The actin nucleator Spir-1 is a virus restriction factor that promotes IRF3 activation

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Abstract

Cellular proteins often have multiple and diverse functions. This is illustrated with protein Spir-1 that is an actin nucleator, but, as shown here, also functions to enhance IRF3 activation downstream of RNA sensing by RIG-I/MDA-5. In human and mouse cells lacking Spir-1, IRF3 activation is impaired, whereas Spir-1 overexpression enhanced IRF3 activation. Furthermore in Spir-1$^{-/-}$ cells, the infectious virus titres and sizes of plaques formed by two viruses that are sensed by RIG-I, vaccinia virus (VACV) and Zika virus, are increased. These observations demonstrate the biological importance of Spir-1 in the response to virus infection. Like cellular proteins, viral proteins also have multiple and diverse functions. Here, we also show that VACV virulence factor K7 binds directly to Spir-1 and that a diphenylalanine motif of Spir-1 is needed for this interaction and for Spir-1-mediated enhancement of IRF3 activation. Thus, Spir-1 is a new virus restriction factor and is targeted directly by an immunomodulatory viral protein that enhances virus virulence and diminishes IRF3 activation.

Author Summary

Infection of cells by viruses is sensed by host molecules called pattern recognition receptors (PRRs) that activate signalling pathways leading to an anti-viral response. In turn, viruses express proteins that negate these host responses to mediate escape from the anti-viral response. Here, we report that protein K7 from a large DNA virus called vaccinia virus (VACV), binds to a host cell protein called Spir-1. Spir-1 is known to regulate the assembly of actin filaments inside cells, but here we show that Spir-1 also functions to activate the host response to virus infection and to limit the replication and spread of both RNA and DNA viruses. Thus, this study has uncovered new functions of cellular protein Spir-1 as an activator of innate immunity and as a restriction factor for diverse viruses. Further, it shows that Spir-1 is targeted by a virus protein during infection.

Introduction

The host innate immune response to viral infection begins with the sensing of pathogen-associated molecular patterns (PAMPs) by pattern recognition receptors (PRRs), such as Toll-like receptors and retinoic acid-inducible gene-I (RIG-I)-like receptors (RLRs) (1, 2). The sensing of virus macromolecules, such as viral DNA or RNA, by PRRs triggers signalling cascades that culminate in the activation of the transcriptional factors interferon regulatory factor (IRF) 3, activator protein (AP) 1 and nuclear factor kappa B (NF-κB) (3). These transcriptional factors translocate to the nucleus where they induce the transcription of genes encoding interferons (IFN), cytokines and chemokines. Once secreted from the cell, IFNs, cytokines and chemokines promote inflammation to restrict virus replication and control the infection. IFNs bind to their receptors on the surface of infected or non-infected cells, and trigger signal transduction via the JAK-STAT pathway leading to expression of interferon-stimulated genes (ISGs) that induce an antiviral state (4).

During the co-evolution with their hosts, viruses have evolved strategies to evade, suppress or exploit the host response to infection by targeting multiple steps of the host immune response (5). Vaccinia virus (VACV), the prototypical orthopoxvirus, is well known as the live vaccine used to eradicate smallpox (6). VACV has a large dsDNA genome of approximately 190 kbp (7), replicates in the cytoplasm (8) and encodes scores of proteins that antagonise innate immunity (9). Interestingly, some cellular pathways, such as those leading to activation of IRF3 or NF-κB, or the JAK-STAT pathway downstream of IFNs binding to their receptors, are targeted by multiple different VACV proteins. Moreover, some of these viral antagonists are multifunctional and inhibit more than one host innate immune pathway (9).

VACV protein K7 is one such antagonist of innate immunity. K7 is a small, intracellular protein that is non-essential for virus replication in cell culture, yet contributes to virulence in both intradermal and intranasal mouse models of infection (10). Functionally, K7 was reported to suppress NF-κB activation by binding to interleukin-1 receptor-associated kinase-like 2 (IRAK2) and tumour necrosis factor (TNF) receptor-associated factor 6 (TRAF6) (11). K7 also inhibits IRF3 activation and binds to the DEAD-box RNA helicase 3 (DDX3) (11). Another study reported that K7 affected regulation of histone methylation during VACV infection, by an unknown mechanism (12). Two unbiased proteomic searches identified cellular binding partners of K7 (13, 14), suggesting that K7 may have additional functions. The identification of cellular proteins targeted by viral proteins has been a useful approach to identify cellular factors that function in the recognition and restriction of virus infections (15, 16). In this study, by investigating the interaction between K7 and the cellular protein Spir-1 (14), we identified new functions for Spir-1 as an activator of innate immunity and as a restriction factor for both DNA and RNA viruses.

The protein spire homolog 1 (Spir-1, also known as SPIRE1) was first described to affect *Drosophila* embryogenesis (17). Spir-1 has actin-binding domains (18) through which it nucleates actin filaments, an activity shared with the Arp2/3 complex and the formins (19). Spir-1 is organised in multiple functional domains. The N-terminal region contains the kinase non-catalytic C-lobe domain (KIND), which mediates Spir-1 interaction with other proteins, such as the formins (20). Spir-1 and the formins cooperate during actin nucleation (21-29). The KIND domain is followed by four actin-binding Wiskott-Andrich syndrome protein homology domain 2 (WH2) domains that are responsible for actin nucleation (19, 30, 31). The C-terminal region of Spir-1 contains a globular tail domain-binding motif (GTBM), which is responsible for binding to myosin V (32). Next, there is a Spir-box (SB) domain that is conserved within the Spir protein family. Due to its similarity to a helical region of the rabphilin-3A protein that interacts with the GTPase Rab3A, it is thought that the Spir-box domain is involved in the association of Spir-1 and Rab-GTPases (24, 33-35). Following the SB domain, there is a modified

93 FYVE zinc finger domain that interacts with negatively-charged lipids in membranes. The membrane
94 targeting specificity is mediated via the interaction of Spir-1 with other membrane-bound proteins such
95 as the Rab-GTPases (29).
96
97 In adult mice, Spir-1 is expressed preferentially in neuronal and hematopoietic cells (36, 37) and in
98 humans the brain also has high Spir-1 expression (38). In general, Spir-1 is involved in several actin-
99 dependent cellular functions such as vesicle trafficking (24, 34, 35, 39), DNA repair (40), mitochondrial
100 division (41), and development of germ cells (17, 23, 42) but a role in innate immunity has not been
101 described. Interestingly, a genome-wide association study found a single nucleotide polymorphism in
102 Spir-1 that correlated with a different antibody response to smallpox vaccination (43).
103
104 Here, Spir-1 is shown to promote IRF3 activation and this activity depends upon a diphenylalanine
105 motif that is also necessary for the direct interaction of Spir-1 with VACV virulence factor K7. Using
106 gain-of-function and loss-of-function cell lines, Spir-1 is shown to diminish VACV and ZIKV replication
107 and/or spread and is therefore a viral restriction factor.
108
109
110 ## Results
111
112 ***Vaccinia virus protein K7 co-precipitates with the C terminal region of Spir-1***
113 A previous proteomic study identified Spir-1 as a cellular interacting partner of VACV protein K7
114 although this interaction was not validated (14). Mammals have two *Spire* genes, *Spire1* and *Spire2*
115 that encode closely related proteins (overall 42% identity and 58% similarity in humans), especially
116 within the WH2 and Spir-box domains (37, 44). The Uniprot database for human Spir-1 (Q08AE8)
117 describes five Spir-1 isoforms and splicing before the GTBM (Exon 9) and SB (Exon 13) domains has
118 been demonstrated (45). Among Spir-1 isoforms, Spir-1 known as isoform 2 that doesn't contain Exon
119 9 or Exon 13, is the most abundant form in the brain and small intestine tissues (45) and is the form
120 studied here. To confirm if K7 co-precipitates with Spir-1, HEK293T cells were transfected with
121 plasmids encoding Myc-tagged human Spir-1, Spir-2, β-TrCP, or Myc-GFP, together with plasmids
122 expressing FLAG-tagged, codon-optimised K7 or another Bcl-2-like VACV protein, A49 (46).
123 Immunoprecipitation with anti-Myc or anti-FLAG affinity resins showed that K7 was co-precipitated by
124 Myc-Spir-1 (Fig 1A), but not by Myc-Spir-2, Myc-β-TrCP or Myc-GFP. In contrast, A49 interacted with
125 β-TrCP as reported (47), but not with the other proteins. Reciprocally, FLAG-K7 co-precipitated Spir-
126 1 (Fig 1B), but not the other Myc-tagged proteins, whilst β-TrCP only interacted with A49.
127

To investigate if the actin-binding domains of Spir-1 were needed for interaction with K7, two Myc-tagged truncations of Spir-1 were generated: an N-terminal region (amino acid residues 1-390), containing the four actin-binding WH2 domains and the KIND domain; and a C-terminal region, containing the SB and FYVE domains (amino acid residues 391-742, Fig 1C). These truncations, Spir-1 and Spir-2 were co-expressed with FLAG-K7 and Myc-tagged immunoprecipitation showed that the C terminus of Spir-1 was sufficient for interaction with K7, whereas the actin-binding domains were dispensable (Fig 1D, middle panel). The reciprocal IP gave the same conclusion and FLAG-K7 co-precipitated full-length Spir-1 and its C-terminal region (Fig 1D, right panel). As controls, the N-terminal region co-precipitated endogenous actin via its WH2 domains, and the C-terminal region interacted with 14-3-3, another binding partner of Spir-1 (48, 49).

