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8	Construction of a recombinant rhinovirus accommodating fluorescent marker expression
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19	Abstract
20	Background: Rhinovirus (RV) causes the common cold and asthma exacerbations. The RV
21	genome is a 7.3 kb single-strand positive-sense RNA. Objective: Using minor group RV1A as a
22	backbone, we sought to design and generate a recombinant RV1A accommodating fluorescent
23	marker expression, thereby allowing tracking of viral infection. Method: Recombinant RV1A
24	infectious cDNA clones harboring the coding sequence of green fluorescent protein (GFP),
25	Renilla luciferase or iLOV (for light, oxygen or voltage sensing) were engineered and
26	constructed. The resulting recombinant RV1A-GFP and RV1A-iLOV, as well as parental virus,
27	were used for infection in vitro and in vivo. RV-infected cells were determined by flow
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28 cytometry, immunohistochemistry and immunofluorescence microscopy. Results: RV1A-GFP showed a cytopathic effect in HeLa cells but failed to express GFP or Renilla luciferase due to 29 partial-deletion. The smaller fluorescent protein construct, RV1A-iLOV, was stably expressed in 30 infected cells. RV1A-iLOV expression was used to examine the antiviral effect of bafilomycin in 31 HeLa cells. in vitro. In vivo studies showed that, Compared to parental virus, RV1A-iLOV 32 infection of BALB/c mice vielded a similar viral load and level of cytokine mRNA expression. 33 However, imaging of fixed lung tissue failed to reveal a fluorescent signal, likely due to the 34 oxidation and bleaching of iLOV-bound flavin mononucleotide. We therefore employed an anti-35 iLOV antibody for immunohistochemical and immunofluorescence imaging. The iLOV signal 36 was identified in airway epithelial cells and CD45+CD11b+ lung macrophages. Conclusions: 37 These results suggest that RV1A-iLOV is a useful molecular tool for studying RV pathogenesis. 38 The construction strategy for RV1A-iLOV could be applied to other RV serotypes. However, 39 detection of iLOV-expressing RV in fixed tissue required the use of an anti-iLOV antibody, 40 limiting the value of this construct. Key words: Picornavirus; rhinovirus; reverse genetics; 41 fluorescent tag; iLOV 42

## 43 Introduction

Rhinovirus (RV) is the most frequent viral infectious agent of the respiratory tract in
humans and is the predominant cause of the common cold<sup>1</sup>. More importantly, RV has emerged
as the most frequent pathogen associated with asthma exacerbations in infants, children and
adults<sup>2-4</sup>.

RV is placed in the *Picornaviridae* family, genus *Enterovirus*, with three species based 48 on phylogenetic sequence criteria<sup>5, 6</sup>. Clinical specimens collected from in the 1960s and 1970s 49 yielded approximately 100 different species A and B strains which were subsequently serotyped 50 <sup>7,8</sup>. More recently, a diverse group of previously unrecognized human viruses from species C 51 were found to be common causes of respiratory illness <sup>4</sup>. To understand RV pathogenesis, human 52 53 and animal models have been developed. Human studies have employed experimental infection with RV-A16<sup>9,10</sup>. Mouse studies have used RV-A1B wild-type mice<sup>11</sup> or RV-A16 in mice that 54 are transgenic for human intercellular adhesion molecule-1<sup>12</sup>. These models have been 55 particularly useful in studying RV-induced exacerbations of allergic airways disease. To detect 56 RV in the tissues, investigators have employed the monoclonal antibody R16-7<sup>9, 13, 14</sup>. This 57 antibody, originally developed by Wai-Ming Lee at the University of Wisconsin, binds to the 58

59 VP2 capsid protein of the closely related RV-A16 and RV-A1 strains <sup>6</sup>, but not to RV-A2, RV-

60 B14, or RV-A49<sup>15</sup>. Because the presence of more than 100 different RV serotypes makes it

infeasible to develop a cross-reactive antibody for RV, we sought to develop a recombinant virus
with a fluorescent marker that could be used for tracking of RV infection *in vivo*.

Similar to other picornaviruses, RV is icosahedral, non-enveloped particle which is 63 composed of 60 copies each of four capsid proteins, VP1, VP2, VP3, and the small myristoylated 64 VP4<sup>16, 17</sup>. The capsid encases a positive sense single-stranded RNA (ssRNA) genome of 65 approximately 7,200 nucleotides <sup>18</sup>. Following virus entry and genome release into the host cell 66 cytoplasm, the RV ssRNA is translated into a single polyprotein that undergoes proteolytic 67 cleavage by viral proteases  $2A^{\text{pro}}$  and  $3C^{\text{pro }8, 19, 20}$ , with the exception of the autocatalytic 68 cleavage of precursor VP0 into VP2 and VP4 in the presence of viral RNA during the assembly 69 process<sup>21</sup>. 70

RV infectious cDNA clones have been constructed and used as a molecular tool to study 71 RV viral protein function and mutation-phenotype association, as well as a vaccine vector for 72 foreign gene expression <sup>17, 22-25</sup>. In the current study, we engineered a recombinant RV1A 73 (RV1A-iLOV) with insertion of the coding sequence for iLOV (for light, oxygen or voltage 74 sensing), a small-size fluorescent marker <sup>26</sup>. RV1A-iLOV is viable and its expressed iLOV 75 protein is trackable both in vitro and in vivo, suggesting that RV1A-iLOV may be a useful tool in 76 the study of RV pathogenesis. However, detection of iLOV-expressing RV in fixed tissue 77 78 required the use of an anti-iLOV antibody, limiting the value of this construct.

79 Materials and Methods

80 *Cells and Reagents.* H1-Hela and THP-1 cells were purchased from ATCC (Manassas, VA). Plasmids pEGFP-N1 (Clontech, Mountain View, CA), pRL (Renilla luciferase; Promega, 81 82 Madison, WI) and pUC18-ilOV (GenScript, Piscataway, NJ) were used to amplify the DNA fragments of green fluorescent protein (GFP), Renilla luciferase (RL) and iLOV, respectively. 83 (For the detailed iLOV nucleotide sequence, see Supplemental Table S1.) Antibody to RV 84 VP2/VP0 was obtained from QED Biosciences (San Diego, CA). Anti-GFP Ab was purchased 85 from Thermo Fisher Scientific (Waltham, MA). A synthesized peptide fragment of iLOV 86 (CLGRNARFLQGPETD) was generated and used to generate anti-iLOV antibody (GenScript). 87 Bafilomycin was purchased from Merck Millipore (Burlington, Massachusetts). 88 Design and construction of recombinant RV1A-iLOV cDNA clone. The RV infectious 89

