1	Species-specific pathogenicity of severe fever with thrombocytopenia syndrome virus is
2	determined by anti-STAT2 activity of NSs
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4	Rokusuke Yoshikawa ^{1,2§} , Saori Sakabe ^{1,3§} , Shuzo Urata ^{1,2} , and Jiro Yasuda ^{1,2,3*}
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6	¹ Department of Emerging Infectious Diseases, Institute of Tropical Medicine
7	(NEKKEN), ² National Research Center for the Control and Prevention of Infectious
8	Diseases (CCPID), ³ Graduate School of Biomedical Sciences and Program for
9	Nurturing Global Leaders in Tropical and Emerging Communicable Diseases, Nagasaki
10	University, 1-12-4 Sakamoto, Nagasaki 852-8523, Japan.
11	
12	[§] Equal contributions
13	*Corresponding author: Jiro Yasuda
14	Department of Emerging Infectious Diseases, Institute of Tropical Medicine
15	(NEKKEN), Nagasaki University, 1-12-4 Sakamoto, Nagasaki 852-8523, Nagasaki,
16	Japan.
17	Phone: +81-95-819-7848, FAX: +81-95-819-7848, E-mail: j-yasuda@nagasaki-u.ac.jp
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19 Running title: Species-specific pathogenicity of SFTSV

21 ABSTRACT

22 Severe fever with thrombocytopenia syndrome virus (SFTSV) is a novel emerging virus that has been identified in China, South Korea, and Japan, and induces 23 thrombocytopenia and leukocytopenia in humans with a high case fatality rate. SFTSV 24 is pathogenic to humans, while immunocompetent adult mice and golden Syrian 25 26 hamsters infected with SFTSV never show apparent symptoms. However, mice 27 deficient for the gene encoding the α chain of the interferon (IFN) α and β receptor (Ifnar $1^{-/-}$ mice) and golden Syrian hamsters deficient for the gene encoding signal 28 transducer and activator of transcription 2 ($Stat2^{-/-}$ hamsters) are highly susceptible to 29 30 SFTSV infection, with infection resulting in death. The nonstructural protein (NSs) of 31 SFTSV has been reported to inhibit the type I IFN response through sequestration of 32 human STAT proteins. Here, we demonstrated that SFTSV induces lethal acute disease 33 in STAT2-deficient mice, but not in STAT1-deficient mice. Furthermore, we discovered 34 that NSs cannot inhibit type I IFN signaling in murine cells due to an inability to bind to murine STAT2. Taken together, our results imply that the dysfunction of NSs in 35 antagonizing murine STAT2 can lead to inefficient replication and the loss of 36 37 pathogenesis of SFTSV in mice.

38

IMPORTANCE

40	Severe fever with thrombocytopenia syndrome (SFTS) is an emerging infectious
41	disease caused by SFTS virus (SFTSV), which has been reported in China, South Korea,
42	and Japan. Here, we revealed that mice lacking STAT2, which is an important factor for
43	antiviral innate immunity, are highly susceptible to SFTSV infection. We also show that
44	SFTSV NSs cannot exert its anti-innate immunity activity in mice due to the inability of
45	the protein to bind to murine STAT2. Our findings suggest that the dysfunction of
46	SFTSV NSs as an IFN antagonist in murine cells confers a loss of pathogenicity of
47	SFTSV in mice.

KEYWORDS: SFTSV, NSs, animal model, mouse, STAT2

51 **INTRODUCTION**

52 Severe fever with thrombocytopenia syndrome (SFTS) is an emerging infectious disease caused by the SFTS virus (SFTSV), which is a novel Phlebovirus of the 53 54 Phenuiviridae family. SFTSV was first isolated in rural areas of central China in 2011 and subsequently identified in South Korea and Japan (1-4). Moreover, another 55 emerging phlebovirus genetically close to SFTSV, Hartland virus, was found in the 56 57 United States (5). SFTS is clinically characterized by fever, vomiting, diarrhea, thrombocytopenia, leukocytopenia, and elevated serum levels of enzymes, such as 58 59 creatine kinase (CK), aspartate aminotransferase (AST), alanine transaminase (ALT), and lactate dehydrogenase (LDH) (6-8). However, the pathogenesis of SFTSV in 60 61 humans is still poorly understood, and no effective vaccines or antiviral drugs are 62 currently available for treatment of SFTS. The SFTSV genome is composed of three negative-strand RNA segments (S, M, 63

- and L). The L segment encodes the viral RNA-dependent RNA polymerase (L), the M
 segment encodes the glycoprotein precursors (Gn and Gc), and the S segment encodes
 the nucleocapsid protein (N) and nonstructural protein (NSs).
- 67 The innate immune response, including the type I interferon (IFN) response, is 68 important for preventing viral infection (9). Antiviral innate immunity is initiated by the

69	recognition of viral infection through cellular pattern recognition receptors (PRRs), such
70	as transmembrane toll-like receptor 3 (TLR3), cytosolic RIG-I-like receptors, and
71	MDA5 (10). Upon recognition, this signal cascade leads to the induction of type I IFN.
72	The activation of the IFN signaling pathway by the binding of secreted IFN to IFN
73	receptors results in the phosphorylation of STAT1 and STAT2. The heterodimer or
74	homodimer of phosphorylated STAT forms heterotrimeric interferon-stimulated gene
75	factor 3 (ISGF3) with IRF-9. The translocation of ISGF3 into the cell nucleus results in
76	the activation of antiviral IFN-stimulated genes (ISGs) by its binding to an
77	IFN-stimulated response element (ISRE) (11). However, during a phlebovirus infection,
78	viral NSs is thought to play a major role in repressing the innate immune response by
79	targeting the IFN response pathway as an IFN antagonist (12-15). Previous studies have
80	reported that NSs of SFTSV inhibits type I and III IFN responses through sequestration
81	of human STAT2 protein in viral replication complexes (13-15).

SFTSV infections do not cause severe disease in immunocompetent mice and golden Syrian hamsters, while type I IFN receptor knock-out (*Ifnar1*^{-/-}) mice, which lack the gene encoding the α chain of the IFN α and β receptor, and STAT2-deficient golden Syrian hamsters are highly susceptible to SFTSV, with infection resulting in death (16-19). This suggests that efficient replication of SFTSV in mice and hamsters is

87	prevented by antiviral innate immunity and that NSs of SFTSV does not inhibit IFN
88	signaling in murine and hamster cells. STAT1 and STAT2 are important factors for
89	antiviral innate immunity. However, the relationship between SFTSV pathogenicity and
90	STAT function remains unknown. In this study, to investigate the role of STAT1 and
91	STAT2 in the pathogenesis and replication of SFTSV in mice, we examined the
92	pathogenicity of SFTSV in $Stat1^{-/-}$ and $Stat2^{-/-}$ mice and measured the antagonistic
93	activities of NSs against IFN signaling in murine cells.