To determine if Spir-1 and K7 interacted at endogenous levels, cells were either mock-infected or infected with VACV expressing HA-tagged K7 (vHA-K7) (10) or B14 (vHA-B14) (50). HA-immunoprecipitation confirmed that K7 interacts with endogenous Spir-1, whilst B14 does not (Fig 1E). As reported, K7 also co-precipitated with DDX3 (11), and B14 interacted with IKKβ (51). Altogether, these results indicate that Spir-1, but not Spir-2, interacts with K7 via its C-terminal region and independent of its actin-binding domains.

Ectopic Spir-1 increases IRF3-dependent gene expression

Since the interaction of Spir-1 with K7 is independent of its actin-binding domains, and K7 is a VACV immunomodulator and virulence factor, we hypothesised that Spir-1 might have an unknown function in antiviral immunity. To test this, the impact of Spir-1 on innate immune signalling pathways was assessed by luciferase reporter gene assays. First, cells were transfected with a reporter plasmid in which the expression of firefly luciferase is driven by the IFNβ promoter. IFNβ expression was induced by Sendai virus (SeV) infection, which is sensed by RIG-I (52). Myc-Spir-1 expression alone did not affect IFNβ-dependent gene activation, however, Spir-1 augmented activation induced by SeV infection (Fig 2A). In contrast, Myc-tagged GFP had no effect, and VACV protein C6 was inhibitory as described (53). Spir-1 did not affect activation of ISRE-dependent gene expression downstream of type I IFN, whereas C6, but not N1, was inhibitory (54) (Fig 2B). Similarly, Spir-1 did not affect NF-κB activation in response to TNF-α, whilst B14 inhibited it (51) and VACV protein N2 had no effect (55) (Fig 2C). Further analysis using an IRF3-specific reporter plasmid (*ISG56.1* or *IFIT1* promoter) showed Spir-1 caused a dose-dependent increase in IRF3 activation induced by the CARD domain of RIG-I (Fig 2D, 2E). As controls, VACV protein N2 inhibited IRF3 activation as described (55) while A49, an NF-κB inhibitor (47), did not. Unlike Spir-1, Spir-2 did not enhance IRF3 activation whereas DDX3 did, as described (11) (Fig 2E).

164 To map at which stage in the IRF3 pathway Spir-1 was acting, further *ISG56.1* reporter assays were
165 performed in which the pathway was stimulated by expression of its different components. Spir-1
166 activated the IRF3 pathway in a dose-response manner when MAVS (mitochondrial antiviral-
167 signalling protein) was used as stimulant (Fig 2F), but not when downstream components such as
168 TBK1 (Fig 2G), IKKε (S1 Fig) or the constitutively active IRF3-5D (Fig 2H) were expressed. These
169 findings indicate Spir-1 enhances IRF3 activation at or downstream of MAVS and upstream of IKKε
170 or TBK1. Finally, N- and C-terminal fragments of Spir-1 were tested following stimulation by RIG-I
171 CARD. Neither half of Spir-1 activated the pathway fully, but the C-terminal region had greater activity
172 than the N-terminal region (Fig 2I).
173
174 ***Spir-1 interaction with K7 is direct, independent of DDX3, and requires a diphenylalanine motif***
175 K7 interacts directly with DDX3 (56, 57), an adaptor protein in the IRF3 pathway (58, 59). To
176 investigate whether K7 binding to Spir-1 was via DDX3, cells stably expressing an inducible shRNA
177 targeting DDX3 (shDDX3) (59) were used. Knockdown, rather than knockout, of DDX3 was utilised
178 because *DDX3* encodes an essential protein (60). Cells expressing a non-silencing control (NSC)
179 shRNA were used in parallel. DDX3 knockdown was induced by incubation with doxycycline (DOX)
180 for 48 h as described (59), prior to transfection with either FLAG-tagged K7 or A49 for 24 h. Viral
181 proteins were immunoprecipitated via their FLAG tag, followed by immunoblotting for endogenous
182 Spir-1. DDX3 levels were reduced greatly in shDDX3 cells following DOX treatment, but not in control
183 cells (Fig 3A). Despite this, Spir-1 co-precipitation by K7 was unaffected (Fig 3A). A49 did not co-
184 precipitate either DDX3 or Spir-1 (Fig 3A). Next, the shDDX3 cells were used to determine if DDX3
185 contributed to Spir-1-induced IRF3 activation. After DDX3 knockdown, there was no significant
186 difference in IRF3 stimulation by Spir-1 (Fig 3B). Notably, K7 inhibited IRF3 activation when DDX3
187 was knocked down, showing K7 had another IRF3 inhibitory mechanism independent of DDX3 (Fig
188 3B). Moreover, the presence of K7 reversed the activation of the pathway by Spir-1 (Fig 3B). In
189 summary, Spir-1 interaction with K7 and its function in the IRF3 pathway are independent of DDX3.
190
191 Since both DDX3 and Spir-1 bind to K7 and activate IRF3, their amino acid sequences were
192 compared. The structure of K7 bound to a DDX3 peptide and subsequent structure-based
193 mutagenesis showed that a diphenylalanine (FF) motif in DDX3 is essential for binding K7 and for
194 IRF3 activation (57). An alignment of the C terminus of Spir-1 and the minimal ten-amino acid peptide
195 from DDX3 (residues 81-90) needed for binding K7, showed a similar FF motif in Spir-1 (Fig 3C). To
196 determine if this was important for Spir-1 binding to K7, the phenylalanines were mutated to alanines
197 (FFAA) and the mutant was expressed in cells together with FLAG-tagged K7. Wild-type (WT) Myc-
198 Spir-1 and Myc-GFP were also expressed. Anti-Myc or anti-FLAG immunoprecipitation showed that
199 the FFAA mutation impaired Spir-1 interaction with K7 (Fig 3D), although it still precipitated both actin

200 and 14-3-3, indicating normal folding. Notably, the FFAA mutant no longer activated IRF3 (Fig 3E).
201
202 To determine if the K7 interaction with Spir-1 was direct, these proteins were expressed by *in vitro*
203 transcription and translation and immunoprecipitated alongside Myc-tagged TAB2 and FLAG-tagged
204 VACV protein F12 (61) as controls. Both Spir-1 and DDX3 interacted directly with K7, whereas Spir-
205 1 did not interact with F12, and K7 did not interact with TAB2 (Fig 3F, 3G). Taken together, this
206 demonstrated that Spir-1 binds directly to K7 and shares with DDX3 a conserved diphenylalanine
207 motif, which is required for its function in the IRF3 pathway.
208
209 ***K7 uses the same amino acid residues to target both Spir-1 and DDX3***
210 K7 binds to the DDX3 peptide through a hydrophobic pocket within a negatively-charged face (56,
211 57). Thus, interactions between K7 and the DDX3 peptide involve hydrophobic contacts, hydrogen
212 bonds and electrostatic interactions, of which electrostatic contacts between R88 of DDX3 with both
213 D28 and D31 of K7 are notable. D31 also forms a hydrogen bond with DDX3 S83 (57). Using this
214 information, K7 mutants were generated in an attempt to distinguish between K7 binding to Spir-1
215 and DDX3. K7 D28 and D31 were changed singly or together to alanine (D28A, D31A) and expressed
216 alongside WT K7 or GFP, and together with Myc-tagged Spir-1 and HA-tagged DDX3.
217 Immunoprecipitation showed that K7 D28A still bound both Spir-1 and DDX3, whilst K7 D31A had
218 impaired binding to both proteins, especially DDX3 (Fig 4A). Furthermore, the double mutant (DDAA)
219 had further reduced binding to Spir-1 and no detectable binding to DDX3 (Fig 4A). Importantly, all
220 mutants still interacted with COPε (Fig 4A), another K7 binding partner (13), suggesting normal K7
221 folding. Co-precipitation of endogenous Spir-1 with FLAG-tagged K7 and mutants gave similar
222 conclusions (Fig 4B). Notably, the K7 D31A mutant inhibited IRF3 activation poorly compared to the
223 WT or D28A (Fig 4C). Altogether, these data indicate that K7 requires D31 for interacting with both
224 DDX3 and Spir-1 and via each interaction it inhibits the IRF3 pathway.
225
226 ***IRF3 activation is reduced in the absence of Spir-1***
227 To investigate Spir-1-mediated activation of IRF3 further, Spir-1 knockout (KO) HEK293T cell lines
228 were generated by CRISPR-Cas9-mediated targeting of *SPIRE1* exon 3, which is conserved in all
229 Spir-1 isoforms (Fig 5A). After single cell selection, HEK293T cell lines were confirmed to lack Spir-1
230 by immunoblotting (Fig 5B) and by sequencing of both *Spire-1* alleles (Fig 5A). A clone that lacked
231 Spir-1 protein expression and in which the *Spire-1* open reading frame was disrupted by frameshift
232 mutations in both alleles, and that lacked WT sequence, was selected. Additionally, a vector
233 expressing Myc-tagged Spir-1 was used to rescue Spir-1 expression in the KO cell line following
234 lentiviral transduction. In parallel, both WT and KO cells were transduced with a control empty vector
235 (EV) lentivirus. Spir-1 WT cells transduced with EV, and Spir-1 KO cells transduced with EV or Myc-
236 Spir-1 were infected with SeV to activate the IRF3 pathway. Supernatants were collected for ELISA

