $n = 5$ each (**b–d**; $n = 4$ each in **e**) for SARS-CoV-2-infected and treated animals, $n = 2$ for healthy (mock) control. **f**, Constellation plots of COVID-19 patients⁵² before (day 0) and after 7 days of standard care (SC) only, or Quercetin plus SC. Variables (Extended Data Table 2) were simultaneously analyzed by agglomerative hierarchical clustering to visualize similarity (distance) between patients and separation of the cohorts after treatment. $n = 21$ for each group. All quantifications are mean $\pm$ s.d. All photomicrographs in this figure are representative with scale bars indicating 50 μ m (except as indicated in **c**).

Methods

Cell culture and virus production

Cell lines were maintained according to the guideline of suppliers. Human diploid fibroblast (HDF) IMR90, WI38, Tig3 were described previously²². Human cell lines RPE1 (hTERT RPE1), A549 and HUVEC were purchased from ATCC. Primary human nasal or bronchial epithelial cells (HNEpC and HBEpC) were purchased from PromoCell. HNEpC cells with exogenous ACE2 expression (HNEpC-hACE2) were generated by lentiviral infection (hACE2 lentivirus, BPS Bioscience). THP-1 cells were kindly provided by Anna Walter (Charité). Senescence-incapable cell lines were generated by transduction with lentiviruses encoding JMJD2C or *shp53* as previously described^{22,55}.

All viruses used in this work are tagged with GFP, with the exception of HCoV-NL63 and SARS-CoV-2, and infection efficiency was monitored by detecting fluorescence in infected cells. Retrovirus was produced by transfecting Phoenix packaging cells with a murine stem cell virus (MSCV) GFP plasmid⁵⁶. Lentivirus was produced by transfecting 293T cells with psPAX2, pMD2.G (Addgene nr. 12260 and 12259) and pCDH-CMV-MCS-EF1-GFP plasmids²². AAV was obtained from the Charité Viral Core Facility. Caco-2 cell-adapted wild-type HCoV-NL63 virus at a titer of 3×10^6 pfu/ml was provided by the M.L. lab. VSV-GFP was a kind gift from W. Brune (Heinrich Pette Institute, Hamburg, Germany). VSV-ΔG* GFP (Kerafast) and plasmids encoding SARS-CoV spike (pKS SARS St19; kindly provided by S. Fukushi, National Institute of Infectious Disease, Tokyo, Japan), SARS-CoV-2 spike (Wuhan SARS-CoV-2 spike deltaCT28; kindly provided by C. Ratswohl and K. de la Rosa, MDC), SARS-CoV-2 spike variants Alpha and Beta (pCDH-CMV-spike-B117-EF1-puro and pCDH-CMV-spike-B1351-EF1-puro synthesized by GENEWIZ, China) proteins were used to generate mutant pseudotypes. SARS-CoV-2 (hCoV-19/Germany/BY-ChVir-984/2020, sequence reference EPI_ISL_406862) was propagated for *in vitro* applications in Vero E6 cells (ATCC CRL-1586) and genome-sequenced to exclude stocks with mutations from further experiments. Infection was monitored by PCR, detecting viral genomic RNA in the supernatant 48 or 72 h p.i., as previously described⁵⁷. Experiments were conducted under appropriate biosafety conditions with enhanced respiratory personal protection equipment in the BSL-3 facility at the Institute for Virology, Charité, Berlin. Self-made virus stocks were concentrated 10-times using virus concentrations kit (TaKaRa Bio and Abcam). High-titer virus infection to induce VIS reflect MOI of 50 for replication-incompetent retrovirus and lentivirus, 10 for replication-incompetent AAV and VSV-ΔG*, 10 as well for replication-competent HCoV-NL63, 1 for replication-competent VSV, and 0.1 for replication-competent SARS-CoV-2. VIS features were assessed on day 5 (retrovirus, lentivirus), day 3 (HCoV-NL63, VSV-ΔG*, SARS-CoV-2) or day 2 (VSV) p.i.

COVID-19 patients, non-COVID-19 patients and healthy donor material

Upper (nasopharyngeal) and lower airway (lung) tissue FFPE samples were derived from deceased SARS-CoV-2-infected COVID-19 patients as well as archive material from patients who passed away without significant clinical signs of a respiratory infection prior to October 2019 (*i.e.* non-COVID-19 patients), blood samples of SARS-CoV-2-infected and hospitalized patients in the course of their COVID-19 disease, or blood samples from healthy volunteers were used based on approval by the local ethics commission of the Johannes Kepler University (reference number 1070/2020). All COVID-19 patients were PCR-proven SARS-CoV-2-positive, however, SARS-CoV-2 RNA was detectable in 4/5 COVID-19 cases shown in Fig. 2a. All participants gave informed consent. In addition, we conducted re-analyses of additional patient and control materials that were obtained before and published elsewhere^{30,34,51,52}.

Flow cytometry, immunoblotting, immunofluorescence, and immunohistochemical analysis

Flow cytometry, immunoblotting (IB), immunofluorescence (IF), and immunohistochemical analysis (IHA) were performed as described previously^{24,58}. Surface antigen detection by flow cytometry was carried out with fluorescence-conjugated antibodies against human CD86-PE-Cy7 (BioLegend, #374209, 1:200), CD13-APC-Cy7 (BioLegend, #301709, 1:200), CD62P-PE (BioLegend, #304905, 1:200). Antigen detection by IB was carried out with antibodies against BCL2 (Cell Signaling Technology [CST], #15071, 1:1000), BCLXL (CST, #2764, 1:1000), BCLW (CST, #2724, 1:1000), MCL1 (CST, #39224, 1:1000), phospho-p65-Ser536 (CST, #3033, 1:1000), phospho-IRF3-Ser386 (CST, #37829, 1:1000), phospho-Rb-Ser807/811 (CST, #8516, 1:1000), p21^{CIP1} (Santa Cruz Biotechnology [SCBT], #sc-6246, 1:200), p16^{INK4a} (SCBT, #sc-1661, 1:200), H3K9me3 (Abcam, #ab8898, 1:2000), phospho-Akt (Thr308) (CST, #13038T, 1:2000), phospho-p38 MAPK (Thr180/Tyr182) (CST, #4511T, 1:1000), phospho-p70 S6 Kinase (Thr389) (CST, #9234T, 1:1000), phospho-Src (Tyr416) (CST, #6943T, 1:1000) and α-Tubulin (Sigma, #T5168, 1:2000). Anti-mouse or anti-rabbit horseradish peroxidase-conjugated antibodies were used as secondary antibodies (GE Healthcare, #RPN4301 and #NA931V, respectively). Antigen detection by IF was performed with antibodies against phospho-H2A.X (Cell Signaling, #9718, 1:400), p16^{INK4a} (Abcam, #ab211542, 1:250), Csb-9 (SCBT, #sc-58935, 1:250), anti-mouse-Cy3 secondary antibody (Thermo Fisher, #A10521, 1:1000), anti-rabbit-594 secondary antibody (Thermo Fisher, #A11012, 1:1000). Antigen detection by IHA was performed using the HiDef Detection HRP Polymer System (Cell Marque, #954D-30) with antibodies against p21^{CIP1} (SCBT, #sc-6246, 1:200), IL-8 (Abcam, #ab18672, 1:200), H3K9me3 (Abcam, #ab8898, 1:2000), BCL2L2 (Abcam, #ab190952, 1:1000), CD86 (Antibodies-online, ABIN736701, 1:100).

Original scans of the immunoblot information presented in Fig. 1f, 4a, with molecular weight markers and crop area indicated, are shown in Supplementary Information.

In situ hybridization (ISH)

ISH was performed as previously described⁴⁶ using the ViewRNA™ Tissue Assay Core Kit (Invitrogen, #19931) and the ViewRNA™ Tissue Assay Blue Module (Invitrogen, #19932) according to the manufacturer's instructions. For the detection of SARS-CoV-2, ViewRNA™ Type 1 Probe Set COVID19 polyprotein (Invitrogen, #CVX-06, Assay ID VPNKRHH) and ViewRNA™ Type 6 Probe Set Human ACTB (Invitrogen, #VX-06, Assay ID VA6-10506) were used. Following hybridization, sections were counterstained with hematoxylin and mounted with ProLong™ Glass Antifade Mountant (Invitrogen, #P36982). Images were taken using the Olympus Slide Scanner VS200.

Quantification of gene transcription

Quantitative reverse transcriptase PCR (qRT-PCR): RNA isolated from cell pellets using Trizol (Invitrogen) was transcribed to cDNA using SuperScript II reverse transcriptase (Invitrogen). Individual gene expression was analyzed by qRT-PCR using Taqman assays from Applied Biosystems. A list of Taqman assays used here is available in Supplementary Information.

RNA sequencing: Total RNA was isolated using the RNeasy Mini kit (Qiagen) and sequenced at the BGI Genomics. Single-cell RNA sequencing (scRNA-seq) was conducted as described⁵⁹. Further processing of the raw sequencing data is described in 'Statistics and data analysis'.

Oligonucleotide hybridization-based transcriptome profiling: RNA was extracted from FFPE tissue sections with the PureLink™ FFPE RNA Isolation Kit (Thermo Fisher Scientific, Cat. No.: K156002), hybridized with the probe set of the NanoString nCounter® Human Tumor Signaling 360 Panel (Cat. No.: XT-CSPS-H-T360-12), and analyzed on the NanoString nCounter® SPRINT.

Quantification of protein expression

Multiplex bead-based protein detection (MAGPIX): MAGPIX assays were conducted according to the manufacturer's manual with following bead panels: Custom Procartaplex 19-plex (Thermo Fisher Scientific, PPX-19, Assay ID MXAACDR), Custom Procartaplex 4-plex (Thermo Fisher Scientific, PPX-04, Assay ID MXCE4XN), Bio-Plex Pro™ Rat Cytokine 23-Plex Assay (Bio-Rad, 12005641). The assay was measured with the BioPlex® Magpix™ Multiplex Reader (Bio-Rad) and analyzed with a 5PL algorithm provided by the Bio-Plex Manager™ software (Version 6.1). Detailed procedures for sample preparation and measurement are described in Supplementary Information. Of note, due to a different normalization procedure, values cannot be cross-read between different panels, e.g. Fig. 1d vs. Fig. 3b.

Mass spectrometry-based proteome: Detailed protocol of sample preparation, mass spectrometry and data processing were previously described³⁴, for further details see also Supplementary Information. Briefly, serum samples were reduced, alkylated, digested and conditioned on a Biomek i7 workstation, and approximately 5 µg of peptides per injection were used for the gradient LC-MS/MS analysis. The raw data were processed using DIA-NN 1.7.12.

VIS assays *in vitro*

Growth curve analysis: HDF IMR90, WI38 or Tig3 cells were infected with MSCV retrovirus at day 0 and day 3, and SA-β-gal activity were measured at day 5. For growth curve analyses, 2×10^4 cells were seeded into 12-well plates and cell numbers were counted at day 3, 6 and 9.

2'3'-cGAMP ELISA assay: Cell cytoplasmic 2'3'-cGAMP concentration was measured using the Caymanchem ELISA kit. Briefly, cells were lysed in M-PER extraction reagent (Thermo Fisher) and 10 µg protein lysate was used to determine 2'3'-cGAMP content.

Analysis of cell viability and senescence: Viability and cell numbers were analyzed by trypan blue dye exclusion or Guava Viacount (Millipore). SA-β-gal activity at pH 6.0 (for human cells) or pH 5.5 (for rodent cells) as a senescence marker in fresh or cryo-preserved cells was assessed as described⁶⁰. *In situ* detection of lipofuscin as a senescence marker in FFPE samples was carried out with the SenTraGor™ reagent (Lab Supplies Scientific; kindly provided by Vassilis G. Gorgoulis, University of Athens) according to the manufacturer's instructions.

ROS detection: 20 µM Dihydroethidium (DHE, MedChemExpress) was directly added to cells and incubated at 37 °C for 20 minutes. DHE was then washed away with PBS. Cells were fixed in 4% paraformaldehyde and staining intensity was analyzed with Nikon fluorescent microscope.

VIS supernatant transfer and secondary, paracrine senescence

Conditioned medium was then collected from proliferating and VIS cells after 24 hours of incubation and centrifuged at 5,000 rpm for 5 minutes, and the SN (SN_{prol.} or SN_{VIS}, respectively) was transferred to HUVEC or THP-1 cells for further analysis. For the SN transfer from SARS-CoV-2-infected HNEpC, self-made neutralizing antibodies against SARS-CoV-2 (provided by the H.S. lab) were mixed in to block secondary infection.

NET formation assay

NET formation was measured by the concentration of NET-DNA bound to myeloperoxidase (MPO). Neutrophils were isolated from whole blood of four healthy donors. NET were quantified as previously described⁶¹. Briefly, 10 µg/ml myeloperoxidase (MPO) antibody (Abcam; #ab25989) was immobilized on the surface of black MaxiSorp-treated plates (Thermo Scientific). The plate was subsequently washed with PBS and blocked with 5% non-fat milk for 2 hours at RT. Neutrophils incubated for 4 hours at 37°C in RPMI medium from proliferating or VIS WI-38 or IMR-90 cells were pipetted onto the MPO-coated plate and incubated for 1h at RT. NET quantification was performed using the MPO-DNA PicoGreen assay according to the manufacturer's instructions (Quant-iT

PicoGreen dsDNA Assay Kit, Invitrogen). Sample fluorescence was measured using the GloMax Discover microplate reader (Promega).

