

A recombinant murine rotavirus with Nano-Luciferase expression reveals tissue tropism, replication dynamics, and virus transmission

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ABSTRACT

Rotaviruses (RVs) are one of the main causes of severe gastroenteritis, diarrhea, and death in children and young animals. Although suckling mice prove to be highly useful small animal models of RV infection and pathogenesis, direct visualization tools are lacking to track the temporal dynamics of RV replication and transmissibility *in vivo*. Here, we report the generation of the first recombinant murine RV that encodes a Nano-Luciferase reporter (NLuc) using a newly optimized RV reverse genetics system. The NLuc-expressing RV was replication-competent in cell culture and both infectious and virulent in neonatal mice *in vivo*. Strong luciferase signals were detected in the proximal and distal small intestines, colon, and mesenteric lymph nodes. We showed, via a noninvasive *in vivo* imaging system, that RV intestinal replication peaked at day 2 and day 5 post infection. Moreover, we successfully tracked RV transmission to uninoculated littermates as early as 3 days post infection, 1 day prior to clinically apparent diarrhea and 3 days prior to detectable fecal RV shedding in the uninoculated littermates. We also observed significantly increased viral replication in *Stat1* knockout mice that lack the host interferon signaling. Our results suggest that the NLuc RV represents a non-lethal powerful tool for the studies

of tissue tropism and host and viral factors that regulate RV replication and spread, as providing a new mechanism to facilitate the testing of prophylactic and therapeutic interventions in the future.

Key words: Rotavirus, *In vivo* imaging system, Transmission, Nano-luciferase, Tissue tropism

INTRODUCTION

Rotavirus (RV) is one of the leading causes of severe diarrhea in infants and young children. Although there are multiple safe and effective RV vaccines currently available, RV infection still results in the death of more than 128, 500 children per year [1]. Suckling mice provide a pathologically relevant small animal model for studying infection, protection, and immune responses because homologous murine RVs are a natural mouse pathogen and cause a similar diarrheal diseases as seen in human infants and many other mammalian species [2; 3]. Using this model, we and others have previously reported an important role of the type I and type III interferon (IFN) responses as well as local and systemic antibody responses in controlling RV replication in the host intestine [4; 5; 6; 7].

RV predominantly infects the host gastrointestinal tract, in particular the small intestine. However, whether RV replicates in extra-intestinal tissues such as the central nervous system, liver, and respiratory tract remains controversial [8; 9; 10; 11; 12; 13; 14]. In addition, although fecal-oral transmission is clearly the primary means of RV spread, it is technically challenging and labor intensive to follow the events of virus transmitted to naïve animals prior to the appearance of diarrheal diseases. Bioluminescent reporter systems provide extreme convenience and sensitivity to visualize intra- and inter-host viral dynamics in real time. Although fluorescent proteins and luciferase enzymes have been widely used in the studies of a variety of viral infections, including influenza virus, herpes simplex virus type 1, dengue virus, Sindbis virus, Sendai virus, and adenovirus [15; 16; 17; 18; 19; 20; 21; 22; 23], most

64 recombinant viruses are significantly attenuated, genetically unstable, and only a few
65 are fully applicable for *in vivo* imaging.

66 A plasmid-based RV reverse genetics system has recently been established and
67 optimized by our labs and others, thereby enabling the recovery of low-titer
68 recombinant reporter viruses and hard-to-rescue RV strains [24; 25; 26; 27].
69 Intragenic sequence duplications in NSP1, NSP3 and NSP5/6 gene segments have
70 been observed in natural RV variants, leading to the production of viral proteins of
71 unusual length and making them ideal targets to accommodate foreign gene
72 expression [28; 29; 30]. NSP5 and NSP6 are encoded from the same gene segment,
73 thereby introducing complications for genetic manipulation. NSP3 is expressed at
74 higher levels than NSP1 in infected cells, rendering NSP3-based fluorescent proteins
75 brighter and easier to detect [26]. Nano-luciferase (NLuc) is a novel bioluminescent
76 protein and offers several advantages over the existing platforms (Firefly, Gaussia,
77 Renilla, etc.), including enhanced stability, smaller size, and increased luminescence
78 [31]. Hence, we take advantage of a highly efficient RV reverse genetics system that
79 we recently developed [27] to generate a recombinant murine RV D6/2-2g strain that
80 encodes NLuc in the RV NSP3 gene segment (rD6/2-2g-NLuc). The NLuc RV is
81 genetically stable, replication-competent, pathogenic, and transmissible *in vivo*. Using
82 this powerful virological tool and a well-established neonatal model of RV infection,
83 we have begun to investigate several fundamental and important questions of RV
84 biology including tissue tropism, replication dynamics, and virus transmission.

85

86 **RESULTS**

87 **Generation of a recombinant NLuc-expressing murine RV**

88 To generate rD6/2-2g-NLuc, we first constructed a T7 plasmid that expresses the
89 NLuc reporter in the RV gene segment 7 that encodes NSP3 (pT7-NSP3-NLuc). The
90 monomeric NLuc gene was placed downstream of the NSP3 open reading frame that
91 is followed by a P2A self-cleaving peptide to permit separate gene expression (**Fig.**
92 **1A**). BHK-T7 cells transfected with T7-NSP3-NLuc produced the NLuc protein (**Fig.**

93 **1B**). We further confirmed by an NLuc substrate assay that strong luciferase activity
 94 was detected in T7-NSP3-NLuc-transfected cells (**Fig. 1C**). We successfully rescued
 95 the parental murine RV rD6/2-2g strain and rD6/2-2g-NLuc viruses using our
 96 optimized RV reverse genetic system [27]. NLuc expression was verified in
 97 rD6/2-2g-NLuc-infected MA104 cells (**Fig. 1D**). The identity of rD6/2-2g-NLuc was
 98 further validated by a unique electrophoretotype by RNA polyacrylamide gel
 99 electrophoresis analysis (**Fig. 1E**). The edited dsRNA of RV gene segment 7 migrated
 100 slower than the wild-type gene segment 7 due to the NLuc insertion (**Fig. 1E**). In
 101 addition, we quantified the luciferase activity in rD6/2-2g-NLuc-infected cells and
 102 found that we were able to detect signals even at the 10^5 dilution factor (**Fig. 1F**).
 103 Taken together, we successfully generated a murine RV NLuc reporter virus that
 104 produces robust luciferase activity in infected cells.

105

106 **Characterization of rD6/2-2g-NLuc replication *in vitro***

107 We next sought to determine the replication kinetics of rD6/2-2g-NLuc as compared
 108 to the parental rD6/2-2g *in vitro*. Despite slightly lower intracellular mRNA levels and
 109 virus titers than those of rD6/2-2g at 24, 48, and 72 hours post infection (hpi) (**Fig. 2A**
 110 **and 2B**), rD6/2-2g-NLuc replicated well in MA104 cells and produced substantial
 111 cytopathic effects (data not shown). The plaque size of rD6/2-2g-NLuc was
 112 approximately half of that of rD6/2-2g (**Fig. 2C**). We performed serial passage of
 113 rD6/2-2g-NLuc in MA104 cells to assess the genetic stability. Importantly,
 114 luminescence was still highly detectable after 8 passages and we observed no loss of
 115 luciferase signals over time (**Fig. 2D**), suggesting that the NLuc gene was functionally
 116 maintained in the viral genome and that the reporter virus is infectious and stable *in*
 117 *vitro*.

118

119 **Tissue tropism of rD6/2-2g-NLuc *in vivo***

120 To leverage the high sensitivity of NLuc and investigate RV tissue tropism, we orally
 121 inoculated five-day-old 129sv pups with 1.3×10^6 foci forming units (FFUs) of

122 rD6/2-2g-NLuc. We observed 100% diarrheal development in infected pups at 1 day
 123 post infection (dpi) (**Fig. 3A**). The diarrhea occurrence remained more than 50% from
 124 2 to 5 dpi (**Fig. 3A**). We euthanized one mouse on each day and harvested different
 125 organs to measure luciferase activities. As expected, we found strong luciferase
 126 signals throughout the lower gastrointestinal tract. We detected more robust activity in
 127 the distal small intestine (SI) than proximal SI (**Fig. 3B and 3C**). We also detected
 128 high NLuc activity in the colon and the mesenteric lymph nodes (**Fig. 3D and 3E**),
 129 suggestive of active RV replication at these sites. On the other hand, the pancreas and
 130 the liver had weak to non-detectable signals (**Fig. 3F and 3G**). These results suggest
 131 that murine RV primarily targets the lower gastrointestinal tract (SI and colon) and
 132 does not actively replicate in extra-intestinal organs such as the liver.

