SARS-CoV-2 induces double-stranded RNA-mediated innate immune responses in respiratory epithelial derived cells and cardiomyocytes

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Summary

Coronaviruses are adept at evading and/or antagonizing double-stranded RNA-induced host antiviral pathways, including interferon signaling, OAS-RNase L and PKR while robust cytokine responses characterize severe coronavirus disease. Knowledge of how newly emerged SARS-CoV-2 interacts with these pathways is minimal. SARS-CoV-2 readily infects patient-derived nasal epithelial cells and induced pluripotent stem cell-derived alveolar type 2 cells(iAT2) and cardiomyocytes(iCM). Robust activation of interferons or RNase L is not observed, while PKR activation is evident in iAT2 and iCM. In SARS-CoV-2 infected Calu-3 and A549^{ACE2} lung derived cell lines, activation of all pathways is observed, similar to a mutant MERS-CoV lacking innate immune antagonists. Moreover, increased replication in *RNASEL* knockout A549^{ACE2} cells, implicates RNase L in restricting SARS-CoV-2. Finally, while SARS-CoV-2 is less adept at antagonizing these host defense pathways compared to other coronaviruses, the innate immune response is still generally weak. These host-virus interactions may contribute to the unique pathogenesis of SARS-CoV-2.

Keywords: SARS-CoV-2; interferon, OAS-RNase L, PKR, viral accessory proteins

Introduction

Severe acute respiratory syndrome coronavirus (SARS-CoV)-2 emerged in China in late 2019, causing the COVID-19 pandemic with extensive morbidity and mortality, leading to major changes in day-to-day life in many parts of the world. This was the third lethal respiratory coronavirus, after SARS-CoV in 2002 and Middle East respiratory coronavirus (MERS-CoV) in 2012, to emerge from bats in the twenty first century. Although these viruses are all members of the *Betacoronavirus* genus (Llanes et al., 2020), each has caused a somewhat different pattern of pathogenesis and spread in humans (Fehr and Perlman, 2015); therefore it is important to understand how these viruses interact with their host. Additionally, recent reports indicate that ancestors of SARS-CoV-2 as well as other SARS-CoV-like viruses have been circulating in bats for decades, suggesting potential future instances of direct spread to humans (Boni et al., 2020).

Coronaviruses are enveloped viruses with large, positive-sense single-stranded (ss)RNA genomes of around 30kb that can infect a diverse range of mammals and other species. Coronaviruses use much of their genomes, including their approximately 20 kb Orf1ab replicase locus comprising the 5' two thirds of the genome, to encode proteins that antagonize host cell responses (Perlman and Netland, 2009). As a result they are remarkably adept at antagonizing host responses, in particular the double-stranded RNA (dsRNA)-induced pathways that are essential components of the host innate immune response (Cruz et al., 2011; Dedeurwaerder et al., 2014; Koetzner et al., 2010; Kopecky-Bromberg et al., 2007; Weiss and Navas-Martin, 2005). In addition, interspersed among the structural genes encoded in the 3' third of the genome are lineage-specific genes encoding accessory proteins, which are non-essential for RNA replication and variable among CoV lineages that further divide the *Betacoronavirus* genus (Cui et al., 2019). These accessory proteins often have functions in antagonizing host cell responses and thus likely contribute to discrepancies in pathogenesis and tropism observed among the different lineages (Comar et al., 2019; Kikkert, 2020; Zhao et al., 2012).

Like other RNA viruses, coronaviruses produce double-stranded RNA (dsRNA) early on during the infection cycle as a result of genome replication and mRNA transcription (Sola et al., 2015). Host cell pattern recognition receptors (PRRs) sense viral dsRNA as pathogenic non-self and respond by activating several antiviral pathways critical for early defense against viral invasion. DsRNA sensing by cytosolic PRRs can be divided into three key pathways – interferon (IFN) production, ribonuclease L (RNase L) activation, and protein kinase R (PKR) activation (**Fig 1**) (Hur, 2019). Detection of dsRNA by MDA5 during coronavirus infection (Roth-Cross et al., 2008), leads to the production of type I (α/β) and type III (λ) IFN. Upon binding to its specific cell surface receptor, IFN triggers phosphorylation of STAT1 and STAT2 transcription factors, which then induce expression of interferon stimulated genes (ISGs) with antiviral activities (Lopusna et al., 2013; Platanias, 2005). In parallel, dsRNA is also sensed by oligoadenylate synthetases (OASs), primarily OAS3, which synthesize 2',5'-linked oligoadenylates (2-5A)(Li et al., 2016; Whelan et al., 2019). Generation of 2-5A induces dimerization and activation of ribonuclease L (RNase L), leading to degradation of viral and host ssRNA. Finally, dsRNA sensing by protein kinase R (PKR) will induce PKR autophosphorylation, permitting PKR to then phosphorylate the translation initiation factor eIF2α, which results in protein synthesis shutdown and restriction of viral replication (Sadler and Williams, 2008). While RNase L and PKR antiviral activity are not dependent on IFN production (Whelan et al., 2019), the genes encoding OASs and PKR are ISGs, therefore these pathways can be activated and/or reinforced by IFN production. Similarly, RNase L and PKR activation can promote IFN production, cellular stress, inflammation, and/or apoptotic death (Banerjee et al., 2014; Castelli et al., 1997; Chakrabarti et al., 2015; Kang and Tang, 2012; Malathi et al., 2007; Zhou et al., 1997), thus further reducing host cell viability.

Induction and inhibition of innate immune responses during infection with SARS-CoV-2 have yet

to be fully characterized. Furthermore, while it is well understood that SARS-CoV-2 enters the human body through the upper respiratory tract, it is unclear which cell types of the upper and lower respiratory system contribute to sustained infection and resulting disease in the airways and elsewhere. We have performed SARS-CoV-2 infections of primary nasal epithelial cells, induced pluripotent stem cell (iPSC)-derived alveolar type 2 cells (iAT2), and iPSC-derived cardiomyocytes (iCM), which together represent the host tissues likely affected by clinical SARS-CoV-2 infection (Hou et al., 2020; Sharma et al., 2020). We assessed viral replication in these cell types as well as the degree of ensuing dsRNA-sensing responses. We also employed two respiratory tract derived immune-competent cells lines, Calu-3 cells and A549 cells, to investigate dsRNA-induced pathway activation during SARS-CoV-2 infection. In addition, we compared host responses to SARS-CoV-2 with those of MERS-CoV and MERS-CoV-ΔNS4ab, a mutant lacking expression of two dsRNA-induced innate immune pathway antagonists that we have characterized previously (Comar et al., 2019).

Results

SARS-CoV-2 replicates efficiently in cells derived from upper and lower respiratory tract. We compared the replication of SARS-CoV-2 and MERS-CoV in nasal epithelia-derived cells, a relevant site of infection *in vivo*, from four different donors (**Fig 2A**). For each virus, replication was similar in cells from all four individuals, although the extent of replication was somewhat variable. The trends in replication kinetics, however, were significantly different between SARS-CoV-2 and MERS-CoV infections. Replication of SARS-CoV-2 increased until 96hpi, but then plateaued at nearly 10^6 plaque-forming units (PFU)/ml. MERS-CoV replication peaked at 96hpi, at a lower titer than SARS-CoV-2. Nasal epithelial cell cultures were stained with antibodies to identify ciliated cells (anti-type IV β-tubulin), a key feature of this cell type, and either SARS-CoV-2 or MERS-CoV nucleocapsid expression (anti-N protein) (**Fig 2B**). We detected abundant N expressed in both SARS-CoV-2 and MERS-CoV infected cells, indicating that these cells were

sufficiently infected at 48 hours post infection (hpi). Interestingly, robust replication occurred in these cultures, despite a very low level of ACE2 protein expression in cells from the three individuals examined (**Fig 2C**).

We measured dsRNA-induced host responses to SARS-CoV-2 infection, including type I and type III IFN mRNA induction, RNase L activation, and PKR activation, in the nasal cells. For RT-qPCR analysis, we extracted RNA from SARS-CoV-2 infected cultures from four different donors at 120hpi. We verified that virus was replicating by quantifying viral genome copies from intracellular RNA (**Fig S1A**). We then quantified mRNA expression of IFN-β (type I IFN), IFN-λ (type III IFN), select ISGs induced downstream of IFN production (*OAS2*, *IFIT1*, *IFIH1*), and the neutrophil attracting chemokine IL-8 (*CXCL8*), which has been implicated in nasal inflammation during viral infection (Mukaida, 2003; Turner et al., 1998) (**Fig 2D**)**.** The data shown represents the average of cells from three donors. There was some induction of type I and to a lesser extent type III IFN mRNA, and minimal induction of the ISG mRNAs examined. Similarly, *CXCL8* encoding IL-8 was barely induced. Interestingly, this may be at least partially due to high basal levels of IFN (notably IFN-λ) and ISG (notably OAS2) mRNAs compared with other cell types examined below, which would result in reporting of weak fold changes in mRNA levels compared with mock infected cells (**Fig S2**). To further investigate this very weak ISG induction, using cells from the same donors as the IFN/ISG mRNA quantification, we assessed the phosphorylation of STAT1, a transcription factor that is itself encoded by an ISG, which is primarily a key mediator of type I and type III IFN signaling. Upon infection, STAT1 is phosphorylated before complexing with STAT2 and IRF9 to form ISGF3, which translocates to the nucleus where it mediates the activation of ISG transcription (Stark and Darnell, 2012). Consistent with the weak activation of ISGs, there was no evidence of phosphorylation of STAT1, likely due to low levels or transient phosphorylation (**Fig 2C**). In addition, we did not detect PKR activation, as indicated by the absence of phosphorylated

PKR and eIF2α in SARS-CoV-2 infected cells, while PKR and eIF2α were clearly expressed (**Fig 2C**). We also assessed activation of the OAS-RNase L pathway during SARS-CoV-2 infection of cells from two of the same four donors. Since 28S and 18S ribosomal RNAs (rRNAs) are targeted for degradation by activated RNase L, we can evaluate 28S and 18S rRNA integrity using a Bioanalyzer as a readout for RNase L activation. The absence of any rRNA degradation in SARS-CoV-2 infected cells (**Fig 2E**) indicated that RNase L was not activated despite abundant RNase L protein expression (**Fig 2C**).

Next, we sought to examine host innate immune responses during infection of alveolar type 2 cells (AT2), a major target of SARS-CoV-2 infection in humans (Hou et al., 2020; Ng et al., 2016; Qian et al., 2013). Initially, we attempted infections in lung organoid cultures, however they were not sufficiently permissive to SARS-CoV-2. Thus, we employed induced pluripotent stem cell (iPSC)-derived iAT2 cells (SPC2 line), expressing tdTomato from the endogenous locus of surfactant protein-C (SFTPC), an AT2 cell specific marker (Jacob et al., 2019). As in nasal cells, virus replicated efficiently, reaching a titer of 10^6 PFU/ml by 48hpi (**Fig 3A**). Staining of cultures with an anti-N antibody showed that most of the iAT2 cells were infected, without obvious cytopathic effect (CPE) during infection (**Fig 3B**). Notably, SARS-CoV-2 infection of iAT2 cells was robust despite ACE2 expression being below the level of detection by immunoblotting (**Fig 3C**). We observed activation of the PKR pathway as indicated by both PKR and eIF2α phosphorylation by immunoblotting (**Fig 3C**). We extracted RNA from infected iAT2 cells for RT-qPCR analysis, verified these cells were replicating virus by quantifying genome RNA copies (**Fig S1B**), and assessed IFN/ISG induction. As with the nasal cells, we observed weak induction of IFN-β and IFN-λ mRNA from mock infected and infected cells (**Fig 3D**), while MDA5 (Roth-Cross et al., 2008) a dsRNA sensor in the pathway leading to IFN production during coronavirus expression, is not detected (**Fig 3C)**. We used the alphavirus Sindbis virus (SINV) as a positive

control, which we have previously shown induces robust activation of all dsRNA-induced pathways (Comar et al., 2019). Surprisingly, we observed greater increases in OAS2 and IFIT mRNA expression by SARS-CoV-2 compared with SINV (**Fig 3D**), but with minimal induction of IFIH1 mRNA or protein (MDA5) (**Fig 3C&D)**. However, we did not observe phosphorylation of STAT1 (**Fig 3C**), as in the nasal cells above. Additionally, we did not observe any degradation of rRNA in SARS-CoV-2 infected cells, and only slight degradation by SINV despite ample expression of RNase L (**Fig 3E**), suggesting minimal activation of RNase L in iAT2 cells in general.

SARS-CoV-2 replicates and induces innate immune responses in iPSC-derived cardiomyocytes. Since many COVID-19 patients experience cardiovascular symptoms and pathology (Lindner et al., 2020; Shi et al., 2020), we investigated SARS-CoV-2 infection of iPSC derived-cardiomyocytes (iCM). SARS-CoV-2 replicated robustly in these cells reaching titers of approximately 10^6 PFU/ml by 48hpi (**Fig 4A**), similar to replication in nasal and iAT2 cells. Cells were stained with an antibody against cardiac troponin-T (cTnT) as a marker for cardiomyocytes, and an antibody against the viral N protein to identify infected cells (**Fig 4B**). In addition, we detected clear cytopathic effect (CPE), in iCM, which differed from infected nasal and iAT2 cells. This CPE included syncytia resulting from cell-to-cell fusion, which is typical of coronaviruses and a result of intracellular cleavage of the viral spike protein by the host enzyme furin (Belouzard et al., 2009; de Haan et al., 2004; Gombold et al., 1993; Qiu et al., 2006; Yamada and Liu, 2009). Interestingly, while we observed detectable ACE2 protein expression in mock infected cells in two independent experiments, we observed loss of ACE2 expression upon SARS-CoV-2 infection, consistent with a recent study (Sharma et al., 2020) (**Fig 4C**)**.** We extracted RNA from mock infected cells and cells infected with SARS-CoV-2 or SINV, verified that virus was replicating by quantifying viral genome in intracellular RNA (**Fig S1C**), and quantified expression of mRNAs for IFNs and select ISGs. We found low levels of IFN/ISGs transcript in iCM similar to the nasal and iAT2 cells (**Fig D**), perhaps due to the undetectable levels of MDA5 and MAVS protein expression

in these cells (**Fig 4C**). SINV also induced host mRNAs weakly, with the exception of IFN-λ, in these cells (**Fig 4D**). We observed no degradation of rRNA, suggesting an absence of RNase L activation in iCM with SARS-CoV-2 or SINV (**Fig 4E**), despite clear infection with either virus (**Fig S1C**). This was not surprising as there was no RNase L detectable by immunoblot in these cells (**Fig 4C**). Finally, as in iAT2 cells, we observed phosphorylation of PKR and eIF2α, indicating that the PKR antiviral pathway is activated (**Fig 4C**).

SARS-CoV-2 replicates in respiratory epithelial cell lines and induces dsRNA responsive pathways.

We aimed to further characterize the relationship between SARS-CoV-2 and dsRNA-induced host response pathways, which were activated to variable levels in the different primary and iPSC derived cells evaluated. We chose two respiratory epithelium-derived human cell lines, A549 and Calu-3, both of which are immune competent and have been used for studies of SARS-CoV (Blanco-Melo et al., 2020) and MERS-CoV (Comar et al., 2019; Thornbrough et al., 2016). A549 cells were not permissive to SARS-CoV-2, which correlated with undetectable levels of the SARS-CoV-2 receptor ACE2 (**Fig S3**)**.** Therefore, we generated A549 cells expressing the ACE2 receptor ($A549^{ACE2}$) by lentiviral transduction, and used two single cell clones, C44 and C34, for all experiments (**Fig S3**)**.** Both $A549^{ACE2}$ clones express high levels of ACE2 greater than the endogenously expressed ACE2 in Calu-3 cells (**Fig S3**) and in the primary cells discussed above (**Fig 2-4**).