Rotational thromboelastometry

To measure clotting time, a rotational thromboelastometry assay was performed on a ROTEM® delta (Werfen) device according to manufacturer's instructions. INTEM captures intrinsic, platelet-dependent and EXTEM extrinsic, non-platelet-dependent clotting. Whole blood samples of healthy donors were spiked with the SN of WI38 in proliferation or VIS. Exclusion criteria for the healthy donors were coagulation disorders and clotting-affecting medication. Gender distribution was equal among the donors.

Platelet activation and ADP release measurement by VIS supernatant

Platelet activation was measured by flow cytometry as percentage of CD62/P-selectin-positive cells in whole blood. To measure VIS-evoked ADP release, 2×10^6 platelets from healthy donors were resuspended in 200 µl conditioned medium and incubated at 37 °C for 1 hour. Supernatant was collected by centrifugation at $2,000 \times g$ for 5 minutes, and ADP concentration was measured using the ADP Colorimetric Assay Kit II (BioVision) according to the manufacturer's instruction.

Complement-mediated cytotoxicity in HUVEC endothelial cells

500 µl normal human serum of healthy donors was incubated with proliferating or VIS HDF (Fig. 3i, j) or HNEpC (Fig. 4f, Extended Data Fig. 5h) in 5 ml medium at 37 °C for 30 minutes. Heat-inactivated (56 °C for 30 minutes) serum was used as a control. Supernatant was collected and incubated with HUVEC endothelial cells at 37 °C. 2 hours after incubation, HUVEC cells were fixed in 4% paraformaldehyde, and C5b-9 immunofluorescent staining was carried out. Alternatively, 24 hours after incubation, a cytotoxicity assay was performed using the CyQUANT LDH Cytotoxicity commercial kit (Invitrogen).

Senolytic treatment *in vitro* and secondary viral infection

VIS cells were treated with Venetoclax (1 µM), Navitoclax (1 µM), Fisetin (20 µM), D/Q (20 µM, reflecting 2 µM Dasatinib + 20 µM Quercetin) or AT-101 (1 µM) for 48 hours and cell viability was determined by trypan blue staining using the Countess™ II FL Automated Cell Counter (Thermo Fisher). To generate the SN used for secondary viral infection, wild-type MEF were infected with VSV for 6 hours and treated with 1 µM Navitoclax for 24 hours. SN was centrifuged and filtered through a 0.22 µm PVDF filter and added to THP-1 cells. After 24 hours, secondary infectivity was measured by counting GFP-positive THP-1 cells.

SARS-CoV-2-driven COVID-19 animal models

In vitro and *in vivo* work related to hamsters was conducted under appropriate biosafety conditions in the BSL-3 facility at the Institute for Virology, Freie Universität Berlin, Germany. All hamster experimentation was approved by the relevant state authority (Landesamt für Gesundheit und Soziales Berlin, Germany [permit number 0086/20]), and performed in compliance with national and international guidelines for care and humane use of animals. Preparation of SARS-CoV-2 virus stock and intranasal infection of Syrian hamsters (*Mesocricetus auratus*) as a faithful *in vivo*-model for COVID-19 lung disease were previously described⁴⁶. Briefly, a SARS-CoV-2 wild-type isolate (BetaCoV/Munich/BavPat2-ChVir984-ChVir1017/2020) was grown in Vero E6 cells. To ensure genetic integrity, passage 3 stocks were genome-sequenced, results showed conformity with the published sequence (GenBank MT270112.1) and confirmed the presence of the furin cleavage site essential for *in vivo* pathogenesis. Anaesthetized male and female hamsters at 6-10 weeks of age were inoculated with 1×10^5 pfu SARS-CoV-2 in a total volume of 60 µl cell culture medium. Control animals were mock infected with the same volume of cell culture medium. One day after infection, animals were randomized and half of the animals ($n = 5$)

received a daily single 85 mg/kg body weight dose of Navitoclax in solvent (60% Phosal PG, 30% PEG 300, 20% ethanol) intraperitoneally for six consecutive days. The other half of infected animals ($n = 5$) received the same volume of solvent only. The control group ($n = 3$) did neither receive virus nor treatment. On day 7 p.i., one day after the last treatment, all hamsters were euthanized, and tissue and peripheral blood samples were prepared for further analyses.

The Roborovski dwarf hamster (*Phodopus roborovskii*), a species highly susceptible to a severe course of SARS-CoV-2 infection, was used under the permit mentioned above. Infections were performed as previously described⁴⁸. Female Roborovski dwarf hamsters at 5-7 weeks of age underwent the procedure described above for Syrian hamsters with the exception that the total volume of the inoculum was reduced to 20 μ l. The same virus stock was used. Animals were randomly distributed into three treatment groups ($n = 5$) and one non-infected, non-treated group ($n = 2$). From 6 h hours p.i. on, animals were treated once daily with oral application of Navitoclax at 85 mg/kg, D/Q at 5/50 mg/kg dissolved in 60% Phosal PG, 30% PEG 300, 20% ethanol and mixed 1:1 with strawberry syrup, the placebo-treatment group received the same solvent/syrup combination without drug. On Day 4 p.i., animals were sacrificed and tissue as well as peripheral blood specimens were collected for downstream analyses.

Infection of *K18-hACE2* mice (Jax strain 034860) with SARS-CoV-2 was performed according to the approval by the Institutional Animal Care and Use Committee (IACUC) of Icahn School of Medicine at Mount Sinai (ISMMS) as previously reported⁶². Briefly, 6-week old female mice were infected with 1×10^4 pfu SARS-CoV-2 (USA-WA1/2020, BEI resources NR-52281) grown in Vero E6 cells and validated by genome sequencing, and randomly distributed into three treatment groups ($n = 5$ each) and one solvent control group ($n = 5$). From one day after infection, randomly chosen animals were treated with oral application of Navitoclax at 85 mg/kg, D/Q at 5/50 mg/kg, and Fisetin at 100 mg/kg dissolved in 60% Phosal PG, 30% PEG 300, 20% ethanol every other day. On Day 6 p.i. (one day after the last treatment), animals were sacrificed and tissue specimens were collected for histopathological analyses.

Hamster and mouse lung tissues were processed for histopathology as described⁴⁷ and analyzed by board-certified veterinary pathologists following suggested standard criteria⁶³. Transmission electron microscopy was performed with trachea tissue from infected and treated Syrian golden hamsters. Fixation and further processing of the samples, as well as image acquisition procedures are described in Supplementary Information.

Statistics and data analysis

Based on previous experience^{22,24,41,47,50,53,54,57}, sample sizes typically reflect three to five, in some experiments also much higher numbers of individual primary material as biological replicates. All quantifications from staining reactions were carried out by an independent and blinded second examiner and reflect at least three samples with at least 100 events counted (typically in three different areas) each. For patients and animal models, IHA quantification was carried out in SARS-CoV-2-affected areas. Regarding Fig. 5, Extended Data Fig. 6 and 7, quantification of the indicated features was based on the following numbers of individual photomicrographs from animals as indicated in legend and text: Fig. 5a – nasopharynx H3K9me3 ($n = 3$ for mock, $n = 6$ for solvent and Navitoclax), lung H3K9me3 and lipofuscin ($n = 3$ for mock, $n = 5$ for solvent and Navitoclax); Fig. 5b – H3K9me3 ($n = 5$ for solvent and Navitoclax, $n = 6$ for D/Q), lipofuscin ($n = 5$ for all three groups); Extended Data Fig. 7e – p16^{INK4a} ($n = 5$ for solvent, Navitoclax and D/Q, $n = 4$ for Fisetin), H3K9me3 ($n = 4$ for solvent and Navitoclax, $n = 5$ for Fisetin and D/Q), lipofuscin ($n = 5$ for solvent and Navitoclax, $n = 4$ for Fisetin, $n = 7$ for D/Q).

Data analysis was performed with GraphPad Prism 9. For statistical comparisons, a *t*-test was applied. Unless otherwise stated, a *p*-value < 0.05 was considered statistically significant. For multiple testing

corrections the method by Benjamini & Hochberg (BH) to control for false discovery rate was applied⁶⁴. Bioinformatics Analysis was performed in R, version 4.0.3, and Bioconductor 3.12 using various R packages as described in the Supplementary Information in greater detail. High-performance computation has been performed on the Research/Clinic cluster of the Berlin Institute of Health. For further analyses of COVID-19 patient clinical data^{51,52} as presented in Fig. 5f and Extended Data Fig. 8a, b, JMP Pro 14 (SAS Institute) was used for agglomerative hierarchical clustering, GraphPad Prism9 was used for Fisher's exact test for *p*-values, and a Haldane-Anscombe correction was applied to calculate relative risks. Lipofuscin (SenTraGor®) staining was quantified with the pixel counting function of the ImageJ program (bundled with Java 1.8.0_172, NIH)⁶⁵.

Reporting summary

Further information on research design is available in the Nature Research Reporting Summary linked to this paper.

Data availability

The WI38 VIS- and OIS-derived raw RNA-seq data (Fig. 1b and Extended Data Fig. 1b) were deposited at the Gene Expression Omnibus (GEO) repository of the National Center for Biotechnology Information (NCBI) under accession number GSE165532. Gene expression data of human AEC cells infected with SARS-CoV-2 (Fig. 1k) are publicly available from at the NCBI GEO under the accession number GSE148729. Raw sequencing data of NHBE, Calu-3 and A549 cells infected with SARS-CoV-2 (Extended Data Fig. 2k) are publicly available at the NCBI GEO under the accession number GSE147507⁴. Seurat objects comprising scRNA-seq datasets of nasopharyngeal, protected specimen brush, and bronchial lavage samples of 19 COVID-19 patients and five healthy controls³⁰, comprising a total of 36 samples that were analyzed in this study (Fig. 2b), are available at FigShare (<https://doi.org/10.6084/m9.figshare.12436517>; covid_nbt_main.rds, covid_nct_loc.rds). The mass spectrometry-based proteome data of serum from COVID-19 patients and healthy donors in Fig. 2f are described³⁴. Patient proteomics data (Fig. 2g, Extended Data Fig. 3e) are publicly available at <https://www.who.int/teams/blueprint/covid-19>, in which disease severity was defined: g3 = hospitalized, no oxygen therapy; g4 = oxygen by mask or nasal prongs; g5 = non-invasive ventilation or high-flow oxygen; g6 = intubation and mechanical ventilation; g7 = ventilation and additional organ support. scRNA-seq data of hamsters infected with SARS-CoV-2 (Extended Data Fig. 6a, b) are available (GSE162208)⁵⁹. All information related to the two randomized trials on early Quercetin intervention in COVID-19 patients (NCT04578158 and NCT04861298) can be found in the respective publications^{51,52} and in Extended Data Table 2.

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Competing interests M.U. contributed to this article as an employee of Mount Sinai and the views expressed do not necessarily represent the views of Regeneron Pharmaceuticals Inc. F.D.P. is a member of the Scientific Board of Pharmextracta S.p.A., the vendor of Quevir®, a dietary supplement containing Quercetin in a sunflower lecithin formulation. The A.G.-S. laboratory has received research support from Pfizer, Senhwa Biosciences, Kenall Manufacturing, Avimex, Johnson & Johnson, Dynavax, 7Hills Pharma, Pharmamar, ImmunityBio, Accurius, Nanocomposix and Merck. A.G.-S. has consulting agreements for the following companies involving cash and/or stock: Vivaldi Biosciences, Contrafact, 7Hills Pharma, Avimex, Vaxalto, Pagoda, Accurius, Esperovax, Farmak and Pfizer. A.G.-S. is inventor on patents and patent applications on the use of antivirals and vaccines for the treatment and prevention of virus infections, owned by the Icahn School of Medicine at Mount Sinai, New York.

