

# 1 Interferon alpha-based combinations suppress SARS- 2 CoV-2 infection in vitro and in vivo

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27 **Running title:** Antiviral IFNa2a-based drug combinations

28 **Keywords:** antivirals; antiviral drug combinations; broad-spectrum antivirals; virus; interferon

29 **Abstract:** There is an urgent need for new antivirals with powerful therapeutic potential and tolerable  
30 side effects. In the present study, we found that recombinant human interferon-alpha (IFNa) triggers  
31 intrinsic and extrinsic cellular antiviral responses, as well as reduces replication of severe acute  
32 respiratory syndrome coronavirus 2 (SARS-CoV-2) in vitro. Although IFNa alone was insufficient to  
33 completely abolish SARS-CoV-2 replication, combinations of IFNa with remdesivir or other antiviral  
34 agents (EIDD-2801, camostat, cycloheximide, or convalescent serum) showed strong synergy and  
35 effectively inhibited SARS-CoV-2 infection in human lung epithelial Calu-3 cells. Furthermore, we  
36 showed that the IFNa-remdesivir combination suppressed virus replication in human lung organoids,  
37 and that its single prophylactic dose attenuated SARS-CoV-2 infection in lungs of Syrian hamsters.  
38 Transcriptome and metabolomic analyses showed that the combination of IFNa-remdesivir  
39 suppressed virus-mediated changes in infected cells, although it affected the homeostasis of  
40 uninfected cells. We also demonstrated synergistic antiviral activity of IFNa2a-based combinations  
41 against other virus infections in vitro. Altogether, our results indicate that IFNa2a-based combination  
42 therapies can achieve higher efficacy while requiring lower dosage compared to monotherapies,  
43 making them attractive targets for further pre-clinical and clinical development.

#### 44 **Introduction**

45 Viral diseases continue to pose a serious threat to public health due to a paucity of effective, rapidly  
46 deployable, and widely available control measures [1, 2]. Viruses are submicroscopic agents that  
47 replicate inside living organisms. When viruses enter and replicate in the cells, viral pathogen-  
48 associated molecular patterns (PAMPs) are recognized, and signals are transduced to activate intrinsic  
49 and extrinsic immune responses [3]. Pattern recognition receptors (PRRs), including Toll-like receptors  
50 (TLRs), RIG-I-like receptors (RLRs) and cytoplasmic DNA receptors sense incoming viruses and

51 activate transcription of IFN genes via NFkB and other pathways. IFNs launch expression of IFN-  
52 stimulated genes (ISGs) in infected cells as well as in nearby non-infected cells, protecting them from  
53 potential viral invasion. This activation of innate immune response, combined with contributions from  
54 adaptive immune response in the host, is often sufficient for elimination of most viruses.

55 IFNs are a large class of host proteins that are activated during innate antiviral immune response  
56 [4, 5]. They are classified into three types, according to the cellular receptor they bind [6] (Fig. S1). Type  
57 I IFNs consist of IFN-alpha (IFN $\alpha$ ), IFN-beta (IFN $\beta$ ), IFN-epsilon, IFN-kappa and IFN-omega (IFN $\omega$ )  
58 and bind to the IFN-alpha/beta receptor (IFNAR1/2). Type II IFNs consist of IFN-gamma (IFN $\gamma$ ) and  
59 interact with the IFN-gamma receptor (IFNGR1/2). Finally, type III IFNs, consisting of IFN-lambda-  
60 1/IL29 (IFN1), IFN-lambda-2/IL28A (IFN2), IFN-lambda-3/IL28B (IFN3) and IFN-lambda-4 (IFN4),  
61 pass signals through a receptor complex consisting of interleukin 10 receptor 2 (IL10R2) and IFN-  
62 lambda receptor (IFNLR1) [7].

63 Different IFNs induce transcription of different sets of ISGs, which participate in intrinsic antiviral  
64 and extrinsic immune responses. For example, ISGs like IFIT1 and OASL activate Ribonuclease L  
65 (RNaseL), which leads to the degradation of viral RNA [8]. Moreover, ISGs such as interleukins (ILs),  
66 C-X-C and C-C motif chemokines (CXCLs and CCLs) recruit immune cells to the site of infection.  
67 Notably, mutations in IFN-signaling pathway genes have resulted in increased susceptibility to viral  
68 infections and reduced patient survival [9-12]. However, the exact role of each IFN pathway and their  
69 crosstalk remain unclear.

70 The use of recombinant human IFNs has been approved for treatment of hepatitis C virus (HCV)  
71 and hepatitis B virus (HBV) infections [13]. Additionally, IFNs have been shown to be effective against  
72 a variety of other viruses in clinical trials and in laboratory settings (Fig. S2) [14-16]. Unfortunately,  
73 IFNs possess limited efficacy when administered as antiviral treatments [17, 18] and can cause adverse  
74 effects when used at established doses [19].

75 IFN-related toxicity can be reduced by combining IFNs with other antiviral drugs that act  
76 synergistically, thus allowing for the use of smaller doses of each component (Fig. S3). Moreover,

77 synergistic combinations can often have higher efficacy against viral infections than individual  
78 components administered as monotherapies, even at lower doses. Indeed, combination treatment of  
79 IFNa and ribavirin was the “gold standard” for treatment of chronic HCV infection for more than  
80 decade. Similarly, several rhIFN-based drug combinations have been tested against COVID-19. Of note,  
81 combinations of IFNb1b/lopinavir–ritonavir/ribavirin, IFNa2b/IFNg, and IFNa/umifenovir were all  
82 shown to be effective for treatment of patients with COVID-19 [20-23]. However, despite these  
83 promising data, the mode in which IFNs can be optimally combined with other drugs to maximize  
84 antiviral and minimize side effects remains unclear.

85 Here, we have identified several novel synergistic IFNa2a-based drug combinations against SARS-  
86 CoV-2, HCV, HEV, FluAV and HIV-1 infections. These treatment combinations are effective at lower  
87 concentrations compared to monotherapies. These combinations have powerful treatment potential,  
88 which can be leveraged for use in response to imminent viral threats including the emergence and re-  
89 emergence of viruses, immune-evading or drug-resistant variants, and viral co-infections.

## 90 **Results**

### 91 *Type I IFNs reduce SARS-CoV-2 replication more efficiently than type II and III IFNs*

92 Although dexamethasone has been shown to improve survival of patients with severe or critical  
93 COVID-19 [24], there are currently no curative therapies against SARS-CoV-2. However, previous  
94 studies have uncovered several potent antiviral agents, including IFNs, against SARS-CoV-2 *in vitro*  
95 and *in vivo* [14, 15, 25]. Here, we tested type I, II, and III IFNs against wild type SARS-CoV-2  
96 (multiplicity of infection (moi) 0.01) in Calu-3 and Vero-E6 cells using cell viability and virus plaque  
97 reduction assays as readouts. We observed that type I IFNs rescued both cell types from virus-mediated  
98 death and reduced SARS-CoV-2 replication more efficiently than type II and III IFNs. However, the  
99 rescue was only partial, and virus replication was reduced only by 2-3 common logarithms (Fig. 1).

100 To identify the type I IFN with most activity against SARS-CoV-2 infection, we infected IFN-  
101 treated and untreated Calu-3 cells with SARS-CoV-2-mCherry (moi 0.01) and collected media from the

102 cells (p1) after 48 h. The media were diluted 25-fold and applied to noninfected cells for another 48 h  
103 (p2). Mock-infected cells were used as controls (Fig. 2a). Fluorescence microscopy, fluorescence  
104 intensity analysis, and cell viability assay of p1 and p2 cells showed that IFN $\alpha$ 1b, IFN $\alpha$ 2a and IFN $\omega$ 1  
105 were more effective inhibitors of SARS-CoV-2 infection than IFN $\beta$ 1a. However, none of the IFNs tested  
106 were able to inhibit virus infection completely (Fig. 2b-d).

107 Type I IFNs are encoded by multiple genes and vary slightly from one another in their protein  
108 structure. In basic research, IFN $\alpha$ 2a is widely used to elucidate the biological activities, structure, and  
109 mechanism of action of such type I IFNs. Thus, we next tested IFN $\alpha$ 2a against various doses of SARS-  
110 CoV-2-mCherry and different time of drug addition. The Calu-3 cells were treated with 1  $\mu$ g/mL IFN $\alpha$ 2a  
111 at indicated time points, then infected with SARS-CoV-2-mCherry at indicated moi. After 48 h,  
112 fluorescence intensity and cell viability analysis were performed. We found that efficacy of IFN $\alpha$ 2a  
113 treatment in preventing SARS-CoV-2 infection is dependent on virus load, decreasing in efficacy as moi  
114 increases (Fig. 3a) as well as on time of addition, showing more efficacy when given prior virus infection  
115 than following infection (Fig. 3b).