133

134 **Infectivity and pathogenicity of rD6/2-2g-NLuc *in vivo***

135 To investigate whether we can use rD6/2-2g-NLuc for studies of intestinal RV
 136 infection, we inoculated five-day-old 129sv mice with a low inoculum (3.5×10^3
 137 FFUs) of rD6/2-2g-NLuc via oral gavage. We observed that 50% of mice developed
 138 diarrhea at 1 dpi and about 80% developed diarrhea by 2 dpi (**Fig. 4A**). We found
 139 high levels of fecal shedding of infectious RVs from 4 to 10 dpi (**Fig. 4B**). Importantly,
 140 we recorded the bioluminescence signals from day 0 to day 12 post infection and
 141 observed strong luciferase in the abdominal cavity as early as 1 dpi using the *in vivo*
 142 imaging system (IVIS) (**Fig. 4C**). The luminescence intensity was over to 10^6
 143 p/sec/cm²/sr and remained high until 7 dpi (**Fig. 4D**). These results demonstrate that
 144 our reporter virus provides extreme sensitivity and temporal resolution of
 145 intra-intestinal RV infection multiple days prior to the detection of RV shedding in the
 146 fecal specimens.

147

148 **Characterization of RV transmission by IVIS**

149 To further quantitatively track RV transmission, an important but under-studied aspect
 150 of RV biology, we co-housed 6 infected and 6 uninfected littermates in the same cage.

151 Compared to the RV-inoculated mice (**Fig. 4A**), diarrhea was first observed in the
152 naïve animals at 4 dpi and reached over 80% at 7 dpi (**Fig. 5A**). We also quantified
153 RV fecal shedding by an FFU assay. The originally uninoculated mice had detectable
154 virus shedding briefly between 6 to 8 dpi (**Fig. 5B**), albeit at a similar level as the
155 infected mice (**Fig. 4B**). Remarkably, we observed strong luminescence as early as 3
156 dpi (**Fig. 5C and 5D**), preceding the first appearance of clinical symptoms at 4 dpi
157 and fecal shedding at 6 dpi. These data indicate that RV transmission readily occurred
158 3 days after co-housing and that rD6/2-2g-NLuc is a highly sensitive and convenient
159 tool for following RV infection and spread in real time *in vivo*.

160

RV infection of *Stat1* knockout mice

162 To determine whether IVIS represents an ideal system to study the role of host factors
163 in RV intestinal replication, which is enhanced in immunodeficient mice, we orally
164 infected five-day-old *Stat1* knockout (KO) mice with 3.5×10^3 FFUs of
165 rD6/2-2g-NLuc, at the same dose as in wild-type 129sv mice (**Fig. 4**). We observed
166 that about 30% of mice developed diarrhea at 1 dpi and 100% developed diarrhea
167 from 2 until 6 dpi (**Fig. 6A**). As expected, *Stat1* KO pups had high levels of fecal
168 shedding of infectious virus particles at 1 to 3 dpi (**Fig. 6B**), much earlier than that
169 observed in the wild-type animals (**Fig. 4B**). Moreover, IVIS revealed that the
170 luminescence intensity was significantly increased (approximately 10-fold higher, up
171 to 10^7 p/sec/cm²/sr) with the lack of host interferon signaling (**Fig. 6C-E**).
172 Collectively, these results demonstrate the utility and effectiveness of rD6/2-2g-NLuc
173 in objectively reflecting RV replication and studying host immunity *in vivo*.

174

DISCUSSION

176 Reporter viruses prove to be important tools for visualizing and monitoring viral
177 replication dynamics *in vitro* and *in vivo*. Although the plasmid-based RV reverse
178 genetics system was reported in 2017 and several fluorescent and luminescent
179 protein-encoding RVs (primarily in the backbone of simian RV SA11 strain) have

180 been reported [24; 25; 26], murine viruses are difficult to rescue, precluding further
 181 manipulation and heterologous expression of foreign genes. In this study, we take
 182 advantage of a more efficient RV reverse genetics system that we recently developed
 183 [27] and generate a murine rD6/2-2g-NLuc strain. This virus was functionally stable
 184 even after 8 passages (**Fig. 2D**). The combinatorial use of rD6/2-2g-NLuc reporter
 185 virus and IVIS enabled the detection of RV replication in different organ systems (**Fig.**
 186 **3**). It is noteworthy that we found strong luciferase signals in the colon (**Fig. 3D**).
 187 There is controversy in the literature regarding RV infection of the large intestine
 188 including cecum and colon [32; 33; 34; 35; 36; 37]. With the limitation that we cannot
 189 distinguish real infection of colon epithelium from NLuc activities from infected shed
 190 but still alive cells, our data suggest a strong possibility that RV also replicates in the
 191 colon. It is also interesting that we transiently detected strong luciferase signals in the
 192 mesenteric lymph node (**Fig. 3E**), composed predominantly of hematopoietic cells.
 193 Furthermore, our system allowed us to assess RV transmission to uninoculated
 194 co-caged littermates (**Fig. 5**) and the effect of host factors and signaling pathways on
 195 RV intestinal replication *in vivo* (**Fig. 6**), which is easily extendable to the role of
 196 other host innate and adaptive antiviral signaling in RV infection, pathogenesis, and
 197 transmission.

198 Given the modular nature and small size of the NLuc reporter construct, this
 199 approach is broadly applicable to the studies of other RV isolates and other enteric
 200 viruses (murine norovirus, enterovirus D68, etc.). The replication of simian RVs is
 201 severely limited in immunocompetent suckling mice. To that end, we can rescue
 202 NLuc reporter in the backbone of simian RV RRV strain, which we expect to be
 203 attenuated in 129sv mice but to cause a lethal biliary disease in *Stat1* deficient or
 204 intra-peritoneally inoculated newborn mice [38]. We can apply traditional virological
 205 approaches (reassortment with gene swapping and/or deletion) to examine the relative
 206 contribution of individual RV gene product in intestinal replication and transmission.
 207 Another interesting aspect is that the host genetic background dictates RV
 208 pathogenicity. Compared to 129sv pups, diarrhea in C57Bl/6 mice is highly attenuated.

209 Thus, one could use NLuc virus to desegregate RV replication from diseases and help
210 dissect the role of RV-encoded products in this process.

211 Finally, reporter viruses have emerged as powerful tools in small-molecule
212 compound screening [39; 40], antibody identification [16], and vaccine efficacy
213 analysis [41]. We envision that our NLuc reporter RV and IVIS will provide a rapid,
214 non-lethal and real-time quantitative means to assess viral replication, spread and
215 facilitate the rationale design and development of novel antiviral therapeutics and
216 new-generation safe and efficacious RV vaccines, to be tested in pre-clinical small
217 animal models.

218

219 **MATERIAL AND METHOD**

220 **Cell culture and viruses**

221 MA104 cells (ATCC CRL-2378) were cultured in Medium 199 (M199,
222 Sigma-Aldrich) supplemented with 10% heat-inactivated fetal bovine serum (FBS),
223 100 I.U. penicillin/ml, 100 µg/ml streptomycin and 0.292 mg/ml L-glutamine
224 (complete medium). The BHK-T7 cell line [42] was provided by Dr. Ursula Buchholz
225 (Laboratory of Infectious Diseases, NIAID, NIH, USA) and cultured in completed
226 DMEM supplemented with 0.2 µg/ml of G-418 (Promega). MA104 N*V cells were
227 cultured in complete M199 in the presence of 3 µg/ml puromycin and 3 µg/ml of
228 blasticidin (InvivoGen, San Diego, CA).

