SAMHD1 promotes SARS-CoV-2 infection by enhancing HNF1-dependent ACE2 expression in lung epithelial cells

Short title: SAMHD1 promotes SARS-CoV-2 entry via HNF1-dependent ACE2 expression

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Abstract

Sterile alpha motif and HD domain-containing protein 1 (SAMHD1) restricts a board spectrum of viruses through multifaceted mechanisms. It also limits spontaneous- and virus-induced innate immune responses by suppressing proinflammatory cytokine and type-I interferon (IFN-I) production. Some viruses escape SAMHD1 restriction by utilizing SAMHD1-mediated innate immune suppression to establish effective infection through viral antagonism. Our previous studies showed that SAMHD1 is a proviral factor facilitating replication of severe acute respiratory syndrome coronavirus (SARS-CoV-2) in human macrophages, monocytic THP-1 and epithelial-like HEK293T cell lines by suppressing IFN responses. However, it is unclear about the function of SAMHD1 in lung epithelial cells during SARS-CoV-2 infection. Here, we report that SAMHD1 facilitates SARS-CoV-2 replication in lung epithelial Calu-3 cells by enhancing endogenous expression of the viral receptor angiotensin-converting enzyme 2 (ACE2) via hepatocyte nuclear factor 1-alpha (HNF1α) and HNF1β. Using pseudotyped SARS-CoV-2 and lentiviral vectors, we found that SARS-CoV-2 spike protein-mediated viral entry was suppressed in Calu-3 cells with SAMHD1 knockout (KO). SAMHD1 KO repressed ACE2 expression in Calu-3 cells at mRNA and protein levels. Functional analyses revealed that HNF1α and HNF1β were crucial for the endogenous ACE2 expression in Calu-3 cells. Additionally, SAMHD1 KO led to a reduction in the expression levels and ACE2-promoting function of HNF1α and HNF1β. Inhibition of IFN antiviral

37 response by baricitinib, a Janus kinase 1 and 2 (JAK 1/2) inhibitor, did not revert the suppression
38 of SARS-CoV-2 in SAMHD1 KO Calu-3 cells. Our findings demonstrate that SAMHD1 facilitates
39 HNF1-mediated ACE2 expression and SARS-CoV-2 replication in Calu-3 cells via a novel
40 mechanism beyond its IFN-suppressive function.
41

42 **Author Summary**

43 During viral infection, SAMHD1 acts as a viral restriction factor and a suppressor of the innate
44 immune system, controlling viral replication while also ensuring immune homeostasis. The innate
45 immune suppressive function of SAMHD1 can be proviral for some viruses. SAMHD1 has been
46 shown to facilitate SARS-CoV-2 infection in human macrophages, THP-1 and HEK293T cell lines
47 by promoting IFN antagonism, but its role in lung epithelial cells is unclear. Here, we demonstrated
48 that SAMHD1 promotes SARS-CoV-2 replication in human lung epithelial Calu-3 cells by
49 enhancing expression of the major viral receptor ACE2. We found that SAMHD1 facilitated HNF1-
50 medaited ACE2 expression that was required for spike protein-mediated SARS-CoV-2 entry.
51 However, inhibiting IFN signaling in SAMHD1 KO Calu-3 cells was not sufficient to revert SARS-
52 CoV-2 replication. Our findings shed light on the differential proviral function of SAMHD1 in ACE2
53 expressing cells and suggest that SAMHD1 can facilitate SARS-CoV-2 infection beyond
54 enhancing IFN antagonism.

55

56 **Introduction**

57 SAMHD1 is the only deoxynucleoside triphosphohydrolase (dNTPase) of mammalian cells
58 to be a restriction factor against human immunodeficient virus type 1 (HIV-1) infection in resting
59 $CD4^+$ T cells and terminally differentiated immune cells, such as macrophages and dendritic cells
60 [1-3]. Increasing evidence suggests that SAMHD1 restricts different viruses including human T
61 cell leukemia virus type 1 [4], DNA viruses such as herpesviruses (herpes simplex virus 1, human
62 cytomegalovirus and Epstein-Barr virus), hepatitis B virus, human papillomavirus and poxviruses
63 [5-10] as well as RNA viruses including influenza A virus, enteroviruses, and flaviviruses [11-13].
64 The viral restriction functions of SAMHD1 encompass both dNTPase-dependent and -
65 independent mechanisms according to the target virus and the contexts of the host cells such as
66 cell type, differentiation status, IFN-I response and the expression of other host restriction factors
67 that cooperate with SAMHD1 in cells [14].

68 SAMHD1 suppresses innate immune responses [15]. Loss-of-function mutation of SAMHD1
69 correlates with the development of the Aicardi-Goutières syndrome which is an autoimmune
70 disease implicating central nervous system [16]. SAMHD1 prevents spontaneous activation of
71 innate immune responses to self-RNA and self-DNA species that respectively activate retinoic
72 acid-inducible gene I (RIG-I)-like receptor signaling and cyclic GMP-AMP synthase (cGAS)-

73 stimulator of interferon genes (STING) signaling [17-24]. Similarly, SAMHD1 prevents
74 inflammation- or virus-induced innate immune responses [25, 26]. SAMHD1 suppresses pattern
75 recognition receptor signal pathways by interacting with various signal proteins such as
76 mitochondrial antiviral-signaling protein (MAVS), inhibitor of nuclear factor kappa-B kinase
77 subunit alpha (IKKα), IKKβ, IKKε as well as transcription factors including p100 and p105 in the
78 NF-κB pathway which drives proinflammatory cytokine expression and interferon regulatory factor
79 7 (IRF7) which promotes IFN-I expression [25, 27, 28].

80 SARS-CoV-2 caused the COVID-19 pandemic, claiming more than 7 million lives worldwide
81 [29, 30]. SARS-CoV-2 suppresses IFN antiviral responses through multiple strategies to facilitate
82 viral infection [31]; however, the precise mechanisms remain to be elucidated. Previously, we
83 reported that SARS-CoV-2 infection was suppressed upon depletion of SAMHD1 expression in
84 HEK293T, differentiated THP-1 cells, and primary human macrophages [32]. Suppression of IFN
85 signaling of SAMHD1-defective HEK293T cells by baricitinib, a JAK1/2 inhibitor, alleviated the
86 repression of SARS-CoV-2 replication, suggesting that SARS-CoV-2 exploits SAMHD1 for IFN
87 antagonism, thereby facilitating its infection [32]. It remains to be determined if SAMHD1-
88 mediated immunosuppression promotes SARS-CoV-2 replication in the primary target cell type,
89 such as epithelial cells expressing the major viral entry factors ACE-2 and transmembrane
90 protease, serine 2 (TMPRSS2) [33, 34].

91 In this study, we found that SAMHD1 KO in Calu-3 cells conferred resistance to SARS-CoV-
92 2 infection, independent of IFN signaling, by reducing the expression of transcription factors
93 HNF1α and HNF1β, which in turn lowered ACE2 levels and inhibited S-mediated viral entry. Our
94 findings shed light on a novel function of SAMHD1 in upregulating ACE2 expression to facilitate
95 SARS-CoV-2 infection in human lung epithelial cells.
96

97 **Results**

98 **Generation and characterization of stable SAMHD1 KO Calu-3 cell lines**

99 To generate SAMHD1 KO Calu-3 cells, CRISPR/Cas9 technology based on the
100 lentiCRISPRv2 system was employed [35]. Two target sequences of the single guide RNAs
101 (sgRNAs) were obtained from CHOPCHOP v3 with no off-target effect at less than four
102 mismatches [36]. With sgRNA 1 and sgRNA 2, the *Streptococcus pyogenes* Cas9 nuclease
103 (SpCas9) was targeted to the SAMHD1 gene, resulting in cleavage sites that encode ^{11}Lysine
104 and ^{150}Leucine, respectively (Fig. 1A). ^{11}Lysine was the first residue of the nuclear localizing signal
105 (NLS) of SAMHD1 protein and ^{150}Leucine was in the HD domain before the dNTPase active site.
106 Calu-3 cells were transduced with the lentiviral vectors, selected by puromycin and clonal
107 purified with limiting dilution. Several purified cell clones were obtained and tested for SAMHD1
108 protein expression (Fig. 1B). We obtained clone 4 and clone 3 of the respective cell populations

109 treated with sgRNA1 or sgRNA2 having the lowest expression of SAMHD1 compared with the
110 Ctrl clones (Fig. 1B). Therefore, clone 1 of the Ctrl population, clone 4 of the sgRNA1-treated
111 population and clone 3 of the sgRNA2-treated population were used for the subsequent study
112 and named Ctrl, KO1 and KO2, respectively.

113 The genomic DNA sequences at the SpCas9 cleavage sites of KO1 cells (Fig. S1A) and
114 KO2 cells (Fig. S1B) were obtained through sanger sequencing and compared with Ctrl cells. We
115 found that a single nucleotide insertion occurred near the SpCas9 cleavage sites, which
116 frameshifted the SAMHD1 coding sequence thereafter (Red arrows, Fig. S1A and S1B). It was
117 noted that multiple signal peaks were observed after the SpCas9 cleavage sites of KO1 and KO2
118 which may indicate the existence of more than one mutant in the clonal purified population.

119 To confirm whether SAMHD1 KO functionally affected intracellular dNTP levels, cellular
120 dATP levels were measured (Fig. S1C) as an example [37]. We found that the mean values of
121 the intracellular dATP levels of KO1 and KO2 were 8.9- and 7.8- fold more than that of the Ctrl
122 cells (Fig. S1C). This result suggests that KO1 and KO2 were deprived of dNTPase activity of
123 SAMHD1.

124 SAMHD1 depletion may enhance innate immune response even in the absence of extrinsic
125 stimuli depending on cell types [19, 24, 25, 32, 38-40]. To examine if SAMHD1 KO promoted
126 innate immune responses of Calu-3 cells, the mRNA levels of proinflammatory cytokine *IL-6* as

127 well as *IFNβ* and two IFN-stimulated genes (ISGs) *OAS1* and *ISG15* of KO1 and KO2 were
128 detected by RT-qPCR and compared with Ctrl cells (Fig. 1C). We found that KO1 and KO2 cells
129 constitutively expressed higher levels of IL-6 in the absence of any extrinsic stimuli. Interestingly,
130 we found that the expression levels of *IFNβ*, *OAS1* and *ISG15* were significantly upregulated in
131 KO2, but not in KO1 clone (Fig. 1C). Thus, SAMHD1 KO promoted proinflammatory cytokine
132 production from Calu-3 cells in both KO1 and KO2 clones, while strong constitutive IFN-I response
133 was only observed in KO2 clone.

134 **SAMHD1 promotes SARS-CoV-2 replication independent of IFN signaling**

135 To test if SAMHD1 affected SARS-CoV-2 replication in Calu-3 cells, kinetics of ancestral
136 SARS-CoV-2 (Wuhan-Hu-1) replication was examined in Ctrl, KO1 and KO2 cells. We found that
137 the kinetics of infectious virus production was suppressed in both KO1 and KO2 (Fig. 2A) despite
138 only KO2 cells having a higher constitutive IFN-I response than Ctrl cells (Fig. 1C). Similarly,
139 significant suppression of the levels of released viral genome was observed in both KO1 and KO2
140 clones (Fig. 2B). The expressions of intracellular viral nucleoprotein (N) and spike protein (S)
141 were significantly reduced in the infected KO1 and KO2 cells (Fig. 2C). Moreover, intracellular
142 viral RNA levels were suppressed in the infected KO1 and KO2 cells which did not produce higher
143 levels of IFNβ, IFNλ or OAS1 in response to SARS-CoV-2 infection (Fig. 2D). To confirm if IFN
144 signaling contributed to the hindered replication of SARS-CoV-2 in SAMHD1 KO Calu-3 cells,

145 infected cells were treated with or without baricitinib to test if suppressing IFN signaling can rescue
146 SARS-CoV-2 replication in KO1 and KO2 cells. We found that baricitinib did not rescue SARS-
147 CoV-2 replication in Calu-3 cells in terms of released infectious viral titer (Fig. 2E), intracellular
148 viral N protein (Fig. 2F), and intracellular viral *N* mRNA, although baricitinib efficiently suppressed
149 virus-induced *OAS1* expression in Ctrl and KO2 cells (Fig. 2G) as well as virus-induced protein
150 expression of STAT1 and Ser727-phosphorylated STAT1 (Fig. 2F). Therefore, SAMHD1
151 expression is required for SARS-CoV-2 replication in Calu-3 cells independent of its suppressive
152 function to IFN.

153 **SAMHD1 facilitates spike protein-mediated viral entry of SARS-CoV-2**

154 To understand how SAMHD1 promoted SARS-CoV-2 infection, we employed a previously
155 developed single cycle SARS-CoV-2 which was S-defective and pseudotyped with vesicular
156 stomatitis virus glycoprotein (VSV-G), namely, ΔS-VRP(G) [41]. ΔS-VRP(G) infection bypasses
157 S-protein mediated viral entry and infects cell types that do not support authentic SARS-CoV-2
158 infection. Firstly, we confirmed that remdesivir, a nucleoside analogue inhibiting viral RNA-
159 dependent RNA polymerase (RdRP) [42], can efficiently suppress intracellular viral RNA levels
160 (N and E genes) of ΔS-VRP(G) in Calu-3 Ctrl cells, suggesting that ΔS-VRP(G) infection
161 depended on RdRP activity (Fig. 3A). Next, we asked if SAMHD1 deficiency suppressed ΔS-
162 VRP(G) infection similarly as that observed in the authentic SARS-CoV-2 infections (Fig. 2).

163 Interestingly, we found that the intracellular viral N and E RNA levels of ΔS-VRP(G) were not
164 suppressed in KO1 or KO2 cells compared with Ctrl cells at 24 and 48 hrs post-infection (hpi)
165 (Fig. 3B). Comparatively, we observed that intracellular viral N protein expression by ΔS-VRP(G)
166 infection was minimally affected in KO1 cells but was slightly reduced in KO2 cells (Fig. 3C),
167 although the difference was much less than that observed in the authentic SARS-CoV-2 infection
168 (Fig. 2C). ΔS-VRP(G) expresses a dual reporter gene (*Gaussia* luciferase-T2A-neon GFP)
169 through the transcriptional regulatory sequence of S gene [41]. Detection to the *Gaussia*
170 luciferase activity reflects the infectivity of ΔS-VRP(G) [41]. We found that ΔS-VRP(G) infection
171 produced similar levels of *Gaussia* luciferase in Ctrl, KO1 and KO2 cells (Fig. 3D). Although ΔS-
172 VRP(G) infection had a trend of producing less *Gaussia* luciferase in KO2 cells than KO1 and
173 Ctrl, we did not observe significant reductions in both KO1 and KO2 cells (Fig. 3D). Therefore,
174 unlike authentic SARS-CoV-2, SAMHD1 deficiency did not inhibit ΔS-VRP(G) infection.

175 One possible explanation for the selective suppression of authentic SARS-CoV-2 infection
176 but not ΔS-VRP(G) in SAMHD1 KO cells was due to abolished S-protein-mediated viral entry,
177 which was not required for ΔS-VRP(G) infection. To validate the possibility, we employed a SARS-
178 CoV-2 S protein-pseudotyped HIV-1-based reporter virus, namely HIV-1-spike-Luc/ZsGreen [43,
179 44]. Successful infection of HIV-1-spike-Luc/ZsGreen depended on S-protein mediated viral entry
180 and the subsequent viral gene expression driven by HIV-1 single-cycle infection. The infectivity

181 of HIV-1-spike-Luc/ZsGreen can be measured by detecting the expression of the firefly luciferase
182 2 [43, 44]. We found that HIV-1-spike-Luc/ZsGreen infected KO1 or KO2 cells produced
183 significantly less luciferase activity than the Ctrl cells (Fig. 3E). This suggested that SAMHD1
184 expression promoted S protein-mediated viral entry, which in turn facilitated infection of authentic
185 SARS-CoV-2 and HIV-1-spike-Luc/ZsGreen but not ΔS-VRP(G).

186 **SAMHD1 maintains the expression of viral receptor ACE2 of Calu-3 cells**

187 To gain mechanistic insight into how SAMHD1 facilitated spike-protein mediated viral entry,
188 the transcriptomic profiles of Ctrl, KO1 and KO2 cells were obtained by mRNA-Sequencing
189 (mRNA-seq). Firstly, principal component analysis (PCA) was performed to cluster Ctrl, KO1 and
190 KO2 cells. Biological triplicate experiment was performed. Nine PCs were therefore obtained, in
191 which PC1 (61%) and PC2 (37%) covered 98% of the total variance (Fig. S2A). Ctrl, KO1 and
192 KO2 cells were well clustered based on PC1 and PC2 (Fig. S2B). Along PC1 axis, KO1 and KO2
193 cells were clearly clustered and separated from Ctrl cells in the same direction. KO2 cells were
194 separated from KO1 and Ctrl cells along the PC2 axis which however minimally distinguished
195 KO1 and Ctrl cells, suggesting clonal specific transcriptomic profile for KO2.

196 A PCA biplot on the top ten most influential loading genes for the PCA clustering was plotted
197 (Fig. S2C). The PCA biplot indicated that the major loading contributors of PC1 were cell surface
198 proteins (CEACAM6, LGALS4 (or Galectin 4), and GJA1) and proteins implicating extracellular

199 matrix (CST6 (Cystatin E/M) and FAM20C). For PC2, the expression changes of ISGs including
200 OAS2, IFI27, IFITM1 and IF16 as well as MHC class II β-chain component HLA-DPB1
201 distinguished KO2 from Ctrl and KO1 but had minimal contribution to PC1 axis (Fig. S2C). In
202 summary, KO1 and KO2 were distinguished from Ctrl along PC1 which was mainly influenced by
203 the mRNA expression of genes implicating cell surface and extracellular matrix while KO2 was
204 further distinguished from Ctrl and KO1 along PC2 which was mainly influenced by the
205 expressions of ISGs.