116 *IFN $\alpha$ 2a reduces the SARS-CoV-2 RNA synthesis and promotes virus-mediated induction of type III IFNs, IFN $\beta$ 1*  
117 *and ISGs*

118 To shed new light on the mechanism of action of IFN $\alpha$ 2a, we evaluated their effect on expression  
119 of cellular genes and transcription of viral RNA in mock- and SARS-CoV-2-infected Calu-3 cells. For  
120 this, cells were treated with 1  $\mu$ g/mL of IFN $\alpha$ 2a, other type I IFNs, or vehicle; then infected with virus  
121 or mock. After 24 h, we analyzed polyadenylated RNA using RNA-sequencing. We found that IFN $\alpha$ 2a  
122 and other type I IFNs attenuated production of viral RNA (Fig. 4a), while increasing expression of many  
123 ISGs in cells, regardless of virus- or mock-infection (Fig. 4b). These ISGs include IFIT1, IFIT2 and IFIT3,  
124 which play a role in recognition of viral RNA; OASL and OAS2, which are involved in RNase L-  
125 mediated RNA degradation; and IDO1, which is essential for kynurenine biosynthesis [26-29].  
126 Interestingly, IFN $\alpha$ 2a and other type I IFNs boosted virus-activated expression of type III IFNs (IFN $\lambda$ 1,

127 IFN $\beta$ 2, IFN $\beta$ 3 and IFN $\beta$ 4) as well as IFN $\beta$ 1, which belongs to type I IFN. These results indicate that  
128 IFN $\alpha$ 2a does not only trigger expression of ISGs, but also amplifies expression of other IFNs usually  
129 activated by viral infections, creating a positive feedback loop of IFN signaling during SARS-CoV-2  
130 infection.

131 Next, we studied the effect of IFN $\alpha$ 2a on the metabolism of mock- and SARS-CoV-2-infected Calu-  
132 3 cells. A total of 93 mainly polar metabolites were quantified at 24 hpi (Fig. S4). We found that tyrosine  
133 and 4-hydroxyproline levels were substantially lowered during viral infection ( $\log_2FC < -2$ ).  
134 Additionally, administration of IFN $\alpha$ 2a or other type I IFNs lowered the levels of several metabolites  
135 including tryptophan while increasing kynurenine, regardless of viral infection ( $\log_2FC > 3$ ; Fig. 4c). This  
136 indicates that IFN $\alpha$ 2a activates IDO1-mediated kynurenine biosynthesis, which could be associated  
137 with adverse reactions such as suppression of T-cell responses, pain hypersensitivity and behavior  
138 disturbance [30].

### 139 *Synergistic IFN $\alpha$ 2a-based combinations against SARS-CoV-2 infection in vitro and in vivo*

140 Next, we examined whether IFN $\alpha$ 2a in combinations with known SARS-CoV-2 inhibitors  
141 remdesivir, EIDD-2801, camostat, cycloheximide, or convalescent serum [31-35] can protect cells from  
142 virus infection more efficiently and at lower concentrations than IFN $\alpha$ 2a alone. Remdesivir and EIDD-  
143 2801 are nucleoside analogues which inhibit viral RNA synthesis [33, 36]. Camostat, a serine protease  
144 inhibitor, reduces SARS-CoV-2-cell membrane fusion by binding host TMPRSS2 [37]. In addition,  
145 camostat possesses some potential beneficial immunomodulatory effects by interfering with the  
146 bradykinin/kallikrein pathways [38]. Cycloheximide inhibits translation elongation and, thereby,  
147 reduces SARS-CoV-2 replication [32]. Convalescent serum contains neutralizing antibodies which bind  
148 S protein of SARS-CoV-2 preventing virus entry into the cells [16].

149 We first confirmed antiviral activities of these known viral inhibitors on Calu-3 cells using SARS-  
150 CoV-2-mCherry (Fig. 5a, Fig. S5a). Then, we tested the antiviral efficacy and toxicity of these agents in  
151 combination with IFN $\alpha$ 2a in Calu-3 cells by monitoring virus-mediated mCherry expression and cell

152 viability (CTG). Each drug combination was tested in a 6×6 dose-response matrix, where 5 doses of  
153 single drugs are combined in a pairwise manner. As a result, we obtained dose-response matrices  
154 demonstrating virus inhibition and cell viability achieved by each combination (Fig 5c,d; Fig. S5b-e).  
155 We plotted synergy distribution maps, showing synergy (higher than expected effect) at each pairwise  
156 dose. For each drug pair, we calculated average ZIP synergy scores for the whole 6×6 dose-response  
157 matrices and for most synergistic 3×3 dose-regions, summarizing combination synergies into single  
158 metrics (Fig. 5e). We observed that all combinations showed a strong synergy (synergy scores >10) at  
159 various combination doses. Thus, the observed synergy allows us to substantially decrease the  
160 concentration of both components to achieve antiviral efficacy that was comparable to those of  
161 individual drugs at high concentrations.

162 Both remdesivir and *rhIFNa2a* (Pegasys) were approved for the treatment of COVID-19 infection  
163 in several countries. Therefore, we evaluated the antiviral effect of IFNa2a-remdesivir combination on  
164 iPSC-derived lung organoids (LOs). Thirty-day-old LOs were treated with 5 ng/mL IFNa2a, 0.5 μM  
165 remdesivir, or a combination thereof, then infected with SARS-CoV-2-mCherry. At 72 hpi, the  
166 organoids were analyzed for viral reporter protein expression (mCherry) and cell death  
167 (CellToxGreen). We found that IFNa2a-remdesivir substantially attenuated virus-mediated mCherry  
168 expression without affecting cell viability (Fig. 6a).

169 We also evaluated the effect of the combination treatment on viral and cellular RNA expression in  
170 LOs. RNA-sequencing revealed that at 48 hpi IFNa2a-remdesivir substantially reduced production of  
171 viral RNA by contrast to single agents (Fig. 6b). Treatment with IFNa2a-remdesivir also led to elevated  
172 levels of ACE2 and other genes involved in lipid metabolism (APOA4, ADH4, CYP3A7, PON3, FADS6,  
173 SDR16C5, ENPP7, FABP2, CUBN, and SERPINA6) [39, 40], for which transcription was substantially  
174 down-regulated during SARS-CoV-2 infection (Fig. S6, Fig. 6c). Importantly, the set of IFNa2a-induced  
175 ISGs in LOs is consistent to what we observed in Calu-3 cells (Fig. S6).

176 Furthermore, we studied the effect of IFNa2a-remdesivir on the metabolism of SARS-CoV-2- and  
177 mock-infected LOs. A total of 82 metabolites were quantified in LO culture supernatants at 48 hpi.

178 Administration of IFNa2a-remdesivir prevented virus-mediated alteration of metabolism, excluding  
179 kynurenine biosynthesis (Fig. S7, Fig. 6d), which is in line with the results obtained on IFNa2a-  
180 stimulated Calu-3 cells.

181 Next, we examined whether IFNa and remdesivir can affect the replication of SARS-CoV-2 *in vivo*.  
182 Four groups of 8 six-week-old female Syrian hamsters were injected IP with recombinant mouse IFNa,  
183 remdesivir, IFNa-remdesivir combination or vehicle thereof. After 2 h of drug treatment, animals  
184 received SARS-CoV-2 intranasally. After 3 days, animals were anesthetized and euthanized, and the  
185 lungs were collected (Fig. 7a). Virus titers from hamster lung homogenates in each treatment group  
186 were determined using plaque reduction assays (Fig. 7b). In addition, viral RNA was extracted and  
187 sequenced. Sequencing results were validated using RT-qPCR (Fig. 7c,d). The IFNa-remdesivir  
188 combination attenuated the SARS-CoV-2 production and the synthesis of some viral RNAs more  
189 efficiently than individual agents.

#### 190 *Synergistic IFNa2a-based combinations against other viral infections*

191 To extend our findings beyond SARS-CoV-2, we tested IFNa2a in combination with known HCV  
192 inhibitors, sofosbuvir and telaprevir, using GFP-expressing HCV in infected Huh-7.5 cells. Sofosbuvir  
193 is a nucleoside analogue, which inhibits viral RNA synthesis, whereas telaprevir is an orally available  
194 peptidomimetic that targets the HCV serine protease and disrupts processing of viral proteins and  
195 formation of a viral replication complex. Eight different concentrations of the compounds alone or in  
196 combination were added to virus- or mock-infected cells. HCV-mediated GFP expression and cell  
197 viability were measured after 72 hpi to determine compound efficacy and toxicity. Both IFNa2a-  
198 sofosbuvir and IFNa2a-telaprevir lowered GFP-expression without detectable cytotoxicity at indicated  
199 concentrations with synergy scores of 3 and 5 (the most synergistic area scores: 14 and 16), respectively  
200 (Fig. S8, Fig. 8).

201 Next, we studied IFNa2a in combination with known HEV inhibitors, NITD008 and ribavirin,  
202 against HEV infection in Huh-7.5 cells (Fig. S9, Fig. 8). Both NITD008 and ribavirin are nucleoside



203 analogs which inhibit viral RNA synthesis. We observed that IFNa2a-NITD008 and IFNa2a-ribavirin  
204 were synergistic against HEV infection (ZIP synergy scores: 11 and 8; the most synergistic area scores:  
205 14 and 19, respectively) while remaining nontoxic at synergistic doses for either drug.