95 **RESULTS**

96 SFTSV infection to *Ifnar1^{-/-}* mice.

97	It has been reported that <i>Ifnar1</i> ^{-/-} mice are highly susceptible to SFTSV strains
98	YL-1 and SPL010, with infection resulting in death (16-17). In this study, we used the
99	YG-1 strain isolated from the first SFTS patient reported in Japan (4). Wild-type
100	C57BL/6 mice and Ifnar1 ^{-/-} mice were intradermally (id) inoculated with 10 focus
101	forming units (FFU) of the SFTSV (YG-1). All infected wild-type mice survived
102	without any clinical signs (Fig. 1A). In contrast, all infected Ifnar1 ^{-/-} mice died 5 to 8
103	days after infection (Fig. 1A). Moreover, all Ifnar1 ^{-/-} mice infected with SFTSV showed
104	severe body weight loss, leukocytopenia, and thrombocytopenia 1-7 days postinfection
105	(pi) (Fig. 1B-D). The titers of SFTSV in the organs (brains, lungs, livers, spleens,
106	kidneys, and intestines) and plasma of infected $Ifnar1^{-/-}$ and wild-type mice were also
107	measured by focus forming assay at 3, 5, and 7 days pi. As shown in Fig. 2, efficient
108	viral replication in <i>Ifnar1</i> ^{-/-} mice was observed in the spleen and plasma at 3 days pi, all
109	organs at 5 days pi, and the spleen, kidney, and intestine at 7 days pi. In contrast, we
110	could not detect infectious SFTSV in the plasma or organs of wild-type mice.

111 The results show that the SFTSV (YG-1) induces lethal acute infection 112 accompanied by thrombocytopenia in $IfnarI^{-/-}$ mice.

114 SFTSV causes lethal infection in *Stat2^{-/-}* mice, but not *Stat1^{-/-}* mice.

Next, to investigate the roles of STAT1 and STAT2 in SFTSV infection, Stat1-/-, 115 Stat2^{-/-}, and Ifnar1^{-/-} mice were infected with YG-1 strain. None of the infected Stat2-/-116 mice survived, while all of the $Stat1^{-/-}$ mice infected with YG-1 survived (Fig. 1A). As 117 shown in Fig. 1B, $Stat2^{-/-}$ mice lost body weight at 1–7 days pi, while $Stat1^{-/-}$ mice lost 118 body weight at 1-5 days pi, and then recovered. Unlike in Ifnar1^{-/-} mice, the number of 119 white blood cells in $Stat1^{-/-}$ and $Stat2^{-/-}$ mice transiently decreased after infection and 120 then recovered to normal values (Fig. 1C). Both $Stat1^{-/-}$ and $Stat2^{-/-}$ mice infected with 121 SFTSV showed thrombocytopenia regardless of survival (Fig. 1D). This implies that the 122 123 lethality of SFTSV is not associated with thrombocytopenia. Next, we measured the titers of SFTSV in organs (brains, lungs, livers, spleens, kidneys, and intestines) and 124 plasma of infected $Stat1^{-/-}$ and $Stat2^{-/-}$ mice by focus forming assay at 3, 5, and 7 days pi. 125 In $Stat2^{-/-}$ mice, SFTSV was detected in the plasma, spleen, and kidney at 3 days pi, the 126 plasma and all organs at 5 days pi, and the spleen and kidney at 7 days pi. In Stat1^{-/-} 127 mice, SFTSV replicated in the lung, spleen, kidney, intestine, and plasma; however, the 128 maximum titers of SFTSV in these organs and plasma were lower than those in Stat2^{-/-} 129 mice (Fig. 2). 130

131 These results indicate that $Stat2^{-/-}$ and $Ifnar1^{-/-}$ mice, but not $Stat1^{-/-}$ mice, are 132 highly susceptible to SFTSV infection, which suggests that STAT2 plays a critical role 133 in the suppression of SFTSV replication in mice.

134

135 SFTSV NSs cannot suppress type I IFN signaling in murine cells.

136 It has been reported that SFTSV suppress type I IFN signaling in human cells (13). 137 Therefore, we hypothesized that SFTSV cannot suppress type I IFN signaling in murine cells, and IFN-mediated innate immunity restricts SFTSV replication in mice. To 138 139 address this possibility, the ISRE activation by SFTSV infection was examined in 140 human-derived HEK293T cells and mouse-derived NIH3T3 cells using dual-luciferase 141 reporter (DLR) gene assay. As shown in Fig 3A, SFTSV infection did not induce the 142 ISRE activation in HEK293T cells, while the ISRE activation was induced by SFTSV infection in NIH3T3 cells. These results suggest that SFTSV cannot inhibit type I IFN 143 144 signaling in murine cells. 145 Recently, SFTSV NSs has been reported to function as an IFN antagonist (13-15).,

Therefore, the effects of NSs on ISRE activation in HEK293T cells and NIH3T3 cells were examined by DLR gene assay. In this experiment, the VP40 protein of mouse-adapted Marburg virus (mMARV), which functions as an IFN signaling inhibitor

149	in murine cells, was used as a positive control (20). As shown in Fig. 3B, IFN- α A/D
150	treatment induced strong ISRE activation in both HEK293T and NIH3T3 cells. As
151	expected, the expression of SFTSV NSs significantly inhibited the ISRE activation
152	driven by IFN- $\alpha A/D$ in HEK293T cells, while NSs expression did not suppress this
153	activation in NIH3T3 cells (Fig. 3B). We also confirmed that the ISRE activation driven
154	by IFN- α A/D in NIH3T3 cells was suppressed by the expression of mMARV VP40 (Fig.
155	3C). These results suggest that SFTSV NSs cannot interfere with type I IFN signaling in
156	murine cells.
157	We also examined the effect of NSs on IFN- α A/D-induced expression of mRNA
158	for two ISGs, ISG56 and oligoadenylate synthetase 1 (OAS1), by real-time qPCR. The
159	induction of both ISGs by IFN in HEK293T cells was suppressed by NSs expression,
160	whereas NSs did not suppress induction in NIH3T3 cells (Fig. 3D).
161	
162	NSs does not interact with murine and hamster STAT2.
163	SFTSV NSs inhibits type I IFN signaling by the interaction with human STAT1
164	(hSTAT1) and STAT2 (hSTAT2) (13-15). However, the interaction with hSTAT1 is
165	weaker than that with hSTAT2 (15). We also showed here that mice deficient for STAT2.
166	but not STAT1, were highly susceptible to SFTSV infection and progressed to severe

disease (Fig1). Therefore, we suggest that NSs cannot interact with murine STAT2 andthus cannot antagonize IFN signaling in murine cells.