206 Next, by analyzing the differential expressed genes (DEGs) implicated in both KO1 and KO2
207 having more than 2-fold change and with false discovery rate (FDR)-adjusted P values < 0.01
208 (Table S1), we found that 806 DEGs were commonly observed in KO1 and KO2 compared with
209 Ctrl cells (Fig. 4A). Among the 806 DEGs, 681 DEGs were of the same direction of change (Table
210 S2). We searched for known and validated entry factors of SARS-CoV-2 infection. We found that
211 the expressions of ACE2 and TMPRSS2 were decreased in both KO1 and KO2 (Fig. 4B). Both
212 ACE2 and TMPRSS2 transcripts were more suppressed in KO1 than in KO2. Other known SARS-
213 CoV-2 entry factors were, however, not on the list. Those included alternative receptors
214 Transmembrane protein 106B (TMEM106B) [45], transferrin receptor [46], CD147 [47], AXL
215 receptor tyrosine kinase (AXL) [48], kringle containing transmembrane protein 1 (KREMEN1), and
216 asialoglycoprotein receptor 1 (ASGR1) [49], attachment factors Neuropilin-1 [50], Niemann-Pick

217 C1 (NPC1) [51], lectin receptors [52], and endosomal protease cathepsin L [53] (Table S2).
218 Interestingly, we noticed both KO1 and KO2 had enhanced expression of furin protease (Fig. 4B),
219 which may facilitate S protein priming in infected cells [54].

220 Finally, ACE2 and TMPRSS2 mRNA and protein expressions were validated respectively by
221 RT-qPCR (Fig. 4C) and Western blot (Fig. 4D). For ACE2, we designed a primer pair targeting
222 the full-length isoforms but not the N-terminally truncated ACE2 (dACE2) that is not a functional
223 receptor to SARS-CoV-2 [55]. We employed a monoclonal ACE2 antibody that detected an N-
224 terminal region (peptide sequence surrounding Asp201) that is absent in dACE2. For TMRPSS2,
225 we designed a primer pair that can detect isoform 1 to 3. We employed a monoclonal TMPRSS2
226 antibody that detected the protease domain which is present in both zymogen (~ 55 kDa) and
227 active form (~ 31 kDa).

228 We found that the full length ACE2 mRNA and protein expressions were significantly reduced
229 in KO1 and KO2 cells (Fig. 4C and 4D). We confirmed the decreased full length ACE2 mRNA
230 expression in KO1 and KO2 by another qPCR primer pair [55] (Fig. S3A). Interestingly, we found
231 that KO2, but not KO1 cells, expressed significantly higher levels of dACE2 (Fig. S3B), which is
232 known to be induced by IFN-I [55, 56]. In contrast, we found that TMPRSS2 mRNA and protein
233 expressions were only downregulated in KO1 but not in KO2 cells (Fig. 4C and 4D). Indeed,
234 mRNA-seq results showed that TMPRSS2 transcripts were marginally defined as DEG in KO2

235 cells with log_2 fold change equal to -1.01 (Fig. 4B, right panel). Therefore, only the expression of
236 full-length ACE2 but not TMPRSS2 was confirmed to be commonly repressed in SAMHD1 KO
237 Calu-3 cells. This suggested that SAMHD1 expression was important to maintain full length ACE2
238 expression that facilitated S protein-mediated viral entry and SARS-CoV-2 infection.

239 **SAMHD1 expression does not affect ACE2 mRNA stability**

240 ACE2 mRNA levels were downregulated in SAMHD1 KO cells (Fig. 4B-4C, S3A). To test
241 whether SAMHD1 KO affected ACE2 mRNA stability, an actinomycin D (actD) treatment assay
242 was performed [57, 58]. Ctrl, KO1 and KO2 cells were treated with actD that inhibited transcription.
243 At various time points following the treatment, the ACE2 mRNA levels were measured by three
244 specific qPCR primer pairs: the same qPCR primer pair used in Fig. 4C for full length ACE2
245 targeting exon 2/3 junction and exon 4 (Fig. 5A, primer pair 1 in Table S5), a qPCR primer pair
246 targeting the 5' end of ACE2 mRNA at exon 1/2 junction (Fig. 5B, primer pair 2 in Table S5), and
247 a qPCR primer pair targeting the 3' end of ACE2 mRNA at exon 19 (Fig. 5C, primer pair 3 in Table
248 S5). We found that ACE2 mRNA was relatively stable over time that more than 50% of it remained
249 by 8 hrs of actD treatment (Fig. 5A-5C), similar to the observation by others [59].

250 We included additional controls to validate the actD treatment assay. The mRNA stability of
251 a proapoptotic gene BCL-2 interacting killer (BIK) is suppressed by La-related protein 1 (LARP1),
252 a protein highly expressed in cancer cells [60, 61]. We found that BIK mRNA in Calu-3 Ctrl cells

253 exhibited rapid decay following actD treatment, with levels decreasing to below 50% by 4 hrs and
254 approximately 10% remaining at 8 hrs (Fig. 5D). Comparatively, 18S ribosomal RNA, which is a
255 structural component of ribosome and more stable than mRNA, was found to remain above 50%
256 of the initial levels during the actD treatment assay (Fig. 5E). These results confirmed that the
257 actD treatment assay was valid in distinguishing unstable RNA species. We found that ACE2
258 mRNA in actD-treated KO1 or KO2 cells were similarly stable as compared with that of the Ctrl
259 cells with over 50% of *ACE2* mRNA remaining in both KO1 and KO2 cells (Fig. 5A-5C). Therefore,
260 SAMHD1 expression does not affect ACE2 mRNA stability.

261 **SAMHD1 maintains HNF1α, HNF1β and HNF4α expressions in Calu-3 cells**

262 Next, we questioned how SAMHD1 KO affected *ACE2* transcription. The *ACE2* promoter is
263 a bipartite promoter that is controlled by various transcription factors depending on cell types [62].
264 Analysis of human lung tissues and immortalized lung 16HBE cells revealed STAT3
265 transcriptionally controlled ACE2 expression [63]. HNF1α and HNF1β were found to cooperate
266 and promote ACE2 expression transcriptionally in HEK293 and pancreatic islet cells [64, 65].
267 HNF4α was found to be a transcription repressor or activator of ACE2 expression depending on
268 different cell types and experiment settings [66-68]. Sp1 was found to transcriptionally promote
269 ACE2 expression in immortalized human type II alveolar epithelial cells [68]. FOXA2 was found
270 to promote ACE2 transcription in 832/13 insulinoma cells or mouse pancreatic islets [69]. Ikaros

271 was found to drive ACE2 expression in human cardiac fibroblasts in response to Ang II stimulation
272 by binding to ATTTGGA sequence of the proximal promoter [70].

273 The exact transcription factors regulating endogenous ACE2 expression in Calu-3 cells
274 remain unclear. To the best of our knowledge, GATA6 was the only experimentally identified
275 transcription factor in Calu-3 cells promoting ACE2 expression and facilitating SARS-CoV-2
276 infection [71]. GATA6 was identified by CRISPR/Cas9-KO library screening for surviving cells
277 upon SARS-CoV-2 infection. Two additional independent studies identified HNF1β as a significant
278 candidate to reduce surviving cells upon SARS-CoV-2 infection by CRISPR/Cas9-activation
279 library screening [72, 73]. However, unlike GATA6, the role of HNF1β in regulating ACE2
280 expression in Calu-3 cells was not further validated. Other known ACE2 transcription factors as
281 mentioned above were not on the candidate list of the three screening studies [71-73]. Our RT-
282 qPCR analysis revealed that the mRNA levels of HNF1β were reduced in KO1 and KO2 cells
283 (Fig. 6B), while GATA6 mRNA level was unchanged in KO1 and KO2 cells compared to Ctrl cells
284 (Fig. 6D).

285 HNF1α, HNF1β, and HNF4α are core transcription factors that establish a complex and
286 interdependent regulatory network during liver and pancreas development [74, 75]. Particularly in
287 hepatocytes, HNF1α and HNF1β can transcriptionally promote the expression of HNF4α [76]. In
288 return, HNF4α promotes HNF1α's expression [77, 78] and transcriptional activity [79]. This

289 network in lung cells is unclear. We found that the mRNA levels of HNF1α (Fig. 6A) and HNF4α
290 (Fig. 6C) were also downregulated in KO1 and KO2 cells. Western blot analysis showed that the
291 protein levels of HNF1α, HNF1β and HNF4α were reduced in KO1 and KO2 cells compared to
292 Ctrl cells (Fig. 6E). These results suggest that endogenous SAMHD1 maintains the expression of
293 the HNF1α, HNF1β and HNF4α in Calu-3 cells.

294 **HNF1α and HNF1β promote endogenous ACE2 expression in Calu-3 cells**

295 Whether HNF1α, HNF1β and HNF4α controlled the endogenous ACE2 expression in Calu-
296 3 cells was unclear. To address this question, HNF1α, HNF1β and HNF4α were knocked down
297 individually in Calu-3 cells. Dicer-substrate siRNAs (DsiRNA) transfection efficiently reduced the
298 target gene expression by more than 50% (Fig. 7A-7C and S4A). We noticed that knocking down
299 HNF1β, but not HNF1α, suppressed HNF4α mRNA and protein expression in Calu-3 cells.
300 Knocking down HNF4α suppressed HNF1α mRNA but not protein (Fig. 7B and 7C). Regarding
301 endogenous ACE2 expression, we found that knocking down HNF1α and HNF1β, but not HNF4α,
302 significantly suppressed ACE2 protein expression (Fig. 7A-7B and S4A). Interestingly, only
303 knocking down HNF1α led to a significant reduction of ACE2 mRNA expression (Fig. 7C).
304 Knocking down HNF1β suppressed ACE2 protein expression (Fig. 7A-7B, S4A) but not mRNA
305 expression in Calu-3 cells (Fig. 7C). Finally, we found that knocking down either HNF1α or HNF1β
306 significantly suppressed SARS-CoV-2 infection in Calu-3 cells (Fig. 7D). Therefore, HNF1α and

307 HNF1β are required to promote the expression of ACE2 and support SARS-CoV-2 infection in
308 Calu-3 cells.

309 **HNF1-dependent ACE2 expression is suppressed in SAMHD1 KO Calu-3 cells**

310 We hypothesized that the functions of HNF1α and HNF1β in promoting endogenous ACE2
311 expression was suppressed in the SAMHD1 KO Calu-3 cells. To test the hypothesis, transient
312 HNF1α and HNF1β knockdown was performed in SAMHD1 KO cells to examine if the ACE2
313 expression was less dependent on HNF1α and HNF1β when their expression was suppressed
314 upon SAMHD1 deficiency. We found that HNF1α and HNF1β protein expression in KO1 and KO2
315 cells could still be suppressed by DsiRNA knockdown despite their lower expression levels
316 compared to Ctrl cells (Fig. 8A-8C and S4B). Knocking down HNF1α and HNF1β significantly
317 reduced ACE2 protein expression in Ctrl cells (Fig. 8A, 8D and S4B). In the case of KO1 and KO2
318 cells, the suppression of ACE2 protein expression by HNF1α and HNF1β knockdown was
319 mitigated. Knocking down HNF1α, but not HNF1β, reduced ACE2 mRNA expression in Ctrl cells
320 (Fig. 8E). In contrast, HNF1α knockdown was less potent in further suppressing ACE2 mRNA in
321 KO1 and KO2 cells (Fig. 8E). Given that endogenous ACE2 expression was more dependent on
322 HNF1α and HNF1β in Calu-3 Ctrl cells (Fig. 8D and 8E), our data suggest that SAMHD1
323 expression promotes HNF1-dependent ACE2 expression in Calu-3 cells.

324

325 **Discussion**

326 In this study, we investigated the role of SAMHD1 in SARS-CoV-2 infection of Calu-3 cells,
327 which expressed endogenous ACE2 and supported productive viral replication. Similar to our
328 previous study using other cell types [32], SARS-CoV-2 replication was enhanced in SAMHD1
329 expressing Calu-3 cells. Previous study showed that inhibition of IFN signaling by the JAK1/2
330 inhibitor baricitinib alleviated the replication restraint of SARS-CoV-2 in HEK293T cells with
331 SAMHD1 KO [32], while in the current study, baricitinib treatment did not promote SARS-CoV-2
332 replication in SAMHD1 KO Calu-3 cells. We noticed that baricitinib treatment promoted the
333 intracellular viral N RNA and protein levels of SARS-CoV-2 in Calu-3 Ctrl cells but did not change
334 the production of infectious progeny viruses. In contrast, baricitinib treatment enhanced neither
335 the viral RNA nor viral protein levels in SAMHD1 KO1 and KO2 cells, suggesting that some
336 fundamental mechanisms to SARS-CoV-2 replication were disrupted in KO1 and KO2 cells rather
337 than IFN signaling.

338 HEK293T cells support productive replication of SARS-CoV-2 despite negligible expression
339 of ACE2 and TMPRSS2 [80-82]. Through a CRISPR/Cas9 KO library screen, an alternative viral
340 receptor TMEM106B was found to be required for SARS-CoV-2 replication in HEK293T cells [82].
341 In contrast, SARS-CoV-2 infection in Calu-3 cells exhibits a strong dependence on ACE2
342 expression, as evidenced by multiple CRISPR/Cas9 library screens where ACE2 was consistently

343 the most critical host factor identified [71-73]. We found that compared to other known viral entry
344 factors, ACE2 expression was significantly reduced in SAMHD1 KO Calu-3 cells, with consistent
345 results observed in both the KO1 and KO2 lines. SAMHD1 KO significantly hindered SARS-CoV-
346 2 S protein-mediated viral entry in Calu-3 cells; however, once this barrier was bypassed by VSV-
347 G pseudotyping, the single-cycle infection of SARS-CoV-2 replicon was restored. Therefore,
348 SAMHD1 KO abolished ACE2-dependent and S-mediated viral entry which is required for SARS-
349 CoV-2 infection of Calu-3 cells, but not HEK293T cells.

350 We questioned how SAMHD1 promoted ACE2 expression in Calu-3 cells. We found that
351 SAMHD1 KO repressed ACE2 mRNA expression in Calu-3 cells, but ACE2 mRNA stability was
352 unaffected. This suggests that SAMHD1 KO might pre-transcriptionally or transcriptionally
353 suppress ACE2 mRNA expression. We found that SAMHD1 KO suppressed the expression levels
354 of HNF1α and HNF1β, which in turn downregulated the expression of ACE2 and SARS-CoV-2
355 infection. We functionally validated the inhibition of HNF1-mediated endogenous ACE2
356 expression in SAMHD1 KO Calu-3 cells. To the best of our scope, this is the first study functionally
357 confirming the role of HNF1α and HNF1β in promoting ACE2 expression in lung epithelial cells.
358 Interestingly, although HNF1α and HNF1β were previously defined to be transcription factors of
359 ACE2 by binding to the HNF1 response element of the proximal promoter [64, 65], we found that
360 only HNF1α was required for ACE2 mRNA expression in Calu-3 cells. HNF1β was however

361 required for ACE2 protein but not mRNA expression. These findings implied that SAMHD1 KO
362 contributed to suppress ACE2 mRNA and protein levels through downregulation of HNF1α and
363 HNF1β expression, respectively (summarized mechanisms in Fig. 9).

364 It is still in question how SAMHD1 promotes the expression and activity of HNF1α and
365 HNF1β in driving ACE2 expression. SAMHD1 is a nuclear protein that has not been identified to
366 have direct transcriptional function. SAMHD1 mainly interacts with single-stranded RNA or DNA
367 but had low affinity to double-stranded DNA [83, 84]. It is possible that SAMHD1 depletion may
368 have created some cellular stresses that inhibit the expression of HNF1α and HNF1β. We found
369 that SAMHD1 KO Calu-3 cells spontaneously express higher IL-6 than Ctrl cells. Indeed, the
370 expression of several proinflammatory cytokines including IL-1α, IL-1β, CSF2 and IL-11 were also
371 upregulated in both KO1 and KO2 clones (Table S2). Some studies suggest that HNF1α and
372 HNF1β expressions are suppressed upon inflammation. Firstly, the expression of HNF1α in
373 hepatocytes was suppressed through a positive feedback circuit when mice were treated with
374 dimethylnitrosamine that induced liver inflammation followed by hepatic fibrogenesis [85].
375 Secondly, the expression of HNF1β was downregulated by IFN-γ in kidney cells HK-2, while
376 lipopolysaccharide injection downregulated HNF1β expression in mouse kidney cells [86]. Thirdly,
377 we found that HNF4α knockdown reduced HNF1α mRNA expression in Calu-3 cells although the
378 protein change was not observed (Fig. 7A-7C). One recent study suggests HNF4α is

379 transcriptionally suppressed by inflammatory stimuli such as IL-6 and IL-1β in differentiated
380 HepaRG cells [87]. It is possible that the enhanced expression of proinflammatory cytokines of
381 SAMHD1 KO Calu-3 cells suppresses HNF4α expression, thereby decreasing the expression of
382 HNF1α. We also found that HNF1β positively regulated HNF4α expression (Fig. 7B-7C). It is
383 possible that HNF1β plays an upstream role in the expression of HNF1α and HNF4α in Calu-3
384 cells. SAMHD1 expression prevents spontaneous proinflammatory cytokine production mainly
385 through inhibition of NF-kB signaling [25, 28] and preventing RIG-I like receptor signaling and
386 cGAS-STING activation by self-RNA or self-DNA species [17-24]. Therefore, SAMHD1
387 expression maintains innate immune homeostasis, which sustains the endogenous expressions
388 of HNF1α and HNF1β to support ACE2 expression. Further investigation is needed to confirm the
389 idea.

390 We noticed that several cell surface proteins and proteins related to extracellular matrix
391 distinguished SAMHD1 KO Calu-3 cells from Ctrl cells through the PCA (Fig. S2C). Similarly,
392 gene ontology (GO) enrichment analysis (GOEA) of cellular components to the 681 common
393 DEGs of SAMHD1 KO Calu-3 cells suggest that cell periphery was the best enriched term having
394 the lowest FDR-adjusted P value (Fig. S5 and table S3). Among the top ten GO terms, four terms
395 were correlated with cell surface membranes in addition to cell periphery (including plasma
396 membrane, apical plasma membrane and cell surface) while five terms were correlated with

397 extracellular matrix (including extracellular matrix, external encapsulating structure, extracellular
398 region, extracellular space, collagen-containing extracellular matrix). Although we did not observe
399 any validated SARS-CoV-2 entry factors on the 681 common DEGs except ACE2, TMPRSS2
400 and furin in which only ACE2 was found to be consistently downregulated in both KO1 and KO2
401 clones, it might be possible that the changes in cell surface and extracellular matrix structures
402 contribute to the suppressed SARS-CoV-2 infection and viral entry in SAMHD1 KO Calu-3 cells.
403 Any combinatorial effects of the DEGs contributing to the changes in cell surface and extracellular
404 structures that may potentially suppress SARS-CoV-2 infection shall be valuable in future
405 investigation (Table S4).