229

230 The rRV strains used in this study include rD6/2-2g and rD6/2-2g-NLuc and were
231 propagated in MA104 cells. Prior to infection, all RV inocula were activated with 5
232 µg/ml of trypsin (Gibco Life Technologies, Carlsbad, CA) for 30 min at 37 °C.

233

234 **Plasmid construction**

235 The murine D6/2 rescue plasmids: pT7-D6/2-VP2, pT7-D6/2-VP3, pT7-D6/2-VP4,
236 pT7-D6/2-VP6, pT7-D6/2-VP7, pT7-D6/2-NSP1, pT7-D6/2-NSP2, pT7-D6/2-NSP3,
237 and pT7-D6/2-NSP5 were prepared as described previously [27] while

238 pT7-SA11-VP1 and pT7-SA11-NSP4 were originally made by Dr. Takeshi Kobayashi
239 (Research Institute for Microbial Diseases, Osaka University, Japan) [24] and
240 obtained from Addgene. The C3P3-G1 plasmid [43] was kindly provided by Dr.
241 Philippe H Jaïs. To generate pT7-D6/2-NSP3-NLuc, which encodes a full-length
242 NLuc gene (GenBank: KM359774.1) and the self-cleaving P2A peptide gene of
243 porcine teschovirus-1, the P2A-NLuc gene cassette was amplified by PCR and
244 inserted between nucleotides in the NSP3 gene via Gibson assembly (NEBuilder HiFi
245 DNA Assembly kit). Purification of all the plasmids was performed using QIAGEN
246 Plasmid Maxiprep kit per the manufacturer's instructions.

247

248 **Generation of recombinant rotaviruses**

249 rD6/2-2g was generated using the following pT7 plasmids: pT7-SA11-VP1 and
250 -NSP4, pT7-D6/2-VP2, -VP3, -VP4, -VP6, -VP7, -NSP1, -NSP2, -NSP3 and -NSP5
251 according to the optimized entirely plasmid-based RG system [27]. The
252 pT7-D6/2-NSP3 plasmid was replaced by the pT7-D6/2-NSP3-NLuc to generate
253 rD6/2-2g-NLuc. The rescued rRVs were propagated for two passages in MA104 cells
254 in a 6-well plate, and then both rRVs were plaque purified twice in MA104 cells.

255

256 **Western blot**

257 BHK-T7 cells were transfected with 1µg pT7 vector or 1 and 2 µg pT7-NSP3-NLuc
258 plasmids for 48 hours and MA104 cells were infected by rD6/2-2g or rD6/2-2g-NLuc
259 at an MOI of 0.1 for 24 h. Then, cells were washed twice with ice-cold
260 phosphate-buffered saline (PBS; Thermo Scientific) and lysed in RIPA buffer
261 (150mM NaCl, 1.0% IGEPAL CA-630, 0.5% sodium deoxycholate, 0.1% SDS,
262 50mM Tris, pH 8.0; Sigma-Aldrich) supplemented with 1× protease inhibitor
263 cocktail (Thermo Scientific) for 30min at 4°C. After that, cell debris was removed
264 by centrifugation at 12,000×g for 10min at 4°C. Samples were resolved in
265 precast SDS-PAGE gels (4 to 15%; Bio-Rad) and transferred to a nitrocellulose
266 membrane (0.45µm; Bio-Rad). The membrane was incubated with blocking buffer

(5% bovine serum albumin [BSA] diluted in PBS supplemented with 0.1% Tween 20) for 1 h at room temperature. Then, the membrane was incubated with anti-NLuc rabbit monoclonal antibody (Promega; catalog no. N7000; 1 µg/ml) diluted in SuperBlock blocking buffer, 4 °C overnight, anti-RV VP6 mouse monoclonal antibody (Santa Cruz Biotechnology; sc-101363; 1:1,000), and anti-glyceraldehyde-3-phosphate dehydrogenase (GAPDH) rabbit monoclonal antibody (CST; catalog no. 2118; 1:1,000), followed by incubation with anti-mouse IgG (CST; catalog no. 7076; 1:5,000) or anti-rabbit IgG (CST; catalog no. 7074; 1:5,000) horseradish peroxidase (HRP)-linked antibodies. The antigen-antibody complex was detected using Clarity Western ECL substrate (Bio-Rad) and the ChemiDoc MP imaging system according to the manufacturer's manuals.

278

279 **RT-qPCR.**

The total RNA of the MA104 cells infection with recombinant rD6/2-2g and rD6/2-2g-NLuc virus was extracted by TRIzol. Total RNA was reverse transcribed to cDNA using a high-capacity cDNA reverse transcription kit with RNase inhibitor (Applied Biosystems) according to the user guide. Briefly, 0.8 µg of RNA, 2 µl of 10× reverse transcription (RT) buffer, 0.8 µl of 100 mM deoxynucleoside triphosphate (dNTP) mix, 2 µl of RT random primers, 0.1 µl of RNase inhibitor, 0.1 µl of MultiScribe reverse transcriptase, and a flexible amount of nuclease-free H₂O were added to the 20 µl reaction mixture. The reverse transcription thermocycling program was set at 25°C for 10 min, 37°C for 2 h, and 85°C for 5 min. The expression level of housekeeping gene GAPDH was quantified by 2× SYBR green master mix (Applied Biosystems), and NSP5 was measured by 2× TaqMan Fast Advanced master mix (Applied Biosystems). The primers used in this study were as follows: human GAPDH forward primer, 5'-GGAGCGAGATCCCTCCAAAAT-3', and reverse primer, 5'-GGCTGTTGTCATACTTCTCATGG-3'; and NSP5 forward primer, 5'-CTGCTTC AAACGATCCACTCAC-3', reverse primer, 5'-TGAATCCATAGACACGCC-3', and

296 probe, 5'-CY5/TCAAATGCAGTTAAGACAAATGCAGACGCT/IABRQSP-3'. The
297 y axis stands for the percentage of NSP5 mRNA levels relative to GAPDH levels.

298

299 **Plaque assay**

300 Activated virus samples were serially diluted 10-fold and added to monolayers of
301 MA104 cells for 1 h at 37°C. Inocula were removed and replaced with 0.1% (w/v)
302 agarose (SeaKem® ME Agarose, Lonza) in FBS-free M199 supplement with 0.5
303 µg/ml of trypsin. Cultures were incubated for 7 days at 37°C in a 5% CO₂ incubator.
304 Random plaques were picked by pushing the 200 µl tip through the overlay agarose,
305 and then were propagated in MA104 cells as described above. To quantify the plaque
306 diameter, cultures at 7 dpi were fixed with 10% formaldehyde and stained with 1%
307 crystal violet (Sigma-Aldrich). The diameter of at least 25 randomly selected plaques
308 from 2 independent plaque assays was recorded using an ECHO microscope and then,
309 diameters were measured with the annotation tool of the microscope.

310

311 **Focus-Forming assay**

312 Activated virus samples from cell culture or mouse stool specimens were serially
313 diluted 2- or 10-fold and added to confluent monolayers of MA104 cells seeded in
314 96-well plates for 1 h at 37°C. Inocula were removed and replaced with M199
315 serum-free and then incubated for 16 to 18 h at 37 °C. Cells were then fixed with 10%
316 paraformaldehyde and permeabilized with 1% Tween 20. Cells were incubated with
317 rabbit hyperimmune serum to rotavirus (anti-DLPs) produced in our laboratory and
318 anti-rabbit HRP-linked secondary antibody. Viral foci were stained with
319 3-amino-9-ethylcarbazole (AEC substrate kit, Vector Laboratories) per manufacturer's
320 instructions and enumerated visually.

321

322 **Luciferase assay**

323 MA104 cells seeded in 96-well plates were infected with 50 µL of 10-fold serial
324 dilution of rRVs at 37°C for 48 h and freeze-thawed 2 times before 50 µL/well of

325 Nano-Glo Luciferase Assay Reagent (Promega) was added per manufacturer's
326 instructions. After 5 minutes incubation at room temperature, relative luminosity units
327 were measured using a 20/20n Luminometer (Turner Biosystems). 100 µL of mouse
328 tissues homogenates were mixed with 50 µL of Nano-Glo working substrate solution
329 and processed as described above.

