AAC Accepted Manuscript Posted Online 5 July 2016 Antimicrob, Agents Chemother, doi:10.1128/AAC.00814-16 Copyright © 2016, American Society for Microbiology. All Rights Reserved.

- 1 A Safe and Sensitive Antiviral Screening Platform Based on Recombinant
- 2 Human Coronavirus OC43 Expressing the Luciferase Reporter Gene
- Liang Shen<sup>1</sup>, Yang Yang<sup>1</sup>, Fei Ye<sup>1</sup>, Gaoshan Liu<sup>1</sup>, Marc Desforges<sup>2</sup>, Pierre J. Talbot<sup>2,\*</sup> 4
- Wenjie Tan<sup>1, \*</sup> 5
- 6

11

13

3

- 7 1 Key Laboratory of Medical Virology, Ministry of Health, National Institute for Viral
- Disease Control and Prevention, China CDC, Beijing 102206, China; 8
- 2. Laboratory of Neuroimmunovirology, INRS-Institut Armand-Frappier, Université 9
- 10 du Québec, Laval, Québec, Canada.
- 12 Running title: Recombinant HCoV- OC43 Expressing Reporter
- \*Corresponding Authors: Wenjie Tan, Key Laboratory of Medical Virology, 14
- 15 Ministry of Health, National Institute for Viral Disease Control and Prevention, China

- CDC 155 Changbai Road, ChangPing District, Beijing 102206, China, Tel/Fax: 16
- 86-10-5890 0878, E-mail: tanwj28@163.com; Pierre J. Talbot, Laboratory of 17
- Neuroimmunovirology, INRS-Institut Armand-Frappier, Université du Québec, Laval, 18
- 19 Québec, Canada, E-mail: pierre.talbot@iaf.inrs.ca

#### Abstract

20

40

Human coronaviruses (HCoVs) cause 15-30% of mild upper respiratory tract 21 infections. However, no specific antiviral drugs are available to prevent or treat HCoV 22 infections to date. Here, we developed four infectious recombinant HCoVs-OC43 23 24 (rHCoVs-OC43), which express the Renilla luciferase (Rluc) reporter gene. Among these four rHCoVs-OC43, rOC43-ns2DelRluc (generated by replacing ns2 with the 25 Rluc gene) showed robust luciferase activity with only a slight impact on its growth 26 characteristics. Additionally, this recombinant virus remained stable for at least 10 27 passages in BHK-21 cells. The rOC43-ns2DelRluc was comparable with its parental 28 wild-type virus (HCoV-OC43-WT) with respect to the quantity of the antiviral 29 activity of chloroquine and ribavirin. We showed that chloroquine strongly inhibited 30 HCoV-OC43 replication in vitro, with an IC<sub>50</sub> of 0.33 μM. However, ribavirin showed 31 inhibition on HCoV-OC43 replication only at high concentrations which may not be 32 applicable to humans in clinical treatment, with an IC<sub>50</sub> of 10 μM. Furthermore, using 33 34 a luciferase-based small interfering RNA (siRNA) screening assay, we identified double-stranded RNA-activated protein kinase (PKR) and DEAD-box RNA helicases 35 (DDX3X) that exhibited antiviral activities, which were further verified by the use of 36 37 HCoV-OC43-WT. Therefore, rOC43-ns2DelRluc represents a promising safe and 38 sensitive platform for high throughput antiviral screening and quantitative analysis of viral replication. 39

### Introduction

41

42

43

44

45

46

47

48

49

50

51

52

53

54

55

56

57

58

59

60

61

62

Coronaviruses (CoVs) belong to the family Coronaviridae in the order Nidovirales (1). They have a positive-sense RNA genome ~30 kb in length, the largest found in any RNA viruses. CoVs infect avian species and a wide range of mammals, including humans (2). Currently, six CoVs that are able to infect humans have been identified; four circulating strains HCoV-229E, -OC43, -HKU1, NL63 and two emergent strains severe acute respiratory syndrome coronavirus (SARS-CoV) and Middle East respiratory syndrome coronavirus (MERS-CoV). Indeed, in 2003, an outbreak of severe acute respiratory syndrome (SARS) first demonstrated the potentially lethal consequences of zoonotic CoV infections in humans. In 2012, a similar, previously unknown CoV emerged, MERS-CoV, which has thus far caused over 1,650 laboratory-confirmed infections, with a mortality rate of about 30% (3, 4). However, to date, no effective drug has been identified for the treatment of HCoV infections and few host factors have been identified that restrict the replication of HCoV. The emergence of these highly pathogenic HCoVs has reignited interest in studying HCoV biology and virus-host interactions. Therefore, a safe and sensitive screening model is required for rapid identification of potential drugs and screening antiviral host factors capable of inhibiting HCoV infection. The introduction of a reporter gene into the viral genome provides a powerful tool for initial rapid screening and evaluation of antiviral agents. The unique CoV transcription mechanism allows efficient expression of reporter genes by inserting

reporter genes under the control of transcription regulatory sequence (TRS) elements.

To date a number of reporter CoVs have been generated (5-11) and several reporter 63 CoVs have been applied to antivirals screening assay (10-14), but most of them are 64 65 animal CoVs which cause disease in only one animal species and are generally not susceptible to humans. Among these reporter CoVs, only one reporter CoV 66 (SARS-CoV-GFP) was based on HCoV and applied to a small interfering RNA 67 (siRNA) library screening (14). However, the SARS-CoV-GFP assay lacks sensitivity 68 and requires a high infectious dose (multiplicity of infection [MOI] of 10) for 69 quantitative screening. Moreover, experiments with this reporter virus require a 70 BSL-3 facility, which is costly and labor-intensive. Thus, it is critical to generate a 71 safe and sensitive reporter HCoV for high-throughput screening (HTS) assays. 72 Moreover, generation of a reporter HCoV was more suitable to screen drugs for 73 74 clinical treatment than the reporter animal CoVs. HCoV-OC43 shows promise as a reporter virus for screening anti-HCoVs drugs or identifying host factors. 75 HCoV-OC43 was first isolated from a patient with upper respiratory tract disease in 76 the 1960s, together with severe Beta-CoVs (SARS-CoV and MERS-CoV), all belong 77 to the Betacoronavirus genus (15, 16), and these three virus strains have a high level 78 of conservation for some essential functional domains, especially within 3CLpro, 79 RdRp, and the RNA helicase, which represent potential targets for broad-spectrum 80 81 anti-HCoVs drug design (17, 18). Moreover, unlike SARS-CoV or MERS-CoV, HCoV-OC43 usually causes a mild respiratory tract disease and can be used for 82 83 screening antivirals in a BSL-2 facility. Furthermore, a small animal model of HCoV-OC43 has been developed and used successfully for antiviral trials (18, 19). 84

86

87

88

89

90

91

92

93

94

95

96

97

98

99

100

101

102

103

104

105

106

HCoV-OC43 encodes two accessory genes, ns2 and ns12.9 (20). The ns2 gene, located between nsp13 and HE gene loci, encodes a protein of unknown function. The ns12.9 gene, located between the S and E structural genes, encodes a protein that was recently demonstrated as a viroporin involved in HCoV-OC43 morphogenesis and pathogenesis (21). In this study, four infectious recombinant HCoVs-OC43 (rHCoVs-OC43) were generated based on the ATCC VR-759 strain of HCoV-OC43 by genetic engineering of the two accessory genes. Successfully rescued viruses were characterized and subsequently investigated for genetic stability. One reporter virus, rOC43-ns2DelRluc, showed robust Rluc activity and had similar growth kinetics to the parental wild-type HCoV-OC43 (HCoV-OC43-WT). Furthermore, this reporter virus was used successfully to evaluate the antiviral activity of Food and Drug Administration (FDA)-approved drugs and siRNA screening assays. Our study indicated that the replacement of accessory ns2 gene represents a promising target for the generation of reporter HCoV-OC43 and provides a useful platform for identifying

Downloaded from http://aac.asm.org/ on September 6, 2016 by INRS-Institut Armand-Frappie

Materials and methods

Plasmid construction. The infectious full-length cDNA clone pBAC-OC43<sup>FL</sup> (22), containing a full-length cDNA copy of the HCoV-OC43, was used as the backbone to generate four rHCoVs-OC43 (Fig. 1). The Rluc gene was amplified from pGL4.75hRluc/CMV vector (Promega) and introduced into the plasmid pBAC-OC43<sup>FL</sup> by standard overlapping polymerase chain reaction (PCR). Modified

anti-HCoVs drugs and host factors relevant to HCoV replication.

127

128

LI-COR Biosciences.