First, to examine whether NSs interacts with murine STAT2 (mSTAT2), we performed co-immunoprecipitation (co-IP) assays using lysates from cells transfected with a NSs expression plasmid. As shown in Fig. 4A, co-IP of STAT2 with NSs was observed only in the lysates from HEK293T cells, but not from NIH3T3 cells, suggesting that NSs interact with hSTAT2 but not with mSTAT2. It was also indicated that NSs bound to hSTAT1, but not to murine STAT1 (mSTAT1) (Fig. 4A).

We also examined the interaction of NSs with hamster STAT2 (hamSTAT2) by co-IP assay, since *Stat2*^{-/-} hamsters, like *Stat2*^{-/-} mice, are highly susceptible to SFTSV infection (19). As shown in Fig. 4B, the interaction of NSs with hamSTAT2, as well as mSTAT2, was not observed.

The interaction of NSs with STAT2 was also examined by subcellular colocalization of the proteins. The NSs expression plasmid was cotransfected with the expression plasmids for hSTAT2, mSTAT2, or hamSTAT2 into HEK293T, NIH3T3, or BHK-21 cells, respectively, and subcellular localizations of proteins were observed. Cytoplasmic inclusion bodies (IBs), mainly formed by NSs, were also observed in HEK293T, NIH3T3, and BHK-21 cells (Fig. 4C). In HEK293T cells, hSTAT2 colocalizes with NSs, consistent with previous reports (13-15). On the other hand, in
NIH3T3 and BHK-21 cells, colocalization of NSs with mSTAT2 or hamSTAT2 was not
observed (Fig. 4C). These findings indicate that NSs interacts with hSTAT2, but not
mSTAT2 and hamSTAT2.

189

190 The N-terminal region of hSTAT2 is important for binding to NSs.

To investigate the difference in NSs binding between human and murine STAT2, we prepared a series of chimeric proteins from hSTAT2 and mSTAT2 (Fig. 5A). The interactions between NSs and the chimeric STAT2 proteins were examined by co-IP assay. All chimeric proteins efficiently expressed in NIH3T3 cells (Fig. 5B). As shown in Fig. 5B, NSs interacted with hSTAT2, HHM, HMM, H(101–315)MM, and H(101– 315)HM, but not mSTAT2, MHH, MMH, H(1–100)MM, H(1–221)MM and H(222– 315)MM.

We also confirmed the results by observation of colocalization of the proteins (Fig. 5C). NSs colocalized with hSTAT2, HHM, HMM, H(101–315)MM and H(101– 315)HM, while mSTAT2, MHH, MMH, H(1–100)MM, H(1–221)MM, and H(222– 315)MM, did not colocalize with NSs. These results are consistent with those from the co-IP assay. It has been reported that SFTSV NSs interacts with the DNA-binding

203	domain (DBD: amino acid position 316-485) of hSTAT2 (13). Taken together, these
204	results suggest that region 101-315 of hSTAT2 is important for the binding to NSs in
205	addition to the DBD, or that this region of mSTAT2 interferes with the binding to NSs.
206	To further examine whether MHH and MMH, which cannot bind to NSs, function
207	as STAT2 proteins in the presence of NSs, ISRE activation by MHH or MMH in the
208	presence of NSs was investigated by the DLR assay in HEK293T cells. ISRE activation
209	was reduced by NSs in the absence of exogenous STAT2, and overexpression of
210	exogenous hSTAT2 slightly compensated for this reduction induced by NSs (Fig. 6). In
211	contrast, the suppression of ISRE activation by NSs was significantly recovered by
212	mSTAT2, MMH, and MHH, suggesting that MMH and MHH, as well as mSTAT2,
213	activate ISRE as a functional STAT2 protein in the presence of NSs in HEK293T cells.
214	
215	Type I IFN induces the phosphorylation of mSTAT2 in the presence of NSs.
216	Tyrosine phosphorylation of STAT2 is important for its function as a transcription
217	factor in the type I IFN signaling pathway (21). To assess whether type I IFN signaling
218	can phosphorylate mSTAT2 in the presence of NSs, HEK293T and NIH3T3 cells were
219	transfected with empty vector or the NSs-HA expression plasmid, and then treated with
220	IFN- $\alpha A/D$. The expression levels of hSTAT2 and mSTAT2 were stable regardless of

221	NSs expression (Fig. 7A). In the absence of NSs, IFN induced the phosphorylation of
222	hSTAT2 and mSTAT2. hSTAT2 phosphorylation in HEK293T cells was significantly
223	downregulated by NSs in a concentration-dependent manner. In contrast, mSTAT2 in
224	NIH3T3 cells was phosphorylated irrespective of NSs expression (Fig. 7A). These were
225	also observed in SFTSV infected cells (Fig. 7B). It is likely that NSs cannot interfere
226	with the phosphorylation of mSTAT2, since NSs cannot bind to mSTAT2.

228 **DISCUSSION**

229 Previous studies in animal models of SFTSV infection indicated the importance of the type I IFN response in mice and STAT2 in hamsters to prevent disease 230 progression (16-17, 19). Both STAT1 and STAT2 have been found to be key factors in 231 232 the IFN signaling pathway (21). In this study, we demonstrated that STAT2-deficient 233 mice, as well as type I IFN receptor-deficient mice, are more susceptible to SFTSV than 234 STAT1-deficient mice and wild-type mice. Moreover, our results indicate that NSs has no ability to suppress the IFN signaling pathway in murine cells because NSs, which 235 236 binds hSTAT1 and hSTAT2, cannot interact with mSTAT1 and mSTAT2. The SFTSV growth in the organs of $Stat1^{-/-}$ mice were much less efficient than those in $Stat2^{-/-}$ and 237 Ifnar1^{-/-} mice, although SFTSV could grow in Stat1^{-/-} mice (Fig. 2). In addition, SFTSV 238 infection induced milder symptom in $Stat 1^{-/-}$ mice than in $Stat 2^{-/-}$ and $I fnar 1^{-/-}$ mice (Fig. 239 240 1). These suggests that innate immunity dependent on STAT2, but not STAT1, strongly 241 inhibits the replication of SFTSV in mice. In several human cell lines, the expression of 242 some ISGs is upregulated by STAT2, independent of STAT1 (22). For example, the 243 expression levels of several ISGs including APOBEC3G, PKR, ISG15, and Mx1 are 244 increased by type I IFN stimulation regardless of STAT1 expression in the human liver cell lines, Huh7 and Hep3B. However, when the expression of STAT2 is suppressed, the 245

