

A screen of FDA-approved drugs with minigenome identified tigecycline as an antiviral targeting nucleoprotein of Crimean-Congo hemorrhagic fever virus

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Abstract

Crimean-Congo hemorrhagic fever virus (CCHFV) belongs to the genus *Orthonairovirus* and is the causative agent of a viral hemorrhagic disease with a case fatality rate of 30%. However, limited studies have been conducted to explore antiviral compounds specific to CCHFV. In this study, we developed a minigenome system of orthonairoviruses, CCHFV and Hazara virus to analyze viral replication and screened an FDA-approved compound library. The transfection of the minigenome components induced marked increase in luciferase expression, indicating the sufficient replication and translation of reporter RNA. Compound library screening identified 14 candidate compounds that significantly decreased luciferase activity. Some of the compounds also inhibited the replication of the infectious Hazara virus. The mechanism of inhibition by tigecycline was further analyzed, and a decrease in the interaction between the viral N protein and RNA by tigecycline was observed. This work provides a basis for validation using animal models and the design of chemical derivatives with stronger activity in future studies on the development of an antiviral against CCHFV.

Keywords:

Crimean-Congo hemorrhagic fever virus, Minigenome, Drug screening, Tigecycline, Nucleoprotein

Highlights:

- Minigenome of CCHFV Hoti strain and HAZV JC280 strain was developed.
- Library screening of FDA-approved compounds identified 14 candidate compounds.
- Compounds including tigecycline showed inhibition at 10 μ M concentration.
- Tigecycline treatment dissociated the interaction between CCHFV N protein and RNA: a new target of antiviral development.

2 **1. Introduction**

3 Crimean-Congo hemorrhagic fever virus (CCHFV) belongs to the genus *Orthonairovirus* and has
4 tri-segmented negative-sense RNAs as genome (Bente et al., 2013; Knipe and Howley, 2013). S,
5 M, and L segments of the viral genomic RNAs encode nucleoprotein (N), glycoprotein precursor,
6 and large (L) protein, respectively. The 5' and 3' non-coding sequences (NCS) of the genomic
7 RNAs are essential for genome replication and acting as a promoter that is recognized by viral L
8 protein for the synthesis of complementary strands (Flick et al., 2003; Matsumoto et al., 2019). N
9 and viral genomic RNA form filamentous ribonucleoprotein complexes (Wang et al., 2016). L
10 has RNA-dependent RNA polymerase (RdRp) activity for the synthesis of mRNA and
11 complementary RNA (Devignot et al., 2015; Mirza et al., 2019). In a recent study, the ovarian
12 tumor protease domain of L was found to regulate the host innate immune response (Scholte et
13 al., 2017). The interaction between N and L is essential for viral genome replication (Macleod et
14 al., 2015).

15

16 CCHFV is an arthropod-borne virus, or arbovirus (Bente et al., 2013; Spengler et al., 2016) and
17 is widely distributed in Africa, the Middle East, southern Europe, and Asia, overlapping with the
18 distribution of the major tick vector, *Hyalomma* spp. (Bente et al., 2013). CCHFV is the causative
19 agent of Crimean-Congo hemorrhagic fever (CCHF), a viral hemorrhagic disease with a case
20 fatality rate of 30%. Humans can be infected through tick bites or exposure to the blood or tissue
21 of infected animals (Bente et al., 2013). Human-to-human transmission has also been reported
22 among healthcare workers in patient care (Altaf et al., 1998; Maltezou et al., 2009). After three to
23 seven days of incubation, CCHF begins to manifest influenza-like symptoms and develops into
24 hemorrhage and acute liver and kidney failure, followed by sharp mood swings and confusion
25 (Akıncı et al., 2013; Bente et al., 2013). Disease outcome in CCHF has been correlated with the

26 level of viremia, decreased platelet counts, elevated liver enzymes, and others (Akıncı et al., 2013).

27

28 The treatment of patients with CCHF is primarily supportive, and there is currently no FDA-

29 approved vaccine or specific antiviral therapeutics (Dai et al., 2021). Ribavirin, a well-known

30 small molecule with broad antiviral activity, has been reported to inhibit viral replication *in vitro*

31 and *in vivo* (Johnson et al., 2018; Paragas et al., 2004; Watts et al., 1989). Additional nucleotide

32 analogs, favipiravir and 2'-deoxy-2'-fluorocytidine, showed antiviral activity (Hawman et al.,

33 2018; Welch et al., 2017); however, their efficacy in clinical settings has yet to be fully evaluated.

34 Due to CCHFV being a biosafety level-4 pathogen, there have been a limited number of studies

35 on targeted antiviral compounds against CCHFV infection and their mechanisms.

36

37 The minigenome is an experimental system used to analyze viral replication, including CCHFV,

38 by the exogenous introduction of minimal viral proteins and genomic RNA elements (Bergeron

39 et al., 2010; Hoenen et al., 2011). Viral RNA transcription and translation can be inferred via the

40 expression of a reporter protein encoded in the RNA with viral sequence. It provides high-

41 throughput quantitative data, which is ideal for antiviral screening (Jasenosky et al., 2010; Ozawa

42 et al., 2013). In this study, we developed minigenome systems of CCHFV Hoti strain which was

43 isolated from a patient with the hemorrhagic disease in the Balkans (Duh et al., 2008), and Hazara

44 virus (HAZV), a close relative of CCHFV used as a model of infection (Dowall et al., 2012).

45 Using those systems, we explored antiviral compounds against CCHFV with an FDA-approved

46 compound library.

47

48

49 **2. Materials and methods**

50 *2.1 Cell culture*

51 Baby hamster kidney-21 (BHK-21) cells were cultured at 37°C in a minimum essential medium
52 (MEM, Fujifilm Labchem Wako, Osaka, Japan) supplemented with 8% (v/v) fetal bovine serum
53 (FBS) and penicillin/streptomycin. Human embryonic kidney 293T (HEK293T) cells and human
54 small-cell carcinoma SW-13 cells were grown at 37°C in Dulbecco's modified Eagle's medium
55 (Fujifilm Labchem Wako) containing 10% (v/v) FBS and penicillin/streptomycin.

56

57 *2.2 Plasmids and RNA*

58 To construct the pCAG-Hyg-CCHFV L and pCAG-Hyg-HAZV L plasmids, coding sequences
59 (CDS) of the L gene of the CCHFV Kosova Hoti strain (GenBank accession no. [EU044832](#)) and
60 HAZV JC280 strain ([DQ076419](#)) were optimized for human codon usage and were synthesized
61 *in vitro* (Integrated DNA Technologies, Inc., Coralville, IA and Azenta Life Sciences, South
62 Plainfield, NJ). These were then subcloned into pCAG-Hyg vector (Fujifilm Labchem Wako).
63 pCAG-Hyg-CCHFV N and pCAG-Hyg-HAZV N were constructed in the same manner. Strep-
64 Tag or His-Tag sequences were inserted at the 3' terminus of the CDS of L or N, respectively.
65 CDS of green fluorescent protein (GFP) with a self-cleavage peptide of *thoesa asigna* virus was
66 inserted upstream of the reading frame of CCHFV N to construct pCAG-Hyg-GFP-T2A-CCHFV
67 N. To construct pGEM-3Z-secNluc with CCHFV L segment NCS and that with HAZV S segment
68 NCS, the CDS of the viral gene was replaced with that of secretory NanoLuc (secNluc) and spacer
69 sequences, and was synthesized *in vitro* (Integrated DNA Technologies). For the synthesis of the
70 reporter RNA, the T7-promoter was inserted upstream of the 5' NCS. pGEM-3Z-mCherry with
71 CCHFV L segment NCS was constructed by the replacement of the CDS with that of mCherry
72 gene. Mutation at the amino acid position of 2517D-to-A was introduced using In-Fusion HD
73 Cloning kit (Takara Bio, Kusatsu, Japan) to construct pCAG-Hyg-CCHFV L (Δ RdRp).

74

75 To synthesize reporter RNAs, pGEM-3Z-secNluc with viral NCS was linearized and subjected to
76 transcription using MEGAscript T7 Transcription kit (Thermo Fisher Scientific, Waltham, MA)
77 according to manufacturer's protocol.

78

79 *2.3 Antibodies, Strep-Tactins, and compounds*

80 Anti-His-tag mAb was purchased from IBA-lifescience (Göttingen, Germany). Anti-His-tag
81 mAb-HRP-DirectT was purchased from Medical & Biological Laboratories Co. (Tokyo, Japan).
82 Anti-GAPDH monoclonal antibody conjugated with peroxidases was purchased from Fujifilm
83 Labchem Wako. Precision Strep Tactin-HRP Conjugate was purchased from Bio-Rad (Hercules,
84 CA).