21,523 and 22,915 nucleotides, inclusively) or in-frame insertion of the Rluc gene into 108 the ns2 gene (between nucleotides 21,517 and 21,518, inclusively), were generated by 109 overlapping PCR and cloned into Narl/PmeI-digested pBAC-OC43FL to generate 110 pBAC-OC43-ns2DelRluc or pBAC-OC43-ns2FusionRluc. The same strategies were 111 employed for replacing the ns12.9 gene with Rluc gene or in-frame insertion of the 112 Rluc gene into the ns12.9 gene, resulting in plasmids pBAC-OC43-ns12.9StopRluc 113 and pBAC-OC43-ns12.9FusionRluc, respectively. Further details are available on 114 request. All final constructs were verified by Sanger sequencing. 115 Cells and antibodies. BHK-21, HEK-293T, and Huh7 cells were grown in 116 Dulbecco's modified Eagle medium (DMEM) (Gibco) supplemented with 10% fetal 117 118 bovine serum (FBS) (Gibco), 2 mM L-glutamine (Sigma-Aldrich) and incubated at 37°C with 5% CO<sub>2</sub>. 119 anti-Renilla luciferase (ab185925), anti-PKR 120 The (ab32052) anti-phosphorylated PKR (ab81303) rabbit monoclonal antibodies were purchased 121 122 from Abcam. The anti-Flag (F7425) rabbit polyclonal antibody was purchased from Sigma-Aldrich. The anti-eIF2α (D7D3), anti-phosphorylated-eIF2α (Ser51) (D9G8), 123 anti-DDX3X (D19B4) and anti-β-actin (13E5) rabbit monoclonal antibodies were 124 125 obtained from Cell Signaling Technology. The infrared IRDye 800CW-labeled goat anti-mouse IgG (H+L) and IRDye 680RD goat anti-rabbit IgG were purchased from 126

Generation and titration of recombinant viruses. The reporter viruses

Downloaded from http://aac.asm.org/ on September 6, 2016 by INRS-Institut Armand-Frappie

fragments of HCoV-OC43 cDNA, for replacing the ns2 gene with Rluc gene (between

129 rOC43-ns2DelRluc, rOC43-ns2FusionRluc, rOC43-ns12.9StopRluc and rOC43-ns12.9FusionRluc were rescued from the infectious cDNA clones 130 131 pBAC-OC43-ns2DelRluc, pBAC-OC43-ns2FusionRluc, pBAC-OC43ns12.9StopRluc and pBAC-OC43-ns12.9FusionRluc, respectively. In brief, BHK-21 132 cells grown to 80% confluence were transfected with 4 µg of pBAC-OC43<sup>FL</sup>, 133 134 pBAC-OC43-ns2DelRluc, pBAC-OC43-ns2FusionRluc, pBAC-OC43-ns12.9StopRluc or pBAC-OC43-ns12.9FusionRluc using 135 X-tremeGENE HP DNA Transfection Reagent (Roche) according to 136 manufacturer's instructions. After incubation for 6 h at 37°C in a humidified 5% CO<sub>2</sub> 137 138 incubator, the transfected cells were washed three times with DMEM and maintained in DMEM supplemented with 2% FBS for 72 h at 37°C and an additional 96 h at 139 140 33°C. Next, the rHCoVs-OC43 were harvested by three freeze-thaw cycles followed by centrifugation at  $2,000 \times g$  for 20 min at 4°C. The HCoV-OC43-WT was obtained 141 from the full-length cDNA clone pBAC-OC43<sup>FL</sup>. All viruses were propagated in 142 143 BHK-21 cells in DMEM supplemented with 2% FBS. The titers of rHCoVs-OC43 were determined by indirect immunofluorescence 144 assay (IFA). Briefly, BHK-21 cells in 96-well plates were infected with 10-fold 145 diluted viruses. The viral titers were determined at 72 h post-infection (hpi) by IFA 146 and expressed as median tissue culture infective dose (TCID<sub>50</sub>)/mL, according to the 147 Reed and Münch method (23). 148 149 **Determination of viral growth kinetics.** BHK-21 cells seeded on 48-well plates

were infected with HCoV-OC43-WT or rHCoVs-OC43 at an MOI of 0.01. After 2 h

152

153

154

155

156

157

158

159

160

161

162

163

164

165

166

167

168

169

170

171

172

of incubation at 33°C, cells were washed with PBS, and replaced with fresh medium before incubation at 33°C. The supernatants (150 μL) were harvested at 24, 48, 72, 96, 120, 144 and 168 hpi, and 150 μL of fresh media were added to the cells. The titer for each virus at the indicated time point was determined by IFA, as described above.

Rluc activity assay. Analysis of Rluc expression was performed in 48- or 96-well plates. Briefly, BHK-21 cells or HEK-293T cells in plates were infected with rHCoVs-OC43 at an MOI of 0.01. At the various time-points post-infection, the cells in each well were assayed for relative light units (RLUs) using the Renilla-Glo Luciferase Assay System (Promega) according to the manufacturer's instructions.

Dual luciferase reporter assay system. HEK-293T cells were seeded in 24-well plates at a cell density of  $2.5 \times 10^5$  cells per well. The next day, cells were transfected with plasmids expressing DDX3X or TBK1 (150 or 300 ng), along with IFN-β-Luc and Rluc internal reference reporter plasmids. At 24 h post-transfection, cells were lysed and analyzed with the Dual-Luciferase Reporter Assay System (Promega) according to the manufacturer's protocol.

Downloaded from http://aac.asm.org/ on September 6, 2016 by INRS-Institut Armand-Frappie

Western blot analysis. Infected or uninfected cells were washed twice with PBS, lysed with NP-40 buffer (50 mM Tris [pH 7.5], 150 mM NaCl, 0.5% NP-40, and 0.5 mM EDTA) containing 1 mM phenylmethylsulfonyl fluoride (PMSF) and 1 mg/mL protease inhibitor cocktail (Roche) for 30 min at 4°C. An equal volume of each sample was separated by sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) and transferred to nitrocellulose membranes (Pall). The membranes were blocked with 5% skim milk in PBS containing 0.5% Tween (PBST) for 1 h at

173 room temperature and incubated with primary antibody overnight at 4°C. After washes with PBST, the membranes were further incubated for 1 h with infrared 174 IRDye 800CW-labeled goat anti-mouse IgG (H+L) (1:10,000) (LI-COR) or IRDye 175 680RD goat anti-rabbit IgG (H+L) (1:10,000) (LI-COR), blots were scanned on the 176 177 Odyssey Infrared Imaging System (LI-COR). 178 RNA isolation and reverse transcription PCR (RT-PCR). Total RNA was extracted from virus-infected BHK-21 cells using TRIzol reagent (Invitrogen) and 179 treated with DNase I to remove potential genomic DNA. The RNA concentration was 180 quantified using a NanoDrop 2000 Series spectrophotometer (Thermo Scientific). For 181 182 RT-PCR, two sets of primer pairs flanking the inserted reporter gene were used: one pair for rOC43-ns2FusionRluc and rOC43-ns2DelRluc (5'-GTG TAA GCC CAA 183 GGT TGA GAT AG-3') / (5'-GTC GTT CAG ATT GTA ATC ATA TTG -3'), and 184 another for rOC43-ns129FusionRluc and rOC43-ns129DelRluc (5'-CAT ATG AAT 185 ATT ATG TAA AAT GGC -3')/ (5'-GCC ATA AAC ATT TAA CTC CTG TC -3'). The 186 187 PCR products were subjected to electrophoresis on a 1% agarose gel. Real-time PCR. Semi-quantitative PCR was performed using the One Step 188 SYBR PrimeScript RT-PCR Kit (Takara) according to the manufacturer's instructions. 189 Fold-induction values were calculated using the  $2^{-\Delta\Delta Ct}$  method and mRNA expression 190 191 was normalized to GAPDH. Genomic RNA copies of HCoV-OC43-WT or rOC43-ns2DelRluc was quantified using a previously described quantitative RT-PCR 192 193 as described previously (24). All primers are available in Table S1.

Stability of rHCoVs-OC43. To examine the stability of the inserted Rluc genes,

196

197

198

199

200

201

202

203

204

205

206

207

208

209

216

rHCoVs-OC43 and their parental HCoV-OC43-WT were passaged 13 times in BHK-21 cells (Fig. 3A). Briefly, cells in a 25-cm<sup>2</sup> flask were infected with the rescued rHCoVs-OC43 and HCoV-OC43-WT (defined as P0) at an MOI of 0.01. At 120 hpi, 300 μL of cell culture supernatants from the passaged virus (P1) were added to naïve cells to generate passage 2 virus (P2). After 13 rounds of serial passage, viral RNA was extracted from the supernatant of infected cells of each passage (P0 to P13) and the stability of the inserted reporter genes was detected by RT-PCR as described above and cloned into the pMD18-T vector (Takara) for Sanger sequencing (four clones were sequenced for each passage). The titers of rHCoVs-OC43 from P1 to P13 were determined using IFA. In addition, BHK-21 cells in 48-well plates were infected with each passage of rHCoVs-OC43 at an MOI of 0.01 and measured the Rluc activity at 72 hpi using the Renilla-Glo Luciferase Assay System. Cell viability assay. The cell viability assay was performed using a Cell Titer-Glo Luminescent Cell Viability Assay kit (Promega). Briefly, cells were seeded in 96-well plates in triplicate. After 24 h, various concentrations of chloroquine (0–80

Downloaded from http://aac.asm.org/ on September 6, 2016 by INRS-Institut Armand-Frappie

μM) and ribavirin (0–320 μM) (Sigma-Aldrich) were added to the medium. At 72 h, 210 the plates were equilibrated at room temperature for 60 min, and 100 µL of 211 212 Celltiter-Glo reagent was added to the medium. The plates were subsequently shaken on a shaker for 2 min to induce cell lysis. After a final incubation for 10 min at room 213

temperature, the luminescence was measured using a GLOMAX Luminometer system 214

215 (Promega).

Antiviral drug assay. For the viral RNA load-based antiviral assay, confluent

217 BHK-21 cells in 48-well culture plates were infected in triplicate with HCoV-OC43-WT or rOC43-ns2DelRluc at an MOI of 0.01. After 2 h adsorption at 218 33°C, the inoculum was removed and the cells were washed three times with DMEM. 219 Subsequently, complete DMEM containing various concentrations of chloroquine (0-220 221  $80 \mu M$ ) or ribavirin (0–320  $\mu M$ ) were added to the cells. Cells were incubated for 72 h at 33°C in a humidified 5% CO<sub>2</sub> incubator. The supernatants of cells infected with 222 HCoV-OC43-WT or rOC43-ns2DelRluc were collected, and the viral RNA loads were 223 determined using quantitative RT-PCR as described above. For the luciferase-based 224 antiviral assay, BHK-21 cells in 96-well culture plates were infected with 225 rOC43-ns2DelRluc followed by incubation with chloroquine or ribavirin for 72 h; 226 then the Rluc activity was measured as described above. 227 228 RNA interference (RNAi) screening. We designed siRNA pools targeting eight potential host antiviral restriction factors for screening, and each individual siRNA 229 pool consisted of three siRNAs targeting the same gene. A non-targeting siRNA 230 231 having no matches to the viral or human genome served as a blank control. The specific siRNAs targeting antiviral host factors were synthesized by GenePharma 232 (sequences provided upon request). 233 For testing of siRNA pools, HEK-293T cells plated in poly-L-lysine 234 235 (PLL)-coated 48-well plates were transfected with siRNA pools using X-tremeGene siRNA Transfection Reagent (Roche) at a final concentration of 300 nM. After 236 237 incubation for 24 h, cells were subsequently infected in triplicate with

rOC43-ns2DelRluc at an MOI of 0.01. At 60 hpi, the Rluc activity was measured as

described above.