90 cDNA clone encoding replication-competent RV-1A, pMJ3-RV1A, was kindly provided by W. T. Jackson, University of Maryland<sup>27</sup> and served as a backbone for either GFP-, RL-, or iLOV-91 expressing viruses. GFP, RL and iLOV open reading frames (ORFs) were designed to be flanked 92 by the edited nucleotide sequences encoding the viral 2A<sup>pro</sup> cleavage site with silent mutations 93 introduced as described previously <sup>24</sup> (Figure 1A, Table S2). Respective GFP, RL, and iLOV 94 inserts were PCR amplified from existing clones using the primers listed in Table S1. The PCR 95 products, which contained Apa I restriction enzyme cleavage sites on the 5' and 3' ends were 96 digested with Apa I, ligated to pMJ3-RV1A and transformed in E. coli (DH5a, Thermo Fisher 97 Scientific). The resultant clones were sequenced to confirm the correct orientation of the inserts. 98 Generation of recombinant RV. Infectious cDNA clones encoding RV1A, RV1A-GFP, 99 RV1A-RL, and RV1A-iLOV were linearized by *Mlu I* restriction enzyme digestion. To produce 100 replication competent virus, full-length viral RNA transcripts were generated using the 101 MEGAscript T7 Transcription Kit (Thermo Fisher Scientific) and transfected into H1-HeLa cells 102 using Lipofectamine MessengerMAX (Thermo Fisher Scientific). After 48 h, cells underwent 103 three freeze-thaw cycles and were subjected to centrifugation at 12,000 rpm for supernatant 104 105 collection. The virus-containing supernatant stocks were designated as passage 0 (P0). H1-HeLa cells were subsequently used to passage the virus for subsequent in vitro virus stability and in 106 vivo studies. RV1A-GFP and RV1A-RL underwent plaque purification for insert analysis. RV 107 was concentrated and partially purified from infected HeLa cell lysates by ultrafiltration using a 108 100 kDa cut-off filter, as described <sup>11</sup>. Viral quantity was determined by plaque assay <sup>28</sup> or 109 quantitative one-step real-time polymerase chain reaction for positive-strand viral RNA using 110 RV-specific primers and probes (forward primer: 5'-GTGAAGAGCCSCRTGTGCT-3'; reverse 111 primer: 5'-GCTSCAGGGTTAAGGTTAGCC-3'; probe: 5'-FAM-112 TGAGTCCTCCGGCCCCTGAATG-TAMRA-3')<sup>29</sup>. The limit of detection for this viral copy 113 number analysis is between 0-10 copies. Presence of the GFP, RL and iLOV inserts was 114 determined using RV-specific flanking primers (forward primer: 5'-115 CATTCTGTTGTCATCACAACACA-3'; reverse primer: 5'-116 CACCTATAGTGTTTGTGCGGT-3'). iLOV insert quantity was measured by quantitative real-117 time PCR using specific primers encoding for iLOV (forward primer: 5'-118 GATTCCTGCAAGGACCAGAG-3'; reverse primer: 5'-CCGCTCTTGGTGTAGTTGAT-3'). 119 iLOV immunofluorescence of cultured cells. H1-HeLa cells were infected with RV1A-120

iLOV at a multiplicity of infection (MOI) of 0.1 for 24 h. Infected cells were then subjected to

122 fluorescent microscopy. In selected experiments, RV1A-iLOV-infected cells were fixed and

stained with Alexa Fluor 555–conjugated mouse anti-RV VP2/VP0 (clone R16-7; QED

124 Bioscience). Images were visualized using an Olympus IX71inverted phase/epifluorescence

125 microscope and digital CCD camera.

126 Animals and RV infection. Animal usage followed guidelines set forth in the Principles of 127 Laboratory Animal Care from the National Society for Medical Research. Six day-old or 8-10 128 week-old BALB/c mice (Jackson Laboratories, Bar Harbor, ME) were treated intranasally with 129 15 or 50  $\mu$ l of 10<sup>8</sup> plaque forming units of virus and harvested 24 h later.

130 Histology, immunohistochemistry and immunofluorescence microscopy. For histology, mouse lungs were perfused through the pulmonary artery with PBS containing 5 mM EDTA and 131 fixed with 4% paraformaldehyde overnight. For immunohistochemistry, lung sections were 132 stained with rabbit anti-iLOV, then incubated with biotinylated secondary goat-IgG, ABC 133 reagent (Vector Laboratories, Burlingame, CA), diaminobenzidine (DAB, Sigma-Aldrich) and 134 Gill's hematoxylin (Fisher Scientific, Kalamazoo, MI). For fluorescence microscopy, slides were 135 136 incubated with Alexa Fluor 488-conjugated iLOV, Alexa Fluor 555-conjugated mouse anti-RV VP2/VP0, and Cy5–anti-mouse CD68 (Biolegend, San Diego, CA). Nuclei were stained with 137 4',6-diamidino-2-phenylindole (DAPI). Images were acquired with a Zeiss ApoTome confocal 138 microscope (Microscopy and Image Analysis Core, University of Michigan). 139 140 Quantitative real-time PCR of lung cytokines. Lung RNA was extracted with TRIzol Reagent (Thermo Fisher Scientific) combined with on-column digestion of genomic DNA 141 (QIAGEN, Valencia, CA). cDNA was synthesized from 1 µg of RNA and subjected to 142 quantitative real-time PCR using specific mRNA primers encoding for IL-1 $\beta$ , IFN- $\beta$ , IFN- $\gamma$ , 143 144 CXCL1, CXCL2, CXCL10, CCL2, CCL5, and IL-10 (Table S2). For each sample, the level of gene expression was normalized to its own GAPDH mRNA. 145 Flow cytometric analysis. HeLa cells were infected with sham, RV1A or RV1A-iLOV at 146 an MOI of 0.1 for 24 hours. Cells were subjected to flow cytometry and analyzed on an LSR 147 Fortessa (BD Biosciences, San Jose, CA). For in vivo experiments, lungs from sham-, RV1A-, 148 149 and RV1A-iLOV-treated BALB/c mice were perfused with PBS containing EDTA, minced and digested in collagenase IV. Cells were filtered and washed with RBC lysis buffer, and deadcells 150

151 were stained with Pac-Orange Live/Dead fixable dead staining dye (Invitrogen). To identify

152 iLOV-positive cells, cells were stained for surface markers with anti-CD45 (BioLegend) and

anti-CD11b (Biolegend). Cells were then fixed, permeabilized and incubated with the Cy3-

tagged anti-iLOV prior to flow cytometry. Data were collected and analyzed using FACSDiva

155 (BD Biosciences) and FlowJo software (TreeStar, Ashland, OR).

156 *Data analysis.* Data are represented as mean  $\pm$  SE. Statistical significance was assessed 157 using an unpaired *t* test or one-way ANOVA, as appropriate. Group differences were pinpointed 158 by a Tukey multiple-comparison test.