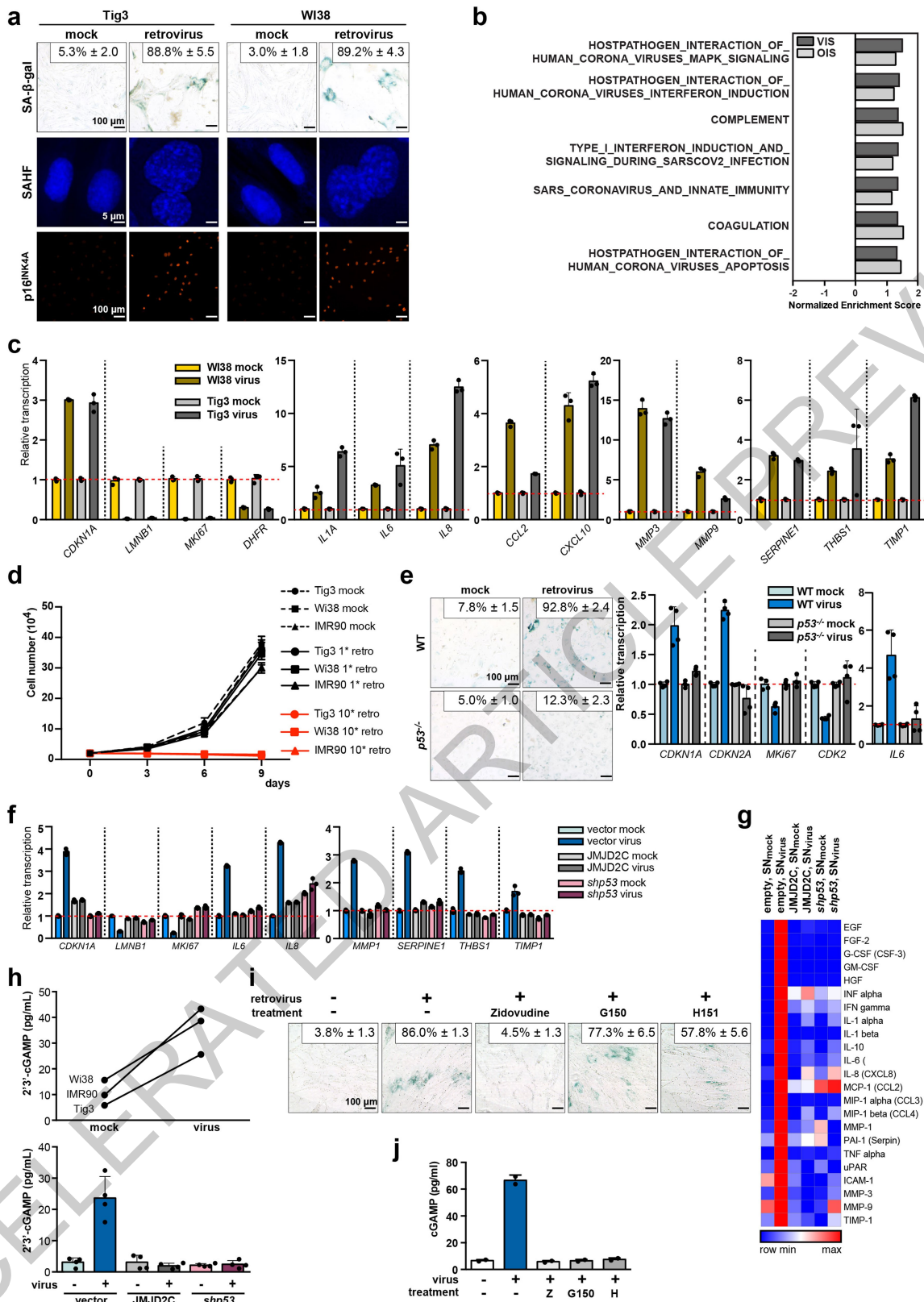
Additional information

Supplementary information The online version contains supplementary material available at <https://doi.org/10.1038/s41586-021-03995-1>.

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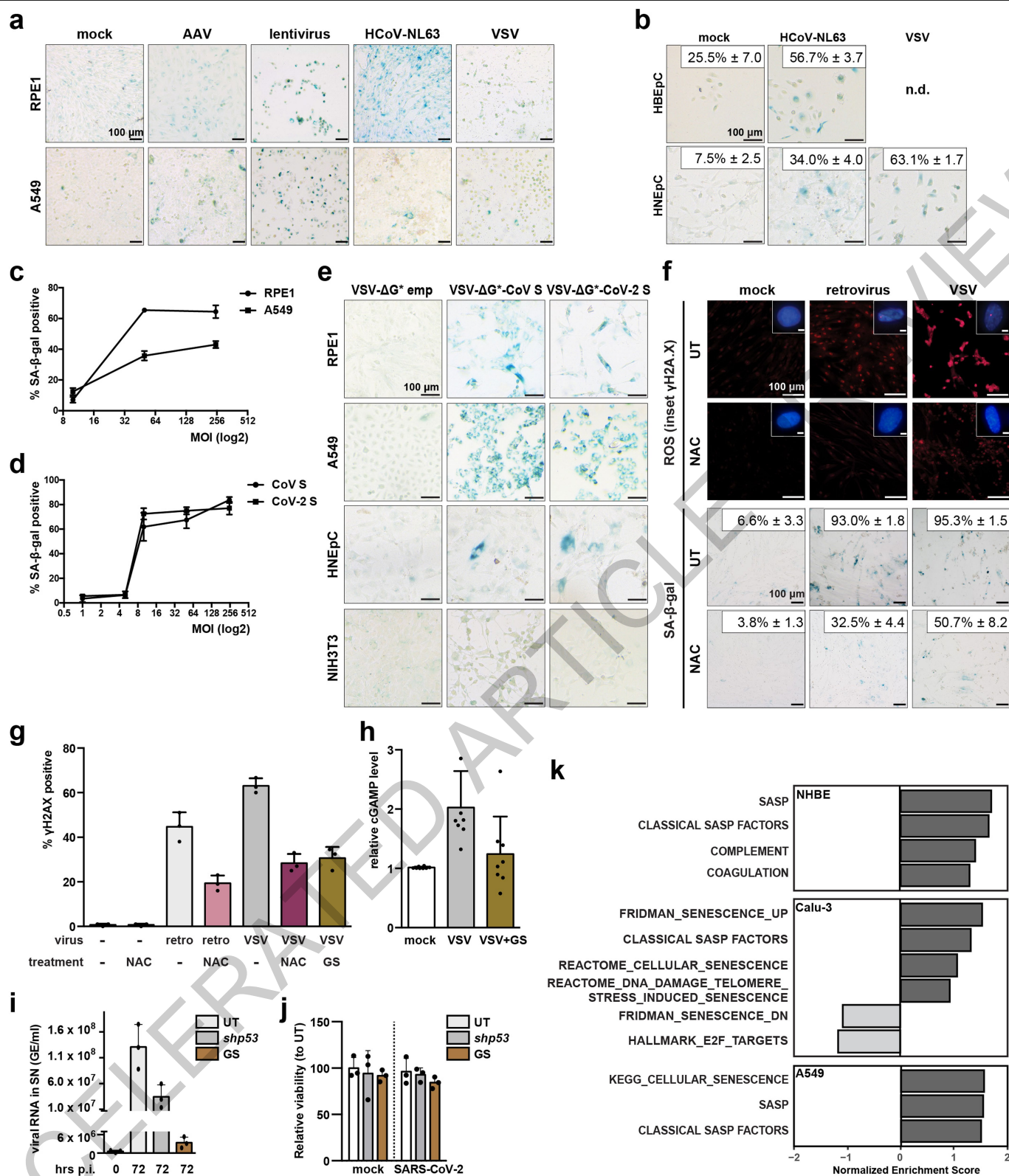


Extended Data Fig. 1 | See next page for caption.

Extended Data Fig. 1 | Additional biological properties of retroviral VIS.

a, SA- β -gal staining, SAHF formation by DAPI, and p16^{INK4a} staining of HDFs (Tig3 and WI38) five days after retroviral infection or mock control. Representative photomicrographs of $n = 3$ independent experiments. **b**, Gene set enrichment analysis (GSEA) of virus infection-relevant GO terms probing RNA-seq datasets of WI38 HDF in VIS and OIS. Positive normalized enrichment scores (NES) indicate enrichment in VIS (dark grey bars) or OIS (light grey bars) compared to proliferating counterparts (mock infection for VIS, or empty vector control for OIS). NES with FDR q -value ≤ 0.1 are considered statistically significant and presented (for individual q -values, see Supplementary Information); $n = 3$ biological replicates each. **c**, Gene expression analysis for core senescence and SASP genes by quantitative RT-PCR in WI38 and Tig3 as in **a**. Mean relative transcript level compared to mock control $\pm$ s.d. of $n = 3$ independent experiments are shown. **d**, Growth curve analyses of HDF infected with retrovirus at different MOI as indicated, showing that high-titer virus induced VIS, reflected by stable cell numbers over time, while lower virus titer remained compatible with exponential cell growth. $n = 3$ independent experiments are presented as mean cell numbers $\pm$ s.d.. **e**, SA- β -gal staining (left) and gene expression analysis of the indicated transcripts by qRT-PCR (right) in wild-type (WT) or senescence-defective $p53^{-/-}$ MEF, five days after

infection with high-titer retrovirus or mock as a control. Representative photomicrographs with fractions of SA- β -gal-positive cells, and mean relative transcript levels normalized to mock control $\pm$ s.d. of $n = 4$ independent experiments are shown. **f**, Gene expression analysis of the indicated transcripts by qRT-PCR in IMR90 cells expressing JMJD2C, *shp53*, or control vector as in Fig. 1e. **g**, Multiplex bead-based protein analysis of SN of senescence-incapable IMR90 as in Fig. 1e. SN_{mock} = SN of mock-infected cells; SN_{virus} = SN of retrovirus-infected cells. Mean expression levels of $n = 3$ biological replicates are shown. **h**, cGAS/STING activation upon viral infection, as evidenced by a higher induction of cyclic guanosine monophosphate-adenosine monophosphate (2'3'-cGAMP) by ELISA analysis in matched pairs of HDF after either mock or retrovirus infection (mean of $n = 4$ independent experiments for each cell line, upper panel). Mean cGAMP levels $\pm$ s.d. for senescence-incapable IMR90 as in Fig. 1e ($n = 4$ independent experiments, lower panel). **i**, SA- β -gal staining of IMR90 cells, treated with reverse transcriptase inhibitor azidothymidine Zidovudine (50 μ M), cGAS inhibitor G150 (5 μ M), STING inhibitor H-151 (1 μ M), or DMSO. Mock infection and DMSO solvent treatment as negative controls. Representative photomicrographs and quantification of positively stained cells as mean $\pm$ s.d. of $n = 3$ independent experiments are shown. **j**, 2'3'-cGAMP ELISA analysis of VIS IMR90 cells as in **i**.



Article

Extended Data Fig. 2 | Additional biological properties of VIS exerted by a variety of viruses. **a**, SA- β -gal staining in human cell lines (RPE1, A549) infected with AAV, lentivirus, HCoV-NL63, and VSV as in Fig. 1g. **b**, SA- β -gal staining of human primary bronchial or nasal epithelial cells (HBEpC and HNEpC, respectively) infected with HCoV-NL63 and VSV. Mock infected cells as negative control. Quantification of positive cells for $n = 3$ independent experiments is shown as mean $\pm$ s.d.; scale bar = 100 μ m. **c**, Quantification result of SA- β -gal-positive cells (RPE1, A549) after lentiviral infection at MOI as indicated are shown as mean percentage $\pm$ s.d. for $n = 3$ independent experiments. Note that MOI 50 was chosen for VIS induction. **d**, Quantification result of SA- β -gal-positive RPE1 cells after infection with VSV- Δ G*-CoV-S or VSV- Δ G*-CoV-2-S at MOI as indicated are shown as mean percentage $\pm$ s.d. for $n = 3$ independent experiments. Note that MOI 10 was chosen for VIS induction. **e**, SA- β -gal staining in human cell lines (RPE1, A549) and primary HNEpC infected with VSV- Δ G*-CoV-S, VSV- Δ G*-CoV-2-S, or VSV- Δ G*/empty vector (VSV- Δ G*-emp) as in Fig. 1g. NIH3T3 as ACE2-negative, infection-resistant control. **f**, Fluorescence detection of ROS in IMR90 after infection with retrovirus or VSV and treatment with NAC as indicated (upper panels). SA- β -gal staining and quantification of corresponding samples (lower panels). Mock infection or solvent treatment controls (UT) are shown. Representative photomicrographs and quantification are shown as mean percentages $\pm$ s.d. for $n = 3$ independent experiments. Scale bar for ROS and SA- β -gal = 100 μ m; for γ H2A.X (insets; pink