406 Why SAMHD1 depletion affected the expression of so many genes encoding cell surface
407 and extracellular matrix proteins remains unclear. One study suggests SAMHD1 expression
408 promotes focal adhesion kinase (FAK) signaling by binding to cortactin, and in turn activated Rac
409 family small GTPase 1 (Rac1)-mediated lamellipodia formation in human clear cell renal cell
410 carcinoma [88]. It is possible that SAMHD1 KO Calu-3 had lower activity of FAK and Rac-1.
411 Interestingly, Rac-1 was found to promote SARS-CoV-2 entry via macropinocytosis in ACE2-
412 expressing cells [89]. Thus, SAMHD1 may enhance SARS-CoV-2 infection by macropinocytosis
413 through cortactin, FAK and Rac-1, in addition to promoting HNF1-mediated ACE2 expression.
414 Further investigation is required for the detailed mechanism by which SAMHD1 promotes SARS-

415 CoV-2 infection in physiologically relevant cell types.

416 We were surprised to find that only KO2 but not KO1 clone had spontaneous IFN-I responses
417 (Fig. 1C). Indeed, based on PCA, KO2 cells were clustered away from Ctrl and KO1 cells mainly
418 by several ISGs (Fig. S2C). IFN-I production requires activation of IRF3/7 in addition to NF-κB
419 signal pathway [90]. KO1 cells exhibited complete absence of SAMHD1 protein since expression
420 was abolished with sgRNA1 frameshifting exon 1 at ^{11}Lysine (Fig. 1A, 1B and S1A). KO2 cells
421 may express a truncated protein consisting of the first 1-149 amino acids of SAMHD1. Whether
422 the truncated SAMHD1 protein (aa. 1-149) contributes to IFN-I activation and ISG expression in
423 Calu-3 cells is unclear and will require further investigation.

424 In summary, we found that SAMHD1 is a proviral factor to SARS-CoV-2 infection in Calu-3
425 cells by enhancing S protein-mediated viral entry through maintaining HNF1-mediated ACE2
426 expression. Our study shed light on a novel function and mechanism of SAMHD1 in facilitating
427 SARS-CoV-2 infection in lung epithelial cells.

428

429 **Materials and Methods**

430 **Cell culture**

431 Cell culture was performed as previously described [91, 92]. The original wildtype Calu-3
432 cells were obtained from ATCC (HTB-55™). Wild-type Calu-3 cells as well as Ctrl, KO1 and KO2

433 cells were maintained in DMEM/F12 (ThermoFisher Scientific, Cat. no. 11320033) with 20% FBS,
434 100 U/mL penicillin (Gibco, Cat. no. 15140122), and 100 µg/mL streptomycin (Gibco, Cat. no.
435 15140122). Huh7.5 cells were kindly provided by Dr. Balaji Manicassamy (University of Iowa)
436 [41]. Vero-hTMPRSS2 cells were cultured in DMEM (ThermoFisher Scientific, Cat. no. 11965092)
437 with 10% FBS, 100 U/mL penicillin, 100 µg/mL streptomycin and 5 µg/mL blasticidin (Gibco, Cat.
438 no. A1113903) as previously described [93]. Huh7.5 cells were cultured in DMEM with 10% FBS,
439 100 U/mL penicillin, 100 µg/mL streptomycin. Actinomycin D (SellekChemicals, Cat. no. S8964),
440 remdesivir (MCE, Cat. no.: HY-104077) and baricitinib (MCE, Cat. no.: HY-15315) were dissolved
441 in dimethyl sulfoxide (DMSO) and stored at -20°C.

442 **Generation of SAMHD1 KO Calu-3 cells**

443 SAMHD1 KO Calu-3 cells were generated similarly as previously described with some
444 modifications [91, 92]. Briefly, third generation lentiviral particles were rescued from HEK293T
445 cells (1 x 10^{7}) transfected with lentiCRISPR v2-puro empty vector, lentiCRISPR v2-puro-sgRNA1,
446 or lentiCRISPR v2-puro-sgRNA2 together with psPAX2, and pMD2.G (ratio 4:3:1) by PEI (1:5
447 ratio). The target sequence of sgRNA 1 guided SpCas9 cutting at exon 1 of SAMHD1 gene (chr20:
448 36,951,611/36,951,612) while that of sgRNA 2 targeted SpCas9 for exon 4 (chr20:
449 36,935,087/36,935,088). The template sequence for sgRNA1 was *5'-*
450 *GTCATCGCAACGGGGACGCTTGG* and sgRNA2 was *5'-CTTCGATACATCAAACAGCTGGG*.

451 At 24 hrs post-transfection (hpt), the culture supernatant was replenished with fresh media. At 72
452 hpt, the 12 mL culture supernatant was cleared by 500 x g 5 min centrifugation followed with 0.45
453 µm filtering and concentrated by lenti-concentrator (ORIGENE, Cat. no TR30026) into 1mL media.
454 A day before transduction, 4 x 10^5 Calu-3 cells were seeded in 12 well plates. On the day of
455 transduction, the culture supernatant of the Calu-3 cells was replaced with the 1mL concentrated
456 virus. At 24 hpi, the culture supernatant was replaced with fresh DMEM/F12 with 20% FBS, 100
457 U/mL penicillin, and 100 µg/mL streptomycin. At 72 hpi, cells were selected against 1 µg/mL
458 puromycin. The survival cells of the transduced populations were purified by limited dilution on a
459 96 well plate. Finally, the purified cell clones were verified for expression of SAMHD1 and
460 genotyping.

461 **RNA interference and transfection**

462 DsiRNAs were oligo-duplex and the sequences were predesigned by Integrated DNA
463 Technologies (IDT) [94]. Cells were transfected with DsiRNA with Lipofectamine RNAiMAX
464 Reagent (ThermoFisher Scientific, Cat. no. 13778150). In brief, equal volume of OPTIMEM-
465 (Gibco, Cat. no. 31985070) diluted DsiRNA (150 µl for 24 well format and 300 µl for 12 well format)
466 and OPTIMEM-diluted lipofectamine RNAiMAX (1:3 ratio) were mixed and incubated for 20 min
467 at room temperature. Cell suspension (0.5 mL in 24 well format and 1 mL in 12 well format) was
468 mixed with the 600 µl DsiRNA/lipofectamine RNAiMax complex. At 24 hpt, culture supernatant

469 was replaced with fresh medium. Cells were harvested at indicated time points. The DsiRNA
470 sequences used in the current study were listed in Table S5.

471 **Virus stocks**

472 Authentic SARS-CoV-2 (Wuhan-Hu-1) was rescued from Vero-hTMPRSS2 transfected with
473 bacterial artificial chromosome carrying SARS-CoV-2 genome (BAC-SARS-CoV-2) as previously
474 described with some modifications [95]. In brief, 1 x 10^7 Vero-hTMPRSS2 cells were seeded in a
475 T75 flask a day before transfection without blasticidin. Vero-hTMPRSS2 cells were transfected
476 with 10 μg BAC-SARS-CoV-2 with lipofectamine 3000 (ThermoFisher Scientific, Cat. no.
477 L3000008). At 24 hpi, the culture supernatant was replaced with serum-free DMEM. At 72 hpi,
478 80% cytopathic effect was observed. The crude culture supernatant was collected for one freeze-
479 thaw cycle. Then, the supernatant was cleared by pelleting debris at 2,000 x g, 10 min, 4°C. The
480 viral containing supernatant was aliquoted and frozen at -80°C for subsequent studies.

481 ΔS-VRP(G) was rescued from Huh7.5 transfected with BAC carrying spike-defective SARS-
482 CoV-2 genome (BAC-ΔS-Gluc-T2A-nGFP) together with VSV-G expression plasmid similarly as
483 previously described [41, 96].

484 HIV-1-spike-Luc/ZsGreen (BEI resources, Cat. no. NR-53818) was a generous gift donated
485 by Dr. Jesse Bloom (Fred Hutchinson Cancer Center) and Dr. Alejandro Benjamin Balazs
486 (Harvard University) and available on BEI resources. The titration of the stock batch (Lot:

487 70042784) was 4.99 × 10^5 relative luciferase tissue culture infectious dose 50% ($TCID_{50}$) units in

488 HEK293-hACE2 cells at 48 hpi.

489 **Virus infection assays**

490 For authentic SARS-CoV-2, cells were seeded a day prior to infection. The culture

491 supernatant was replaced with serum free DMEM prior to infection. Then, the cells were incubated

492 with SARS-CoV-2 at appropriate MOI for 1 hr. Then, the virus inoculum was aspirated. The cells

493 were washed twice with DPBS (Gibco, Cat. no. 14190144). Then, cells were replenished with

494 serum free DMEM. The culture supernatants or infected cells were harvested at indicated time

495 points.

496 For ΔS-VRP(G), cells were infected as previously described [41, 96] and similarly as that of

497 the authentic SARS-CoV-2 but with 2 hr virus inoculation instead of 1 hr. After virus inoculation,

498 infected cells were washed twice with DPBS. Cells were then replenished with DMEM/F12 with

499 20% FBS, 100 U/mL penicillin, and 100 μg/mL streptomycin. The culture supernatants or infected

500 cells were harvested at indicated time points.

501 For HIV-1-spike-Luc/ZsGreen, cells were infected as previously described [43, 44]. Cells

502 were incubated with the virus in the presence of 5 μg/ml polybrene for 1 hr in DMEM/F12 with

503 20% FBS, 100 U/mL penicillin, and 100 μg/mL streptomycin. Then, virus inoculum was removed.

504 Fresh DMEM/F12 with 20% FBS, 100 U/mL penicillin, and 100 μg/mL streptomycin was added.

505 At 48 hpi, infected cells were harvested for downstream analysis.

506 **Plaque assay**

507 A day before infection, 4 x 10^5 or 8 x 10^5 Vero-hTMPRSS2 cells were seeded respectively
508 on 12- or 6- well plates. Vero-hTMPRSS2 cells were infected with serially diluted viral stocks for
509 1 hr. Then, the virus inoculum was removed. Infected cells were overlayed with 1% agarose in
510 DMEM/ DPBS (1:1). At 72 hpi, infected cells were overnight fixed with 4% paraformaldehyde/PBS
511 (ThermoFisher Scientific, Cat. no. J19943.K2). Then, the overlay was removed, and the cells
512 were stained with 0.5% crystal violet in 10% methanol for at least 5 min. Plaques were visualized.
513 Virus concentration was calculated based on the number of plaques in the countable dilution.

514 **Viral copy number detection**

515 Viral RNA was extracted by RNeasy Plus kit (QIAGEN, Cat. no. 74134) in which viral
516 containing solutions and RLT plus lysis buffer was in 1:4 ratio. Viruses were lysed in RLT plus
517 lysis buffer for 10 min at room temperature. The purified viral RNA was reverse transcribed using
518 the iScript cDNA Synthesis Kit (BIO-RAD, Cat. no. 1708891). Viral RNA was detected by the
519 qPCR primer pair targeting the viral RdRP (Table S5) with iTaq™ Universal SYBR® Green
520 Supermix (BIO-RAD, Cat. no.1725124) [97, 98]. Standard curve for the number of single stranded
521 DNA against Ct value was generated using the BAC-SARS-CoV-2 DNA. The copy number of
522 single stranded RNA was estimated from the copy number of cDNA in each sample.

523 **Genomic DNA sequencing**

524 The genome DNA of Ctrl, KO1 and KO2 cells were purified with DNeasy Blood and Tissue
525 Kits for DNA Isolation (QIAGEN, Cat. no. 69504). Exon 1 and exon 4 regions encompassing the
526 Cas9 cleavage sites were amplified by Phusion High-Fidelity DNA Polymerase (NEB, Cat. no.
527 M0530L). The sequences of the PCR primer pair for amplifying exon 1 was *5'-*
528 *CGAAGGGCTCAACTGTCAGT* (forward) and *5'-CTCGGGTCTTCCTTTCCTCG* (reverse) and
529 that of exon 4 was *5'-TGATCTGTCTGGTAGTGATACCT* (forward) and *5'-*
530 *CGATTGTGTGAAGCTCCTGG* (reverse). Then, the PCR products were submitted for sanger
531 sequencing services provided by Genomics Division of Iowa Institute of Human Genetics
532 (University of Iowa) using the forward primers.

533 **Cellular dATP detection**

534 Cellular dATP levels were measured by a single nucleotide RT incorporation assay
535 previously described [37, 40, 92]. In brief, 2 x 10^6 cells were harvested for dNTP extraction with
536 50% methanol. Methanol extract was dried at 80°C for 1 hr and then reconstituted in reaction
537 buffer at appropriate dilution within linear range of the assay as previously described for dATP
538 levels detection. The levels of cellular dATP were calculated by extrapolating the relative band
539 intensity to the standard curve created by the parallel reactions.

540 **Western blot analysis**

541 Upon harvest, cells were washed once with DPBS and lysed with 1 x cell lysis buffer (Cell
542 Signaling Technology, Cat. no. 9803) with phosphatase and protease inhibitor (ThermoFisher
543 Scientific, Cat. no. A32961) for 10 to 30 min until complete lysis. Cell debris was removed by
544 centrifugation at 16.1 kg for 10 min at 4°C. Total protein concentration was estimated by Pierce™
545 BCA Protein Assay Kit (ThermoFisher Scientific, Cat. no. 23225). Protein samples with
546 normalized total protein levels were mixed with 5 x protein sample buffer (0.25 M Tris-Cl pH 6.8,
547 20% glycerol, 10% SDS and 1% saturated bromophenol blue) to the final concentration of 1 x and
548 heat-denatured at 98°C for 10 min. Cellular protein (10 to 25 μg) was loaded onto polyacrylamide
549 gels for Western blot analysis as previous described [91]. Primary antibodies used were as follows:
550 Anti-GAPDH (BIORAD, Cat. no. AHP1628), anti-viral N (BEI resources, Cat. no. NR-56223), anti-
551 viral S (ThermoFisher Scientific, Cat. no. PA5114451), anti-SAMHD1 (Abcam, Cat. no. ab117908),
552 anti-STAT1 (Cell Signaling Technology, Cat. no. 9172T), anti-p-STAT1 (Cell Signaling
553 Technology, Cat. no. 8826T), anti-ACE2 (Cell Signaling Technology, Cat. no. 92485T), anti-
554 TMPRSS2 (Santa Cruz Biotechnology, Cat. no. sc-515727), anti-HNF1α (Cell Signaling
555 Technology, Cat. no. 89670T), anti-HNF1β (Proteintech, Cat no. 12533-1-AP) and anti-HNF4α
556 (Cell Signaling Technology, Cat. no.3113T). For secondary antibody, goat anti-mouse IgG (H+L)
557 HRP (Promega, Cat. no. W4021) or goat anti-rabbit IgG (H+L) HRP (Promega, W401B) was used.
558 Immunoblots were developed with Odyssey Fc Imager. Protein band intensity was quantified by

559 Image Studio™.

560 **RNA extraction and RT-qPCR**

561 Cellular RNA extraction was performed with RNeasy Plus Kits according to the
562 manufacturer's instructions. Upon harvest, cells were washed once with DPBS and lysed with
563 RLT plus lysis buffer. After column purification, 1 μg of purified RNA was used for reverse
564 transcription through iScript cDNA Synthesis Kit. The cDNA product was used for qPCR
565 quantification with iTaq Universal SYBR Green supermix. SYBR signal was quantified by
566 QuantStudio™ 3 Real-Time PCR or CFX Duet Real-Time PCR System. The qPCR primer pairs
567 were either previously designed (including Viral E [99], 18S RNA [100] , IL-6 [25], OAS1 [101],
568 ACE2 and dACE2 [55]), predesigned by PrimerBank [102] or designed in-house based on NCBI
569 primer-BLAST with Primer3 adjustment (Table S5).

570 **Luciferase detection**

571 To detect secreted *Guassia* luciferease activity, 20 μl of culture supernatant was incubated
572 with 50 μl of the working solution of Pierce™ Gaussia Luciferase Flash Assay Kit (ThermoFisher
573 Scientific, Cat. no. 16158) for quantification of the resulting chemiluminescence following
574 manufacturer's instruction. To detect cellular firefly luciferase 2 activity, cells were washed once
575 with DPBS and lysed in 1 x passive lysis buffer (Promega, Cat. no. E1941) supplemented with
576 phosphatase and protease inhibitor. At 30 min lysis, cell debris were removed by centrifugation

577 at 16.1 kg for 10 min at 4°C. Total protein concentration was estimated by Pierce™ BCA Protein
578 Assay Kit. 10 µl of the PLB lysate was incubated with 100 µl of LAR-II substrate reagent of the
579 Dual-Luciferase® Reporter Assay System following manufacturer's instruction to quantify the
580 resulting chemiluminescence (Promega, Cat. no. E1980). The cellular firefly luciferase 2 activities
581 were calculated as follow: ($RLU_{infected}$ per one microgram protein) – ($RLU_{uninfected}$ per one
582 microgram protein).

583 **mRNA-sequencing**

584 Calu-3 Ctrl, KO1 and KO2 cells (8 x 10^5) were seeded in 6 well plates in biological triplicate.
585 Cells were cultured in 2 mL DMEM/F12 with 20% FBS, 100 U/mL penicillin, and 100 µg/mL
586 streptomycin. At 20 hrs after seeding, cells were washed once with DPBS and lysed with RLT
587 plus lysis buffer. Cellular RNA was purified with RNeasy Plus kit following manufacturer's
588 instructions. All RNA samples got RNA integrity Number (RIN) scores equal to or more than 9.9
589 as determined by Agilent BioAnalyzer by Genomics Division of Iowa Institute of Human Genetics
590 (University of Iowa). The subsequent steps of the mRNA-Seq were performed by the Genomics
591 Division using manufacturer recommended protocols. Briefly, at least 500 ng of DNase I-treated
592 total RNA was used to prepare sequencing libraries using the Illumina stranded mRNA library
593 preparation kit (Illumina, Cat. no. 20040534). Barcoded libraries were quantified using a Qubit
594 fluorometer (ThermoFisher Scientific) and pooled together to give the same molar concentration

595 per sample. The pooled libraries were sequenced on the Element AVITI24 sequencing platform
596 on a Cloudbreak FS 150 cycle (2 x 75 bp) medium output sequencing flow cell (Element
597 Biosciences, Cat. no. 860-00014) to generate at least 30M paired-end sequencing reads per
598 sample. The raw base files were converted to FASTQ files using the Bases2fastq v2.1 tool. The
599 mRNA-seq data have been deposited in the Gene Expression Omnibus (GEO) and an accession
600 number will be obtained.