We performed single step growth curves to measure replication of SARS-CoV-2 over the course of one infectious cycle in $A549^{ACE2}$ cells, simian Vero-E6 cells, which are commonly used to prepare SARS-CoV-2 stocks, and Calu-3 cells (clone HTB-55). SARS-CoV-2 replicated robustly in $A549^{ACE2}$ and Vero-E6 cells (**Fig 5A**) but in comparison viral yields were lower in Calu-3 cells (**Fig 5B**). Since Calu-3 cells also support MERS-CoV infection, we compared SARS-CoV-2

234 replication to that of MERS-CoV (WT) and MERS-CoV-ΔNS4ab, a mutant deleted in host cell
235 antagonists NS4a, a dsRNA-binding protein, and NS4b, a 2'5'-phosphodiesterase that prevents
236 RNase L activation and nuclear translocation of NF-κB (Canton et al., 2018; Comar et al., 2019).
237 Consistent with our previous work (Comar et al., 2019), MERS-CoV-ΔNS4ab reduced viral titers
238 from WT MERS-CoV levels, although they remained higher than SARS-CoV-2 titers (**Fig 5B**). To
239 further understand the replication of SARS-CoV-2, we stained A549, Calu-3 and Vero-E6 cells at
240 24 hpi with antibodies against viral N protein and viral dsRNA, including additional Calu-3 staining
241 at 48 hpi since replication kinetics are slower (**Fig 5C**). We observed cytopathic effect in all three
242 cell types, with N staining in the cytoplasm. Syncytia were observed in $A549^{ACE2}$ and Calu-3 cells,
243 but not in Vero cells (**Fig 5C**). We also observed viral dsRNA localized to perinuclear foci as we
244 and others have described during infection with other coronaviruses (Comar et al., 2019; Knoops
245 et al., 2008; Lundin et al., 2014; Rabouw et al., 2016).
246
247 We used RT-qPCR to quantify the induction of type I and type III IFNs and select ISGs at 24 and
248 48 hpi (**Fig 6A**), as well as the intracellular viral genome copies to verify replication (**Fig 6B**) in
249 $A549^{ACE2}$ cells. Using SINV as a positive control, we found relatively low levels of both IFNβ and
250 IFNλ mRNA at 24 and 48 hpi by SARS-CoV-2, compared to SINV (**Fig 6A**). Notably, IFN induction
251 was greater than observed in the nasal, iAT2, or iCM cells, possibly due to lower basal levels of
252 IFNβ, but not IFNλ, mRNA in the $A549^{ACE2}$ cells, which allow for greater fold changes over mock
253 infected cells (**Fig S2**). As observed previously with SINV and MERS-CoV, SARS-CoV-2 induced
254 more IFNλ than IFNβ, typical of A549 cells (Comar et al., 2019). Levels of ISG mRNAs were
255 variable, with SARS-CoV-2 inducing moderate levels of OAS2 and IFIT1 mRNAs, but only late in
256 infection (48 hpi), similar to those induced by SINV at 24 hpi **(Fig 6A**). We observed minimal
257 effects on mRNA levels of IFIH1 and the cytokine CXCL8 at both timepoints (**Fig 6A**).
258 Furthermore, we did not detect any STAT1 phosphorylation at 24 hpi (**Fig 6C**), which correlates

with weak ISG expression, suggesting defective IFN signaling downstream of IFN production. The data shown in Fig 6 were derived from A549^{ACE2} clone C44; similar data were obtained for a second clone, C33 **(Fig S4)**.

We evaluated IFN/ISG responses in Calu-3 cells, which provided a second lung-derived cell line that additionally supports both SARS-CoV-2 and MERS-CoV infection, allowing us to compare host responses between the two lethal CoVs. We compared SARS-CoV-2 responses to both WT MERS-CoV and mutant MERS-CoV-ΔNS4ab (**Fig 7A**). Although we observed reduced MERS-CoV-ΔNS4ab infectious virus production compared with WT MERS-CoV (**Fig 5B**)**,** we detected similar intracellular viral genome levels of all three viruses (**Fig 7B**). We found previously that MERS-CoV-ΔNS4ab induces higher levels of IFNs and ISGs compared to WT MERS-CoV, and also activates RNase L and PKR (Comar et al., 2019). Herein, in Calu-3 cells, we observed greater SARS-CoV-2 induction of IFN mRNAs as compared to A549^{ACE2} cells (**Fig 6A&S4B**). Interestingly, SARS-CoV-2 induced higher IFN mRNA levels than WT MERS-CoV at 24 and 48 hpi, which more closely resemble those induced by the IFN antagonist-deficient mutant MERS-CoV-ΔNS4ab by 48hpi (**Fig 7A**). Similarly, SARS-CoV-2 generally induced more ISG mRNA than WT MERS-CoV, and even more OAS2 mRNA than MERS-ΔNS4ab (**Fig 7A**)**.** Induction of CXCL8 was weak for all viruses (**Fig 7A**). Notably, SARS-CoV-2 induced ISG mRNAs in Calu-3 (24hpi) without the delay observed in A549^{ACE2} cells. Consistent with earlier ISG mRNA induction during infection, SARS-CoV-2 infection promotes phosphorylation of STAT1 in Calu-3 cells (**Fig 7C**) as recently reported (Lokugamage et al., 2020). SARS-CoV-2 induction of pSTAT1 as well as rapid IFIT1 and OAS2 mRNA induction suggests a similar host response to SARS-CoV-2 as that observed during mutant MERS-CoV-ΔNS4ab infection, and not that of WT MERS-CoV infection.

SARS-CoV-2 infection activates RNase L and PKR. We assessed activation of the RNase L pathway by analyzing intracellular rRNA from infected cells for RNA integrity, as described above.

We found that SARS-CoV-2 promotes rRNA degradation minimally at 24 hpi and more clearly at 48 hpi in A549^{ACE2}, using SINV as a positive control (**Fig 8A**). Evaluation of RNase L activation in SARS-CoV-2, WT MERS-CoV, and MERS-CoV-ΔNS4ab infected Calu-3 cells showed SARS-CoV-2 activation of RNase L to a similar extent as MERS-CoV-ΔNS4ab, which lacks both a dsRNA binding protein and a RNase L-specific antagonist (Comar et al., 2019; Siu et al., 2014) (**Fig 8B**). In contrast, as we previously reported, WT MERS-CoV failed to activate RNase L (Comar et al., 2019; Thornbrough et al., 2016) (**Fig 8B**). We also observed activation of PKR as indicated by phosphorylation of PKR and downstream eIF2α, in both A549^{ACE2} cells (**Fig 8C**) and Calu-3 cells (**Fig 8D**) infected with SARS-CoV-2. In Calu-3 cells, SARS-CoV-2 induced PKR phosphorylation to a similar extent as MERS-CoV-ΔNS4ab, while WT MERS-CoV failed to induce a response**.** These data are consistent with IFN/ISG induction data described above, suggesting that SARS-CoV-2 may not antagonize dsRNA pathways as efficiently as MERS-CoV, but instead induces host responses similar to those observed during MERS-CoV-ΔNS4ab infection.

The A549^{ACE2} cells were valuable in that they provided a system with intact innate immune responses that was also amenable to CRISPR-Cas9 engineering. Thus, we used the A549^{ACE2} cells to construct additional cell lines with targeted deletions of *MAVS*, *RNASEL*, or *PKR*, as we have done previously for parental A549 cells (Li et al., 2017; Li et al., 2016). We could then use these cells to determine whether activation of IFN, RNase L, and/or PKR resulted in attenuation of SARS-CoV-2 replication (Li et al., 2017; Li et al., 2016). We validated the knockout (KO) A549^{ACE2} cell lines by western blot (**Fig 9A**) and compared replication of SARS-CoV-2 in *MAVS* KO, *RNASEL* KO and *PKR* KO cells with levels in WT A549^{ACE2} cells (**Fig 9B**). Interestingly, there was little effect on SARS-CoV-2 replication with MAVS or PKR expression absent. In *RNASEL* KO cells at 48 hpi, virus replication was two- to four-fold higher compared to WT A549^{ACE2} cells **(Fig 9B**). While the difference in replication between *RNASEL* KO and WT was not extensive, it

was statistically significant in three independent experiments. Additionally, infected *RNASEL* KO cells exhibited strikingly more CPE as compared with WT, *PKR* KO, or *MAVS* KO cells, as demonstrated by crystal violet-staining of infected cells (**Fig 9C**). We also assessed rRNA degradation and, as expected, found that rRNA remained intact in the *RNASEL* KO A549^{ACE2} cells, which further validated these cells. However, rRNA was degraded in *PKR* or *MAVS* KO cells, indicating RNase L activation in both of these cell types (**Fig 9D**). These data are consistent with our previous findings that activation of the RNase L pathway does not depend on MAVS signaling in A549 cells infected with SINV or Zika virus (ZIKV) (Li et al., 2019; Whelan et al., 2019). RNase L activation instead occurs in parallel with IFN production (**Fig 1**), and is likely dependent on basal levels of OAS gene expression (Birdwell et al., 2016).

Discussion

SARS-CoV-2 is the causative agent of the severe acute respiratory, COVID-19. SARS-CoV-2 infection begins in the ciliated cells of the nasal epithelium and spreads to the lower respiratory tract, possibly by aspiration of infectious nasal secretions, infecting alveolar type 2 (AT2) cells and causing acute respiratory distress syndrome (ARDS) (Hou et al., 2020). Despite this typical axis of infection, many infected individuals exhibit symptoms and pathology in other organ systems, including the cardiovascular system (Puelles et al., 2020; Shi et al., 2020). Here, we present data expanding our understanding of cellular responses from each one of these critical areas. We focused on understanding the early host-viral interactions that trigger activation of the dsRNA-sensing pathways, including the RNase L, PKR, and type I and III IFN pathways. We evaluated responses to SARS-CoV-2 infection in primary nasal epithelia-derived upper airway cells and iPSC-derived type II airway (iAT2) cells, which represent major sites of infection during COVID-19 disease, as well as iPSC-derived cardiomyocytes (iCM), another likely target of infection (Sharma et al., 2020). To complement these studies, we used two lung derived

transformed cell lines, Calu-3 cells and two different A549^{ACE2} clones, to more mechanistically dissect activation and antagonism of these pathways by SARS-CoV-2. We found that the extent of IFN induction and signaling is variable among the primary cell types and cell lines used, but is consistently only poorly induced. Interestingly, we show that SARS-CoV-2 infection results in more IFN signaling (phosphorylation of STAT1 and IFN/ISG expression) when compared to MERS-CoV in Calu-3 cells. We also found that SARS-CoV-2 activates RNase L and PKR in both cell lines used and PKR in iAT2 cells and iCM, but not in primary nasal cells. Using KO cell lines, we demonstrate that RNase L expression significantly impacts SARS-CoV-2 viral titers and CPE observed during infection. These data suggest that while SARS-CoV-2 is generally a weak activator of dsRNA-induced responses in cells of the respiratory and cardiovascular systems, SARS-CoV-2 is less adept at antagonizing host responses than MERS-CoV.

Nasal cells are the initial replication site of SARS-CoV-2 and MERS-CoV. In quantifying virus replication in infected nasal cell culture, we found that SARS-CoV-2 replicates to higher titer than MERS-CoV, and the time period for shedding of virus is much longer (**Fig 2A**). We suggest that this longer period of replication in nasal cells and stronger immune responses in Calu-3 cells may in part explain why SARS-CoV-2 is less virulent, yet more contagious than MERS-CoV. Indeed for SARS-CoV-2, R_0=5.7 (Sanche et al., 2020) while for MERS-CoV, (R_0=0.45)(Oh et al., 2016).

Infection of all three primary cell types – nasal cells, iAT2 cells, and iCM – resulted in high levels of SARS-CoV-2 replication, while only cardiomyocytes exhibited obvious CPE (**Figs 2-4**). It was easily observed with syncytia formation in both lines, but the kinetics of viral spread were slower in Calu-3 (**Fig 5**). IFA staining with viral dsRNA-specific antibody (J2) showed SARS-CoV-2 dsRNA localized to perinuclear areas in A549^{ACE2} and Calu-3 cells, which is typical of coronavirus infection (**Fig 5**). The protein expression level of the SARS-CoV-2 host receptor ACE2 (Lu et al., 2020; Wan et al., 2020; Zhou et al., 2020) in primary cells and Calu-3 cells was either low or

undetectable, indicating that high levels of receptor are not necessary for productive infection (**Fig 2-4&S3**). This is similar to previous observations in the murine coronavirus (MHV) system where viral receptor CEACAM1a is very weakly expressed in the mouse brain, a major site of infection, and particularly in neurons, the most frequently infected cells, as measured by RT-qPCR for mRNA and antibody staining for protein (Bender et al., 2010).

The canonical IFN production and signaling pathways activated by the sensing of dsRNA, an obligate intermediate in viral genome replication and mRNA transcription, provide a crucial early antiviral response (**Fig 1**). The role of IFN responses during coronavirus infection is complex and at times contradictory. For example, SARS-CoV induces poor IFN signaling during early infection in mice, and treatment with IFN improves outcome. However, IFN production later in infection has a pathogenic effect (Channappanavar and Perlman, 2017). Similarly, weak IFN responses have been observed during initial stages of SARS-CoV-2 infection, but IFN produced later may contribute to the strong inflammatory responses and resulting immunopathology observed during SARS-CoV-2 infection cytokine storms (Giamarellos-Bourboulis et al., 2020; Hadjadj et al., 2020). Furthermore, murine coronavirus (MHV) induces minimal levels of IFN in cell culture and *in vivo*, yet IFNα/β receptor (IFNAR) KO mice lacking type I IFN signaling responses experience ectopic virus spread and rapid death (Roth-Cross et al., 2008).

While IFNs may contribute to pathogenesis later on in infection, coronaviruses, including the lethal human viruses, often prevent these responses early on during infection in both animal models and humans (Arabi et al., 2017; Channappanavar et al., 2016; Channappanavar et al., 2019). Antagonism of dsRNA-induced antiviral pathways has been well characterized for lineage a betacoronaviruses (subgenera embeco; for example, murine coronavirus MHV) (Zhao et al., 2012) and lineage c betacoronaviruses (merbeco; MERS-CoV and other related bat viruses) (Comar et al., 2019), however there is less known about lineage b (sarbeco) betacoronaviruses,

including SARS-CoV (2002) and SARS-CoV-2. A recent report described a cohort of COVID-19 patients with impaired IFN and innate immune responses that correlated with enhanced disease severity, suggesting that subversion of these host responses is important for severe SARS-CoV-2-mediated clinical outcomes (Hadjadj et al., 2020). Thus, it is important to understand the basic biology of SARS-CoV-2 interaction with the host innate immune system.

We and others have previously found that both MHV (lineage a) and MERS-CoV (lineage c) betacoronaviruses induce only minimal type I and type III IFNs, and fail to activate RNase L or PKR pathways (Rabouw et al., 2016; Thornbrough et al., 2016; Ye et al., 2007; Zhao et al., 2012; Zhao et al., 2011). We found that SARS-CoV-2, like other betacoronaviruses, induced limited amounts of type I and type III IFN mRNAs, although this was somewhat variable among the cell types examined. Using SINV as a control for robust activation of IFN, we detected low levels of type I and type III IFN mRNA in nasal cell, iAT2 cells, and iCM (**Fig 2-4**). However, we observed higher levels of OAS2, an ISG, relative to SINV in iAT2 cells (**Fig 3D**). As we have observed among murine cells, we saw vastly different levels of basal expression of both IFN and ISG mRNAs among the cell types infected (**Fig S2**) (Li and Weiss, 2016; Zhao et al., 2013; Zhao et al., 2011). It is understood that higher basal levels of innate immune response mRNAs typically result in a lower threshold for activation of corresponding responses. Interestingly, we observed significantly higher basal levels, especially IFNλ, in (uninfected) nasal cells as compared to iAT2 cells and iCM (**Fig S2A**). As major barrier cells, we speculate that this may be important for protection as these cells are more exposed to infectious agents in the environment. Indeed, it is well documented that type III IFNs serve as an added defense for epithelial cells, which may perhaps explain some of the differences observed in basal gene expression between nasal cells and iCM (Ank et al., 2008; Forero et al., 2019; Galani et al., 2017). As previously reported in heart tissue, the iCM expressed undetectable levels of both MAVS and RNase L, (Uhlén et al., 2015; Zhou et al., 1997), which is possibly to protect the heart from excessive inflammation.

In A549^{ACE2} cells, SARS-CoV-2 induced low levels of IFNλ and IFNβ mRNAs and somewhat higher ISG mRNA by 48 hpi, as compared with SINV (**Fig 6A**). We observed greater increases in IFN induction in Calu-3 compared to A549^{ACE2} (**Fig 7A**), which may be at least partially due to higher basal levels of IFNs in the Calu-3 cells (**Fig S2**). Calu-3 cells were employed to directly compare the host response to SARS-CoV-2 infection with that of MERS-CoV and mutant MERS-CoV-ΔNS4ab, which lacks the NS4a and NS4b proteins that inhibit IFN production and signaling (Canton et al., 2018; Comar et al., 2019; Rabouw et al., 2016). In Calu-3 cells, SARS-CoV-2 induced more IFN mRNA than WT MERS-CoV, closer to the level of MERS-CoV-ΔNS4ab (**Fig 7A**). Furthermore, SARS-CoV-2 induced higher levels of ISG mRNAs than MERS-CoV and, in the case of OAS2, higher than MERS-CoV-ΔNS4ab as well. Consistent with this, in Calu-3 cells SARS-CoV-2 and MERS-CoV-ΔNS4ab, but not WT MERS-CoV, promoted STAT1 phosphorylation (**Fig 7C**), which leads to ISG transcription and antiviral responses. Overall, our results displayed a trend of relatively weak IFN responses induced by SARS-CoV-2 in airway epithelial cells with limited ISG induction, when compared with host responses to viruses from other families. Additionally, our data show that enhanced IFN/ISG responses in Calu-3 cells restrict virus production, while lower host responses in A549^{ACE2} cells correlate with higher viral titers (**Fig 5**). Considering how robust ACE2 expression appears dispensable for infection of some cell types (nasal, iAT2, Calu-3), these data also indicate that stronger innate immune responses may be more effective at restricting SARS-CoV-2 replication than low ACE2 expression level.