85

86 Minocycline hydrochloride was purchased from Fujifilm Labchem Wako. Tetracycline,
87 doxycycline hyclate, minocycline hydrochloride, tigecycline, dihydroergotamine mesylate,
88 ergotamine tartrate, and promethazine hydrochloride were purchased from Tokyo Chemical
89 Industry (Tokyo, Japan). Minocycline hydrochloride and nisoldipine were purchased from
90 Fujifilm Labchem Wako.

91

92 *2.4 Virus and viral titration*

93 HAZV JC280 strain (Begum et al., 1970) was kindly provided by Prof. Roger Hewson, Public
94 Health England's Porton Down Institute. The working stock of the virus was propagated in SW-
95 13 cells.

96

97 For viral titration, the monolayers of SW-13 cells prepared in multi-well plates were incubated

98 with serial dilutions of viruses for one hour (h) and were overlaid with MEM containing 2% (v/v)
99 FBS and 0.7% (w/v) UltraPure Agarose (Thermo Fisher Scientific). Following incubation for four
100 days, the cells were fixed with ethanol containing 16% (v/v) acetic acid and stained with 1% (w/v)
101 Amido black in phosphate-buffered saline. Viral titers were expressed as plaque-forming units
102 (PFU)/mL.

103

104 *2.5 Western blotting*

105 HEK293T cells in 12 well plates were co-transfected with pCAG-Hyg-CCHFV L and pCAG-
106 Hyg-CCHFV N, or those of HAZV using X-tremeGene HP DNA transfection reagent (Merck
107 KGaA, Darmstadt, Germany). At 48 h post-transfection (h.p.t.), the cells were lysed with Cell
108 Lysis Buffer M (Fujifilm Labchem Wako). SDS-PAGE and western blotting were performed with
109 ePAGEL HR Gel (Atto, Tokyo, Japan), anti-His Tag antibody, anti-GAPDH antibody, and Strep-
110 Tactin conjugated with HRP. The bands were visualized with Immobilon Western
111 Chemiluminescent HRP Substrate (Merck) and taken with LuminoGraph I (Atto).

112

113 *2.6 Minigenome assay and strand-specific reverse transcription and qPCR (RT-qPCR)*

114 HEK293T cells cotransfected with CCHFV or HAZV expression plasmids were further
115 transfected with the reporter RNA using Lipofectamine MessengerMAX (Thermo Fisher
116 Scientific) six hours later. At 24 or 48 h.p.t., luciferase expression was evaluated using Nano-Glo
117 Luciferase Assay System (Promega, Madison, WA) with SpectraMax iD5 (Molecular Devices,
118 San Jose, CA) according to the manufacturer's instructions.

119

120 Total RNA was extracted from HEK293T cells with the minigenome at 48 h.p.t. using ISOSPIN
121 Cell&Tissue RNA (Nippon Gene Co., Ltd., Tokyo, Japan). cDNA was synthesized by reverse

122 transcription using SuperScript III (Thermo Fisher Scientific) and gene-specific primers against
123 mRNAs of secNluc (5'catacggcgcgtccgaaata3') and GAPDH (5'gcccaatacagaccaaattcc3'). qPCR
124 was conducted using KAPA SYBR FAST qPCR Kit (KAPA Biosystems, Wilmington, MA),
125 primers targeting secNluc (Fw: 5'attgtcctgagcggtgaaa3', Rv: cacagggtacaccaccttaaa3') and
126 GAPDH (Fw: 5'agccacatcgctcagacac3', Rv: 5'gcccaatacagaccaaattcc3'), and StepOnePlus Real
127 Time PCR system (Thermo Fisher Scientific). The relative RNA abundance of the reporter RNA
128 against GAPDH was calculated using the CT value.

129

130 *2.7 Drug screening*

131 BHK-21 cells with the minigenome were prepared on 96 well plates. At 1.5 h.p.t., compounds of
132 FDA-approved Drug Library, Japan version (Enzo Life Sciences, Farmingdale, NY) or positive
133 control ribavirin were added at a final concentration of 20 µg/ml in the culture medium with 1%
134 (v/v) DMSO. Luciferase assay was conducted at 48 h.p.t., and cell viability was measured using
135 Resazurin Cell Viability Assay Kit (Biotium, Fremont, CA) according to the manufacturer's
136 instructions. After the log₁₀ conversion of luminescence, Dunnett's test of multiple-comparison
137 against DMSO treated samples was conducted to reduce the rate of type II error in the
138 determination of compounds that significantly decreased the luciferase activity. The control plates
139 were used to calculate the Z-factor. To compare the distribution of the data, the data of the treated
140 plates were converted to Robust Z-score, also known as the median absolute deviation method
141 (Chung et al., 2008; Huber and Rochetti, 2009).

142

143 *2.8 Dose-response analysis and calculation of concentration of 50% Inhibition*

144 BHK-21 cells with the minigenome were prepared, and the compounds were added to the culture
145 medium with 1% (v/v) DMSO at a final concentration from 0 to 50 µM. Luciferase assay was

146 conducted at 48 h.p.t., and the relative luciferase signal (%) was calculated in relation to the
147 control wells. A fitting curve with non-linear regression was conducted based on triplicate results,
148 and the concentration of 50% inhibition was measured using GraphPad Prism (GraphPad
149 Software, San Diego, CA).

150

151 SW-13 cells were infected with HAZV at an multiplicity of infection (MOI) of 0.005 for one h
152 and cultured with the compounds. At 48 h.p.i., the viral titer in the supernatant was measured. The
153 concentration of 50% inhibition was calculated as described above.

154

155 *2.9 Influence of tigecycline on the binding of N to reporter RNA*

156 HEK293T cells transfected with CCHFV expression plasmids were lysed with Cell Lysis Buffer
157 M at 48 h.p.t. The lysate containing 80 µg of total protein was incubated with 100 µM ribavirin
158 or tigecycline, and the mixture was further incubated with 50 ng of synthesized reporter RNA. To
159 precipitate N, the mixtures were incubated with Cell Lysis Buffer M containing Ab-Capcher Extra
160 beads (ProteNova, Kagawa, Japan) with 4 µg of anti-His antibody. Half of the beads were used
161 for western blotting. The RNAs co-precipitated with the beads were extracted from the remainder
162 of the beads using ISOSPIN Cell&Tissue RNA. Following the reverse transcription reaction with
163 random primers, qPCR was performed. The experiments were repeated three times.

164

165 *2.10 Statistical analysis*

166 Data are expressed as the mean ± standard deviation (SD). Following the F-test to analyze
167 variances, the unpaired two-sided Student's *t*-test was used to determine the statistical
168 significance of the mean values of the luminescent intensity between the two conditions (Figs.
169 1C, S1, S6B, and C). Dunnett's multiple comparison tests were performed for the multiple

170 comparisons against the control condition after one-way analysis of variance tests (ANOVA)
171 (Figs.2A, B, C, 3B, and S6A). Following ANOVA, the Tukey–Kramer test was used for multiple
172 comparisons of statistical significance (Figs. 2D, 5B, S2A, B, and S6D). Statistical analyses were
173 performed with GraphPad Prism: *: $p \leq 0.05$, **: $p \leq 0.01$, ***: $p \leq 0.001$, and ****: $p < 0.0001$.

174

175

176 **3. Results**

177 *3.1 Establishment of the minigenome of orthonairoviruses.*

178 Our orthonairovirus minigenome consists of three components: a reporter RNA encoding secNluc
179 and two plasmids expressing viral L or N (Fig. 1A). We employed the *in vitro*-transcribed RNA
180 for the reporter to avoid non-specific transcription/translation of positive-strand RNA from the
181 plasmid. The reporter RNA was designed with NCS of the CCHFV Hoti strain L segment (Duh
182 et al., 2008) or the HAZV JC280 strain S segment (Begum et al., 1970) because of the high
183 reporter activities in previous reports (Bergeron et al., 2010; Matsumoto et al., 2019). After the
184 transfection of the reporter RNA to cells infected with a helper virus, a marked increase in the
185 luciferase signal was observed (Fig. S1), indicating that reporter RNAs were functionally
186 sufficient. Next, we confirmed the protein expression from the constructed plasmids, and the
187 tagged proteins were expressed in the expected size (Fig. 1B). Transfection of the reporter RNAs
188 induced a significant increase in luciferase activity in cells transfected with the expression
189 plasmids (Fig. 1C). These results showed that our minigenome worked well.

190

191 *3.2 Analysis of the requirements of minigenome replication.*

192 We analyzed the requirements for viral replication using the established minigenome. HEK293T
193 cells with both L and N plasmids showed the highest luciferase activity in both CCHFV and

194 HAZV minigenome, whereas transfection with only L plasmid slightly increased luciferase
195 activity (Fig. 2A). The abundance of positive strands of the reporter RNA significantly increased
196 in cells with both L and N (Fig. 2B), consistent with the results of the luciferase activity. These
197 results indicated that both L and N were required for the efficient transcription of orthonairovirus
198 reporter RNAs.