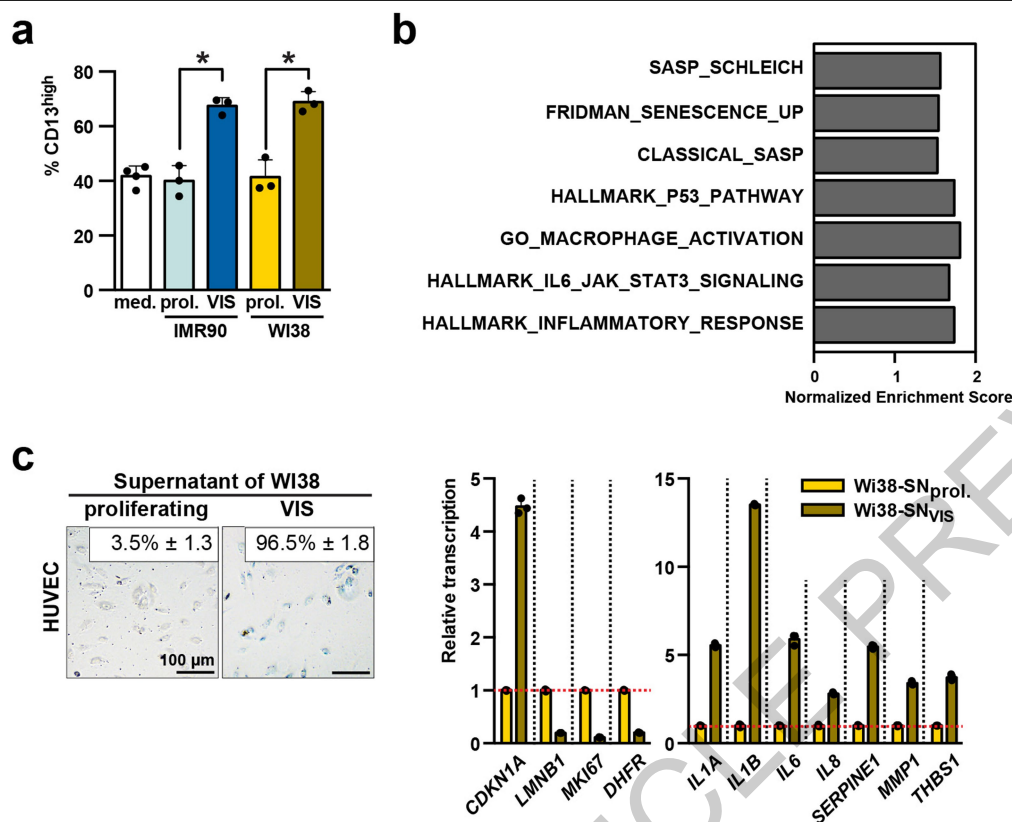
dots reflect foci) 5 μ m. **g**, Quantification of γ H2A.X-positive IMR90 cells as in **f**. $n = 3$ independent experiments is shown as mean $\pm$ s.d. **h**, 2'3'-cGAMP ELISA analysis of IMR90 infected and treated with GS-441524 as in **g**. $n = 8$ independent experiments is shown as mean $\pm$ s.d. **i**, Viral RNA detection in the supernatant of primary nasal epithelial cells with exogenous hACE2 expression (HNEpC-hACE2) infected with SARS-CoV-2, at the indicated time-points. *shp53* renders cells senescence-incapable, but, unlike treatment with 10 μ M GS-441524 (GS), does not block viral replication. Data are shown as mean values $\pm$ s.d. for $n = 3$ independent experiments. **j**, Relative viability of the indicated conditions, each compared to the corresponding untreated (UT) control of SARS-CoV-2-infected or mock-infected cells as in **i**, 72 hours p.i. Data are shown as mean values $\pm$ s.d. for $n = 3$ independent experiments. **k**, GSEA probing selected senescence-related gene sets⁶⁶ by RNA-seq (GSE147507) analysis of NHBE, Calu-3, and A549 cells infected with SARS-CoV-2, compared to corresponding mock-infected controls. Positive NES indicate enrichment in virus-infected cells (dark grey bars), negative NES indicate downregulation in virus-infected cells (light grey bars). NES of FDR q -value < 0.05 are considered statistically significant and presented (for individual q -values, see Supplementary Information). Biological replicates comprise $n = 7$ control and $n = 3$ infected regarding NHBE, $n = 3$ for each condition regarding Calu-3, and $n = 5$ control and $n = 3$ infected regarding A549.



Extended Data Fig. 3 | Vignettes of VIS in human COVID-19 lung specimens.

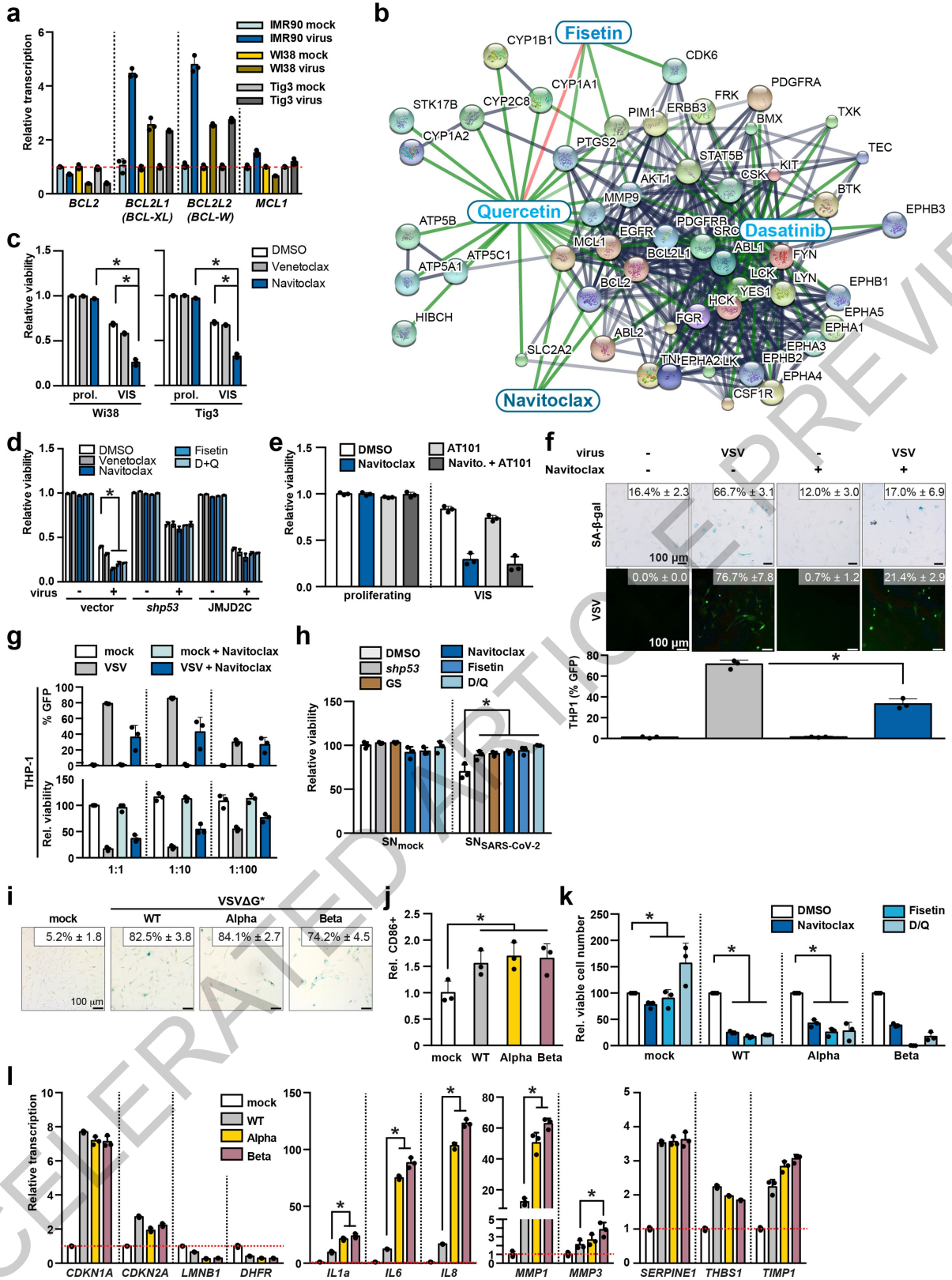
a, IHA of senescence markers in autopsy lung specimens from non-COVID-19 individuals (with no obvious airway pathology) *vs.* SARS-CoV-2-PCR-proven COVID-19 patients. Representative photomicrographs and quantification of affected area as mean percentages of positive cells $\pm$ s.d. or mean percentage of positive area $\pm$ s.d. (only for lipofuscin) of COVID-19 patients (lipofuscin, p21^{CIP1}, H3K9me3, BCL2L2, $n=5$; IL-8, $n=9$; SARS-CoV-2 RNA, $n=4$) and Non-COVID-19 individuals ($n=2$). Note that *in situ* hybridization of SARS-CoV-2 RNA was occasionally, but not consistently positive in COVID-19 samples at autopsy (2/4). Scale bars represent 50 μ m. **b**, scRNA-sequencing-based expression analysis of *CDKN2A* and targets of Navitoclax (*BCL2L1* and *BCL2L2*) in bronchiolar protected specimen brushes (PS), and bronchoalveolar lavages (BL) of COVID-19 patients with critical course of the disease ($n=4$). UMAPs of cell types (top). Orange color code marks cells expressing *CDKN2A*, purple *BCL2L1* (lower left) or *BCL2L2* (lower right), and red for both. **c**, Gene expression profile (GEP) indicating elevated transcript expression of cytokines and markers related to M1 macrophage polarization and activation^{32,33} by oligonucleotide-based transcript hybridization of lung specimens as in **a** ($n=3$ each). **d**, CD62/P-selectin-marked platelet activation by flow cytometry in whole blood samples of healthy donors ($n=7$) or COVID-19 patients ($n=10$).

Mean $\pm$ s.d. with individual values as dots. * $p=0.0368$ by unpaired t-test (two-tailed). **e**, Volcano plot of proteins differentially ($p<0.05$) expressed in COVID-19 patient serum; SASP factor SERPINA3⁶⁷ highlighted in red as presented in Fig. 2g. Combined clinical COVID-19 severity WHO grade 3 and grade 4 ($n=86$ patients) *vs.* grade 7 ($n=52$ patients) are compared. Log2-fold changes are plotted against log10 adjusted (Benjamini-Hochberg) p -values. Vertical red lines indicate log-fold change cutoffs -0.5/0.5, horizontal red line indicates a significance cutoff $p=0.05$. Analysis was performed using the DEqMS software package. **f**, Scatter plot showing average level of 16 SASP factors measured as in Fig. 2e and fibrinogen concentration in the serum (y-axis) of the same individual patients. $n=3$ severe, $n=5$ moderate, and $n=18$ mild COVID-19 patients and healthy control ($n=6$) are shown as color-coded dots. Correlation coefficient (Pearson) $r=0.4139$ with $p=0.0103$. **g**, Expression levels of senescence-related transcripts (gene sets: Reactome_SASP and SASP_Schleich⁶⁸) by oligonucleotide-based transcript hybridization of nasopharyngeal and lung specimens of COVID-19 patients ($n=3$) separated by their histopathological microthrombosis status. Shown are genes with fold-change >1.5 . **h**, Percentages of IL-8-positive cells in COVID-19 lung specimens as in **a**, now stratified by their microthrombosis status (positive, $n=4$; negative $n=5$), are shown as mean values $\pm$ s.d.. $p=0.0397$ by unpaired t-test (two-tailed).



Extended Data Fig. 4 | Additional COVID-19-relevant biological features evoked by the VIS-associated secretome. **a**, Percentage of CD13⁺ THP-1 macrophages exposed to SN from retroviral VIS *vs.* proliferating HDF as indicated and shown in Fig. 3a. $n = 3$ ($n = 4$ for medium control) independent experiments; shown are mean percentages $\pm$ s.d.. “*” indicates $p = 0.0017$ for IMR90 and 0.0029 for WI38 by unpaired t-test (two-tailed). **b**, GSEA of SN_{VIS}-primed macrophages unveiled vignettes of senescence and inflammation in the CD86⁺ population by probing of selected senescence- or macrophage activation-related GO terms and gene sets^{66,68} in RNA-seq analyses

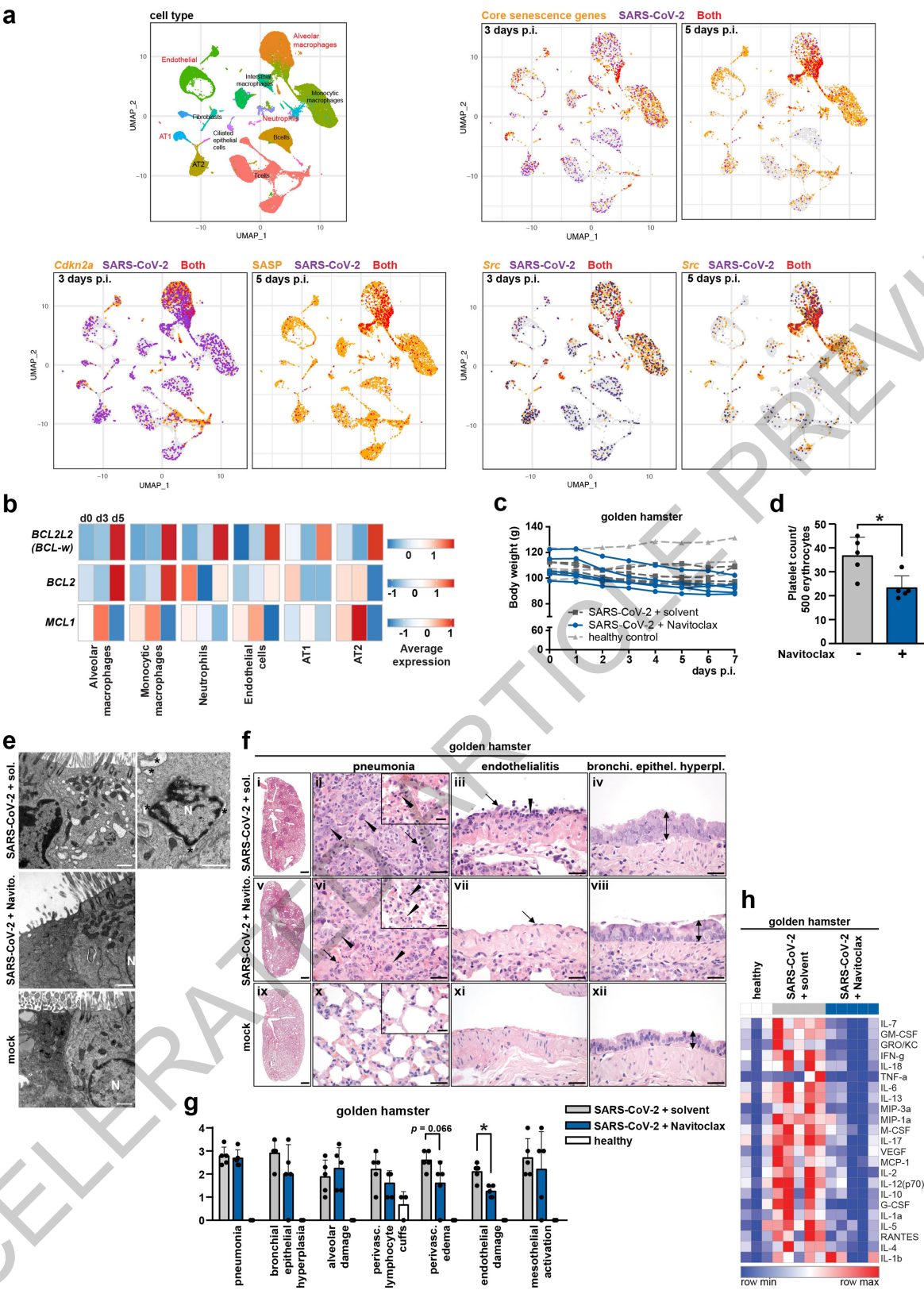
of THP-1 macrophages incubated with IMR90 SN_{VIS} and sorted by CD86 expression status (as in Fig. 3c, left). $n = 2$ for each condition. Gene sets with FDR q -value ≤ 0.05 are shown. **c**, SA- β -gal staining (left) and gene expression analysis by qRT-PCR (right) of HUVEC endothelial cells that entered secondary, paracrine senescence upon exposure to SN_{VIS} of WI38 as indicated. Representative photomicrographs and quantification of $n = 3$ independent experiments; shown are mean percentages $\pm$ s.d.. Relative expression levels of core senescence-related transcripts (left panel) and SASP transcripts (right panel) are shown as mean values $\pm$ s.d.