We found that SARS-CoV-2 was unable to prevent activation of RNase L and PKR, although to different extents among the cell types, unlike two other betacoronaviruses, MHV and MERS-CoV, which shut down these pathways (Comar et al., 2019; Ye et al., 2007; Zhao et al., 2012). We

observed PKR activation as indicated by phosphorylation of PKR and eIF2α in SARS-CoV-2 infected iAT2 (**Fig 3C**) and iCM (one/two experiments) (**Fig 4C**), but not in nasal cells (**Fig 2C**). However, we did not detect rRNA degradation indicative of RNase L activation in these cell types (**Fig 2E, 3E, 4E**). Activation of both RNase L and PKR were observed in A549^{ACE2} and Calu-3 cells during infection with SARS-CoV-2 (**Fig 8**). In Calu-3 cells, this contrasted MERS-CoV and was more similar to MERS-CoV-ΔNS4ab. Previous studies have shown that MERS-CoV NS4a restricts phosphorylation of PKR by binding dsRNA, reducing its accessibility to PKR (Comar et al., 2019; Rabouw et al., 2016). Additionally, MERS-CoV NS4b, a 2'-5' phosphodiesterase, prevents RNase L activation by degrading 2-5A, the small molecular activator of RNase L (Comar et al., 2019; Thornbrough et al., 2016). Current understanding of SARS-CoV-2 protein function infers an absence of these types of protein antagonists, therefore it is not surprising that both of these pathways are activated during infection of both A549^{ACE2} and Calu-3. Indeed, MERS-CoV-ΔNS4ab attenuation compared to WT MERS-CoV, as well as lower SARS-CoV-2 titers than those of MERS-CoV (**Fig 5B**), may be at least in part due to RNase L and PKR activation in addition to IFN/ISG induction in Calu-3 cells.

Consistent with previous studies involving the alphavirus SINV, we found that neither MERS-CoV-ΔNS4ab nor SARS-CoV-2 activated dsRNA-induced pathway responses as robustly as SINV (Li et al., 2016; Whelan et al.). We suggest this may be due to CoV antagonists encoded by the nsp genes of the replicase locus. For CoVs, conserved replicase proteins have been identified as important modulators of innate immune invasion, including nsp1, nsp14, nsp15, and nsp16 (Gordon et al., 2020; Kindler et al., 2017; Perlman and Netland, 2009; Volk et al., 2020). Most notably, nsp15 encodes an endoribonuclease (EndoU) that has been shown in the MHV system to restrict dsRNA accumulation and thus limit activation of both RNase L and PKR (Deng et al., 2017; Kindler et al., 2017). A very recent report using a replicon system concludes that SARS-

CoV-2 nsp1 and nsp6 are more effective antagonists than the homologous proteins of SARS-CoV or MERS-CoV (Xia et al., 2020). Nevertheless, increased, albeit modest, replication and enhanced cell death in SARS-CoV-2 infected *RNASEL* KO cells indicates that this pathway is activated and indeed restricts replication and downstream cell death caused by SARS-CoV-2 infection (**Fig 9B&C**). In contrast, we found that *PKR* KO had no effect on viral titer. This is consistent with our previous finding that MERS-CoV infection inhibits host protein synthesis independent of PKR, so that PKR phosphorylation during MERS-CoV-ΔNS4ab infection did not lead to further reduction (Comar et al., 2019). Finally, KO of *MAVS* and the consequent loss of IFN production had no significant effect on viral titer or cell death. This is similar to our previous findings demonstrating that RNase L activation can occur independent of virus-induced IFN production with other viruses (SINV) (Li et al., 2019) and ZIKV (Whelan et al., 2019) in A549 cells, as well as for MHV in murine bone marrow-derived macrophages (Birdwell et al., 2016). This underscores the importance of the RNase L and PKR antiviral pathways, which can be activated early in infection upon concurrent dsRNA sensing by OAS, PKR, and MDA5 receptors before IFN is produced. Alternatively, these pathways can be activated in cells infected by virus that produce low levels of IFN only late in infection, as we observe here with SARS-CoV-2. Further studies are required to determine whether activation of PKR or RNase L during SARS-CoV-2 infection results in functional outcomes characteristic of these pathways, including inhibition of protein synthesis, induction of apoptosis, cleavage of viral RNA, or induction of inflammatory responses (**Fig 1**). Interestingly, we observed possible RNase L-induced apoptosis in the SARS-CoV-2 infected A549^{ACE2} WT, *MAVS* KO, and *PKR* KO cells, when compared with mock infected counterparts (**Fig 9C**). However, *RNASEL* KO cells displayed the most cell death among the four cell lines, suggesting that virus-induced cell lysis in the *RNASEL* KO cells where viral titers are highest (**Fig 9B**) is more detrimental to cells than RNase L-induced programmed cell death.

There have been few studies on the interaction of the prototype lineage b betacoronavirus, SARS-CoV (2002), with these dsRNA-induced pathways, with most of the studies describing IFN antagonists involving overexpressed protein and overexpressed artificial IFN promoter sequences for readouts. In this way, it was reported that Orf3b, Orf6 and nucleocapsid (N) protein are antagonists of IFN production and signaling (Kopecky-Bromberg et al., 2007). The role of the SARS-CoV Orf6 encoded protein as an IFN antagonist was subsequently confirmed in the context of virus infection, and further defined as Orf6 binding to host nuclear importins to prevent translocation of STAT1 and other transcription factors, thus impairing induction of antiviral ISGs (Frieman et al., 2007; Sims et al., 2013). SARS-CoV-2 encodes an Orf6 protein with 69% homology to SARS-CoV Orf6 (Lokugamage et al., 2020), as well as a similar, truncated Orf3b which has been shown by overexpression studies to antagonize IFN mRNA transcription (Konno et al., 2020). Strikingly, recent work using overexpression systems of SARS-CoV-2 Orf6 found that it interacts with host KPNA2, the same target of the SARS-CoV Orf6 protein (Xia et al., 2020). However, further investigation is required to determine how similarly the proteins from the two viruses function in the context of infection.

We have shown that SARS-CoV-2 activates dsRNA-induced innate immune responses to levels similar to those of a MERS-CoV mutant lacking two accessory proteins that antagonize these pathways, which highlights the distinctions among coronaviruses in interacting with these pathways. However, like MERS-CoV and MHV, SARS-CoV-2 induces limited and late IFN/ISG responses, indicating that proteins antagonizing innate immune responses are likely encoded. Our future studies will focus on identifying specific innate immunity antagonists among lineage b betacoronavirus accessory proteins as well as conserved nsp proteins. The recent development of reverse genetics systems for SARS-CoV-2 (Hou et al., 2020; Thi Nhu Thao et al., 2020; Xie et al., 2020) will allow us to study these proteins during viral infection. This will provide a system complete with coronavirus-mediated alterations of cellular architecture typically nonexistent in

517 overexpression systems, which is critical to fully appreciate the functions of these proteins
518 (Knoops et al., 2008; Lundin et al., 2014; Sola et al., 2015). Our future studies will reveal key
519 features of SARS-CoV-2 biology, as well as those of other currently circulating SARS-related
520 viruses with pandemic potential.
521
522 **Materials and Methods**
523 **Viruses.** SARS-CoV-2 (USA-WA1/2020 strain) was obtained from BEI and propagated in Vero-
524 E6 cells. The genome RNA was sequenced was found to be identical to GenBank: MN985325.1**.**
525 Recombinant MERS-CoV and MERS-CoV-ΔNS4ab were described previously (Comar et al.,
526 2019) and were propagated in Vero-CCL81 cells. Sindbis virus Girdwood (G100) was obtained
527 from Dr. Mark Heise, University of North Carolina, Chapel Hill, and was prepared as previously
528 described (Suthar et al., 2005). Sendai virus (SeV) strain Cantell (Basler et al., 2003) was
529 obtained from Dr. Carolina B. Lopez (University of Pennsylvania).
530
531 **Cell lines**. African green monkey kidney Vero cells (E6) or (CCL81) (obtained from ATCC) were
532 cultured in Dulbecco's modified Eagle's medium (DMEM; Gibco catalog no. 11965),
533 supplemented with 10% fetal bovine serum (FBS), 100 U/ml of penicillin, 100 µg/ml streptomycin,
534 50 µg/ml gentamicin, 1mM sodium pyruvate, and 10mM HEPES. Human A549 cells(Verified by
535 ATCC) were cultured in RPMI 1640 (Gibco catalog no. 11875) supplemented with 10% FBS, 100
536 U/ml of penicillin, and 100 µg/ml streptomycin. Human HEK 293T cells were cultured in DMEM
537 supplemented with 10% FBS and 1 mM sodium pyruvate. Human Calu-3 cells (clone HTB-55)
538 were cultured in MEM supplemented with 20% FBS without antibiotics.
539
540
541 **Primary cell cultures**
542

Human sinonasal air liquid interface (ALI) cultures. Sinonasal mucosal specimens were acquired from residual clinical material obtained during sinonasal surgery subsequent to approval fromm The University of Pennsylvania Institutional Review Board. ALI cultures were established from enzymatically dissociated human sinonasal epithelial cells (HSEC) as previously described (Lee et al., 2017; Lee et al., 2014) and grown to confluence with bronchial epithelial basal medium (BEBM; Lonza, Alpharetta, GA) supplemented with BEGM Singlequots (Lonza), 100 U/ml penicillin and 0.25 µg /ml amphotericin B for 7 days. Cells were then trypsinized and seeded on porous polyester membranes (2-3× 10^4 cells per membrane) in cell culture inserts (Transwell-clear, diameter 12 mm, 0.4 µm pores; Corning, Acton, MA). Five days later the culture medium was removed from the upper compartment and the epithelium was allowed to differentiate by using the differentiation medium consisting of 1:1 DMEM (Invitrogen, Grand Island, NY) and BEBM (Lonza), supplemented with BEGM Singlequots (Lonza) with 0.1 nM retinoic acid (Sigma-Aldrich), 100 UI/ml penicillin, 0.25 µg /ml amphotericin B and 2% Nu serum (Corning) in the basal compartment. Cultures were fed every three days for 6 weeks prior to infection with SARS-CoV-2. The day prior infection, the cells were fed and the apical side of the cultures were washed with 100µl of warm PBS X 3.

Alveolar organoids and 2D cultures. iPSC (SPC2 iPSC line, clone SPC2-ST-B2, Boston University) derived alveolar epithelial type 2 cells (iAT2s) were differentiated and maintained as alveolospheres embedded in 3D Matrigel in CK+DCI media, as previously described (Jacob et al., 2019). iAT2s were passaged approximately every two weeks by dissociation into single cells via the sequential application of dispase (2mg/ml, Thermo Fisher Scientific, 17105-04) for 1h at 37°C and 0.05% trypsin (Invitrogen, 25300054) for 15min at 37°C and re-plated at a density of 400 cells/µl of Matrigel (Corning, 356231) in CK+DCI media supplemented with ROCK inhibitor for the first 48h, as previously described (Jacob et al., 2019). For generation of 2D alveolar cells for viral infection, alveolospheres were dispersed into single cells, then plated on pre-coated 1/30

Matrigel plates at a cell density of 125,000 cells/cm2 using CK+DCI media with ROCK inhibitor for the first 48h and then the medium was changed to CK+DCI media at day 3 and infected with SARS-CoV-2 virus.

Cardiomyocytes. Experiments involving the use of human iPSCs were approved by the University of Pennsylvania Embryonic Stem Cell Research Oversight Committee. The iPSC line (PENN123i-SV20) used for cardiomyocyte generation was derived by the UPenn iPSC core as previously described (Pashos et al., 2017; Yang et al., 2015). This line has been deposited at the WiCell repository (Wicell.org). iPSCs were maintained on Geltrex (Thermofisher Scientific)-coated plates in iPS-Brew XF (Miltenyi Biotec) media at 37°C in 5% CO_2/5% O_2/90% air humidified atmosphere. Cells were passaged every 5-7 days using Stem-MACS Passaging Solution (Miltenyi Biotec). Differentiation of SV20 into cardiomyocytes (iCMs) was performed using previously described protocols (Laflamme et al., 2007; Palpant et al., 2017). In general, iCMs were >95% positive for cardiac Troponin T staining by FACS. Day 18-25 differentiated cells were replated and used for viral infection experiments.

Generation of A549^{ACE2} cells. A549^{ACE2} cells were constructed by lentivirus transduction of *hACE2*. The plasmid encoding the cDNA of *hACE2* was purchased from Addgene. The cDNA was amplified using forward primer 5′-ACTCTAGAATGTCAAGCTCTTCCTGGCTCCTTC-3′ and reverse primer 5′-TTGTCGACTTACGTAGAATCGAGACCGAGGAGAGGGTTAGGGATAGGCTTACCAAAGGAG GTCTGAAC ′-3(Contained V5 tag sequences). The fragment containing hACE2-V5 was digested by the XbaI and SalI restriction enzymes from the hACE2 cDNA and was cloned into pLenti-GFP (Addgene) in place of green fluorescent protein (GFP), generating pLenti-hACE2-V5. The resulting plasmids were packaged in lentiviruses pseudotyped with vesicular stomatitis virus glycoprotein G (VSV-G) to establish the gene knock-in cells. Supernatants harvested 48 hours

595 post-transfection were used for transduction into A549 cells. Forty-eight hours after transduction,
596 cells were subjected to hygromycin (1 mg/ml) selection for 3 days and single-cell cloned. Clones
597 were screened for ACE2 expression and susceptibility to SARS-CoV-2 replication.
598
599 **CRISPR/Cas9 engineered cells**. *RNASEL*, *PKR* and *MAVS* KO A549^{ACE2} cells were constructed
600 using the same Lenti-CRISPR system and guide RNA sequences as previously described (Li et
601 al., 2017; Li et al., 2016).
602 **Viral growth kinetics**. The nasal ALI cultures were apically infected with SARS-CoV-2(MOI=5),
603 MERS-CoV(MOI=5)**.** Briefly, viral stocks were diluted in nasal cell media, 50μl was added to each
604 well, the cells were incubated in 37°C for one hour, then the virus was removed and the cells were
605 wash three times with 200μl of PBS. For viral growth curves, at indicated time points, 200 μl of
606 PBS was added to the apical surface, collected 5 minutes later and frozen for subsequent analysis
607 of shed virus by plaque assay. The inserts were transferred to new 24-well plates with fresh media
608 after each collection. For iAT2 or iCM, cells were plated in 12 or 6-well plates, 4X10^5 cells (iAT2)
609 or 6.25X10^5 cells per well (iCM), cells were infected with SARS-CoV-2 at MOI=5 (iAT2) or
610 MOI=1(iCM). At 6, 24, 48 hours postinfection, 200μl of supernatant were harvested and stored
611 in -80°C for infectious virus titration. For infections, Cell lines were plated in 12-well plates, A549
612 and Vero-E6 at 5X10^5 cells per well) and Calu-3 at 3X10^5 cells per well). Viruses were diluted in
613 serum-free RPMI (A549 infections) or serum-free DMEM (Vero infections) or serum-free MEM
614 (Calu-3 infections) and added to cells for absorption for 1 hour at 37°C. Cells were washed three
615 times with PBS and fed with DMEM or RPMI +2% FBS for Vero and RPMI infections, respectively,
616 or 4% FBS in MEM for Calu-3 infections (Thornbrough et al., 2016). For virus titration 200 μl of
617 supernatant was collected at the times indicated and stored at -80°C for plaque assay on Vero-
618 E6 (SARS-CoV-2) or Vero-CCL81 (MERS-CoV) cells as previously described (Scobey et al.,
619 2013).

620

621 **Plaque assay.** Briefly virus supernatant was 10-fold serial diluted and inoculum was absorbed on
622 Vero cells for 1 hour at 37°C. Inoculum was overlaid with DMEM plus agarose (either 0.7% or
623 0.1%) and incubated for 3 days at 37°C. Cells were fixed with 4% paraformaldehyde and stained
624 with 1% crystal violet for counting plaques. All infections and virus manipulations were conducted
625 in a biosafety level 3 (BSL-3) laboratory using appropriate and approved personal protective
626 equipment and protocols.