237 and cells lysates were used for either RNA extraction or immunoblotting, which confirmed that cells
238 did or did not express Spir-1 (Fig 5B). The expression of Myc-Spir-1 increased in the presence of
239 SeV, but this was not observed for endogenous Spir-1 (Fig 5B). One possible explanation is that Myc-
240 Spir-1 expression is driven by the human cytomegalovirus immediate early promoter (62) that
241 contains binding sites for transcription factors such as NF-κB (63), which can also be activated during
242 SeV infection. The phosphorylation of IRF3 at S396 (p-IRF3), a hallmark of IRF3 activation (64),
243 increased greatly 24 h after SeV infection of WT cells (Fig 5B) but was reduced in the absence of
244 Spir-1 and restored in the KO cells expressing Myc-Spir-1 (Fig 5B). Moreover, after SEV infection,
245 Spir-1 KO cells produced lower levels of mRNAs for *ISG56/IFIT1* (Fig 5C), *IFNB1* (Fig 5D) and
246 *CXCL10* (Fig 5E), and secreted less CXCL-10 (Fig 5F), as measured by RT-qPCR and ELISA,
247 respectively. Importantly, the absence of Spir-1 did not change the levels of CXCL-10 secreted in
248 response to TNF-α, a specific agonist of the NF-κB pathway (Fig 5G).
249
250 Immortalised mouse embryonic fibroblasts (MEFs) from mice with a terminator (gene trap) between
251 exons 3 and 4 of the *Spire1* gene (65) were used to investigate the contribution of Spir-1 to IRF3
252 activation in cells from a different mammal. After stimulation of IRF3 by either poly I:C or SeV infection,
253 MEFs were lysed for immunoblotting or RNA analysis and supernatants were collected for ELISA. A
254 reduction in p-IRF3 was seen in Spir-1 KO cells (Fig 6A, 6B) and this was quantified (bottom graphs
255 in Fig 6A, 6B). The Spir-1 KO MEFs also expressed less mRNAs for cytokines and chemokines upon
256 stimulation with poly I:C or SeV infection than their WT controls (Fig 6C, 6D, 6E, 6F, 6G, 6H). Likewise,
257 CXCL-10 and IL-6 secretion were lower from Spir-1 KO cells (Fig 6I, 6J, 6K, 6L). However, the levels
258 of CXCL-10 and IL-6 secreted after stimulation with IL-1β were not reduced in Spir-1 KO MEFs (Fig
259 6M, 6N); indeed, there was a small increase in IL-6 levels in KO cells (Fig 6N). In summary, in both
260 mouse and human cells lacking Spir-1 there is a defect in IRF3 activation downstream of RIG-I/MDA5,
261 whilst other immune signalling pathways were largely unaltered.
262
263 ***Spir-1 is a viral restriction factor***
264 Given that Spir-1 interacts with VACV protein K7 and enhances IRF3 activation, which is critical for
265 the host response to viral infection, the impact of Spir-1 on VACV replication and spread was
266 assessed. Spir-1 WT and KO HEK293T cells and the derivative cell line in which Spir-1 expression
267 was restored in the KO cells, were infected with A5-GFP-VACV, a VACV strain expressing GFP fused
268 to capsid protein A5 (66), and 2 days (d) later plaque diameters were measured (Fig 7A, 7B). A
269 significant increase in plaque size was seen in the absence of Spir-1 compared to both WT and
270 rescued cells (Fig 7B), suggesting that Spir-1 restricts VACV spread and/or replication. Lastly, virus
271 growth on those cells was assessed. Cells were infected with 0.001 plaque-forming unit (PFU)/cell of
272 VACV strain WR and 2 d later the virus yield was determined by plaque assay. Spir-1 KO cells yielded

273 higher viral titres compared to both WT and Spir-1-complemented cells (Fig 7C).
274
275 The IRF3 pathway also restrict RNA viruses, therefore the impact of Spir-1 in restricting Zika virus
276 (ZIKV), a single-stranded RNA virus, was also assessed. HEK293T Spir-1 WT, KO and Spir-1-
277 rescued cells were infected with ZIKV-mCherry with 0.01 PFU/cell. Three days later, the mCherry
278 signal was visualised by live-cell imaging and showed a greater signal in the KO cells compared to
279 controls (Fig 7D), suggesting an increased ZIKV replication in these cells. To address that possibility,
280 the virus yield in the supernatant of infected HEK293T cells was determined by plaque assay in VERO
281 E6 cells (Fig 7E). In the absence of Spir-1, there is an increase in ZIKV titres compared to the WT
282 and Spir-1 restored KO cells. Collectively, loss of Spir-1 caused an increase in both virus plaque size
283 and yield of infectious virus, showing that Spir-1 functions as a restriction factor against both a DNA
284 (VACV) and an RNA (ZIKV) virus.
285
286
287 **Discussion**
288
289 During co-evolution with their hosts, viruses have evolved mechanisms to evade the host antiviral
290 responses and thereby replicate and spread efficiently. Such virus proteins are numerous and have
291 diverse functions and, therefore, can be used to gain insight into how the host innate immune system
292 functions. VACV is a poxvirus and encodes scores of immunomodulatory proteins many of which
293 target the innate immune system. In several cases, multiple VACV proteins engage the same
294 pathway, but despite this, these proteins each contributes to virulence indicating non-redundant
295 functions (9). Sometimes a single protein can inhibit multiple pathways (9) or an open reading frame
296 can encode multiple proteins with different functions (67). High-throughput proteomic approaches
297 have been used to identify binding partners of VACV proteins, or cellular proteins that are up or down-
298 regulated during virus infection, and such cellular proteins may have antiviral activity and function in
299 innate immunity (14, 16). For example, histone deacetylases (HDAC) 4 and 5 are each targeted for
300 proteasomal degradation by VACV protein C6 and function as a virus restriction factor (15, 16).
301
302 Here, Spir-1 is characterised as a new cellular protein that is bound by VACV protein K7 (Fig 1), a
303 virulence factor that inhibits NF-κB and IRF3 activation (10, 11). K7 binding to Spir-1 was identified in
304 a proteomic screen for binding partners of virus immunomodulatory proteins (14). Here, this
305 interaction is confirmed, demonstrated to occur at endogenous levels during VACV infection (Fig 1E),
306 and shown to be direct (Fig 3F, 3G).
307
308 Spir-1 belongs to a family of proteins involved in actin organisation (44) but K7 interaction with Spir-1