239

240

241

242

243

244

245

246

247

248

249

250

251

252

253

254

256

257

258

259

260

Mice and infection. 12-day-old female BALB/c mice (Animal Care Centre, Chinese Academy of Medical Science, Beijing, China) were randomly distributed into three groups. Two groups were intracerebral inoculation (IC) with 20 µl of DMEM containing 100 TCID<sub>50</sub> of HCoV-OC43-WT or rOC43-ns2DelRluc and another group was intracerebral inoculation with 20 µl of DMEM. The infected mice were monitored for survival. For the passages of rOC43-ns2DelRluc in BALB/c mice, 12-day-old mice were intracerebral inoculation with 500 TCID<sub>50</sub> of rOC43-ns2DelRluc (P0) in 20 μl of DMEM and sacrificed at 3 days post-inoculation, brains were homogenized in 500 µl of PBS containing 100 U/ml penicillin, 0.1 mg/ml streptomycin and 0.5 µg/ml amphotericin B. Then Brain homogenate were clarified by low-speed centrifugation at 3,000 rpm for 12 min to obtain passage 1 virus (P1). After 5 rounds of serial passages, the rOC43-ns2DelRluc was passaged to P5. Statistical analysis. Differences between groups were examined for statistical significance using Student's t-test. Confidence levels are indicated in the figures as

255

# Results

follows: \*, P < 0.05; \*\*, P < 0.01.

Characterization of rHCoVs-OC43 expressing Rluc. Reporter virus is a valuable screening tool for identifying novel antiviral drugs or host factors. To generate a high expression reporter HCoV-OC43 and evaluate the roles of ns2 and ns12.9 genes in viral production, four rHCoVs-OC43 were obtained following

262

263

264

265

266

267

268

269

270

271

272

273

274

275

276

277

278

279

280

281

282

replacement of the ns2 or ns12.9 genes with Rluc (rOC43-ns2DelRluc and rOC43-ns12.9StopRluc) or in-frame insertion of the Rluc gene into ns2 or ns12.9 genes (rOC43-ns2FusionRluc and rOC43-ns12.9FusionRluc), respectively (Fig. 1). The in vitro growth characteristics of the reporter viruses were analyzed by growth kinetics **BHK-21** cells. rOC43-ns2FusionRluc rOC43-ns12.9FusionRluc showed replication kinetics similar to that of HCoV-OC43-WT, reached a peak titer of 10<sup>6</sup> TCID<sub>50</sub>/mL at 144 hpi (Fig. 2B), indicating that ns2-Rluc or ns12.9-Rluc fusion proteins were likely to retain their biological functions in the life cycle of HCoV-OC43. Moreover, the viral titer of rOC43-ns2DelRluc was only 4-fold lower than that of HCoV-OC43-WT at 144 hpi, indicating that the ns2 gene is nonessential for virus replication (Fig. 2B). By contrast, rOC43-ns12.9StopRluc showed impaired growth kinetics, with a peak titer of 10<sup>4.8</sup> TCID<sub>50</sub>/mL at 144 hpi, which was ~27-fold lower than that of the parental HCoV-OC43-WT (Fig. 2B). This result indicated that the ns12.9 viroporin is important for viral propagation in cell culture. To further explore whether the reduction in virus titers of rOC43-ns2DelRluc was due to the abolishment of ns2 protein expression, we performed a transient complementation assay. An ns2 protein expression vector was constructed, and its expression levels were detected by Western blot analysis (Fig. 2C, left). Compared with the empty vector-transfected cells, ns2-expressing cells exhibited a slight increase in virus titers for HCoV-OC43-WT (Fig. 2C, right). These results confirmed that the loss of infectious virus production by

deletion of ns2 gene could be compensated by transient expression of ns2 in BHK21

cells.

283

285

286

287

288

289

290

291

292

293

294

295

296

297

298

299

300

301

302

303

304

Rluc activity in cells infected with reporter viruses was also characterized. Surprisingly, the viral titer of rOC43-ns2DelRluc was 4-fold lower than that of the rOC43-ns2FusionRluc at 144 hpi, but showed robust Rluc expression levels, with Rluc activity 18-fold higher than that of the rOC43-ns2FusionRluc (Fig. 2D). rOC43-ns12.9StopRluc, although having impaired growth kinetics, showed relatively high Rluc activity, with 10<sup>7</sup> RLUs at 144 hpi. However, rOC43-ns12.9FusionRluc showed faint Rluc activity even though it showed similar replication kinetics with HCoV-OC43-WT (Fig. 2D). Moreover, Western blotting was performed to confirm the Rluc expression levels of the reporter viruses at 72 and 96 hpi. The results showed similar expression levels of N proteins in rOC43-ns2FusionRluc rOC43-ns2DelRluc, but the expression of ns2-Rluc fusion protein rOC43-ns2FusionRluc was significantly reduced compared with Rluc proteins of rOC43-ns2DelRluc (Fig. 2E). In addition, we observed high levels of Rluc proteins in the lysates of cells infected with rOC43-ns12.9StopRluc, but no ns12.9-Rluc fusion proteins were detected in the lysates of rOC43-ns12.9FusionRluc-infected cells, perhaps due to its low Rluc expression levels at 96 hpi (Fig. 2F). These results correlated with the Rluc activity detected at the corresponding hpi (Fig. 2D).

Downloaded from http://aac.asm.org/ on September 6, 2016 by INRS-Institut Armand-Frappie

These observations prompted us to ascertain whether replacement of ns2 or ns12.9 with Rluc gene could enhance the subgenomic (sg) mRNA transcription efficiency when compared with that of ns2-Rluc or ns12.9-Rluc fusion genes, we detected the transcription levels of ns2 (HCoV-OC43-WT), Rluc (rOC43-ns2DelRluc

305 or rOC43-ns12.9StopRluc), ns2-Rluc fusion (rOC43-ns2FusionRluc) and ns12.9-Rluc 306 fusion (rOC43-ns12.9FusionRluc) genes using semi-quantitative PCR. The sg mRNA 307 level of Rluc (rOC43-ns2DelRluc) was only 2.3-fold higher than that of ns2 of HCoV-OC43-WT, and was similar to the sg mRNA level of the ns2-Rluc fusion gene 308 309 (Fig. 2G). Moreover, replacement of ns12.9 gene with Rluc gene or insertion of Rluc 310 gene in frame into the ns12.9 coding region caused a slight reduction in Rluc or ns12.9-Rluc sg mRNA level during infection (Fig. 2G). This result indicated that the 311 312 Rluc activity differences in the two reporter viruses were not due to the transcription level of sg mRNAs. 313 314 Collectively, these results suggested that the ns2 gene is not required for HCoV-OC43 replication and high expression reporter virus can be generated by 315 316 replacing the ns2 gene with Rluc. Stability of rHCoVs-OC43 after multiple passages. To examine the in vitro 317 stability of the four reporter viruses, rHCoVs-OC43 and HCoV-OC43-WT were 318 319 passaged 13 times in BHK-21 cells as described above (see Fig. 3A). As shown in Fig. 3B, titers for all viruses increased over the first four passages and became stable in 320 subsequent passages. Moreover, the Rluc activity of rOC43-ns2DelRluc and 321 rOC43-ns12.9StopRluc at each passage showed no significant fluctuations during the 322 323 passages in **BHK-21** cells. However, rOC43-ns2FusionRluc and rOC43-ns12.9FusionRluc showed 4- to 6-fold reduction in Rluc activity during the 13 324 325 passages (Fig. 3C). To investigate whether mutations were introduced during the

passages, viral RNA was extracted from the supernatant of infected cells of each

328

329

330

331

332

333

334

335

336

337

338

339

340

341

342

343

344

345

346

347

348

passage. The Rluc gene and its flanking sequences were detected by RT-PCR. Surprisingly, the Rluc gene remained intact in the genome of all rHCoVs-OC43 as no smaller PCR product was detected over the 13 passages (Fig. 3D). However, sequence analysis of clones of RT-PCR products identified same mutations (two-nucleotide insertion between position 70 and 71), which resulted in a stop codon in the region of the Rluc expression cassette of three rHCoVs-OC43 (see Fig. S1 and Table S2). It is worth mentioning that the replacement of accessory genes with the Rluc gene resulted in rHCoVs-OC43 with higher genetic stability when compared with in-frame insertions of the Rluc gene (Table S2). Because the rOC43-ns2DelRluc showed robust Rluc activity, with little impact on its replication kinetics and it remained genetically stable during 10 passages in BHK-21 cells. We next evaluated the pathogenicity of rOC43-ns2DelRluc in the mouse model. Unlike previously reported ns12.9 deletion mutant (21), the result showed that BALB/c mice inoculated with 100 TCID<sub>50</sub> of either rOC43-ns2DelRluc or HCoV-OC43-WT showed a severe symptom of twitching limbs at 3 days post-inoculation and caused 100% mortality at 4 days post-inoculation, indicating that deletion of ns2 had no influence on the pathogenicity of rOC43-ns2DelRluc in BALB/c mice (Fig. S2, A and B). rOC43-ns2DelRluc remained genetically stable after 5 passages in mice and the viral titers in brain tissues was 10<sup>7.1</sup> TCID<sub>50</sub>/g at 3 days post-inoculation, further confirmed the applicability of rOC43-ns2DelRluc in vivo (Fig. S2, D and E). Suitability of rOC43-ns2DelRluc for high-throughput antiviral drug

screening. To verify whether rOC43-ns2DelRluc displayed sensitivity similar to the