330

331 **Purification of RV particles by sucrose gradient centrifugation**

332 rRVs were concentrated by pelleting through a sucrose cushion as described [44].
333 Briefly, MA104 grown in 12-well plate were infected and harvested 72 h post
334 infection (hpi), the viral lysates were freeze-thawed three times, and viral particles
335 concentrated by ultracentrifugation for 1 h at 30,000 rpm at 4 °C. Viral pellets were
336 resuspended in TNC buffer (10 mM Tris-HCl [pH 7.5], 140 mM NaCl, 10 mM
337 CaCl₂), extracted with genetron and the aqueous phase pelleted through a 40%
338 sucrose cushion by centrifugation for 1 h at 30,000 rpm at 4°C. The pelleted rRV was
339 resuspended with 1 mL of PBS with Ca²⁺ and Mg²⁺ and this suspension was used to
340 perform mice infections or to obtain genomic dsRNA profiles.

341

342 **Electrophoresis of viral dsRNA genomes**

343 Viral dsRNAs were extracted from sucrose cushion-concentrated rRVs with TRIzol
344 (Invitrogen) according to the manufacturer's protocol and then mixed with Gel
345 Loading Dye, Purple (6x), no SDS (NEB). Samples were subjected to PAGE (10%)
346 for 2h 30 min at 180V and then stained with ethidium bromide (0.1 µg/mL) for 10
347 minutes and visualized by the gel documentation system (Axygen).

348

349 **Mice infection and phenotypic characterization**

350 Wild-type 129sv and *Stat1* KO mice were purchased from the Jackson Laboratory and
351 Taconic Biosciences and bred locally at the Washington University in St. Louis
352 (WUSTL) CSRB vivarium. Wild type 129sv mice were originally purchased from the
353 Jackson Laboratory and maintained in-house in a breeding colony. 5-day-old pups

were orally inoculated with rD6/2-2g-NLuc (1.3×10^6 FFU) or PBS. Diarrhea was scored as previously described (Broome et al). On the indicated day animals were sacrificed and small intestine, colon, mesenteric lymph node, pancreas, and liver were collected, weighed, homogenized in PBS with Ca^{2+} and Mg^{2+} and clarified by centrifugation. Homogenized tissues were subjected to Luciferase activity. Proximal and distal small intestines samples were collected: proximal samples were collected at about 2-3 cm from the pyloric sphincter while distal were collected at about 0.5 cm from the caecum.

362

363 **IVIS**

Wild-type 129sv and *Stat1* KO mice were purchased from the Jackson Laboratory and Taconic Biosciences and bred locally at the Washington University in St. Louis (WUSTL) CSRB vivarium. Five-day-old suckling pups were orally infected with rD6/2-2g-NLuc (3.5×10^3 FFU). Diarrhea was evaluated from day 1 to day 12 post infection. To perform IVIS, we firstly weighted the mice, and oral gavage Nano-Glo™ substrate (1/20 dilution in PBS; to make sure 50 μL per mouse, 1/25-1/57 dilution in PBS) for 3.5 hours and then performed IVIS (exposure time: 1 second) by using the IVIS Spectrum BL.

372

Statistical analysis. All statistical tests were performed as described in the indicated figure legends using Prism 9.0. Statistical significance was determined using a one-way ANOVA when comparing three or more groups. When comparing two groups, a Mann-Whitney test and student t test were performed. The number of an independent experiment performed is indicated in the relevant figure legends.

378

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389

390 **Conflicts of interest**

391 Nothing to report

392

393 **Figure legends**

394 **Fig. 1. Generation and validation of a bioluminescent rD6/2-2g-NLuc.**

395 (A) A schematic diagram of a genetically engineered pT7 plasmid that encodes NLuc
396 with nucleotide positions indicated. UTR, untranslated region; P2A, self-cleaving P2A
397 peptide gene of porcine teschovirus-1.

398 (B) BHK-T7 cells were transfected with pT7-NSP3 and increasing amounts of
399 pT7-NSP3-NLuc for 48 hours, and cell lysates were analyzed by western blot.

400 (C) BHK-T7 cells were transfected with pT7 or pT7-NSP3-NLuc plasmids for 48
401 hours. The luciferase activity was determined by Nano-Glo® luciferase assay. Data
402 are presented as the average of three experiments and error bars indicate standard
403 error of the mean (SEM) (Student t test; *** P < 0.001).

404 (D) MA104 cells were infected with rD6/2-2g and rD6/2-2g-NLuc viruses (MOI=0.1)
405 for 24 hours, and cell lysates were analyzed by western blot.

406 (E) dsRNA profiles. Viral RNA was extracted from sucrose cushion-concentrated
407 virus, separated on a 10% polyacrylamide gel, and then stained with ethidium
408 bromide. The dsRNA segment numbers are indicated and the position of the
409 engineered segment 7 is marked with a yellow arrowhead.

410 (F) Luciferase activity of rD6/2-2g and rD6/2-2g-NLuc. MA104 cells were infected
411 with 10-fold serially diluted rD6/2-2g or rD6/2-2g-NLuc. Cells were harvested at 48

hpi and the luciferase activity was determined by Nano-Glo® luciferase assay. Results are expressed as the mean luminescence of triplicates and error bars show the SEM (one-way ANOVA with Dunnett's test; ns, not significant, * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$, **** $P < 0.0001$).

Fig. 2. Growth kinetics of bioluminescent rD6/2-2g-NLuc in MA104 cells.

(A) MA104 cells were infected with rD6/2-2g or rD6/2-2g-NLuc (MOI=0.01) in the presence of trypsin (0.5 μ g/ml) and harvested at the indicated time points. The viral mRNA level was determined by RT-qPCR assay and normalized to that of GAPDH. Data are the average of three experiments, error bars indicate SEM (two-way ANOVA test; ns, not significant, * $P < 0.05$, ** $P < 0.01$).

(B) Multi-step growth curves of rD6/2-2g-NLuc. MA104 cells were infected with rD6/2-2g or rD6/2-2g-NLuc (MOI=0.01) in the presence of trypsin (0.5 μ g/ml) and harvested at the indicated time points. The viral titers were determined by an immunoperoxidase focus-forming assay. Data are the average of three experiments, error bars indicate SEM (two-way ANOVA test; ns, not significant, * $P < 0.05$, ** $P < 0.01$).

(C) Plaque formation of rD6/2-2g-NLuc. Plaques were generated on MA104 monolayers and detected by crystal violet staining at 7 dpi. The diameter of at least 25 randomly selected plaques from 2 independent plaque assays was measured by a bright-field microscope. Error bars indicate SEM (Student t test; **** $P < 0.0001$).

(D) Functional stability of luciferase activity in rD6/2-2g-NLuc after sequential passage. rD6/2-2g-NLuc was sequentially passaged in MA104 cells. The luciferase activity for passages 3-8 was determined by Nano-Glo® luciferase assay as described. Results are expressed as the mean luminescence of duplicates. Error bars show SEM. Luminescence from NLuc substrate from MA104 cells infected with rD6/2-2g were plotted as a reference.

Fig. 3. Bioluminescence of rD6/2-2g-NLuc in the intestines and the systemic sites

441 **in wild-type 129sv mice.**

442 (A) Five-day-old wild-type 129sv pups (n=5) were orally infected with 1.3×10^6
443 FFUs of rD6/2-2g-NLuc and diarrhea was monitored till 5 days post infection.

444 (B-G) Five-day-old wild-type 129sv pups were orally infected with 1.3×10^6 FFUs
445 of rD6/2-2g-NLuc, then euthanized at indicated days post infection. Bioluminescence
446 from indicated tissue homogenates was determined by Nano-Glo® luciferase assay.
447 Luminescence from NLuc substrate of uninfected mice tissues were plotted as a
448 reference.

449

450 **Fig. 4. Infectivity and pathogenicity of rD6/2-2g-NLuc *in vivo*.**

451 (A) Five-day-old 129sv mice (n=6) were orally inoculated with 3.5×10^3 FFUs of
452 rD6/2-2g-NLuc. The diarrhea rate was monitored from 1 to 12 days post infection.

453 (B) Viral shedding in stool samples was detected by an FFU assay and normalized to
454 the feces weight.