199

200 Next, we analyzed minigenome replication in heterogeneous combinations of L, N, and the
201 reporter RNA between CCHFV and HAZV. The cells with the homogenous pair of L and N
202 proteins showed significantly higher luciferase activity than the negative control cells, while cells
203 with heterogeneous pairs did not (Fig. 2C). In contrast, the reporter RNAs did not require a protein
204 pair that was homogenous with the RNA (Figs. 2C and S2A). A reporter RNA with taxonomically
205 distant virus sequences did not show the sign of replication by the CCHFV L and N proteins (Fig.
206 S2B), suggesting a conserved motif in the non-coding sequences for the orthonairovirus
207 replication.

208

209 To further analyze the requirement for viral replication, we attempted to mutate a protein motif.
210 The active site of RdRp in L was structurally predicted and analyzed using transcriptionally
211 competent virus-like particles (Devignot et al., 2015; Mirza et al., 2019). The RdRp mutation
212 significantly decreased luciferase activity (Figs. 2D and S3). As expected, our minigenome
213 system was capable of analyzing the requirements for viral replication by mutagenesis.

214

215 *3.3 FDA-approved drug screening by CCHFV minigenome system.*

216 To explore the inhibitors of CCHFV replication, a library of 630 FDA-approved compounds were
217 screened. We employed BHK-21 cells for this screening because of the ease of handling. As

218 shown in Fig. 3A, the cells with the CCHFV minigenome were cultured in the presence of 20
219 $\mu\text{g/ml}$ compounds or ribavirin as a positive control. The Z-factors of the three independent
220 experiments were 0.79, 0.64, and 0.85, which were reliable levels, and the data were correlated
221 and distributed similarly (Fig. S4). We set the cut-off values to $p < 0.05$ in comparison to DMSO-
222 treated cells for luciferase activity and Log_{10} 8.1 for cell viability, approximately 40% cell
223 viability of the DMSO-treated cells. Fourteen compounds (Table 1) significantly decreased the
224 luciferase activity among the tested compounds and had little influence on cell viability (Fig. 3B
225 and Supplemental data).

226

227 *3.4 Validation of the inhibitor candidates and their derivatives.*

228 Considering the adverse effects and ease of availability, we selected six compounds and tested
229 their dose-response and cytotoxicity (Figs. 4A and S5). We also analyzed the derivatives of some
230 compounds: minocycline hydrochloride, tigecycline (tetracycline antibiotics), and ergotamine
231 tartrate (ergot alkaloid). Alfacalcidol and ergotamine tartrate showed strong cytopathic effect at
232 $50 \mu\text{M}$ (Fig. S5) and were excluded from the analysis. Tetracycline, doxycycline hyclate,
233 minocycline hydrochloride, and promethazine hydrochloride showed activity equivalent to that
234 of ribavirin (Fig. 4A). Dihydroergotamine mesylate and nisoldipine showed differences in the
235 activity between CCHFV and HAZV: 50% inhibition at $8.58 \mu\text{M}$ v.s. $23.8 \mu\text{M}$ and $12.7 \mu\text{M}$ v.s. $>$
236 $50 \mu\text{M}$, respectively. Tigecycline worked on both minigenome and showed 50% inhibition at a
237 concentration lower than $10 \mu\text{M}$ (Fig. 4A).

238

239 We validated the effect of these compounds on the replication of the infectious virus by using
240 HAZV. Tigecycline showed 50% inhibition at $6.40 \mu\text{M}$, which reflected the results of the
241 minigenome (Fig. 4B). Dihydroergotamine mesylate showed 50% inhibition at $18.6 \mu\text{M}$, which

242 was similar to the result of the minigenome (Fig. 4B).

243

244 *3.5 Effect of tigecycline on the interaction between N and viral RNA.*

245 We attempted to analyze the mechanism of inhibition by tigecycline. A reporter assay showed a
246 limited effect of tigecycline on a protein expression from the transfected plasmid (Fig. S6A). In
247 cells transfected with minigenome or infected with HAZV, RT-qPCR showed decreased RNA
248 abundance in the presence of tigecycline (Fig. S6B and C). These results indicated an influence
249 on the transcription of the viral genome. The combination treatment of tigecycline and ribavirin
250 did not compete with each other, which suggested independent targets of inhibition between them
251 (Fig. S6D). Previously, Sharifi *et al* virtually screened compounds binding to pockets of CCHFV
252 N (Sharifi et al., 2017), which were predicted to bind viral RNA (Jeeva et al., 2017b; Wang et al.,
253 2016). Intriguingly, several compounds, including doxycycline and minocycline, overlapped with
254 our candidates. Therefore, we analyzed the influence of tigecycline on the interaction between N
255 and viral RNA. We mixed the cell lysates expressing viral proteins with an equivalent amount of
256 the reporter RNA in the presence or absence of tigecycline and precipitated N protein. Equivalent
257 amounts of N and L precipitated in the presence of the compounds, suggesting a limited influence
258 on the protein-protein interactions (Fig. 5A). In contrast, treatment with tigecycline significantly
259 decreased the RNA abundance of the reporter RNA that was co-precipitated (Fig. 5B). These
260 results showed the inhibition of the interaction between N and RNA by tigecycline.

261

262

263 **4. Discussion**

264 Our reporter RNA with the CCHFV NCS was replicated under heterogeneous HAZV infection as
265 a helper virus (Fig. S1). Replication of reporter RNAs did not require the expression of

266 homogenous viral proteins (Figs. 2C and S2A). A previous study showed the importance of
267 conserved promoter elements, which were conserved in our reporter RNAs (Fig. S7), for the
268 replication of the HAZV minigenome (Matsumoto et al., 2019). The requirement of NCSs may
269 be flexible except for conserved terminal sequences. In contrast, the reporter RNA did not
270 replicate in the heterogeneous protein pairs (Fig. 2C), indicating that the homogenous interaction
271 between L and N is essential for the formation of a functional complex for genome replication.

272

273 Our screening identified 14 compounds as CCHFV inhibitor candidates (Fig. 3B and Table 1),
274 some of which overlapped with screenings against other viruses in *Bunyavirales* (Benedict et al.,
275 2015; Li et al., 2019). Alfacalcidol, an analog of vitamin D, influences cellular calcium
276 homeostasis. Calcium metabolism participates in the regulation of endoplasmic reticulum stress
277 response and apoptotic signaling (Zhou et al., 2009) and its disturbance could result in the
278 inhibition of CCHFV replication. Nisoldipine, a calcium channel blocker, was shown to inhibit
279 multiple steps of Dabie bandavirus, or SFTSV, replication (Li et al., 2019; Urata et al., 2021) and
280 our data suggested a similar effect on CCHFV replication. A study with the influenza A virus
281 showed that itraconazole, an azole antifungal, induced endolysosomal cholesterol storage,
282 resulting in decreased viral replication (Schloer et al., 2019). CCHFV also required cholesterol
283 for its replication (Simon et al., 2009), and ketoconazole might similarly inhibit CCHFV
284 replication.

285

286 Our results identified tetracyclines, especially tigecycline, as potent inhibitors of
287 orthonairoviruses *in vitro* (Fig. 4). Tigecycline dissociated N and viral RNA (Fig. 5). Wang *et al*
288 proposed a model of RNA binding of N protein via positively charged patches and a groove
289 between these patches (Wang et al., 2016). The occupation of this groove, which is predicted as a

290 binding target of tetracyclines (Sharifi et al., 2017), may result in the inhibition of the interaction
291 and viral replication (Fig. 5). The interaction between N and RNA participates in multiple steps
292 of the viral life cycle. It was suggested that N is involved in 5' Cap-snatching via the interaction
293 with 5' Cap and the 5' sequences of the cellular mRNA (Knipe and Howley, 2013; Mir et al.,
294 2008). However, the RNA used in our RNA-immune precipitation was synthesized without 5'
295 Cap. The 5' Cap-binding activity was not necessary to be affected by tigecycline. A previous study
296 showed that N facilitated the dissociation of the RNA panhandle, which supports viral RNA
297 transcription (Mir and Panganiban, 2006). In addition, N promoted viral protein translation by
298 recruiting the eukaryotic initiation factor (Jeeva et al., 2017a). Tigecycline may disturb these steps
299 of viral transcription and translation. Tetracyclines are antibiotics and inhibitors of the 30S subunit
300 of bacterial ribosomes (Brodersen et al., 2000), although recent studies have reported the effects
301 on mammalian and mitochondrial ribosomes (Chatzispyrou et al., 2015; Mortison et al., 2018).
302 CCHFV mRNAs might be more sensitive to translation distraction than cellular mRNAs. These
303 results showed that the interaction between N and viral RNA could be a target of antiviral agents,
304 such that the design of derivatives with a stronger binding affinity will contribute to the
305 development of CCHFV antiviral in future studies.