350

351

352

353

354

355

356

357

358

359

360

361

362

363

364

365

366

367

368

369

370

antiviral drug screening.

to evaluate of the antiviral activity of chloroquine or ribavirin in parallel. As shown in Fig. 4A, chloroquine treatment had a significant inhibitory effect on HCoV-OC43-WT or rOC43-ns2DelRluc replication at low-micromolar concentrations, while ribavirin showed no inhibitory effect at the same concentrations (Fig. 4B). Moreover, a similar decrease in viral copy numbers was observed in the two viruses in the presence of increasing levels of chloroquine or ribavirin, indicating that deletion of the ns2 gene had no effect on the sensitivity of rOC43-ns2DelRluc to the antiviral drugs. To verify whether the Rluc activity of rOC43-ns2DelRluc could be used for antiviral drug screening, we analyzed the antiviral activity of chloroquine and ribavirin against rOC43-ns2DelRluc in parallel using luciferase-based reporter assays. As expected, Rluc activity was reduced in the presence of increasing levels of chloroquine or ribavirin in a dose-dependent manner (Fig. 4C and Fig. 4D). For chloroquine, an IC<sub>50</sub> of 0.33  $\mu$ M and CC<sub>50</sub> of 397.54  $\mu$ M was observed (see Table 1), which is in line with a previous report (18). By contrast, ribavirin exhibited an inhibitory effect at concentrations of 3 μM or higher, with an IC<sub>50</sub> of 10.00 μM and

CC<sub>50</sub> of 156.16 µM (Table 1). Our validation experiments suggested that the

rOC43-ns2DelRluc-based Rluc assay allows more sensitive and rapid quantification

of viral replication than the traditional quantitative RT-PCR assay, with RLUs of 106.2

in dimethyl sulfoxide (DMSO)-treated cells at 72 hpi (data not shown) and the Rluc

activity could be detected without extracting viral RNA, suggesting its utility for HTS

Downloaded from http://aac.asm.org/ on September 6, 2016 by INRS-Institut Armand-Frappie

parental HCoV-OC43-WT under antiviral drugs treatment, the reporter virus was used

372

373

374

375

376

377

378

379

380

381

382

383

384

385

386

387

388

389

390

391

392

Screening for potential host factors that inhibit HCoV-OC43 replication. To further evaluate the applicability of rOC43-ns2DelRluc for antiviral screening, this reporter virus was employed to screen host factors that inhibit HCoV-OC43 replication. Here, we selected eight potential antiviral host factors that were reported against flaviviruses and tested them in RNAi screening. Among these eight host factors, the tripartite motif protein 56 (TRIM56) served as a positive control as it belongs to a new class of host antiviral restriction factors that confers resistance to HCoV-OC43 (25). The effect of knockdown of the individual gene on rOC43-ns2DelRluc replication was expressed as relative luciferase activity (RLA), which is the ratio of RLUs obtained from cells treated with targeting siRNA pools over that obtained from cells that were treated with a control siRNA (26).

As expected, compared with HEK-293T cells transfected with a control siRNA, knockdown tripartite motif protein 56 (TRIM56; reduced mRNA levels to 37.2% compared to control cells) increased Rluc activity ~1.62-fold (Fig. 5A). In addition, we showed that knockdown double-stranded RNA-activated protein kinase (PKR) or DEAD-box RNA helicases (DDX3X) could significantly enhance Rluc activity, indicating that PKR and DDX3X are potential anti-HCoV-OC43 host factors (Fig. 5A). Moreover, the cell viability assay showed no significant differences between cells transfected with host factor siRNA pools and control cells transfected with scrambled siRNA and efficiency of RNAi-mediated knockdown was assessed using quantitative RT-PCR (Fig. 5B), demonstrating that the validity of these host factors on the replication of the HCoV-OC43.

394

395

396

397

398

399

400

401

402

403

404

405

406

407

408

409

410

411

412

413

414

Validation of PKR and DDX3X as antiviral factors in HCoV-OC43 replication. PKR is the strongest antiviral host factor identified in the primary siRNA screening assay. To further validate the antiviral role of PKR in HCoV-OC43 replication, Huh7 cells were infected with HCoV-OC43-WT at a MOI of 0.05. Cell pellets were collected at 2, 4, 8, 12 and 24 hpi, respectively. As shown in Fig. 6A, cells infected with HCoV-OC43-WT strongly induced PKR activation at 8 and 12 hpi, which decreased dramatically after 24 hpi. This observation was supported by the detection of phosphorylation of eIF2α, the substrate of phosphorylated PKR, showing high basal levels at 8 and 12 hpi and becoming barely detectable at 24 h (Fig. 6A). These results suggested that phosphorylation of PKR and eIF2α were increased at the early stage of infection, but quickly suppressed at 24 hpi. To determine the role of PKR in HCoV-OC43 replication, Huh7 cells were transfected with PKR-specific siRNAs to knockdown PKR or non-targeting siRNA as a negative control. The results showed that two siRNAs (PKR #2 and PKR#3) efficiently reduced endogenous PKR levels compared to control cells (Fig. 6B). The reduction of endogenous PKR (PKR #2 and PKR#3) resulted in an obvious increase in both HCoV-OC43-WT and rOC43-ns2DelRluc replication with a 1.83-fold increase in Rluc activity or virus titer (Fig. 6C and 6D), indicating that PKR plays an antiviral role in HCoV-OC43-infected cells. The observation of rapid dephosphorylation of eIF-2α in HCoV-OC43-infected cells prompted us to examine the expression of GADD34, which is a component of the protein phosphatase 1 (PP1) complex that dephosphorylates eIF- $2\alpha$ . The mRNA level of GADD34 showed a 5-fold increase in HCoV-OC43-infected Huh7 cells at 24

416

417

418

419

420

421

422

423

424

425

426

427

428

429

430

431

432

433

434

435

436

hpi which served as a feedback loop to mediate eIF-2α dephosphorylation at the corresponding time point (Fig. 6E). Interestingly, we also detected a 1.7-fold induction of the GADD34 mRNA level at 2 hpi, this slight increase of GADD34 mRNA level may play an important role in facilitating HCoV-OC43 replication during its invasion period. Okadaic acid (OA) was defined as a protein phosphatase inhibitor, promoting PKR and eIF2α phosphorylation. To further confirm the effect of PP1 activity on HCoV-OC43 replication, cells were incubated in the presence of OA or DMSO followed by infected with HCoV-OC43-WT or rOC43-ns2DelRluc, respectively. As shown in Fig. 7F, in contrast to DMSO-untreated Huh7 cells, in the presence of different concentrations of OA, the Rluc activity of rOC43-ns2DelRluc was significantly decreased at concentrations of 4 nM, with 10-fold inhibition observed at concentrations of 108 nM. This result was further confirmed by the HCoV-OC43-WT, with obviously reduced virus titers (~11-fold) at concentrations of 108 nM (Fig. 6G). Taken together, these results indicated that PKR and eIF2α phosphorylation induce an antiviral effect in HCoV-OC43-infected cells, and this inhibition was blocked by HCoV-OC43-induced GADD34 expression. DDX3X is another potent antiviral host factor identified in the siRNA screening assay. Human DDX3X is a newly discovered DEAD-box RNA helicase. In addition to its involvement in protein translation, cell cycle, apoptosis, nuclear export and eukaryotic gene regulation, human DDX3X is a critical molecule in innate immune signaling pathways and contributes to type I interferon (IFN) induction. A previous

report showed that DDX3X is upregulated upon DENV or PRRSV infection (27, 28).

438

439

440

441

442

443

444

445

446

447

448

449

450

451

452

453

454

455

456

457

458

DDX3X protein levels in Huh7 cells upon HCoV-OC43-WT infection (Fig. 7A). This result was further confirmed by semi-quantitative PCR in HCoV-OC43-WT-infected Huh7 or HEK-293T cells (data not shown). A previous study demonstrated that coexpression of TBK1 with DDX3X rather than overexpression of DDX3X itself led to IFN promoter activation because overexpression of TBK1 causes DDX3X activation (29). Our result showed that silencing of endogenous DDX3X expression using RNAi would significantly affect the transcription level of IFN-β; however, overexpression of DDX3X alone activated the IFN promoter only 2-fold (Fig. 7C and 7D). Moreover, the result showed that the Rluc activity of rOC43-ns2DelRluc or virus titers of HCoV-OC43-WT increased by 1.7-fold in DDX3X-silenced cells (DDX3X #1 or DDX3X #3) compared with control cells at 72 hpi (Fig. 7F and 7G). Furthermore, we performed an overexpression assay and demonstrated that overexpression of DDX3X showed antiviral activity against HCoV-OC43 infection (Fig. 7E). Thus, DDX3X may play an antiviral role during HCoV-OC43 infection through positive regulation of innate immune-signaling processes. These data demonstrated the feasibility of using rOC43-ns2DelRluc for drug

However, contrary to our expectations, Western blotting showed no change in

Discussion

screening and identifying antiviral host factors.