309 does not require its N-terminal actin-binding domain (Fig 1D). VACV induces polymerisation of actin
310 to facilitate virus dissemination from the cell surface and VACV mutants unable to polymerise actin
311 spread poorly and form small plaques (68). However, a mutant lacking K7 produces normal size
312 plaques (10). Given that K7 is an immunomodulatory protein, we hypothesised that Spir-1 might have
313 a function in innate immunity. In reporter gene assays, Spir-1 over-expression enhanced IRF3-
314 dependent gene expression (Fig 2D) but did not affect JAK-STAT signalling induced by type I IFN, or
315 NF-κB activation (Fig 2B, 2C). Conversely, human and murine Spir-1 knockout cell lines showed
316 diminished IRF3 signalling, with reduced IRF3 phosphorylation and reduced transcription and
317 expression of IRF3-responsive genes (Fig 5B, 6A, 6B). Importantly, rescue of Spir-1 expression in
318 Spir-1 KO cells restored phospho-IRF3 and cytokine expression levels (Fig 5).
319
320 To map where Spir-1 influences IRF3 activation, the pathway was activated by different agonists and
321 the influence of Spir-1 examined. Spir-1 enhanced activation induced by SeV infection (Fig 2A, 5 and
322 6), poly I:C transfection (Fig 6), and overexpression of both RIG-I CARD (Fig 2D, 2E) and MAVS (Fig
323 2F), but not overexpression of TBK1, IKKε or a constitutively active IRF3 (Fig 2G and S1). SeV RNA
324 is sensed by RIG-I (69) whilst high molecular weight (HMW) poly I:C is sensed by MDA-5 (52, 70).
325 This suggests Spir-1 acts at or downstream of MAVS, the adaptor molecule recruited downstream of
326 RIG-I and MDA5 activation (71). The association of RIG-I/MDA5 with MAVS results in the recruitment
327 of tumour necrosis factor receptor-associated factors (TRAF), such as TRAF3, leading to the
328 phosphorylation of IRF3 by TBK1/IKKε. Collectively, these data suggest Spir-1 functions at MAVS or
329 TRAF3 level.
330
331 K7 inhibition of IRF3 activation was attributed to direct binding to DDX3, which acts as a
332 multifunctional scaffolding adaptor culminating in IRF3 activation (58, 59). However, data presented
333 here show K7 has additional targets within the IRF3 pathway, since Spir-1 also contributes to IRF3
334 activation and K7 is able to inhibit IRF3 activation even in the absence of DDX3. Furthermore, DDX3
335 and Spir-1 act at different positions in the pathway; DDX3 acts at the TRAF3 and TBK1/IKKε level (9,
336 11, 59, 72), whilst Spir-1 acts upstream of TBK1/IKKε (Fig 2). Interestingly, both DDX3 and Spir-1
337 share a diphenylalanine motif that is responsible for both binding to K7 and their function in the IRF3
338 pathway (Fig 3) (57). Furthermore, the same amino acid residue in K7 (D31) is crucial for its binding
339 to both cellular proteins (Fig 4). This prevented assessment of the relative importance of K7 binding
340 to each cellular protein.
341
342 Nonetheless, Spir-1 has an important antiviral role because cells lacking Spir-1 show enhanced VACV
343 and ZIKV replication and/or spread (Fig 7). Comparable data for DDX3 are lacking, and obtaining
344 such data is complicated by DDX3 being an essential protein (60). Both K7 and Spir-1 localise in the

345 cytoplasm (10, 34). Interestingly, mutations in the FYVE domain and in the diphenylalanine motif in
346 Spir-1 change its sub-cellular localisation from a trans-Golgi network and post-Golgi vesicles
347 localisation to an even cytoplasmic distribution (29, 34). Neither the N- or C-terminal halves of Spir-1
348 were capable of activating the IRF3 pathway as well as full-length protein (Fig 2I), despite comparable
349 expression levels, suggesting that both halves are important. It is possible that Spir-1 is directed to
350 the correct location by its C-terminal domain, whist its N-terminal domain mediates Spir-1 engagement
351 with other proteins to promote IRF3 activation. This might explain why the FFAA Spir-1 mutant is no
352 longer able to activate the IRF3 pathway. Another possibility is that K7 may bind to the Spir-1
353 diphenylalanine motif and displace other proteins or sequester it and prevent it reaching its subcellular
354 location. Spir-1 has several isoforms (45), and one, Spire-1C (also known as Spire1-E13), differs from
355 the canonical isoform by encoding an extra exon sequence (ExonC or E13), which mediates its
356 mitochondrial localisation and regulates mitochondrial division (41). Even though this was not the
357 isoform used in the present study, K7 might regulate Spir-1 trafficking to the mitochondrion, where
358 MAVS is anchored (73).
359
360 RIG-I and MDA5 can sense RNA virus genomes directly, but also RNA generated by infection with
361 DNA viruses (74), leading to IRF3 activation. Therefore, RIG-I/MDA5-triggered antiviral response is
362 antagonised by several RNA and DNA viruses (71, 75). For instance, ZIKV has been shown to be
363 sensed by both RIG-I and MDA-5 depending on the infected cell type (reviewed by (76)). Furthermore,
364 it has long been known that dsRNA is generated during VACV infection (77-79), so it is not surprising
365 that VACV encodes proteins to interfere with cytosolic RNA sensing. For instance, VACV protein E3
366 binds to dsRNA and prevents RIG-I-dependent sensing of RNA products generated via the
367 transcription of AT-rich DNA by RNA polymerase III (80, 81), and the decapping enzymes D9 and
368 D10 prevent the accumulation of dsRNA from viral complementary RNA molecules (82). Downstream
369 of RNA sensing, VACV encodes proteins to inhibit IRF3 activation, such as C6, which acts at
370 TBK1/IKKε activation level (53), N2, which acts downstream of IRF3 translocation to the nucleus (55)
371 and K7, which targets DDX3 (11). Here, we show that Spir-1 also contributes to IRF3 activation, with
372 both Spir-1 and DDX3 sharing a similar motif which binds K7.
373
374 In summary, Spir-1 is a new cellular protein that affects IRF3 activation and is a virus restriction factor.
375 By exploring in detail the function of VACV protein K7, an additional cellular factor that regulates IRF3
376 activation and acts as a viral restriction factor has been characterised.
377
378
379

380 ## Material and Methods

381

382 *Cells lines*

383 Human embryonic kidney (HEK) 293T, HEK293T NSC or shDDX3 (kind gifts from Dr. Martina
384 Schröder, Maynooth University, Ireland), murine embryonic fibroblasts (MEFs) Spir-1 KO and WT
385 (kindly provided by Prof. Dr. Eugen Kerkhoff - University Hospital Regensburg, Germany), BSC-1 and
386 VERO E6 (African Green Monkey) cells were cultured in Dulbecco's modified Eagle's medium
387 (DMEM, Gibco) supplemented with 10% heat-treated (56 ºC, 1 h) foetal bovine serum (FBS, Pan
388 Biotech), 100 U/mL penicillin and 100 µg/mL streptomycin (P/S, Gibco). RK13 cells were grown in
389 minimal essential medium (MEM, Gibco) supplemented with 10% FBS and P/S.

390

391 *Viruses*

392 VACV strain Western Reserve (WR) and derivative strains expressing GFP fused to the capsid protein
393 A5 (A5-GFP-VACV) (66), VACV expressing HA-tagged B14 (50) and VACV expressing HA-tagged
394 K7 (10) were described. VACV strains were grown on RK13 cells and titrated by plaque assay on
395 BSC-1 cells. Sendai virus (SeV) Cantell strain (Licence No. ITIMP17.0612A) was a gift from Prof.
396 Steve Goodbourn (St George's Hospital Medical School, University of London). ZIKV engineered to
397 express a mCherry marker (83) was a kind gift from Dr. Trevor Sweeney (Department of Pathology,
398 University of Cambridge).

399

400 *Plasmids*

401 A plasmid encoding the Myc-tagged human Spir-1 isoform 2 and human Spir-2 (20) constructs were
402 a kind gift of Prof. Dr. Eugen Kerkhoff. Spir-1 N- and C-terminal truncations were constructed by PCR
403 amplification from pcDNA3.1-Myc-Spir-1 and inserted into plasmid pcDNA3.1-Myc. Codon-optimised
404 FLAG-K7 was described (84) and Spir-1 and K7 plasmids were used as templates for site-directed
405 mutagenesis according to the instructions of the QuikChange Site-Directed Mutagenesis Kit (Agilent).
406 All mutations were confirmed by DNA sequencing. Myc-DDX3 and HA-DDX3 (11) were kindly
407 provided by Dr. Martina Schröder. The IFNβ-firefly luciferase reporter plasmid was from T. Taniguchi
408 (University of Tokyo, Japan), NF-κB-firefly luciferase was from R. Hofmeister (University of
409 Regensburg, Germany) and ISG56.1-firefly luciferase was a gift from Ganes Sen (Cleveland Clinic,
410 USA). ISRE-firefly luciferase and pTK-renilla luciferase (pRL-TK) plasmids were from Promega.
411 Vectors expressing MAVS, IKKε, TBK1 and IRF3-5D (53), and RIG-I-CARD domain (85) were
412 described. Lentivirus vector plasmid pLKO.DCMV.TetO.mcs (pLDT) (86) was a gift from Prof. Roger
413 Everett (University of Glasgow, UK) and was used as backbone for sub-cloning the Myc-Spir-1.
414 Plasmids pCMV.dR8.91 (expressing all necessary lentivirus helper functions) and pMD-G (expressing
415 the vesicular stomatitis virus envelope protein G) were from Dr. Heike Laman (University of