306

307 We showed the concentration of 50% inhibition of tigecycline was lower than 10 μ M, which was
308 somehow competitive with that of favipiravir (T705), 7.0 μ M (Oestereich et al., 2014). However,
309 a previous study showed the *in vivo* concentration of tigecycline in serum was ranged from 1.32
310 mg/L (2.25 μ M) to 0.22 mg/L (0.37 μ M) after single 100 mg administration (Rodvold et al., 2006),
311 which did not meet the level of 50% inhibition. It may be acceptable to increase the administration
312 dose in this case of lethal pathogen infection, but, careful validation of the side effect would be
313 required. A combinational treatment of tigecycline and nucleotide analogs might be beneficial, as

314 our data suggested they have independent targets (Fig. S6D).

315

316 In this study, we developed the minigenome of orthonairoviruses and demonstrated its validity in
317 antiviral screening. We identified tigecycline as a potent antiviral against CCHFV via the
318 dissociation of N and viral RNA. Future validation with *in vivo* and the design of the chemical
319 derivatives with stronger levels of activity will facilitate the development of the specific antiviral
320 against CCHFV and its clinical applications in patients.

321

322

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334

Figure legends

Figure 1. Establishment of the minigenome system of orthonairoviruses.

A: Schematic diagram of the minigenome system. The reporter RNA consists of a reverse complement sequence of secNluc CDS with 5' and 3' NCSs of CCHFV or HAZV genomic RNA. For the expression of viral L and N, the plasmids with pCAG-Hyg backbone were constructed. **B:** Western-blotting images of the HEK293T cells co-transfected with/without the L and N expression plasmids. Left panels: CCHFV plasmids, Right panels: HAZV plasmids. **C:** Positive strand synthesis and translation of the orthonairovirus minigenome. HEK293T cells co-transfected with (black) or without (white) the viral protein expression plasmids were transfected with the reporter RNA. The luciferase activity was measured at 24 and 48 h.p.t. Left: CCHFV minigenome, Right: HAZV minigenome.

Figure 2. Analysis of the requirements of the minigenome replication.

A-B: Protein requirements of minigenome replication. HEK293T cells were mock-transfected (white bars) or transfected with L (gray) or N (gray-striped), or co-transfected with both of them (black). After the reporter RNA transfection, the luciferase activity of the supernatants (**A**) and the relative RNA abundance of the luciferase gene against GAPDH (**B**) were measured. **C:** Heterogeneous combinations of proteins and RNA in the minigenome. The HEK293T cells co-transfected with the L and N expression plasmids of CCHFV (C) or HAZV (H) were transfected with the reporter RNAs of the CCHFV L segment (left) or HAZV S segment (right). Minigenome replication was evaluated via the luciferase assay. **D:** Mutagenesis of the RdRp motif of HAZV L. The HEK293T cells were transfected with the plasmids expressing N and L wild type (WT, black) or L RdRp mutant (Δ RdRp, gray). The minigenome replication was evaluated via the luciferase assay after the reporter RNA transfection.

Figure 3. FDA-approved drug screening with CCHFV minigenome.

A: Time course of the experiment. BHK-21 cells were transfected with the CCHFV minigenome on 96 well plates, and then the compound library was added at the final concentration of 20 $\mu\text{g/ml}$. Following incubation for 48 h, the minigenome replication or cell viability was evaluated via the luciferase assay or the resazurin assay, respectively. **B:** Results of drug screening plotted as dot plots. The top graph shows a plot of Log_{10} (Cell viability) in the x-axis and Log_{10} (Luciferase activity) in the y-axis. The bottom graph shows a plot of compound ID in the x-axis and $-\text{log}_{10}$ (p-value) in the y-axis. DMSO- and ribavirin-treated wells were used as negative control (green) and positive control (orange), respectively. The compounds that passed the cut-off values (magenta) are shown as the inhibitor candidates.

Figure 4. Validation of the inhibitor candidates and their derivatives.

A: Dose-response of inhibitor candidates and their derivatives. BHK-21 cells were transfected with the CCHFV (black) or HAZV (white) minigenome, followed by the addition of the inhibitor candidates at a final concentration from 10-50 μM . Minigenome replication was evaluated via the luciferase assay and is shown as relative luciferase against DMSO-treated wells. The black and dotted lines indicate the non-linear regression of the dose-response. CCHFV50 or HAZV50 indicates concentration of 50% inhibition of each minigenome, respectively. **B:** Evaluation of the efficacy of the compounds against infectious HAZV replication. SW-13 cells were infected with HAZV at an MOI of 0.005, and viral replication under the compounds was evaluated by plaque assay and was shown as a relative virus titer against DMSO-treated wells. Gray lines indicate the concentration of the 50% inhibition of HAZV infection.

Figure 5. Analysis of the inhibitory mechanism of tigecycline

A-B: RNA immunoprecipitation of N protein under tigecycline. The cell lysates of HEK293T cells expressing CCHFV L and N were incubated with the reporter RNA under the presence or absence of ribavirin or tigecycline. After the immunoprecipitation of N, the L and N (**A**) and reporter RNA (**B**) were detected by western blotting or RT-qPCR against the luciferase gene, respectively. The representing image of the western-blotting is shown.

Figure S1. Reporter activity under the helper virus infection.

Replication of the reporter RNAs with a helper virus. BHK-21 cells were infected with HAZV at an MOI of 0.005 (black) or mock-infected (white). At 48 hours post-infection (h.p.i.), the cells were transfected with the reporter RNA and were cultured for 24 h. The expression of the luciferase protein was evaluated by the luciferase assay.

Figure S2. Reporter activity of the minigenome with variations.

A: The BHK-21 cells co-transfected with the L and N expression plasmids of CCHFV (C, Black bar) or HAZV (H, Gray bar) were further transfected with the mCherry-expressing reporter RNAs of the CCHFV L segment. Images of the control cells or cells showing mCherry signal were taken with ZOE fluorescent imager (Bio-rad). The fluorescent intensity of five independent images was measured with Image J (Schneider et al., 2012). **B:** Minigenome assay of lymphocytic choriomeningitis virus (LCMV) backbone (Urata et al., 2016). The BHK-21 cells were co-transfected with a plasmid encoding GFP-expressing reporter RNA of LCMV and the L and N expression plasmids of LCMV (LC, Black) or CCHFV (C, Gray). The fluorescent intensities were measured as described above.

Figure S3. Expression of CCHFV L and N with mutations.

Western blotting images of HEK293T cells co-transfected with L and N expression plasmids with or without Δ RdRp mutation.

Figure S4. Data distributions of the FDA-approved drug library screening.

A: Data correlation between the experiments. The Log_{10} (Luciferase activity) was normalized as robust z-scores and plotted as dot plots. DMSO- or ribavirin-treated wells were used as a

negative control (green) and positive control (orange), respectively. The compounds that passed the cut-off points (magenta) are shown as inhibitor candidates. **B:** Histogram representing the distribution of reporter activity or cell viability of the drug screening. The robust z-scores were used to bin the range of values (x-axis, bin center). The counts of the compounds falling into each interval were shown (y-axis, number). blue: Experiment 1, green: Experiment 2, orange: Experiment 3.

Figure S5. Cell viability under the presence of the inhibitor candidates.

The compounds were added to the culture medium of BHK-21 cells with 1% (v/v) DMSO at a final concentration from 0 to 200 μ M. Resazurin assay was conducted at 48 h.p.t., and the relative cell viability (%) against the signal of the control wells was calculated. A fitting curve with non-linear regression was conducted based on triplicate results, and the 50% cytotoxic concentration (CC50) was measured using GraphPad Prism. Selectivity indexes (SI) were calculated from the CC50 divided by the concentration of 50% inhibition of CCHFV minigenome.

Figure S6. Effect of tigecycline on the CCHFV minigenome system.

A: Effect of tigecycline on the expression of the plasmid-derived protein. BHK-21 cells were transfected with pCAG-Hyg-GFP-T2A-CCHFV N. After 6h of incubation, the culture medium was replaced with that contains ribavirin or tigecycline. After 48 h of culture, fluorescent intensities of the expressed GFP were measured with SpectraMax iD5. **B:** Effect on minigenome replication. HEK293T cells with the CCHFV minigenome were cultured with or without the 25 μ M tigecycline for 48 h. Total RNA was extracted with ISOGEN II (Nippon Gene). RNA abundance was measured using strand-specific RT-qPCR. **C:** Effect on infectious

virus replication. SW-13 cells infected with HAZV at an MOI of 0.5 were cultured with or without 25 μ M tigecycline for 24 h. Total RNA was extracted from the cells with ISOSPIN Cell&Tissue RNA. Following the reverse transcription reaction with random primers, qPCR was conducted with primers targeting HAZV S segment (Fw: 5'cgctgctgaggcattact3', Rv: 5'ctgggtactccccaatgga3'), M seg (Fw: 5'aatctgaaggaccggttg3', Rv: 5'tttgtcaacctcaacggta3'), L segment (Fw: 5'atcagcgacttcttaggcg3', Rv: 5'attgcctaggettccagcac3') and GAPDH. The RNA abundance of each segment against GAPDH is shown. **D:** Combination treatment of tigecycline and ribavirin. BHK-21 cells with CCHFV minigenome were treated with 4 μ M tigecycline and/or 32 μ M ribavirin. Luciferase activity was measured at 48 h.p.t., and relative luciferase signal against DMSO treated sample was calculated.