Rapid identification of therapeutics is a high priority as there is currently no specific therapy to treat novel Betacoronavirus (SARS-CoV and MERS-CoV)

460

461

462

463

464

465

466

467

468

469

470

471

472

473

474

475

476

477

478

479

480

with

results

obtained by

the

two

Rluc-fusion reporter viruses

Downloaded from http://aac.asm.org/ on September 6, 2016 by INRS-Institut Armand-Frappie

infections, which can cause high case-fatality rates (30). A marker virus with the introduction of a reporter gene into the viral genome provides a powerful tool to address this problem. To date, only one reporter HCoV (SARS-CoV-GFP) has been generated and applied to siRNA library screening assay (14). However, the SARS-CoV-GFP lacks sensitivity, as it requires a high infectious dose (MOI of 10) for quantitative screening. Moreover, this reporter virus assay must be performed in a BSL-3 facility, which is costly and labor-intensive. Thus, the generation of a safe and sensitive reporter HCoV for HTS assays is urgent. Here, we reported a sensitive antiviral screening platform based on recombinant HCoV-OC43 (rOC43-ns2DelRluc) that expresses Rluc as a reporter gene. Furthermore, using a luciferase-based siRNA screening assay, we identified two host factors (PKR and DDX3X) that exhibit antiviral effects. HCoV-OC43 encodes two accessory genes, ns2 and ns12.9; however, the biological functions of these HCoV-OC43 accessory genes remain poorly understood. In this study, we generated a variety of luciferase-based rHCoVs-OC43 by genetic engineering of the two accessory genes. Among the rHCoVs-OC43, rOC43-ns12.9StopRluc led to a lower virus yield in BHK-21 cells, suggesting that the ion channel activity of ns12.9 is important for the production of infectious virions. A recent study by Freeman et al. showed that in-frame insertion of reporter gene into replicase genes (ns2 or ns3) of murine hepatitis virus (MHV) was tolerated and resulted in similar replication kinetics as MHV-WT (10). These results are consistent

482

483

484

485

486

487

488

489

490

491

492

493

494

495

496

497

498

499

500

501

502

(rOC43-ns2FusionRluc and rOC43-ns12.9FusionRluc), which showed replication kinetics similar to HCoV-OC43-WT. However, our study demonstrated that Rluc fused with the accessory genes of HCoV-OC43 was an ineffective way to generate high expressing reporter HCoV because the two Rluc-fusion reporter viruses showed impaired Rluc activity and genetic instability during passages in vitro. One reporter virus, rOC43-ns2DelRluc, had similar replication kinetics to the parent virus HCoV-OC43-WT, showing robust Rluc activity during infection of BHK-21 cells. Moreover, deletion of the ns2 gene had no influence on the pathogenicity of rOC43-ns2DelRluc in mice and the inserted Rluc gene remained stable both in vitro and in vivo. Thus, rOC43-ns2DelRluc might be a superior reporter virus for screening antivirals in terms of growth characteristics, Rluc expression levels and genetic stability. Recently, a library of FDA-approved drugs used for anti-MERS-CoV screening in cell culture successfully identified four potent inhibitors. Intriguingly, all the screened compounds were broad-spectrum anti-HCoVs drugs that also inhibited the replication of SARS-CoV and HCoV-229E (31). However, the traditional CPE-based viral titration assays were ill-suited for HTS assays as more and more novel antiviral drugs are developed every year. Thus, rOC43-ns2DelRluc would provide a powerful tool for rapid and quantitative screening of broad-spectrum anti-HCoVs drugs. Chloroquine, a clinically approved drug, appeared to be a broad-spectrum CoVs drug, as it blocks the replication of SARS-CoV, HCoV-OC43, MERS-CoV and HCV-229E

in vitro (32, 33). Additionally, clinical experience gained from treating SARS and

504

505

506

507

508

509

510

511

512

513

514

515

516

517

518

519

520

521

522

523

524

(PKR and DDX3X).

interferon (alfacon-1), corticosteroids or a combination of these interventions (34, 35). In our study, rOC43-ns2DelRluc was used to evaluate the antiviral activity of chloroquine and ribavirin in 96-well plates. rOC43-ns2DelRluc with deletion of the ns2 gene showed no impairment in response to drugs treatment compared with HCoV-OC43-WT, showing a similar decrease in viral copy numbers in the presence of increasing concentrations of chloroquine or ribavirin (Fig. 4A and 4B). Moreover, Rluc activity of rOC43-ns2DelRluc was reduced in the presence of increasing levels of chloroquine or ribavirin in a dose-dependent manner, with IC<sub>50</sub> values similar to those with HCoV-OC43-WT. It is worth mentioning that in our study, we demonstrated that ribavirin exhibited inhibitory effect against HCoV-OC43 only at high concentrations and showed a significant cytotoxicity in BHK-21 cells. These data suggest that rOC43-ns2DelRluc represents a superior model for screening broad-spectrum HCoV drugs without the requirement of BSL-3 confinement. In the past decade, reporter viruses have been used widely for screening pooled RNAi to discover host factors that can influence the replication of diverse +RNA viruses. Such reporter viruses have allowed sensitive and quantitative evaluation of antiviral or proviral effects (36–40). However, few host factors have been identified that can restrict the replication of CoV. Here, eight potential antiviral host factors in flavivirus infection were selected for RNAi screening using the reporter rOC43-ns2DelRluc, leading to the identification of two anti-HCoV-OC43 host factors

MERS suggested the effectiveness of a number of interventions including ribavirin,

526

527

528

529

530

531

532

533

534

535

536

537

538

539

540

541

542

543

544

545

546

Many viral families have evolved various regulatory mechanisms that modulate host protein synthesis to maximize the production of progeny viruses. In CoV IBV infection, overexpression of a dominant negative kinase-defective PKR mutant enhanced IBV replication by almost 2-fold (41). In this study, we showed that the basal level of phosphorylated PKR and eIF- $2\alpha$  was unregulated in cells infected with HCoV-OC43 at the early stage of infection. Intriguingly, phosphorylated eIF-2α decreased rapidly via induction of GADD34 expression. Upregulation of eIF-2a phosphorylation using OA significantly reduced HCoV-OC43 replication. These results indicated that PKR plays an antiviral role in HCoV-OC43-infected cells. DDX3X, an alias for DDX3 represented on the X chromosome, belongs to the DEAD-box family of ATP-dependent RNA helicases. It is a multiple-function protein

involved in protein translation, cell cycle, apoptosis, nuclear export, translation and assembly of stress granules. There is growing evidence that DDX3X is a component of the innate immune response against viral infections (42). In our study, using RNA interference and overexpression approach, we first described the antiviral role of DDX3X during HCoV-OC43 infection via regulation of the type I IFN pathway. Other studies have suggested that DDX3X is an important host factor required for HCV and HIV infection (43, 44). The core protein of HCV interacts with DDX3X to manipulate splicing and regulation of transcription or translation, and the helicase activity of DDX3X was required for HIV RNA export. Therefore, DDX3X plays distinct roles in virus-specific situations.

Downloaded from http://aac.asm.org/ on September 6, 2016 by INRS-Institut Armand-Frappie

In summary, we generated a robust and stable luciferase-based recombinant

HCoV-OC43 by replacement of the ns2 gene. This reporter virus can be used for 547 screening anti-HCoVs drugs and host factors. To the best of our knowledge, this is the 548 first construction of a luciferase-based HCoV-OC43 for quantitative antiviral assays. 549 The reporter virus will contribute to future work focused on screening wide-spectrum 550 551 drugs or host factors influencing HCoV replication. 552 Acknowledgments 553 This work was supported by grants from the Megaproject for Infectious Disease 554

Research of China (2014ZX10004001, 2013ZX10004601). The funders had no role in 555 556 study design, data collection and analysis, decision to publish, or preparation of the 557 manuscript.

Downloaded from http://aac.asm.org/ on September 6, 2016 by INRS-Institut Armand-Frappier

558

559

## **Competing Interests**

The authors have declared that no competing interests exist. 560

561

562

### References

- 1. Adams MJ, Lefkowitz EJ, King AM, Carstens EB. 2014. Ratification vote on 563 taxonomic proposals to the International Committee on Taxonomy of Viruses. 564
- 565 Arch Virol 159:2831-2841.
- 2. Perlman S, Netland J. 2009. Coronaviruses post-SARS: update on replication 566 567 and pathogenesis. Nat Rev Microbiol 7:439-450.
- 3. Gralinski LE, Baric RS. 2015. Molecular pathology of emerging coronavirus 568

4. Desforges M, Le Coupanec A, Stodola JK, Meessen-Pinard M, Talbot PJ. 570

infections. J Pathol 235:185-195.

569

- 571 2014. Human coronaviruses: viral and cellular factors involved in
- neuroinvasiveness and neuropathogenesis. Virus Res 194:145-158. 572
- 5. de Haan CA, Haijema BJ, Boss D, Heuts FW, Rottier PJ. 2005. Coronaviruses 573
- 574 as vectors: stability of foreign gene expression. J Virol 79:12742–12751.
- 6. Stirrups K, Shaw K, Evans S, Dalton K, Casais R, Cavanagh D, Britton P. 575
- 2000. Expression of reporter genes from the defective RNA CD-61 of the 576
- coronavirus infectious bronchitis virus. J Gen Virol 81:1687-1698. 577
- 7. Shen H, Fang SG, Chen B, Chen G, Tay FP, Liu DX. 2009. Towards 578
- construction of viral vectors based on avian coronavirus infectious bronchitis virus 579

- 580 for gene delivery and vaccine development. J Virol Methods 160:48–56.
- 8. Bosch BJ, de Haan CA, Rottier PJ. 2004. Coronavirus spike glycoprotein, 581
- extended at the carboxy terminus with green fluorescent protein, is assembly 582
- competent. J Virol 78:7369-7378. 583
- 9. Becares M, Sanchez CM, Sola I, Enjuanes L, Zuñiga S. 2014. Antigenic 584
- structures stably expressed by recombinant TGEV-derived vectors. Virology. 585
- 586 **464-465:**274-286.
- 587 10. Freeman MC, Graham RL, Lu X, Peek CT, Denison MR. 2014. Coronavirus
- replicase-reporter fusions provide quantitative analysis of replication and 588
- 589 replication complex formation. J Virol 88:5319–5327.