206 We also tested IFNa2a in combination with known influenza inhibitor pimodivir against FluAV  
207 infection in A549 cells. Pimodivir (VX-787, JNJ-63623872) is an orally available anti-FluAV agent which  
208 targets viral polymerase basic protein 2, inhibits cap-snatching and has shown promising results in  
209 Phase II clinical trials [41, 42]. Cell viability was measured after 48 h in FluAV- and mock-infected cells  
210 to determine efficiency and toxicity of each compound and their combinations with IFNa2a (Fig. S9,  
211 Fig. 8). We observed that IFNa2a-pimodivir was synergistic against FluAV infection (ZIP synergy score:  
212 22, the most synergistic area score: 43) while remaining nontoxic at synergistic doses for either drug.

213 Finally, we tested IFNa2a in combination with known anti-retroviral agent lamivudine against  
214 HIV-1 in TZM-bl cells. Lamivudine (3TC) is an orally available anti-HIV drug which inhibits viral  
215 reverse transcriptase [43]. Cell viability and HIV-induced luciferase expression were measured for each  
216 compound or their combination with IFNa2a after 48 h. We identified that treatment with IFNa2a and  
217 lamivudine was effective while being nontoxic at synergistic drug concentrations, with ZIP synergy  
218 scores of 6 and ZIP synergy score at the most synergistic area of 11 (Fig. S10, Fig. 8).

## 219 Discussion

220 Currently, combinational therapies are still largely eschewed for the treatment of emerging viral  
221 infections in favor of monotherapies. This is in part due to the fact that many drug-drug interactions  
222 have not been fully explored or understood [44].

223 Here, we have reported several novel IFNa2a-based combination therapies that have better  
224 efficacy and lower toxicity than single drugs. In particular, we report novel *in vitro* activities of IFNa2a  
225 combinations with remdesivir, EIDD-2801, camostat, cycloheximide, and convalescent serum against  
226 SARS-CoV-2, with sofosbuvir or telaprevir against HCV infection, with NITD008 or ribavirin against  
227 HEV infection, with pimodivir against FluAV, as well as with lamivudine against HIV-1 infection. Our

228 results indicate that other IFNa could be as efficient as IFNa2a when combined with these antivirals.  
229 Moreover, they expand the spectrum of antiviral activities of these combinations and emphasize the  
230 potential of IFNa-based combinatorial approach (Fig. 8b). Interestingly, pimodivir, lamivudine,  
231 remdesivir, EIDD-2801, NITD008, ribavirin and sofosbuvir interfere with synthesis of viral nucleic  
232 acids, whereas camostat, cycloheximide, telaprevir and convalescent serum inhibit other steps of viral  
233 replication cycle [33, 36, 41, 45], indicating that IFNa could be combined with virus- and host-directed  
234 agents targeting different stages of virus replication.

235 Based on our experiments, we propose the following mechanism of action of the IFNa-based  
236 combinations (Fig. S11). IFNa induces transcription of ISGs including IFIT1, IFIT2 and IFIT3, which  
237 recognize viral RNA; OASL and OAS2, which are involved in RNase L-mediated RNA degradation;  
238 and IDO1, which catalyzes kynurenine biosynthesis. IFNa also facilitates expression of several  
239 cytokines and virus-activated synthesis of IFNL1, IFNL2, IFNL3, IFNL4, and IFNB1, which alert the  
240 neighboring cells of upcoming infection. Therefore, combination treatments of IFNa and therapies  
241 targeting viral nucleic acid synthesis or other stages of virus replication can inhibit infection within a  
242 virus-host system.

243 Furthermore, we demonstrated anti-SARS-CoV-2 activity of IFNa-remdesivir in human lung  
244 organoids and hamsters. In particular, the combination treatment suppressed viral RNA expression  
245 more effectively than the drugs alone, while inducing transcription of antiviral genes. Thus, we have  
246 identified combination treatments that reduce viral replication at lower concentrations than is required  
247 with monotherapies. The low effective doses of these combination drugs may have several clinical  
248 advantages, including improved patient outcome and fewer adverse events.

249 In conclusion, the potential of using clinical grade IFNs as therapeutics against SARS-CoV-2 and  
250 other viral infections has raised interest recently [46]. It has been demonstrated that administration of  
251 IFNs in patients with early onset and mild symptoms inhibit infection and favor SARS-CoV-2 clearance  
252 [47, 48]. Our work may suggest that IFNa-based combinations with other antiviral agents may favor  
253 treatment of COVID-19 patients at various stages of disease and severity. It is conceivable that

254 particularly vulnerable groups of COVID-19 patients with impaired immunity (i.e., impaired B-cell  
255 response, IFN response and T-cell response) may also benefit from combination of effective antivirals  
256 that are amplified by a dose of IFN $\alpha$  to elicit a clinical host response. We believe further development  
257 of IFN $\alpha$ -based combinations for treatment of SARS-CoV-2 and other viral infections can lead to practical  
258 therapeutic options that are more effective while having potentially reduced side effects than currently  
259 existing treatments. Moreover, the capacity to deliver IFN $\alpha$ -based combinations through different  
260 administration routes could allow for the treatment of patients at different stages of COVID-19 and  
261 other viral diseases [37, 49, 50].

## 262 **Materials and Methods**

### 263 *Drugs, viruses, cells, lung organoids and hamsters*

264 Table S1 lists IFNs and other antiviral agents, their suppliers and catalogue numbers. Lyophilized  
265 IFNs were dissolved in sterile deionized water to obtain 200  $\mu$ g/mL concentrations. Compounds were  
266 dissolved in dimethyl sulfoxide (DMSO; Sigma-Aldrich, Hamburg, Germany) or milli-Q water to  
267 obtain 10 mM stock solutions. The convalescent serum (G614) from a recovered COVID-19 patient has  
268 been described in a previous study [25].

269 The propagation of wild-type SARS-CoV-2 (hCoV-19/Norway/Trondheim-S15/2020), recombinant  
270 mCherry-expressing SARS-CoV-2 strains (SARS-CoV-2-mCherry), wild type human influenza  
271 A/Udorn/307/1972 (H3N2), HCV and HIV-1 have been also described previously [25, 51-55]. SARS-  
272 CoV-2 strain Slovakia/SK-BMC5/2020 was provided by the European Virus Archive global (EVAg) and  
273 propagated in VeroE6/TMPRSS2 cells. To quantitate the production of infectious virions, we titered the  
274 viruses using plaque assays or ELISA [25, 51-54].

275 A plasmid harboring a sub-genomic HEV sequence coupled with a GFP reporter gene (Kernow-  
276 C1 p6 clone, gt3; GenBank Accession No. JQ679013) was used to generate HEV transcripts. Viral capped  
277 RNAs were transcribed *in vitro* from linearized plasmid using mMESSAGE mMACHINE™ T7  
278 Transcription Kit (Thermofisher, USA).  $1.5 \times 10^7$  Huh-7.5 cells/mL in 400  $\mu$ L of Maxcyte electroporation

279 buffer were electroporated with 10 µg of p6-GFP sub-genomic HEV RNA. Electroporation was carried  
280 out with a Gene Pulser system (Bio-Rad, Munich, Germany) and allowed to recover for 30 min in a  
281 37°C incubator. Recovered cells were resuspended in 10 mL prewarmed DMEM complete medium and  
282 maintained in an incubator for 24 h.

283 The propagation of human non-small cell lung cancer Calu-3; human adenocarcinoma alveolar  
284 basal epithelial A549; African green monkey kidney Vero-E6; T-cell like ACH-2 cells, which possess a  
285 single integrated copy of the provirus HIV-1 strain LAI (NIH AIDS Reagent Program); and human  
286 cervical cancer-derived TZM-bl, which express firefly luciferase under control of HIV-1 long terminal  
287 repeat (LTR) promoter allowing quantitation of the viral infection (tat-protein expression by integrated  
288 HIV-1 provirus) using firefly luciferase assay, have been described in our previous studies [25, 51-54].  
289 Human hepatoma cells (Huh-7.5) were cultured in Dulbecco's modified Eagle's medium (DMEM)  
290 (Invitrogen, Karlsruhe, Germany) supplemented with 10% fetal bovine serum (Invitrogen), 1%  
291 nonessential amino acids (Invitrogen), 100 µg/mL of streptomycin (Invitrogen), and 100 IU/mL of  
292 penicillin.