416 Cambridge, UK). pF3A WG plasmid was from Promega. px459 CRISPR-Cas9 plasmid was
417 purchased from Addgene. More information about plasmids and oligonucleotide primers used are
418 given in the reagents table.
419
420 *Antibodies and Reagents*
421 Primary antibodies used were from the following sources: rabbit (Rb) anti-Myc (Cell Signaling, 2278),
422 mouse (Ms) anti-Myc (Cell Signaling, 9B11), Rb anti-Actin (Sigma, A2066), Ms anti-FLAG (Sigma
423 F1804), Rb anti-14-3-3 (Santa Cruz, sc-629), Ms anti -Spir-1 (Santa Cruz, sc-517039), Ms anti- Spir-
424 1 (Abcam, ab57463), Rb anti-DDX3 (Cell Signaling, 2635), Rb anti-IKKβ (Cell Signaling, 2684), Rb
425 anti-HA (Sigma, H6908), Ms anti-α-Tubulin (Millipore, 05-829), Ms anti-GAPDH (Sigma, G8795), Rb
426 anti-IRF3 (Cell Signaling, 4962), Ms anti-COPε (Santa Cruz, sc-133194), Rb anti-phospho-IRF3
427 Ser396 (Cell Signaling, 4947S) and Rb polyclonal anti-C6 (53). For dilutions used for the primary
428 antibodies, see reagents table. Secondary antibodies used (1:10,000 dilution) were IRDye 680RD-
429 conjugated goat anti-rabbit IgG or anti-mouse IgG and IRDye 800CW-conjugated goat anti-rabbit IgG
430 or anti-mouse IgG (LI-COR).
431
432 Reagents used in this study were: Anti-c-Myc Agarose from Santa Cruz Biotechnology, and
433 monoclonal Anti-HA-Agarose, clone HA-7, ANTI-FLAG M2 Affinity Gel and Poly-D-lysine
434 hydrobromide (all from Sigma Aldrich). Human IFNα, human TNF-α and mouse IL-1β were from
435 Peprotech, HMW poly(I:C) and puromycin were from InvivoGen, and doxycycline was from Melford.
436
437 *Reporter Gene Assay*
438 HEK293T cells were seeded in 96-well plates with 1.5×10^4 cells per well. After two days, cells were
439 transfected with 60 ng per well of the firefly luciferase reporter plasmids (IFNβ, ISRE, NF-κB or
440 ISG56.1), 10 ng per well of pTK-renilla luciferase and different amounts of the expression plasmid
441 under test or empty vector (EV) control using polyethylenimine (PEI, CellnTec, 2 µL per 1 µg DNA).
442 When necessary, EV plasmid was added to the transfection so that the final amount of DNA
443 transfected was kept constant. In cases where stimulation was done by transfecting another plasmid,
444 the same amount of EV was transfected to the non-stimulated (NS) control wells. Cells were
445 stimulated as shown in the Figures: (i) infection with SeV for 24 h (IFNβ Luc), (ii) 10 ng/mL of TNF-α
446 for 8 h (NF-κB Luc) or (iii) with 1000 U/mL of IFNα for 8 h (ISRE-Luc). After stimulation, cells were
447 washed with PBS, lysed with 100 uL/well of passive lysis buffer (Promega) and firefly and renilla
448 luciferase activities were measured using a FLUOstar luminometer (BMG). The firefly luciferase
449 activity in each sample was normalised to the renilla luciferase activity and fold inductions were
450 calculated relative to the non-stimulated controls for each plasmid. In all cases, data shown are
451 representative from at least three independent experiments with at least triplicate samples analysed

452 for each condition.
453
454 *Immunoblotting*
455 HEK293T (8 x 10^5) or MEFs (2 × 10^5) cells were seeded in 6-well plates and 24 h later cells were
456 stimulated by infection with SeV or transfection with 5 µg/mL of poly I:C using lipofectamine 2000 (Life
457 Technologies). After stimulation, cells were washed twice with ice-cold PBS, and scrapped into a cell
458 lysis buffer containing 50 mM Tris-HCl pH 8, 150 mM NaCl, 1 mM EDTA, 10% (v/v) glycerol, 1% (v/v)
459 Triton X-100 and 0.05% (v/v) NP-40, supplemented with protease (cOmplete Mini, Roche) and
460 phosphatase inhibitors (PhosSTOP, Roche). Protein concentration was determined using a
461 bicinchoninic acid protein assay kit (Pierce) before being boiled at 100 ºC for 5 min. Proteins were
462 then separated by SDS-polyacrylamide gel electrophoresis and transferred onto a nitrocellulose
463 Amersham Protran membrane (GE Healthcare). Membranes were blocked at room temperature with
464 either 5% (w/v) milk or 5% (w/v) bovine serum albumin (BSA, Sigma) in PBS containing 0.1% Tween
465 20. Then, membranes were incubated with a specific primary antibody diluted in blocking buffer at 4
466 ºC overnight. After washing, membranes were probed with LI-COR secondary antibodies at room
467 temperature followed by imaging using the LI-COR Odyssey imaging system, according to the
468 manufacturer's instructions. Where indicated, protein bands from at least two independent
469 experiments were quantified by using Odyssey software (LI-COR Biosciences).
470
471 *Immunoprecipitation*
472 HEK293T cells were seeded in 10-cm dishes (3.5 × 10^6 cells per dish) and transfected with the
473 plasmids indicated in the Figures using PEI. The following day, cells were washed twice with PSB,
474 lysed in immunoprecipitation (IP) lysis buffer (150 mM NaCl, 50 mM Tris-HCl pH 7.4, 0.5% (v/v)
475 Nonidet P-40 (NP-40) and protease (cOmplete Mini, Roche) and phosphatase inhibitors (PhosSTOP,
476 Roche)) and cleared by centrifugation at 21,000 *g* for 15 min at 4 ºC. Cleared lysates were then
477 incubated with 20 µL of ANTI-FLAG M2 Affinity Gel (Sigma Aldrich) or Anti-HA Agarose (Sigma
478 Aldrich) for 2 h, or with 50 uL of Anti-c-Myc Agarose overnight, at 4 ºC. Alternatively, proteins were
479 expressed by *in vitro* transcription/translation using the TNT SP6 High-Yield Wheat Germ Protein
480 Expression System (Promega) prior to incubation with the affinity resins. Immunoprecipitations were
481 washed 3 or 4 times in IP buffer and bound proteins were eluted in Laemmli SDS-PAGE loading buffer
482 and heated at 100 ºC for 5 min. Samples were then analysed by SDS-PAGE and immunoblotting.
483
484 *RT-qPCR*
485 HEK293T (4 × 10^5) or MEFs (1 × 10^5) cells were seeded in 12-well plates. The next day, cells were
486 stimulated by infection with SeV or transfection with 5 µg/mL of poly I:C using lipofectamine 2000 (Life
487 Technologies). RNA was extracted using the RNeasy kit (QIAGEN) and 500 ng of each RNA sample
488 was used to synthesise cDNA using Superscript III reverse transcriptase according to the

489 manufacturer's protocol (Invitrogen). mRNA was quantified by real-time PCR using a ViiA 7 Real-
490 Time PCR System (Life Technologies), fast SYBR Green Master Mix (Applied Biosystems) and the
491 following primers: human *CXCL10* (Fwd: GTGGCATTCAAGGAGTACCTC, Rev:
492 GCCTTCGATTCTGGATTCAGA), human *IFNB1* (Fwd:ACATCCCTGAGGAGATTAAGCA, Rev:
493 GCCAGGAGGTTCTCAACAATAG), human *IFIT1* (Fwd: CCTGAAAGGCCAGAATGAGG, Rev:
494 TCCACCTTGTCCAGGTAAGT), human *GAPDH* (Fwd: ACCCAGAAGACTGTGGATGG, Rev:
495 TTCTAGACGGCAGGTCAGGT), mouse *Ifit1* (Fwd: ACCATGGGAGAGAATGCTGAT, Rev:
496 GCCAGGAGGTTGTGC), mouse *Il6* (Fwd: GTAGCTATGGTACTCCAGAAGAC. Rev:
497 ACGATGATGCACTTGCAGAA), mouse *Cxcl10* (Fwd: ACTGCATCCATATCGATGAC, Rev:
498 TTCATCGTGGCAATGATCTC) and mouse *Gapdh* (Fwd: ATGGTGAAGGTCGGTGTGAACGG, Rev:
499 TTACTCCTTGGAGGCCATGTAGGC). Gene amplification was normalised to *GAPDH*
500 (glyceraldehyde-3-phosphate dehydrogenase) amplification from the same sample, and the fold
501 induction of genes in stimulated samples was calculated relative to the unstimulated control.
502 Experiments were performed in at least biological duplicate and conducted at least twice.
503
504 *ELISA*
505 HEK293T (4×10^5) or MEFs (1×10^5) cells were seeded in 12-well plates. The following day, cells
506 were stimulated by: (i) infection with SeV; (ii) transfection with 5 µg/mL of poly I:C using lipofectamine
507 2000 (Life Technologies), (iii) 50 ng/mL of human TNF-α or (iv) 50 ng/mL of mouse IL-1β. After
508 stimulation, supernatants were assayed for human or murine CXCL-10 and IL-6 protein using Duoset
509 enzyme-linked immunosorbent assay (ELISA) reagents (R&D Biosystems) according to the
510 manufacturer’s instructions.
511
512 *CRISPR/Cas9-mediated genome editing*
513 Two guide RNAs (gRNAs) were designed using online software (http://tools.genome-engineering.org)
514 to target *SPIRE1* gene exon 3, which is shared by all Spir-1 isoforms. CRISPR/Cas9-mediated
515 genome editing of HEK293T cells was performed as described (87). Briefly, px459 CRISPR/Cas9
516 plasmids with or without gRNA sequence were transfected into HEK293T using TransIT-LT1
517 transfection reagent (Mirus, MIR 2306). Puromycin (1 µg/mL) was added to transfected cells and,
518 after 48 h, puromycin-resistant cells were serially diluted to obtain individual clones. Several clones
519 were amplified, and a few potential knockout clones were selected by immunoblotting and confirmed
520 by genomic DNA sequencing at the gRNA target sites. Only one gRNA was successful and one clonal
521 cell line was confirmed to be knockout after PCR-amplified genomic DNA was cloned into bacterial
522 plasmids and multiple colonies (n = 20) were sequenced. These all contained frameshift mutations.
523 No wild type allele was identified.
524
525 *Lentivirus transductions*