246	expression levels of these ISGs are not increased after type I IFN treatment. These
247	findings suggest that ISGs expression mediated by STAT2, but not STAT1, suppress
248	mainly SFTSV infection in mice.
249	SFTSV causes severe disease in human, while immunocompetent adult mice
250	never show any apparent severe symptoms after SFTSV infection (18). In this study, we
251	showed that mice lacking STAT2 are highly susceptible to SFTSV infection. Moreover,
252	NSs can suppress the phosphorylation of hSTAT2, whereas the phosphorylation of
253	mSTAT2 is not inhibited by NSs due to the inability of NSs to bind to mSTAT2. The
254	data also indicates that NSs cannot interact with hamSTAT2. This result is consistent
255	with a previous report showed that STAT2-deficient hamsters are also highly susceptible
256	to SFTSV infection (19).
257	The relationship between NSs and STAT2 is reminiscent of that of dengue virus
258	NS5 and STAT2 (A23-25). Previous studies reported that innate immunity mediated by
259	mSTAT2 restricts dengue virus replication in mice (25-26). To block the type I IFN
260	signaling pathway in humans, dengue virus NS5 expression leads to the degradation of
261	hSTAT2 (25). However, NS5 cannot suppress type I IFN signaling in mice, because
262	mSTAT2 is resistance to NS5-mediated degradation (23-25). These results demonstrate
263	that STAT2 may be one of the determinants for the species specificity of dengue virus.

264	Here, we elucidated that SFTSV induces lethal disease in STAT2-deficient mice and that
265	NSs cannot interact with mSTAT2. Thus, similar to dengue virus NS5, the anti-STAT2
266	activity of NSs appears to determine the species specificity of SFTSV infection.
267	In this study, chimeric mutants of hSTAT2 and mSTAT2 revealed that residues
268	101-315 of hSTAT2 are required for the interaction with NSs or that these residues in
269	mSTAT2 interfere with the interaction with NSs. We also confirmed that mSTAT2 and
270	all of the chimeric mutants of hSTAT2 and mSTAT2 used in this study can activate
271	ISRE-mediated gene expression as functional STAT2 proteins. Previously, Ning et al.
272	reported that the DBD region (316-485) of hSTAT2 is required for the interaction with
273	NSs (13). However, we showed that mutants possessing the DBD region of mSTAT2,
274	HMM, and H(101-315)MM, can still bind to NSs (Fig. 5). At present, we cannot
275	explain this result, although this discrepancy may be explained by the differences in the
276	three-dimensional protein structure between our mutants and Ning's deletion mutants.
277	Further analyses will be required to clarify this issue.

Taken together, we conclude that the anti-STAT2 activity of NSs determines the species specificity of SFTSV infection. In addition, we show that $Stat2^{-/-}$ mice, as well as *Ifnar1*^{-/-} mice and $Stat2^{-/-}$ hamsters, are highly susceptible to SFTSV infection, which causes lethal disease, suggesting that $Stat2^{-/-}$ mice may be useful as an animal model to 282 develop antiviral drugs against SFTSV infection.

284 MATERIALS AND METHODS

285 **Ethics statement.**

- 286 Our research protocol for the use of mice follows the Nagasaki University Regulations
- for Animal Care and Use, which was approved by the Animal Experiment Committee of
 Nagasaki University (approval number; 151110-1-5).
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Animals.
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B6.129-Dnase2a<tm10sa>Ifnar1<tm1Agt> mouse strain (RBRC04021; *Ifnar1*^{-/-} *Dnase2a*^{+/-}) (27) was provided by RIKEN BRC through the National BioResource Project of MEXT, Japan. *Ifnar1*^{-/-} mice were generated by crossing *Dnase2a*^{+/-} *Ifnar1*^{-/-} parents. *Stat1*^{-/-} mice were provided by Dr. Takayuki Yoshimoto (Tokyo Medical University). *Stat2*^{-/-} mice were purchased from the Jackson Laboratory. The genetical backgrounds of all mice used in this study are C57BL/6.

298 SFTSV infection in mice.

Six- to eight-week-old male or female mice were used in this study. In infection experiments, each mouse was infected with SFTSV by intradermal injection (50 μ L of virus solution for 10 FFU). Mouse survival and body weight changes were monitored

302	daily for 14 days pi. At 1, 3, and 7 days pi, blood was collected, and platelets and
303	leukocytes were counted using a hematology analyzer (Sysmex pocH-100iV; Sysmex or
304	VetScan HMII; Abaxis). Mice were euthanized, and plasma and organs (lungs, livers,
305	spleens, kidneys, intestines, and brains) were collected. Viruses in plasma were titrated
306	by focus forming assay using Vero E6 cells. To determine the titer of SFTSV in organs,
307	mouse organs were collected in a 9-fold volume of minimum essential media
308	(Sigma-Aldrich) and then disrupted through high-speed shaking using TissueLyser II
309	(Qiagen). After centrifugation (700 x g, 5min, 4° C), the amounts of viruses in the
310	homogenates (10% w/v) were determined by focus forming assay in VeroE6 cells. The
311	limit of detection is 100FFU/g.

313 Cell culture and virus.

Human embryonic kidney (HEK) 293T (CRL-11268; ATCC), NIH3T3 (CRL-1658; ATCC), BHK-21 (JCRB9020; Health Science Research Resources Bank (HSRRB)), and Vero E6 (CRL-1586; ATCC) cells were cultured in Dulbecco modified Eagle medium (Sigma-Aldrich) supplemented with 10% heat-inactivated (fetal calf serum) FCS and antibiotics (Thermo Fisher Scientific). The SFTSV (YG1), a field isolate from an SFTS patient in Japan, was kindly provided by Dr. Ken Maeda, Yamaguchi 320 University (28). The virus stocks were prepared from culture supernatants of Vero E6321 cells.

322

323 Focus forming assay.

324 SFTSV titers were determined using a focus forming assay. Briefly, confluent 325 monolayers of Vero E6 cells were inoculated with 10-fold dilutions of SFTSV and 326 incubated at 37°C for 1 hour. The inoculum was removed, and cells were washed and 327 overlaid with MEM (Sigma-Aldrich) containing 0.7% agarose and 0.7% FCS. After 4 328 days, cells were fixed with 4% paraformaldehyde and permeabilized with 329 phosphate-buffered saline (PBS) containing 1% Triton X-100. Cells were blocked with 330 PBS containing 0.1% Triton X-100 and 1% bovine serum albumin (BSA), and then 331 incubated with anti-SFTSV N protein rabbit polyclonal antibody (28). After washing 332 with PBS, the cells were incubated with anti-rabbit IgG conjugated with horseradish 333 peroxidase (Promega). After more washes with PBS, SFTSV-infected cells were detected by using Peroxidase Stain DAB Kit and Metal Enhancer for DAB Stain 334 335 (Nacalai Tesque). The number of SFTSV N positive cells were determined and 336 normalized as FFU/ml.