601 **Bioinformatic analysis for mRNA-sequencing**

602 The bioinformatic analysis to the raw FASTQ data obtained from mRNA-sequencing was
603 performed by Bioinformatics Division, Iowa Institute of Human Genetics (University of Iowa). In
604 brief, PCA including PCA plot, PCA biplot and DEG analysis were generated by SALMON
605 DeSeq2. Pathway analysis including GOEA was performed by iPathwayGuide platform
606 (ADVAITABIO).

607 **Statistical analysis**

608 At least biological triplicate was performed for each experiment throughout the study.
609 Statistical analysis was performed by GraphPad Prism. For the dataset of the mRNA-seq
610 experiment, FDR-adjusted P value was obtained. Only changes that had P values less than 0.05
611 were considered statistically significant.

612

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626

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640

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646

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1048

1049 **Figure legends of 9 main figures**

1050 **Figure 1. Generation and characterization of SAMHD1 KO Calu-3 cell lines.** (A) Schematic
1051 diagram of human SAMHD1 protein domains showing the target sites of sgRNA1 or sgRNA2. (B)
1052 SAMHD1 expression of Calu-3 cells transduced to express SpCas9 without the expression of any
1053 sgRNA (Ctrl, two single clones) or with the expression of sgRNA1 (five single clones) or sgRNA2
1054 (three single clones). GAPDH detection was used as normalization control. The relative band
1055 intensities of SAMHD1 were calculated by dividing them with GAPDH bands and were normalized
1056 to Ctrl clone 1. Clone 1 of Ctrl, clone 4 of sgRNA1- and clone 3 of sgRNA 2- treated groups were
1057 chosen for all subsequent experiments and respectively named Ctrl, KO1 and KO2. (C) Levels of
1058 IL-6, IFNβ, OAS1 and ISG15 mRNA were measured with RT-qPCR. 18S RNA was used as
1059 internal control. Biological sextuplicate experiments were performed. One-way ANOVA multiple
1060 comparisons test was used to evaluate the statistical significance of the difference between Ctrl
1061 and KO1 or KO2. * $P<0.05$, *** $P<0.001$, **** $P<0.0001$. ns, not significant.

1062

1063 **Figure 2. Suppression of SARS-CoV-2 infection by SAMHD1 depletion independent to IFN**
1064 **antiviral response.** (A, B) Calu-3 Ctrl, KO1 or KO2 cells were infected with authentic SARS-CoV-
1065 2 at MOI=0.05. Culture supernatant was collected at 0, 24, 48 or 72 hpi. (A) Infectious titer or (B)
1066 viral copy number of the conditioned media were respectively measured by plaque assay or RT-

1067 qPCR. Statistical comparison was performed at each time point between Ctrl and KO1 or KO2.
1068 (C) Viral N and S proteins of infected Ctrl, KO1 or KO2 cells (SARS-CoV-2, MOI=1) were detected
1069 at 24 hpi. GAPDH was detected as an input control. The relative band intensities of viral N and
1070 viral S were calculated by dividing them with GAPDH bands and were normalized to Ctrl cells.
1071 (D) The levels of viral RNA (N), IFNβ mRNA, IFNλ mRNA and OAS1 mRNA of infected Ctrl, KO1
1072 or KO2 cells (SARS-CoV-2, MOI=1, 0 or 24 hpi) were quantified with RT-qPCR. 18S RNA was
1073 used as internal control. (E, F and G) Calu-3 Ctrl, KO1 or KO2 cells treated with 10 μM baricitinib
1074 or DMSO (added 4 hrs before infection) were infected with authentic SARS-CoV-2 at MOI=1. At
1075 24 hpi, culture supernatant, cellular protein and cellular RNA were harvested and respectively
1076 tested with (E) plaque assay, (F) Western blot or (G) RT-qPCR. For (F), viral N protein, total
1077 STAT1 or S727-phosphorylated STAT1 (p-STAT1) were detected and GAPDH was used as input
1078 control. The relative band intensities of viral N, STAT1, or p-STAT1 were calculated by dividing
1079 them with GAPDH bands and were normalized to Ctrl cells treated with DMSO. For (G), viral N
1080 RNA and OAS1 mRNA were detected. 18S RNA was used as normalization control. For (A), (B),
1081 (D) and (G), biological triplicate experiment was performed. For (E), biological quadruplicate
1082 experiment was performed. For (A), (B), (D), (E) and (G), two-way ANOVA multiple comparisons
1083 test was performed. * $P<0.05$, ** $P<0.01$, *** $P<0.001$, **** $P<0.0001$. ns, not significant.
1084

1085 **Figure 3. SAMHD1 depletion suppresses spike protein-mediated viral entry.** (A) Viral RNA
1086 levels (N and E genes) of Calu-3 Ctrl cells infected with ΔS-VRP(G) at 1.2 x 10^5 copy number per
1087 cell and treated with 5 μM remdesivir (RDV) or DMSO were quantified with RT-qPCR at 24 hpi.
1088 18S RNA was used as normalization control. Biological triplicate experiments were performed.
1089 (B, C and D) Calu-3 Ctrl, KO1 or KO2 cells were infected with ΔS-VRP(G) at 1.2 x 10^5 copy
1090 number per cell. (B) Viral RNA levels (N and E genes) were quantified with RT-qPCR at indicated
1091 time points. 18S RNA was used as normalization control. Biological triplicate experiments were
1092 performed. (C) Viral N protein was detected with Western blot at indicated time points. GAPDH
1093 was used as input control. The relative band intensities of viral N were calculated by dividing them
1094 with GAPDH bands and were normalized to Ctrl cells at 24 hpi. (D) The activities of secreted
1095 *Guassia* luciferase at indicated time points were assayed through Pierce™ *Gaussia* Luciferase
1096 Flash Assay Kit. Biological quadruplicate experiments were performed. (E) Cellular luciferase
1097 activities of HIV-1-spike-Luc/ZsGreen infected Calu-3 Ctrl, KO1 or KO2 cells (12.5 $TCID_{50}$ per
1098 cell) were measured at 48 hpi. Biological sextuplicate experiments were performed. For (A), (B)
1099 and (D), two-way ANOVA multiple comparisons test was performed. For (E), one-way ANOVA
1100 multiple comparisons test was used. * $P<0.05$, ** $P<0.01$, *** $P<0.001$. ns, not significant.
1101
1102 **Figure 4. SAMHD1 depletion downregulates the expression of SARS-CoV-2 receptor ACE2.**

1103 (A) Calu-3 Ctrl, KO1 and KO2 cells were subjected to mRNA-Seq using Element Aviti24.
1104 Biological triplicate was performed. DEGs were identified and selected based on the following
1105 criteria: FDR-adjusted P <0.01 and $\log_2$ fold change >1. The number of DEGs in the three different
1106 comparison groups were plotted on a Venn diagram (i.e. Ctrl vs KO1, Ctrl vs KO2 and KO1 vs
1107 KO2). 681 common DEGs of Ctrl vs KO1 and Ctrl vs KO2 were found to have consistent direction
1108 of change. (B) The 681 DEGs described in (A) were plotted on two volcano plots with FDR-
1109 adjusted P values against $\log_2$ fold change according to the values of KO1 vs Ctrl (left) or KO2 vs
1110 Ctrl (right). Three known viral entry factors ACE2, TMPRSS2 and Furin were identified. The values
1111 of $\log_2$ fold change were labelled adjacent to the corresponding data points. (C) mRNA levels of
1112 ACE2 (primer pair 1, Table S5) and TMPRSS2 of Ctrl, KO1 or KO2 cells were quantified with RT-
1113 qPCR. 18S RNA was used as normalization control. Biological sextuplicate experiments were
1114 performed. (D) Protein levels of ACE2 and TMPRSS2 were measured with Western blot. GAPDH
1115 was used as the input control. Triangle (◁) and asterisk (*) symbols respectively represented the
1116 zymogen (~55 kDa) and active form (~31 kDa) of TMPRSS2. The relative band intensities of
1117 ACE2, TMPRSS2 zymogen and TMPRSS2 active form were calculated by dividing them with
1118 GAPDH bands and were normalized to Ctrl. For (C), one-way ANOVA multiple comparisons test
1119 was used to evaluate the statistical significance of the difference between Ctrl and KO1 or KO2.
1120 **** P<0.0001, ns, not significant.

1121

1122 **Figure 5. SAMHD1 KO does not affect ACE2 mRNA stability.** (A-C) The levels of ACE2 mRNA

1123 of actinomycin D (10 μg/mL) treated Calu-3 Ctrl, KO1 or KO2 cells were quantified with RT-qPCR

1124 using (A) primer pair 1, (B) primer pair 2 or (C) primer pair 3 (Table S5) at indicated time points.

1125 (D) BIK mRNA and (E) 18S RNA were detected with RT-qPCR as controls to the experiment.

1126 Total RNA (1 μg) was used for reverse transcription. mRNA levels were normalized to 0 hr. The

1127 one phase decay curves for KO1 (blue), KO2 (red) and Ctrl cells (black) were plotted.

1128

1129 **Figure 6. SAMHD1 KO decreases the expression HNF1α, HNF1β and HNF4α.** mRNA levels

1130 of (A) HNF1α, (B) HNF1β, (C) HNF4α and (D) GATA6 were measured with RT-qPCR. 18S RNA

1131 was used as normalization control. (E) Protein levels of HNF1α, HNF1β and HNF4α were

1132 detected with Western blot. GAPDH was detected for input control. The relative band intensities

1133 of HNF1α, HNF1β and HNF4α were calculated by dividing them with GAPDH bands and were

1134 normalized to Ctrl cells. For (A)-(D), one-way ANOVA multiple comparisons test was used to

1135 evaluate the statistical significance of the difference between Ctrl and KO1 or KO2. ** $P<0.01$, ***

1136 $P<0.001$, **** $P<0.0001$. ns, not significant.

1137

1138 **Figure 7. Knocking down HNF1α and HNF1β downregulates ACE2 expression and**

1139 **suppresses SARS-CoV-2 infection.** (A) ACE2, HNF1α, HNF1β or HNF4α proteins of Calu-3

1140 cells (4 x 10^5) treated with DsiRNA (24 pmol, 72 hpt) targeting HNF1α, HNF1β, HNF4α or NC

1141 were detected with Western blot. GAPDH was detected for input control. A representative blot

1142 was shown. (B) ACE2, HNF1α, HNF1β or HNF4α protein band intensities of three independent

1143 experiments (i.e. (A) and Supplementary S4A) were quantified by densitometry analysis and

1144 divided by GAPDH and normalized to NC control. (C) Cells were treated similarly as in (A). The

1145 mRNA levels of ACE2 (primer pair 1, Table S5), HNF1α, HNF1β or HNF4α were quantified with

1146 RT-qPCR. 18S RNA was used as normalization control. (D) Calu-3 cells (3.2 x 10^6) transfected

1147 DsiRNA (192 pmol, 72 hpt) targeting HNF1α, HNF1β or NC were infected with authentic SARS-

1148 CoV-2 at MOI=0.05. Released viral progenies in culture supernatants were quantified with plaque

1149 assay. Biological triplicate experiments were performed. For (B-C), unpaired T-test was used to

1150 evaluate the statistical significance of the difference between sample groups and NC. For (D),

1151 two-way ANOVA multiple comparisons test was performed comparing Ctrl and KO1 or KO2 at

1152 various time points. * $P<0.05$, ** $P<0.01$, *** $P<0.001$, **** $P<0.0001$. ns, not significant.

1153

1154 **Figure 8. SAMHD1 deficiency mitigates the effect of HNF1α and HNF1β knockdown in**

1155 **further suppressing ACE2 expression.** (A) ACE2, HNF1α and HNF1β proteins of Ctrl, KO1 or

1156 KO2 cells (2 x 10^5) treated with DsiRNA (12 pmol, 72 hpt) targeting HNF1α, HNF1β or NC were

1157 detected with Western blot. GAPDH was detected for input control. A representative blot was
1158 shown. (B) HNF1α, (C) HNF1β and (D) ACE2 protein band intensities of three independent
1159 experiments (i.e. (A) and Supplementary S4B) were quantified by densitometry analysis, divided
1160 by GAPDH bands and normalized to Ctrl NC. (E) Cells were treated similarly as in (A). The mRNA
1161 levels of ACE2 (primer pair 1, Table S5) were quantified with RT-qPCR. 18S RNA was used as
1162 normalization control. One-way ANOVA multiple comparisons test was used to evaluate the
1163 statistical significance of the difference between sample groups. * $P<0.05$, ** $P<0.01$, *** $P<0.001$,
1164 **** $P<0.0001$. ns, not significant.
1165
1166 **Figure 9. SAMHD1 promotes SARS-CoV-2 infection via HNF1-mediated ACE2 expression.**
1167 SAMHD1 supports the expression of HNF1α and HNF1β which respectively promote mRNA and
1168 protein expression of ACE2 in human lung epithelial cells (Calu-3). Upon infection, SARS-CoV-2
1169 binds to ACE2 receptor via its surface spike protein to initiate viral entry. In the absence of
1170 SAMHD1 expression (i.e. SAMHD1 KO), cellular stresses are induced such as proinflammatory
1171 cytokine expression (thunder symbols). The expression levels of HNF1α and HNF1β are reduced.
1172 In turn, ACE2 expression is reduced which blocks SARS-CoV-2 infection via spike protein-
1173 mediated viral entry. Whether and how proinflammatory cytokines produced by SAMHD1 KO
1174 Calu-3 cells (e.g. IL-6, IL-1, CSF2, or IL-11) suppress HNF-1-mediated ACE2 expression remains

1175 unclear and requires further studies.

1176

1177 **Figure legends of 5 supplementary figures**

1178

1179 **Supplementary Fig. S1. Validation of SAMHD1 deficiency in SAMHD1 KO Calu-3 cells.** (A

1180 and B) The sanger sequencing results to the regions of SpCas9 cleavage sites directed by

1181 respectively sgRNA1 or sgRNA2 of (A) KO1 and (B) KO2 cells were shown and compared with

1182 that of the Ctrl cells. Red arrows indicated one base pair insertion near the SpCas9 cleavage site.

1183 (C) dATP levels of Calu-3 Ctrl, KO1 or KO2 cells were measured with HIV-1 RT based single

1184 nucleotide incorporation assay. For (C), one-way ANOVA multiple comparisons test was used to

1185 evaluate the statistical significance of the difference between Ctrl and KO1 or KO2. ** $P<0.01$. ns,

1186 not significant.

1187

1188 **Supplementary Fig. S2. PCA clustering of Calu-3 Ctrl, KO1 and KO2 cells based on the**

1189 **mRNA-seq profiles.** Nine samples of the mRNA-seq analysis gave nine PCs (i.e. Ctrl, KO1 and

1190 KO2 cells, biological triplicate). The influence of each PC was plotted based on their contributing

1191 variance (%). The cumulative variances from 1 to 9 were plotted above and joined by a curve.

1192 PC1 and PC2 gave 98% coverage of all PCs. (B) Individual samples from Ctrl, KO1 and KO2

1193 cells were plotted along the PC1 and PC2 based on the net scores of loading genes obtained

1194 from PCA. (C) A PCA biplot was generated by top ten loading genes influencing PC1 and PC2.

1195

1196 **Supplementary Fig. S3. Confirming ACE2 and dACE2 mRNA expressions in SAMHD1 KO**

1197 **Calu-3 cells.** The mRNA levels of (A) ACE2 and (B) dACE2 of Ctrl, KO1 and KO2 cells were

1198 measured by RT-qPCR with qPCR primer pairs previously described [55]. For ACE2, primer pair

1199 4 listed in Table S5 was used. Biological triplicate experiment was performed. One-way ANOVA

1200 multiple comparisons test was used to evaluate the statistical significance of the difference

1201 between Ctrl and KO1 or KO2. ** $P<0.01$, *** $P<0.001$. ns, not significant.

1202

1203 **Supplementary Fig. S4. Independent experiments performed for protein band calculation**

1204 **of Fig. 7B and Fig. 8B-8D.** The Western blot results to two more independent experiment

1205 replicates for the same experiment conducted in Fig. 7A and Fig. 8A were respectively shown in

1206 (A) and (B).

1207

1208 **Supplementary Fig. S5. Gene ontology enrichment analysis to cellular components to the**

1209 **common DEGs of SAMHD1 KO Calu-3 cells.** 681 consistent DEGs obtained from SAMHD1 KO

1210 Calu-3 cells as shown in Fig. 4A were used for gene ontology enrichment analysis to the category

1211 of “Cellular component”. Top ten GO terms with the best FDR-adjusted P values were plotted on

1212 a bubble plot against the rich ratio (i.e. number of DEGs per all annotated genes of the GO term).

1213 The number of counts of DEGs was shown in terms of the size of the bubble. The bubble plot was

1214 generated with the online resources SR plot (https://www.bioinformatics.com.cn/srplot).

1215

1216 **Information of supplementary Table S1-S5**

1217 **Supplementary Table S1.** DEGs observed in the mRNA-seq data sets on the three comparison

1218 pairs (Ctrl vs KO1, Ctrl vs KO2 and KO1 vs KO2 cells).

1219

1220 **Supplementary Table S2.** The 681 common DEGs observed in both Calu-3 KO1 and KO2 cells

1221 as shown in Fig. 4A.

1222

1223 **Supplementary Table S3.** All GO terms in the category of “Cellular component” enriched based

1224 on the 681 common DEGs shown in Fig. 4A.

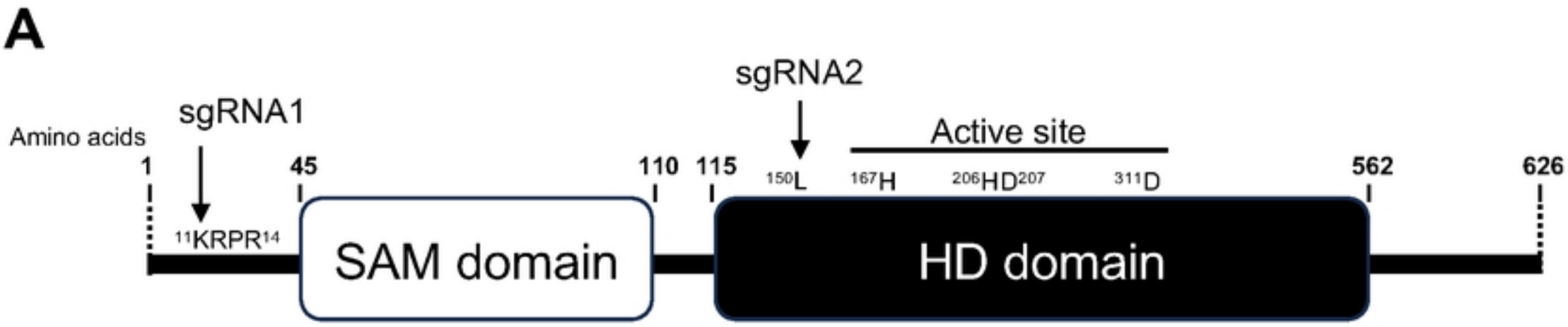
1225

1226 **Supplementary Table S4.** Enriched DEGs of the top ten GO terms as shown in Fig. S5.