Lentivirus particles for transduction were generated after transient co-transfection of HEK293T cells seeded in 6-cm dishes. Cells were transfected with pCMV.dR8.91 and pMD-G vectors together with either pLDT-EV or pLDT-Myc-Spir-1. After 48 h and 72 h, the supernatant was collected and passed through a 0.45 µm filter. Lentivirus-containing supernatant was then used to infect HEK293T Spir-1 WT and KO cells. Transduced cells were selected with 1 µg/mL puromycin followed by clonal selection by serial dilution. Spir-1 expression was assessed by immunoblotting.

Virus Infection

Plaque size analysis were performed in HEK293T Spir-1 WT and KO cells seeded in 6-well plates coated with poly-D-lysine (Sigma). Once confluent, cells were infected with VACV-A5-GFP at 20 PFU per well for 2 d. Virus plaques diameters (n=54) were measured using AxioVision 4.8 software and a ZEISS Axio Vert.A1 fluorescent microscope.

Viral replication was measured by multi-step growth analyses of HEK293T Spir-1 WT and KO cells infected with VACV-WR at 0.001 PFU / cell or ZIKV-mCherry at 0.01 PFU/cell. For VACV, at 48 h post infection, cells were scraped in their medium and collected by centrifugation at 500 *g* for 5 min. Cells were subjected to three rounds of freeze-thawing before the infectious viral titre was determined by plaque assay on BSC-1 cells for 3 days. For ZIKV, at 72 h post infection, supernatants of infected cells were collected, and virus infectivity was determined by plaque assay on Vero E6 cells for 5 days. ZIKV-infected monolayers were also imaged using a Zeiss Axiovert 200M microscope. Images in Figure 7D were processed using Adobe Photoshop 2020 to enhance linearly the mCherry visualisation. SC-1 and VERO E6 cells were then fixed with 4% paraformaldehyde (PFA) and stained with toluidine blue.

Statistical Analysis

Statistical analysis was carried out using one or two-way ANOVA test where appropriate with the Bonferroni post-test, using the GraphPad Prism statistical software (Graph-Pad Software). Statistical significance is expressed as follows: ns = not significant, *P < 0.05, **P < 0.01, ***P < 0.001, ****P < 0.0001.

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562

563 ## Conflicts of Interest

564

565 The authors declare that they have no conflict of interest.

566

567

568 ## Figure Legends

569

570 **Fig 1: Spir-1 co-immunoprecipitates VACV protein K7 via its C-terminal region.** HEK293T cells
571 were transfected (**A**, **B** and **D**) with Myc-tagged and FLAG-tagged plasmids overnight. Cell lysates
572 were immunoprecipitated using either Myc (**A** and **D** – right panel) or FLAG affinity resins (**B** and **D** –
573 middle panel) and analysed by SDS-PAGE and immunoblotting. (**C**) Schematic representations of
574 hSpir-1 isoform 2 full-length (top) and its C- and N-terminal truncations. (**E**) HEK293T cells were either
575 mock-infected or infected at 5 or 10 PFU/cell with vHA-K7 or vHA-B14 for 4 h. Lysates were
576 immunoprecipitated using HA-affinity resin and analysed by SDS-PAGE and immunoblotting. In (**A**),
577 (**B**), (**D**) and (**E**) the positions of molecular mass markers in kDa are shown on the left. Each
578 experiment was done 3 times and representative results are shown.

579

580 **Fig 2**: **Ectopic expression of Spir-1 increases IRF3-dependent gene expression induced by**
581 **other stimuli, at or downstream of MAVS.** HEK293T cells were transfected with IFNβ (**A**), ISRE (**B**)
582 and NF-κB (**C**) firefly luciferase reporter plasmids, together with TK-renilla luciferase and 40 ng of the
583 plasmids for expression of the indicated proteins. After overnight transfection, cells were stimulated
584 with SeV for 24 h (**A**), IFNα (**B**) or TNF-α (**C**) for 8 h. **D-I**) HEK293T cells were transfected with the
585 ISG56.1 firefly luciferase reporter plasmid, TK-renilla luciferase and plasmids for expression of the
586 indicated proteins. Cells were also co-transfected with EV as the non-stimulated (NS) controls or with
587 the 5 ng of CARD-domain of RIG-I (**D**, **E** and **I**), 40 ng of MAVS (**F**), 40 ng of TBK-1 (**G**) and 5 ng of
588 IRF3-5D (**H**) plasmids to activate the IRF3 pathway. EV was added to samples when necessary to
589 keep the final amount of DNA transfected as 40 ng in all samples. Cell lysates were prepared and
590 luciferase expression was measured and normalised to renilla luciferase. At least triplicate samples
591 were analysed for each condition. Data are expressed as the mean (± SEM) fold induction of the
592 firefly luciferase activity normalised to renilla values for the stimulated versus non-stimulated samples.
593 Data shown are representative of three independent experiments. Immunoblots underneath each
594 graph show the expression levels of the different proteins. The positions of molecular mass markers
595 in kDa are shown on the right and the antibodies used are shown on the left. ns = not significant; *P <
596 0.05; ****P < 0.0001.

597

598 **Fig 3: Spir-1 and DDX3 share a conserved diphenylalanine motif that is required for IRF3**
599 **activation and direct binding to K7.** (**A**) DDX3 knockdown was induced in HEK293T cells stably
600 transfected with pTRIPZ-shDDX3 (or a NSC pTRIPZ vector) through incubation with doxycycline for
601 48 h. Twenty-four h after doxycycline addition, cells were transfected with FLAG-tagged plasmids
602 overnight. Cell lysates were immunoprecipitated using FLAG-affinity resin and analysed by SDS-
603 PAGE and immunoblotting. (**B**) DDX3 knockdown was induced in HEK293T shDDX3 cells as in (**A**)
604 and cells were then transfected with ISG56.1-firefly luciferase reporter, TK-renilla luciferase, plasmids
605 for expression of the indicated proteins together with the CARD-domain. Cell lysates were prepared
606 and analysed as in Fig 2. Immunoblots underneath the graph show the expression levels of the
607 different proteins. (**C**) Alignment of amino acid residues of Spir-1 and DDX3 showing the conserved
608 diphenylalanine motif. (**D**) HEK293T cells were transfected overnight with Myc-tagged Spir-1 wild
609 type, GFP or Spir-1 mutant FFAA together with FLAG-K7. Cell lysates were immunoprecipitated using
610 either Myc (middle panel) or FLAG-affinity resins (right panel) and analysed by SDS-PAGE and
611 immunoblotting. (**E**) HEK293T cells were transfected with ISG56.1 firefly luciferase reporter, TK-
612 renilla luciferase, plasmids for expression of the indicated proteins together with the CARD-domain of
613 RIG-I or EV as the NS control. Cell lysates were prepared and analysed as in (**B**). The panel
614 underneath the graph shows immunoblots for the expression level of K7 and GAPDH. (**F**, **G**) Myc or
615 FLAG-tagged proteins were synthesized by *in vitro* transcription/translation. Samples were
616 immunoprecipitated using FLAG- (**F**) or Myc-affinity resins (**G**) and analysed by SDS-PAGE and
617 immunoblotting. For all immunoblots, the positions of molecular mass markers in kDa are shown on
618 the left and the antibodies used on the right. ns = not significant; ****P < 0.0001. HC/LC: IgG heavy
619 chain or light chain, respectively.
620

621 **Fig 4: K7 residue Asp31 is important for binding to Spir-1 and DDX3 and inhibition of IRF3**
622 **activation.** HEK293T cells were transfected with FLAG-tagged GFP, K7 wild type or mutants, Myc-
623 Spir-1 and HA-DDX3 (**A**) or with only FLAG-tagged plasmids overnight (**B**). Cell lysates were
624 immunoprecipitated using FLAG-affinity resin and analysed by SDS-PAGE and immunoblotting. The
625 positions of molecular mass markers in kDa are shown on the left and the antibodies used on the
626 right. (**C**) HEK293T cells were transfected with ISG56.1-firefly luciferase reporter, TK-renilla
627 luciferase, plasmids for expression of the indicated proteins together with the CARD-domain or EV as
628 the NS control. Cell lysates were prepared and analysed as in Fig 2. Statistical analyses compared
629 the fold induction of the mutant sample to its respective K7 wild type. The panel underneath the graph
630 shows immunoblots for the expression levels of the different K7 proteins and α-tubulin. The positions
631 of molecular mass markers in kDa are shown on the right and the antibodies used on the left. ns =
632 not significant; ****P < 0.0001. LC: IgG light chain.
633