455 (C) Representative images of rD6/2-2g-NLuc infected pups (1 to 12 days). The
456 bioluminescent signal is expressed in photons per second per square centimeter per
457 steradian (p/sec/cm²/sr).

458 (D) Quantification of the luminescence in (C). The dashed line indicates the upper
459 limit of detection.

460

461 **Fig. 5. Transmission rD6/2-2g-NLuc *in vivo*.**

462 (A) Five-day-old 129sv mice were co-housed with 6 infected (3.5×10^3 FFUs of
463 rD6/2-2g-NLuc) and 6 uninfected littermates in the same cage. The diarrhea rate was
464 monitored from 1 to 12 days post infection.

465 (B) Viral shedding in stool samples was detected by an FFU assay and normalized to
466 the feces weight.

467 (C) Representative images of naive pups (1 to 12 days). The bioluminescent signal is
468 expressed in photons per second per square centimeter per steradian (p/sec/cm²/sr).

469 (D) Quantification of the luminescence in (C). The dashed line indicates the upper

470 limit of detection.

471

472 **Fig. 6. Characterization of rD6/2-2g-NLuc infection in *Stat1* KO 129sv mice.**

473 (A) Five-day-old *Stat1* KO 129sv mice (n=9) were orally inoculated with 3.5×10^3
474 FFUs of rD6/2-2g-NLuc. The diarrhea rate was monitored from 1 to 12 days post
475 infection.

476 (B) Viral shedding in stool samples was detected by an FFU assay and normalized by
477 to feces weight.

478 (C) Representative images of rD6/2-2g-NLuc infected *Stat1* KO pups (1 to 12 days).
479 The bioluminescent signal is expressed in photons per second per square centimeter
480 per steradian (p/sec/cm²/sr).

481 (D) Quantification of the luminescence in (C). The dashed line indicates the upper
482 limit of detection.

483 (E) Statistical analysis of area under the curve (AUC) comparing data in Fig. 4D and
484 6D. Error bars show the SEM (one-way ANOVA test; ns, not significant, * $P < 0.05$,
485 ** $P < 0.01$).