337

338 Plasmids.

339 The open reading frame (ORF) encoding NSs was amplified by reverse transcription 340 PCR (RT-PCR) from SFTSV (YG-1) viral RNA and inserted into pcDNA3.1 (Invitrogen) with a hemagglutinin (HA) tag using the primers listed in Table 1 to 341 342 produce pcDNA3.1/NSs-HA. To prepare the expression plasmids for 6xHistidine 343 (His)-tagged hSTAT2 (pcDNA3.1/hSTAT2-His), mSTAT2 (pcDNA3.1/mSTAT2-His), 344 and hamSTAT2 (pcDNA3.1/hamSTAT2-His), the desired genes were amplified by RT-PCR using the primers listed in Table 1 from the cDNA of HEK293T, NIH3T3, and 345 346 BHK-21 cells, respectively. The expression plasmids for the series of STAT2 chimeras 347 were constructed using an In-Fusion HD Cloning kit (TaKaRa) with the primers listed 348 in Table 1. The expression plasmid for mMARV VP40 was constructed from MARV VP40 (28) using a KOD-Plus-Mutagenesis Kit (TOYOBO) using the primers listed in 349 350 Table 1.

351

352 **Reporter gene assay.**

HEK293T cells and NIH3T3 cells were cotransfected with ISRE reporter plasmid (450 ng) (Promega) and pRL-TK plasmid [the *Renilla* luciferase control plasmid for the constitutively active herpes simplex virus (HSV)-thymidine kinase (TK) promoter] (100

356	ng) (Promega). Twenty-four hours after transfection, the transfected cells were
357	mock-infected or infected with SFTSV. Two days after infection, luciferase activities
358	were measured with a DLR assay kit (Promega) and a TriStar LB941 system (Berthold).
359	For the reporter gene assays with SFTSV NSs transfection, the ISRE reporter plasmid
360	(500 ng) (Promega) and pRL-TK [the Renilla luciferase control plasmid for the
361	constitutively active herpes simplex virus (HSV)-thymidine kinase (TK) promoter]
362	plasmid (100 ng) (Promega) were transfected into HEK293T and NIH3T3 cells with or
363	without the indicated amount of pcDNA3.1/NSs-HA plasmid or the expression plasmid
364	for mMARV VP40 (800 ng) using LT-1 (Mirus) or Lipofectamine 3000 (Thermo Fisher
365	Scientific) according to the manufacturer's instructions. Twenty-four hours after
366	transfection, cells were treated with IFN- $\alpha A/D$ (500 U/ml) (Sigma-Aldrich) or were left
367	untreated for 18 h. Luciferase activities then were measured with a DLR assay kit
368	(Promega) and a TriStar LB941 system (Berthold).

370 Quantitative real-time reverse transcription PCR (RT-PCR) of IFN-treated cells.

Total RNA was extracted from HEK293T and NIH3T3 cells using an RNeasy Mini kit
(Qiagen). Real-time RT-PCR was performed by using the One Step TB GreenTM
PrimeScriptTM PLUS RT-PCR Kit (TaKaRa) according to the manufacturer's

instructions, and the PCR primers used in this study are listed in Table 1. Relative mRNA levels were calculated by the $2^{-\Delta\Delta CT}$ method with *GAPDH* mRNA as an internal control and are shown as relative fold changes normalized to the untreated control samples.

378

379 Immunoblotting.

380 Protein samples were separated by SDS-PAGE and transferred to nitrocellulose membranes (Millipore). After blocking with 5% skim milk in Tris-buffered 381 382 saline/Tween 20 (TBS-T), the membranes were incubated with each of the following 383 antibodies: anti-HA (18850; QED Biosciences Inc.), anti-His (9F2; Wako), anti-hSTAT2 (A-9; Santa Cruz), anti-mSTAT2 (07-140; Merc), anti-STAT2 (phosphor Y690) 384 385 (ab53132; Abcam), anti-STAT1 (D19KY; Cell signaling) or anti-β actin (AC-15; Sigma-Aldrich). After washing with TBS-T, the membranes were incubated with 386 387 horseradish peroxidase-labeled secondary antibodies, Anti-Mouse IgG-HRP (A2304; Sigma-Aldrich) or Anti-Rabbit IgG-HRP (WA4011; Promega), and then detected using 388 389 ECL prime (GE Healthcare) according to the manufacturer's instructions. Bands were 390 visualized using an image analyzer (LAS-4000 mini; GE Healthcare).

391

392 Co-IP assay.

393 To examine the binding of NSs to endogenous STAT2, the pcDNA3.1/NSs-HA plasmid 394 (15 µg) was transfected into HEK293T and NIH3T3 cells in 10-cm dishes (Thermo 395 Fisher Scientific) using LT-1 or Lipofectamine 3000, respectively. To examine the 396 binding of NSs to exogenous STAT2 or STAT2 derivatives, the pcDNA3.1/NSs-HA 397 plasmid (3 µg) was cotransfected into NIH3T3 cells with each STAT2 expression 398 plasmid (1 µg) in 6-well plates (Thermo Fisher Scientific) using Lipofectamine 3000. 399 Two days after transfection, cells were lysed in lysis buffer (25 mM Tris-HCl, 150 mM 400 NaCl, 1 mM EDTA, and 1% Triton X-100) containing a protease inhibitor cocktail 401 (Roche). To perform the co-IP assay, cell lysates were mixed with magnetic beads 402 conjugated to an anti-His monoclonal antibody (OGHis; MBL) or anti-HA monoclonal 403 antibody (5D8; MBL) and incubated at 4°C for 3 h or overnight, respectively. Then, the 404 magnetic beads were washed with lysis buffer and wash buffer (50 mM Tris-HCl, 1% 405 NP-40, 0.25% deoxycholic acid sodium salt, 150 mM NaCl, and 1 mM EDTA) and 406 analyzed by immunoblotting as described above.