Figure S7. Comparison of NCS between reporter RNAs.

Schematic diagram of the conserved terminal sequence of the reporter RNAs of CCHFV Hoti L segment, HAZV JC280 S segment, and LCMV Armstrong S segment (Outgroup). Magenta: conserved nucleotide sequences.

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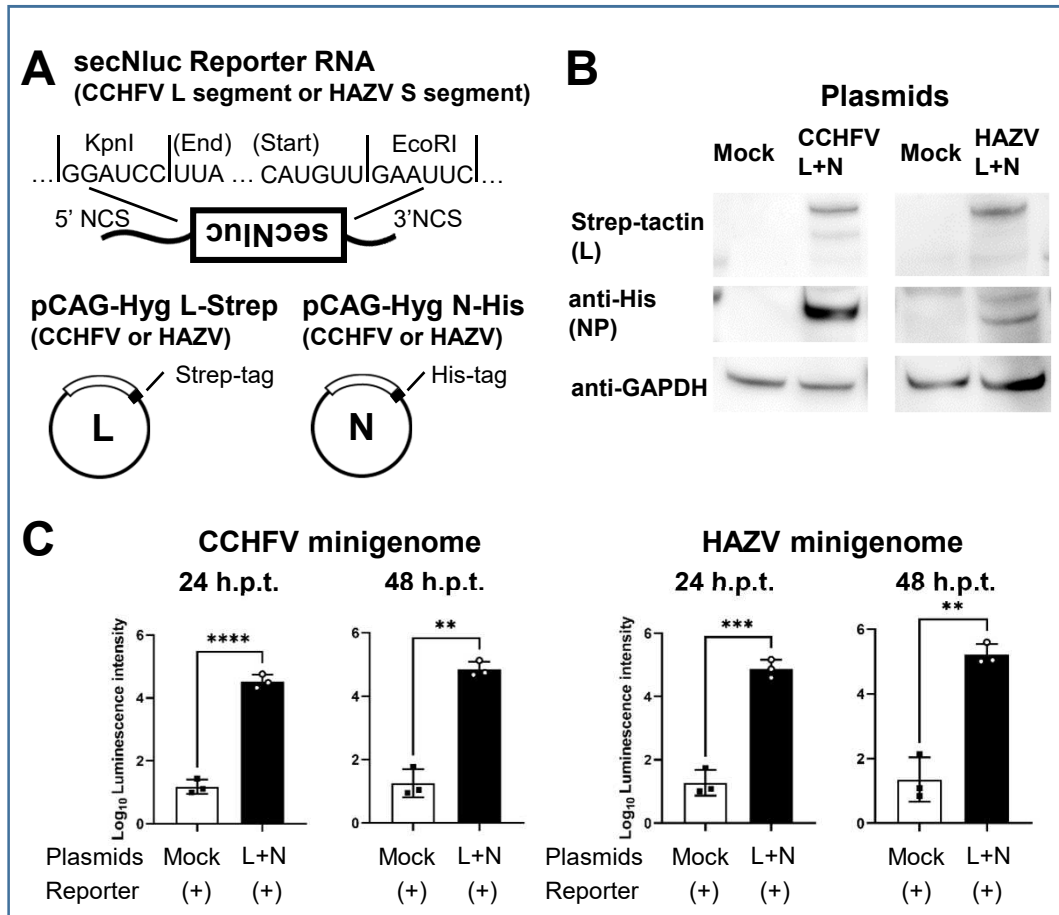
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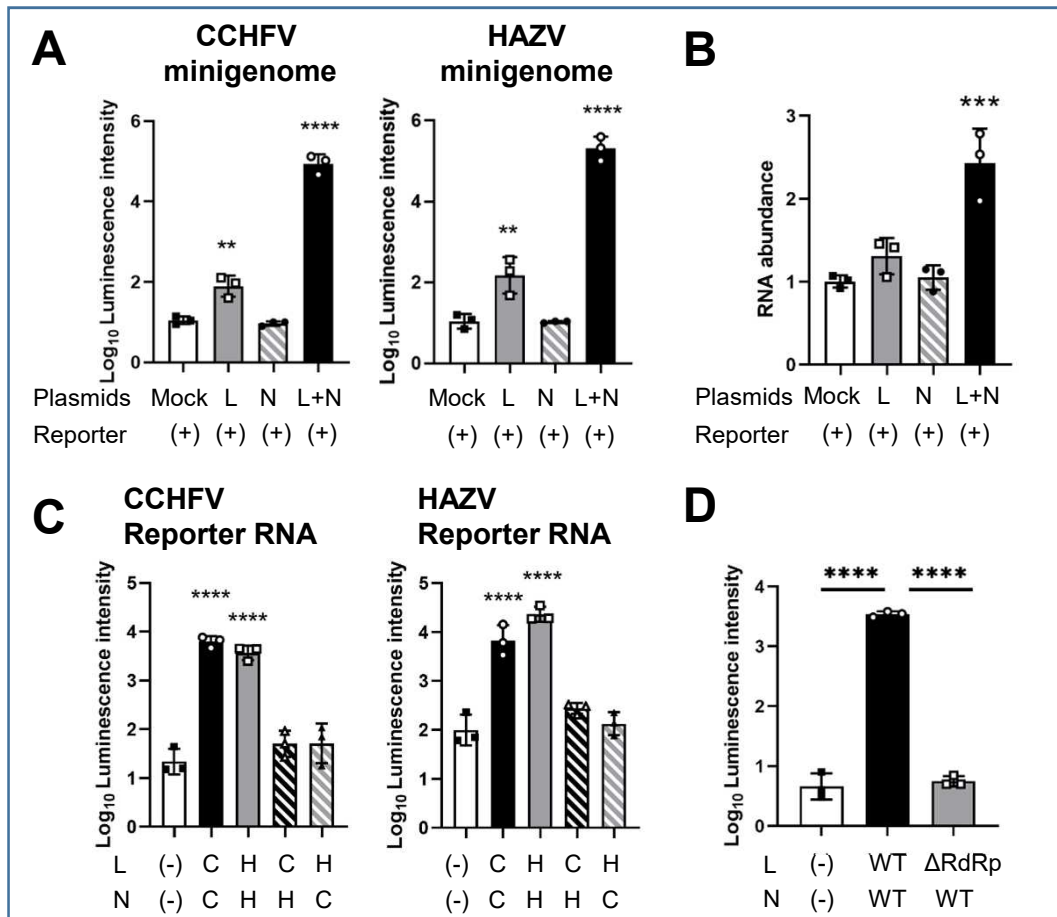
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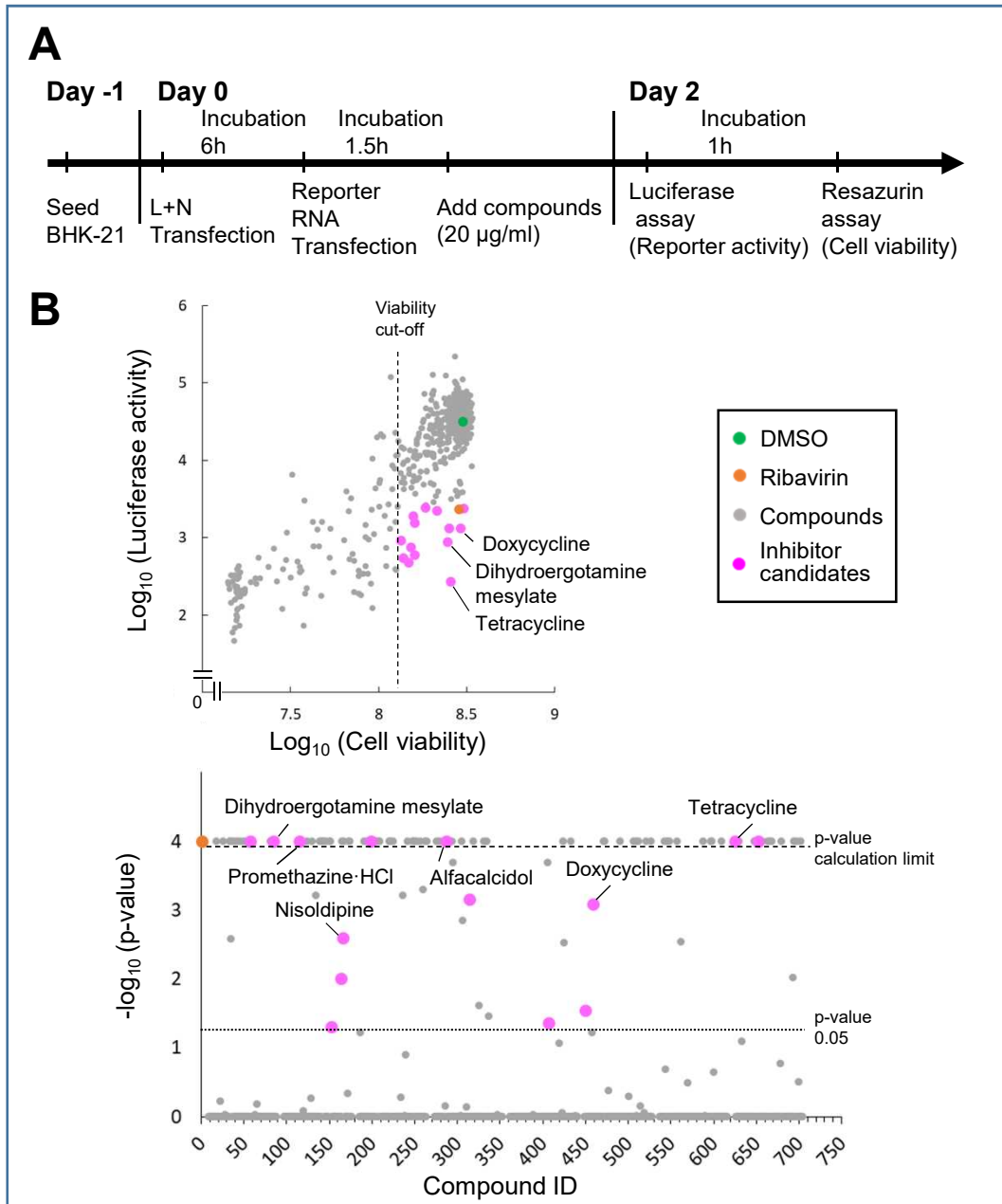
Hirano *et al*, Figure 1 (1.5 Column)