293 The lung organoids (LOs) were generated as described previously (10.3390/v13040651). Briefly,  
294 induced pluripotent stem cells (iPSCs) were subjected to embryoid body induction using embryoid  
295 bodies (EB)/primitive streak media (10 µM Y-27632 and 3 ng/mL BMP4 in serum-free differentiation  
296 (SFD) media consisting of 375 mL Iscove's Modified Dulbecco's Medium (IMDM), 100 mL Ham's F-12,  
297 2.5 mL N2, 5 mL B27, 3,75 mL 7.5% BSA, 5 mL 1% penicillin-streptomycin, 5 mL GlutaMax, 50 µg/mL  
298 ascorbic acid, and 0.4 µM monothioglycerol) in ultra-low attachment plates. After 24 h the media was  
299 replaced with endoderm induction media (10 µM Y-27632, 0.5 ng/mL BMP4, 2.5 ng/mL FGF2, and 100  
300 ng/mL Activin A in SFD media). Extra media was added every day for 3 days. The embryoid bodies  
301 were collected and dissociated using 0.05% Trypsin/EDTA and plated on fibronectin-coated plates with  
302 a cell density of 85,000 cells/cm<sup>2</sup>. Cells were then incubated in anteriorization media-1 (100 ng/mL  
303 Noggin, and 10 µM SB431542 in SFD media), followed by an incubation with anteriorization media-2  
304 (10 µM SB431542, and 1 µM IWP2 in SFD media). The anteriorization media-2 was replaced with

305 ventralization media (3  $\mu$ M CHIR99021, 10 ng/mL FGF10, 10 ng/mL FGF7, 10 ng/mL BMP4, and 50 nM  
306 all-trans Retinoic acid in SFD media) and incubated for two days. The cell monolayer was then lifted  
307 by gentle pipetting, and the suspended cells were transferred to an ultra-low attachment plate where  
308 they would form the lung organoids.

309 Thirty-two 6-week-old healthy female Syrian hamsters were obtained from Janvier Labs. The  
310 animals were maintained in pathogen free health status according to the FELASA guidelines. The  
311 animals were individually identified and were maintained in housing rooms under controlled  
312 environmental conditions: temperature:  $21 \pm 2^\circ\text{C}$ , humidity  $55 \pm 10\%$ , photoperiod (12h light/12h dark),  
313 H14 filtered air, minimum of 12 air exchanges per hour with no recirculation. Each cage was labeled  
314 with a specific code. Animal enclosures provided sterile and adequate space with bedding material,  
315 food and water, environmental and social enrichment (group housing) as described below: IsoRat900N  
316 biocontainment system (Techniplast, France), poplar bedding (Select fine, Safe, France), A04 SP-10 diet  
317 (Safe, France), tap water, environmental enrichment, tunnel, wood sticks. Animal housing and  
318 experimental procedures were conducted according to the French and European Regulations and the  
319 National Research Council Guide for the Care and Use of Laboratory Animals. The animal BSL3 facility  
320 is authorized by the French authorities (Agreement N° D92-032-02). All animal procedures (including  
321 surgery, anesthesia, and euthanasia as applicable) were approved by the Institutional Animal Care and  
322 Use Committee of CEA and French authorities (CETEA DSV – n° 44).

### 323 *Drug Testing and Drug Sensitivity Quantification*

324 Approximately  $4 \times 10^4$  Vero-E6 or Calu-3 cells were seeded per well in 96-well plates. The cells  
325 were grown for 24 h in DMEM or DMEM-F12, respectively, supplemented with 10% FBS and Pen-  
326 Strep. The medium was then replaced with DMEM or DMEM-F12 containing 0.2% BSA, Pen-Strep and  
327 the compounds in 3-fold dilutions at 7 different concentrations. No compounds were added to the  
328 control wells. The cells were infected with SARS-CoV-2 or SARS-CoV-2-mCherry strains at a moi of  
329 0.01 or mock. After 72 or 48 h of infection, a CellTiter-Glo (CTG) assay was performed to measure cell

330 viability. Drug efficacy on SARS-CoV-2-mCherry infected cells was measured on PFA- or acetone-fixed  
331 cells with fluorescence.

332 For testing compound toxicity and efficacy against FluAV, approximately  $4 \times 10^4$  A549 cells were  
333 seeded in each well of a 96-well plate. The cells were grown for 24 h in DMEM supplemented with 10%  
334 FBS and Pen–Strep. The medium was then replaced with DMEM containing 0.2% BSA, Pen–Strep, 0,5  
335  $\mu\text{g}/\text{mL}$  TPSK-trypsin and compounds in three-fold dilutions at seven different concentrations. No  
336 compounds were added to the control wells. The cells were infected with FluAV (moi = 0.5) or mock.  
337 At 48 hpi, the media was removed, and a CTG assay was performed to measure cell viability.

338 For testing compound toxicity and efficacy against HIV-1, approximately  $4 \times 10^4$  TZM-bl cells were  
339 seeded in each well of a 96-well plate in DMEM supplemented with 10% FBS and Pen–Strep. The cells  
340 were grown for 24 h in growth medium. The medium was then replaced with DMEM containing 0.2%  
341 BSA, Pen–Strep and the compounds in 3-fold dilutions at 7 different concentrations. No compounds  
342 were added to the control wells. The cells were infected with HIV-1 (corresponding to 300 ng/mL of  
343 HIV-1 p24) or mock. At 48 hours post-infection (hpi), the media was removed from the cells, the cells  
344 were lysed, and firefly luciferase activity was measured using the Luciferase Assay System (Promega,  
345 Madison, WI, USA). In a parallel experiment, a CTG assay was performed to measure cell viability.

346 We also examined cytotoxicity and antiviral activity of drug combinations using GFP-expressing  
347 HCV in Huh-7.5 cells by following previously described procedures [56]. For testing compound toxicity  
348 and efficacy against HEV, electroporated Huh-7.5 cells were seeded in the 384-well plate ( $3 \times 10^3$   
349 cells/well) with immune-modulators at indicated concentrations for 72 h. HEV replication was  
350 analyzed by determining the number of GFP-positive cells using fully automated confocal microscopy  
351 (Operetta CLS; PerkinElmer Devices).

352 The half-maximal cytotoxic concentration ( $\text{CC}_{50}$ ) for each compound was calculated based on  
353 viability/death curves obtained on mock-infected cells after non-linear regression analysis with a  
354 variable slope using GraphPad Prism software version 7.0a. The half-maximal effective concentrations

355 (EC<sub>50</sub>) were calculated based on the analysis of the viability of infected cells by fitting drug dose-  
356 response curves using four-parameter (4PL) logistic function  $f(x)$ :

$$357 \quad f(x) = A_{min} + \frac{A_{max} - A_{min}}{1 + (\frac{x}{m})^\lambda}, \quad (1)$$

358 where  $f(x)$  is a response value at dose  $x$ ,  $A_{min}$  and  $A_{max}$  are the upper and lower asymptotes (minimal  
359 and maximal drug effects),  $m$  is the dose that produces the half-maximal effect (EC<sub>50</sub> or CC<sub>50</sub>), and  $\lambda$  is  
360 the steepness (slope) of the curve. The relative effectiveness of the drug was defined as selectivity index  
361 ( $SI = CC_{50}/EC_{50}$ ).

362 To quantify each drug responses in a single metric, a drug sensitivity score ( $DSS$ ) was  
363 calculated as a normalized version of standard area under dose-response curve ( $AUC$ ), with the  
364 baseline noise subtracted, and normalized maximal response at the highest concentration (often  
365 corresponding to off-target toxicity):

$$366 \quad DSS = \frac{AUC - t(x_{max} - x_{min})}{(100 - t)(x_{max} - x_{min}) \log_{10} A_{min}}, \quad (2)$$

367 where activity threshold  $t$  equals 10%, and  $DSS \in [0, 50]$ .

### 368 *Drug Combination Testing and Synergy Calculations*

369 Calu-3, A549, TZM-bl or Huh-7.5 cells were treated with different concentrations of two drugs and  
370 infected with SARS-CoV-2-mCherry (moi 0.01), FluAV (moi 0.5), HIV-1 (corresponding to 300 ng/mL  
371 of HIV-1 p24), HCV or mock. In addition, HEV-expressing Huh-7.5 cells were treated with different  
372 concentrations of two drugs. After 48 h, cell viability and reporter protein expression (SARS-CoV-2-  
373 mCherry, HIV-1, HCV-GFP, and HEV-GFP) were measured.

374 To test whether the drug combinations act synergistically, the observed responses were compared  
375 with expected combination responses. The expected responses were calculated based on the ZIP  
376 reference model using SynergyFinder version 2 [57, 58]. Final synergy scores were quantified as average  
377 excess response due to drug interactions (i.e., 10% of cell survival beyond the expected additivity  
378 between single drugs represents a synergy score of 10). Additionally, we calculated most synergistic

379 area scores for each drug combination – the most synergistic 3-by-3 dose-window in dose-response  
380 matrixes.

381 LOs were treated with 0.5  $\mu$ M remdesivir, 5 ng/mL IFNa2a, or their combination and infected with  
382 SARS-CoV-2-mCherry (moi 0.1). No compounds were added to the control wells. At 72 hpi, the LOs  
383 were stained using Cell Toxicity Green reagent (CTxG, Promega), and cell nuclei were stained with  
384 DAPI. Cells were fixed with PFA and imaged using microscopy. Representative images ( $n = 3$ ) were  
385 selected.