611

**78:**8824-8834.

590 11. Roberts RS, Yount BL, Sims AC, Baker S, Baric RS. 2006. Renilla luciferase as a reporter to assess SARS-CoV mRNA transcription regulation and efficacy of 591 anti-SARS-CoV agents. Adv Exp Med Biol 581:597-600. 592 12. Zhao G, Du L, Ma C, Li Y, Li L, Poon VK, Wang L, Yu F, Zheng BJ, Jiang S, 593 **Zhou Y.** 2013. A safe and convenient pseudovirus-based inhibition assay to detect 594 595 neutralizing antibodies and screen for viral entry inhibitors against the novel human coronavirus MERS-CoV. Virol J 10:266. 596 13. Cao J, Forrest JC, Zhang X. 2015. A screen of the NIH Clinical Collection 597 small molecule library identifies potential anti-coronavirus drugs. Antiviral Res 598 599 **114:**1-10. 14. de Wilde AH, Wannee KF, Scholte FE, Goeman JJ, Ten Dijke P, Snijder EJ, 600 601 Kikkert M, van Hemert MJ. 2015. A Kinome-Wide Small Interfering RNA Screen Identifies Proviral and Antiviral Host Factors in Severe Acute Respiratory 602 Syndrome Coronavirus Replication, Including Double-Stranded RNA-Activated 603 604 Protein Kinase and Early Secretory Pathway Proteins. J Virol 89: 8318–8333. 15. McIntosh K, Becker WB, Chanock RM. 1967. Growth in suckling-mouse brain 605 of "IBV-like" viruses from patients with upper respiratory tract disease. Proc Natl 606 607 Acad Sci U S A 58:2268–2273. 608 16. St-Jean JR, Jacomy H, Desforges M, Vabret A, Freymuth F, Talbot PJ. 2004. Human respiratory coronavirus OC43: genetic stability and neuroinvasion. J Virol 609

17. Wang F, Chen C, Tan W, Yang K, Yang H. 2016. Structure of Main Protease

- from Human Coronavirus NL63: Insights for Wide Spectrum Anti-Coronavirus
- 613 Drug Design. Sci Rep **6:**22677.
- 18. Keyaerts E, Li S, Vijgen L, Rysman E, Verbeeck J, Van Ranst M, Maes P.
- 615 2009. Antiviral activity of chloroquine against human coronavirus OC43 infection
- in newborn mice. Antimicrob Agents Chemother **53:**3416–3421.
- 19. Jacomy H, Fragoso G, Almazan G, Mushynski WE, Talbot PJ. 2006. Human
- coronavirus OC43 infection induces chronic encephalitis leading to disabilities in
- 619 BALB/C mice. Virology **349:**335–346.
- **20. Mounir S., Labonte P. & Talbot P. J.** 1993. Characterization of the nonstructural
- and spike proteins of the human respiratory coronavirus OC43: comparison with
- bovine enteric coronavirus. Adv Exp Med Biol **342:**61–67.
- 623 **21. Zhang R, Wang K, Ping X, Yu W, Qian Z, Xiong S, Sun B.** 2015. The ns12.9
- accessory protein of human coronavirus OC43 is a viroporin involved in virion
- morphogenesis and pathogenesis. J Virol **89:**11383–11395.
- 626 22. St-Jean JR, Desforges M, Almazán F, Jacomy H, Enjuanes L, Talbot PJ. 2006.
- Recovery of a neurovirulent human coronavirus OC43 from an infectious cDNA
- 628 clone. J Virol **80:**3670–3674.
- **23. Reed LJ, Münch HA.** 1938. Simple method of estimating fifty percent endpoints.
- 630 Am J Hyg **27:**493–497.
- 631 24. Hu Q, Lu R, Peng K, Duan X, Wang Y, Zhao Y, Wang W, Lou Y, Tan W. 2014.
- Prevalence and genetic diversity analysis of human coronavirus OC43 among
- adult patients with acute respiratory infections in Beijing. PLoS One 9:e100781.

- 634 25. Liu B, Li NL, Wang J, Shi PY, Wang T, Miller MA, Li K. 2014. Overlapping
- and distinct molecular determinants dictating the antiviral activities of TRIM56 635
- against flaviviruses and coronavirus. J Virol 88:13821-13835. 636
- 26. Jiang D, Weidner JM, Qing M, Pan XB, Guo H, Xu C, Zhang X, Birk A, 637
- Chang J, Shi PY, Block TM, Guo JT. 2010. Identification of five 638
- 639 interferon-induced cellular proteins that inhibit west nile virus and dengue virus
- infections. J Virol 84:8332-8341. 640
- 27. Li G, Feng T, Pan W, Shi X, Dai J. 2015. DEAD-box RNA helicase DDX3X 641
- inhibits DENV replication via regulating type one interferon pathway. Biochem 642
- 643 Biophys Res Commun **456:**327–332.
- 28. Chen Q, Liu Q, Liu D, Wang D, Chen H, Xiao S, Fang L. 2013. Molecular 644
- 645 cloning, functional characterization and antiviral activity of porcine DDX3X.
- Biochem Biophys Res Commun 443:1169-1175. 646
- 29. Soulat D, Bürckstümmer T, Westermayer S, Goncalves A, Bauch A, 647
- Stefanovic A, Hantschel O, Bennett KL, Decker T, Superti-Furga G. 2008. 648
- The DEAD-box helicase DDX3X is a critical component of the TANK-binding 649
- kinase 1-dependent innate immune response. EMBO J 27:2135–2146. 650
- 30. Falzarano D, de Wit E, Martellaro C, Callison J, Munster VJ, Feldmann H. 651
- 652 2013. Inhibition of novel β coronavirus replication by a combination of
- interferon-α2b and ribavirin. Sci Rep 3:1686. 653
- 654 31. de Wilde AH, Jochmans D, Posthuma CC, Zevenhoven-Dobbe JC, van
- Nieuwkoop S, Bestebroer TM, van den Hoogen BG, Neyts J, Snijder EJ. 2014. 655

- 656 Screening of an FDA-approved compound library identifies four small-molecule
- inhibitors of Middle East respiratory syndrome coronavirus replication in cell 657
- culture. Antimicrob Agents Chemother 58:4875-4884. 658
- 32. Keyaerts E, Vijgen L, Maes P, Neyts J, Van Ranst M. 2004. In vitro inhibition 659
- 660 of severe acute respiratory syndrome coronavirus by chloroquine. Biochem
- 661 Biophys Res Commun 323:264–268.
- 33. Kono M, Tatsumi K, Imai AM, Saito K, Kuriyama T, Shirasawa H. 2008. 662
- Inhibition of human coronavirus 229E infection in human epithelial lung cells 663
- (L132) by chloroquine: involvement of p38 MAPK and ERK. Antiviral Res 664
- 77:150-152. 665
- 34. Gross AE, Bryson ML. 2015. Oral Ribavirin for the Treatment of Noninfluenza 666
- 667 Respiratory Viral Infections: A Systematic Review. Ann Pharmacother 49:1125-
- 1135. 668
- 35. Groneberg DA, Poutanen SM, Low DE, Lode H, Welte T, Zabel P. 2005. 669
- 670 Treatment and vaccines for severe acute respiratory syndrome. Lancet Infect Dis
- **5:**147–155. 671
- 36. Karlas A, Machuy N, Shin Y, Pleissner KP, Artarini A, Heuer D, Becker D, 672
  - Khalil H, Ogilvie LA, Hess S, Mäurer AP, Müller E, Wolff T, Rudel T, Meyer 673
- 674 TF. 2010. Genome-wide RNAi screen identifies human host factors crucial for
- influenza virus replication. Nature 463:818-822. 675
- 676 37. Hao L, Sakurai A, Watanabe T, Sorensen E, Nidom CA, Newton MA,
- Ahlquist P, Kawaoka Y. 2008. Drosophila RNAi screen identifies host genes 677

- 678 important for influenza virus replication. Nature 454:890–893.
- 38. Zhou H, Xu M, Huang Q, Gates AT, Zhang XD, Castle JC, Stec E, Ferrer M, 679
- Strulovici B, Hazuda DJ, Espeseth AS. 2008. Genome-scale RNAi screen for 680
- host factors required for HIV replication. Cell Host Microbe 4:495-504. 681
- 39. Krishnan MN, Ng A, Sukumaran B, Gilfoy FD, Uchil PD, Sultana H, Brass 682
- 683 AL, Adametz R, Tsui M, Qian F, Montgomery RR, Lev S, Mason PW, Koski
- RA, Elledge SJ, Xavier RJ, Agaisse H, Fikrig E. 2008. RNA interference screen 684
- 685 for human genes associated with West Nile virus infection. Nature 455:242–245.
- 40. Sessions OM, Barrows NJ, Souza-Neto JA, Robinson TJ, Hershey CL, 686
- Rodgers MA, Ramirez JL, Dimopoulos G, Yang PL, Pearson JL, 687
- Garcia-Blanco MA. 2009. Discovery of insect and human dengue virus host 688

- 689 factors. Nature 458:1047-1050.
- 41. Wang X, Liao Y, Yap PL, Png KJ, Tam JP, Liu DX. 2009. Inhibition of protein 690
- kinase R activation and upregulation of GADD34 expression play a synergistic 691
- role in facilitating coronavirus replication by maintaining de novo protein 692
- synthesis in virus-infected cells. J Virol 83:12462-12472. 693
- 42. Schröder M, Baran M, Bowie AG. 2008. Viral targeting of DEAD box protein 3 694
  - 695 reveals its role in TBK1/IKKepsilon-mediated IRF activation. EMBO J 27:2147-
  - 43. Pène V, Li Q, Sodroski C, Hsu CS, Liang TJ. 2015. Dynamic Interaction of
  - Stress Granules, DDX3X, and IKK-α Mediates Multiple Functions in Hepatitis C
- Virus Infection. J Virol 89:5462-5477.