Hirano *et al*, Figure 2 (1.5 Column)



Hirano *et al*, Figure 3 (1.5 column, Color)

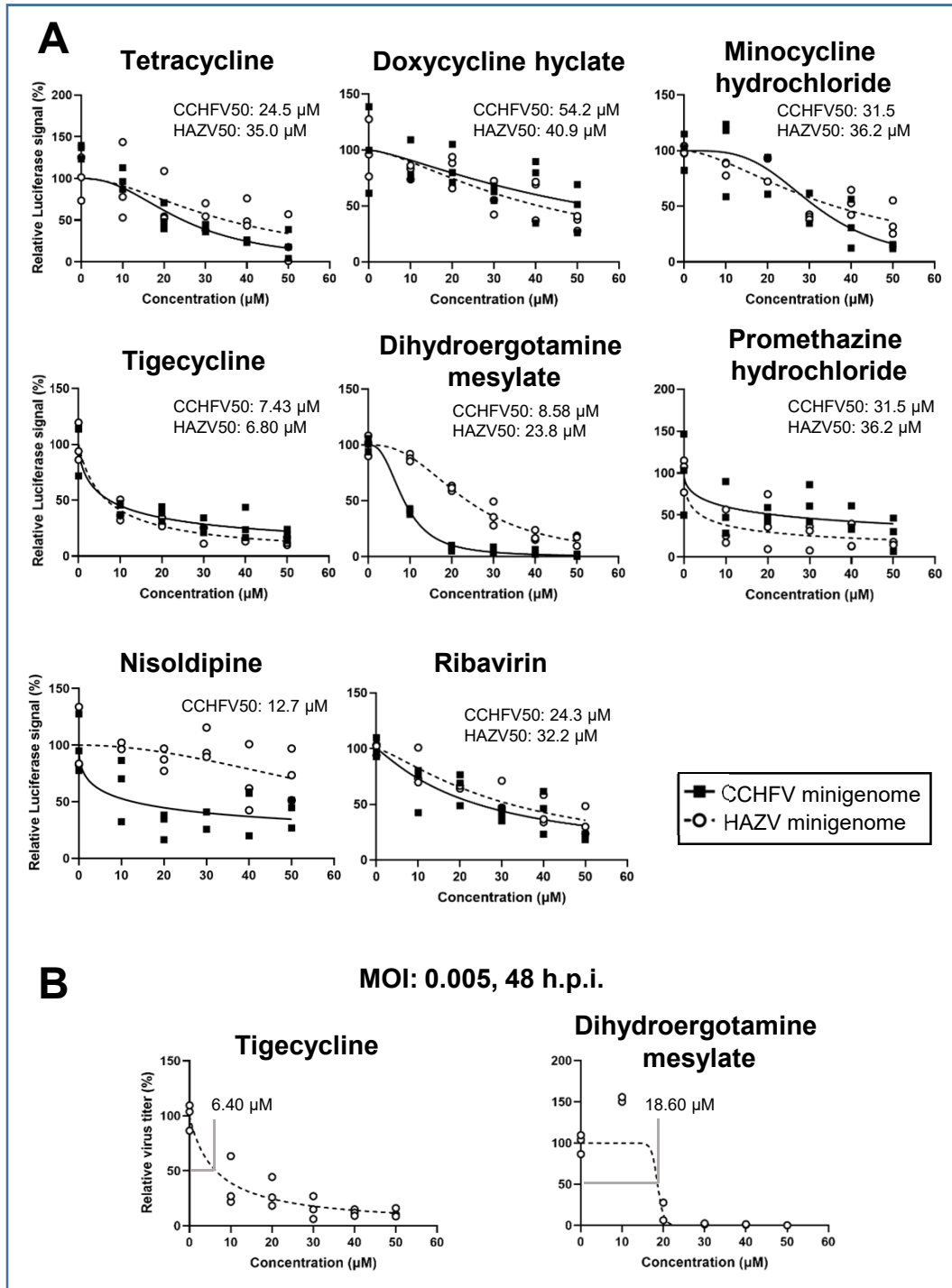


Hirano *et al*, Table 1

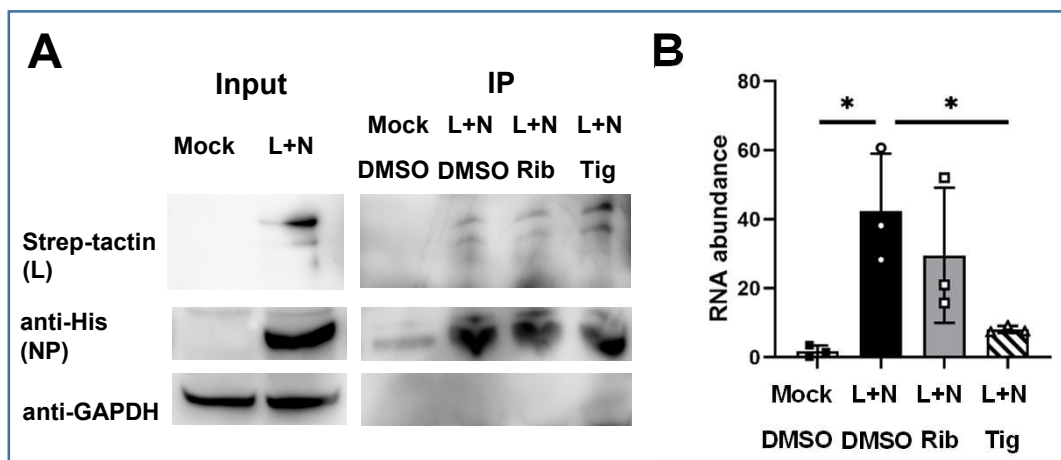
Table 1. List of the inhibitor candidates determined with the CCHFV minigenome.

Name	MW	CAS	Route	Medical use, Mechanism	Adverse effect, Toxicity
Tetracycline	444.4346	60-54-8	Oral, Parental, Topical	Antibiotics. Inhibitor of bacterial 30S ribosomal subunit.	Phototoxicity, stomach or bowel upsets
Lomofungin	314.2497	26786-84-5		Antifungal drug.	Not well characterized
Alfacalcidol	400.6371	41294-56-8	Oral	Analogue of vitamin D.	Hypocalcemia
Dihydroergocristine	611.7305	24730-10-7	Oral	Antihypertensive drug. Partial agonist activity on dopaminergic and alpha-adrenergic receptors.	Narrow therapeutic index
Ketoconazole	531.431	65277-42-1	(Oral), Topical	Antifungal drug. Inhibition of Ergosterol synthesis.	Hepatotoxicity, Cardiotoxicity in oral administration.
Dihydroergotamine mesylate	679.783	11032-41-0	Parental, Topical	Treatment of Migraine. Partial agonist activity on alpha-adrenergic receptors.	Dizziness, Narrow therapeutic index
Promethazine·HCl	320.88	58-33-3	Oral, Parental, Topical	Antihistamine medication. Control of parkinsonism. Antagonist of Histamine H1 receptor.	Tardive dyskinesia, Drowsiness
Suramin	1291.232	129-46-4	Parental	Treatment of African trypanosomiasis.	Skin reaction, Nausea, Headache, Diarrhea
Doxycycline	444.4346	24390-14-5	Oral, Parental, Topical	Antibiotics. Inhibitor of bacterial 30S ribosomal subunit.	Phototoxicity, stomach or bowel upsets
Nisoldipine	388.4144	63675-72-9	Oral	Treatment of hypertension. Calcium channel inhibitor.	Ischemia, Myocardial infarction
Vitamin A acetate	328.4883	127-47-9	Oral	Vital roles in the retina formation and other epithelial differentiation. Formation of rhodopsin.	Headache, Rash
Dehydroepiandrosterone	288.4244	53-43-0	Oral	Treatment of dyspareunia. C19 steroid and Precursor of steroid hormones (androstenedione and others).	Excessive testosterone
Ceftazidime	546.576	72558-82-8	Parental	Antibiotic for multi-drug resistant Gram-negative bacterial pathogens. Non-β-lactam β-lactamase inhibitor.	Abdominal cramps or tenderness, diarrhea
Entacapone	305.286	130929-57-6	Oral	Treatment of Parkinson's disease. Catechol-O-methyl transferase inhibitor.	Dizziness, nausea, diarrhea