634 **Fig 5: Spir-1 contributes to IRF3 phosphorylation and IRF3 stimulated gene expression after**
635 **SeV infection in HEK293T cells.** (**A**) Schematic of CRISPR-Cas9-mediated knockout strategy
636 targeting *Spire1* exon 3 and single allele sequences of HEK293T Spir-1 knockout (KO) cells. (**B-F**)
637 Spir-1 knockout (KO) HEK293T cells were transduced with empty vector (EV) or Myc-Spir-1
638 lentiviruses to rescue Spir-1 expression. Cells lines were either non-infected (NS) or infected with
639 SeV for the indicated times. Cells were then either lysed and analysed by immunoblotting (**B**) or
640 subjected to total RNA extraction followed by RT-qPCR (**C-E**). Supernatants were analysed by ELISA
641 (**F**). (**G**) Spir-1 KO or wild type (WT) HEK293T cells were stimulated overnight with TNF**α** and
642 supernatants were analysed by ELISA. ns = not significant, **P < 0.01, ***P < 0.001, ****P < 0.0001.
643
644 **Fig 6: IRF3 activation is reduced in Spir-1 KO MEFs.** Spir-1 WT or KO MEF cells were transfected
645 with poly I:C (**A, C-E, I-J**) or infected with SeV (**B, F-H, K-L**) for the indicated times. Cells were lysed
646 and analysed by immunoblotting (**A, B**) and phospho-IRF3 bands intensity was quantified and
647 normalised by the intensity of α-tubulin from at least two different experiments (**A**, **B**, bottom graphs).
648 The positions of molecular mass markers in kDa are shown on the left and the antibodies used on the
649 right. Cells were also subjected to total RNA extraction followed by RT-qPCR (C-H) and supernatants
650 were analysed by ELISA (**I-L**). (**M, N**) Spir-1 WT or KO MEF cells were stimulated with IL-1β for 8 h
651 and supernatants were analysed by ELISA. ns = not significant, *P < 0.05, **P < 0.01, ****P < 0.0001.
652
653 **Fig 7: Spir-1 is a cellular restriction factor for VACV and ZIKV.** (**A, B**) Spir-1 WT or KO and Spir-
654 1 KO complemented HEK293T cells were infected with VACV-A5-GFP and plaque diameters were
655 measured at 48 h p.i. (**A**) Representative plaques formed in each cell line. (**B**) Plaques diameter
656 measurements (n=54). (**C**) Spir-1 WT or KO and Spir-1 KO complemented HEK293T cells were
657 infected with VACV WR at 0.001 PFU/cell for 48 h and the virus yield was measured in BSC-1 cells.
658 ns = not significant, *P<0.05, **P < 0.01, ***P < 0.001, ****P < 0.0001. (**D and E)** Spir-1 WT or KO
659 and Spir-1 KO complemented HEK293T cells were infected with ZIKV-mCherry at 0.01 PFU/cell for
660 72 h and ZIKV-infected monolayers were imaged (**D**) or the virus yield was measured in VERO E6
661 cells (**E**). ns = not significant, **P < 0.01, ***P < 0.001.
662
663
664 ## Supporting information
665
666 **S1 Fig: Ectopic expression of Spir-1 doesn't affect IRF3-dependent gene expression induced**
667 **by IKKε.** HEK293T cells was transfected with the ISG56.1 firefly luciferase reporter plasmid, TK-
668 renilla luciferase and plasmids for expression of the indicated proteins. Cells were also co-transfected
669 with EV as the non-stimulated (NS) controls or with the 100 ng of IKKε plasmid to activate the IRF3

670 pathway. EV was added to samples when necessary to keep the final amount of DNA transfected as
671 40 ng in all samples. Cell lysates were prepared and luciferase expression was measured and
672 normalised to renilla luciferase. At least triplicate samples were analysed for each condition. Data are
673 expressed as the mean (± SEM) fold induction of the firefly luciferase activity normalised to renilla
674 values for the stimulated versus non-stimulated samples. Data shown are representative of three
675 independent experiments. Immunoblots underneath each graph show the expression levels of the
676 different proteins. The positions of molecular mass markers in kDa are shown on the right and the
677 antibodies used are shown on the left. ns = not significant; *P < 0.05; ****P < 0.0001.
678
679 **S1 Table.** Plasmids used in the study
680
681 **S2 Table.** Oligonucleotides used in this study
682
683 **S3 Table.** Primary antibodies used in the study
684

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686

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Supporting information

S1 Fig. Ectopic expression of Spir-1 does not affect IRF3-dependent gene expression induced by IKKε (related to Figure 2). HEK293T cells were transfected with the ISG56.1 firefly luciferase reporter plasmid, TK-renilla luciferase and plasmids for expression of the indicated proteins. Cells were also co-transfected with EV as the non-stimulated (NS) controls or with 100 ng of IKKε plasmid to activate the IRF3 pathway. EV was added to samples when necessary to keep the final amount of DNA transfected as 40 ng in all samples. Cell lysates were prepared and luciferase expression was measured and normalised to renilla luciferase. At least triplicate samples were analysed for each condition. Data are expressed as the mean (± SEM) fold induction of the firefly luciferase activity normalised to renilla values for the stimulated versus non-stimulated samples. Data shown are representative of three independent experiments. Immunoblots underneath each graph show the expression levels of the different proteins. The positions of molecular mass markers in kDa are shown on the right and the antibodies used are shown on the left. ns = not significant; *P < 0.05; ****P < 0.0001.

S1 Table. Plasmids used in the study

PLASMID	SOURCE
human nMyc-Spir-1-pcDNA3.1	Gift from Prof. Dr. E. Kerkhoff (University Hospital Regensburg, Germany)
human nMyc-Spir-2-pcDNA3.1	Gift from Prof. Dr. E. Kerkhoff (University Hospital Regensburg, Germany)
mouse nMyc-B-TrCP-pcDNA3.1	(Mansur *et al*, 2013)

GFP-Myc-pCMV	(Neidel *et al*, 2019)
nFlag-coK7-pcDNA4/TO	(Torres *et al*, 2016)
coA49-cFlag-pcDNA3.1	(Neidel *et al.*, 2019)
GFP-cFlag-pcDNA4/TO	Sarah Neidel (Prof. G.L. Smith laboratory)
human nMyc-Spir-1-NT-pcDNA3.1	This study
human nMyc-Spir-1-CT-pcDNA3.1	This study
coN1-cTAP-pcDNA4/TO	(Maluquer de Motes *et al*, 2011)
coC6-cTAP-pcDNA4/TO	(Unterholzner *et al*, 2011)
nTAP-coN2-pcDNA4/TO	(Ferguson *et al*, 2013)
nFlag-coB14-pcDNA4/TO	(Torres *et al.*, 2016)
pcDNA4/TO	Invitrogen
nMyc-DDX3-pCMV	Gift from Dr M. Schröder - (Gu *et al*, 2013)
nHA-DDX3-pCMV	Gift from Dr M. Schröder - (Gu *et al.*, 2013)
IFN-β-luc	Gift from Dr T. Taniguchi (University of Tokyo, Japan)
ISRE-luc	Gift from Dr. A. Bowie (Trinity College, Dublin, Ireland)
NF-κB-luc	Gift from Dr. A. Bowie (Trinity College, Dublin, Ireland)
ISG56.1-luc	Gift from G. Sen (Cleveland Clinic, Cleveland, OH, USA).
TK-Renilla	Promega
Flag-RIG-I-CARD	Gift from A. Garcia-Sastre (Mount Sinai, New York, USA)
HA-MAVS	(Unterholzner *et al.*, 2011)
Flag-TBK1	(Unterholzner *et al.*, 2011)
Flag-IKKe	(Unterholzner *et al.*, 2011)
IRF3-5D	(Unterholzner *et al.*, 2011)
human nMyc-Spir-1-FFAA-pcDNA3.1	This study
pF3A-nFlag-coK7	This study
pF3A-nMyc-Spir-1	This study
pF3A-nMyc-DDX3	This study
pF3A-F12-cFlagd	GLS - unpublished
pF3A-nMyc-TAB2	GLS - unpublished
nFlag-coK7-D28A-pcDNA4/TO	This study
nFlag-coK7-D31A-pcDNA4/TO	This study
nFlag-coK7-DDAA-pcDNA4/TO	This study
pSpCas9(BB)-2A-Puro (px459)	(Ran *et al*, 2013) - Addgene plasmid #62988
px459-Spir-1-sgRNA#2	This study
pLKO.DCMV.TetO.mcs	(Everett *et al*, 2013)
pLKO.DCMV.TetO.Myc-Spir-1	This study
pCMV.dR8.91	Gift from Dr H. Laman (Lomonosov *et al*, 2011)
pMD-G	Gift from Dr H. Laman (Lomonosov *et al.*, 2011)