407

408 Immunofluorescence assay (IFA).

409 The expression plasmids for His-tagged hSTAT2, mSTAT2, hamSTAT2, or a series of

410	STAT2 chimeras were cotransfected into HEK293T, NIH3T3, or BHK-21 cells with the
411	pcDNA3.1/NSs-HA plasmid. Twenty-four hours after transfection, transfected cells
412	were fixed using 4% paraformaldehyde-PBS (Wako), and then the fixed cells were
413	incubated in 1% Triton X-100 in PBS for permeabilization and blocked in 10% FCS in
414	blocking buffer (3% BSA and 0.3% Triton X-100 in PBS). Cells then were treated with
415	primary antibodies (anti-HA (18850; QED Biosciences Inc.) or anti-His (9F2; Wako))
416	overnight at 4°C and stained with secondary antibodies (Anti-Rabbit IgG - H&L (FITC)
417	(ab6009; abcam) or Anti-Mouse IgG (whole molecule) -TRITC (T5393;
418	Sigma-Aldrich)) for 2 h at room temperature with DAPI (Roche) for visualization of
419	nuclei. Image acquisition was performed with a LSM780 microscope (Carl Zeiss)

421 **Statistical analyses.** Significant differences in virus titers in mouse organs among 422 mouse strains were determined by one-way ANOVA following Tukey's multiple 423 comparisons test using GraphPad Prism software. And statistically significant 424 differences in the data of Fig3A, 3B, 3C, 3D and 6 were determined using Student's 425 *t*-test (Fig3A. 3C and 3D) or Dunnett's test (Fig 3B and 6). 426

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555 FIGURE LEGENDS

Fig. 1. Clinical pathologies of mice infected with SFTSV. Wild-type C57BL/6 (WT), *Ifnar1^{-/-}*, *Stat1^{-/-}*, and *Stat2^{-/-}* mice were infected with 10 FFU of SFTSV (YG1). (A)
Survival and (B) body weight changes were observed daily for 14 days pi (n = 10). For
WBC and PLT counts, blood samples were collected from two male and three female
mice at 0, 1, 3, 5, and 7 days pi. The values are shown as mean ± Standard Divisions
(SDs).

Fig. 2. Titers of SFTSV in mouse organs. Mice were inoculated with 10 FFU of SFTSV YG1. Three female mice were euthanized for virus titration at 3, 5, and 7 days pi. The virus titers in the mouse brains, lungs, livers, spleens, kidneys, intestines, and plasma were measured by focus forming assay. The values are shown as mean \pm SDs (n = 3). **P* < 0.05, compared among each mouse strain.



cells with or without the expression plasmid for NSs. Twenty-four hours after transfection, cells were treated with or without IFN-αA/D (500 U/ml) for 18 hours and then were lysed to measure luciferase activity and detect protein expression using immunoblotting. RLU in cells transfected with the empty vector or the indicated amount of NSs expression plasmid in the absence of IFN-αA/D were set as 1. Fold activation by IFN-αA/D are indicated. (C) The experiment done in (B) was repeated using the expression plasmid for mMARV VP40 in NIH3T3 cells. (D) NSs expression plasmid (1 µg or 1.5 µg) or control plasmid was transfected into HEK293T or NIH3T3 cells, respectively. Twenty-four hours after transfection, the cells were treated with IFN-αA/D (200 U/ml) or left untreated for 10 hours. Expression levels of <i>Isg56</i> and <i>Oas1</i> mRNAs in each cell line were measured by real-time qPCR. The mRNA expression levels of ISG56 and OAS1 in IFN-αA/D untreated cells were set as 1. Fold activations by IFN-αA/D are indicated. These assays were independently performed in triplicate. The data represent averages with SDs. **in panel A and B, <i>P</i> < 0.05 versus no NSs.	574	are indicated. (B) The reporter plasmids were transfected into HEK293T or NIH3T3
transfection, cells were treated with or without IFN-αA/D (500 U/ml) for 18 hours and then were lysed to measure luciferase activity and detect protein expression using immunoblotting. RLU in cells transfected with the empty vector or the indicated amount of NSs expression plasmid in the absence of IFN-αA/D were set as 1. Fold activation by IFN-αA/D are indicated. (C) The experiment done in (B) was repeated using the expression plasmid for mMARV VP40 in NIH3T3 cells. (D) NSs expression plasmid (1 µg or 1.5 µg) or control plasmid was transfected into HEK293T or NIH3T3 cells, respectively. Twenty-four hours after transfection, the cells were treated with IFN-αA/D (200 U/ml) or left untreated for 10 hours. Expression levels of <i>Isg56</i> and <i>Oas1</i> mRNAs in each cell line were measured by real-time qPCR. The mRNA expression levels of ISG56 and OAS1 in IFN-αA/D untreated cells were set as 1. Fold activations by IFN-αA/D are indicated. These assays were independently performed in triplicate. The data represent averages with SDs. **in panel A and B, <i>P</i> < 0.05 versus no NSs.	575	cells with or without the expression plasmid for NSs. Twenty-four hours after
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immunoblotting, RLU in cells transfected with the empty vector or the indicated amount of NSs expression plasmid in the absence of IFN-αA/D were set as 1. Fold activation by IFN-αA/D are indicated. (C) The experiment done in (B) was repeated using the expression plasmid for mMARV VP40 in NIH3T3 cells. (D) NSs expression plasmid (1 μ g or 1.5 μ g) or control plasmid was transfected into HEK293T or NIH3T3 cells, respectively. Twenty-four hours after transfection, the cells were treated with IFN-αA/D (200 U/ml) or left untreated for 10 hours. Expression levels of <i>Isg56</i> and <i>Oas1</i> mRNAs in each cell line were measured by real-time qPCR. The mRNA expression levels of ISG56 and OAS1 in IFN-αA/D untreated cells were set as 1. Fold activations by IFN-αA/D are indicated. These assays were independently performed in triplicate. The data represent averages with SDs. **in panel A and B, <i>P</i> < 0.05 versus no NSs.	577	then were lysed to measure luciferase activity and detect protein expression using
579 of NSs expression plasmid in the absence of IFN-αA/D were set as 1. Fold activation by 580 IFN-αA/D are indicated. (C) The experiment done in (B) was repeated using the 581 expression plasmid for mMARV VP40 in NIH3T3 cells. (D) NSs expression plasmid (1 582 µg or 1.5 µg) or control plasmid was transfected into HEK293T or NIH3T3 cells, 583 respectively. Twenty-four hours after transfection, the cells were treated with IFN-αA/D 584 (200 U/ml) or left untreated for 10 hours. Expression levels of <i>Isg56</i> and <i>Oas1</i> mRNAs 585 in each cell line were measured by real-time qPCR. The mRNA expression levels of 586 ISG56 and OAS1 in IFN-αA/D untreated cells were set as 1. Fold activations by 587 IFN-αA/D are indicated. These assays were independently performed in triplicate. The 588 data represent averages with SDs. **in panel A and B, <i>P</i> < 0.05 versus no NSs.	578	immunoblotting. RLU in cells transfected with the empty vector or the indicated amount
IFN-αA/D are indicated. (C) The experiment done in (B) was repeated using the expression plasmid for mMARV VP40 in NIH3T3 cells. (D) NSs expression plasmid (1 μ g or 1.5 µg) or control plasmid was transfected into HEK293T or NIH3T3 cells, respectively. Twenty-four hours after transfection, the cells were treated with IFN-αA/D (200 U/ml) or left untreated for 10 hours. Expression levels of <i>Isg56</i> and <i>Oas1</i> mRNAs in each cell line were measured by real-time qPCR. The mRNA expression levels of ISG56 and OAS1 in IFN-αA/D untreated cells were set as 1. Fold activations by IFN-αA/D are indicated. These assays were independently performed in triplicate. The data represent averages with SDs. **in panel A and B, <i>P</i> < 0.05 versus no NSs.	579	of NSs expression plasmid in the absence of IFN- $\alpha A/D$ were set as 1. Fold activation by
expression plasmid for mMARV VP40 in NIH3T3 cells. (D) NSs expression plasmid (1 μ g or 1.5 μg) or control plasmid was transfected into HEK293T or NIH3T3 cells, respectively. Twenty-four hours after transfection, the cells were treated with IFN-αA/D (200 U/ml) or left untreated for 10 hours. Expression levels of <i>Isg56</i> and <i>Oas1</i> mRNAs in each cell line were measured by real-time qPCR. The mRNA expression levels of ISG56 and OAS1 in IFN-αA/D untreated cells were set as 1. Fold activations by IFN-αA/D are indicated. These assays were independently performed in triplicate. The data represent averages with SDs. **in panel A and B, <i>P</i> < 0.05 versus no NSs.	580	IFN- $\alpha A/D$ are indicated. (C) The experiment done in (B) was repeated using the
582μg or 1.5 μg) or control plasmid was transfected into HEK293T or NIH3T3 cells,583respectively. Twenty-four hours after transfection, the cells were treated with IFN- α A/D584(200 U/ml) or left untreated for 10 hours. Expression levels of <i>Isg56</i> and <i>Oas1</i> mRNAs585in each cell line were measured by real-time qPCR. The mRNA expression levels of586ISG56 and OAS1 in IFN- α A/D untreated cells were set as 1. Fold activations by587IFN- α A/D are indicated. These assays were independently performed in triplicate. The588data represent averages with SDs. **in panel A and B, <i>P</i> < 0.05 versus no NSs.	581	expression plasmid for mMARV VP40 in NIH3T3 cells. (D) NSs expression plasmid (1
respectively. Twenty-four hours after transfection, the cells were treated with IFN-αA/D (200 U/ml) or left untreated for 10 hours. Expression levels of <i>Isg56</i> and <i>Oas1</i> mRNAs in each cell line were measured by real-time qPCR. The mRNA expression levels of ISG56 and OAS1 in IFN-αA/D untreated cells were set as 1. Fold activations by IFN-αA/D are indicated. These assays were independently performed in triplicate. The data represent averages with SDs. **in panel A and B, $P < 0.05$ versus no NSs.	582	μg or 1.5 $\mu g)$ or control plasmid was transfected into HEK293T or NIH3T3 cells,
(200 U/ml) or left untreated for 10 hours. Expression levels of <i>Isg56</i> and <i>Oas1</i> mRNAs in each cell line were measured by real-time qPCR. The mRNA expression levels of ISG56 and OAS1 in IFN-αA/D untreated cells were set as 1. Fold activations by IFN-αA/D are indicated. These assays were independently performed in triplicate. The data represent averages with SDs. **in panel A and B, $P < 0.05$ versus no NSs.	583	respectively. Twenty-four hours after transfection, the cells were treated with IFN- $\alpha A/D$
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ISG56 and OAS1 in IFN-αA/D untreated cells were set as 1. Fold activations by IFN-αA/D are indicated. These assays were independently performed in triplicate. The data represent averages with SDs. **in panel A and B, $P < 0.05$ versus no NSs.	585	in each cell line were measured by real-time qPCR. The mRNA expression levels of
587 IFN- α A/D are indicated. These assays were independently performed in triplicate. The 588 data represent averages with SDs. **in panel A and B, <i>P</i> < 0.05 versus no NSs.	586	ISG56 and OAS1 in IFN- $\alpha A/D$ untreated cells were set as 1. Fold activations by
data represent averages with SDs. **in panel A and B, $P < 0.05$ versus no NSs.	587	IFN- $\alpha A/D$ are indicated. These assays were independently performed in triplicate. The
	588	data represent averages with SDs. **in panel A and B, $P < 0.05$ versus no NSs.