### 386 *Prophylactic Study of Remdesivir, IFN $\alpha$ and Their Combination Against SARS-CoV-2 Infection in Hamsters*

387 Thirty-two animals were weighed and divided into 4 homogenous groups of 8 animals. Group 1  
388 received 5 mL/kg vehicle IP 2h before infection. Group 2 received 40  $\mu$ g/kg (5 mL/kg) mouse  
389 recombinant IFNa IP 2h before infection. Group 3 received 5mg/kg (5 mL/kg) remdesivir IP 2h before  
390 infection. Group 4 received a combination of 5mg/kg remdesivir and 40  $\mu$ g/kg (5 mL/kg) IFNa IP 2h  
391 before infection. All groups received SARS-CoV-2 intranasally. Animal viability, behavior and clinical  
392 parameters were monitored daily. After 3 days animals were deeply anesthetized using a cocktail of 30  
393 mg/kg (0.6 mL/kg) Zoletil and 10 mg/kg (0.5 mL/kg) Xylazine IP. Cervical dislocation followed by  
394 thoracotomy was performed before lung collection. The entire left lungs and superior, middle, post-  
395 caval and inferior lobes of right lungs were put in RNAlater tissue storage reagent overnight at 4°C,  
396 then stored at -80°C until RNA extraction.

### 397 *RT-qPCR Analysis*

398 Viral RNA was extracted using the QIAamp Viral RNA Mini Kit (Qiagen). RT-PCR was performed  
399 using SuperScript™ III One-Step qRT-PCR System kit (commercial kit #1732-020, Life Technologies)  
400 with primers nCoV\_IP2-12669Fw: ATGAGCTTAGTCCTGTTG, nCoV\_IP2-12759Rv:  
401 CTCCTTTGTTGTGTTGT, and nCoV\_IP2-12696bProbe(+): Hex-AGATGTCTTGCTGCCGGTA-  
402 BHQ-1 or nCoV\_IP4-14059Fw: GGTAAGTGGTATGATTTCCG, nCoV\_IP4-14146Rv:  
403 CTGGTCAAGGTTAATATAG, and nCoV\_IP4-14084Probe(+): Fam-TCATACAAACCACGCCAGG-



404 BHQ-1 targeting IP2 and IP4 regions SARS-CoV-2 RdRP gene as well as ORF1ab\_Fw:  
405 CCGCAAGGTTCTTCTTCGTAAG, ORF1ab\_Rv: TGCTATGTTTAGTGTTCCAGTTTTTC,  
406 ORF1ab\_probe: Hex-AAGGATCAGTGCCAAGCTCGTCGCC-BHQ-1 targeting another region on  
407 ORF1ab. RT-qPCR was performed using a Bio-Rad CFX384<sup>TM</sup> and adjoining software. The relative gene  
408 expression differences were calculated using  $\beta$ -Actin as control and the results were represented as  
409 relative units (RU). Technical triplicates of each sample were performed on the same qPCR plate and  
410 non-templates and non-reverse transcriptase samples were analysed as negative controls. Statistical  
411 significance ( $p < 0.05$ ) of the quantitation results was evaluated with t-test. Benjamini-Hochberg method  
412 was used to adjust the p-values.

#### 413 *Gene Expression Analysis*

414 Calu-3 cells, LOs or Syrian hamsters were treated with drugs or vehicles and infected with SARS-  
415 CoV-2, SARS-CoV-2-mCherry or mock. Total RNA was isolated using RNeasy Plus Mini kit (Qiagen,  
416 Hilden, Germany) from Calu-3 cells, LOs or lungs of Syrian hamsters. Polyadenylated mRNA was  
417 isolated from 250 ng of total RNA with NEBNext Poly(A) mRNA magnetic isolation module. NEBNext  
418 Ultra II Directional RNA Library Prep kit from Illumina was used to prepare samples for sequencing.  
419 Sequencing was done on NextSeq 500 instrument (set up: single-end 1 x 76 bp + dual index 8 bp) using  
420 NextSeq High Output 75 cycle sequencing kit (up to 400M reads per flow cell). Reads were aligned  
421 using the Bowtie 2 software package version 2.4.2 to the NCBI reference sequence for SARS-CoV-2  
422 (NC\_045512.2) and to the human GRCh38 genome. The number of mapped and unmapped reads that  
423 aligned to each gene were obtained with the featureCounts function from Rsubread R-package version  
424 2.10. The GTF table for the SARS-CoV-2 reference sequence was downloaded from  
425 [https://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/009/858/895/GCF\\_009858895.2\\_SM985889v3/GCF\\_009858895.2\\_ASM985889v3\\_genomic.gtf.gz](https://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/009/858/895/GCF_009858895.2_SM985889v3/GCF_009858895.2_ASM985889v3_genomic.gtf.gz). The heatmaps were generated using the pheatmap package  
426 (https://cran.r-project.org/web/packages/pheatmap/index.html) based on log<sub>2</sub>-transformed or non-  
427 transformed profiling data.  
428

429 *Metabolic Analysis*

430 Calu-3 cells or LOs were treated with drugs or vehicle and infected with SARS-CoV-2, SARS-CoV-  
431 2-mCherry or mock. Metabolites were extracted from Calu-3 cells and LOs supernatants or from lung  
432 extracts. 100  $\mu$ L of culture medium/lung extracts were mixed with 400  $\mu$ L of cold extraction solvent  
433 (acetonitrile:methanol:water 40:40:20). Subsequently, samples were sonicated for 3 cycles (60 s, power  
434 = 60 and frequency = 37), vortexed for 2 min and centrifuged at 4  $^{\circ}$ C, 15000 g for 10 min. The supernatant  
435 was transferred to autosampler vials for LC-MS analysis. The extracts were analyzed with Thermo  
436 Vanquish UHPLC+ system coupled to a QExactive Orbitrap quadrupole mass spectrometer equipped  
437 with a heated electrospray ionization (H-ESI) source probe (Thermo Fischer Scientific, Waltham, MA,  
438 USA). A SeQuant ZIC-pHILIC (2.1  $\times$  100 mm, 5  $\mu$ m particles) HILIC phase analytical column (Merck  
439 KGaA, Darmstadt, Germany) was used as a chromatographic separation column.

440 Gradient elution was carried out with a flow rate of 0.1 mL/min with 20 mM ammonium carbonate,  
441 adjusted to pH 9.4 with ammonium solution (25%) as mobile phase A and acetonitrile as mobile phase  
442 B. The gradient elution was initiated from 20% mobile phase A and 80% mobile phase B and maintained  
443 for 2 min. Then, mobile phase A was gradually increased up to 80% for 17 min, followed by a decrease  
444 to 20% over the course of 17.1 min. and sustained for up to 24 min.

445 The column oven and auto-sampler temperatures were set to  $40 \pm 3$   $^{\circ}$ C and  $5 \pm 3$   $^{\circ}$ C, respectively.  
446 The mass spectrometer was equipped with a heated electrospray ionization (H-ESI) source using  
447 polarity switching and the following settings: resolution of 35,000, the spray voltages of 4250 V for  
448 positive and 3250 V for negative mode, sheath gas at 25 arbitrary units (AU), the auxiliary gas at 15 AU,  
449 sweep gas flow of 0, Capillary temperature of 275 $^{\circ}$ C, and S-lens RF level of 50.0. Instrument control  
450 was operated with Xcalibur 4.1.31.9 software (Thermo Fischer Scientific, Waltham, MA, USA).  
451 Metabolite peaks were confirmed using the mass spectrometry metabolite library kit MSMLS-1EA  
452 (Sigma Aldrich supplied by IROA Technologies).

453 For data processing, final peak integration was done with the TraceFinder 4.1 software (Thermo  
454 Fisher Scientific, Waltham, MA, USA) and for further data analysis, the peak area data was exported as

455 an Excel file. Data quality was monitored throughout the run using pooled healthy human serum as  
456 Quality Control (QC), which was processed and extracted in the same manner as unknown samples.  
457 After integration of QC data with TraceFinder 4.1, each detected metabolite was checked and %RSD  
458 were calculated, while the acceptance limit was set to  $\leq 20\%$ .

459 Blank samples were injected after every five runs to monitor any metabolite carryover. A carryover  
460 limit of  $\leq 20\%$  was set for each metabolite. Percentage background noise was calculated by injecting a  
461 blank sample at the beginning of the run. The acceptance limit for background noise was set at  $\leq 20\%$   
462 for each metabolite.

463

464 **Ethics approval and consent to participate:** Standard operational procedures were approved by  
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466

467 **Consent for publication:** All authors have read and agreed to the published version of the manuscript.