486

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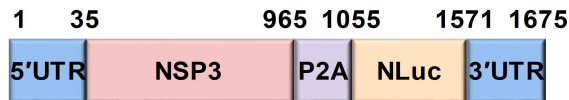
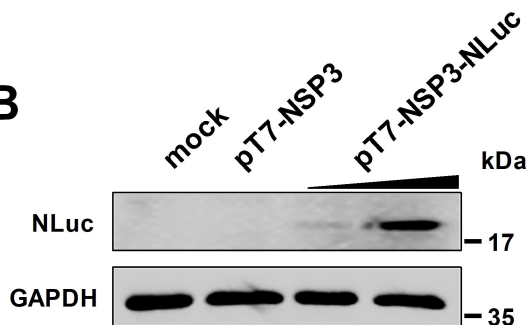
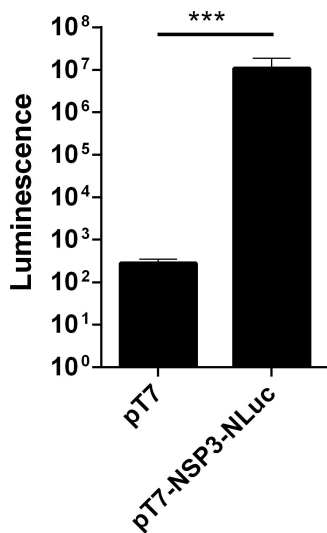
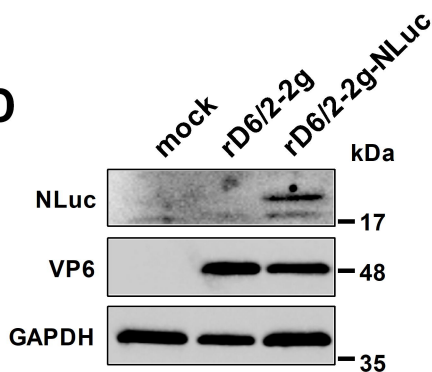
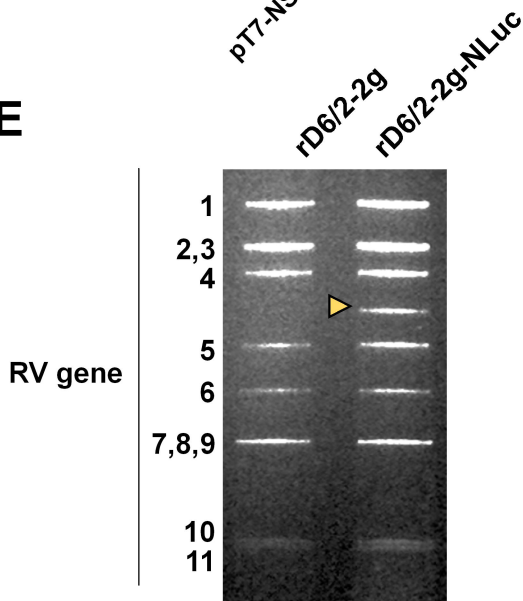
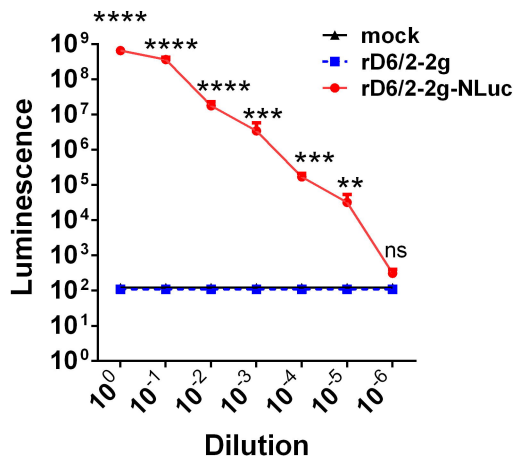
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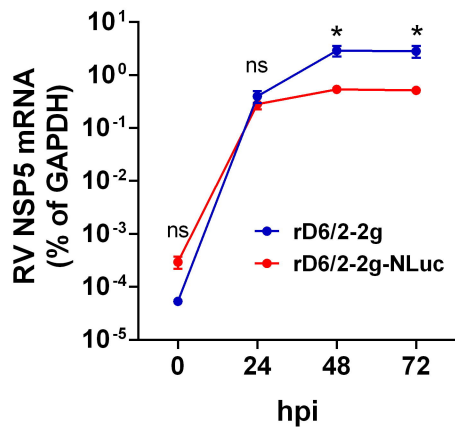
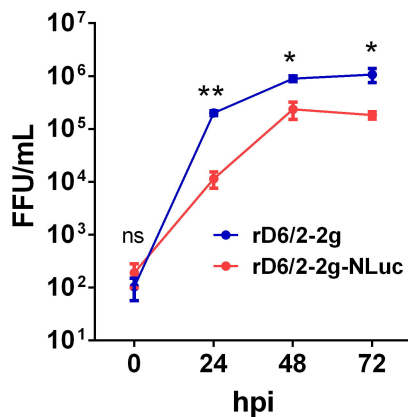
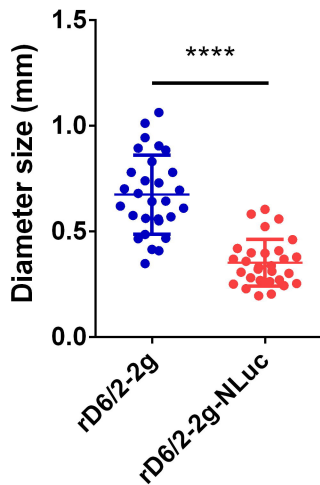
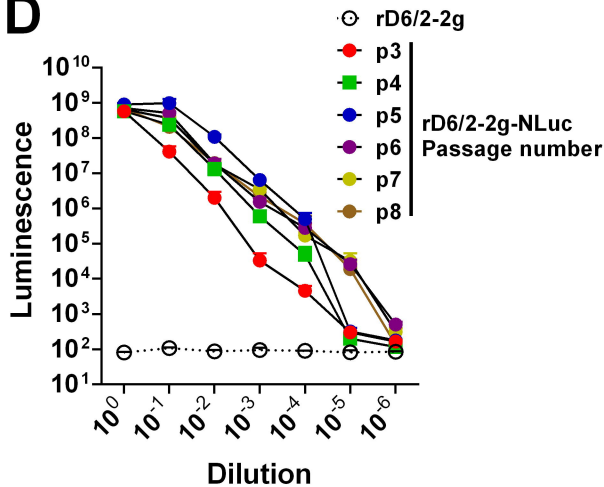
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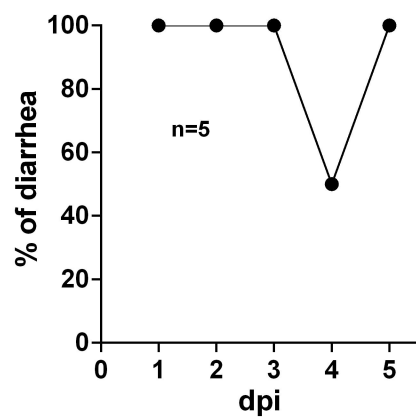
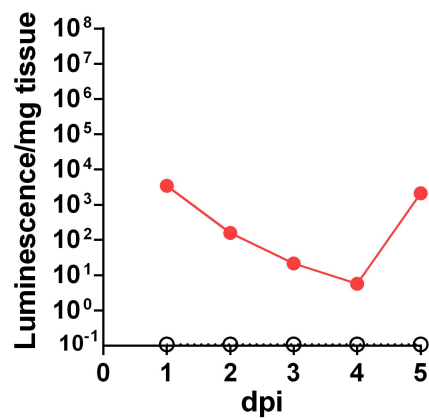
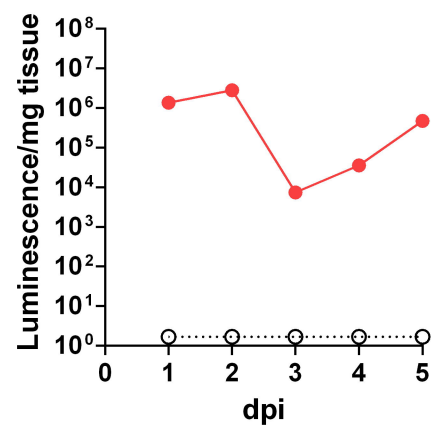