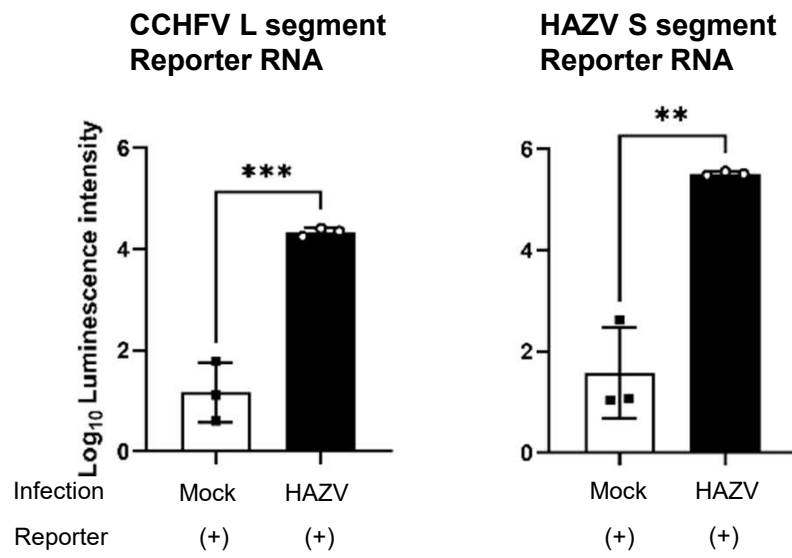
Hirano *et al*, Figure 4 (1.5 column)



Hirano *et al*, Figure 5 (1.5 column)

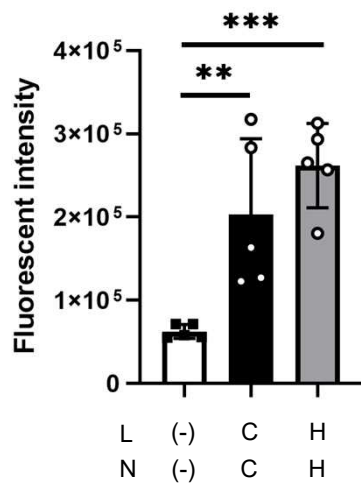


Hirano *et al*, Figure S1

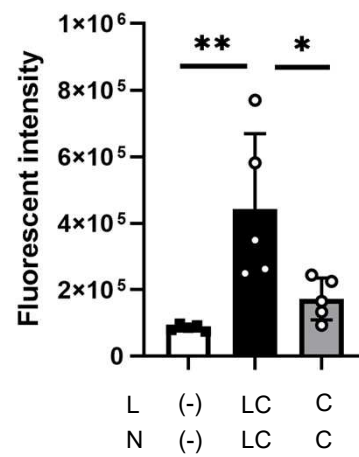


Hirano *et al*, Figure S2

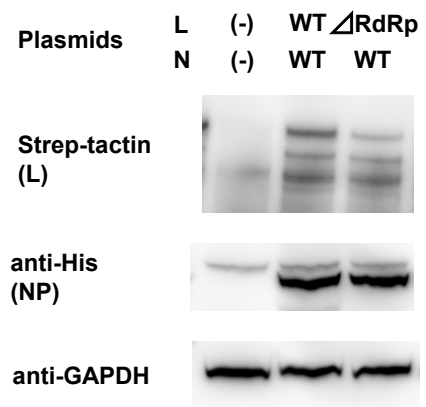
A CCHFV Reporter RNA (mCherry)