468

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471

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473

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485

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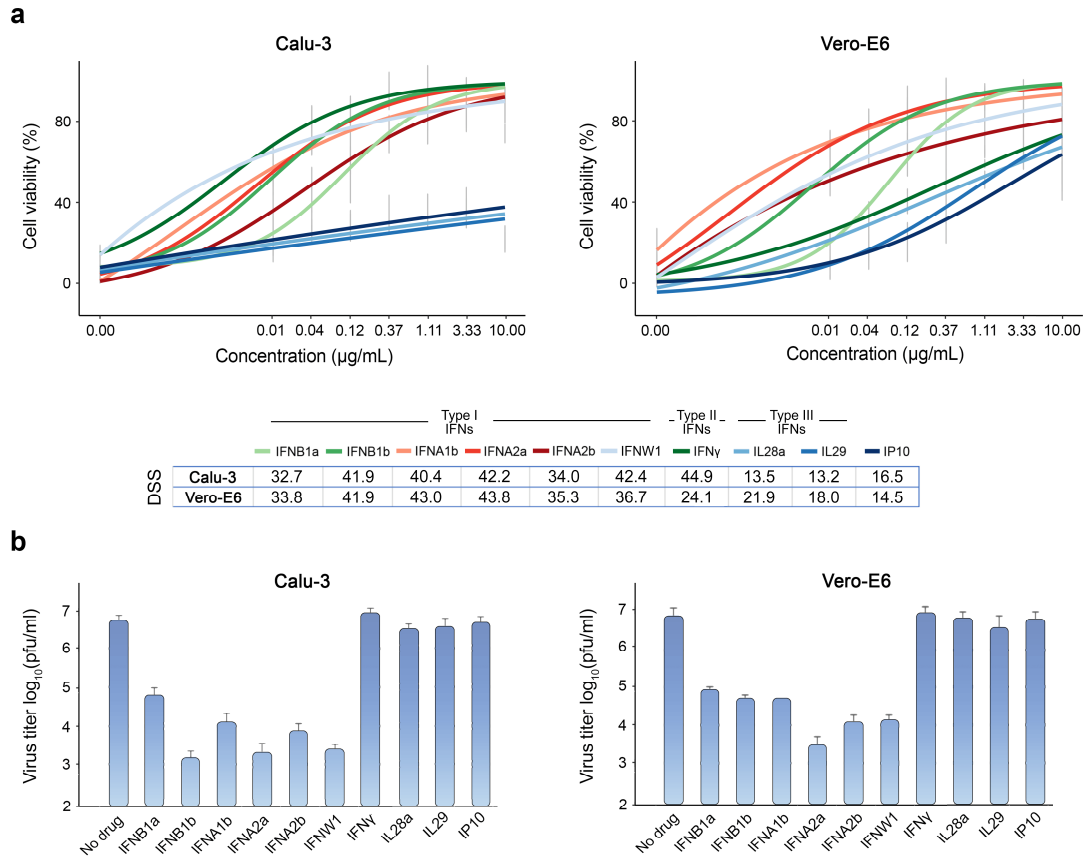
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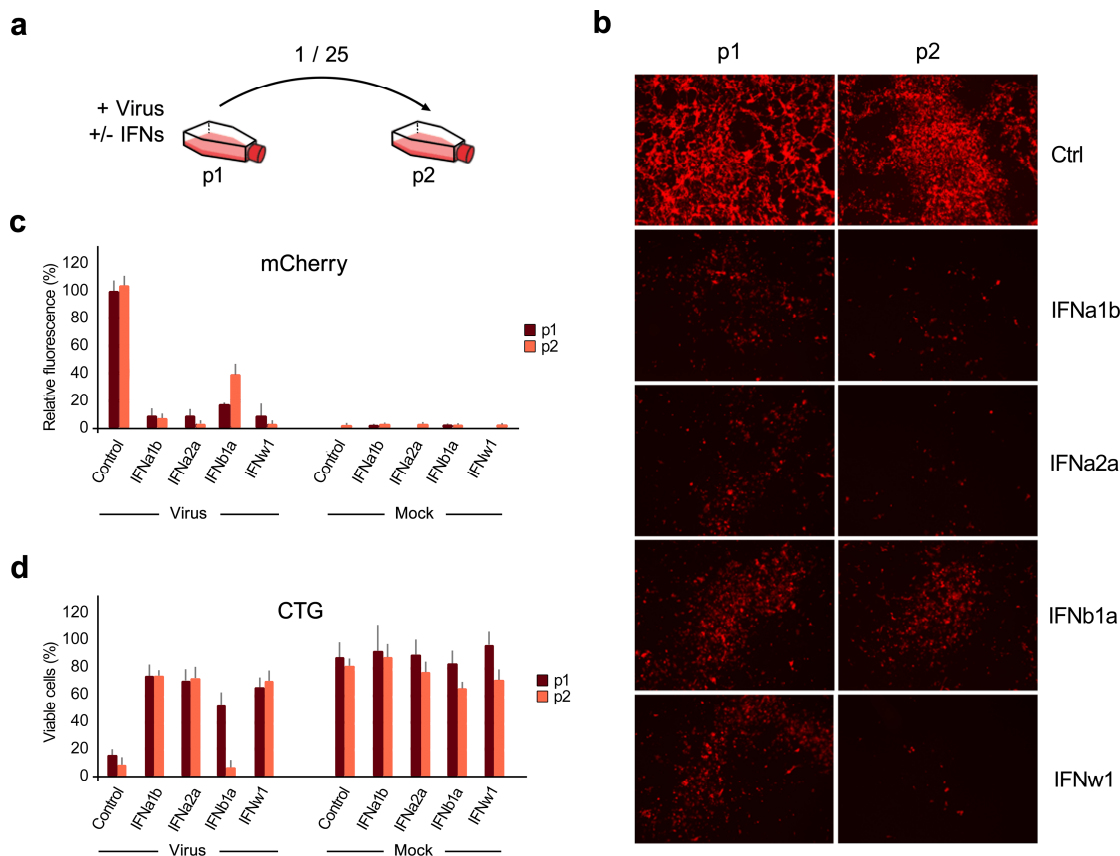
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- 621



622

623 **Figure 1.** Type I IFNs rescue Calu-3 and Vero-E6 cells from SARS-CoV-2-mediated death and attenuate virus  
 624 replication. (a) The effect of different doses of IFNs on viability of SARS-CoV-2-infected (moi = 0.01) Calu3 and  
 625 Vero-E6 cells. Cell viability was determined using the CTG assay at 72 hpi. Mean  $\pm$  SD; n = 3. The anti-SARS-CoV-  
 626 2 activity of the IFNs was quantified using drug sensitivity scores (DSS). (b) The effects of IFNs on viral replication,  
 627 measured by plaque reduction assay. Mean  $\pm$  SD; n = 3.

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629

630 **Figure 2.** IFNα1b, IFNα2a and IFNω1 are more effective than IFNβ1a against SARS-CoV-2-mCherry infection

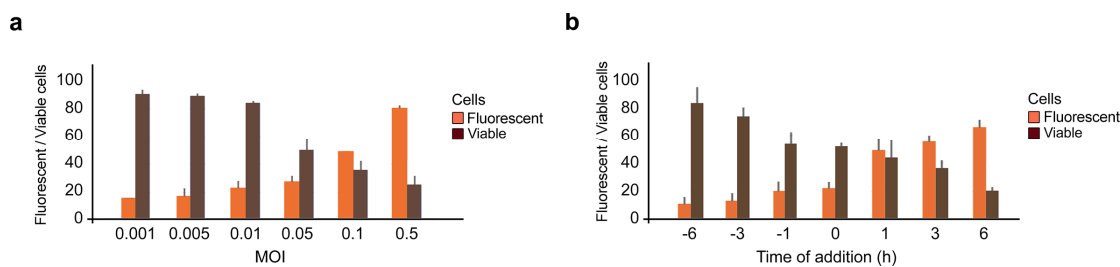
631 in Calu-3 cells. (a) Schematic representation of the experimental setup. (b) Fluorescent images of non-treated

632 (Ctrl) and IFN-treated (1 μg/mL) SARS-CoV-2-mCherry-infected Calu-3 cells (p1) and cells (p2) treated with

633 25-fold diluted media from P1 cells taken at 48 hpi. (c, d) Fluorescence intensity and viability analysis of p1

634 and p2 cells at 48 hpi. Mock-infected cells were used as controls (Mean ± SD; n = 3).