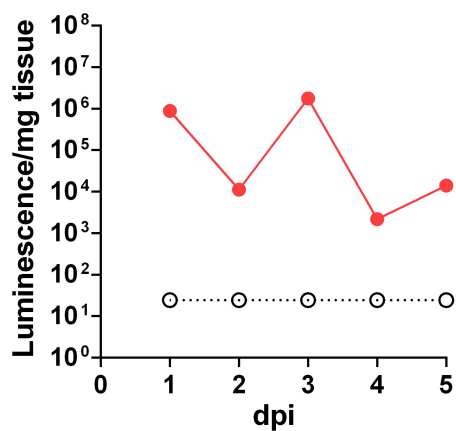
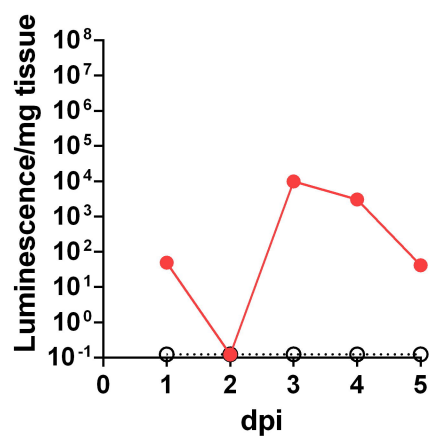
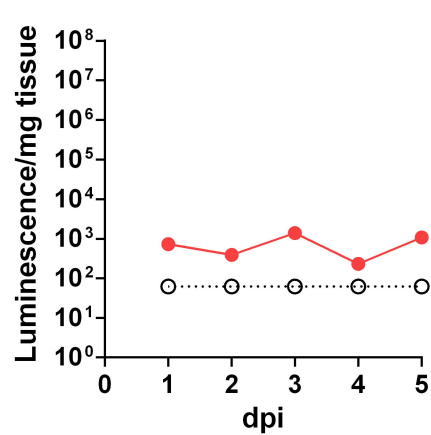
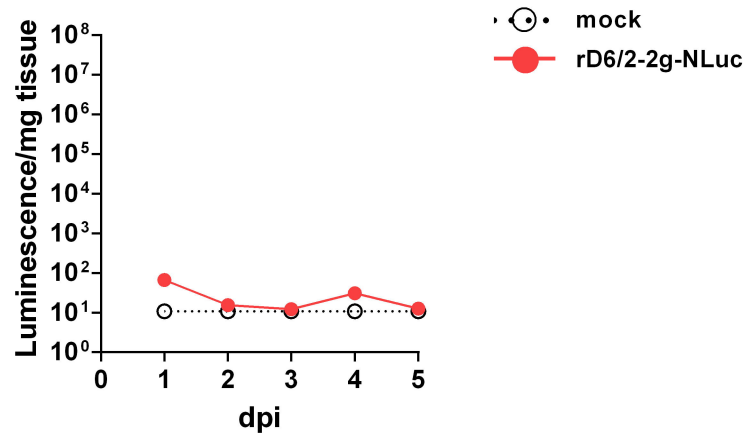
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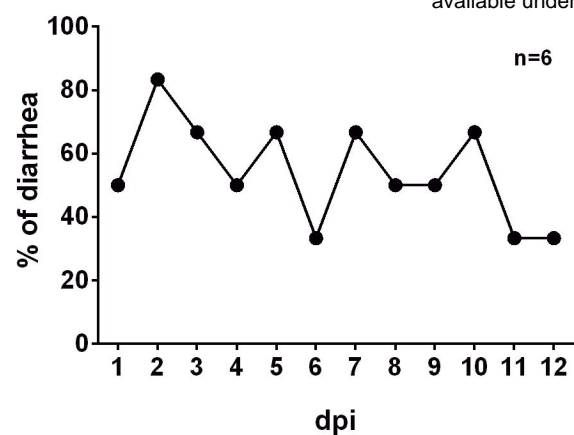
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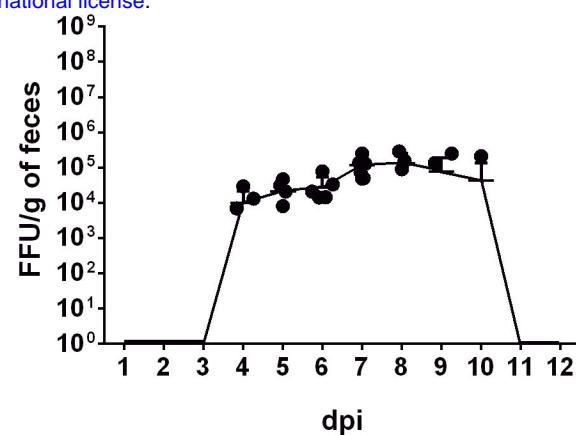
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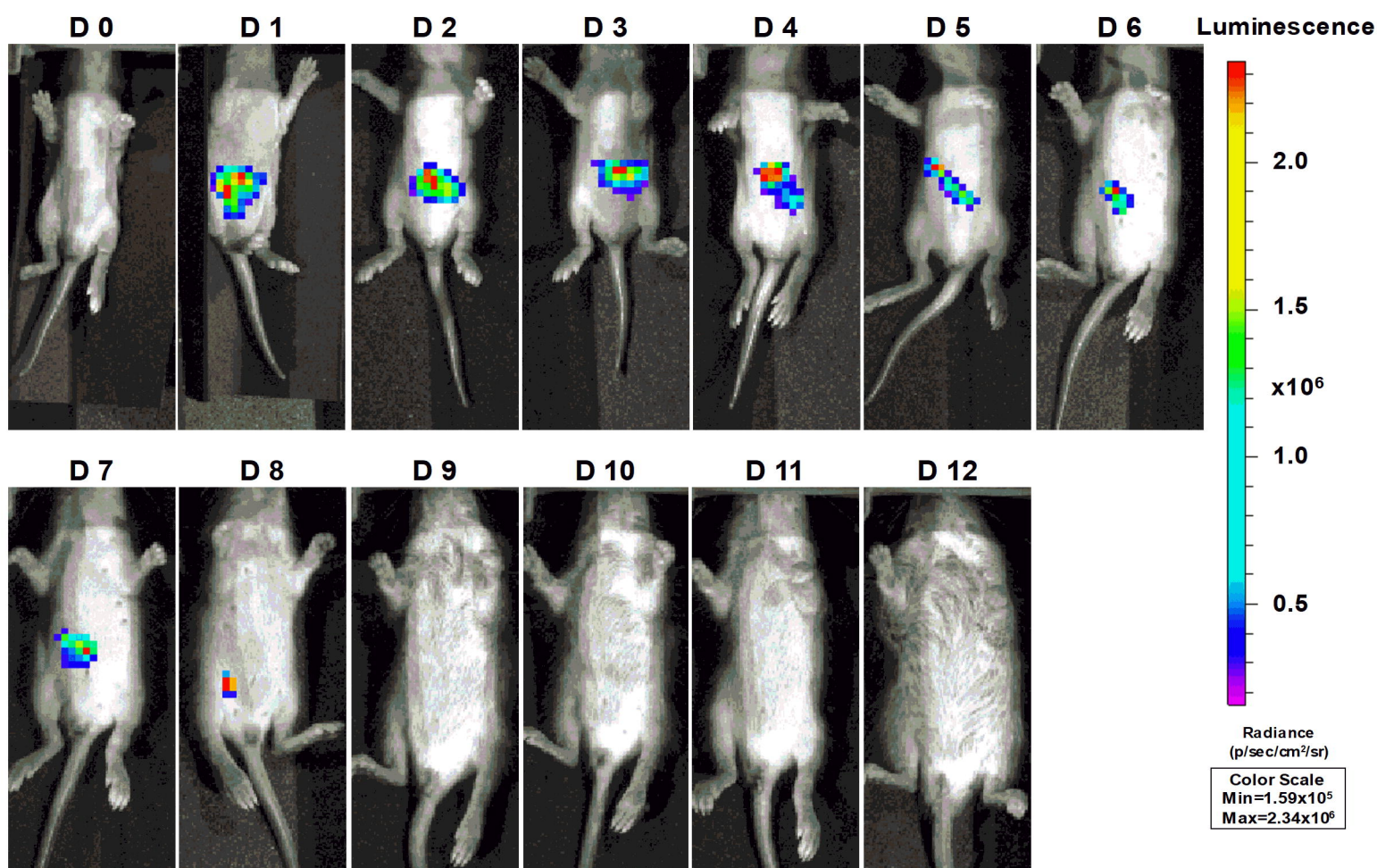
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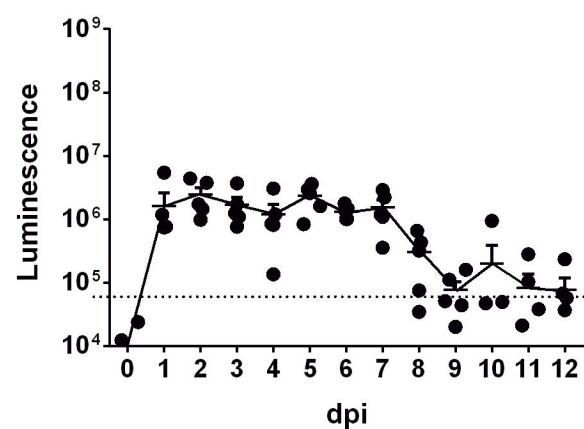
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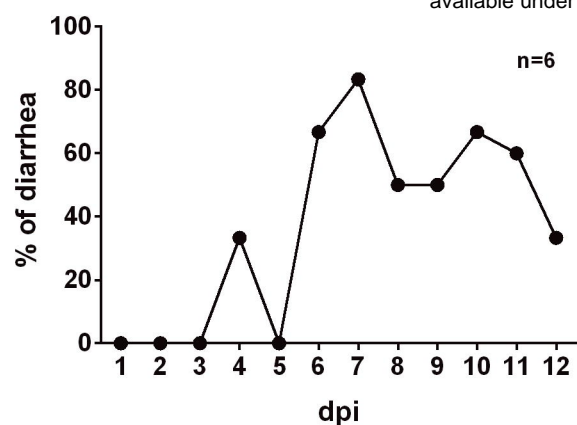