Extended Data Fig. 5 | See next page for caption.

Extended Data Fig. 5 | Targets of senolytic drugs are induced after viral infection and render VIS cells sensitive to senolytics. **a**, Gene expression analysis of BCL2 family transcripts by qRT-PCR in VIS HDF, with mock infection as a control, as indicated. $n = 3$ independent experiments for each cell line and infection. **b**, STITCH plot showing interactions between senolytic drugs (Navitoclax, Fisetin, Dasatinib, Quercetin) and their potential targets. Protein-protein interactions are shown in grey, chemical-protein interactions in green and interactions between chemicals in red. Modified from <http://stitch.embl.de>. Note that all senolytics shown are working in close proximity and have overlapping targets at the level of kinase networks and BCL2-family members. **c**, Relative viability of proliferating or VIS (retrovirus) WI38 and Tig3 HDF as in Extended Data Fig. 1a, 24 hours after treatment with 1 μ M Venetoclax, 1 μ M Navitoclax, or solvent-only (DMSO). $n = 3$ independent experiments. **d**, Relative viability of senescence-incapable IMR90 (as in Fig. 1e, 4b) infected with VSV, and 24 hours after treatment with 1 μ M Venetoclax, 1 μ M Navitoclax, 20 μ M Fisetin, 20 μ M D/Q or solvent-only (DMSO). $n = 3$ independent experiments. **e**, Relative viability of proliferating or VIS IMR90 HDF compared to solvent-only (DMSO) control, two days after treatments with 1 μ M Navitoclax, 1 μ M MCL1 inhibitor AT101, or both. Results shown as mean relative viability $\pm$ s.d. for $n = 3$ independent experiments. Of note, strongly Mcl-1-expressing IMR90 VIS cells (see Fig. 4a) were not more susceptible to combined treatment with Navitoclax plus an Mcl-1 inhibitor as compared to Navitoclax alone. **f**, Secondary viral infectivity by SN transfer. Wild-type MEF that entered VIS in response to replication-competent VSV/GFP (or mock) were treated with 1 μ M Navitoclax before transferring the SN to uninfected THP-1 macrophages, here used as an infectivity reporter line. SA- β -gal staining to illustrate VIS, and GFP detection to visualize VSV infection of MEF. Secondary infectivity was measured as the GFP-positive fraction of THP-1 cells exposed to SN from MEF after Navitoclax or solvent-only treatment (bar plot). Senescence-dependent killing of VIS MEF did not increase GFP-positive THP-1 cells, thereby demonstrating that non-assembled cytoplasmic virus material potentially released upon senolysis does

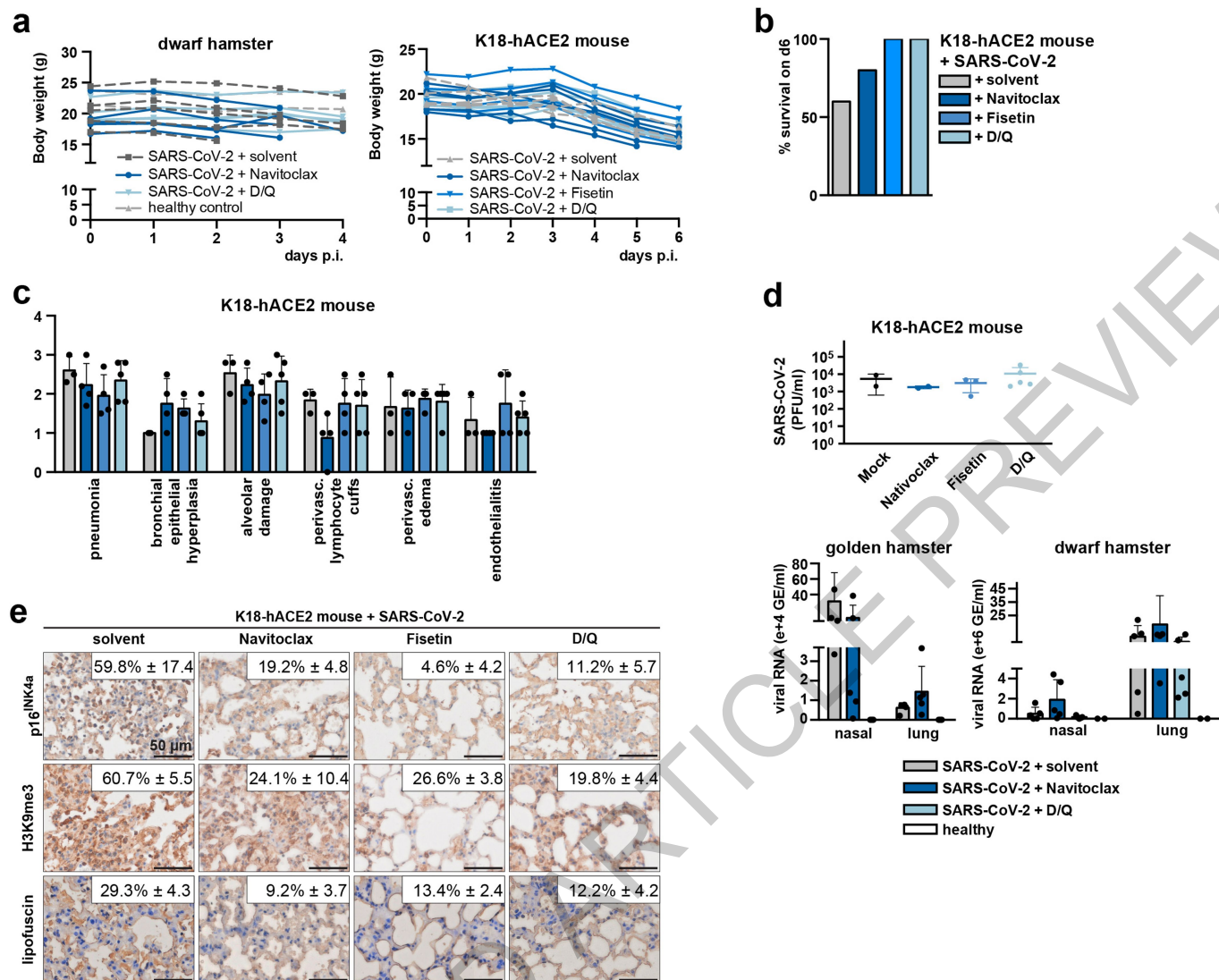
not add to infectivity. $n = 3$ independent experiments. **g**, Secondary viral infectivity (% GFP) and relative viability (Rel. viability) of THP-1 cells after SN transfer from VSV (or mock)-infected MEFs. Dilution of VIS SN as indicated below decreases secondary infection and increases viability. $n = 3$ independent experiments. **h**, Viability of HUVEC endothelial cells after exposure to human serum and SN of proliferating (SN_{prol}) or VIS (SN_{vis}) primary nasal epithelial cells (HNEpC-ACE2) as in Fig. 4f. $n = 3$ independent experiments. **i**–**l**, SARS-CoV-2 spike protein-pseudotyped VSV- Δ G*/CoV-2-S system to probe VIS in response to spike protein-affecting mutations. **i**, SA- β -gal staining of human cell line RPE1 infected with VSV- Δ G*-CoV-2-S (WT), VSV- Δ G*-CoV-2-S variant B.1.1.7 (Alpha), VSV- Δ G*-CoV-2-S variant B.1.351 (Beta), or mock infection as control. No obvious difference in the ability to drive VIS was detected. Representative photomicrographs and quantifications are shown as mean percentages $\pm$ s.d. for $n = 3$ independent experiments. Scale bar represents 100 μ m. **j**, CD86-marked activation of THP-1 cells exposed to SN of RPE1 cells in VIS after infection with VSV- Δ G* pseudotypes as indicated, or mock infection, as in **i**. Fractions of CD86⁺ cells relative to mock are shown, SN of cells infected with either mutant- or wild-type-pseudotyped virus equally enhance the fraction of CD86⁺ THP-1 cells. $n = 3$ independent experiments. **k**, Viability of cells as in **i**, after senolytic treatments as indicated. $n = 3$ independent experiments. All senolytic regimens, Navitoclax, Fisetin and D/Q proved equally effective in selectively eliminating VIS cells induced by the wild-type or the alpha or beta mutants. **l**, Gene expression analysis of senescence-related genes by qRT-PCR in RPE1 cells as in **i**. While transcript profiles of cell-autonomous senescence markers and pro-coagulatory SASP factors were similar between wild-type and mutants, pro-inflammatory cytokines and extracellular matrix-active factors appeared to be significantly higher expressed in the two mutant scenarios compared to wild-type. $n = 3$ independent experiments. All bar plots in this figure show mean results $\pm$ s.d. with individual values as dots. “*” indicates $p < 0.05$ by unpaired t-test (two-tailed) in all panels of this figure.



Extended Data Fig. 6 | See next page for caption.

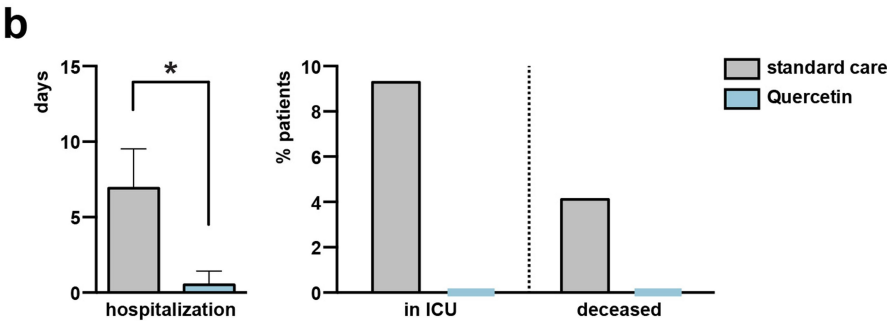
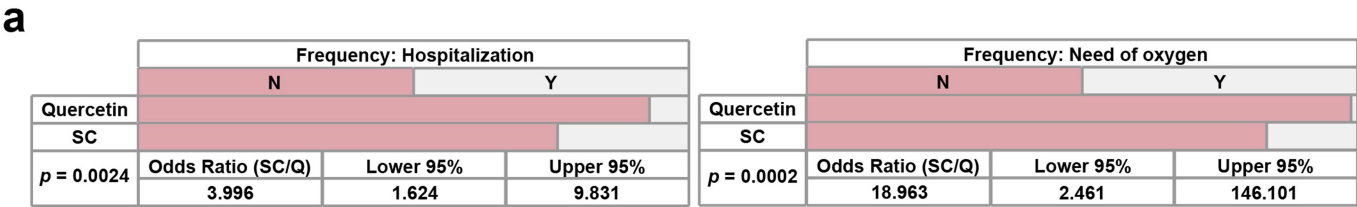
Extended Data Fig. 6 | Senolysis as a novel treatment concept in the COVID-19 golden hamster model. **a**, scRNA-seq-based expression analysis of viral RNA and senescence-associated genes in SARS-CoV-2-infected Syrian golden hamster lungs ($n = 3$ per time-point). UMAPs of cell types (top left, cell types of special interest in red), core senescence genes (top right), *CDKN2A* (bottom left), SASP genes (bottom second from left), and *SRF* (bottom right) on the indicated day p.i.; orange color code marks cells expressing senescence-associated genes, purple viral RNA, and red both. **b**, scRNA-seq-based expression analysis of *BCL-w*, *BCL2* and *MCL1* transcripts in the indicated cell types in SARS-CoV-2-infected Syrian golden hamster lungs ($n = 3$ per time-point) at the indicated days p.i.; average-scaled (z -scores) expression levels are shown in color code. Note that *BCL2* and *MCL1* transcript levels followed no clear trend, while *BCL-w* transcripts were induced at day 5 p.i. in all cell types presented. **c**, Daily body weight assessment of Syrian golden hamsters infected with SARS-CoV-2 (or uninfected healthy controls), and subsequently treated with Navitoclax or solvent-only as in Fig. 5a. $n = 5$ each for SARS-CoV-2-infected solvent-only- and Navitoclax-treated animals; $n = 3$ for the healthy control group. **d**, Number of platelets per 500 erythrocytes in blood smears of golden hamsters infected with SARS-CoV-2 and treated as in c, on day 7 p.i.. Mean counts $\pm$ s.d. of $n = 5$ hamsters per treatment group. $*p = 0.0127$ by unpaired t-test (two-tailed). Note for c and d: Although the Navitoclax group presented with relative weight loss of around nine percent and a reduction of nearly 40% of the initial thrombocyte concentration compared to the infection-only group at the end of therapy, a prominent adverse effect of Navitoclax, no obvious external or internal signs of enhanced hemorrhage was observed.