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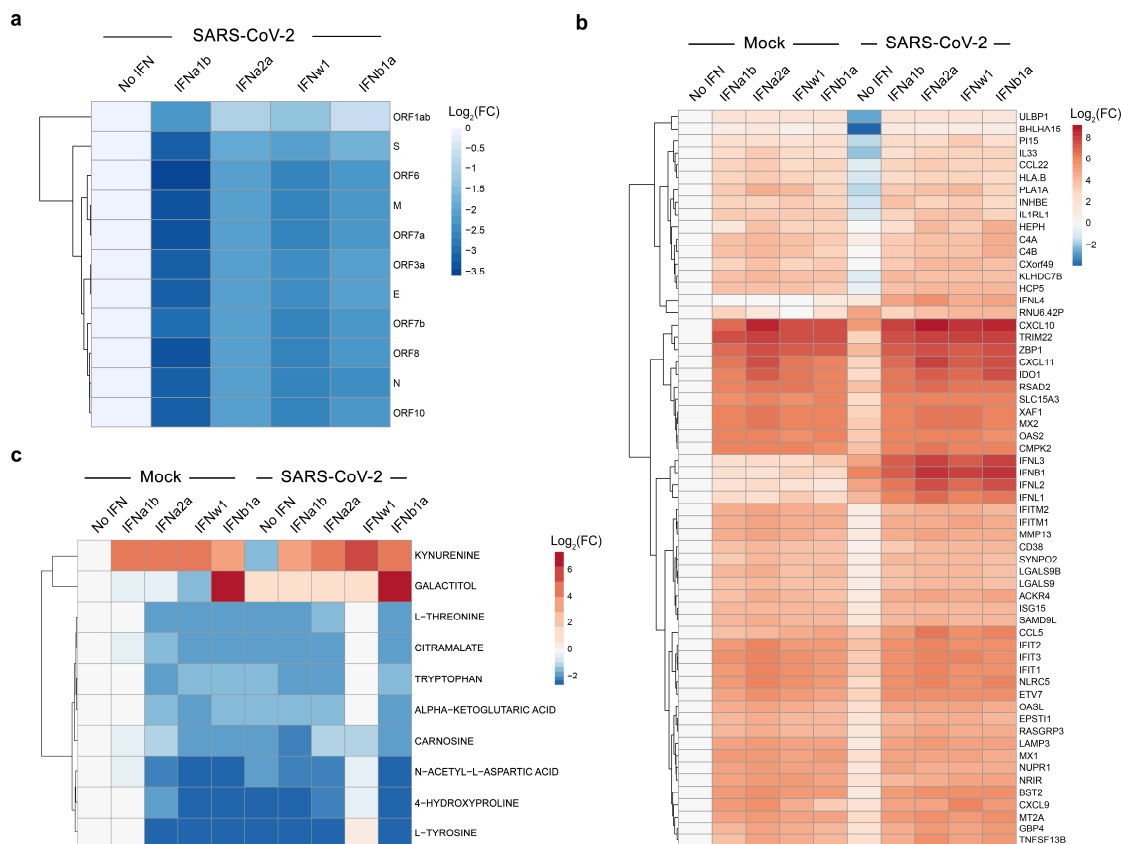


636

637 **Figure 3.** Anti-SARS-CoV-2 activity of IFNα2a depends on moi and time of administration. (a) Calu-3 cells were

638 treated with 1 μg/mL IFNα2a and infected with indicated moi of SARS-CoV-2-mCherry. Fluorescence intensity and

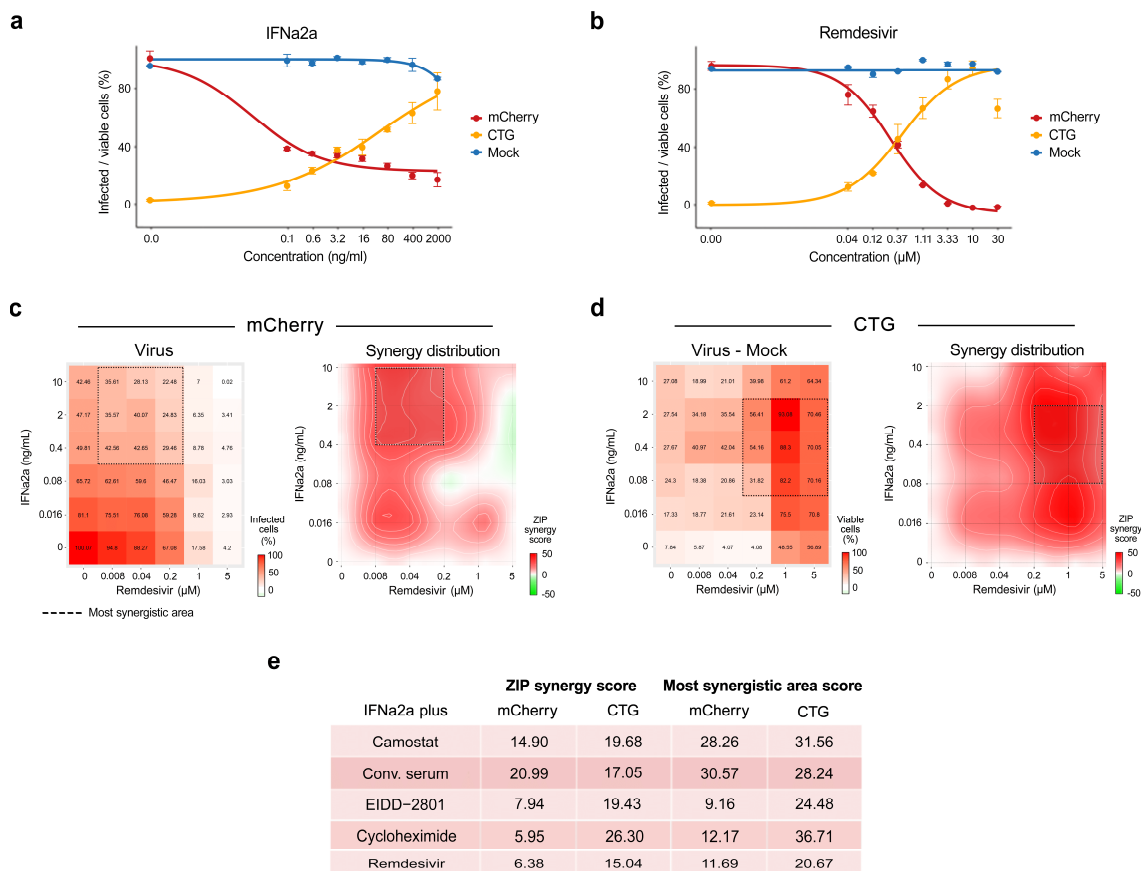
639 cell viability were measured after 48 h (Mean  $\pm$  SD; n = 3). (b) Calu-3 cells were treated with 1  $\mu$ g/mL IFNa2a prior,  
 640 simultaneously or post infection with SARS-CoV-2-mCherry (moi 0.01). Fluorescence intensity and cell viability  
 641 were measured after 48 h (Mean  $\pm$  SD; n = 3).  
 642



643  
 644 **Figure 4.** Transcriptomic and metabolomic analysis of mock- and SARS-CoV-2-infected Calu-3 cells non-  
 645 treated or treated with type I IFNs. (a) Calu-3 cells were stimulated with IFNs (1  $\mu$ g/mL) or non-stimulated  
 646 and infected with SARS-CoV-2 (moi = 0,01). A heatmap of viral RNAs affected by treatment is shown. Each  
 647 cell is colored according to the log<sub>2</sub>-transformed expression values of the samples, expressed as fold-change  
 648 relative to the nontreated control. (b) Calu-3 cells were either stimulated with purified recombinant human  
 649 IFN (1  $\mu$ g/mL) or left untreated with IFN, then infected with either mock or SARS-CoV-2 (moi = 0,01). A  
 650 heatmap of the most variable cellular genes affected by treatment and virus infection is shown. Each cell is  
 651 colored according to the log<sub>2</sub>-transformed expression values of the samples, expressed as fold-change relative  
 652 to the nontreated mock-infected control. (c) Cells were treated as for panel b. After 24 h, the cell culture  
 653 supernatants were collected, and metabolite levels were determined by LC-MS/MS. A heatmap of the most

654 affected metabolites is shown. Each cell is colored according to the log<sub>2</sub>-transformed profiling values of  
 655 samples, expressed as fold-change relative to the mock control.

656



657

658 **Figure 5.** Synergistic IFNa2a-based combinations against SARS-CoV-2-mCherry infection in Calu-3 cells. **(a,b)**

659 Calu-3 cells were treated with increasing concentrations of IFNa2a or remdesivir and infected with the SARS-CoV-

660 2-mCherry or Mock. After 48 h, the virus-mediated mCherry expression was measured (red curves). After 72 h,

661 viability of virus- and mock-infected cells was determined using a CTG assay (yellow and blue curves,

662 respectively). Mean  $\pm$  SD; n = 3. **(c)** The 6  $\times$  6 dose-response matrices and interaction landscapes of IFNa2a and

663 remdesivir obtained using fluorescence analysis of SARS-CoV-2-mCherry-infected Calu-3 cells. ZIP synergy score