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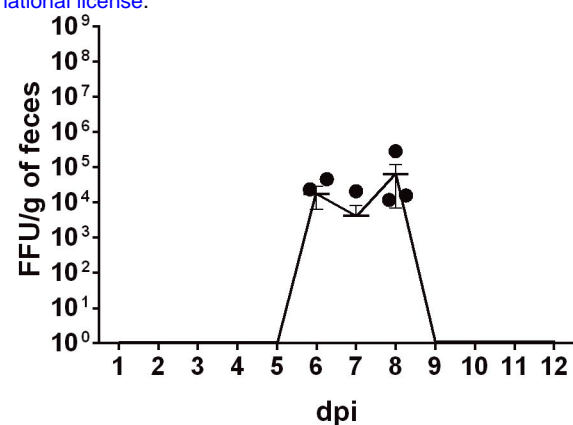
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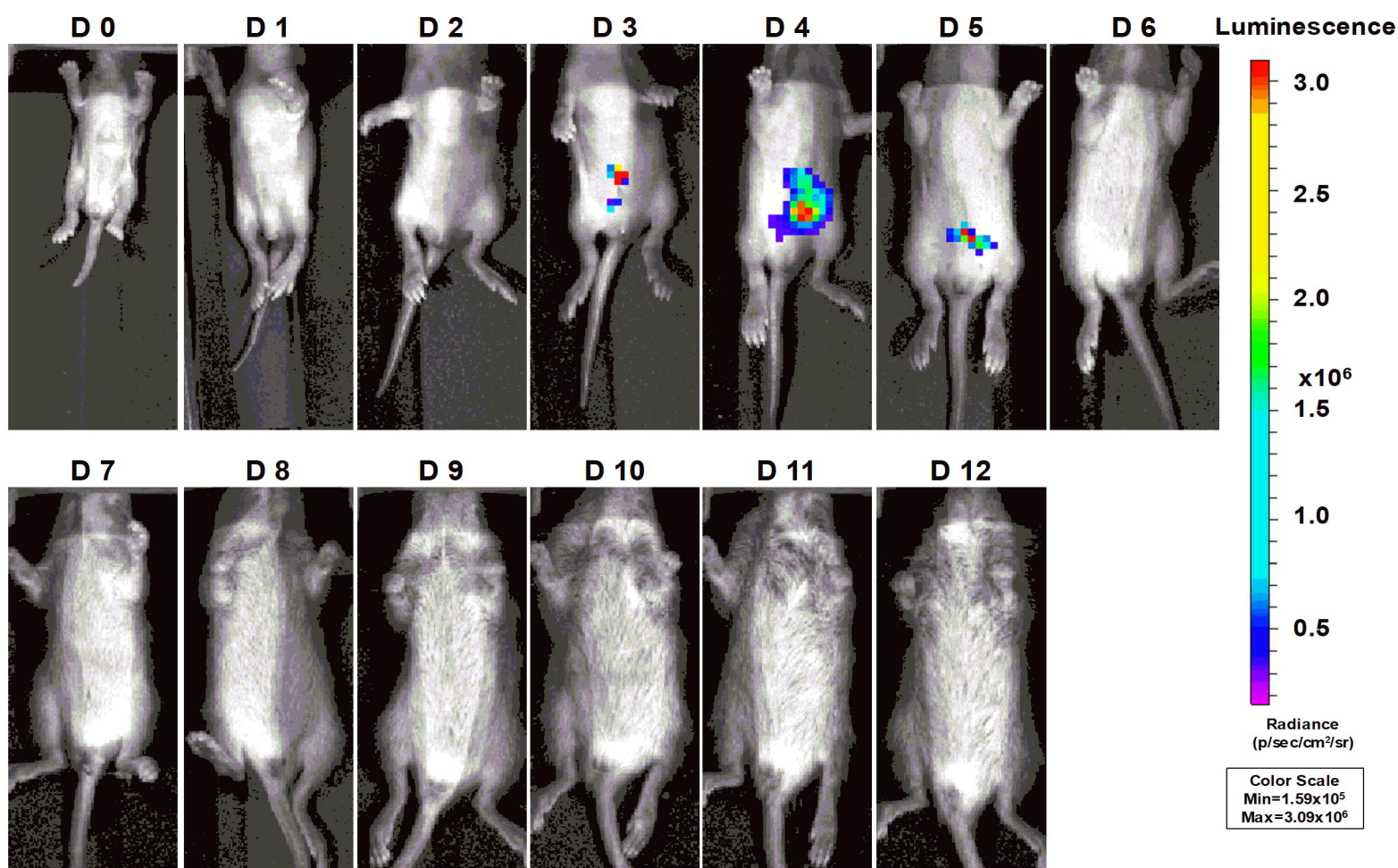
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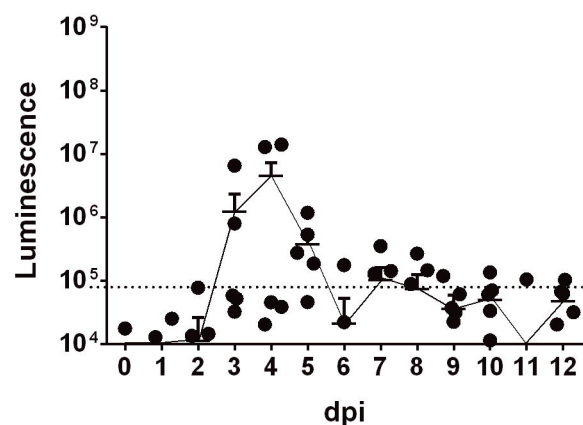
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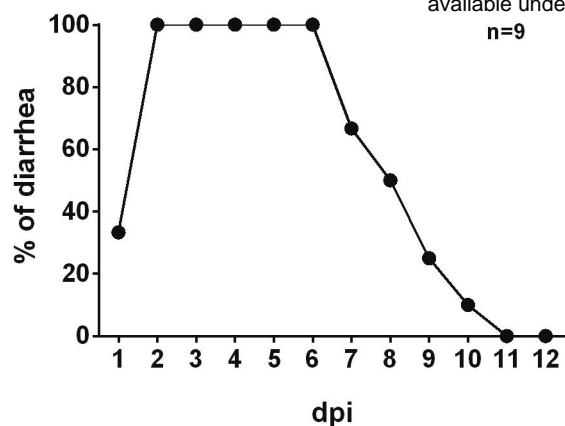
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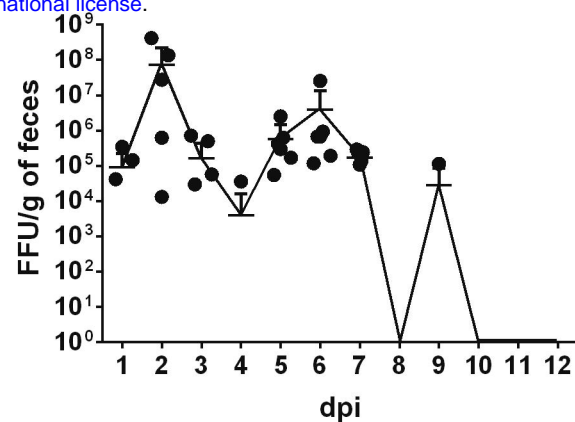
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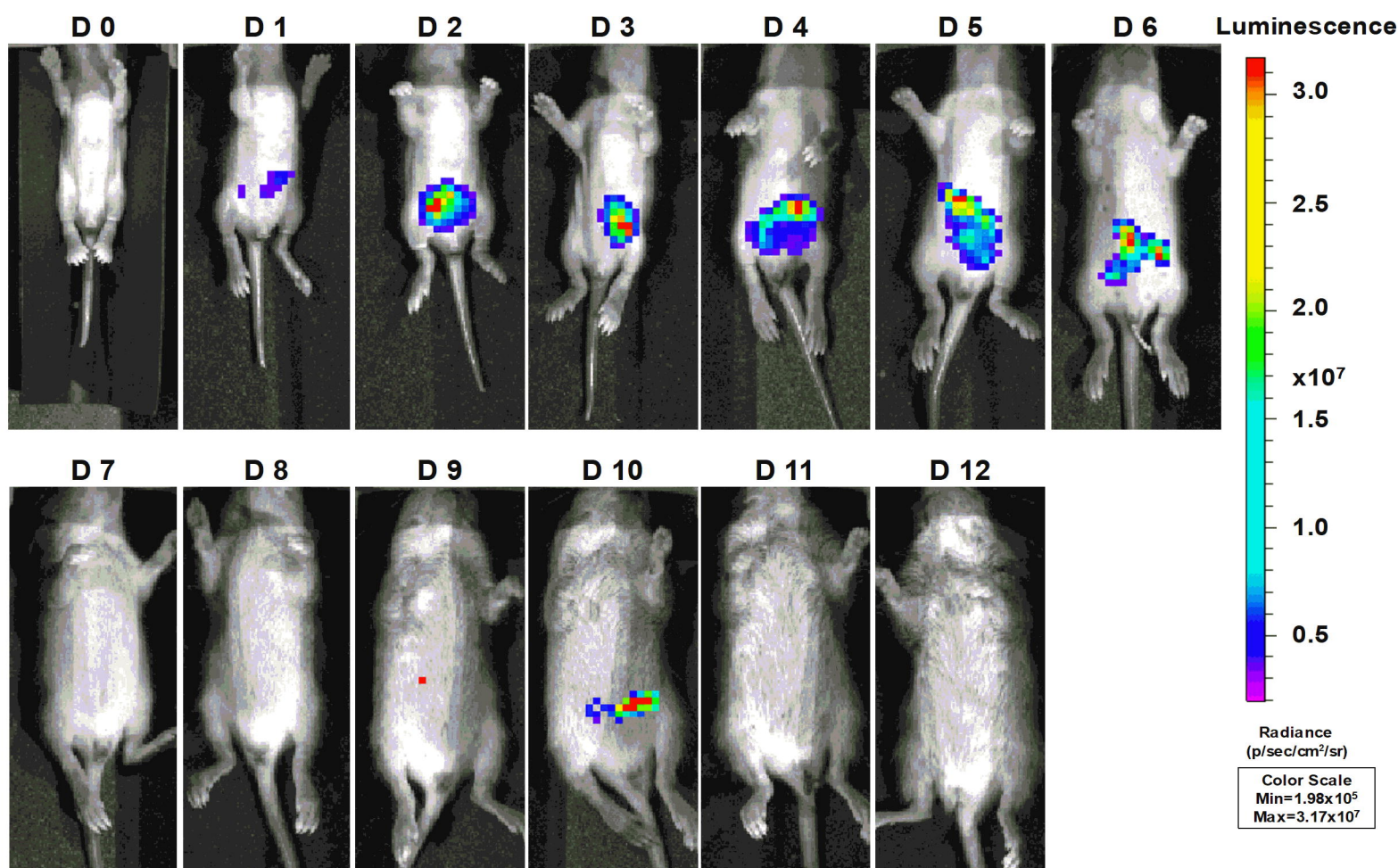
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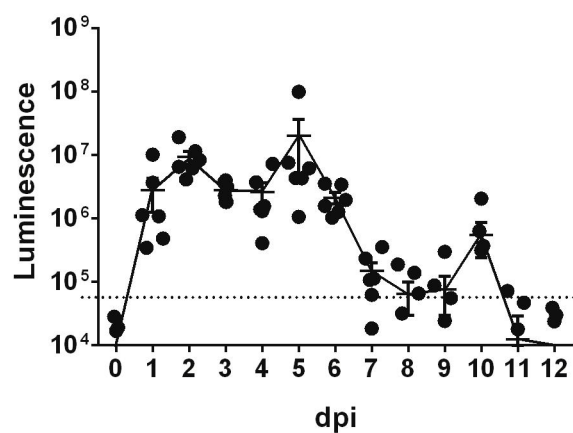
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