e, Transmission electron microscopy analysis of trachea epithelial cells from hamsters as in b and c. In infected and solvent treated animals (with the enlarged photomicrograph of a nucleus on the right), ciliated epithelial cells show senescent features as dilated endoplasmic reticulum (*), disrupted and dilated nuclear envelope (N = nucleus), vacuolization and altered mitochondria. Scale bar = $1\mu\text{m}$. $n = 4$ for SARS-CoV-2 infected groups and $n = 3$ for the mock infection group. **f**, Representative photomicrographs of H/E-stained lung tissue of Syrian golden hamsters as in Fig. 5a and c-e at day 7 p.i.. Lung sections for overview (i, v, ix) with active inflammation (arrow), signs of necrosis (inset, arrowhead), and hyperplasia (arrowheads) of alveolar epithelial cells (AEC) II (ii, vi). Vascular endothelialitis (iii, vii) with sloughing of endothelial cells (arrow), and subendothelial infiltration by lymphocytes (arrowhead). Regeneration of bronchial epithelium (iv, viii; double-headed arrow). Lung of mock-infected, untreated animals as control (ix, x, xi, xii). General signs of inflammation and AEC II hyperplasia in the Navitoclax group were rather similar to untreated animals. While the Navitoclax group presented with a less extensive patchy pneumonia pattern when compared to the solvent-only group (compare f-v to f-i). $n = 5$ each for SARS-CoV-2-infected solvent-only- and Navitoclax-treated animals. $n = 3$ for the healthy control group. Scale bars in i, v, ix = 1 mm , ii-iv, vi-viii, x-xii = $50\mu\text{m}$, insets ii, vi, x = $20\mu\text{m}$. **g**, Quantification of the findings shown in f. $*p = 0.0042$ by unpaired t-test (two-tailed). **h**, Multiplex bead-based protein analysis of golden hamster serum samples at day 7 p.i.; hamsters as in c-g. All bar plots in this figure show mean results $\pm$ s.d. with individual values as dots.



Extended Data Fig. 7 | Senolysis as a novel treatment concept in COVID-19 in additional animal models. **a**, Daily body weight assessment of dwarf hamsters and *K18-hACE2* mice infected with SARS-CoV-2 (or uninfected healthy controls), and subsequently treated with senolytics as in **b-e** and Fig. 5b-e. Dwarf hamsters: $n = 5$ each for SARS-CoV-2-infected solvent-only-, Navitoclax- or D/Q-treated; $n = 2$ for the healthy control group. *K18-hACE2*-transgenic mice: $n = 5$ for solvent, Navitoclax, and D/Q; $n = 4$ for Fisetin. **b**, Survival rate of *K18-hACE2*-transgenic mice on day 6d p.i. with SARS-CoV-2 and subsequent

senolytic treatment as in **a**. **c**, Histological scoring of H/E-stained lung tissue of *K18-hACE2* mice as in **a**. **d**, Viral load in hamster and mouse tissues on day 6 (mouse, as in **a-c**), day 7 (golden hamster, as in Fig. 5a and Extended Data Fig 6), and day 4 (dwarf hamster, as in Fig. 5b-e) p.i.. **e**, IHA of senescence markers (p16^{INK4a}, H3K9me3) and lipofuscin-staining in lung specimens of *K18-hACE2*-transgenic mice as in **a-d**. All bar plots in this figure show mean results + s.d. with individual values as dots.



Extended Data Fig. 8 | Senolysis as a novel treatment concept in COVID-19 patients. a, Frequency (bars) and risk (odds ratio) of COVID-19 patients to be hospitalized or in need of oxygen support after either standard care (SC) or Quercetin plus standard care (Quercetin). $n = 97$ for each group, based on two randomized trials combined and re-analyzed here^{51,52}. **b**, Days of

hospitalization (left) of COVID-19 patients (left; $p < 0.0001$ by unpaired t-test, two-tailed), the fraction of patients admitted to the intensive care unit (ICU; middle) or deceased in the course of the disease (right). Note that there was no patient in ICU or deceased in the Quercetin group. Patients as in n ; $n = 97$ for each group.

Extended Data Table 1 | Histological scoring of COVID-19 features in the SARS-CoV-2-infected hamsters

Roborovski dwarf hamster	Infection	Treatment	Time (dpi)	Pneumonia					Pneumonia score ¹	Bronchial epithelial necrosis	Bronchial inflammation	Bronchial epithelial hyperplasia	Alveolar epithelial necrosis	Alveolar edema	Alveolar damage ²	Perivascular edema	Perivascular lymphocytic cuffing	Hyperplasia ATII	Endothelialitis
				% affected score*	Degree of inflammation**	Lymphocytes	Macrophages	Neutrophils											
ND/Q_1	SARS-CoV-2	solvent	4	3	2-3	2	3	2	2.5	1-2	2	2	2-3	2-3	2.5	1	1	1-2	1
ND/Q_2	SARS-CoV-2	solvent	4	4	3	1	2-3	3	2.7	2-3	2	2-3	3	3	3.0	2	0	1	2
ND/Q_3	SARS-CoV-2	solvent	4	0	1	1	1	1	1.0	0	0	0	0	0	0.0	0	1	0	0
ND/Q_4	SARS-CoV-2	solvent	2	3	2	1-2	2	1-2	2.0	2	2	1	1	1	1.0	0	1	1	1
ND/Q_5	SARS-CoV-2	solvent	3	3	2-3	1	2	2-3	2.2	1-2	2	3	2-3	2	2.3	1-2	0	0	1
ND/Q_6	SARS-CoV-2	navitoclax	4	1	1	1	2	1	1.2	1	1	1	0	0	0.0	1	0	0	0
ND/Q_7	SARS-CoV-2	navitoclax	3	4	3	1	2-3	2	2.5	2	1	2-3	3	3	3.0	2	0	1	1
ND/Q_8	SARS-CoV-2	navitoclax	3	2	2	1	2	2	2.0	3	1	1	2	2	2.0	2	0	1	1
ND/Q_9	SARS-CoV-2	navitoclax	2	2	2-3	1	2	2	1.9	3	1-2	1	2	2	2.0	1	0	1	1-2
ND/Q_10	SARS-CoV-2	navitoclax	3	3	2-3	1	2-3	2	2.2	3	1	1	2	2-3	2.3	1	0	1	1
ND/Q_11	SARS-CoV-2	D/Q	4	0	1	1	2	1	1.2	0	0	0	0	1	0.5	0	0	0	1
ND/Q_12	SARS-CoV-2	D/Q	4	1	1	1	1-2	1	1.1	0	1	1	0	1	0.5	0	0	0	0
ND/Q_13	SARS-CoV-2	D/Q	4	2	1	1	1-2	1-2	1.4	1	1	1	1	1-2	1.3	1	0	0	1
ND/Q_14	SARS-CoV-2	D/Q	4	2	1	1	2	1	1.4	1	1	1	1	1	1.0	0	0	0	0
ND/Q_15	SARS-CoV-2	D/Q	4	2	2	1	2	2	1.8	2	1	1-2	2	2	2.0	1-2	1	1	1-2
ND/Q_16	mock	mock	4	0	1	1	2	1	1.2	0	0	0	0	1	0.5	0	0	0	0
ND/Q_17	mock	mock	4	0	1	1-2	2	1	1.3	0	0	0	0	1	0.5	0	1	0	0

Syrian Golden hamster	Infection	Treatment	Time (dpi)	Pneumonia					Pneumonia score ¹	Bronchial epithelial necrosis	Bronchial inflammation	Bronchial epithelial hyperplasia	Alveolar epithelial necrosis	Alveolar edema	Alveolar damage ²	Perivascular edema	Perivascular lymphocytic cuffing	Hyperplasia ATII	Endothelialitis	Endothelial activation	Endothelial damage ³	Mesothelial activation
				% affected score*	Degree of inflammation**	Lymphocytes	Macrophages	Neutrophils														
NX1	SARS-CoV2	Navitoclax	7	2	2-3	3	2-3	2	2.4	0	1	2	2-3	0	1.3	2	2	3	0	2	1	3
NX2	SARS-CoV2	Navitoclax	7	3	2-3	3	2-3	2	2.6	0	0	3-4	3.5	2	2.8	1-2	1	4	0	3	1.5	4
NX3	SARS-CoV2	Navitoclax	7	2	2-3	2	2-3	3	2.4	0	2	2-3	2-3	0	1.3	0	1	2-3	0	2	1	1
NX4	SARS-CoV2	Navitoclax	7	2	3	2-3	3	3	2.7	0	1	2	3	2	2.5	2	2	3-4	0	3	1.5	0
NX5	SARS-CoV2	Navitoclax	7	3	4	3	3-4	3	3.3	0	0	0	4	2-3	3.3	2-3	2	4	0	2-3	1.25	3
NX6	SARS-CoV2	solvent	7	2	3	3	3	3	2.8	0	1	3	3	2-3	2.8	2-3	2	3	1-2	3	2.25	2-3
NX7	SARS-CoV2	solvent	7	2	2-3	3	2-3	2-3	2.5	0	0	3	2	0	1.0	2-3	2-3	3	0	3	1.5	3
NX8	SARS-CoV2	solvent	7	2	3	3	3	3	2.8	0	0	2	2	2	2.0	3	1	3-4	1-2	3	2.25	2
NX9	SARS-CoV2	solvent	7	3	4	4	3-4	2-3	3.4	0	0	3-4	2	2-3	2.3	3	3	4	2	3	2.5	4
NX10	SARS-CoV2	solvent	7	1	2-3	3	2-3	3	2.4	0	0	3	2-3	0	1.3	2	2-3	3	1	3	2	2
NX11	mock	mock	7	0	0	0	0	0	0.0	0	0	0	0	0	0.0	0	0	0	0	0	0	0
NX12	mock	mock	7	0	0	0	0	0	0.0	0	0	0	0	0	0.0	0	1	0	0	0	0	0
NX13	mock	mock	7	0	0	0	0	0	0.0	0	0	0	0	0	0.0	0	1	0	0	0	0	0

Histopathological scoring of FFPE lung tissue from hamsters infected and treated as indicated.

* % affected score is scaled as (0) not present, (1) present but $\leq 25\%$, (2) > 25 but $\leq 50\%$, (3) > 50 but $\leq 75\%$, (4) $> 75\%$;

** degree of inflammation is scaled as (1) minimal, (2) mild, (3) moderate or (4) severe.

For all other parameters, rating refers to occurrence rate of (1) sporadic, (2) mild, (3) moderate, (4) severe.

¹Pneumonia score is the average of five pneumonia criteria (% affected score, degree of inflammation, occurrence rates of lymphocytes, macrophages, neutrophils).

²Alveolar damage is the average of alveolar epithelial necrosis and alveolar edema.