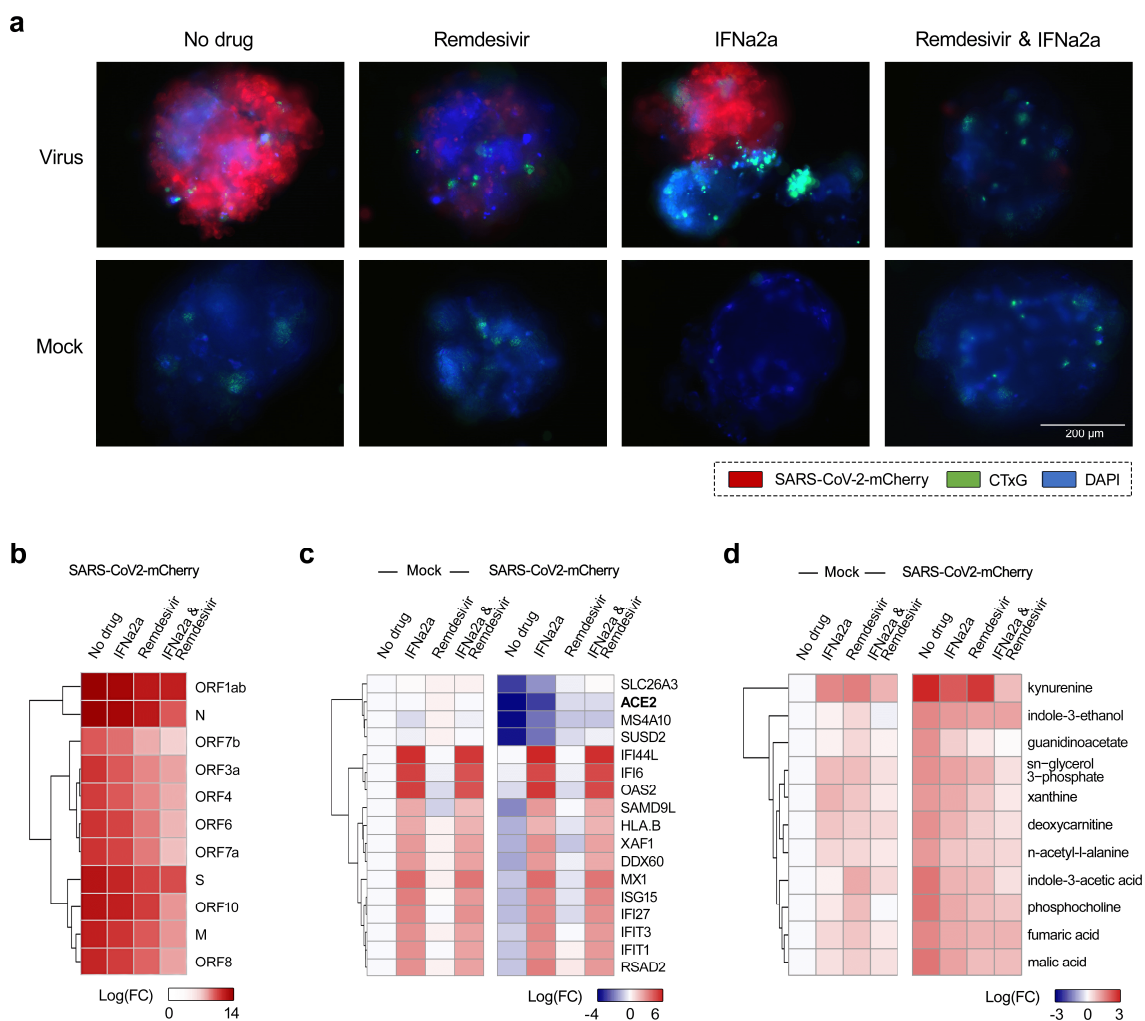
664 was calculated for the drug combinations. **(d)** The 6  $\times$  6 dose-response matrices and interaction landscapes of

665 IFNa2a and remdesivir obtained using a cell viability assay (CTG) on mock-, and SARS-CoV-2-mCherry-infected

666 Calu-3 cells. The selectivity for the indicated drug concentrations was calculated (selectivity = efficacy-(100-

667 Toxicity)). ZIP synergy scores were calculated for indicated drug combinations. **(e)** ZIP synergy scores (synergy

668 score for whole 6×6 dose-response matrices) and the most synergistic area scores (synergy score for most  
 669 synergistic 3×3 dose-regions) calculated for indicated drug combinations.  
 670



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672

673 **Figure 6.** Evaluation of antiviral effect of IFNa2a-remdesivir combination in human lung organoids (LOs). (a)

674 LOs were treated with 0,5  $\mu$ M remdesivir, 5 ng/mL IFNa2a, their combination or vehicle, and infected with

675 SARS-CoV-2-mCherry (moi = 0,1) or mock. Fluorescence of drug- or carrier-treated SARS-CoV-2-mCherry-

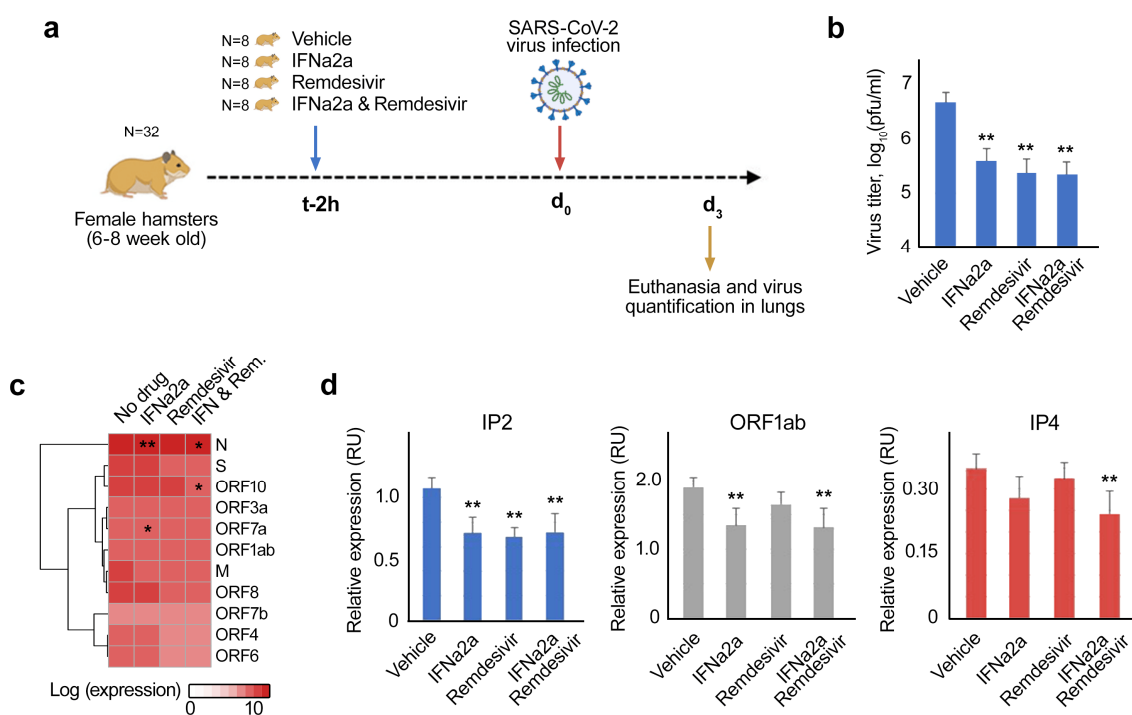
676 infected LOs was detected at 48 hpi. Virus infection, cell nuclei, and cytotoxicity are shown in red, blue, and

677 green, respectively. Scale bars, 200  $\mu$ m. (b) LOs were treated with 0,5  $\mu$ M remdesivir, 5 ng/mL IFNa2a, their

678 combination or vehicle, and infected with SARS-CoV-2-mCherry (moi = 0,1). After 48 h, total RNA was

679 extracted and sequenced. A heatmap of viral RNAs affected by treatment is shown. Each cell is colored

680 according to the log<sub>2</sub>-transformed expression values of the samples, expressed as log<sub>2</sub> fold-change relative  
 681 to the nontreated control. (c) LOs were treated and infected as for panel a. After 48 h, total RNA was extracted  
 682 and sequenced. A heatmap of the most variable cellular genes affected by treatment and virus infection is  
 683 shown. Each cell is colored according to the log<sub>2</sub>-transformed expression values of the samples, expressed as  
 684 fold-change relative to the nontreated mock-infected control. Cut-off - 3.75. (d) Cells were treated as for panel  
 685 a. After 48 h, the cell culture supernatants were collected, and metabolite levels were determined by LC-  
 686 MS/MS. A heatmap of the most affected metabolites is shown. Each cell is colored according to the log<sub>2</sub>-  
 687 transformed profiling values of samples, expressed as fold-change relative to the mock control. Cut-off - 1.5.



688

689 **Figure 7.** Evaluation of antiviral activity of recombinant mouse IFNa-remdesivir combination in vivo. (a)  
 690 Schematic representation of the experimental setup. (b) The effects of IFNa-remdesivir combination on viral  
 691 replication in hamster lungs, measured by plaque reduction assay. Mean  $\pm$  SD; n = 8. (c) A heatmap of viral  
 692 RNAs affected by treatment. Each cell is colored according to the log<sub>2</sub>-transformed expression values of the  
 693 samples, expressed as log<sub>2</sub> fold-change relative to the nontreated control. Mean, n = 8. (d) RT-qPCR analysis  
 694 of selected viral RNA. Expression of viral RNA was normalized to b-actin control. Mean  $\pm$  SD, n = 8.  
 695 Statistically significant differences in viral gene expression between non-treated and treated animals are  
 696 indicated with asterisks (\*\*p<0.05, \*p<0.1, Wilcoxon test).