Fig. 4. Interaction of NSs with STAT1 and STAT2. (A) HEK293T or NIH3T3 cells were
transfected with the expression plasmid for HA-tagged NSs and co-IP assays were

592	performed. (B) NIH3T3 cells were transfected with the expression plasmids for
593	HA-tagged NSs and His-tagged hSTAT2 or hamSTAT2. The protein expression levels in
594	cell lysates (left) and in co-IP assays (right) using an anti-HA or anti-His antibody. (C)
595	Colocalization of NSs with STAT2. HEK293T, NIH3T3, or BHK-21 cells were
596	transfected with the expression plasmid for HA-tagged NSs and the expression plasmid
597	for His-tagged hSTAT2, mSTAT2, or hamSTAT2, respectively. IFA was also performed
598	with NSs, STAT2, and the nuclei shown in green, red, and blue, respectively.

599

600 Fig. 5. Determination of the region of hSTAT2 important for the binding to NSs. (A) 601 Schematic representation of the chimeric mutants of hSTAT2 and mSTAT2. (B) 602 NIH3T3 cells were cotransfected with the expression plasmids for HA-tagged NSs and 603 each of the STAT2 His-tagged chimeras. Representative results from the protein expression check in cell lysates (upper) and the co-IP assays using an anti-His antibody 604 605 (lower) are shown. (C) IFA was also performed with NSs, STAT2, and the nuclei shown 606 in green, red, and blue, respectively.

608 Fig. 6. Function of the NSs binding-deficient STAT2 chimera. The reporter plasmids were cotransfected into HEK293T cells with the expression plasmids for NSs and each 609

610	STAT2 chimera. Twenty-four hours after transfection, cells were treated with or without
611	IFN- $\alpha A/D$ (500 U/ml) for 18 hours and then were lysed to measure luciferase activity
612	(upper figure) or detect protein expression using immunoblotting (lower figure). The
613	ISRE activity was calculated by dividing RLU in IFN- α A/D-treated cells by the units
614	IFN- α A/D untreated cells. The ISRE activity in the absence of NSs was set as 100%.
615	The assays were independently performed in triplicate. The data represent averages with
616	SDs. ** $P < 0.05$ versus hSTAT2.