³Endothelial damage is the average of endothelialitis and endothelial activation

Extended Data Table 2 | Input data for Figure 5f

Patient Nr.	Treatment	Sex	Gender code	Age (years)	CRP d1	CRP d7	CPR d7 - d1	LDH d1	LDH d7	LDH d7 - d1	Symptoms d7 - d1	RT-PCR d1	RT-PCR d7
1	Q	F	0	45	4,05	0,43	-3,62	240	190	-50	-3	Positive	Negative
2	Q	F	0	20	6,7	0,99	-5,71	341	230	-111	-2	Positive	Negative
3	Q	M	1	68	3,54	0,34	-3,2	298	240	-58	-2	Positive	Negative
4	Q	F	0	40	3	0,5	-2,5	220	140	-80	0	Positive	Negative
5	Q	M	1	29	10,2	1,5	-8,7	560	331	-229	-1	Positive	Negative
6	Q	F	0	32	19	0,75	-18,25	605	256	-349	-2	Positive	Negative
7	Q	M	1	38	0,42	0,41	-0,01	175	127	-48	-3	Positive	Negative
8	Q	M	1	30	1	1	0	300	202	-98	-2	Positive	Negative
9	Q	F	0	24	2,1	0,5	-1,6	402	264	-138	-2	Positive	Negative
10	Q	M	1	56	38	55	17	709	678	-31	-3	Positive	Positive
11	Q	F	0	53	5	1	-4	340	220	-120	-3	Positive	Negative
12	Q	M	1	70	37	46	9	300	309	9	-2	Positive	Positive
13	Q	F	0	66	15	3	-12	267	220	-47	-2	Positive	Negative
14	Q	M	1	30	24	5	-19	176	160	-16	-4	Positive	Negative
15	Q	F	0	32	16	21	5	250	274	24	-1	Positive	Positive
16	Q	F	0	34	67	3,1	-63,9	345	213	-132	-4	Positive	Negative
17	Q	M	1	43	45	10	-35	678	248	-430	-3	Positive	Negative
18	Q	M	1	38	60	25	-35	770	279	-491	-2	Positive	Negative
19	Q	F	0	45	80	27	-53	670	370	-300	-3	Positive	Negative
20	Q	F	0	47	75	30	-45	535	270	-265	-3	Positive	Positive
21	Q	M	1	52	60	25	-35	610	450	-160	-2	Positive	Positive
22	Standard	F	0	54	62	40	-22	352	320	-32	-2	Positive	Positive
23	Standard	F	0	56	80	77	-3	512	459	-53	-3	Positive	Positive
24	Standard	M	1	62	55	43	-12	323	310	-13	-3	Positive	Positive
25	Standard	F	0	45	66	48	-18	402	380	-22	-2	Positive	Positive
26	Standard	F	0	59	78	66	-12	612	551	-61	-3	Positive	Positive
27	Standard	M	1	95	17,14	12,2	-4,94	320	280	-40	-2	Positive	Positive
28	Standard	M	1	37	12,5	1,6	-10,9	262	257	-5	-3	Positive	Positive
29	Standard	F	0	33	7,3	2,3	-5	203	285	82	-1	Positive	Negative
30	Standard	F	0	73	16	3,3	-12,7	615	359	-256	-1	Positive	Positive
31	Standard	F	0	57	17,5	5	-12,5	267	231	-36	-2	Positive	Positive
32	Standard	M	1	72	73	5	-68	256	231	-25	-1	Positive	Positive
33	Standard	F	0	57	12	24	12	232	250	18	-2	Positive	Positive
34	Standard	M	1	60	34	11,4	-22,6	640	250	-390	-1	Positive	Positive
35	Standard	M	1	51	48,7	12	-36,7	305	259	-46	-2	Positive	Positive
36	Standard	M	1	73	15	6	-9	347	243	-104	-1	Positive	Positive
37	Standard	M	1	68	4,78	1	-3,78	573	433	-140	-2	Positive	Positive
38	Standard	M	1	50	0,9	0,5	-0,4	344	250	-94	-2	Positive	Positive
39	Standard	M	1	42	0,5	0,5	0	250	253	3	-3	Positive	Negative
40	Standard	F	1	69	5,51	6,2	0,69	358	745	387	-2	Positive	Positive
41	Standard	F	0	42	1	0,5	-0,5	240	320	80	-1	Positive	Positive
42	Standard	F	0	25	33,9	15,2	-18,7	250	214	-36	-2	Positive	Positive

Treatment, sex, age, symptoms, CRP, LDH, RT-PCR were collectively analyzed in a multi-variant analysis by agglomerative hierarchical clustering underlying the constellation plots.

Reporting Summary

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Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a Confirmed

- ☐ ☒ The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement
- ☐ ☒ A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
- ☐ ☒ The statistical test(s) used AND whether they are one- or two-sided
Only common tests should be described solely by name; describe more complex techniques in the Methods section.
- ☐ ☒ A description of all covariates tested
- ☐ ☒ A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
- ☐ ☒ A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
- ☐ ☒ For null hypothesis testing, the test statistic (e.g. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted
Give P values as exact values whenever suitable.
- ☒ ☐ For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
- ☐ ☒ For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
- ☒ ☐ Estimates of effect sizes (e.g. Cohen's d , Pearson's r), indicating how they were calculated

Our web collection on [statistics for biologists](#) contains articles on many of the points above.

Software and code

Policy information about [availability of computer code](#)

Data collection	For multiplex bead-based protein analysis, the assay was measured with the BioPlex Magpix Multiplex Reader (Bio-Rad). For mass-spectrometry, the raw data were processed using the DIA-NN software package 1.7.12.
Data analysis	For multiplex bead-based protein analysis, the data was analyzed with a SPL algorithm provided by the Bio-Plex Manager™ software (Version 6.1). Flow cytometry-based patient data analysis was performed with the CytExpert software (version 2.4, Beckman-Coulter). Heatmaps were generated via online tool Morpheus (https://software.broadinstitute.org/morpheus/). Oligonucleotide hybridization-based transcriptome profiling data was analyzed on the NanoString nCounter® SPRINT, with nSolver analysis software (version 4.0). Data analysis was performed with GraphPad Prism 9. For statistical comparisons, a t-test was applied. Unless otherwise stated, a p-value < 0.05 was considered statistically significant. For multiple testing corrections the method by Benjamini & Hochberg (BH) to control for false discovery rate was applied. Bioinformatics Analysis was performed in R, version 4.0.3, and Bioconductor 3.12 using various R packages as described in the Supplemental Experimental Procedures in greater detail. High-performance computation has been performed on the Research/Clinic cluster of the Berlin Institute of Health. For further analyses of COVID-19 patient clinical data as presented in Fig. 5g and Extended Data Fig. 5m, n, JMP Pro software (version 14.1, SAS Institute) was used for agglomerative hierarchical clustering, GraphPad Prism9 for Fisher's exact test for p-values, and a Haldane-Anscombe correction was applied to calculate relative risks. Lipofuscin (SenTraGor®) staining was quantified with the pixel counting function of the ImageJ program (bundled with Java 1.8.0_172, NIH). Gene set enrichment analyses were performed using GSEA. Custom signatures were analyzed along with hallmarks gene sets (h.all.v7.2.symbols.gmt) as in the list below. Signal2Noise metric for ranking of the genes was used, unless less than three samples per group were available. In these cases, ratio of classes was used as ranking metric. RNA-sequencing: Transcripts were quantified using salmon74 and imported using tximeta75 or tximport packages76. Differential expression analysis was performed using DESeq277. scRNA-seq data were explored, analyzed with Seurat package, and visualized using ggplot278. Packages used for visualization: library(ggplot2), library(ComplexHeatmap), library(cowplot), library(pheatmap) for scRNA: library(Seurat)

for bulk RNA-Seq: library(tximport), library(tximeta), library(DESeq2)
 other: library(plyr), library(dplyr), library(tibble), library(reshape), library(tidyr)

Custom terms used:

CLASSICAL SASP (BGN, CCL2, CCL20, COL1A1, CXCL12, DCN, EGF, EFEMP1, FGF2, FGF7, FN1, CSF1, CTGF, CXCL1, GDNF, IGFBP2, IGFBP6, IFNA1, IFNB1, IFNG, IL1A, IL1B, IL6, IL7, CXCL8, IL13, IL15, KITLG, CCL2, CCL9, MMP2, MMP3, MMP9, SERPINE1, TGFB1, THBS1, TIMP2, TNF, VEGFA)

SASP_SCHLEICH66 (ANG, AREG, ATF4, BHLHE40, CCL1, CCL11, CCL12, CCL2, CCL20, CCL25, CD55, CD55B, CD9, CPE, CSF2, CSF2RB, CSF2RB2, CSF3, CTSB, CXCL1, CXCL12, CXCL13, CXCL2, CXCL5, CXCR2, EGF, EGFR, EREG, ETS1, ETS2, FAS, FGF2, FGF7, FN1, GEM, GMFG, HGF, ICAM1, ID1, IFNG, IGF1, IGF2, IGF2R, IGFBP1, IGFBP2, IGFBP3, IGFBP4, IGFBP5, IGFBP6, IGFBP7, IL13, IL15, IL1A, IL1B, IL6, IL6ST, IL7, ITGA2, ITPKA, KITLG, MIF, MMP10, MMP12, MMP14, MMP1A, MMP3, NGF, PECAM1, PIGF, PLAT, PLAU, PLAUR, PTGES, SERPINB2, SERPINE1, TGFB1, TIMP1, TIMP2, TNFRSF11B, TNFRSF1A, TNFRSF1B, VEGFA)

SUVARNess_SCHLEICH66 (FKBP9, F2R, FSTL1, PLPP3, NCKAP1, CTSC, WLS, PRRX1, MMP9, ITGAM, GPX8, SGPL1, SGK1, FKBP10, GAS1, SDC2, CDH2, CD274, FAM114A1, SNX7, XAF1, CD38)

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Data

Policy information about [availability of data](#)

All manuscripts must include a [data availability statement](#). This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

The WI38 VIS- and OIS-derived raw RNA-seq data (Fig. 1b and Extended Data Fig. 1b) were deposited at the Gene Expression Omnibus (GEO) repository of the National Center for Biotechnology Information (NCBI) under accession number GSE165532. Gene expression data of human AEC cells infected with SARS-CoV-2 (Fig. 1k) are publicly available from at the NCBI GEO under the accession number GSE148729. Raw sequencing data of NHBE, Calu-3 and A549 cells infected with SARS-CoV-2 (Extended Data Fig. 1u) are publicly available at the NCBI GEO under the accession number GSE147507 (Blance-Melo, D. et al. doi:10.1016/j.cell.2020.04.026). Seurat objects comprising scRNA-seq datasets of nasopharyngeal, protected specimen brush, and bronchial lavage samples of 19 COVID-19 patients and five healthy controls(Chua, R.L. et al. doi:10.1038/s41587-020-0602-4), comprising a total of 36 samples that were analyzed in this study (Fig. 2b), are available at FigShare: <https://doi.org/10.6084/m9.figshare.12436517>. The mass spectrometry-based proteome data of serum from COVID-19 patients and healthy donors in Fig. 2f are described(Messner, C.B. et al. doi:10.1016/j.cels.2020.05.012). Patient proteomics data (Fig. 2g, Extended Data Fig. 2e) are publicly available at <https://www.who.int/teams/blueprint/covid-19>. scRNA-seq data of hamsters infected with SARS-CoV-2 (Extended Data Fig. 5a and b) is available at the NCBI GEO (GSE162208)(Nouailles, G et al. , doi:10.1101/2020.12.18.423524). All information related to the two randomized trials on early Quercetin intervention in COVID-19 patients (NCT04578158 and NCT04861298) can be found in the respective publications(Di Pierro, F. et al. <https://doi.org/10.2147/IJGM.S318720>)(Di Pierro, F. et al. doi: 10.2147/IJGM.S318720).

Field-specific reporting

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☒ Life sciences ☐ Behavioural & social sciences ☐ Ecological, evolutionary & environmental sciences

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Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	Based on previous experience using both animal and human patient material (references in Methods, Statistics and Data Analysis), sample sizes typically reflect three to five, in some experiments also much higher numbers of individual primary material as biological replicates. All quantifications from staining reactions were carried out by an independent and blinded second examiner and reflect at least three samples with at least 100 events counted (typically in three different areas) each.
Data exclusions	No data was excluded.
Replication	For all experiments, sample size and number of individual experiment replicated or biological replicates are mentioned in corresponding figure legend. Most or replications were successful and the variations of assay results are described in the text, as well as in the form of statistical parameters such as standard deviation.
Randomization	Hamster and mouse model: animals were randomly assigned to each group for treatment. Patients in Quercetin trial were randomized (Block Randomization Algorithm).
Blinding	All quantifications from immunohistochemistry analysis were carried out by an independent and blinded second examiner. Hamster and mouse tissues were processed and analyzed by board-certified veterinary pathologists (blinded about the treatment) following standard

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
☐	☒ Antibodies
☐	☒ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☐	☒ Animals and other organisms
☐	☒ Human research participants
☐	☒ Clinical data
☒	☐ Dual use research of concern

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☐	☒ Flow cytometry
☒	☐ MRI-based neuroimaging

Antibodies

Antibodies used

Flow cytometry, immunoblotting (IB), immunofluorescence (IF), and immunohistochemistry (IHC) were performed as described previously^[Schmitt, 1999 #1684;Jing, 2011 #3545]. Surface antigen detection by flow cytometry was carried out with fluorescence-conjugated antibodies against human CD86-PE-Cy7 (BioLegend, #374209, 1:200), CD13-APC-Cy7 (BioLegend, #301709, 1:200), CD45-BV510 (BioLegend, #368525, 1:200), CD42b-FITC (BioLegend, #303903, 1:200), CD62P-PE (BioLegend, #304905, 1:200). For MACS-column separation, biotinylated anti-CD86 antibody (Miltenyi Biotech #130-114-096, 1:10) was used. Antigen detection by IB was carried out with antibodies against BCL2 (Cell Signaling Technology [CST], #15071, 1:1000), BCLXL (CST, #2764, 1:1000), BCLW (CST, #2724, 1:1000), MCL1 (CST, #39224, 1:1000), phospho-p65-Ser536 (CST, #3033, 1:1000), phospho-IRF3-Ser386 (CST, #37829, 1:1000), phospho-Rb-Ser807/811 (CST, #8516, 1:1000), p21CIP1 (Santa Cruz Biotechnology [SCBT], #sc-6246, 1:200), p16INK4a (SCBT, #sc-1661, 1:200), H3K9me3 (Abcam, #ab8898, 1:2000), phospho-Akt (Thr308) (CST, #13038T, 1:2000), phospho-p38 MAPK (Thr180/Tyr182) (CST, #4511T, 1:1000), phospho-p70 S6 Kinase (Thr389) (CST, #9234T, 1:1000), phospho-Src (Tyr416) (CST, #6943T, 1:1000) and α -Tubulin (Sigma, #T5168, 1:2000). Anti-mouse or anti-rabbit horseradish peroxidase-conjugated antibodies were used as secondary antibodies (GE Healthcare, #RPN4301 and #NA931V, respectively). Antigen detection by IF was performed with antibodies against phospho-H2A.X (Cell Signaling, #9718, 1:400), p16INK4a (Abcam, #ab211542, 1:250), C5b-9 (SCBT, #sc-58935, 1:250), anti-mouse-Cy3 secondary antibody (Thermo Fisher, #A10521, 1:1000), anti-rabbit-594 secondary antibody (Thermo Fisher, #A11012, 1:1000). Antigen detection by IHC was performed using the HiDef Detection HRP Polymer System (Cell Marque, #954D-30) with antibodies against p21CIP1 (SCBT, #sc-6246, 1:200), IL-8 (Abcam, #ab18672, 1:200), H3K9me3 (Abcam, #ab8898, 1:2000), BCL2L2 (Abcam, #ab190952, 1:1000), CD86 (Antibodies-online, ABIN736701, 1:100).