159 **Results** 

Incompatibility of RV1A genome with GFP insert. GFP with flanking 2A<sup>pro</sup> cleavage sites 160 was designed to be inserted between the RV genomic sequences encoding the VP1 and 2A 161 proteins (Fig. 1A). To stabilize the genome, silent mutations were introduced into the coding 162 sequences of both the flanking 2A<sup>pro</sup>cleavage sites (see Supplemental Table 1), as described 163 previously<sup>24</sup>. To generate viral stocks, genomic RNA transcripts made from the RV1A-GFP 164 165 infectious clone were transfected into H1-HeLa cells followed by three consecutive passages (P1-P3). A cytopathic effect (CPE) was observed in HeLa cells infected RV1A-GFP (Fig. 1B). 166 167 However, we were unable to detect GFP expression by Western blot (Fig. 1C) or immunofluorescence (Fig. 1D). We also constructed recombinant RV1A-expressing Renilla 168 169 luciferase (RL) protein to determine if the size of the GFP insert exceeded the limited packaging 170 capacity of RV. To examine the presence of intact GFP and RL ORFs from RV1A-GFP and 171 RV1A-RL, RT-PCR was performed for plaque-purified RV1A-GFP and RV1A-RL using RVspecific flanking primers primers. Results showed that the GFP and RL sequences were deleted 172 173 (Fig. 1E). Sequence analysis of inserts confirmed these results (data not shown). Generation and characterization of RV1A-iLOV. We reasoned that the approximately 753 174 175 nt GFP and 1005 nt RL ORFs (including engineered flanking sequences) exceeded the limited packaging capacity of RV<sup>24</sup>. We therefore chose an alternative smaller fluorescent protein, 176 iLOV (~366 nt). RV1A-iLOV was generated following the design and generation procedure of 177 RV1A-GFP. CPE and growth kinetics of RV1A-iLOV were determined in HeLa cells. In 178 comparison with the parental virus, the RV1A-iLOV displayed a slightly reduced cytopathic 179 180 effect and growth rate (Fig. 2A and 2B). By immunofluorescence, iLOV signal (green) appeared in RV1A-iLOV infected cells only, further confirming the expression of iLOV (Fig 2C). Western 181 blot analysis using rabbit sera recognizing the iLOV protein showed expression of a product of 182

the predicted molecular weight in RV1A-iLOV infected cells (Fig 2D), while viral capsid
proteins VP0 and VP2 were detected in both RV1A and RV1A-iLOV infected cells.

*Genetic stability of RV1A-iLOV in cell culture*. Next we examined the genetic stability of
 RV1A-iLOV in HeLa cells. iLOV expression was observed in RV1A-iLOV P1- and P5-infected

187 HeLa cells by live cell imaging and flow cytometry (Fig 3A-3D). All VP2/0-positive cells were

iLOV-positive. Analysis of the P1 and P5 RV1A-iLOV stocks by RT-PCR revealed that

189 exogenous iLOV DNA was stably retained within the RV genome over five passages (P1 to P5)

(Fig. 3E). Sequence analysis of the iLOV insert confirmed these results and revealed nomutations (data not shown).

Assessment of anti-viral effects using RV1A-iLOV in vitro. We explored the application of 192 RV1A-ilOV to antiviral drug screening. Bafilomycin has previously been shown to inhibit RV 193 infection <sup>30</sup>. We infected HeLa cells with RV1A-iLOV at an MOI of 0.1 for 24 hours in the 194 presence of different concentrations of bafilomycin. iLOV expression was examined using flow 195 cytometry (Fig. 4A). Consistent with previous work <sup>30</sup>, bafilomycin completely inhibited iLOV 196 expression at a concentration of 0.1 µM (Fig. 4A and 4B) and significantly reduced the viral 197 titers of both RV1A and RV1A-iLOV (Fig. 4C). These results demonstrate the potential utility 198 of the iLOV construct to measure RV protein expression in vitro. 199

Induction of cytokines in RV1A-iLOV infected mice. We previously showed RV1B, a 200 minor group virus, triggers inflammation and cytokine expression in mice<sup>11</sup>. We therefore tested 201 202 whether the iLOV insert influences RV replication and RV-induced inflammatory responses in vivo. Eight-week-old mice were infected with RV1A and RV1A-iLOV for up to four days, and 203 lungs were harvested at different time points after infection and processed for positive-strand 204 viral RNA. Measurement of RV copy number and viral titers showed no statistical difference in 205 viral load between RV1A-iLOV and the parental RV1A at each of the indicated time points (Fig. 206 5A). 207

Studies in coxsackievirus have shown that large insertions at the analogous capsid protein P-1D protease 2A junction may delete readily <sup>31, 32</sup>. iLOV stability *in vivo* was therefore examined by RT-PCR at each of the indicated time points (Fig. 5B). The intact iLOV fragment (~600 bp band) along with a size-reduced band (~300bp) appeared in RV1A-iLOV infected mice. Sequence analysis of the size-reduced band revealed the deletion of the coding sequence for intact iLOV plus three nucleotides from 2A<sup>pro</sup> (see sequence in Table S1). Retention of the iLOV insert was approximately 90% at the indicated time points (Fig. 5B and 5C).

215 We next examined cytokine mRNA expression in RV1A-iLOV infected mice. Lungs

216 were harvested one day after infection. Similar to the parental RV1A virus, RV1A-iLOV

217 increased lung mRNA levels of *Il1b*, *Ifnb1*, *Ifng*, *Cxcl1*, *Cxcl10*, *Cxcl2* and *Ccl2* (Fig. 5D).

However, *Ifng* and *Cxcl10* mRNA expression were decreased for RV1A-iLOV compared to

219 RV1A, perhaps because of the slightly reduced growth rate. No induction of *Ccl5* or *Il10* were

220 observed for either RV1A or RV1A-ilOV.

Detection of iLOV in lungs of infected mice. HeLa cells were plated on coverslips,
 infected with RV1A-iLOV and fixed in 4% paraformaldehyde. A fluorescent signal was

visualized, but the signal was rapidly quenched, likely due to the oxidation and bleaching of

iLOV-bound flavin mononucleotide. Similarly, imaging of fixed lung tissue from RV1A-iLOV-

infected mice failed to reveal a fluorescent signal. We therefore employed an anti-iLOV antibody

226 for immunohistochemical staining and immunofluorescence imaging. We infected mice with

227 RV1A-iLOV and harvested lungs one day post-infection. We have previously shown that,

besides airway epithelial cells, RV colocalizes with CD68+ macrophages  $^{13, 14}$ .

Immunohistochemical staining with anti-iLOV showed signal in both the epithelium and

230 macrophages (Fig. 6A). Immunofluorescence similarly indicated localization in the airway

epithelium, as well as colocalization of iLOV (green) with VP2/0 (red) and a macrophage

232 marker, CD68 (blue, Fig. 6B).