1227

1228 **Supplementary Table S5.** DsiRNA and RT-qPCR primer sequences and related information.

Fig. 1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sgRNA1
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Active site
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150L
167H
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311D
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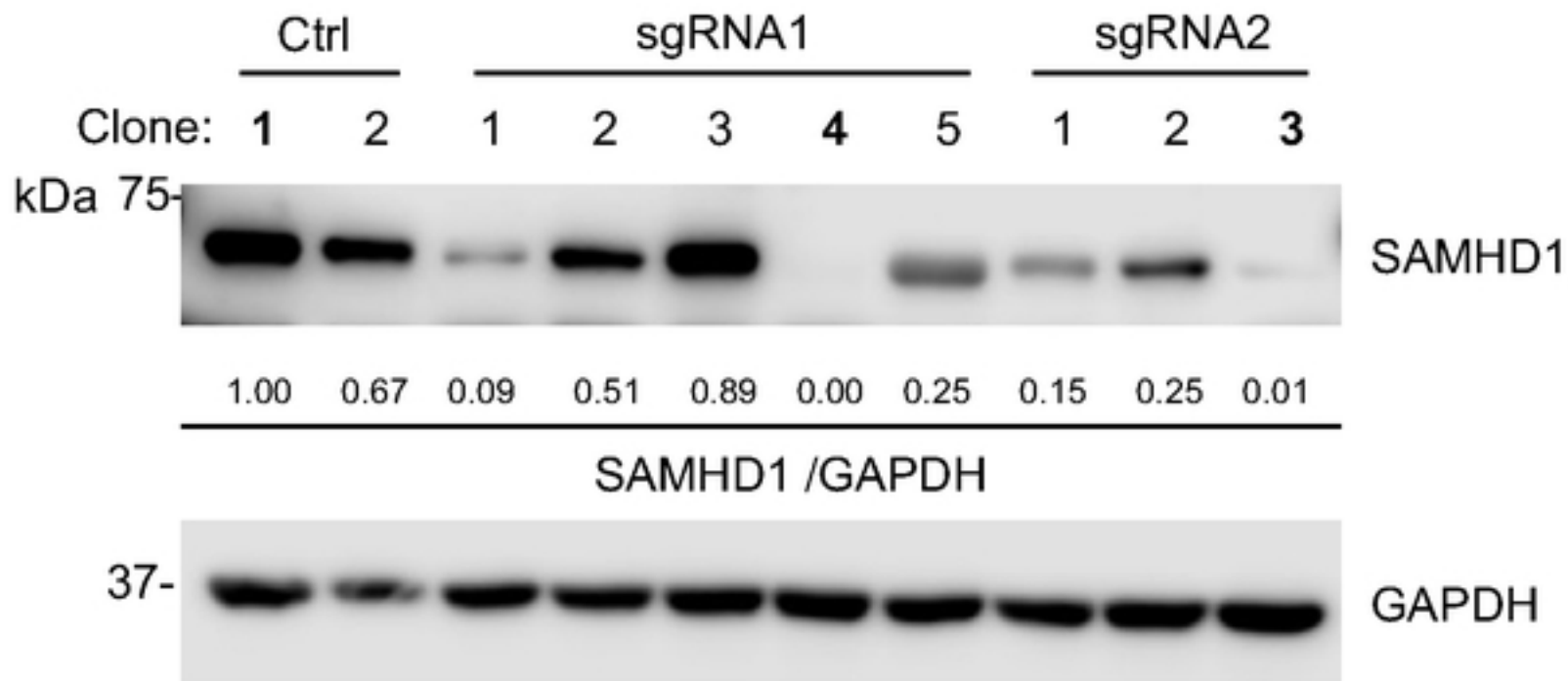
11KRPR14
SAM domain
HD domain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Clone: 1 2 1 2 3 4 5 1 2 3
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SAMHD1
1.00 0.67 0.09 0.51 0.89 0.00 0.25 0.15 0.25 0.01
SAMHD1 /GAPDH
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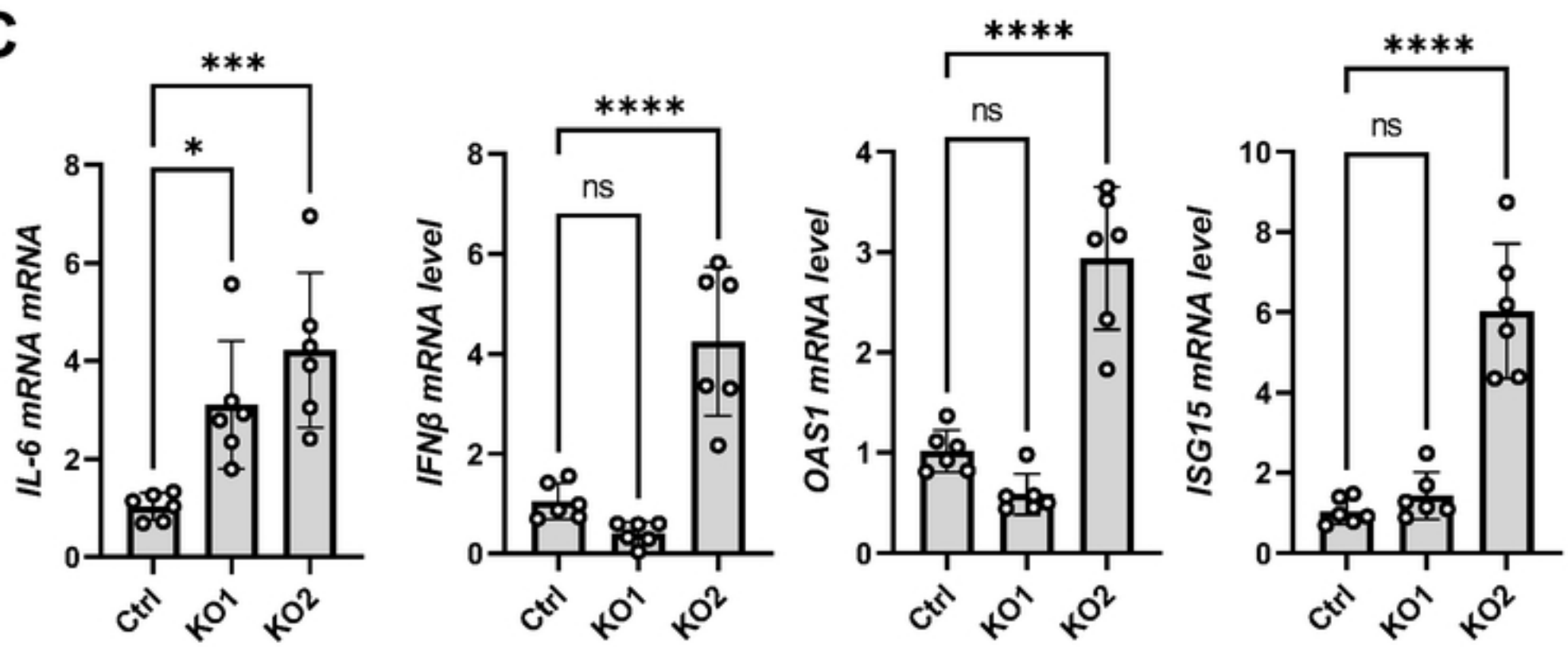
GAPDH


C
IL-6 mRNA mRNA
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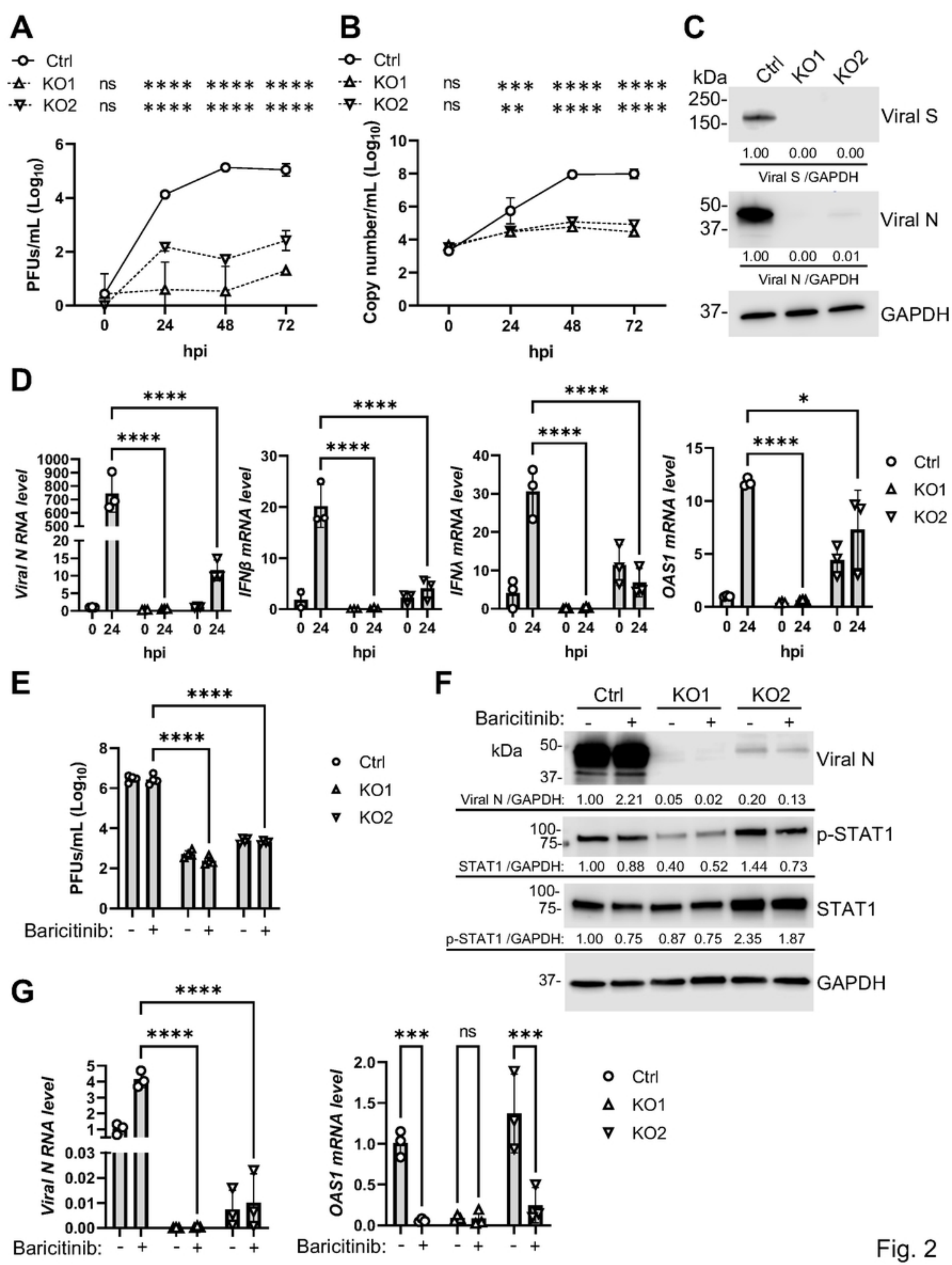
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KO1 ns **** **** ****
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250-
150-
Viral S
1.00 0.00 0.00
Viral S /GAPDH
50-
37-
Viral N
1.00 0.00 0.01
Viral N /GAPDH
37-
GAPDH
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Viral N RNA level
IFNβ mRNA level
IFNλ mRNA level
OAS1 mRNA level
hpi
Ctrl
KO1
KO2
E
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STAT1 /GAPDH: 1.00 0.88 0.40 0.52 1.44 0.73
100-
75-
STAT1
p-STAT1 /GAPDH: 1.00 0.75 0.87 0.75 2.35 1.87
37-
GAPDH
G
Viral N RNA level
Baricitinib: - + - + - +
OAS1 mRNA level
*** ns ***
Baricitinib: - + - + - +
Ctrl
KO1
KO2

Fig. 2

Fig. 3

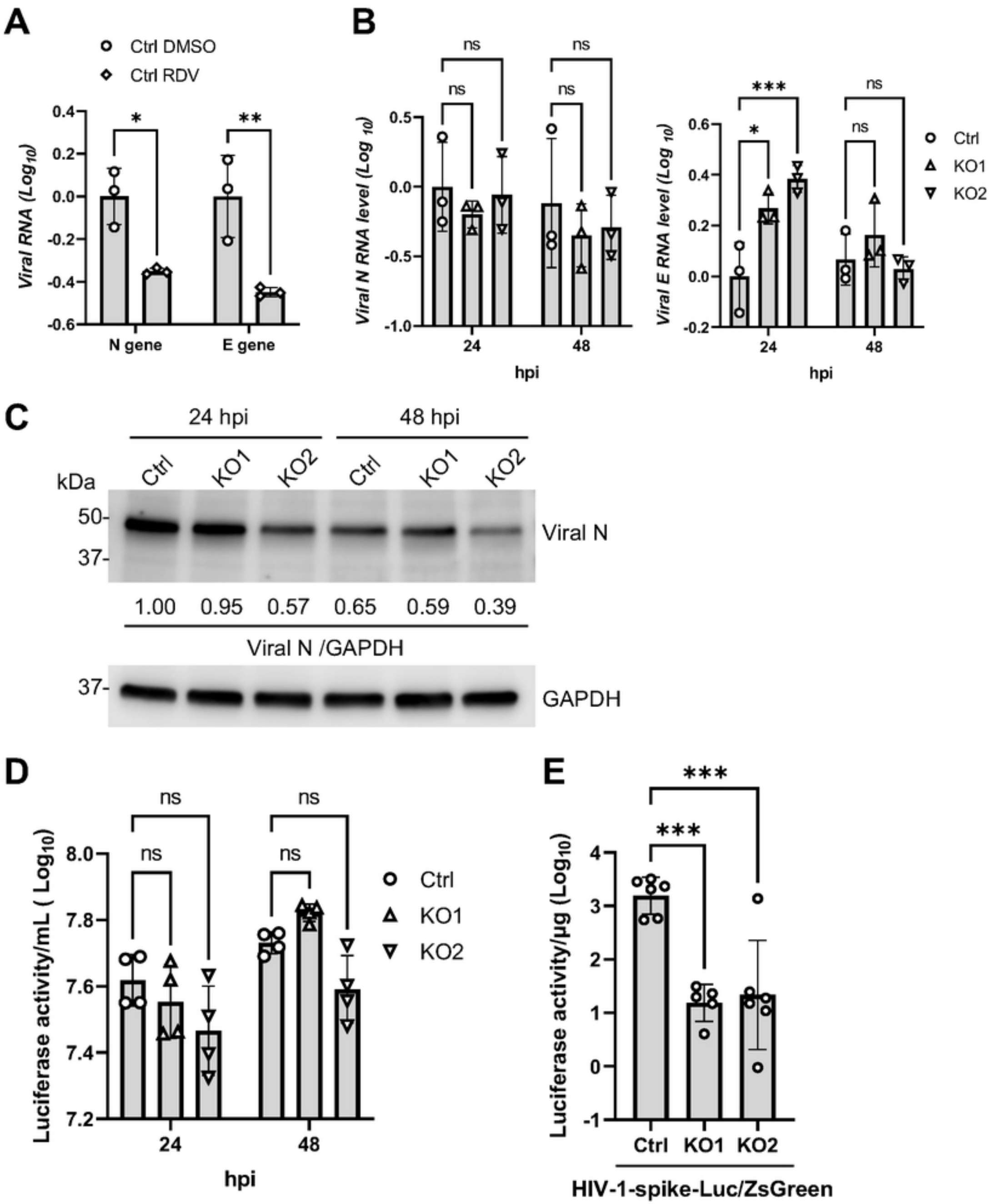

A
Ctrl DMSO
Ctrl RDV
Viral RNA (Log10)
N gene
E gene
B
Viral N RNA level (Log 10)
Viral E RNA level (Log 10)
24
48
hpi
Ctrl
KO1
KO2
C
24 hpi
48 hpi
kDa
Ctrl
KO1
KO2
50-
37-
Viral N
1.00 0.95 0.57 0.65 0.59 0.39
Viral N /GAPDH
37-
GAPDH
D
Luciferase activity/mL (Log10)
24
48
hpi
Ctrl
KO1
KO2
E
Luciferase activity/μg (Log10)
Ctrl
KO1
KO2
HIV-1-spike-Luc/ZsGreen