Validation

CD86-PE-Cy7 (BioLegend, #374209): reactive to human (H). Application flow cytometry. <https://www.biolegend.com/en-us/products/pe-cyanine7-anti-human-cd86-antibody-15545>
 CD13-APC-Cy7 (BioLegend, #301709): reactive to H, Baboon, Chimpanzee, Cotton-topped Tamarin. Application flow cytometry. <https://www.biolegend.com/en-us/products/apc-cyanine7-anti-human-cd13-antibody-3963>
 CD62P-PE (BioLegend, #304905): reactive to H, chimpanzee. Application flow cytometry. <https://www.biolegend.com/en-us/products/pe-anti-human-cd62p-p-selectin-antibody-595>
 biotinylated anti-CD86 antibody (Miltenyi Biotech #130-114-096): reactive to H and non-H primates. Application flow cytometry. <https://www.miltenyibiotec.com/CA-en/products/cd86-antibody-anti-human-fm95.html#gref>
 CD45-BV510 (BioLegend, #368525): reactive to H. Application flow cytometry. <https://www.biolegend.com/en-us/products/brilliant-violet-510-anti-human-cd45-antibody-14685?GroupID=BLG14850>
 BCL2 (Cell Signaling Technology [CST], #15071): reactive to H. Application IB, IHC. <https://media.cellsignal.com/coa/15071/7/15071-lot-7-coa.pdf>
 BCLXL (CST, #2764): reactive to H, mouse (M), rat (R), monkey (MK). Application IB, IHC, IF. <https://media.cellsignal.com/coa/2764/11/2764-lot-11-coa.pdf>
 BCLW (CST, #2724), reactive to H, M, R. Application IB. <https://media.cellsignal.com/coa/2724/3/2724-lot-3-coa.pdf>
 MCL1 (CST, #39224), reactive to H. Application IB, IHC, IF. <https://media.cellsignal.com/coa/39224/4/39224-lot-4-coa.pdf>
 phospho-p65-Ser536 (CST, #3033), reactive to H, M, R, hamster (Hm), Mk, Pig (Pg). Application, IB, IF. <https://media.cellsignal.com/coa/3033/17/3033-lot-17-coa.pdf>
 phosphor-IRF3-Ser386 (CST, #37829), reactive to H. Application IB, IF. <https://media.cellsignal.com/coa/37829/3/37829-lot-3-coa.pdf>
 phosphor-Rb-Ser807/811 (CST, #8516), reactive to H M R Mk. Application IB, IHC, IF. <https://media.cellsignal.com/coa/8516/8/8516-lot-8-coa.pdf>
 p21CIP1 (Santa Cruz Biotechnology [SCBT], #sc-6246), reactive to H, M, R. Application IB. <https://datasheets.scbt.com/sc-6246.pdf>
 p16INK4a (SCBT, #sc-1661), reactive to H, M, R. Application IB, IHC, IF. <https://datasheets.scbt.com/sc-1661.pdf>
 H3K9me3 (Abcam, #ab8898), reactive to H, M, R, yeast. Application IB, IHC, IF. <https://www.abcam.com/histone-h3-tri-methyl-k9-antibody-chip-grade-ab8898.html>
 phospho-Akt (Thr308) (CST, #13038T), reactive to H, M, R, MK. Application IB, IP, IF, F. <https://media.cellsignal.com/coa/13038/7/13038-lot-7-coa.pdf>
 phospho-p38 MAPK (Thr180/Tyr182) (CST, #4511T), reactive to H, M, R, Mk, Mink (Mi), Pg, yeast. Application IB, IP, IHC, IF, F. <https://media.cellsignal.com/coa/4511/13/4511-lot-13-coa.pdf>
 phospho-p70 S6 Kinase (Thr389) (CST, #9234T), reactive to H, M, R, Mk. Application IB. <https://media.cellsignal.com/>

coa/9234/12/9234-lot-12-coa.pdf.
 phospho-Src (Tyr416) (CST, #6943T), reactive to H, M, R, Mk. Application IB, IP. <https://media.cellsignal.com/coa/6943/4/6943-lot-4-coa.pdf>.
 a-Tubulin (Sigma, #T5168), reactive to H, M, R, Mk, bovine, chicken. Application IB, IF. <https://www.sigmaaldrich.com/catalog/product/sigma/t5168?lang=de®ion=DE>.
 phospho-H2A.X (Cell Signaling, #9718), reactive to H, M, R, Mk. Application IB, IHC, IF, F. <https://media.cellsignal.com/coa/9718/17/9718-lot-17-coa.pdf>
 p16INK4a (Abcam, #ab211542), reactive to M. Application IB, IF, flow cytometry. <https://www.abcam.com/cdkn2ap16ink4a-antibody-epr20418-ab211542.html>.
 C5b-9 (SCBT, #sc-58935), reactive to H, Pg. Application IG, ELISA. <https://datasheets.scbt.com/sc-58935.pdf>.
 IL-8 (Abcam, #ab106350), reactive to H. Application IB, IHC. <https://www.abcam.com/il-8-antibody-ab106350.html>.
 BCL2L2 (Abcam, #ab190952), reactive to H. Application IB, IHC. <https://www.abcam.com/bcl2l2-antibody-ab190952.html>.
 CD86 (Antibodies-online, ABIN736701) reactive to H, M, R. Application IB, IHC, IF. <https://www.antibodies-online.com/antibody/736701/anti-CD86+Molecule+CD86+AA+130-180+antibody/>

Eukaryotic cell lines

Policy information about [cell lines](#)

Cell line source(s)	Human cell lines RPE1 (hTERT RPE1), A549 and HUVEC were purchased from ATCC. Primary human nasal or bronchial epithelial cells (HNEpC and HBEpC) were purchased from PromoCell. THP-1 cells were provided by Anna Walter (Charité).
Authentication	Purchased cell lines were authenticated by the commercial provider, e.g. STR profiling or cell marker expression e.g. cytokeratin for HNEpC and HBEpC. THP-1 cells were not authenticated. information added to the new reporting summary.
Mycoplasma contamination	All cell lines were tested mycoplasma negative.
Commonly misidentified lines (See ICLAC register)	No commonly misidentified cell line was used.

Animals and other organisms

Policy information about [studies involving animals](#); [ARRIVE guidelines](#) recommended for reporting animal research

Laboratory animals	6 - 10 weeks old Mesocricetus auratus (Syrian golden hamster) of mixed gender, 5 - 7 weeks old female Phodopus roborovskii (Roborovski dwarf hamster), and 6 weeks old female Mus musculus (house mouse), specifically, K18-hACE2 transgenic (Jax strain 034860) were used. All animals were kept in BSL3 facility for virus infection and treatment, with normal chow diet and water ad libitum. Hamsters were maintained under a natural light cycle, ambient temperature (22 - 25°C), and 50 -60% humidity. Mice were housed under specific pathogen-free conditions in individually ventilated cages and fed irradiated food and filtered water.
Wild animals	This study did not involve wild animals.
Field-collected samples	This study did not involve samples collected from the field.
Ethics oversight	Hamster experiments: Local governmental Office for Health and Social Affairs: Landesamt für Gesundheit und Soziales (LaGeSo) Berlin, Berlin, Germany Mouse experiments: Institutional Animal Care and Use Committee (IACUC) of Icahn School of Medicine at Mount Sinai (ISMMS), New York, USA

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Human research participants

Policy information about [studies involving human research participants](#)

Population characteristics	Upper (nasopharyngeal) and lower airway (lung) tissue FFPE samples were derived from deceased SARS-CoV-2-infected COVID-19 patients as well as archive material from patients who passed away without significant clinical signs of a respiratory infection prior to October 2019 (i.e. non-COVID-19 patients), blood samples of SARS-CoV-2-infected and hospitalized patients in the course of their COVID-19 disease, or blood samples from healthy volunteers were used based on approval by the local ethics commission of the Johannes Kepler University, Linz, Austria (reference number 1070/2020). No significant difference in the age distribution between deceased COVID-19 patients and non-COVID-19 patients were noted. Healthy blood donors – typically health care personnel and cancer research staff – were slightly younger than the COVID-19 patients in the various cohorts presented. All participants gave informed consent. In addition, we conducted re-analyses of additional patient and control materials that were obtained before and published elsewhere(30,33,51,52). Beyond the data reported here and therein, no genotypic profiles of the human participants are currently known, and no detailed medical information outside the COVID-19-centered data collection was recorded for the purpose of this study. 30 Chua, R. L. et al. COVID-19 severity correlates with airway epithelium-immune cell interactions identified by single-cell analysis. Nat Biotechnol 38, 970-979, doi:10.1038/s41587-020-0602-4 (2020). 33 Messner, C. B. et al. Ultra-high-throughput clinical proteomics reveals classifiers of COVID-19 infection. Cell Syst 11, 11-24 e14, doi:10.1016/j.cels.2020.05.012 (2020).
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51 Di Pierro, F. et al. Possible therapeutic effects of adjuvant Quercetin supplementation against early-stage COVID-19 infection: A prospective, randomized, controlled, and open-label study. *Int J Gen Med* 14, 2359-2366, doi:10.2147/ijgm.S318720 (2021).

52 Di Pierro, F. et al. Potential clinical benefits of Quercetin in the early stage of COVID-19: Results of a second, pilot, randomized, controlled and open-label clinical trial. *Int J Gen Med* 14, 2807-2816 (2021).

Recruitment

COVID-19 patients and control participants were recruited according to availability on an outpatient or inpatient basis, or as healthy volunteers, and based on informed consent on a continuous basis, hence include patients across the spectrum of COVID-19 disease severity, or as reported and published elsewhere^{30,33,51,52} (see respective references above and in the manuscript). Due to the somewhat younger age of healthy blood donors and an impossible match between the extent of systemic inflammation in COVID-19 patients vs. non-COVID-19 patients (actually selected for no obvious respiratory infection) deceased prior to the beginning of the pandemic a bias in such inflammatory parameters (e.g. cytokine levels) cannot be ruled out or is actually intrinsic to the subject of the comparison presented here. No other potential investigator-based biases apply to the best of our knowledge.

Ethics oversight

Ethics commission of the Johannes Kepler University, Linz, Austria

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Clinical data

Policy information about [clinical studies](#)

All manuscripts should comply with the ICMJE [guidelines for publication of clinical research](#) and a completed [CONSORT checklist](#) must be included with all submissions.

Clinical trial registration NCT04578158 and NCT04861298

Study protocol We do not provide more detailed information (beyond Extended Table 2) here, because both trials are published elsewhere.

Data collection See references 51 and 52 in our manuscript. Our manuscript is not the primary publication of these trials.

Outcomes See Fig. 5f, Extended Data Fig. 5n, o and the references above.

Flow Cytometry

Plots

Confirm that:

- ☒ The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).
- ☒ The axis scales are clearly visible. Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).
- ☒ All plots are contour plots with outliers or pseudocolor plots.
- ☐ A numerical value for number of cells or percentage (with statistics) is provided.

Methodology

Sample preparation Cells were washed once with PBS and resuspended in 50 µl of ice-cold FACS buffer containing FcR blocking reagent (Miltenyi Biotec, #130-059-901) with antibody.

Instrument Cytoflex flow cytometer (Beckman-Coulter) equipped with 405, 488 and 633 nm lasers for excitation and 13 fluorescence detection channels.

Software CytExpert software (Beckman-Coulter).

Cell population abundance DAPI-negative live cells were analyzed. For THP-1 cells, usually more than 90% were alive.

Gating strategy THP-1 cells: DAPI- and CD45+ events were gated and analyzed for CD86 and CD13 expression.

☒ Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.