627

628 **Immunofluorescent staining.** For nasal ALI culture, following 48 hours of infection, the cultures
629 were fixed in 4% paraformaldehyde at room temperature for 30 minutes. The transwell supports
630 were washed 3 times with PBS prior to excision of the membrane containing the cells. The cells
631 were permeabilized with 0.2% Triton X-100 in PBS and then immersed in PBS with 0.2% Triton
632 X-100, 10% normal donkey serum, and 1% BSA for 60 min at room temperature. Primary
633 antibody incubation was incubated overnight at 4 ºC (Type IV tubulin, Abcam ab11315, rabbit anti
634 SARS-CoV-2 Nucleocapsid protein, GeneTex, Irvine, CA). Visualization was carried out with Alex
635 Fluor®-conjugated donkey anti-mouse or anti-rabbit IgGs(Thermo-Fisher) (1:1000; 60 min
636 incubation at room temperature). Confocal images were acquired with an Olympus Fluoview
637 System (Z-axis step 0.5µm; sequential scanning). For iAT2, the cell monolayer was fixed using
638 4% paraformaldehyde (PFA) for 30min, 1X PBS was used to removed PFA and proceed with
639 antibody staining. Fixed cells were treated with a blocking solution containing 0.1% Triton X-100
640 and 5% donkey serum in 1X PBS for 30min. Immunostaining was performed for SARS-CoV-2
641 nucleocapsid protein expression using the SARS-CoV-2 nucleocapsid antibody at 1:1000 dilution
642 in blocking solution incubated for 30min. After washing primary antibody away, a secondary Alexa
643 fluor 488 donkey anti-rabbit IgG(H+L) antibody(Thermo-Fisher) was used at 1:400 dilution in
644 blocking solution and incubated for 30min. Secondary antibody was washed away with 1X PBS

and DAPI was used for nuclear staining at 2.5μg/ml. iCM were fixed in 4% paraformaldehyde and permeabilized with 0.1% Triton X-100 for 15min. Cells were blocked with 10% normal donkey serum (Sigma D9663) in 0.2% Tween 20 (Biorad 170-6531) for 1hr. Antibodies against cardiac troponin T (cTnT, Abcam ab8295; 1:100 mouse) and SARS-CoV-2 nucleocapsid were incubated with cells in blocking solution overnight at 4 °C. Donkey anti-mouse Alexa Fluor 647 (Invitrogen A31571) and Donkey anti-rabbit Alexa Fluor 488 (Invitrogen A21206) were diluted 1:250 in blocking solution and incubated with cells for 2hr at RT. Slides were mounted in Slowfade Gold anti-fade reagent with DAPI (Invitrogen S36939). Images were acquired with BZ-X710 all-in-one fluorescence microscope equipped with BZ-X Viewer software (Keyence Corporation). At the indicated times post-infection cells were fixed onto glass coverslips (Calu-3 coverslips were coated with rat tail collagen type-1: Cell Applications, Inc. Cat. # 122-20) with 4% paraformaldehyde for 30 minutes at room temperature. Cells were then washed three times with PBS and permeabilized for 10 minutes with PBS+0.1% Triton-X100. Cells were then blocked in PBS and 3% BSA for 30-60 minutes at room temperature. Primary antibodies were diluted in block buffer and incubated on a rocker at room temperature for one hour. Cells were washed three times with block buffer and then incubated rocking at room temperature for 60 minutes with secondary antibodies diluted in block buffer. Finally, cells were washed twice with block buffer and once with PBS, and nuclei stained with DAPI diluted in PBS (2ng/uL final concentration). SARS-CoV-2 nucleoprotein and dsRNA (J2,1:1000, Scions) were detected. Secondary antibodies were from Invitrogen: goat anti-mouse IgG AlexaFluor594 (A-11005) for J2 and goat anti-rabbit IgG AlexaFluor488 (A-11070) for nucleocapsid. Coverslips were mounted onto slides for analysis by widefield microscopy with Nikon Eclipse Ti2 using a Nikon 40x/0.95NA Plan APO objective and NikonDS-Qi1Mc-U3 12 bit camera. Images were processed using Fiji/Image J software.

Western immunoblotting. Cells were washed once with ice-cold PBS and lysates harvested at the indicated times post infection with lysis buffer (1% NP40, 2mM EDTA, 10% glycerol, 150mM NaCl, 50mM Tris HCl) supplemented with protease inhibitors (Roche – complete mini EDTA-free protease inhibitor) and phosphatase inhibitors (Roche – PhosStop easy pack). After 5 minutes lysates were harvested, incubated on ice for 20 minutes, centrifuged for 20 minutes at 4°C and supernatants mixed 3:1 with 4x Laemmli sample buffer. Samples were heated at 95°C for 5 minutes, then separated on 4-15% SDS-PAGE, and transferred to polyvinylidene difluoride (PVDF) membranes. Blots were blocked with 5% nonfat milk or 5% BSA and probed with antibodies (table below) diluted in the same block buffer. Primary antibodies were incubated overnight at 4°C or for 1 hour at room temperature. All secondary antibody incubation steps were done for 1 hour at room temperature. Blots were visualized using Thermo Scientific SuperSignal west chemiluminescent substrates (Cat #: 34095 or 34080). Blots were probed sequentially with antibodies and in between antibody treatments stripped using Thermo scientific Restore western blot stripping buffer (Cat #: 21059).

Primary Antibody	Antibody species	Blocking buffer	Dilution	Catalog number
p-PKR (phospho-T446) [E120]	rabbit	5% milk/TBST	1 : 1000	Abcam 32036
PKR (D7F7)	rabbit	5% milk/TBST	1:1000	Cell Signaling Technology 12297S
p-eif2α (S51)	rabbit	5% BSA/TBST	1:1000	Cell Signaling Technology 9721S
eif2α	rabbit	5% BSA/TBST	1:1000	Cell Signaling Technology 9722S
GAPDH (14C10)	rabbit	5% milk/TBST	1:2000	Cell Signaling Technology 2118S
SARS-CoV-2 N	rabbit	5% milk/TBST	1:2000	GTX135357 (Gentex)
MERS-CoV N	mouse	5% milk/TBST	1:2000	40068-MM10 (Sino Biological)
pSTAT1 (Tyr701)	rabbit	5% BSA/TBST	1:1000	Cell Signaling Technology 7649

STAT1	mouse	5% BSA/TBST	1:1000	Santa Cruz (C136): SC-464
ACE2	rabbit	5% milk/TBST	1:1000	Cell Signaling Technology 4355S
MAVS	rabbit	5% milk/TBST	1:1000	Cell Signaling Technology 24930S
V5	rabbit	5% milk/TBST	1:1000	Cell Signaling Technology 13202S
RNase L	mouse	5% milk/TBST	1:1000	gift from Dr. Robert Silverman (Cleveland Clinic)
MDA5	rabbit	5% milk/TBST	1:1000	Cell Signaling Technology 5321S
Secondary Antibody				
goat anti-rabbit IgG	HRP linked	same as primary	1:3000	Cell Signaling Technology 7074S
goat anti-mouse IgG	HRP linked	same as primary	1:3000	Cell Signaling Technology 7076S

Quantitative PCR (RT-qPCR).

A549, Calu-3, and iAT2 cells were lysed at indicated times post infection in RLT buffer and DNase-treated before total RNA was extracted using the RNeasy Plus Mini Kit (Qiagen). RNA from iCM and nasal cells was extracted using TRIzol-LS (Ambion), and DNase-treated using the DNA-*free*™ Kit (Invitrogen). RNA was reverse transcribed into cDNA with a High Capacity cDNA Reverse Transcriptase Kit (Applied Biosystems). cDNA was amplified using specific RT-qPCR primers (see Table below), iQ™ SYBR® Green Supermix (Bio-Rad), and the QuantStudio™ 3 PCR system (Thermo Fisher). Host gene expression displayed as fold change over mock-infected samples was generated by first normalizing cycle threshold (C_T) values to 18S rRNA to generate ΔC_T values (ΔC_T = C_T gene of interest - C_T 18S rRNA). Next, $\Delta(\Delta C_T)$ values were determined by subtracting the mock-infected ΔC_T values from the virus-infected samples. Technical triplicates were averaged and means displayed using the equation $2^{-\Delta(\Delta CT)}$. For basal expression levels, C_T values were normalized to 18S rRNA to generate ΔC_T values (ΔC_T = C_T gene of interest - C_T 18S rRNA), and displayed as $2^{-\Delta Ct}$. Basal expression levels were also calculated as fold change over $A549^{ACE2}$ clone 44 using the equation $2^{-\Delta(\Delta CT)}$. $\Delta(\Delta C_T)$ values were calculated by subtracting ΔC_T

values from each cell type from the ΔC_T value of $A549^{ACE2}$ clone 44. Absolute quantification of SARS-CoV-2 and MERS-CoV genomes was calculated using a standard curve generated from serially diluted known concentrations of a digested plasmid containing the region of interest. For SARS-CoV-2, construct pcDNA6B-nCoV-NSP12-FLAG encoding the RDRP gene (gift from Dr. George Stark, Cleveland Clinic) was digested with Xho1 and purified by Qiagen QIAquick PCR Purification Kit to be used as a standard in the RT-qPCR reaction. For MERS-CoV, cDNA MERS-D1 (Scobey et al., 2013) containing basepairs 12259–15470 of the MERS-CoV genome was digested with BglI and purified by Qiagen QIAquick PCR Purification Kit to be used as a standard in the RT-PCR reaction. Copy numbers were generated by standard curve analysis in the QuantStudio™ 3 software, and copy numbers per ug RNA were calculated based on the volume of cDNA used in the qPCR reaction, and concentration of RNA used to generated cDNA. Primer sequences are as follows:

	Forward primer (5' to 3')	Reverse primer (5' to 3')
IFNL1	CGCCTTGGAAGAGTCACTCA	GAAGCCTCAGGTCCCAATTC
OAS2	TTCTGCCTGCACCACTCTTCACGAC	GCCAGTCTTCAGAGCTGTGCCTTTG
IFIT1	5'-TGGTGACCTGGGGCAACTTT	AGGCCTTGGCCCGTTCATAA
IFNB	GTCAGAGTGGAAATCCTAAG	ACAGCATCTGCTGGTTGAAG
GAPDH	GCAAATTCCATGGCACCGT	TCGCCCCACTTGATTTTGG
IFIH1	GCACAGAGCGGTAGACCCTGCTT	AGGCCTTGGCCCGTTCATAA
CXCL8	GAGAGTGATTGAGAGTGGACCAC	CACAACCCTCTGCACCCAGTTT
18S rRNA	TTCGATGGTAGTCGCTGTGC	CTGCTGCCTTCCTTGAATGTGGTA
SARS-CoV-2 genome (nsp12/RdRp)	GGTAACTGGTATGATTTCG	CTGGTCAAGGTTAATATAGG

MERS-CoV genome (nsp7)	GCACATCTGTGGTTCTCCTCTCT	AAGCCCAGGCCCTACTATTAGC

715

716

717 **Analyses of RNase L-mediated rRNA degradation.** RNA was harvested with buffer RLT
718 (Qiagen RNeasy #74106) or Trizol-LS (Ambion) and analyzed on an RNA chip with an Agilent
719 Bioanalyzer using the Agilent RNA 6000 Nano Kit and its prescribed protocol as we have
720 described previously (Cat #: 5067-1511).

721

722 **Statistical analysis.** All statistical analyses and plotting of data were performed using GraphPad
723 Prism software (GraphPad Software, Inc., CA). SARS-CoV-2 and MERS-CoV replication trends
724 in nasal cells were analyzed by two-way ANOVA comparing averaged titers from all four donor
725 cells for each virus at each timepoint. MERS-CoV and MERS-CoV-ΔNS4ab viral replication and
726 primary cell RT-qPCR gene expression between SARS-CoV-2 and SINV were analyzed by paired
727 Student *t* test. RT-qPCR analysis in $A549^{ACE2}$ cells was analyzed by one-way ANOVA, comparing
728 SARS-CoV-2 at each timepoint to SINV. RT-qPCR analysis in Calu-3 cells was analyzed by two-
729 way ANOVA, comparing SARS-CoV-2 at each timepoint to MERS-CoV and MERS-CoV-ΔNS4ab.
730 SARS-CoV-2 replication in $A549^{ACE2}$ WT cells compared with $A549^{ACE2}$ KO cells was analyzed by
731 two-way ANOVA. Displayed significance is determined by p-value (P), where * = $P < 0.05$; ** = P
732 < 0.01; *** = $P < 0.001$; **** = $P < 0.0001$; ns = not significant.

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Declaration of Interests

The authors declare no competing interests.

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Figure Legends

Figure 1. Double-stranded RNA induced innate immune responses during SARS-CoV-2 infection. Coronavirus double-stranded RNA (dsRNA) is produced through replication and transcription and recognized by cytosolic OAS, MDA5, or PKR host receptors to activate innate immune pathways. MDA5 signals through MAVS, leading to type I and type III IFN production and release from the cell where it binds to cell surface receptors, which induces phosphorylation and heterodimerization of STAT1 and STAT2 that then prompt ISG transcription and cytokine responses. OASs produce 2'-5'-oligoadenylates (2-5A) that bind RNase L, leading to homodimerization and catalytic activation of RNase L, which cleaves host and viral ssRNA to trigger apoptosis and inflammation. PKR autophosphorylates before phosphorylating eIF2α, which leads to translational arrest, cell death, and inflammatory responses. Graphic was created with Biorender.com

Figure 2. Infection of nasal epithelia-derived cells by SARS-CoV-2 and MERS-CoV. Nasal cells were cultured in air-liquid trans-wells, and mock infected or infected with SARS-CoV-2 (MOI=5), MERS-CoV (MOI=5) , or Sendai Virus (SeV) apically at MOI=10. (A) At indicated times, apically released virus was collected and quantified by plaque assay on Vero-E6 cells. Values are means ± SD (error bars). Statistical significance (not displayed) was determined by two-way

ANOVA (*, $P < 0.05$). One experiment was performed using four separate donors. (B) At 48 hpi, nasal cells were fixed with 4% PFA and permeabilized. Expression of nucleocapsid (N) protein (red) of SARS-CoV-2 and MERS-CoV was detected with an anti-N antibody, and cilia (green) with an anti-type IV β-tubulin antibody by immunofluorescence assay (IFA). One representative image is shown from at least three independent experiments, with four donors for each virus infection shown. Scale bar = 100μm. (C) At 120 hpi, cells were lysed, and proteins were analyzed by immunoblotting with antibodies as indicated. One experiment using three separate donors was performed. (D) At 120 hpi, total RNA was harvested, and the mRNA expression level of *IFNB, IFNL1, OAS2, IFIT1, IFIH1, CXCL8* was quantified by RT-qPCR. Cycle threshold (C_T) values were normalized to 18S rRNA to generate ΔC_T values (ΔC_T = C_T gene of interest - C_T 18S rRNA). Fold change over mock values were calculated by subtracting mock infected ΔC_T values from virus infected ΔC_T values, displayed as $2^{-\Delta(\Delta Ct)}$. Technical replicates were averaged, the means for each replicate displayed, ± SD (error bars). One experiment was performed using three separate donor samples. (E) Total RNA was harvested from two donors at 120 hpi and rRNA integrity determined by Bioanalyzer. The position of 28S and 18S rRNA and indicated. Data shown are from one representative experiment of two independent experiments. (See also Figures S1A&S2).

Figure 3. Infection of iPSC-derived AT2 cells (iAT2) by SARS-CoV-2. iAT2 cells were mock infected or infected with SARS-CoV-2 at MOI=5 or SINV at MOI=1. (A) At indicated times, supernatants were collected and infectious virus was quantified by plaque assay on Vero-E6 cells. Values are means ± SD (error bars). Data shown are one representative experiment from at least three independent experiments. (B) At 48 hpi, cells were fixed with 4% PFA and permeabilized. Expression of nucleocapsid (N) protein (green) of SARS-CoV-2 and the expression of SFTPC promoter control tdTomato fluorescent protein (AT2 marker in red) was examined by IFA. Channels are merged with DAPI nuclear staining. Images shown are representative from at least

three independent experiments. Scale bar = 100μm. (C) At 48 hours post infection, cells were lysed and proteins were analyzed by immunoblotting with antibodies as indicated. Data shown are from one representative experiment of two independent experiments. (D) At 16 (SINV) or 48 (SARS-CoV-2) hpi, total RNA was harvested, and the mRNA expression level of *IFNB, IFNL1, OAS2, IFIT1, IFIH1, CXCL8* was quantified by RT-qPCR. C_T values were normalized to 18S rRNA to generate ΔC_T values (ΔC_T = C_T gene of interest - C_T 18S rRNA). Fold change over mock values were calculated by subtracting mock infected ΔC_T values from virus infected ΔC_T values, displayed as $2^{-\Delta(\Delta Ct)}$. Technical replicates were averaged, the means for each replicate displayed, ± SD (error bars). Statistical significance was determined by Student *t* test (*, P < 0.05; **, P < 0.01; ***, P < 0.001). Data shown are from one representative experiment of two independent experiments. (E) Total RNA was harvested at 16 (SINV) or 48 (SARS-CoV-2) hpi and rRNA integrity determined by Bioanalyzer. The position of 28S and 18S rRNA and indicated. Data shown are from one representative experiment of two independent experiments. (See also Figures S1B&S2).

Figure 4. Infection of iPSC-derived cardiomyocytes (iCM) by SARS-CoV-2. iCM were mock infected or infected at MOI=1 with SARS-CoV-2 or SINV. (A) At indicated times, supernatants were collected and virus quantified by plaque assay on Vero-E6 cells. Values are means ± SD (error bars). Data shown are one representative experiment from at least three independent experiments. (B) At 48 hpi, iCM were fixed with 4% PFA and permeabilized, the expression of SARS-CoV-2 N (green) of and of cTnT protein (cardiomyocyte marker, red) was examined by IFA. Channels are merged with DAPI nuclear staining. Images shown are representative from three independent experiments. Scale bar = 50μm. (C) At 16 (SINV) or 48 (SARS-CoV-2) hpi, cells were lysed and proteins were analyzed by immunoblotting with antibodies as indicated. Immunoblots were performed at least two times and one representative blot is shown. (D) At 16 (SINV) or 48 (SARS-CoV-2) hpi, total RNA was harvested, the mRNA expression level of *IFNB,*

IFNL1, OAS2, IFIT1, IFIH1, CXCL8 was quantified by RT-qPCR. C_T values were normalized to 18S rRNA to generate ΔC_T values (ΔC_T = C_T gene of interest - C_T 18S rRNA). Fold change over mock values were calculated by subtracting mock infected ΔC_T values from virus infected ΔC_T values, displayed as $2^{-\Delta(\Delta Ct)}$. Technical replicates were averaged, the means for each replicate displayed, ± SD (error bars). Statistical significance was determined by Student *t* test (*, $P < 0.05$; ****, $P < 0.0001$; ns = not significant). Data shown are from one representative experiment of two independent experiments. (E) Total RNA was harvested at 16 (SINV) or 48 (SARS-CoV-2) hpi, and rRNA integrity determined by Bioanalyzer. The position of 28S and 18S rRNA and indicated. Data shown are from one representative experiment of two independent experiments. (See also Figures S1C&S2).