We have previously shown that RV infection induces lung infiltration with CD11bpositive, M2-polarized exudative macrophages <sup>33</sup>. For the analysis of intracellular iLOV, aliquots of lung mince were fixed, permeabilized and incubated with the Cy3-tagged anti-iLOV prior to flow cytometry. Flow cytometric analysis showed similar increases in the percentage for CD45+ CD11b+ cells in both RV1A- and RV1A-iLOV-infected mice (Fig. 6C), confirming the colocalization of lung macrophages and RV. However, a signal was detected in CD45+CD11b+ cells only in RV1A-iLOV infected mice. Taken together, these results suggest RV1A-iLOV as a

240 potential tool to study RV-induced responses in immature mice.

241 **Discussion** 

In the present study, we sought to design and generate a recombinant RV1A

243 accommodating fluorescent marker expression, thereby allowing tracking of viral infection *in* 

244 vivo. Using reverse genetics, we engineered and constructed recombinant RV1A infectious

245 cDNA clones harboring the coding sequences of GFP, RL, or iLOV. GFP and RL were not expressed in cultured cells due to deletion during replication, consistent the limited packaging 246 247 capability of other picornaviruses. On the other hand, the smaller fluorescent protein construct, iLOV, was stably expressed in RV1A-iLOV-infected cells both in vitro and in vivo. Evaluation 248 of iLOV expression was used to assess the antiviral effects of bafilomycin in RV1A-iLOV 249 infected cells in vitro. Further, in vivo studies showed that, compared to parental virus, RV1A-250 251 iLOV yielded a similar viral load and level of cytokine mRNA expression in the lungs of infected mice. These results suggest RV1A-iLOV may be a useful molecular tool for studying 252 the life cycle and pathogenesis of RV. 253

Construction of recombinant viruses expressing fluorescent markers, especially GFP, has 254 been applied through reverse genetics to RNA viruses including influenza virus <sup>34</sup>, Zika virus <sup>35</sup>, 255 West Nile virus <sup>36</sup>, respiratory syncytial virus <sup>37</sup>, murine coronavirus <sup>38</sup> and porcine reproductive 256 and respiratory syndrome virus <sup>39</sup>. However, insertion of large fluorescent protein coding 257 sequences into the genome of the picornaviruses, a group of small RNA viruses whose genome 258 sizes range from 7.2-8.5 kb, has been problematic. Insertion of the GFP ORF into poliovirus 259 severely impaired viral replication and was deleted in the course of cell culture serial passage <sup>40</sup>. 260 In addition, an attempt to construct a recombinant foot-and-mouth disease virus (FMDV) 261 expressing GFP or Renilla luciferase protein failed, likely due to the limited packaging capability 262 <sup>41</sup>. Subsequent construction of viruses containing increasingly larger inserts suggested 300–400 263 264 nt as the maximum size to be inserted into FMDV genome. Consistent with this, RV1A has been used to express a 393 nt-long fragment of HIV gag gene <sup>24</sup>. Shorter antigenic tags have also been 265 inserted into the nonstructural proteins of poliovirus <sup>42</sup>. 266

Compared to GFP, fluorescent proteins based on flavin-binding LOV (light, oxygen, or 267 268 voltage sensing) domain offer advantages owing to their smaller size (354 nt), pH and thermal stability <sup>43</sup>. iLOV was created from the LOV2 domain of the phototropin 2 plant blue light 269 receptor of *Arabidopsis thaliana*<sup>26</sup>. Unlike GFP-based fluorescent proteins which are inherently 270 fluorescent, LOV domains specifically function as photosensory modules and typically bind 271 272 flavin mononucleotide as an ultraviolet blue light-absorbing chromophore. Accordingly, iLOV has been used as a reporter gene in recombinant FMDV<sup>41</sup> and reovirus<sup>44</sup>. However, in the latter 273 studies, iLOV expression was only examined in cultured mammalian cells, not in vivo 274 experiments. We now show that iLOV is expressed in RV1A-iLOV-infected cells in vivo. 275

276 Though some deletion occurs during *in vivo* infection, over 90% of the recombinant RV1A-

277 iLOV retains the iLOV sequence. However, while iLOV was readily detectable in cultured HeLa

- cells, the iLOV fluorescence was rapidly lost in fixed cells and lung tissue, likely due to the
- oxidation and bleaching of iLOV-bound flavin mononucleotide. We therefore required the use ofanti-iLOV antibody to detect RV1A-iLOV.
- Similar to viral proteins, iLOV protein is released from the RV polyprotein through viral proteinase-mediated auto-cleavage during viral protein production, an early step of viral replication. Detection of iLOV in mouse tissue is therefore highly suggestive of viral replication, particularly in the airway epithelium. However, it remains unclear whether iLOV signal in macrophages represents replication or engulfment of the virus by phagocytosis. Viral replication in cultured macrophages is limited <sup>45</sup>, though it has recently been shown that airway epithelial cells promote rhinovirus replication in monocytic cells <sup>46</sup>.
- Because there are more than 100 different RV serotypes (in species A and B alone), it is 288 infeasible to develop a cross-reactive antibody for RV. Until now, only one antibody has been 289 available for this purpose, the monoclonal antibody R16-7. This antibody binds to the VP2 290 capsid protein of the closely related RV-A16 and RV-A1 strains <sup>6</sup> but not to RV-A2, RV-B14, or 291 RV-A49<sup>15</sup>. We developed a recombinant virus with a fluorescent marker that could be used for 292 tracking of RV infection in vivo. We designed the iLOV sequence to be flanked with 2A<sup>pro</sup> 293 cleavage sites and then inserted between the RV genomic sequences encoding the VP1 and 2A 294 proteins. 2A<sup>pro</sup> mediates auto-cleavage between VP1 and 2A proteins <sup>20, 47</sup>. Since self-catalytic 295 cleavage is a characteristic of picornavirus replication, this design should allow extension of our 296 technique to all human RVs. Given the fact that iLOV sequence was stably maintained within 297 RV1A genome during consecutive passages, it is plausible that other RVs serotypes would 298 accommodate and maintain the stability of iLOV sequence. Though the 2A<sup>pro</sup> cleavage sites of 299 numerous RV serotypes are heterogeneous <sup>48</sup>, designing the flanked 2A<sup>pro</sup> cleavage sequence to 300 301 be serotype-specific would guarantee the release of iLOV. Besides VP1-2A cleavage site, the junction site between 5'UTR and the N-terminus of VP4 has been used to insert GFP in the 302 genome of coxsackie A16 virus <sup>49</sup>; however, the insertion impaired viral replication. Taken 303 together, these data suggest that the construction strategy for RV1A-iLOV could be applied to 304 other RV serotypes for studying the life cycle of RV in cultured cells, screening for antiviral 305 drugs and for pathogenesis of RV. 306