Fig. 4

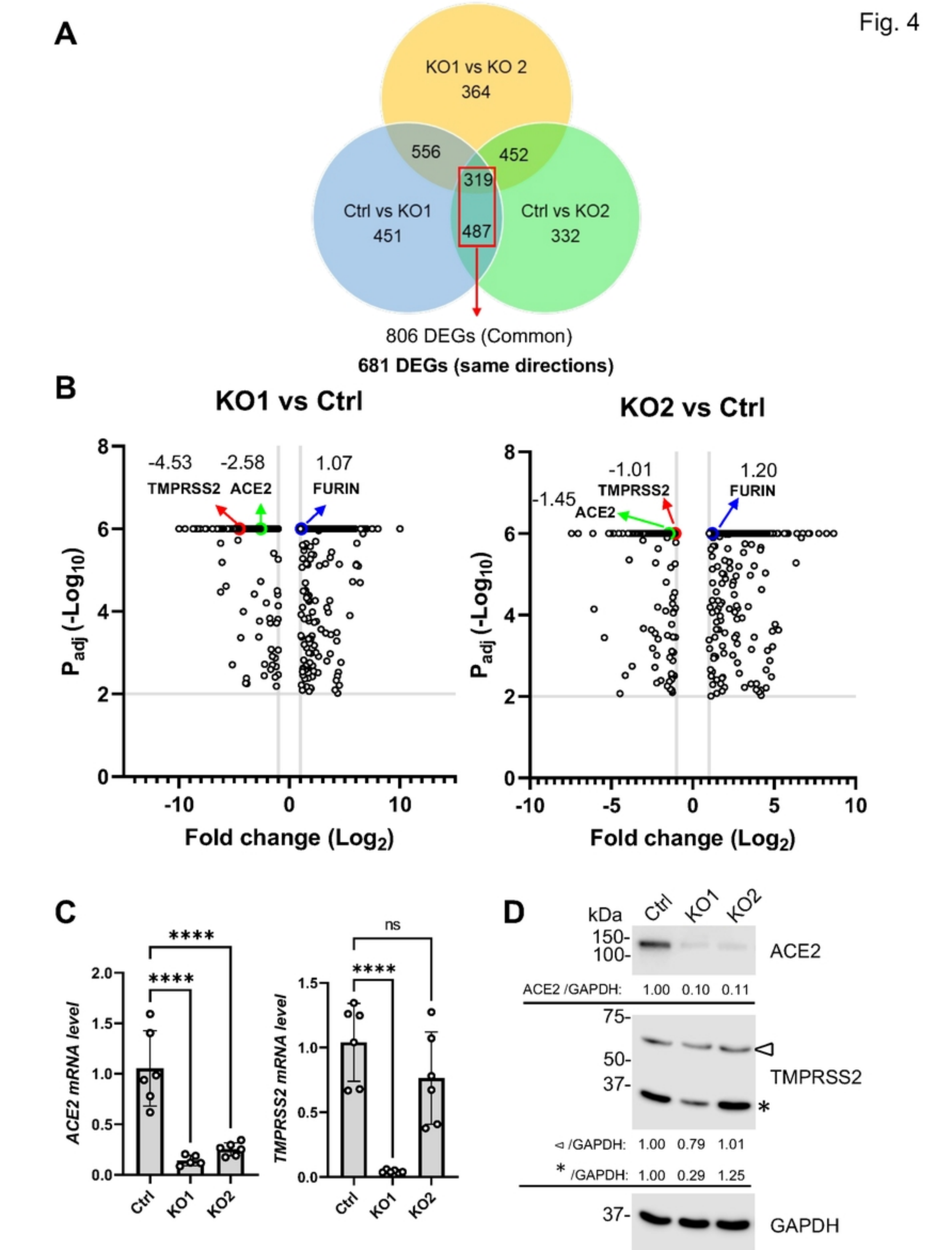

A
KO1 vs KO 2
364
556
452
319
Ctrl vs KO1
451
487
Ctrl vs KO2
332
806 DEGs (Common)
681 DEGs (same directions)
B
KO1 vs Ctrl
-4.53
-2.58
1.07
TMPRSS2
ACE2
FURIN
Padj (-Log10)
Fold change (Log2)
KO2 vs Ctrl
-1.01
1.20
-1.45
TMPRSS2
ACE2
FURIN
Padj (-Log10)
Fold change (Log2)
C
****
****
ACE2 mRNA level
Ctrl
KO1
KO2
ns
****
TMPRSS2 mRNA level
Ctrl
KO1
KO2
D
kDa
Ctrl
KO1
KO2
150-
100-
ACE2
ACE2 /GAPDH: 1.00 0.10 0.11
75-
50-
37-
TMPRSS2
◁ /GAPDH: 1.00 0.79 1.01
* /GAPDH: 1.00 0.29 1.25
37-
GAPDH

Fig. 5

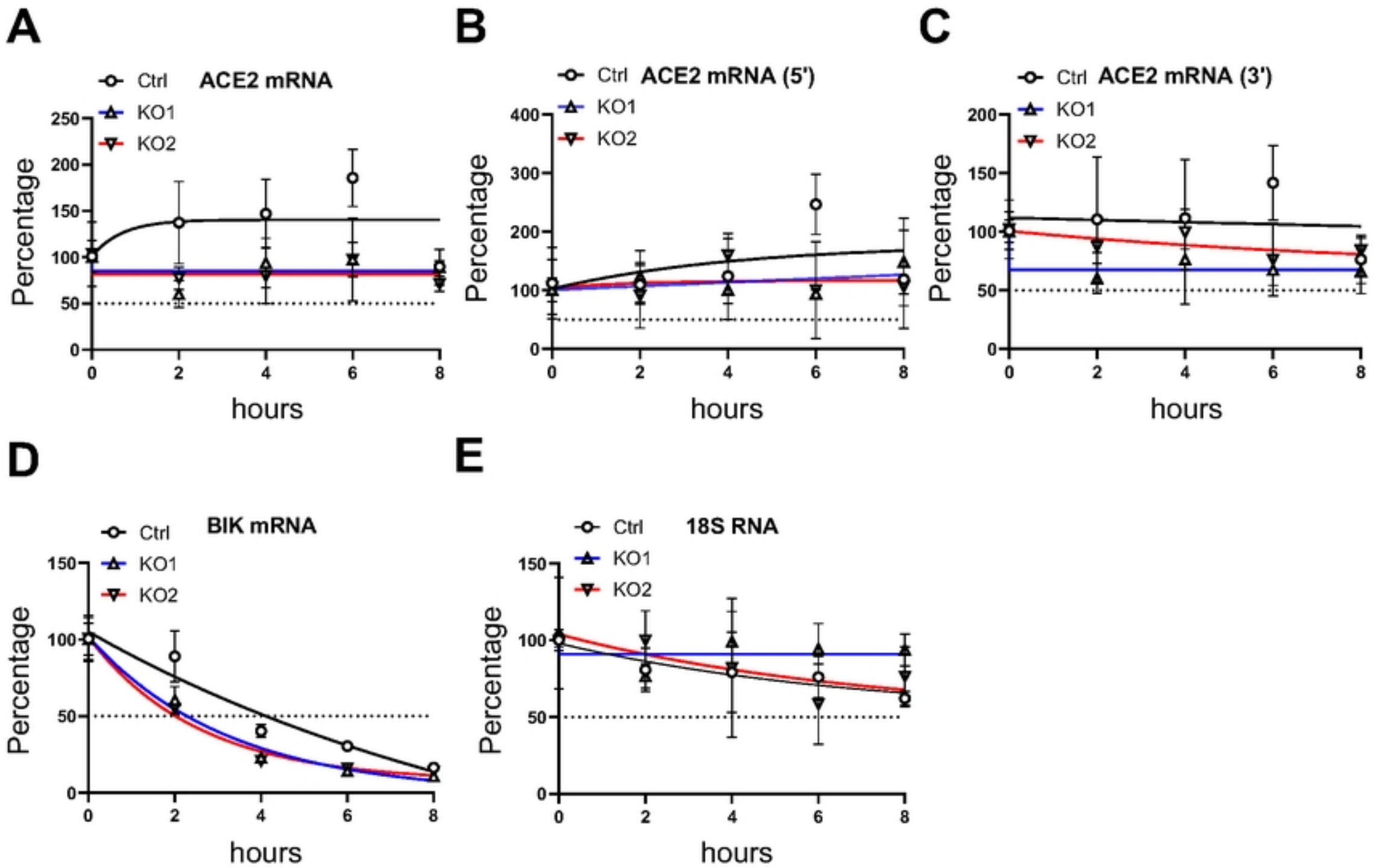

A
ACE2 mRNA
Ctrl
KO1
KO2
Percentage
hours
B
ACE2 mRNA (5')
Ctrl
KO1
KO2
Percentage
hours
C
ACE2 mRNA (3')
Ctrl
KO1
KO2
Percentage
hours
D
BIK mRNA
Ctrl
KO1
KO2
Percentage
hours
E
18S RNA
Ctrl
KO1
KO2
Percentage
hours

Fig. 6

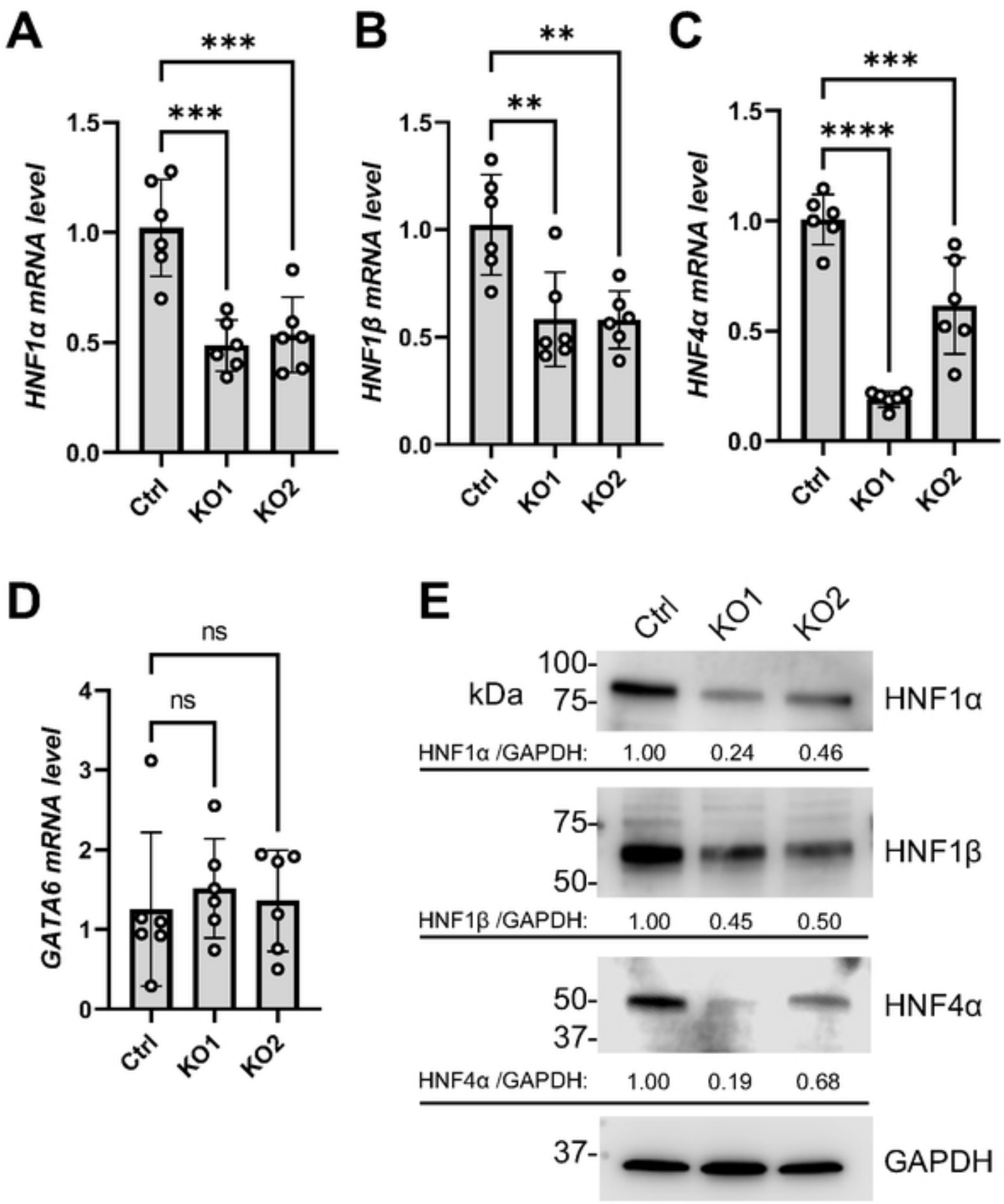

A
B
C
D
E
HNF1α mRNA level
HNF1β mRNA level
HNF4α mRNA level
GATA6 mRNA level
Ctrl
KO1
KO2
***
**
****
ns
kDa
100-
75-
50-
37-
HNF1α
HNF1β
HNF4α
GAPDH
HNF1α /GAPDH: 1.00 0.24 0.46
HNF1β /GAPDH: 1.00 0.45 0.50
HNF4α /GAPDH: 1.00 0.19 0.68

Fig. 7

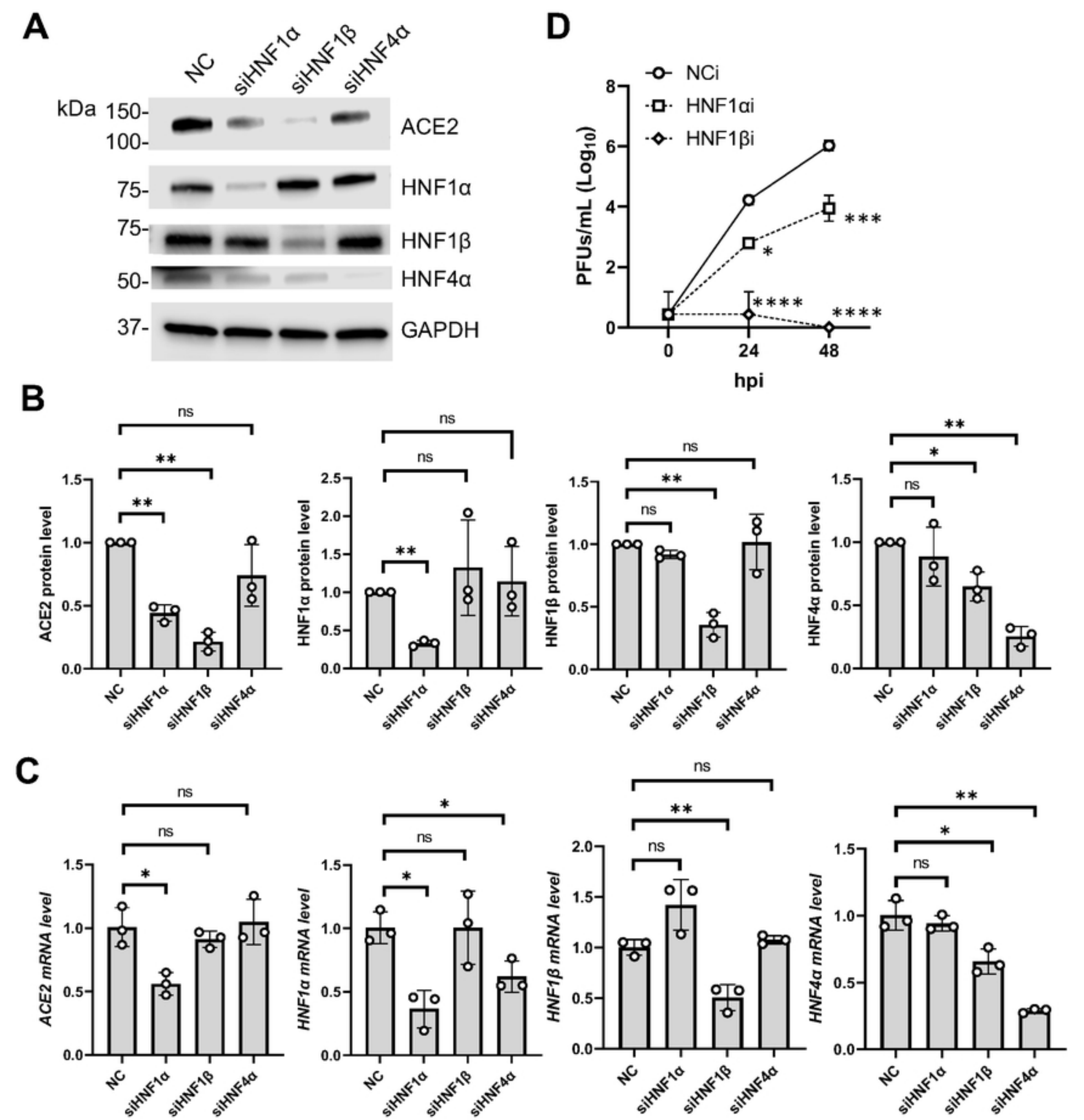

A
NC
siHNF1α
siHNF1β
siHNF4α
kDa
150-
100-
75-
75-
50-
37-
ACE2
HNF1α
HNF1β
HNF4α
GAPDH
D
NCi
HNF1αi
HNF1βi
PFUs/mL (Log10)
hpi
B
ACE2 protein level
HNF1α protein level
HNF1β protein level
HNF4α protein level
C
ACE2 mRNA level
HNF1α mRNA level
HNF1β mRNA level
HNF4α mRNA level
ns
*
**
***
****