Figure 5. Replication of SARS-CoV-2 in A549^{ACE2} and Calu-3 cell lines. (A) Vero-E6 or A549^{ACE2} cells were infected with SARS-CoV-2 at MOI=1. At the indicated times, supernatant was collected and virus quantified by plaque assay on Vero-E6 cells. Values are means ± SD (error bars). (B) Calu-3 cells were infected with SARS-CoV-2, MERS-CoV or MERS-CoV-ΔNS4ab at MOI=1. Supernatant was collected at the indicated times and virus quantified by plaque assay on Vero-E6 cells (SARS-CoV-2) or VeroCCL81 cells (MERS-CoV and MERS-CoV-Δ4ab). Values represent means ± SEM (error bars). Statistical significance was determined by Student *t* test (**, $P < 0.01$). Data shown are one representative experiment of three independent experiments. (C) Vero-E6, A549^{ACE2}, and Calu-3 cells were grown on untreated (Vero-E6 and A549^{ACE2}) or collagen-coated (Calu-3) glass coverslips before infection with SARS-CoV-2 at MOI = 1. At indicated hpi, cells were fixed with 4% PFA and permeabilized for N (green) and dsRNA (red) expression detection by IFA using anti-N and J2 antibodies, respectively. Channels are merged with DAPI nuclear staining. Images shown are representative from two independent experiments. Scale bar = 25μm. (See also Figure S3&S4A).

Figure 6. SARS-CoV-2 IFN responses in the lung epithelia-derived A549^{ACE2} cell line. A549^{ACE2} cells were mock infected or infected with SINV (MOI=1) or SARS-CoV-2 (MOI=5). (A) Total RNA was harvested at 24 and 48 hpi. Expression of *IFNB, IFNL1, OAS2, IFIT1, IFIH1,* and *CXCL8* mRNA was quantified by RT-qPCR. C_T values were normalized to 18S rRNA to generate ΔC_T values (ΔC_T = C_T gene of interest - C_T 18S rRNA). Fold change over mock values were calculated by subtracting mock infected ΔC_T values from virus infected ΔC_T values, displayed as $2^{-\Delta(\Delta Ct)}$. Technical replicates were averaged, the means for each replicate displayed, ± SD (error bars). (B) Viral genome copies per ug of total RNA were calculated at 24 and 48hpi by RT-qPCR standard curve generated using a digested plasmid encoding SARS-CoV-2 nsp12. Values are means ± SD (error bars). Statistical significance was determined by one-way ANOVA (*, P < 0.05; **, P < 0.01; ***, P < 0.001; ****, P < 0.0001; ns = not significant). (C) At 24 hpi, A549^{ACE2} cells were lysed and proteins harvested. Protein expression was analyzed by immunoblot using the indicated antibodies. All data are one representative experiment of three independent experiments. (See also Figures S2 and S4B&C).

Figure 7. SARS-CoV-2 and MERS-CoV IFN responses in the lung-derived Calu-3 cells. Calu-3 cells were mock treated or infected with SARS-CoV-2, MERS-CoV or MERS-CoV-ΔNS4ab at MOI=5. (A) At 24 or 48 hpi, total RNA was harvested. Expression of *IFNB, IFNL1, OAS2, IFIT1, IFIH1,* and *CXCL8* mRNA was quantified by RT-qPCR. C_T values were normalized to 18S rRNA to generate ΔC_T values (ΔC_T = C_T gene of interest - C_T 18S rRNA). Fold change over mock values were calculated by subtracting mock infected ΔC_T values from virus infected ΔC_T values, displayed as $2^{-\Delta(\Delta Ct)}$. Technical replicates were averaged, the means for each replicate displayed, ± SD (error bars). Statistical significance was determined by two-way ANOVA (*, P < 0.05; **, P < 0.01; ***, P < 0.001; ****, P < 0.0001; ns = not significant). (B) Viral genome copies per ug of

total RNA were calculated by RT-qPCR standard curve generated using a digested plasmid encoding SARS-CoV-2 nsp12 or plasmid encoding a region of MERS-CoV orf1ab. Values are means ± SD (error bars). Statistical significance was determined by two-way ANOVA (*, $P < 0.05$; **, $P < 0.01$; ns = not significant). (C) At 24 hpi, Calu-3 cells were lysed and proteins harvested. Proteins were analyzed by immunoblotting using the indicated antibodies. All data are one representative experiment of three independent experiments. (See Figure S2).

Figure 8. SARS-CoV-2 infection leads to activation of RNase L and PKR in A549^{ACE2} and Calu-3 cells. A549^{ACE2} and Calu-3 cells were mock infected or infected with SARS-CoV-2, MERS-CoV, or MERS-CoV-ΔNS4ab at MOI=5. Total RNA was harvested from A549^{ACE2} cells (A) or Calu-3 cells (B) at 24 and 48 hpi. 28S and 18S rRNA integrity was assessed by Bioanalyzer. 28S and 18s rRNA bands are indicated. At 24 hpi, A549^{ACE2} cells (C) or Calu-3 cells (D) were lysed and proteins harvested for analysis by immunoblotting using the indicated antibodies. All data are one representative experiment of three independent experiments. (See also Figure S4D&E).

Figure 9. Replication of SARS-CoV-2 is restricted by RNase L independent of PKR or MAVS. Indicated genes were knocked out (KO) from one clone of A549^{ACE2} cells using CRISPR-Cas9 engineering. (A) KO cell lines were grown in culture with or without 1000U IFN-α treatment for 24 hours. Cells were lysed and proteins harvested for analysis by immunoblotting using indicated antibodies. (B) Indicated cell lines were infected with SARS-CoV-2 at MOI=1. At the indicated time points, supernatant was collected and virus quantified by plaque assay on Vero-E6 cells. Values represent mean ± SD (error bars). Statistical significance was determined by two-way ANOVA (****, $P < 0.0001$; ns = not significant). Data are one representative experiment from at least three independent experiments. (C) Indicated cell lines were mock treated or infected with SARS-CoV-2 at MOI=1. At 48 hpi, cells were fixed with 4% PFA and stained with 1% crystal violet as a marker for live cells. The image is one representative experiment from two independent

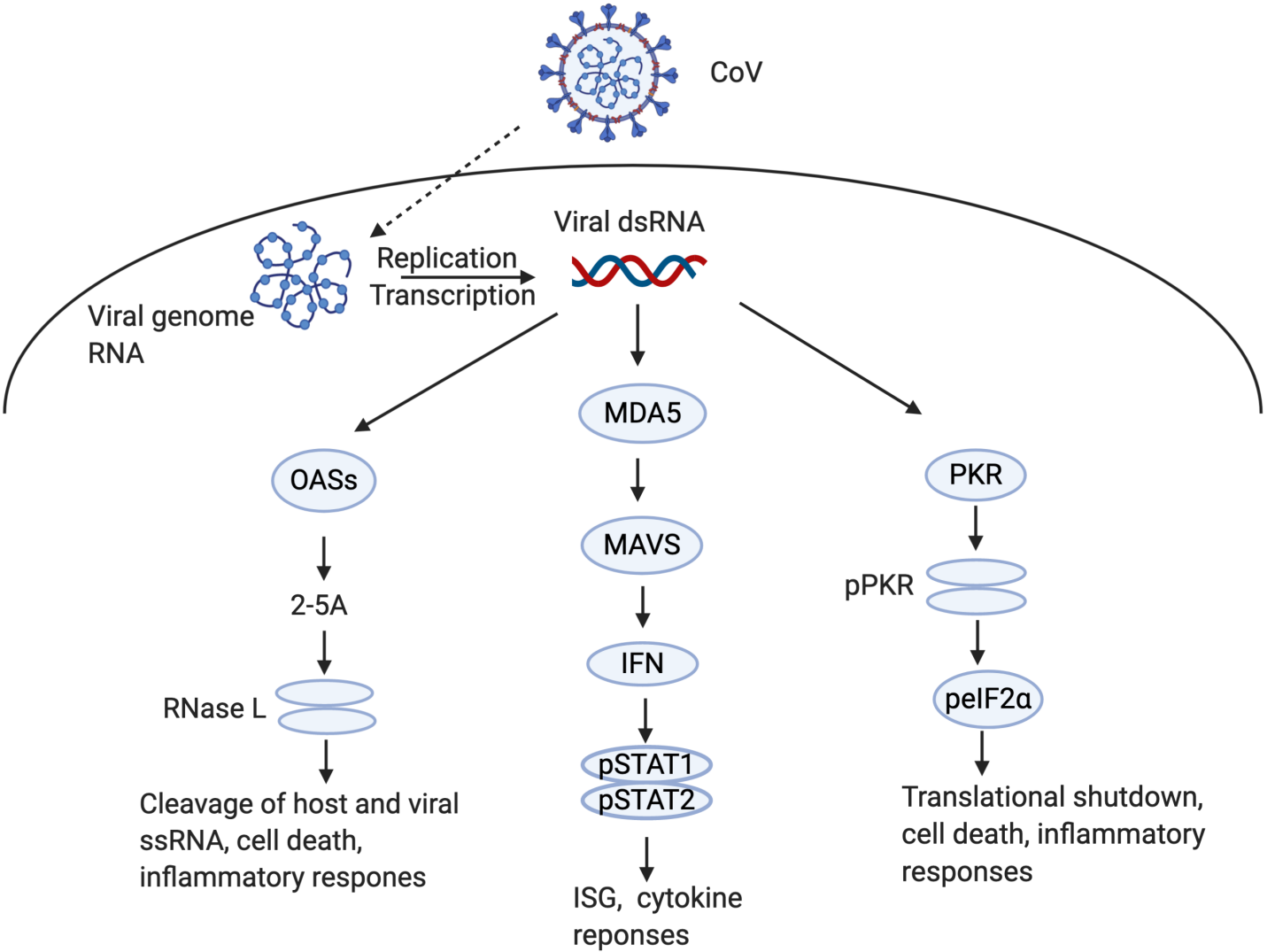
experiments. (D) The indicated cell lines were mock infected or infected with SARS-CoV-2 or SINV at MOI=1. RNA was harvested 24 hpi (SINV) or 24 and 48 hpi (SARS-CoV-2). Integrity of rRNA was assessed by Bioanalyzer. 28S and 18S rRNA bands are indicated. Data is one representative experiment of two independent experiments.

Figure S1. Genome replication in nasal cells, iAT2, and iCM. Nasal (A) and iAT2 cells (B) were infected at MOI=5 with SARS-CoV-2, and (C) iCM at MOI=1 with SARS-CoV-2 or SINV. Total RNA was harvested at 48 hpi(SARS-COV-2) or 16 hpi(SINV) for iAT2 and iCM cells and 120 hpi for nasal cells. Viral genome copies per ug of harvested RNA were calculated by RT-qPCR standard curve generated using a digested plasmid encoding SARS-CoV-2 nsp12. Values are means ± SD (error bars). For SINV (C), cycle threshold (C_T) values of SINV nsP4 polymerase sequences were normalized to 18S rRNA to generate ΔC_T values (ΔC_T = C_T gene of interest - C_T 18S rRNA). Technical triplicates were averaged and displayed using the equation $2^{-(\Delta CT)}$. Data are from one representative experiment of two independent experiments.

Figure S2. Host basal mRNA expression of uninfected cells. Total RNA was harvested from mock treatment from all indicated cell types after 24 hours incubation. mRNA expression levels of *IFNB, IFNL1, OAS2, IFIT1, IFHI1,* and *CXCL8* were quantified by RT-qPCR. C_T values were normalized to 18S rRNA to generate ΔC_T values (ΔC_T = C_T gene of interest - C_T 18S rRNA). (A) Basal level of gene expression is displayed for nasal cells, iAT2 and iCM, Calu-3 cells and two clones of $A549^{ACE2}$ cells, displayed as $2^{-\Delta Ct}$. (B) Fold expression over $A549^{ACE2}$ C44 values were calculated by subtracting ΔC_T values from the indicated cell line from $A549^{ACE2}$ C44 ΔC_T values, displayed as $2^{-\Delta(\Delta CT)}$. Biological replicates were averaged and values are means ± SD (error bars). Data were generated from at least two independent experiments.

Figure S3. ACE2 protein expression in A549^{ACE2} and Calu-3 cell lines. Parental A549 cells, two A549^{ACE2} clones, and Calu-3 cells were grown in culture before lysis and protein harvest. Protein expression was analyzed by immunoblotting using the indicated antibodies.