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313	Refer	rences:
314	1.	Makela MJ, Puhakka T, Ruuskanen O, et al. Viruses and bacteria in the etiology of the
315		common cold. J Clin Microbiol 1998; 36:539-42.
316	2.	Nicholson KG, Kent J, Ireland DC. Respiratory viruses and exacerbations of asthma in
317		adults. BMJ. 1993; 307:982-6.
318	3.	Johnston SL, Pattemore PK, Sanderson G, et al. Community study of role of viral
319		infections in exacerbations of asthma in 9-11 year old children. BMJ 1995; 310:1225-9.
320	4.	Lee WM, Kiesner C, Pappas T, et al. A diverse group of previously unrecognized human
321		rhinoviruses are common causes of respiratory illnesses in infants. PLoS One 2007;
322		2:e966.
323	5.	Lamson D, Renwick N, Kapoor V, et al. MassTag polymerase-chain-reaction detection of
324		respiratory pathogens, including a new rhinovirus genotype, that caused influenza-like
325		illness in New York State during 2004-2005. J Infect Dis 2006; 194:1398-402.
326	6.	Palmenberg AC, Spiro D, Kuzmickas R, et al. Sequencing and analyses of all known
327		human rhinovirus genomes reveal structure and evolution. Science 2009; 324:55-9.
328	7.	Conant RM, Hamparian VV. Rhinoviruses: basis for a numbering system. II. Serologic
329		characterization of prototype strains. J Immunol 1968; 100:114-9.
330	8.	Palmenberg AC, Rathe JA, Liggett SB. Analysis of the complete genome sequences of
331		human rhinovirus. J Allergy Clin Immunol 2010; 125:1190-9.
332	9.	Mosser AG, Vrtis R, Burchell L, et al. Quantitative and qualitative analysis of rhinovirus
333		infection in bronchial tissues. Am J Respir Crit Care Med. 2005; 171:645-51.
334	10.	Papadopoulos NG, Bates PJ, Bardin PG, et al. Rhinoviruses infect the lower airways. J
335		Infect Dis 2000; 181:1875-84.

- Newcomb DC, Sajjan US, Nagarkar DR, et al. Human rhinovirus 1B exposure induces
   phosphatidylinositol 3-kinase-dependent airway inflammation in mice. *Am J Respir Crit Care Med* 2008; 177:1111-21.
- Bartlett NW, Walton RP, Edwards MR, et al. Mouse models of rhinovirus-induced
  disease and exacerbation of allergic airway inflammation. *Nat Med* 2008; 14:199-204.
- 13. Nagarkar DR, Bowman ER, Schneider D, et al. Rhinovirus infection of allergensensitized and -challenged mice induces eotaxin release from functionally polarized
  macrophages. J. Immunol. 2010; 185:2525-35.
- Bentley JK, Sajjan US, Dzaman MB, et al. Rhinovirus colocalizes with CD68- and
  CD11b-positive macrophages following experimental infection in humans. *J Allergy Clin Immunol* 2013; 132:758-61 e3.
- Mosser AG, Brockman-Schneider R, Amineva S, et al. Similar frequency of rhinovirusinfectible cells in upper and lower airway epithelium. *J Infect Dis* 2002; 185:734-43.
- 34916.Hadfield AT, Lee WM, Zhao R, et al. The refined structure of human rhinovirus 16 at
- 2.15 angstrom resolution: Implications for the viral life cycle. *Structure* 1997; 5:427-41.
- 17. Lee WM, Monroe SS, Rueckert RR. Role of maturation cleavage in infectivity of
  picornaviruses: activation of an infectosome. *J Virol* 1993; 67:2110-22.
- Stanway G, Hughes PJ, Mountford RC, et al. The complete nucleotide sequence of a
  common cold virus: human rhinovlrus 14. *Nucl Acids Res.* 1984; 12:7859-75.
- Cordingley MG, Callahan PL, Sardana VV, et al. Substrate requirements of human
  rhinovirus 3C protease for peptide cleavage in vitro. *J Biol Chem* 1990; 265:9062-5.
- Toyoda H, Nicklin MJ, Murray MG, et al. A second virus-encoded proteinase involved in
  proteolytic processing of poliovirus polyprotein. *Cell* 1986; 45:761-70.
- 35921.Basavappa R, Syed R, Flore O, et al. Role and mechanism of the maturation cleavage of
- VP0 in poliovirus assembly: structure of the empty capsid assembly intermediate at 2.9 A
  resolution. *Protein Sci* 1994; 3:1651-69.
- 362 22. Mizutani S, Colonno RJ. In vitro synthesis of an infectious RNA from cDNA clones of
  363 human rhinovirus type 14. *J Virol* 1985; 56:628-32.
- 364 23. Skern T, Torgersen H, Auer H, et al. Human rhinovirus mutants resistant to low pH.
  365 *Virology* 1991; 183:757-63.

- Tomusange K, Yu WB, Suhrbier A, et al. Engineering human rhinovirus serotype-A1 as
  a vaccine vector. *Virus Res* 2015; 203:72-6.
- 368 25. Schibler M, Piuz I, Hao WD, et al. Chimeric rhinoviruses obtained via genetic
- engineering or artificially induced recombination are viable only if the polyprotein
  coding sequence derives from the same species. *J Virol* 2015; 89:4470-80.
- Chapman S, Faulkner C, Kaiserli E, et al. The photoreversible fluorescent protein iLOV
  outperforms GFP as a reporter of plant virus infection. *Proc Natl Acad Sci USA* 2008;
  105:20038-43.
- Quiner CA, Jackson WT. Fragmentation of the Golgi apparatus provides replication
  membranes for human rhinovirus 1A. *Virology* 2010; 407:185-95.
- 376 28. Martin S, Casasnovas JM, Staunton DE, et al. Efficient neutralization and disruption of
  377 rhinovirus by chimeric ICAM-1/immunoglobulin molecules. *J Virol* 1993; 67:3561-8.
- 29. Contoli M, Message SD, Laza-Stanca V, et al. Role of deficient type III interferonlambda production in asthma exacerbations. *Nat Med* 2006; 12:1023-6.
- 380 30. Suzuki T, Yamaya M, Sekizawa K, et al. Bafilomycin A(1) inhibits rhinovirus infection
  in human airway epithelium: effects on endosome and ICAM-1. *Am J Physiol Lung Cell*382 *Mol Physiol* 2001; 280:L1115-L27.
- 383 31. Höfling K, Tracy S, Chapman N, et al. Expression of an antigenic adenovirus epitope in a
  384 group B coxsackievirus. *J Virol* 2000; 74:4570-8.
- 385 32. Chapman NM, Kim K-S, Tracy S, et al. Coxsackievirus expression of the murine
  386 secretory protein interleukin-4 induces increased synthesis of immunoglobulin G1 in
  387 mice. *J Virol* 2000; 74:7952-62.
- 388 33. Chung Y, Hong JY, Lei J, et al. Rhinovirus infection induces IL-13 production from
  389 CD11b-positive, M2-polarized exudative macrophages. *Am J Respir Cell Mol Biol*390 2015;52:205-16.
- 391 34. Pan W, Dong Z, Li F, et al. Visualizing influenza virus infection in living mice. *Nat*392 *Commun* 2013; 4:2369.
- 393 35. Gadea G, Bos S, Krejbich-Trotot P, et al. A robust method for the rapid generation of
   recombinant Zika virus expressing the GFP reporter gene. *Virology* 2016; 497:157-62.
- 395 36. Pierson TC, Diamond MS, Ahmed AA, et al. An infectious West Nile virus that
  a expresses a GFP reporter gene. *Virology* 2005; 334:28-40.