Fig. 8

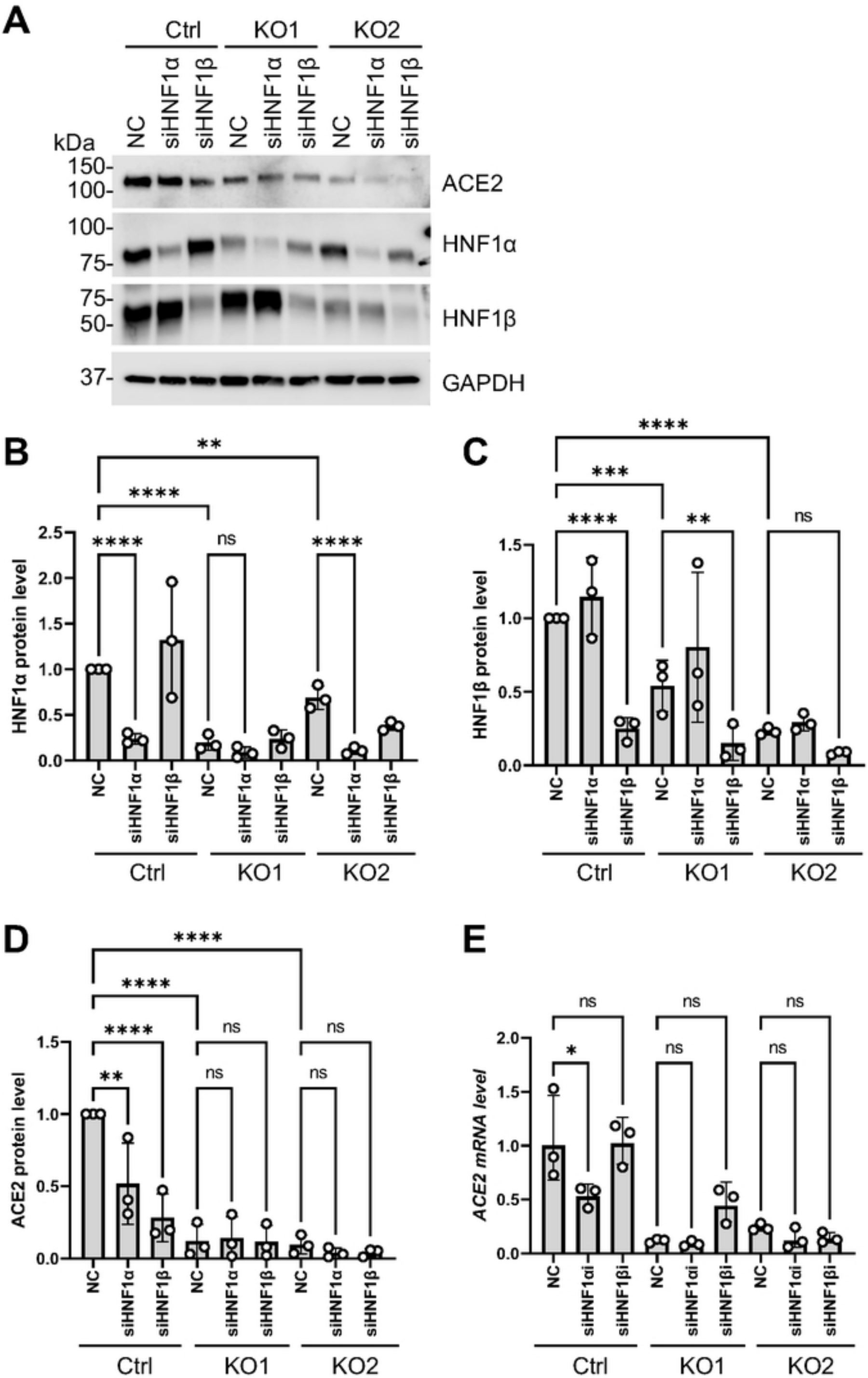
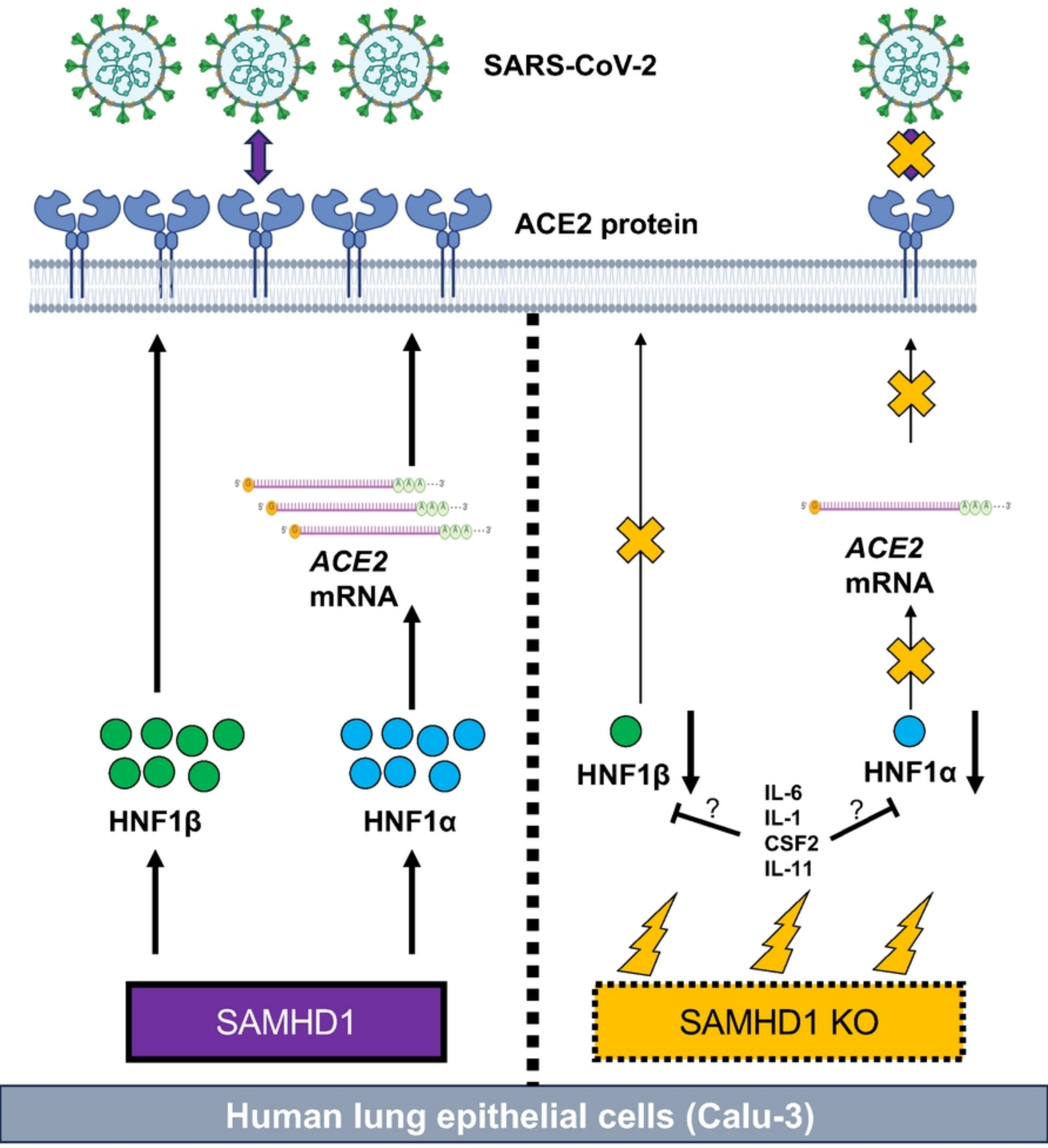
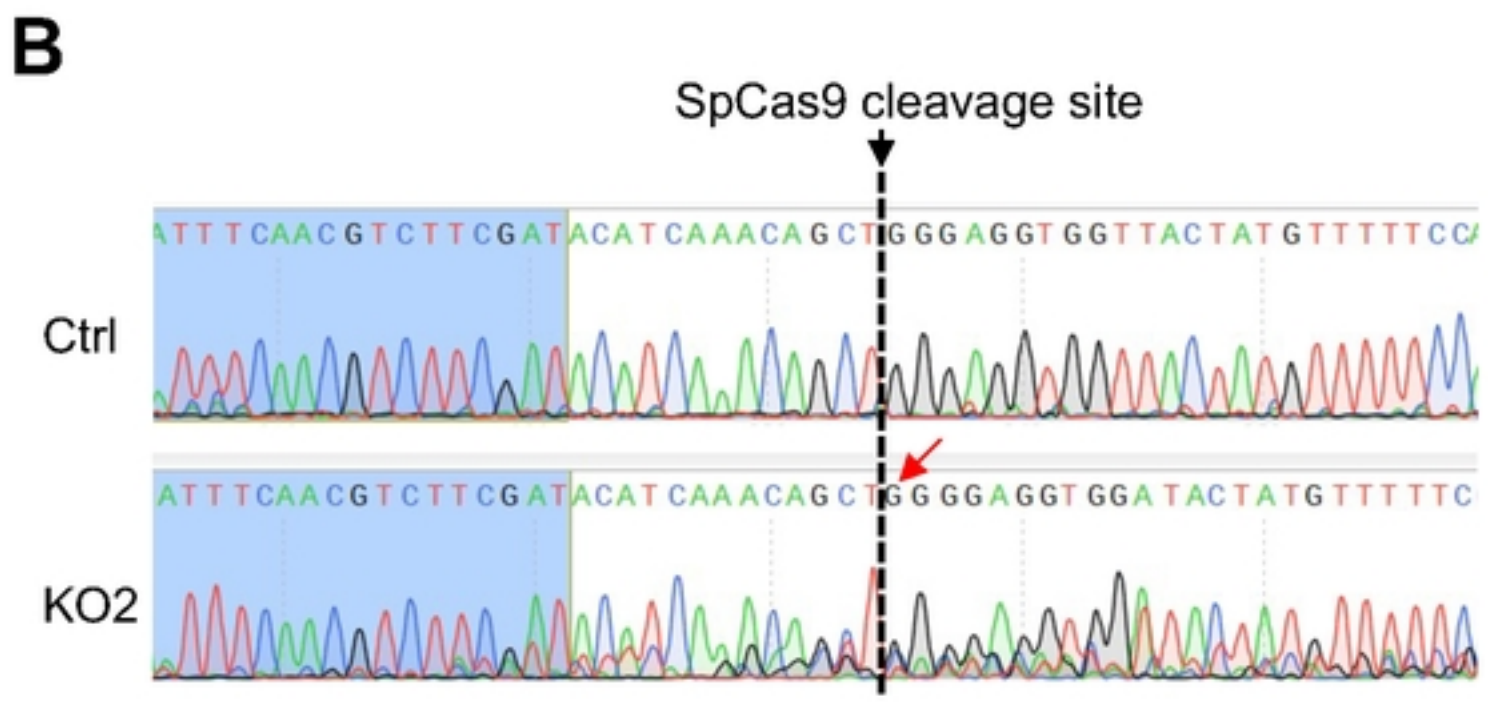
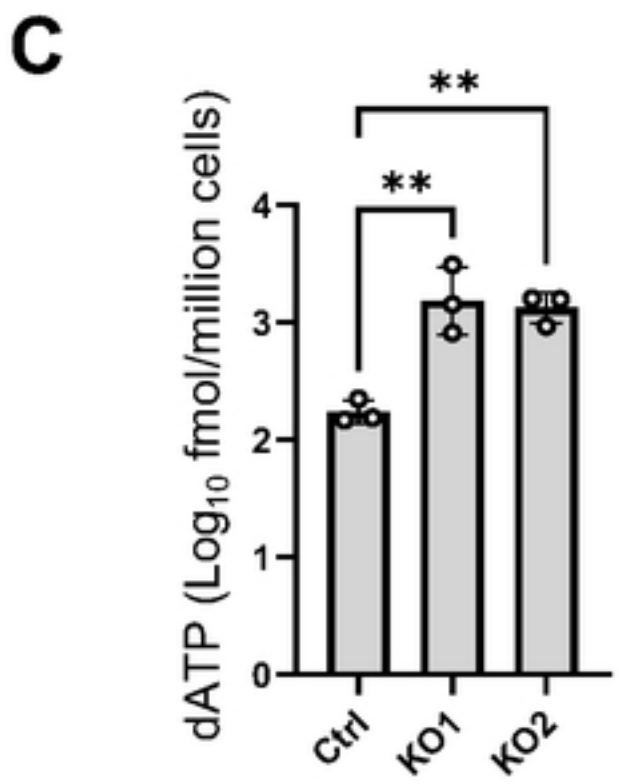

A
Ctrl
KO1
KO2
NC
siHNF1α
siHNF1β
kDa
150-
100-
ACE2
100-
75-
HNF1α
75-
50-
HNF1β
37-
GAPDH
B
HNF1α protein level
2.5
2.0
1.5
1.0
0.5
0.0
****
ns
**
C
HNF1β protein level
1.5
1.0
0.5
0.0
***
D
ACE2 protein level
1.5
1.0
0.5
0.0
E
ACE2 mRNA level
2.0
1.5
1.0
0.5
0.0
*
siHNF1αi
siHNF1βi

Fig. 9

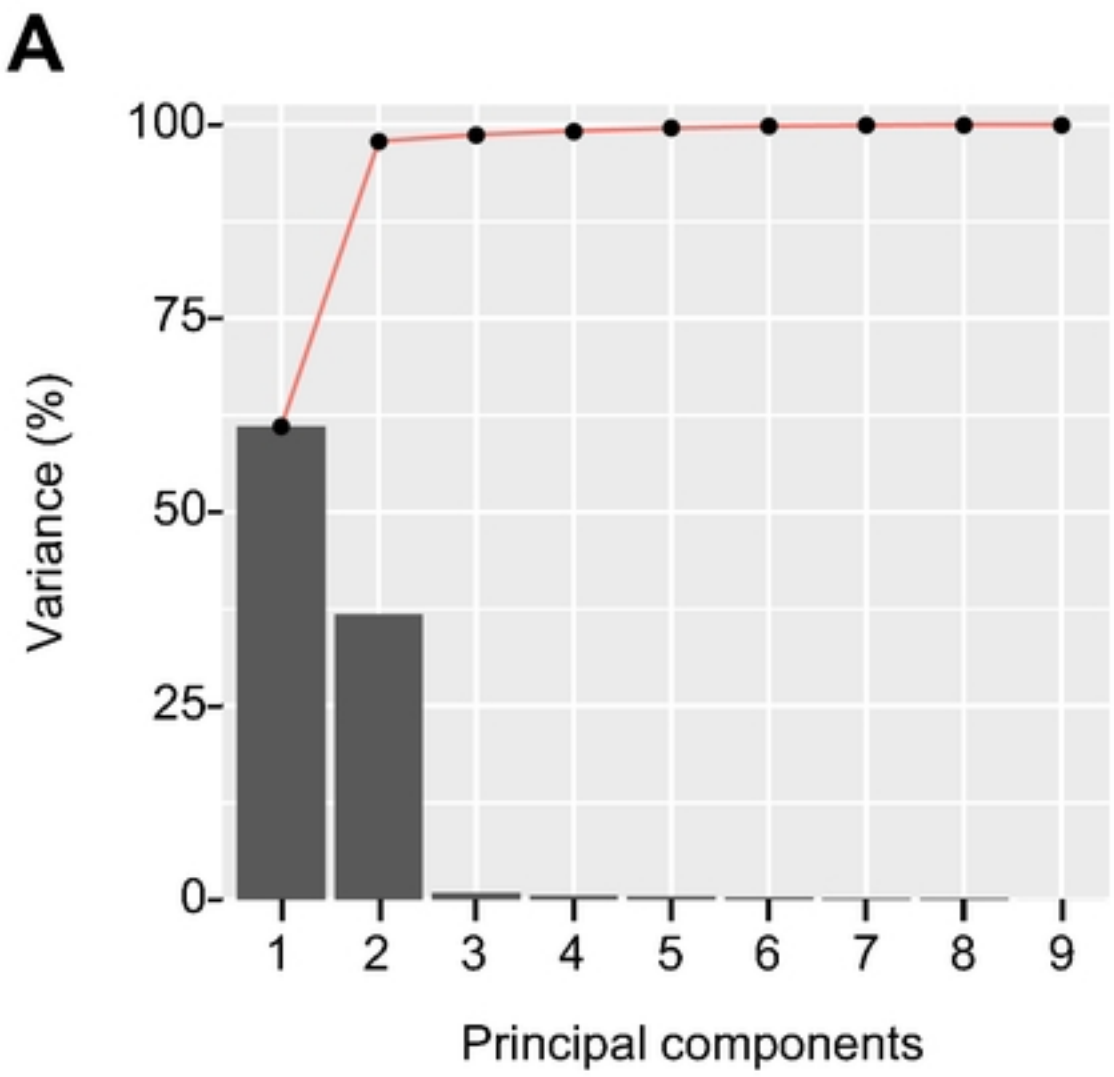

SARS-CoV-2
ACE2 protein
ACE2
mRNA
ACE2
mRNA
HNF1β
HNF1α
HNF1β
HNF1α
?
IL-6
IL-1
CSF2
IL-11
?
SAMHD1
SAMHD1 KO
Human lung epithelial cells (Calu-3)