709

710

711

712

713

714

715

716

717

718

719

720

721

44. Yedavalli VS, Neuveut C, Chi YH, Kleiman L, Jeang KT. 2004. Requirement 700 701 of DDX3 DEAD box RNA helicase for HIV-1 Rev-RRE export function. Cell 702 119:381-392. 703 704 705 Figure legends 706 Fig. 1. Development of human coronaviruses-OC43 (HCoV-OC43) reporter 707

systems. Schematic representation of the cDNA clone pBAC-OC43<sup>FL</sup> and recombinant cDNA clones of HCoV-OC43 harboring the Renilla luciferase (Rluc) gene, which was introduced into the accessory genes by overlapping polymerase chain reaction (PCR) as described in the Materials and methods. The Rluc gene (green) is depicted. Expanded regions show the transcription regulatory sequence (TRS) control of Rluc gene expression.

The N protein of recombinant HCoVs-OC43 (rHCoVs) examined by indirect immunofluorescence assay (IFA). At 72 h postinfection, virus-infected BHK-21 cells were incubated with anti-OC43-N mouse polyclonal antibodies and then stained with fluorescein isothiocyanate (FITC)-labeled goat anti-mouse IgG. Cells were analyzed under a fluorescence microscope. (B) Growth kinetics of rHCoVs. BHK-21 cells were infected with rHCoVs and HCoV-OC43-WT at a multiplicity of infection (MOI) of

Fig. 2. Characterization of reporter viruses using engineered accessary genes. (A)

723

724

725

726

727

728

729

730

731

732

733

734

735

736

737

738

739

740

741

742

743

0.01. Viral titers from culture supernatants at the indicated time points were determined by indirect IFA. Data represent three independent experiments and are shown as means ± standard deviation. (C) Complementation of rOC43-ns2DelRluc infection in BHK-21 cells expressing ns2. Cells were transfected with a plasmid expressing ns2-EGFP or a control vector using the X-tremeGENE HP DNA Transfection Reagent, and the expression levels of ns2-EGFP were analyzed by Western blot using anti-GFP antibody (left). After 24 h post-transfection, BHK-21 cells were infected with HCoV-OC43-WT or rOC43-ns2DelRluc at an MOI of 0.01. Cell supernatants were collected at 72 h post-infection, and the viral titers were determined by IFA (right). (D) Time-course analysis of the reporter gene expression. The Rluc activity represented as relative light units (RLU) was measured in BHK-21 cells infected with rHCoVs at the indicated time points (MOI = 0.01). Data represent three independent experiments and are shown as means  $\pm$  standard deviation. (E and F) Western blot analysis of reporter gene expression. Proteins in cell lysates of BHK-21 cells infected with rHCoVs and HCoV-OC43-WT were analyzed by Western blot using anti-OC43-N, anti-Rluc and anti-β-actin antibodies. Cell lysates from uninfected cells (Mock) served as a negative control. (G) The effect of inserted reporter gene on subgenomic (sg) RNA synthesis. 72 h post-infection (MOI = 0.01), total cellular mRNAs were extracted and subjected to RT-PCR to determine the mRNA level of ns2 (HCoV-OC43-WT), Rluc (rOC43-ns2DelRluc and rOC43-ns12.9StopRluc), ns2-Rluc (rOC43-ns2FusionRluc) and (rOC43-ns12.9FusionRluc). HCoV-OC43-WT was used as control. Data were

normalized to the levels of internal mouse GAPDH mRNA. Error bars indicate means and standard deviations of three independent experiments.

746

747

748

749

750

751

752

753

754

755

756

757

758

759

760

761

762

763

744

745

Fig. 3. Analysis of genetic stability of the reporter viruses. (A) Illustration of the virus passage procedure in BHK-21 cells. rHCoVs rescued from transfected cells were defined as P0. Culture supernatants from the transfected cells (P0) were added to näive cells to obtain passage 1 virus (P1). After 13 rounds of serial passages, the reporter viruses were passaged to P13. (B) Viral titers of reporter viruses during passages. Reporter viruses were passaged 13 times in BHK-21 cells, and the supernatants were collected from the virus-infected cells of each passage and titrated using the IFA-based viral titration assay. Data represent three independent experiments and are shown as means ± standard deviation. (C) Rluc activity of reporter viruses of each passage. BHK-21 cells were infected with reporter viruses (MOI = 0.01) of each passage in 48-well plates and assayed for the Rluc activity in RLUs at 72 h post-infection. Data represent mean values of three independent experiments with error bars representing the standard deviations of the means. (D) Analysis of genetic stability of the reporter viruses after several passages in BHK-21 cells. Viral RNA was extracted from culture supernatants of each passage, and RT-PCR was performed with a primer set flanking the Rluc gene. The resulting RT-PCR products were resolved by 1% agarose gel electrophoresis.

Downloaded from http://aac.asm.org/ on September 6, 2016 by INRS-Institut Armand-Frappie

764

765

Fig. 4. Replication of HCoV-OC43 in response to drugs treatment in BHK-21

767

768

769

770

771

772

773

774

775

776

777

778

779

780

781

782

783

784

785

786

cells. (A and B) Effect of chloroquine or ribavirin on the replication of HCoV-OC43-WT or rOC43-ns2DelRluc. BHK-21 cells seeded in 48-well plates were infected with HCoV-OC43-WT or rOC43-ns2DelRluc at an MOI of 0.01 for 2 h and subsequently treated with chloroquine or ribavirin at the indicated concentrations. At 72 h post-infection, supernatants were removed and subsequently analyzed for viral load by real time quantitative RT-PCR. Error bars indicate means and standard deviations of three independent experiments. (C and D) Chloroquine or ribavirin inhibition of Rluc activity of rOC43-ns2DelRluc and cell cytotoxic effects. The inhibition assay was performed as described in the Materials and methods. Rluc activity of chloroquine- or ribavirin-treated cells was normalized to dimethyl sulfoxide (DMSO)-treated control cells and measured relative to DMSO-treated cells. Viable cell numbers were used to determine the percentage cytotoxic effect in drug-treated cells relative to DMSO-treated cells. Error bars indicate means and standard deviations of three independent experiments. (E and F) The antiviral effect of chloroquine or ribavirin on HCoV-OC43-WT N protein synthesis.

Downloaded from http://aac.asm.org/ on September 6, 2016 by INRS-Institut Armand-Frappie

Fig. 5. Screening of host factors influencing HCoV-OC43 replication using rOC43-ns2DelRluc. (A) HEK-293T cells were transfected with various small interfering RNA (siRNA) pools, followed by infection with rOC43-ns2DelRluc at an MOI of 0.01 in 48-well plates, and assayed for Rluc activity. The relative luciferase activity (RLA) represents the mean  $\pm$  the standard deviation (n = 3) of the ratio of

relative light units (RLUs) obtained from cells treated with targeting siRNAs to the 787

RLUs obtained from cells that were treated with a nontargeting siRNA (siControl), which had no adverse effect on the viruses and cells. (B) Real-time RT-PCR was used to quantitate the knockdown effect of the indicated siRNA pools at 36 h post-transfection (gray bars) and the effect of siRNA transfection on cell viability was analyzed in parallel (black bars), and values were normalized to those of nontargeting siRNA-transfected cells (100%). Error bars indicate means and standard deviations of three independent experiments. \*, P < 0.05; \*\*, P < 0.01.

795

796

797

798

799

800

801

802

803

804

805

806

807

808

809

788

789

790

791

792

793

794

Fig. 6. Validation of PKR as an antiviral factor in HCoV-OC43 replication. (A) HCoV-OC43 infection induced the phosphorylation of PKR and eIF2α. Huh7 cells were infected with HCoV-OC43 or mock infected at an MOI of 0.05 and harvested at 2, 4, 8, 12 and 24 hpi. The cell lysates were collected and analyzed by Western blot with anti-PKR, anti-p-PKR, anti-eIF2α, and anti-p-eIF2α (S51) antibodies. β-actin was used as a protein loading control. (B) Knockdown of PKR expression at 48 h post transfection. (C and D) Knockdown PKR induced the replication of HCoV-OC43 in Huh7 cells. The Rluc activity of rOC43-ns2DelRluc and titers of HCoV-OC43-WT were determined at 72 hpi. Data represent three independent experiments and are shown as means ± standard deviation. (E) Induction of GADD34 expression in HCoV-OC43-infected Huh7 cells at 12 h post infection. (F and G) Reduction of HCoV-OC43 replication by inhibition of PP1 activity with okadaic acid (OA) in HCoV-OC43-infected Huh7 cells. Huh7 cells were treated with OA or DMSO after infected with rOC43-ns2DelRluc or HCoV-OC43-WT. The Rluc activity of

rOC43-ns2DelRluc and titers of HCoV-OC43-WT were determined at 72 hpi. Data represent three independent experiments and are shown as means  $\pm$  standard deviation. \*, P < 0.05; \*\*, P < 0.01.