Figure S4. SARS-CoV-2 replication and host responses in a second lung epithelia-derived A549^{ACE2} cell line clone (C34). (A) Vero-E6 or A549^{ACE2} cells were infected with SARS-CoV-2 at MOI=1 and supernatant harvested at indicated times post infection. Infectious virus was quantified by plaque assay on Vero-E6 cells. Values are means ± SD (error bars). (B) A549^{ACE2} cells (C34) were mock infected or infected with SARS-CoV-2 or SINV at MOI=5 and total RNA total RNA harvested at 24 (SINV) or 24 and 48 (SARS-CoV-2) hpi. Expression of *IFNB, IFNL1, OAS2, IFIT1, IFIH1,* and *CXCL8* mRNA was quantified by RT-qPCR. C_T values were normalized to 18S rRNA to generate ΔC_T values (ΔC_T = C_T gene of interest - C_T 18S rRNA). Fold change over mock values were calculated by subtracting mock infected ΔC_T values from virus infected ΔC_T values, displayed as $2^{-\Delta(\Delta Ct)}$. Statistical significance for each gene was determined by one-way ANOVA (***, P < 0.001; ****, P < 0.0001; ns = not significant). Technical replicates were averaged, the means for each replicate displayed, ± SD (error bars). (C&D) A549^{ACE2} cells were infected at MOI=5, lysed at 24 hpi, and proteins harvested for analysis by immunoblotting using the indicated antibodies. (E) A549^{ACE2} cells were infected at MOI=1 (SINV) or MOI=5 (SARS-CoV-2) and total RNA harvested at 24 (SINV) or 24 and 48 (SARS-CoV-2) hpi. Integrity of rRNA was assessed by Bioanalyzer. 28S and 18s rRNA bands are indicated. All data are representative of two or three independent experiments.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Replication
Transcription
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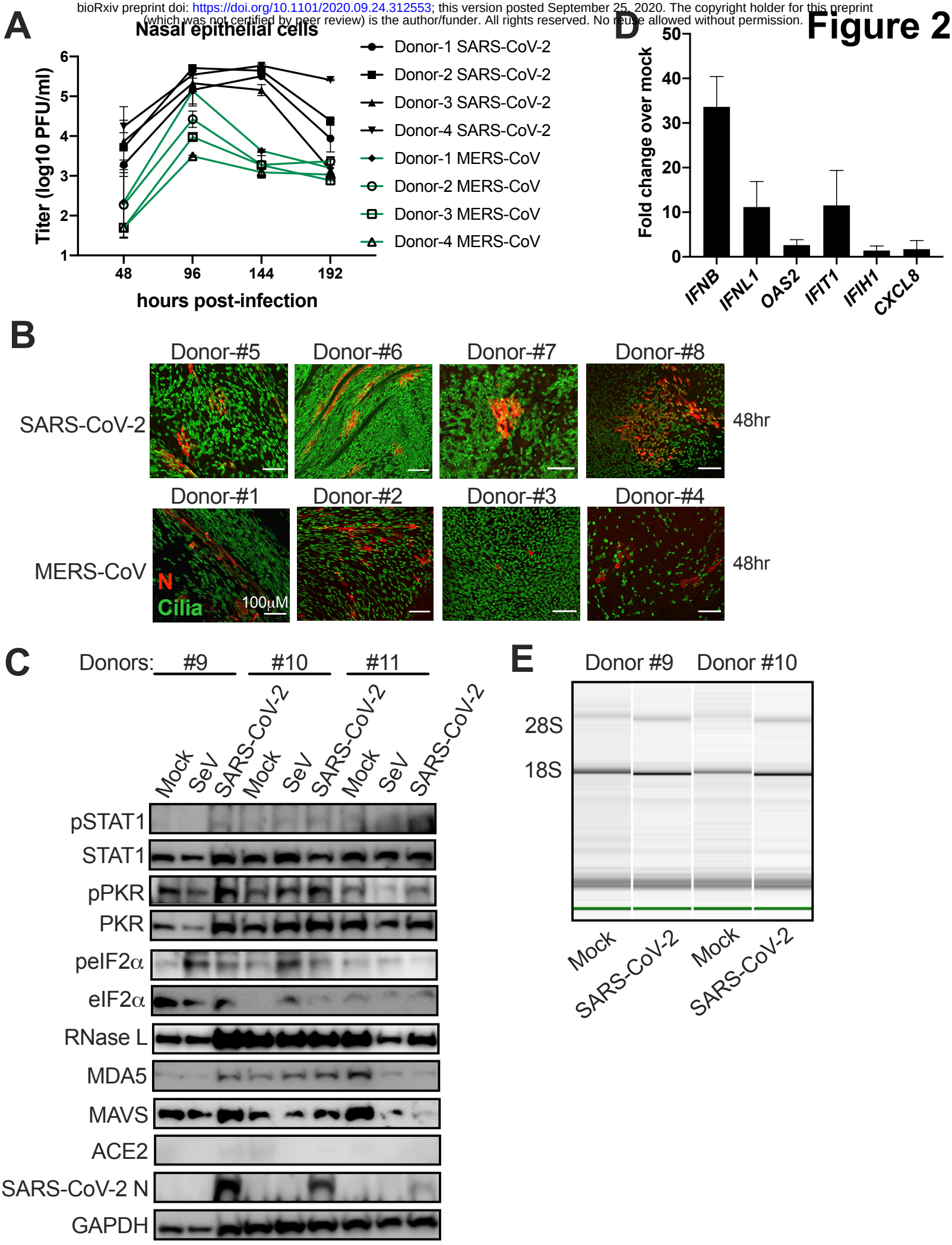
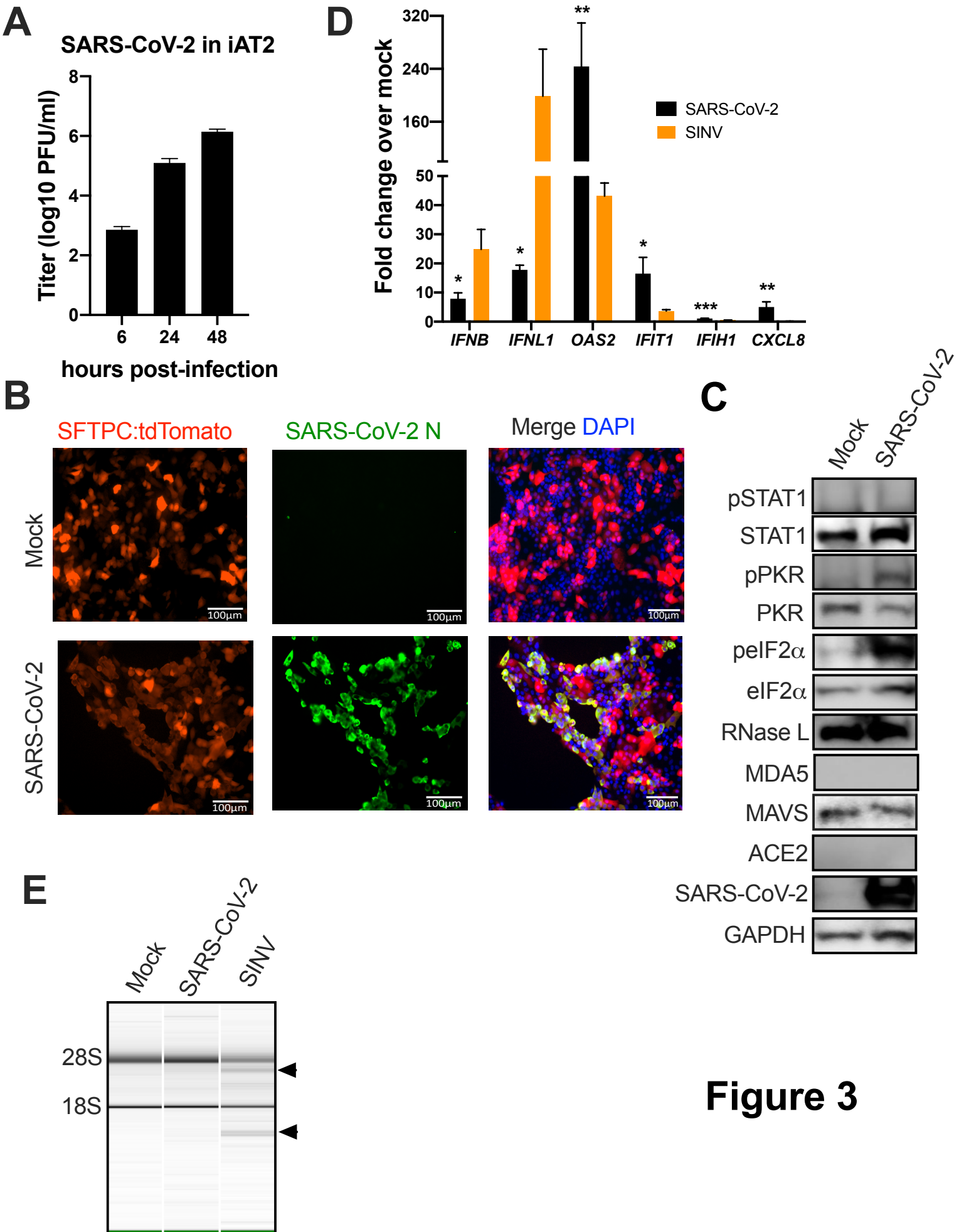
RNA
MDA5
OASs
PKR
MAVS
2-5A
pPKR
IFN
RNase L
pSTAT1
pSTAT2
peIF2α
Cleavage of host and viral ssRNA, cell death, inflammatory respones
ISG, cytokine reponses
Translational shutdown, cell death, inflammatory responses

Figure 2

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6
4
2
0
6
24
48
hours post-infection
D
Fold change over mock
320
240
160
50
40
30
20
10
0
SARS-CoV-2
SINV
IFNB
IFNL1
OAS2
IFIT1
IFIH1
CXCL8
B
SFTPC:tdTomato
SARS-CoV-2 N
Merge DAPI
Mock
SARS-CoV-2
100µm
C
Mock
SARS-CoV-2
pSTAT1
STAT1
pPKR
PKR
peIF2α
eIF2α
RNase L
MDA5
MAVS
ACE2
SARS-CoV-2
GAPDH
E
Mock
SARS-CoV-2
SINV
28S
18S

Figure 3

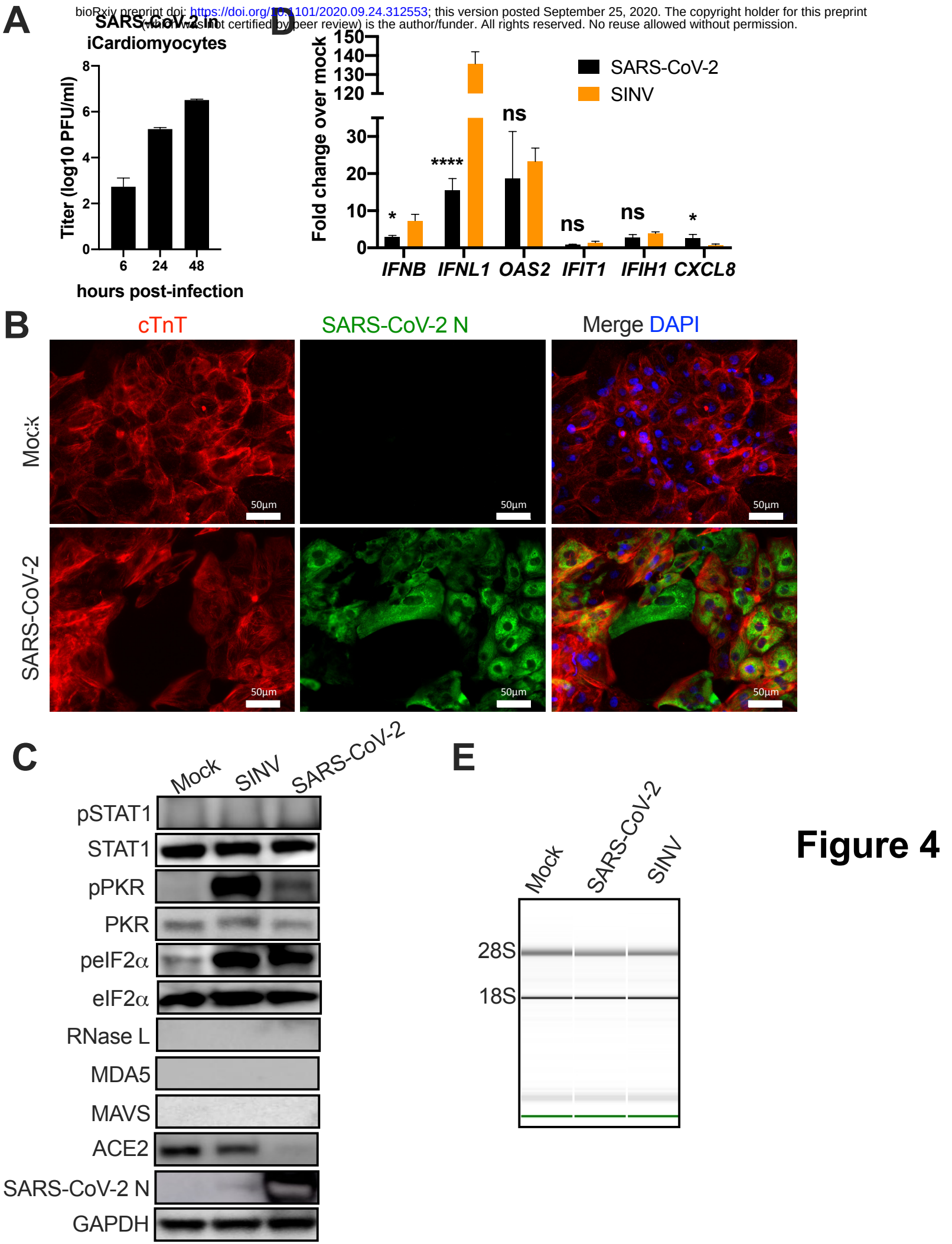
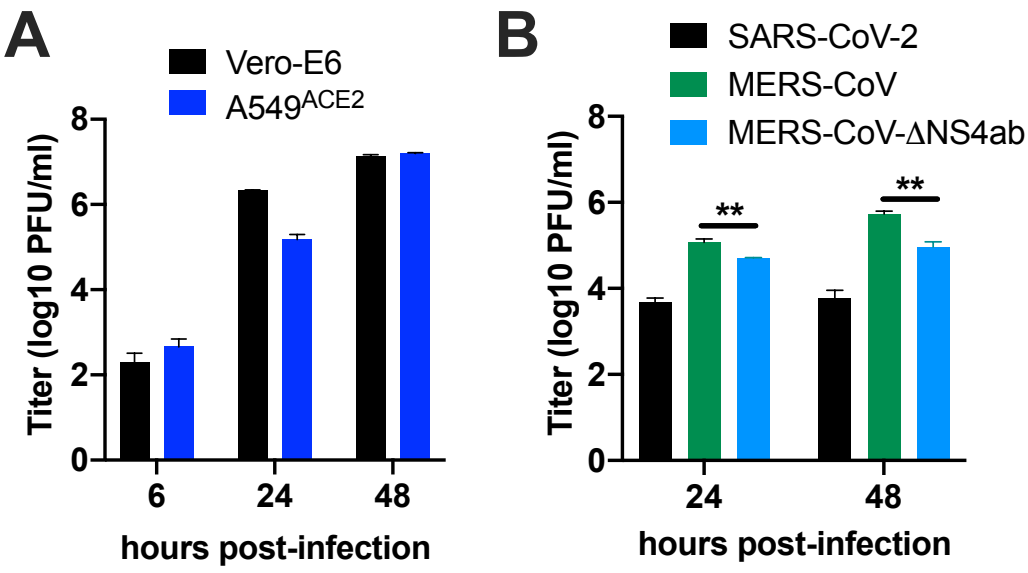


Figure 4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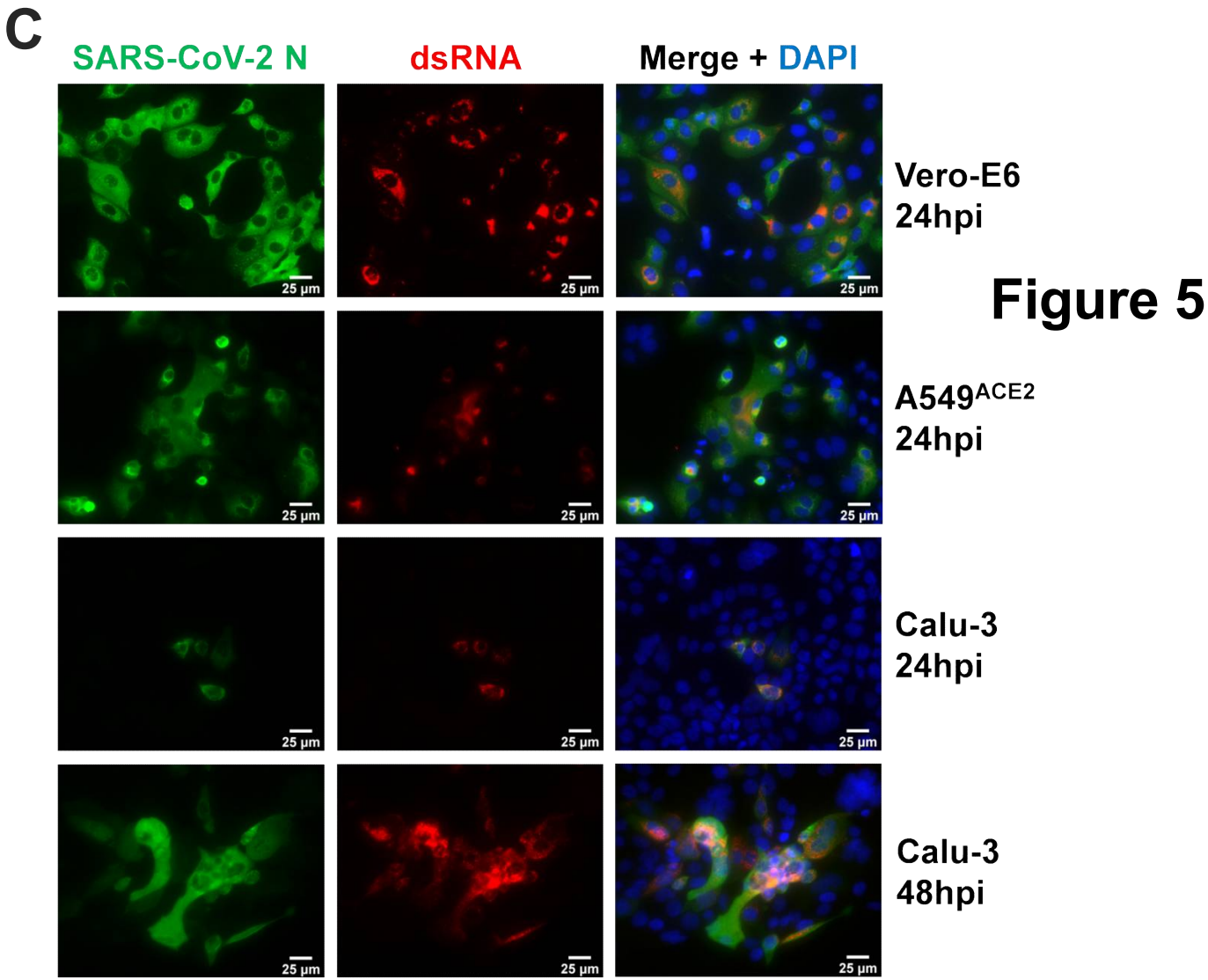
Vero-E6
A549ACE2
Titer (log10 PFU/ml)
0
2
4
6
8
6
24
48
hours post-infection
B
SARS-CoV-2
MERS-CoV
MERS-CoV-ΔNS4ab
Titer (log10 PFU/ml)
**
**
0
2
4
6
8
24
48
hours post-infection