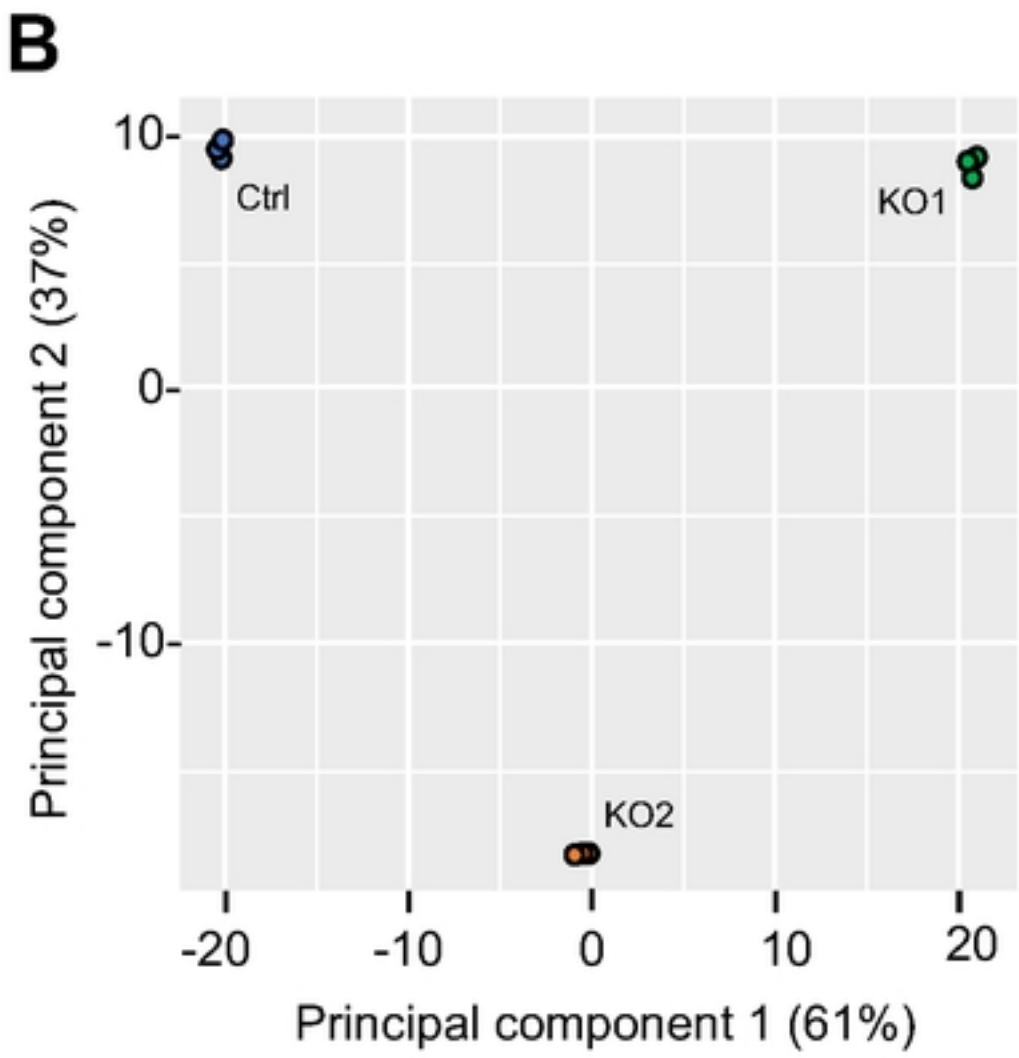
Supplementary Fig. S1

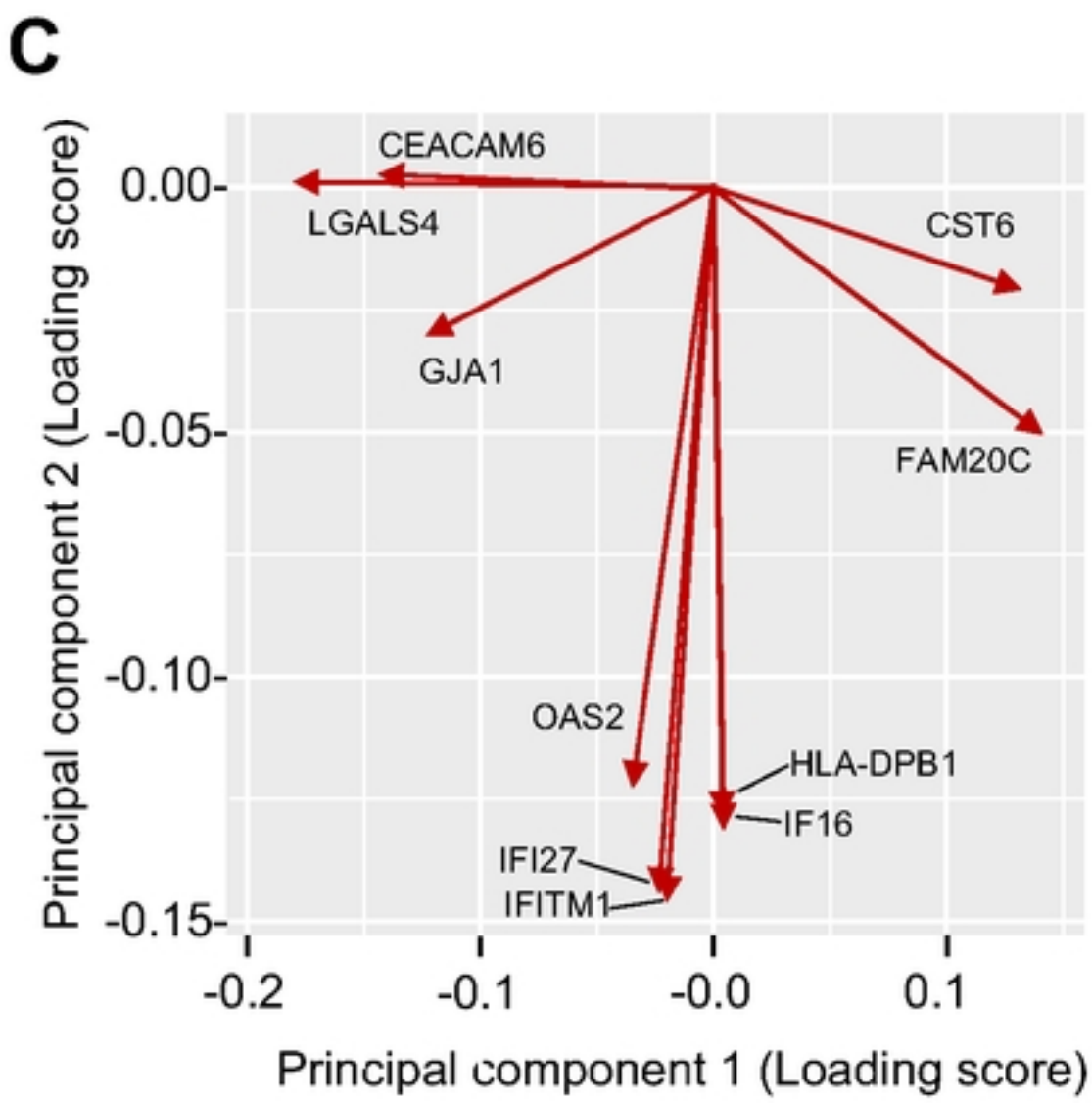




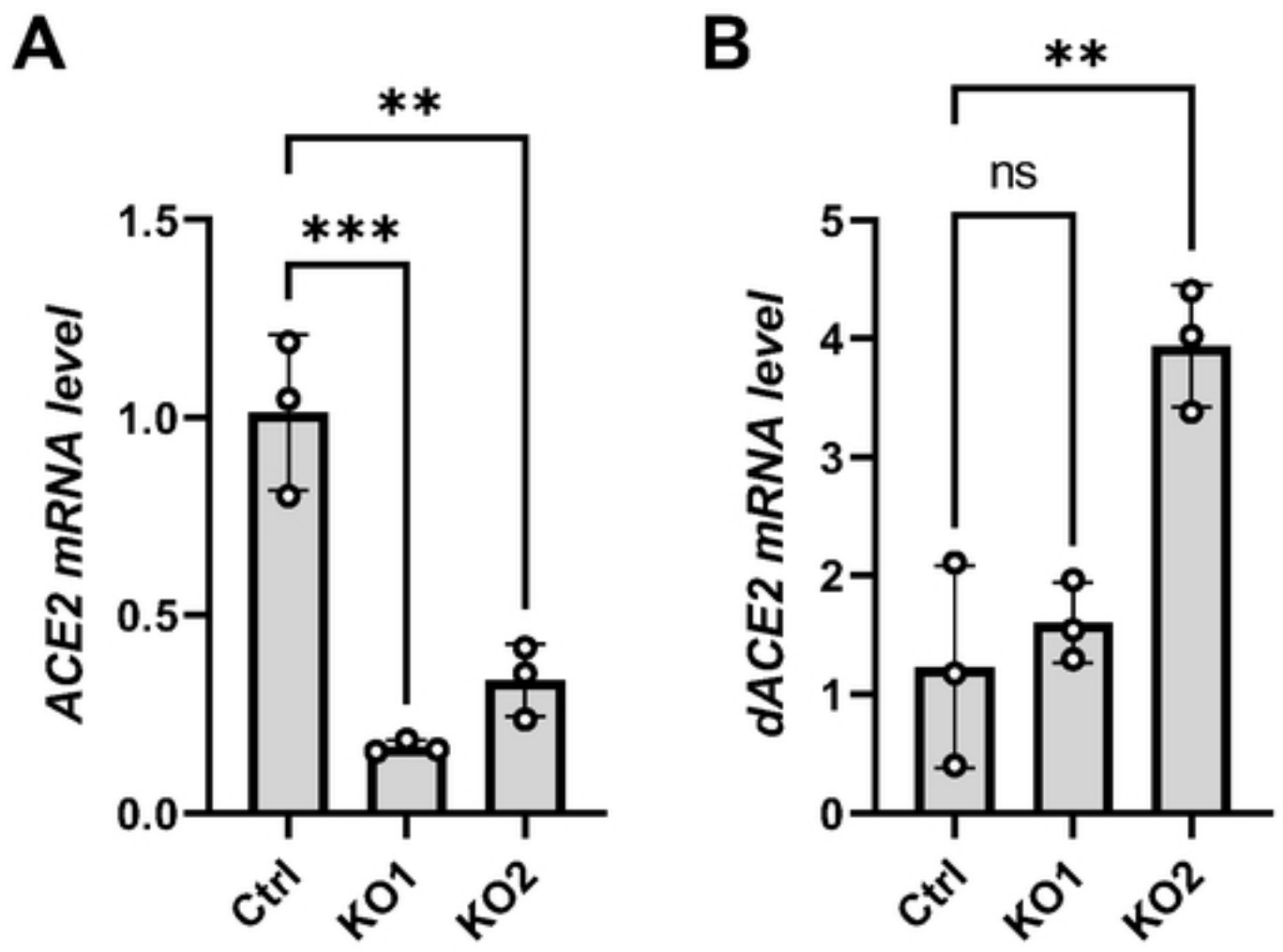
Supplementary Fig. S2



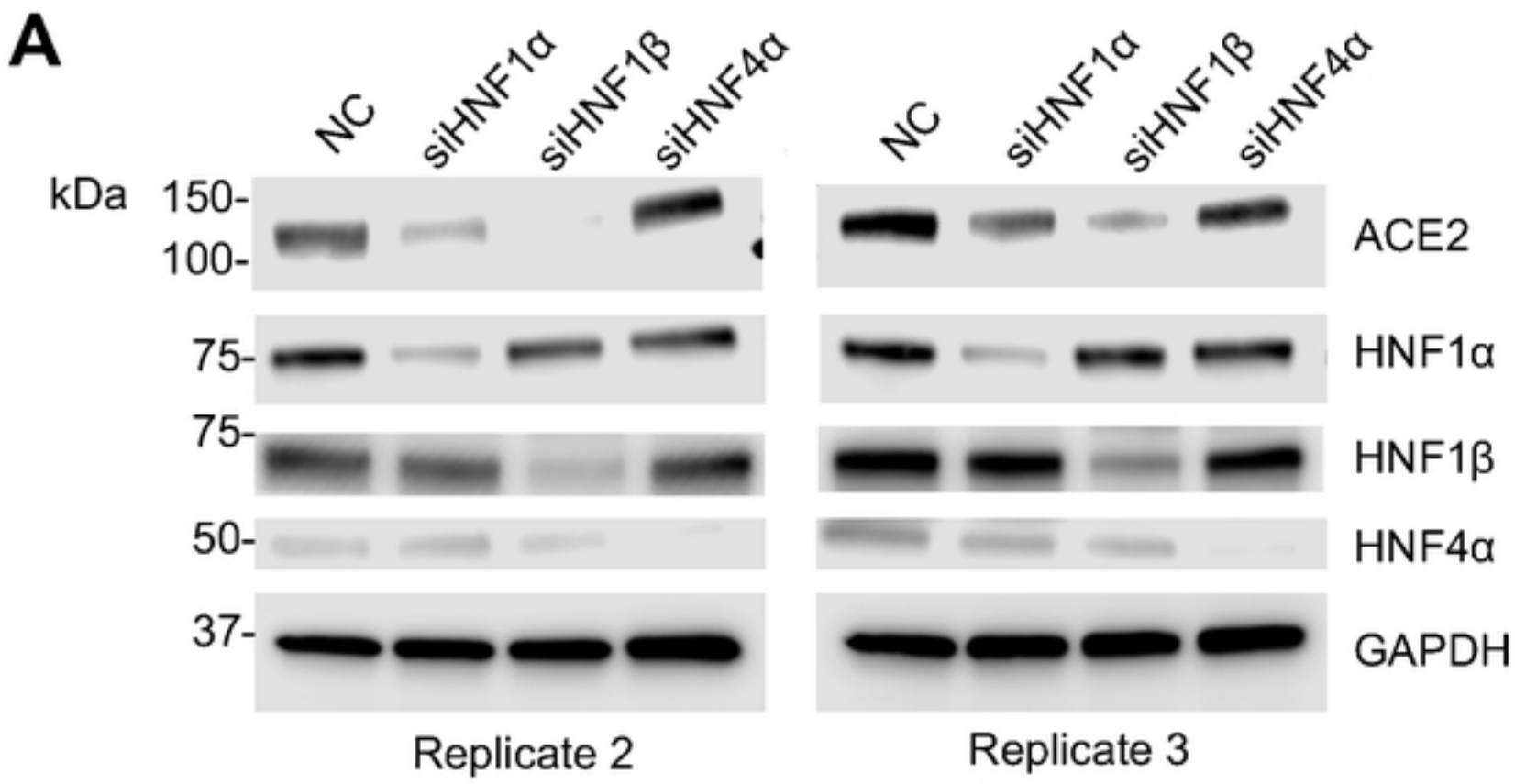


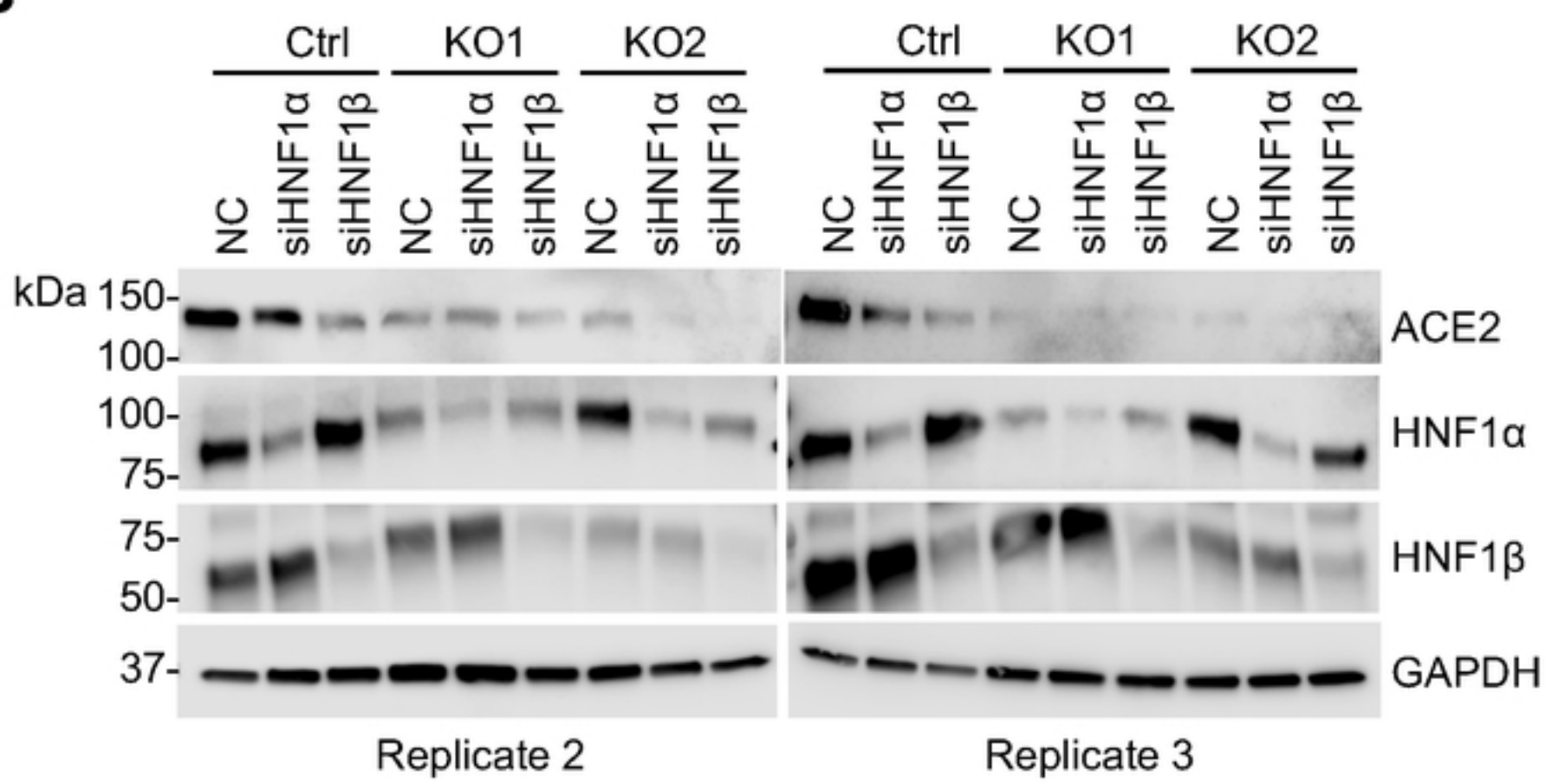
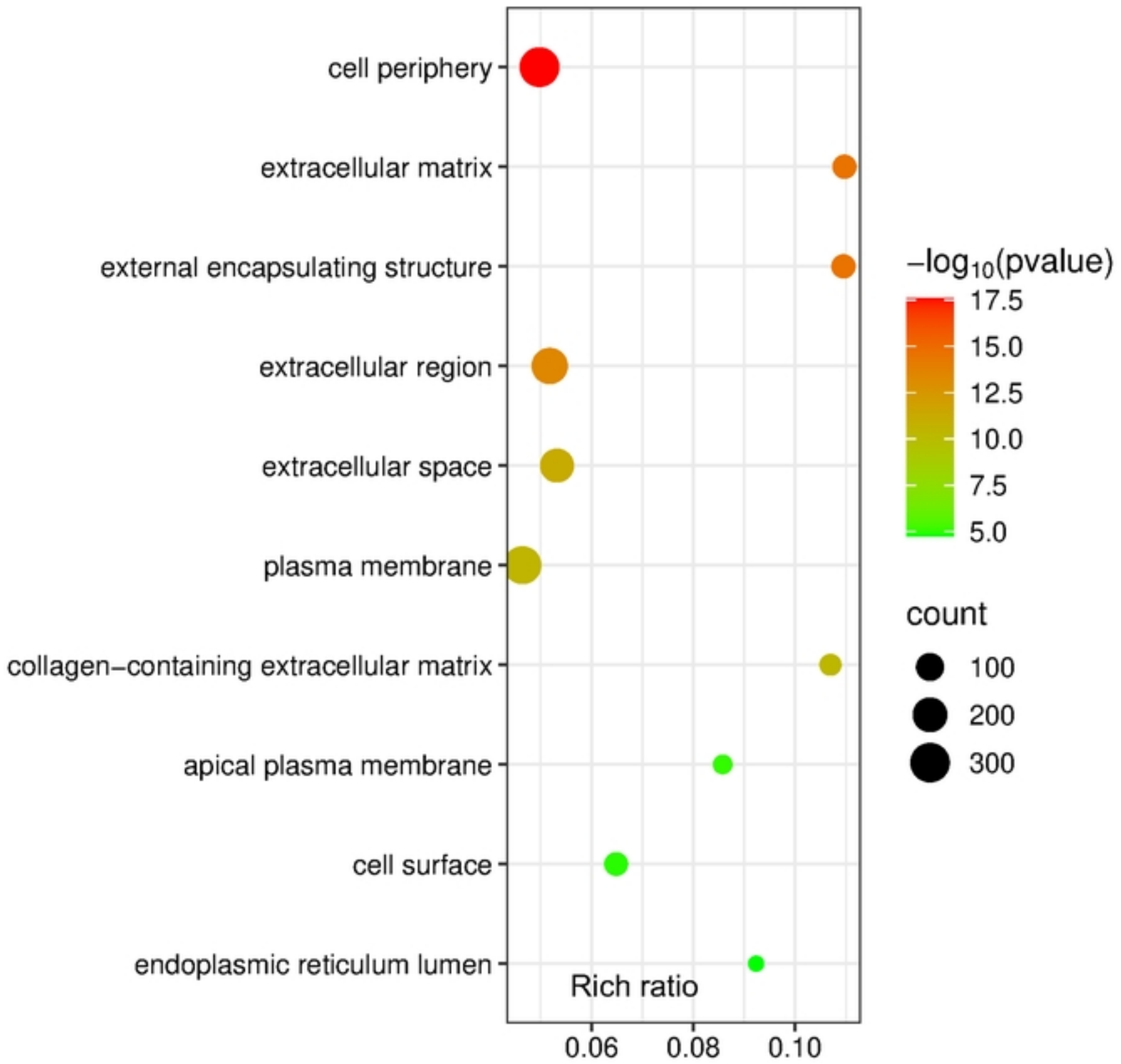


Supplementary Fig. S3



Supplementary Fig. S4





Supplementary Fig. S5