B LCMV Reporter plasmid

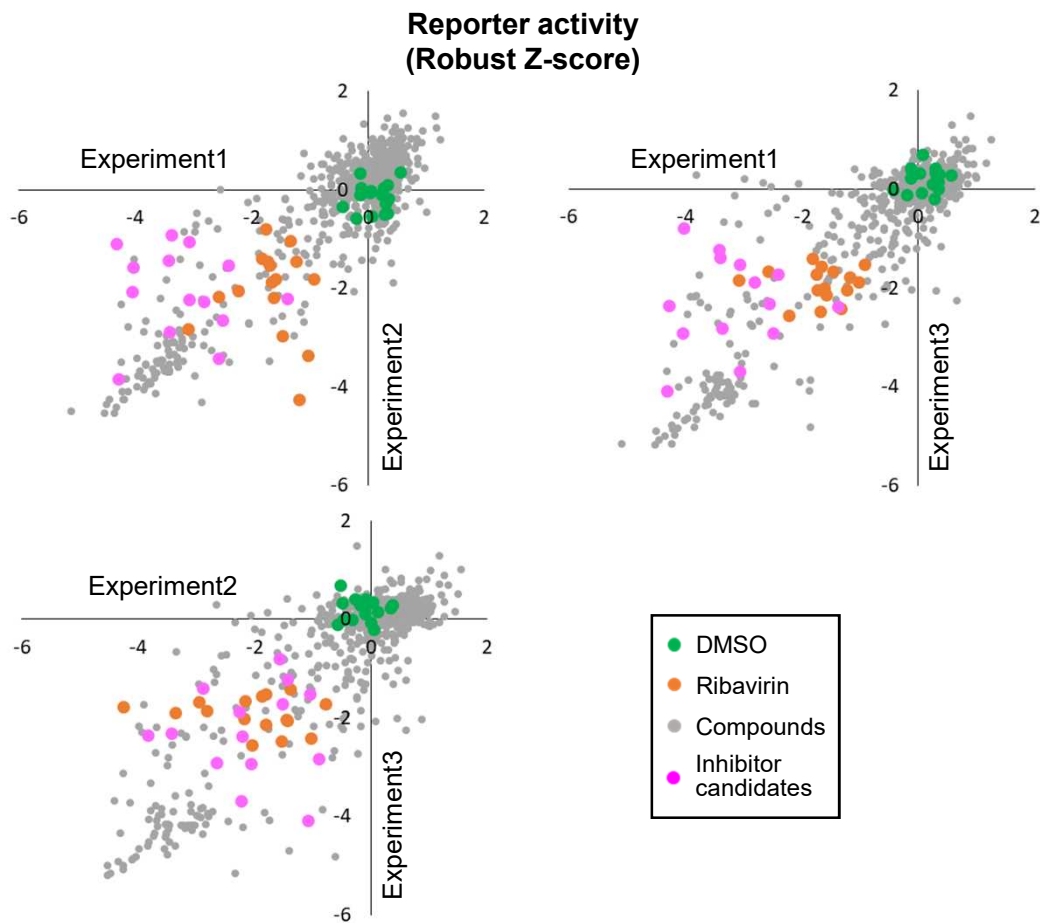


Hirano *et al*, Figure S3

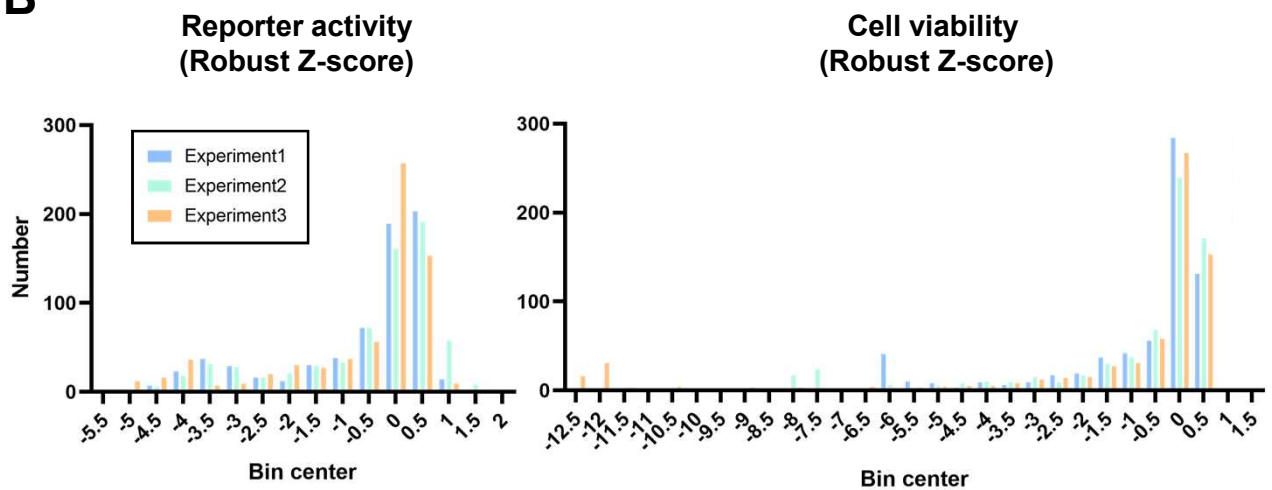


Hirano *et al*, Figure S4

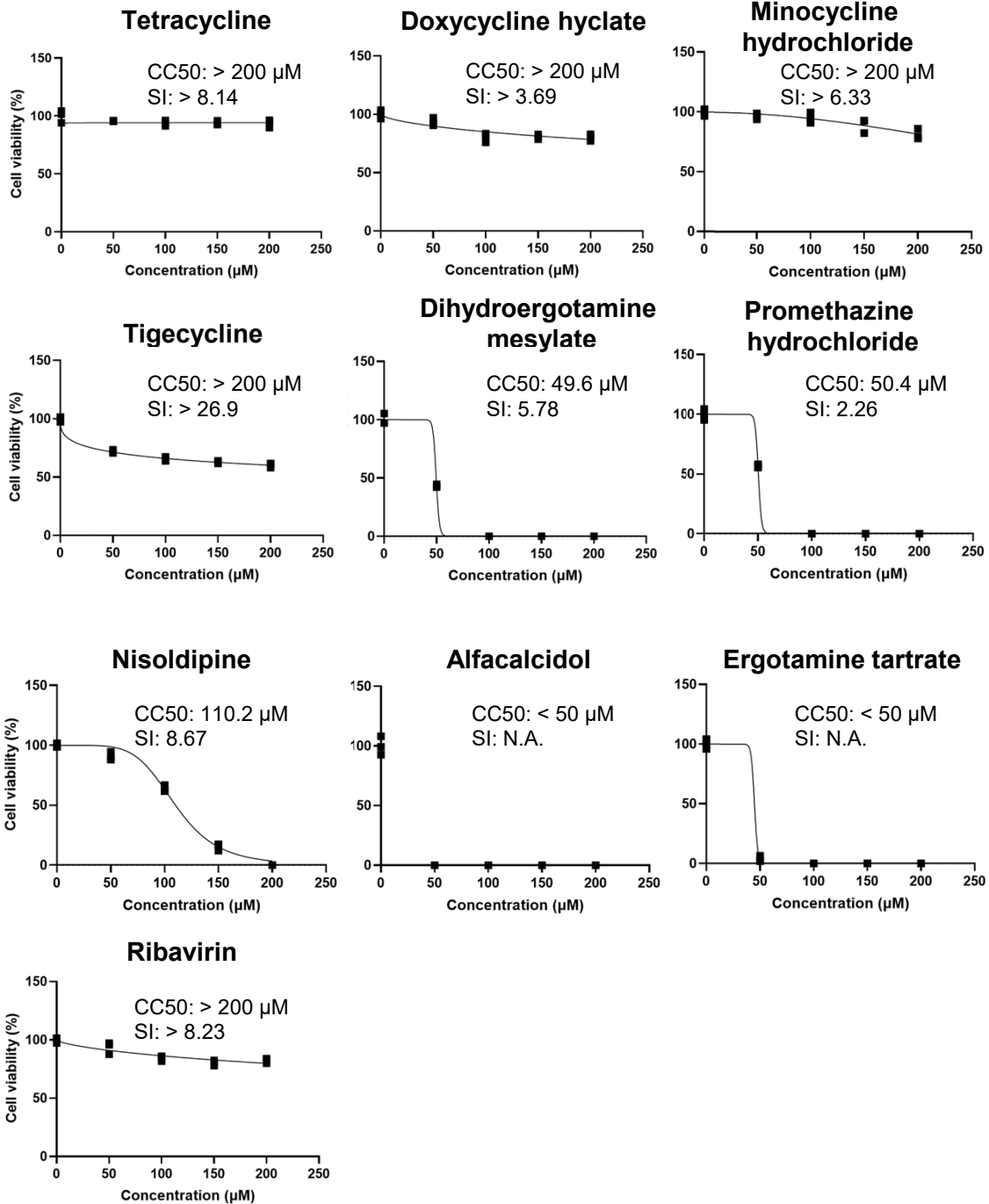
A



B

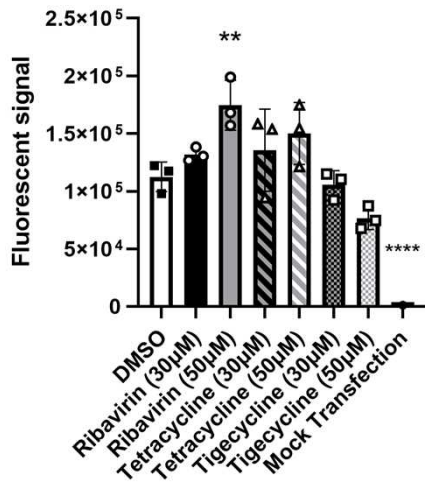


Hirano *et al*, Figure S5

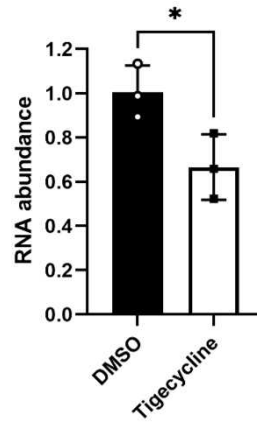


Hirano *et al*, Figure S6

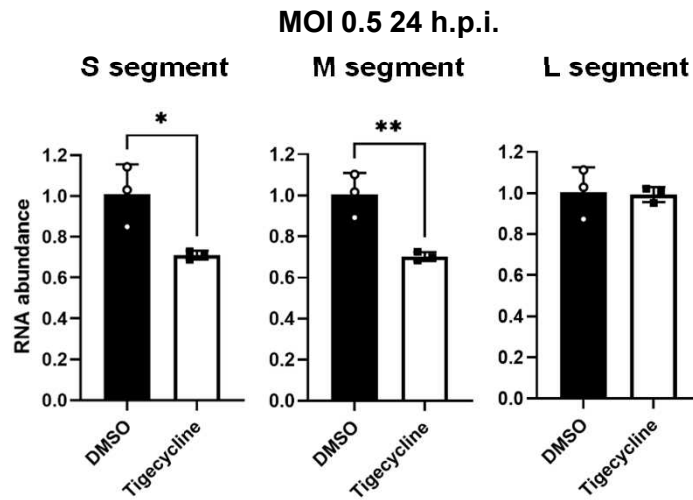
A



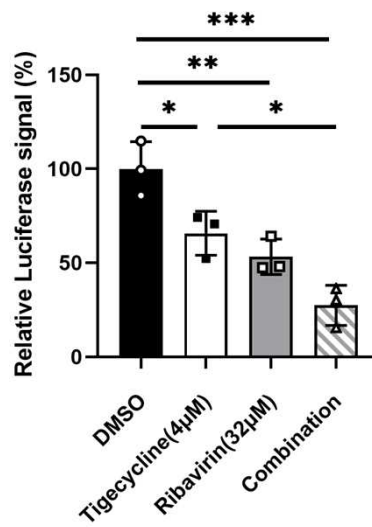
B



C



D



Hirano *et al*, Figure S7

CCHFV Hoti
L segment 5' NCS
HAZV JC280
S segment 5' NCS

1 10 20 30 40

5' GUCUCAAGAAAU CGUUC CCCCCACACCCUUUAAA UAAUG

5' GUCUCAAGAU AU CGUUC CCCCCACACCCCAAUUU UAAUC

LCMV Armstrong
S segment 5' NCS
(Out group)

5' CGCACAGUGGAUCCUAGGCAUUUGAUUGCGCAUUUGUCU

CCHFV Hoti
L segment 3' NCS
HAZV JC280
S segment 3' NCS

40 30 20 10 1

UGUGUCAACGUGGGUAAAGGGGGGAUUGAUUAUCUUUGAGA 3'

--- GUUAACUUGGGGAUAAGGGGGA- UGAUGUCUUUGAGA 3'

LCMV Armstrong
S segment 3' NCS
(Out group)

AGAGGAAAGCGCAAUCCAAAAAGCCUAGGAUCCCCGGUGCG 3'