C
SARS-CoV-2 N
dsRNA
Merge + DAPI
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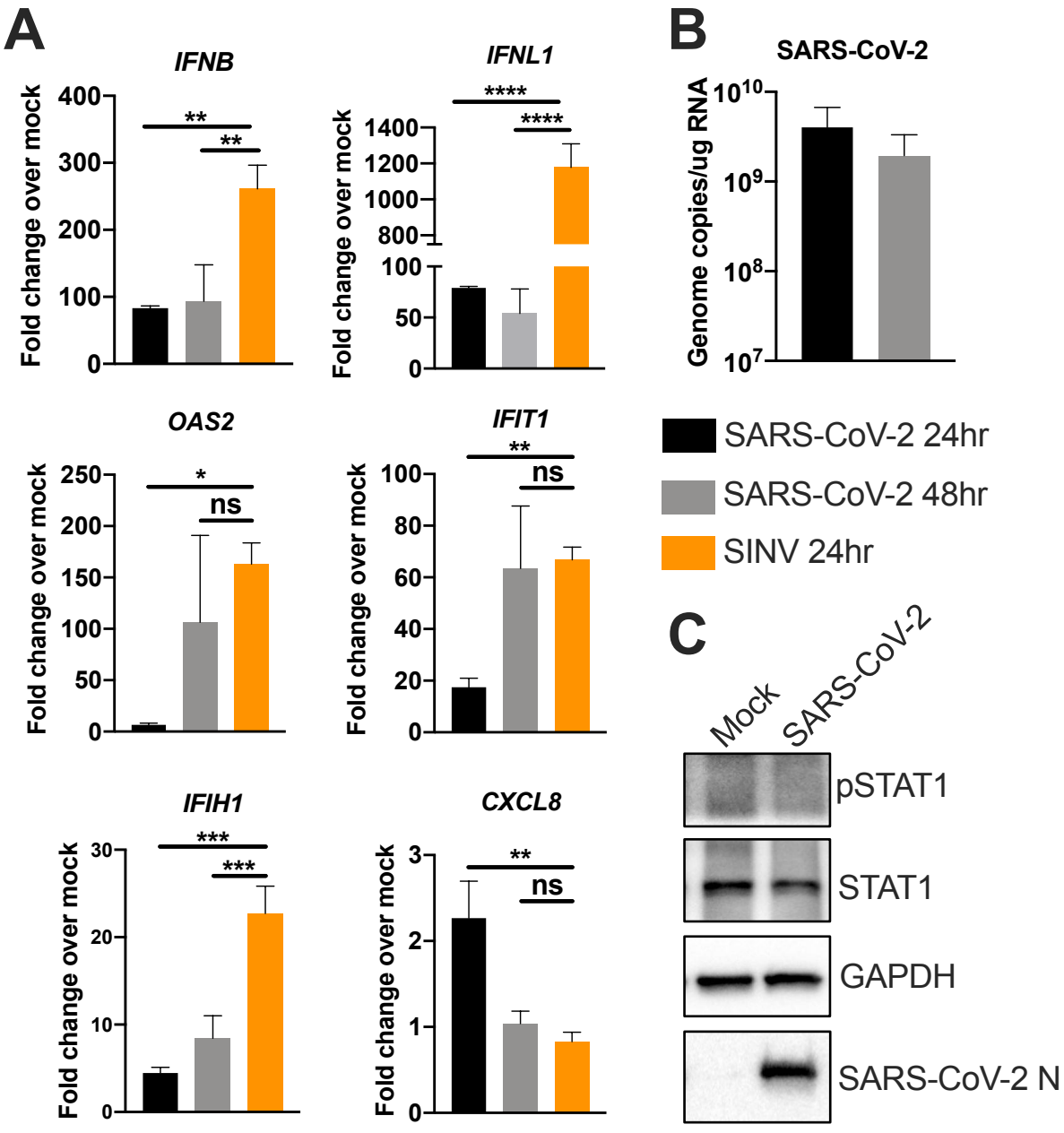
Vero-E6
24hpi
A549ACE2
24hpi
Calu-3
24hpi
Calu-3
48hpi

Figure 5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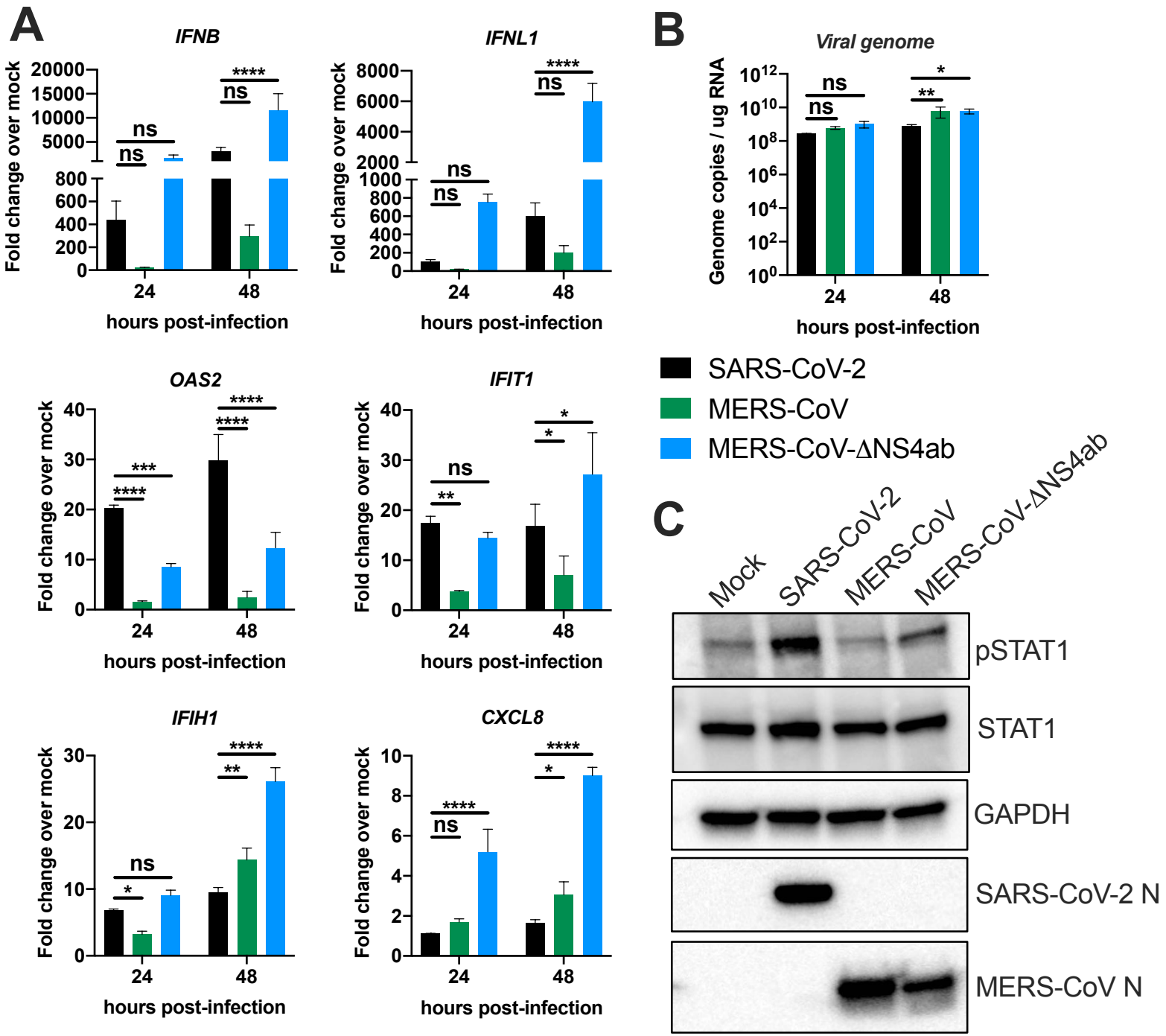
Fold change over mock
400
300
200
100
0
**
**
IFNL1
Fold change over mock
1400
1200
1000
800
100
50
0
****
****
OAS2
Fold change over mock
250
200
150
100
50
0
*
ns
IFIT1
Fold change over mock
100
80
60
40
20
0
**
ns
IFIH1
Fold change over mock
30
20
10
0
***
***
CXCL8
Fold change over mock
3
2
1
0
**
ns
B
SARS-CoV-2
Genome copies/ug RNA
10^{10}
10^{9}
10^{8}
10^{7}
SARS-CoV-2 24hr
SARS-CoV-2 48hr
SINV 24hr
C
Mock
SARS-CoV-2
pSTAT1
STAT1
GAPDH
SARS-CoV-2 N

Figure 6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OAS2
IFIT1
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CXCL8
Fold change over mock
hours post-infection
24
48
ns
B
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Genome copies / ug RNA
SARS-CoV-2
MERS-CoV
MERS-CoV-ΔNS4ab
C
Mock
SARS-CoV-2
MERS-CoV
MERS-CoV-ΔNS4ab
pSTAT1
STAT1
GAPDH
SARS-CoV-2 N
MERS-CoV N

Figure 7

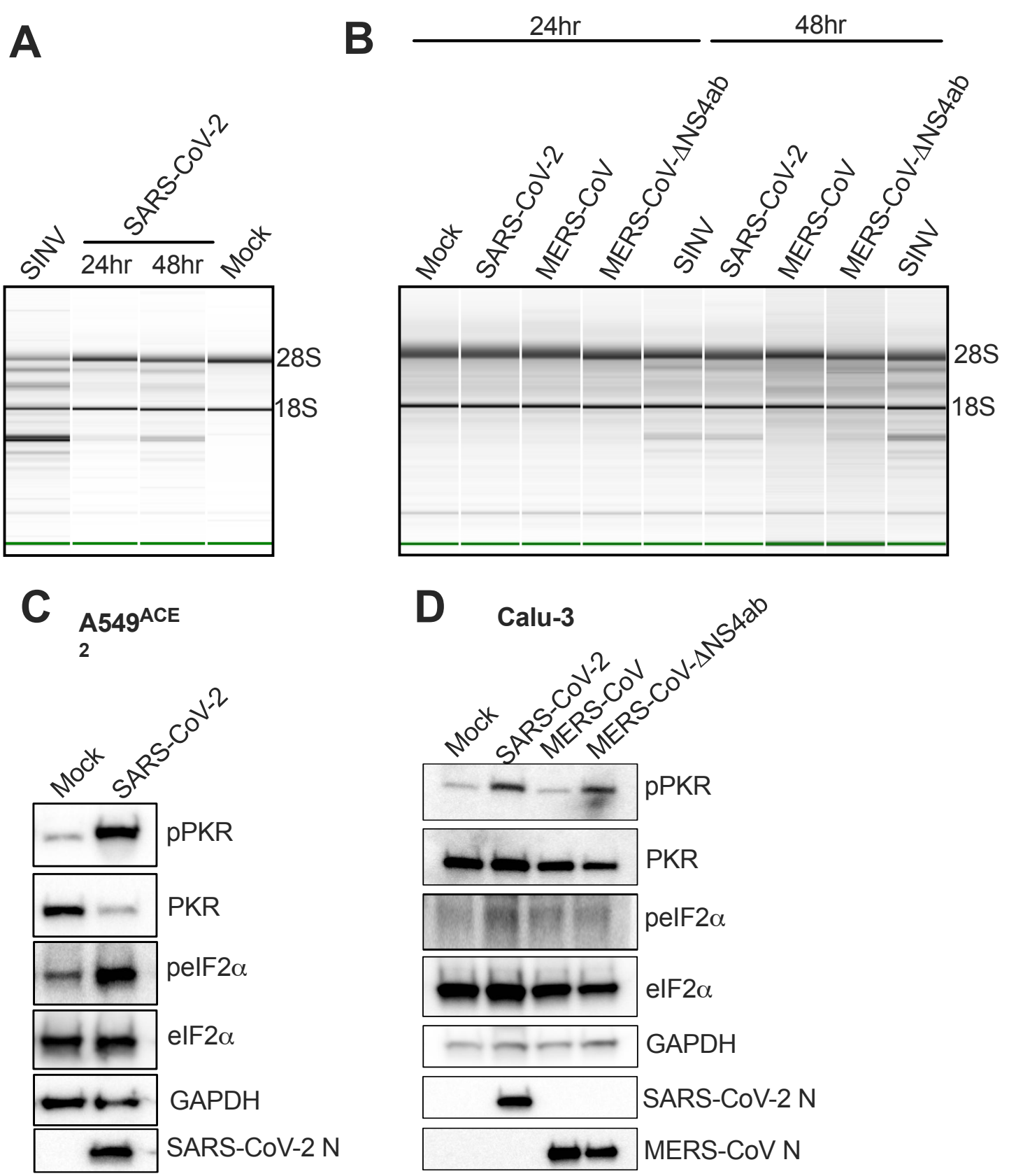
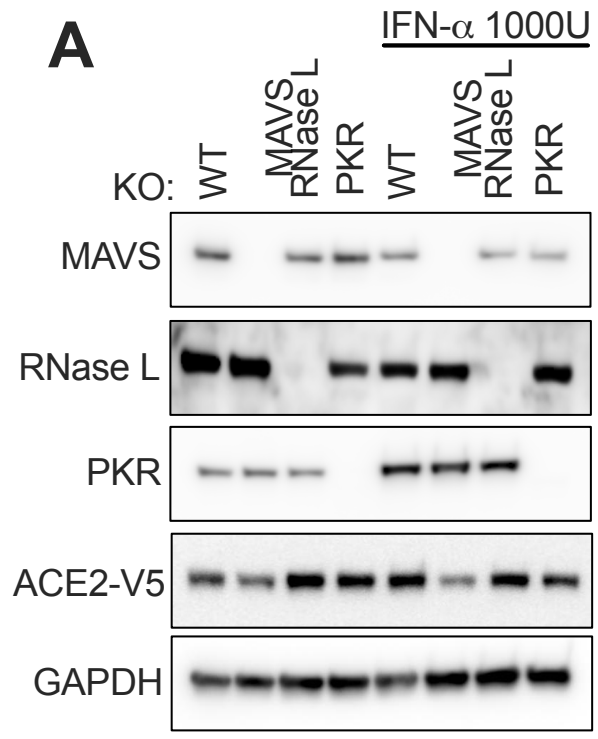

A
SINV
SARS-CoV-2
24hr
48hr
Mock
28S
18S
B
24hr
48hr
Mock
SARS-CoV-2
MERS-CoV
MERS-CoV-ΔNS4ab
SINV
SARS-CoV-2
MERS-CoV
MERS-CoV-ΔNS4ab
SINV
28S
18S
C
A549ACE2
Mock
SARS-CoV-2
pPKR
PKR
peIF2α
eIF2α
GAPDH
SARS-CoV-2 N
D
Calu-3
Mock
SARS-CoV-2
MERS-CoV
MERS-CoV-ΔNS4ab
pPKR
PKR
peIF2α
eIF2α
GAPDH
SARS-CoV-2 N
MERS-CoV N

Figure 8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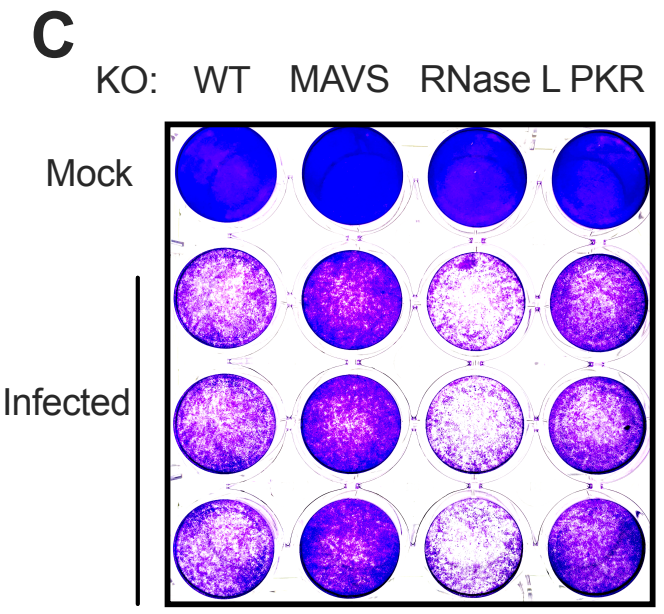
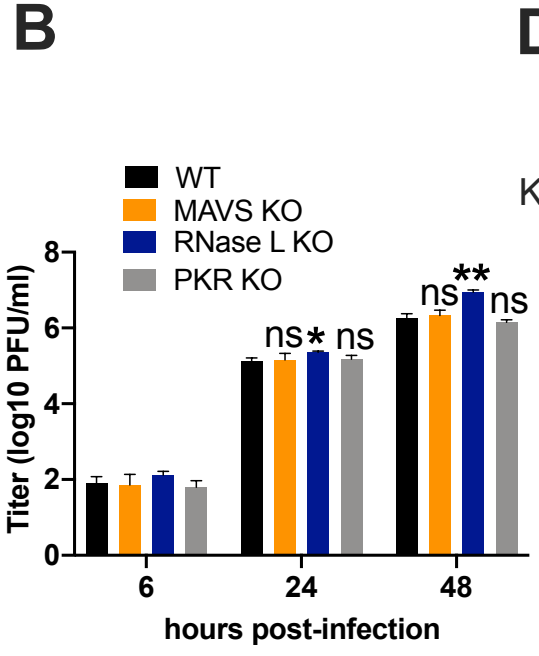
IFN-α 1000U
KO:
WT
MAVS
RNase L
PKR
WT
MAVS
RNase L
PKR
MAVS
RNase L
PKR
ACE2-V5
GAPDH


C
KO:
WT
MAVS
RNase L
PKR
Mock
Infected


B
WT
MAVS KO
RNase L KO
PKR KO
Titer (log10 PFU/ml)
0
2
4
6
8
ns
*
ns
ns
**
ns
6
24
48
hours post-infection