397 37. Lemon K, Nguyen DT, Ludlow M, et al. Recombinant subgroup B human respiratory
398 syncytial virus expressing enhanced green fluorescent protein efficiently replicates in
399 primary human cells and is virulent in cotton rats. *J Virol* 2015; 89:2849-56.

- 38. Das Sarma J, Scheen E, Seo SH, et al. Enhanced green fluorescent protein expression
  may be used to monitor murine coronavirus spread in vitro and in the mouse central
  nervous system. *J Neurovirol* 2002; 8:381-91.
- 403 39. Pei YL, Hodgins DC, Wu JQ, et al. Porcine reproductive and respiratory syndrome virus
  404 as a vector: Immunogenicity of green fluorescent protein and porcine circovirus type 2
  405 capsid expressed from dedicated subgenomic RNAs. *Virology* 2009; 389:91-9.
- 40. Mueller S, Wimmer E. Expression of foreign proteins by poliovirus polyprotein fusion:
  407 analysis of genetic stability reveals rapid deletions and formation of cardioviruslike open
  408 reading frames. *J Virol* 1998; 72:20-31.
- 409 41. Seago J, Juleff N, Moffat K, et al. An infectious recombinant foot-and-mouth disease
  410 virus expressing a fluorescent marker protein. *J Gen Virol* 2013; 94:1517-27.
- 411 42. Teterina NL, Pinto Y, Weaver JD, et al. Analysis of poliovirus protein 3A interactions
  412 with viral and cellular proteins in infected cells. *J Virol* 2011; 85:4284-96.
- 413 43. Buckley AM, Petersen J, Roe AJ, et al. LOV-based reporters for fluorescence imaging.
  414 *Curr Opin Chem Biol* 2015; 27:39-45.
- 415 44. van den Wollenberg DJM, Dautzenberg IJC, Ros W, et al. Replicating reoviruses with a
  416 transgene replacing the codons for the head domain of the viral spike. *Gene Therapy*417 2015; 22:267-79.
- 418 45. Laza-Stanca V, Stanciu LA, Message SD, et al. Rhinovirus replication in human
  419 macrophages induces NF-{kappa}B-dependent tumor necrosis factor alpha production. *J.*420 *Virol.* 2006; 80:8248-58.
- 46. Zhou X, Zhu LX, Lizarraga R, et al. Human airway epithelial cells direct significant
  rhinovirus replication in monocytic cells by enhancing ICAM1 expression. *Am J Respir Cell Mol Biol* 2017; 57:216-25.
- 424 47. Hellen CU, Lee CK, Wimmer E. Determinants of substrate recognition by poliovirus 2A
  425 proteinase. *J Virol* 1992; 66:3330-8.
- 426 48. Sousa C, Schmid EM, Skern T. Defining residues involved in human rhinovirus 2A
  427 proteinase substrate recognition. *FEBS Lett* 2006; 580:5713-7.

- 428 49. Deng C, Li X, Liu S, et al. Development and characterization of a clinical strain of
  429 Coxsackievirus A16 and an eGFP infectious clone. *Virol Sin* 2015; 30:269-76.
- 430

## 431 Figure Legends

FIG 1. GFP ORF insertion into the rhinovirus genome is deleted. A. Schematic presentation 432 of the insertion GFP into RV genome. RV proteins are presented in boxes. 2A<sup>pro</sup> cleavages at 433 points indicated by yellow solid triangles separates RV structural from non-structural proteins 434 and releases GFP proteins. Solid blue arrows indicate 3C<sup>pro</sup> cleavage sites. **B.** Plaque morphology 435 of HeLa cells infected with parental wild-type RV1A or RV1A-GFP. C. Western blot analysis of 436 whole-cell lysates from HeLa cells infected with RV1A or RV1A-GFP. Samples were probed for 437 the presence of GFP and the RV structural proteins VP0 and VP2. GFP input was made from 438 whole cell lysate of pEGFP-N1 transfected HeLa cells. D. Detection of RV1A-GFP infected cells 439 by live-cell imaging and immunofluorescence staining. HeLa cells were infected at an MOI of 440 0.1 with either sham, parental-RV1A or RV1A-GFP for 16 hours. HeLa cells were transfected 441 with pEGFP-N1 for 16 hours (bar, 50 µm). RV VP2/0 protein was detected using AF555-442 conjugated anti-VP2/0 Ab (red); iLOV (green) was directly detected by blue laser; nuclei were 443 stained by DAPI (shown in black; bar, 50 µm). E. RT-PCR analysis of RV-GFP and RV-RL 444 445 genomes. RV-GFP and RV-RL genomic RNA were isolated from HeLa cells infected with P3 plaque-purified virus stocks. RV1A-GFP and RV1A-RL infectious cDNA clones were used as 446 447 template for amplification of complete GFP or RL sequence.

448

FIG 2. Construction of the infectious recombinant rhinovirus-iLOV. A. Plaque morphology 449 of HeLa cells infected with parental wild-type RV1A or RV1A-iLOV. iLOV (green) expression 450 was directly detected by blue laser for RV plaques. B. Viral copy number and titers in RV-451 infected HeLa cells. Cells were infected with RV1A or RV1A-iLOV at an MOI of 0.1. At 452 453 specified times, cells were harvested for analysis. Viral copy number was analyzed by quantitative polymerase chain reaction. Viral titer was determined by TCID<sub>50</sub> (n = 3, mean  $\pm$ 454 SD). C. Fluorescence imaging for RV-iLOV. HeLa cells were infected with parental wild-type 455 RV1A or RV1A-iLOV for 24 hours at an MOI of 0.1. RV VP2/0 protein was detected using 456 AF555-conjugated anti-VP2/0 Ab (red); iLOV (green) was directly detected by blue laser; nuclei 457 were stained by DAPI (shown in black; bar, 50 µm). D. Western blot assay to detect the 458

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459 expression of iLOV.