Fig. 7. Suppression of STAT2 phosphorylation by NSs. (A) HEK293T or NIH3T3 cells transfected with the expression plasmid for HA-tagged NSs were treated with IFN- α A/D (2000 U/ml) or left untreated for 45 minutes and were then lysed for detection of each protein expression by immunoblotting. (B) HEK293T or NIH3T3 cells infected with SFTSV at an MOI of 10 were treated with IFN- α A/D (2000 U/ml) or left untreated for 45 minutes and were then lysed for detection of each protein expression by immunoblotting.

Primer name	Primer sequence	Remarkes	
pcDNA-NSsHA-RV-F	atccaccatotcoctoaocaaatoctccaac		
	octrootaceteaaocotaatetooaacateotat	For the construction of	
pcDNA-NSsHA-Kpn-R	goatagaceteetteggaaggteace	pcDNA3.1/NSs-HA	
humanSTAT2hisF	atccaccatggcgcagtgggaaatgctg	·	
	activetacctcaateeteateeteateateacce	For the construction of	
humanSTAT2hisR	gatgcatattgaagtcagaaggcatcaagggtcc	pcDNA3.1/hSTAT2-His	
mouseSTAT2hisF	atccaccatggcgcagtgggagatgttg		
	gcttggtacctcaatggtgatggtgatgatgaccg	For the construction of	
mouseSTAT2hisR	gtatgcatattgaaggtatcaagagtccatcccaa	pcDNA3.1/mSTAT2-His	
hamSTAT2F	atccaccatggcgcagtgggagacactg	For the construction of	
hamSTAT2hicP	gcttggtacctcaatggtgatggtgatgatgaccg	ncDNA3 1/hamSTAT2-His	
	gtatgcatattgtcatcagaaggaatcaagggtcc		
mSTAT2-hDBD-veF	gttcttctgccaagctccgaaag		
HMM-HHM-inR	accggtatgcatattgaaggtatc	For the construction of	
hmSTAT2DBDveF	aatatgcataccggtcatcatcac	pHHM(#1)	
mSTAT2-hDBD-inR	gcttggcagaagaactgctggttctgaagg		
hSTAT2-mDBD-inF	acagagcctttgtagtagaaacccagccctg		
HMM-HHM-inR	accggtatgcatattgaaggtatc	For the construction of	
hmSTAT2DBDveF	aatatgcataccggtcatcatcac	pHMM(#2)	
hSTAT2-mDBD-veR	ctacaaaggctctgtggagcag		
mSTAT2-hDBD-inF	aaaggtcctttgtggtagaaacccagccc		
MMH-MHH-inR	accggtatgcatattgaagtcag	For the construction of	
hmSTAT2DBDveF	aatatgcataccggtcatcatcac	pMHH(#3)	
mSTAT2-hDBD-veR	ccacaaaggacctttggagcagac		
hSTAT2-mDBD-veF	gttcttctccaaccccccaag		
MMH-MHH-inR	accggtatgcatattgaagtcag	For the construction of	
hmSTAT2DBDveF	aatatgcataccggtcatcatcac	pMMH(#4)	
hSTAT2-mDBD-inR	gggttggagaagaactgctggttcttggg		
H(1-100)MMinF	cccaggatcctacccagttggctgagatg		
HMM-HHM-inR	accggtatgcatattgaaggtatc	For the construction of	
hmSTAT2DBDveF	aatatgcataccggtcatcatcac	pH(1-100)MM(#5)	
H(1-100)MMVeR	gggtaggatcctgggaaaagggctgaatg		
H(1-221)MMinF	cactgctaggccgattaaccaccctgg		
HMM-HHM-inR	accggtatgcatattgaaggtatc	For the construction of	
hmSTAT2DBDveF	aatatgcataccggtcatcatcac pH(1-221)MM(#6)		
H(1-221)MMVeR	atcggcctagcagtgctttggaggcatc		

Table 1. List of the primers used in this study

Table	1. ((Continued)
		· · · · · · · · · · · · · · · · · · ·

Primer name	Primer sequence	Remarkes
H222-315inF	gactggttggccgattaactaccctaatcg	
hSTAT2-mDBD-veR	ctacaaaggetetgtggageag	For the construction of pH(222-315)MM(#7)
hSTAT2-mDBD-inF	acagagcctttgtagtagaaacccagccctg	
H222-315veR	atcggccaaccagtcctttggagatgtcc	
MH(101-315)MMinF	cccaatggccctacccagttggctgagatg	
hSTAT2-mDBD-veR	ctacaaaggetetgtggageag	For the construction of
hSTAT2-mDBD-inF	acagagcctttgtagtagaaacccagccctg	pH(101-315)MM(#8)
MH(101-315)MMveR	ggtagggccattgggaaaggtctgaatatc	
MH(101-315)MMinF	cccaatggccctacccagttggctgagatg	
HMM-HHM-inR	accggtatgcatattgaaggtatc	For the construction of
hmSTAT2DBDveF	aatatgcataccggtcatcatcac	pH(101-315)HM(#9)
MH(101-315)MMveR	ggtagggccattgggaaaggtctgaatatc	
MARV VP40 S15PF	cttgaacccccctccttatgctgatcacgg	
MARV VP40 S15PR	tattgcatgtatgtgttgtaattgctggaactggcc	For the construction of
MARV VP40 G79SF	gttccggcatggctgcctcttgg	pmMARV VP40
MARV VP40 G79SR	gcttttgactgttcgctcgttatatgcagatatgtc	
hISG56F	cctccttgggttcgtctaca	For the Real-time RT-PCR
hISG56R	ggetgatatetgggtgeeta	detection of human ISG56 (Ref 13)
mISG56F	accatgggagagaatgctgat	For the Real-time RT-PCR
mISG56R	gccaggaggttgtgc	detection of mouse ISG56 (Ref: 30)
hOAS1realF	catccgcctagtcaagcactg	For the Real-time RT-PCR
hOAS1realR	caccacccaagtttcctgtag	detection of human OAS1 (Ref: 13)
mOAS1realF	gcctggtcacgcactggta	For the Real-time RT-PCR
mOAS1realR	aagccctgggctgtgttg	detection of mouse OAS1 (Ref: 31)
hGAPDH-F	atgggaaggtgaaggtcgg	For the Real-time RT-PCR
hGAPDH-R	ttactccttggaggccatgtg	detection of human GAPDH
mGAPDH-F	aggtcggtgtgaacggatttg	For the Real-time RT-PCR
mGAPDH-R	tgtagaccatgtagttgaggtca	detection of mouse GAPDH (Ref: 32)





Fig.2





Mock



С







NIH3T3







IFN (-)

IFN(+)





В