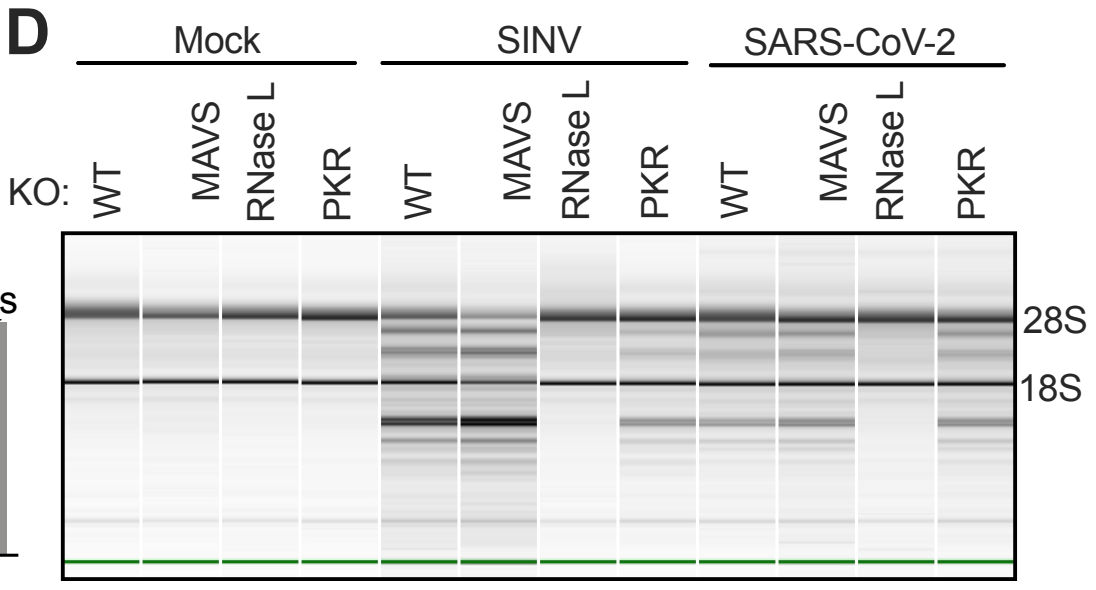

D
Mock
SINV
SARS-CoV-2
KO:
WT
MAVS
RNase L
PKR
WT
MAVS
RNase L
PKR
WT
MAVS
RNase L
PKR
28S
18S

Figure 9

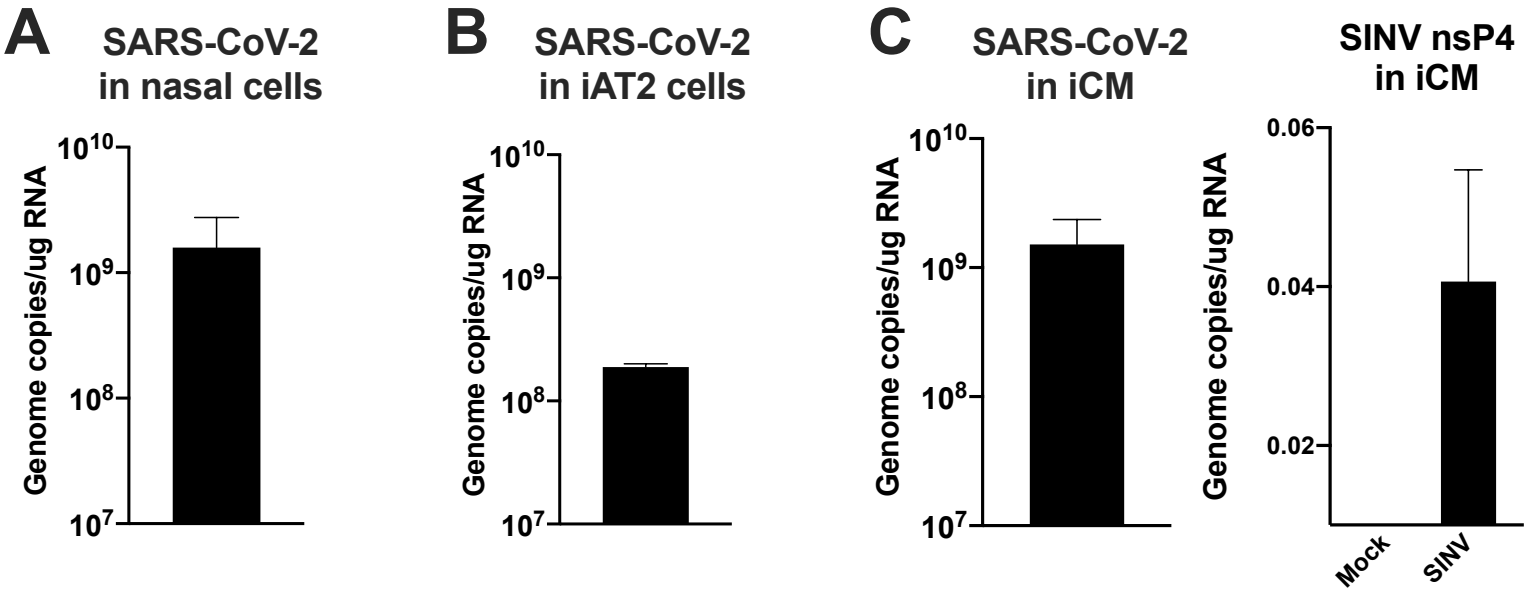
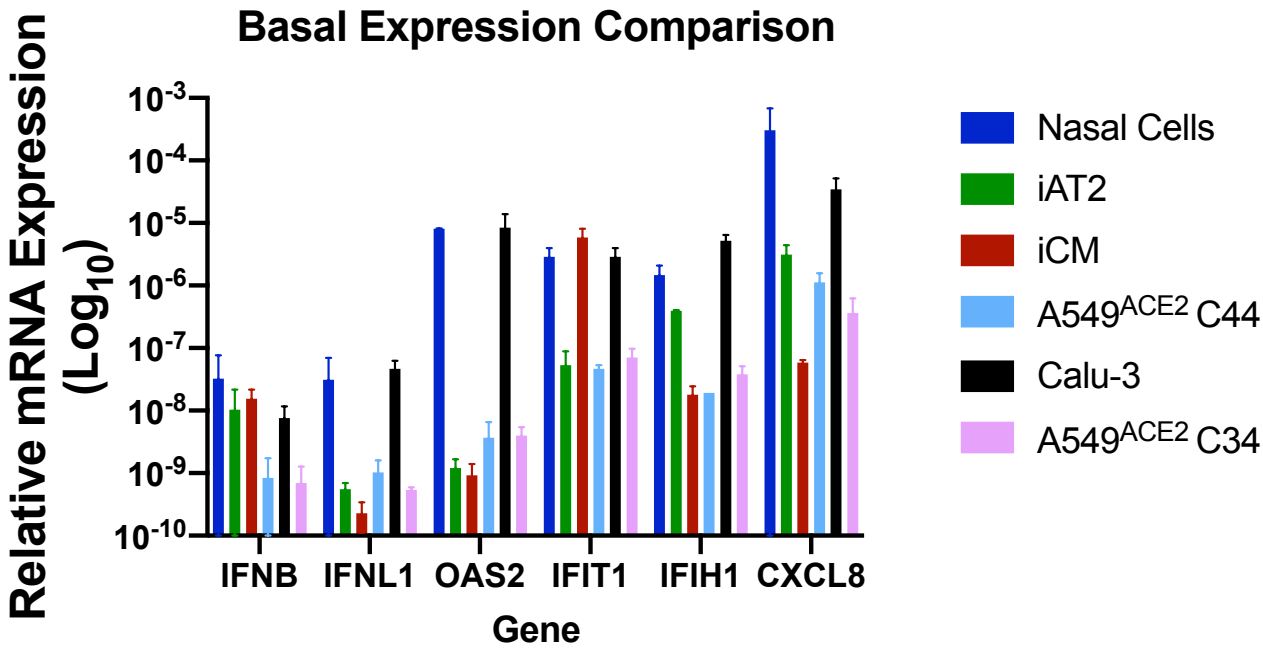

A
SARS-CoV-2
in nasal cells
Genome copies/ug RNA
10^{10}
10^{9}
10^{8}
10^{7}
B
SARS-CoV-2
in iAT2 cells
Genome copies/ug RNA
10^{10}
10^{9}
10^{8}
10^{7}
C
SARS-CoV-2
in iCM
Genome copies/ug RNA
10^{10}
10^{9}
10^{8}
10^{7}
SINV nsP4
in iCM
Genome copies/ug RNA
0.06
0.04
0.02
Mock
SINV

Figure S1

A


Basal Expression Comparison
Relative mRNA Expression (Log10)
10-3
10-4
10-5
10-6
10-7
10-8
10-9
10-10
IFNB
IFNL1
OAS2
IFIT1
IFIH1
CXCL8
Gene
Nasal Cells
iAT2
iCM
A549ACE2 C44
Calu-3
A549ACE2 C34

B

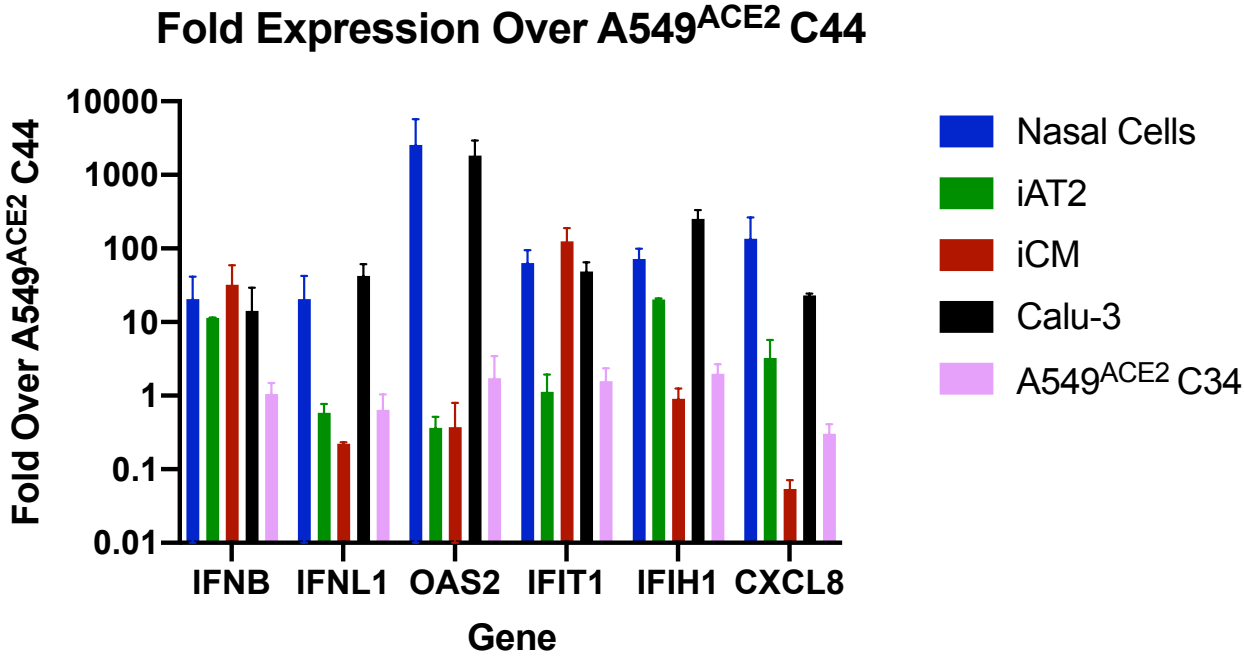

Fold Expression Over A549ACE2 C44
Fold Over A549ACE2 C44
10000
1000
100
10
1
0.1
0.01
IFNB
IFNL1
OAS2
IFIT1
IFIH1
CXCL8
Gene
Nasal Cells
iAT2
iCM
Calu-3
A549ACE2 C34

Figure S2

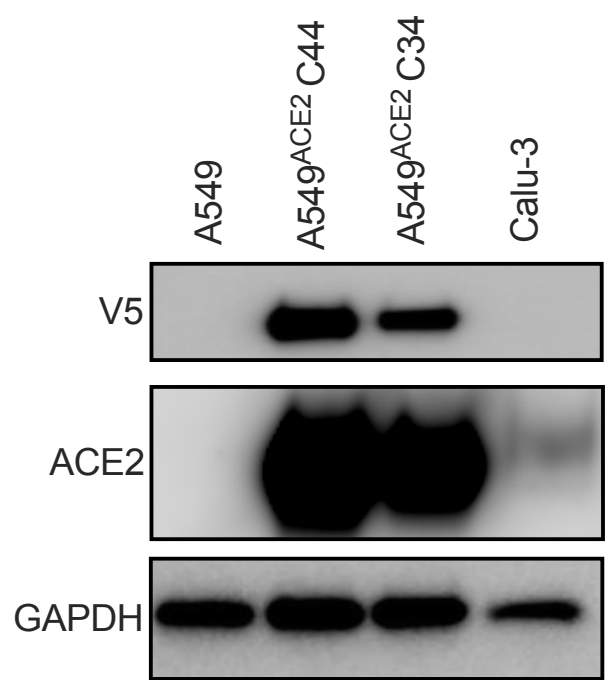


Figure S3

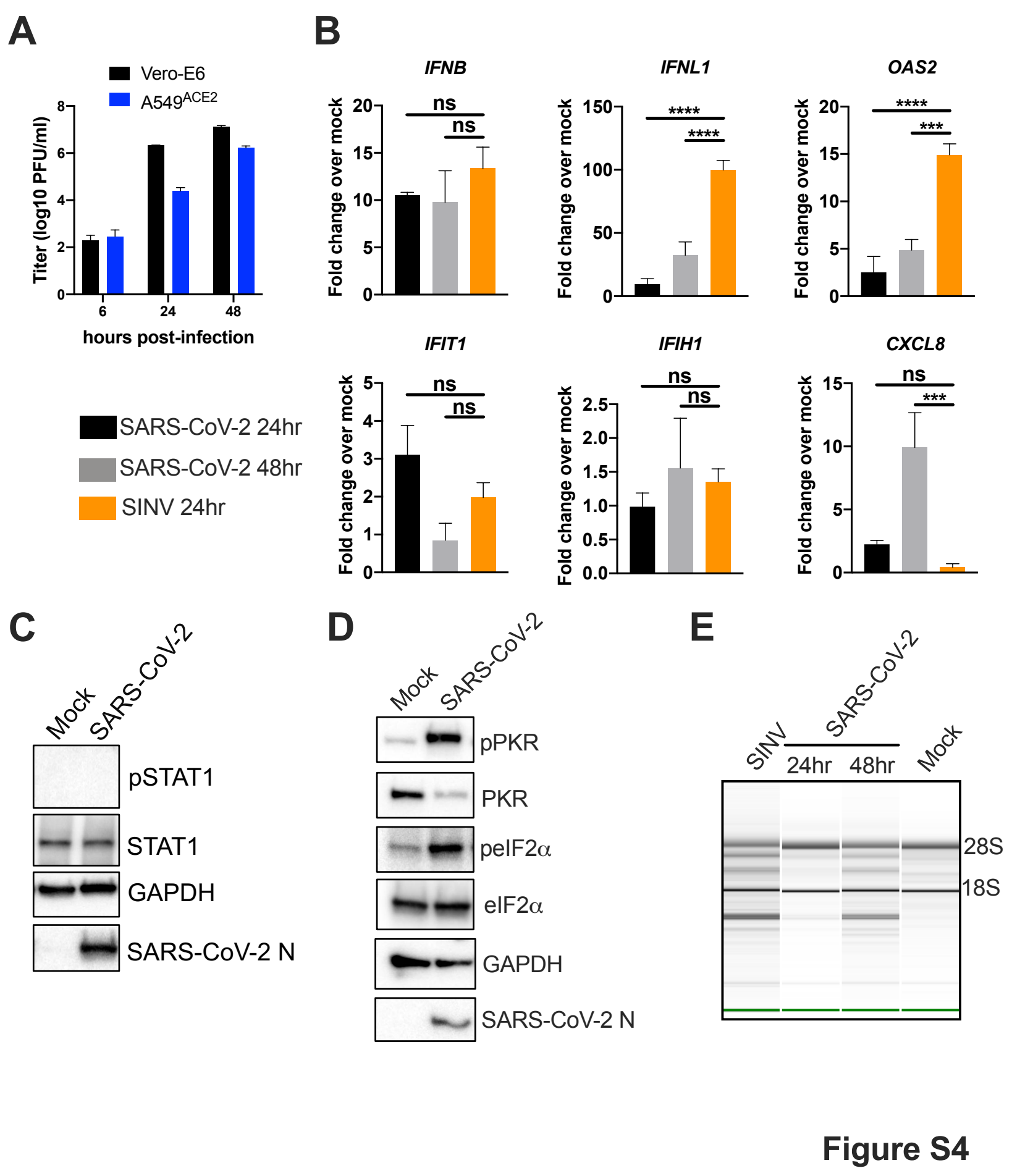

A
Vero-E6
A549ACE2
Titer (log10 PFU/ml)
hours post-infection
6
24
48
B
IFNB
IFNL1
OAS2
IFIT1
IFIH1
CXCL8
Fold change over mock
ns
****
***
SARS-CoV-2 24hr
SARS-CoV-2 48hr
SINV 24hr
C
Mock
SARS-CoV-2
pSTAT1
STAT1
GAPDH
SARS-CoV-2 N
D
pPKR
PKR
peIF2α
eIF2α
E
SINV
24hr
48hr
28S
18S

Figure S4