460

461	FIG 3. Stability of RV1A-iLOV. A. Live-cell imaging and immunofluorescence staining of
462	RV1A-iLOV infected HeLa cells. HeLa cells were infected with P1 and P5 of RV1A-iLOV for
463	24 hours at an MOI of 0.1 RV VP2/0 protein was detected using AF555-conjugated anti-VP2/0
464	Ab (red); iLOV (green) was directly detected by blue laser; nuclei were stained by DAPI (shown
465	in black, bar, 50 $\mu$ m). <b>B.</b> The number of iLOV positive cells out of 50 VP2/0 positive cells was
466	counted. All VP2/0-positive cells were iLOV-positive. C and D. iLOV detection in HeLa cells
467	by flow cytometry. Cells were transfected with pXJ41-iLOV or infected with RV1A or RV1A-
468	iLOV, harvested 24 hours later and analyzed as a percentage of single cells (n = 3, mean $\pm$
469	SEM). E. RT-PCR analysis of RV1A-iLOV genomes. Parental RV1A or RV1A-iLOV genomic
470	RNA was isolated from HeLa cells infected with P1 or P5 virus stocks. The RV1A-iLOV
471	infectious cDNA clone was used as template for amplification of complete iLOV sequence.
472	
473	FIG 4. Assessment of anti-viral role of bafilomycin using RV1A-iLOV. HeLa cells were
474	infected with sham or RV1A-iLOV for 24 hours. Selected cells were treated with $0.01\mu M$ , $0.1$
475	$\mu$ M, or 0.2 $\mu$ M of bafilomycin. iLOV positive cells were analyzed as a percentage of single cells
476	(n = 3, mean $\pm$ SEM). Viral titers were calculated as TCID <sub>50.</sub>
477	
478	FIG 5. Viral load and cytokine expression of RV1A-iLOV in vivo infection. Eight-week-old
479	BALB/c mice were inoculated with sham, RV1A or RV1A-iLOV. A Whole lung was harvested
480	at the indicated time points and used for measuring viral copy number and titer. <b>B</b> RT-PCR
481	analysis of RV1A-iLOV genomes. Parental RV1A or RV1A-iLOV genomic RNA was isolated
482	from infected mice at indicated time points. The RV1A-iLOV infectious cDNA clone was used
483	as template for amplification of complete iLOV sequence. C iLOV/RV copy ratio in RV1A-
484	iLOV infected mice. Total lung RNA (1 $\mu$ g) from RV1A-iLOV infected mice harvested at the
485	indicated time points was used for measuring iLOV and RV genome copy numbers. $D$ Whole
486	lung mRNA expression was measured one day post-infection. (N=4, mean±SEM, *different
487	from RV1A, one-way ANOVA.)
488	

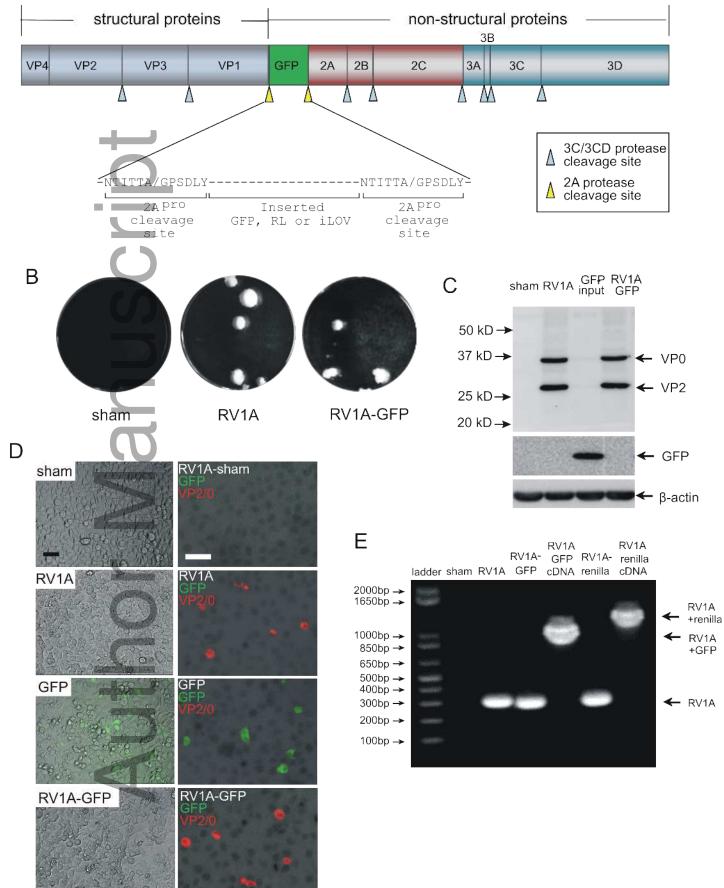
## 489 FIG 6. Presence of iLOV signal in the airway epithelium and lung macrophages of RV1A-

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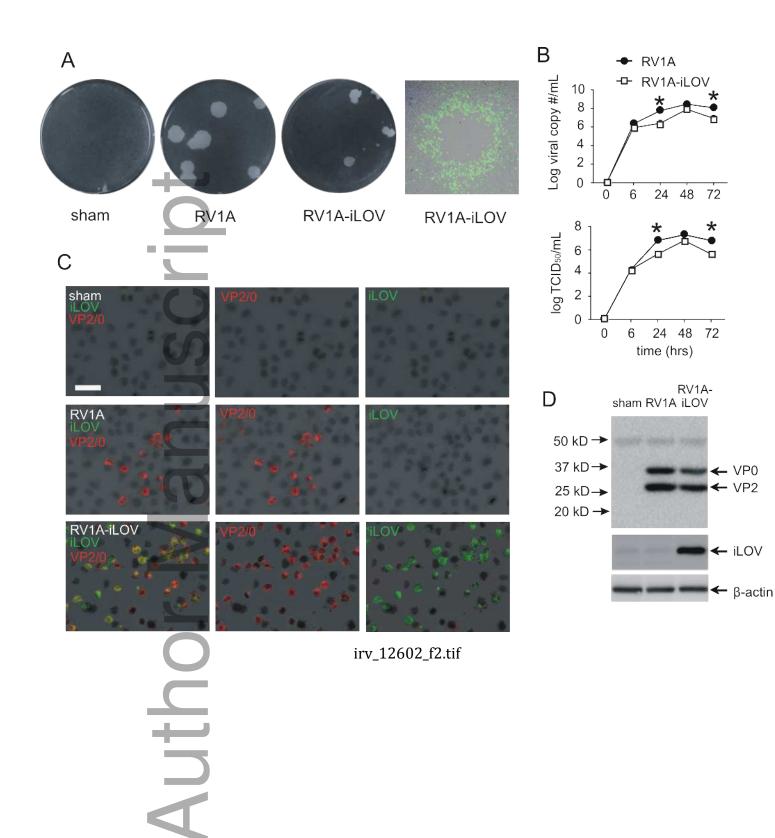
## 490 iLOV infected mice.