813

814

815

816

817

818

819

820

821

822

823

824

825

826

827

828

829

830

831

810

811

812

Fig. 7. Validation of DDX3X as an antiviral factor in HCoV-OC43 replication. (A)

The expression level of DDX3X was unchanged in HCoV-OC43-infected Huh7 cells. Huh7 cells were infected with HCoV-OC43 or mock infected at an MOI of 0.05 and harvested at 2, 4, 8, 12 and 24 hpi. Cell lysates were collected and analyzed by Western blot with anti-DDX3X antibody. β-actin was used as a protein loading control. (B and C) DDX3X is required for IFN-β induction. siRNA-treated HEK-293T cells were infected with Sendai virus (Sev). Induction of IFN-β mRNA was measured by semi-quantitative PCR. (D) Overexpression of DDX3X alone was insufficient to activate the IFN promoter. HEK-293T cells were transfected with 500 ng of plasmids encoding DDX3X or TBKI, co-transfected with plasmids TBK1 (500 ng) and DDX3X (100 or 300 ng), together with 500 ng of IFN-β-Luc reporter plasmid and an internal control plasmid pRL-TK (20 ng) as indicated. (E) Overexpression of DDX3X showed weak antiviral activity against HCoV-OC43. Huh7 cells were transfected with pFlag-DDX3X or empty vector. 24 h post-transfection, cells were infected with HCoV-OC43 an MOI of 0.05 and titers of HCoV-OC43-WT were determined at 72 hpi. (F and G) siRNA-mediated DDX3X silencing induced HCoV-OC43 replication. The Rluc activity of rOC43-ns2DelRluc and titers of HCoV-OC43-WT were determined at 72 hpi. Data represent three independent experiments and are shown as

means  $\pm$  standard deviation. \*, P < 0.05; \*\*, P < 0.01. 832

Figure 1

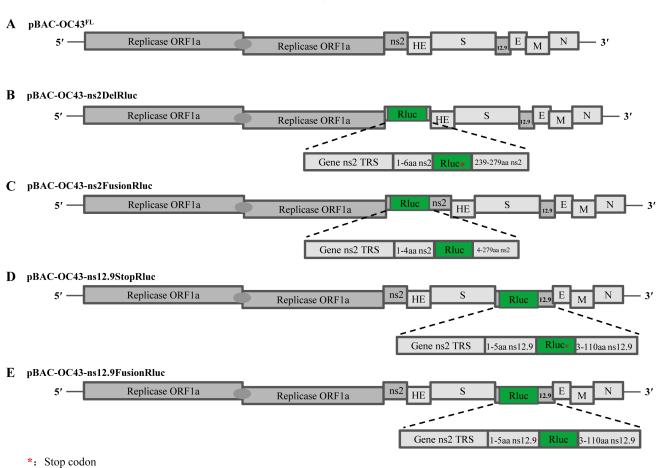
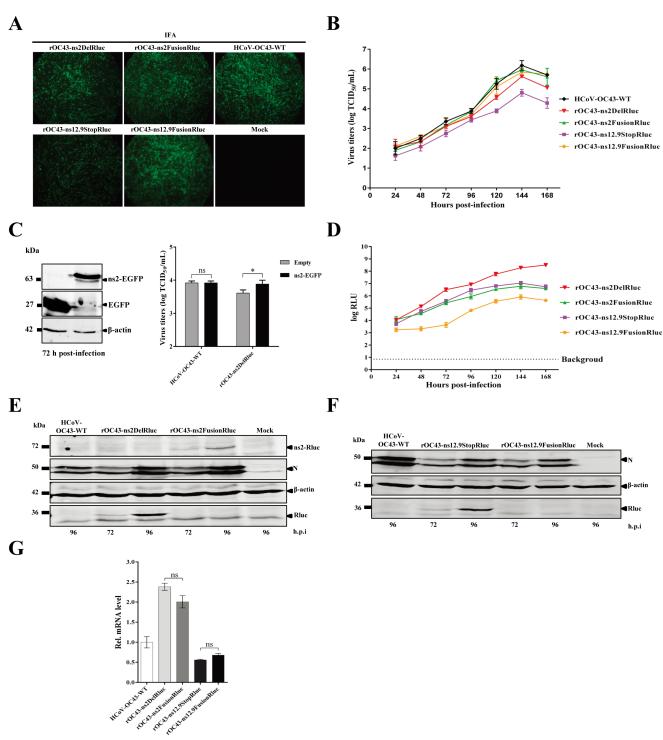


Figure 2





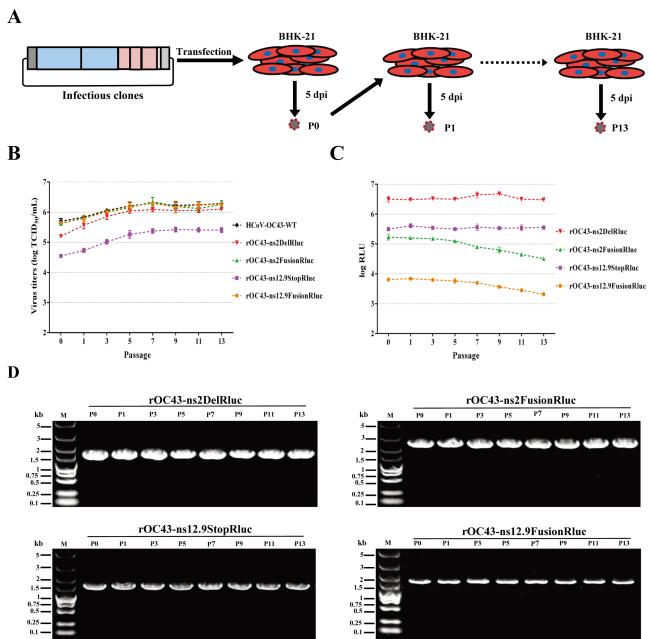


Figure 4

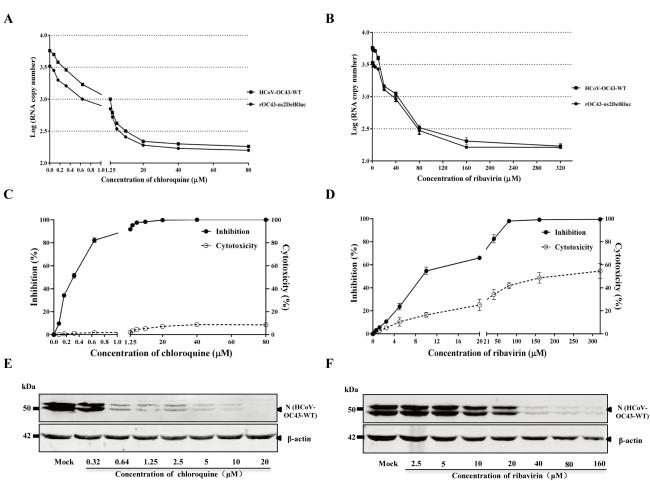
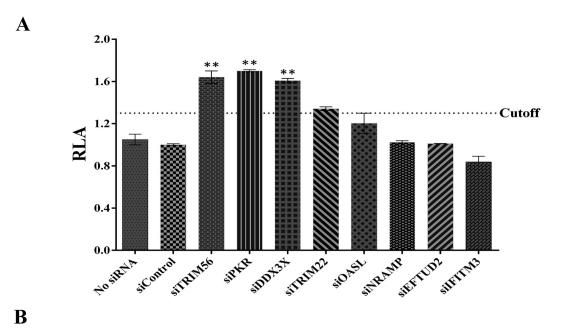
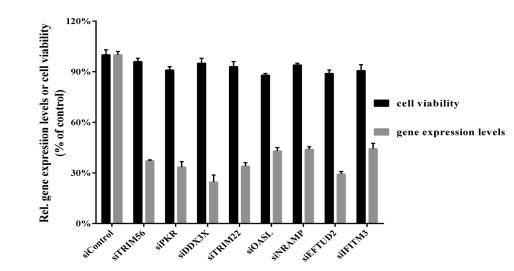


Figure 5







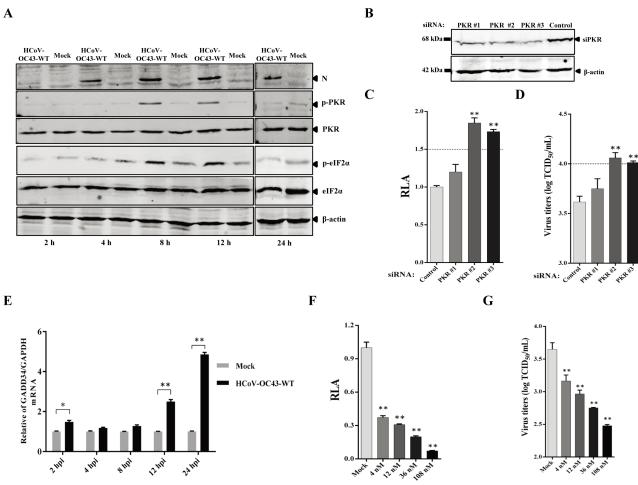


Figure 7

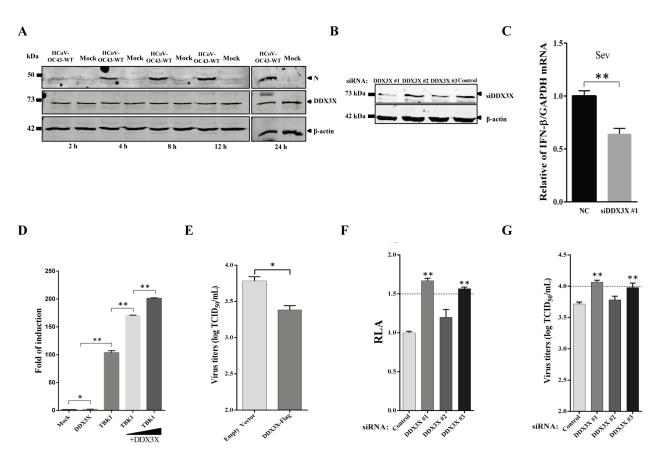


TABLE 1. Antiviral activity of chloroquine or ribavirin in BHK-21 cells

Drugs	CC <sub>50</sub> , μM	IC <sub>50</sub> , μΜ
Chloroquine	397.54	0.33
Ribavirin	156.16	10.00

Data represent mean values for three independent experiments. IC50, 50% effective concentration of chloroquine or ribavirin for the inhibition of rOC43-ns2DelRluc. CC50, 50% cytotoxic concentration of chloroquine or ribavirin for mock-infected BHK-21 cells.