- 491 *A*. Twenty-four hours after infection, lungs were fixed in formaldehyde overnight, embedded in
- 492 paraffin, sectioned at 5 μm, and incubated with a 1:1000 dilution of anti-iLOV or isotype control
- 493 IgG (bar, 50 μm). **B.** Lung sections were costained with AF-488-conjugated anti-iLOV (green),
- 494 AF-555-conjugated anti-VP2/0 (red) and Cy5-conjugated CD68 (far red optical spectrum, shown
- in blue). *C*. Lung CD45+, CD11b+, iLOV+ cells from RV-infected BALB/c mice were identified
- 496 one day post-infection and analyzed as a percentage of CD45+ cells (n = 4 from one
- 497 experiment). Data are presented as mean  $\pm$  SEM (\*different from sham, P < 0.05; one-way
- 498 ANOVA.)

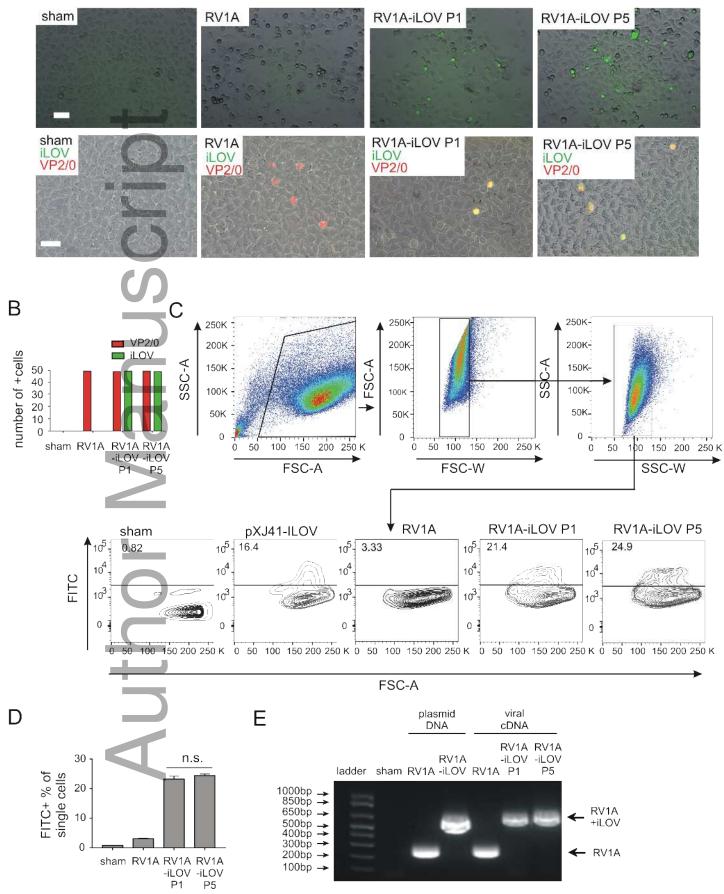
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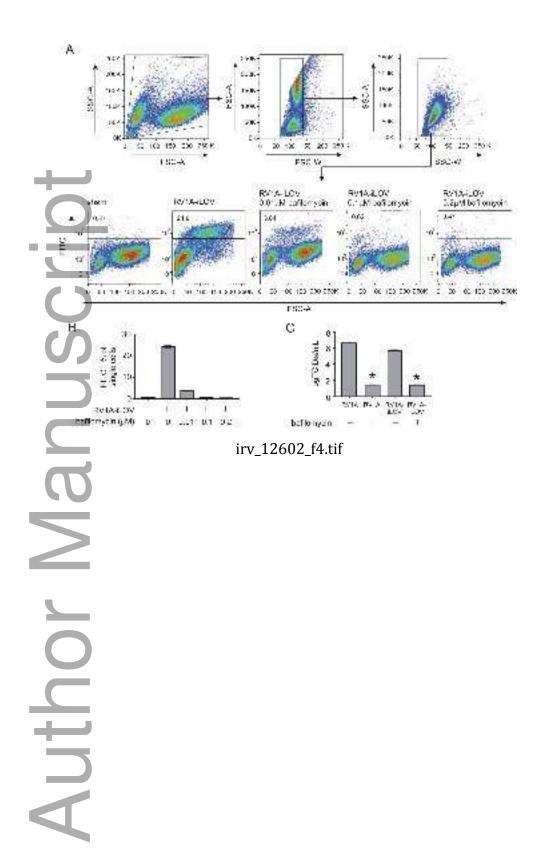
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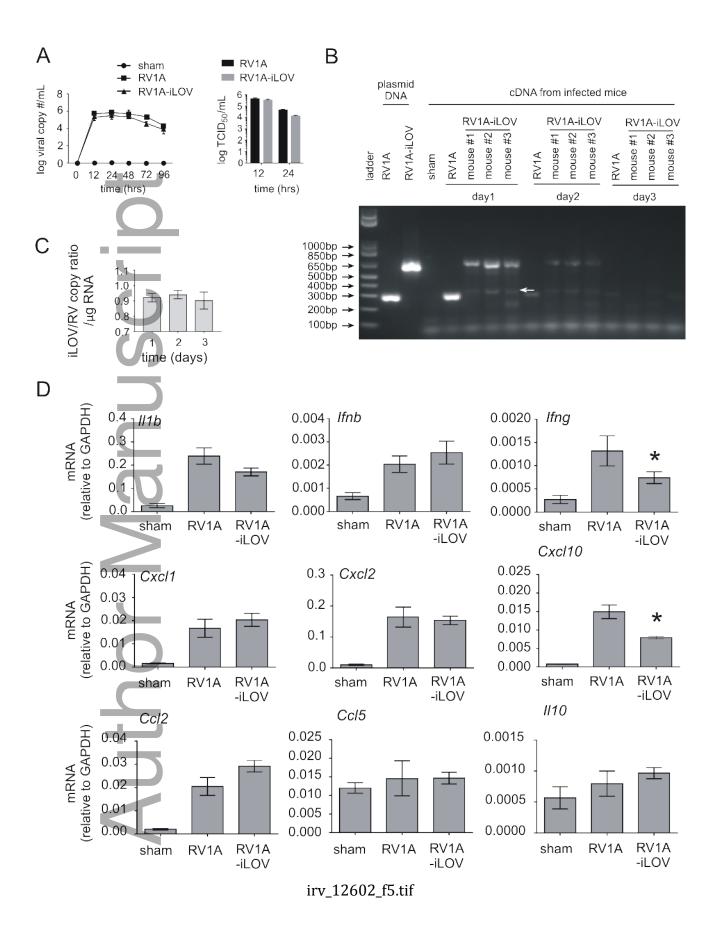


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