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926
927 **S2 Table. Oligonucleotides used in this study**
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PLASMID CONSTRUCTION	**PRIMER**
human nMyc-Spir-1-CT-pcDNA3.1	AAAAGCGGCCGCCAGTGTGATGGATGGGTCAGATCTCACTGAT
	AAAAGGATCCGCCGCCGCCATGGAGCAGAAGCTGATCTCCGAGGAG GACCTGGCT
human nMyc-Spir-1-NT-pcDNA3.1	AAAAGCGGCCGCCAGTGTGATGGATGGGTCACTCCTCTGGTGATACA GGCCGCAGCT
	AAGCTTGGTACCGAGCTCGGATCCGCCG
pLKO.DCMV.TetO. Myc-Spir-1	AAAAACGCGTGCCGCCAGTGTGATGGATGGGTCAGATCTCACTGATC GTCCT
	AAAAGCTAGCGCCGCCGCCATGGAGCAGAAGCTGATCTCCGAGGAG GA
human nMyc-Spir-1-FFAA-pcDNA3.1	TTGCCGAACCAGGAGGTTTTCCGCCGCCACTTGGTCTTATACCTGTCA G
	CTGACAGGTATAAGACCAAGTGGCGGCGGAAAACCTCCTGGTTCGGC AA
nFlag-coK7-D28A-pcDNA4.1/TO	CGGGACAGCATCATCGCCCTGATCGACGAGTAC
	GTACTCGTCGATCAGGGCGATGATGCTGTCCCG
nFlag-coK7-D31A-pcDNA4.1/TO	GCATCATCGACCTGATCGCCGAGTACATCACCTGGCG
	CGCCAGGTGATGTACTCGGCGATCAGGTCGATGATGC
nFlag-coK7-DDAA-pcDNA4.1/TO	CGGGACAGCATCATCGCCCTGATCGCCGAGTAC
	GTACTCGGCGATCAGGGCGATGATGCTGTCCCG
pF3A-nFlag-coK7	AAAAGCGATCGCATGGACTACAAAGACGATGACGACAAG
	AAAATTTAAACTCAGTTCAGCTTCTTTTCCAGGAA
pF3A-nMyc-Spir-1	AAAAGCGATCGCATGGAGCAGAAGCTGATCTCCGA
	AAAATTTAAACTCAGATCTCACTGATCGTCCTCTC
pF3A-nMyc-DDX3	AAAAGTTTAAACTCAGTTACCCCACCAGTCAACCC
	AAAAGCGATCGCATGGAGCAGAAGCTGATCTCAGAGGA
CRISPR/Cas9 gRNA targeting region	**gRNA SEQUENCE**
Spire1 exon 3	AGAGCAGCTTATCGATCACA
SEQUENCING PRIMERS	
Forward primer for exon 3 of human *Spire1*	TGGGAAATGTGGAAAATCAACTCG
Reverse primer for exon 3 of human *Spire1*	AAAAATAACAGCTTGGACACAGTGG

929
930
931 **S3 Table. Primary antibodies used in the study**
932

ANTIBODIES	**SOURCE**	**DILUTION**
Rb anti-Myc	Cell Signaling, 2278	1 in 1000

Ms anti-Myc	Cell Signaling, 9B11	1 in 1000
Rb anti-Actin	Sigma, A2066	1 in 1000
Ms anti-Flag	Sigma, F1804	1 in 1000
Rb anti-14-3-3	Santa Cruz, sc-629	1 in 1000
Ms anti-Spir-1	Santa Cruz, sc-517039	1 in 500
Ms anti-Spir-1	Abcam, ab57463	1 in 1000
Rb anti-DDX3	Cell Signaling, 2635	1 in 1000
Rb anti-IKKb	Cell Signaling, 2684	1 in 1000
Rb anti-HA	Sigma, H6908	1 in 1000
Rb anti-C6	(Unterholzner *et al.*, 2011)	1 in 1000
Ms anti-alpha-Tubulin	Millipore, 05-829	1 in 5000
Ms anti-GAPDH	Sigma, G8795	1 in 1000
Rb anti-IRF3	Cell Signaling, 4962	1 in 1000
Ms anti-COPe	Santa Cruz, sc-133194	1 in 500
Rb anti-p-IRF3	Cell Signaling, 4947S	1 in 1000

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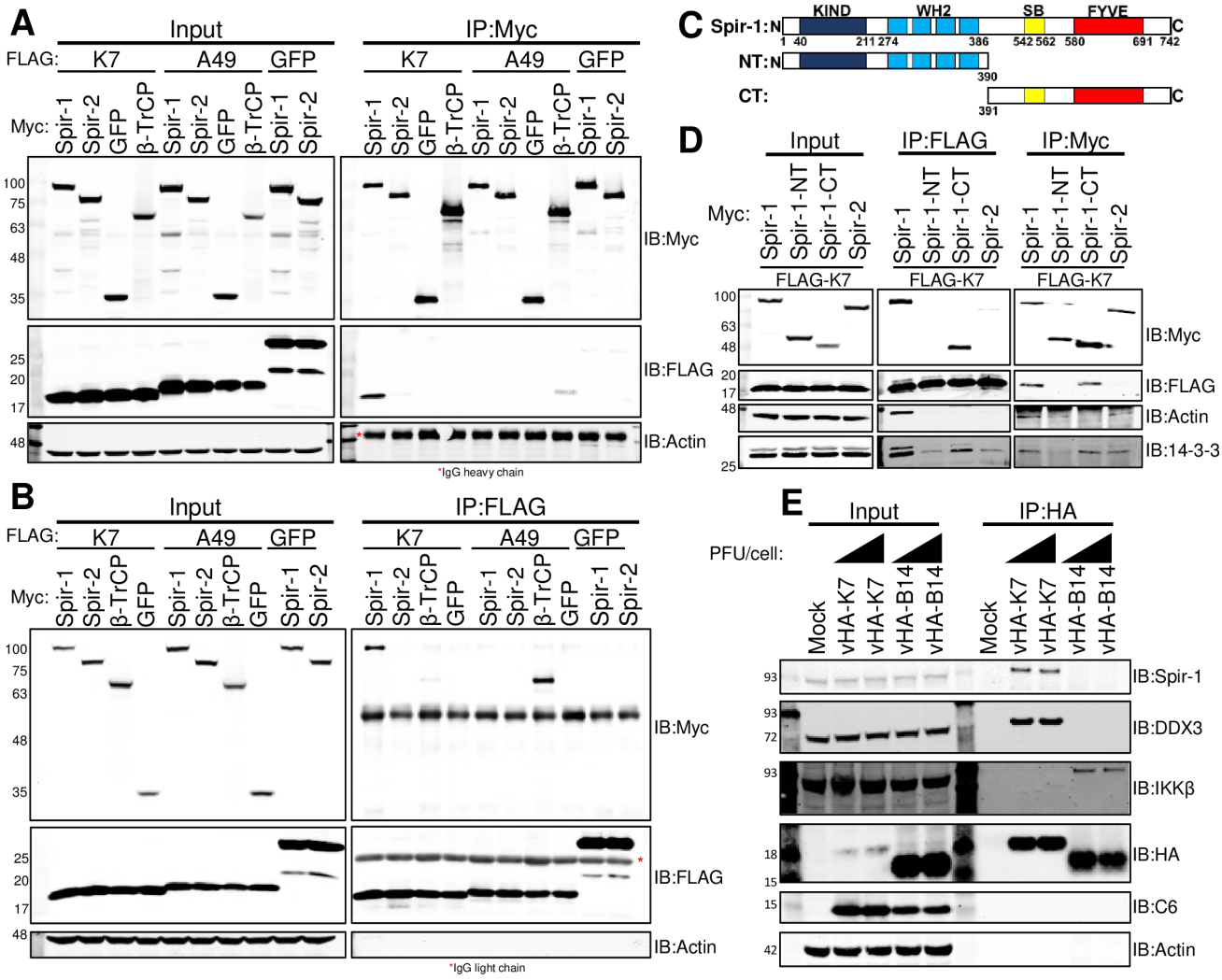
967 Fig 1


A
Input
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FLAG:
K7
A49
GFP
Myc:
Spir-1
Spir-2
GFP
β-TrCP
IB:Myc
IB:FLAG
IB:Actin
*IgG heavy chain
B
Input
IP:FLAG
IB:Myc
IB:FLAG
IB:Actin
*IgG light chain
C
Spir-1:N
KIND
WH2
SB
FYVE
NT:N
CT:
D
Input
IP:FLAG
IP:Myc
Spir-1-NT
Spir-1-CT
FLAG-K7
IB:Myc
IB:FLAG
IB:Actin
IB:14-3-3
E
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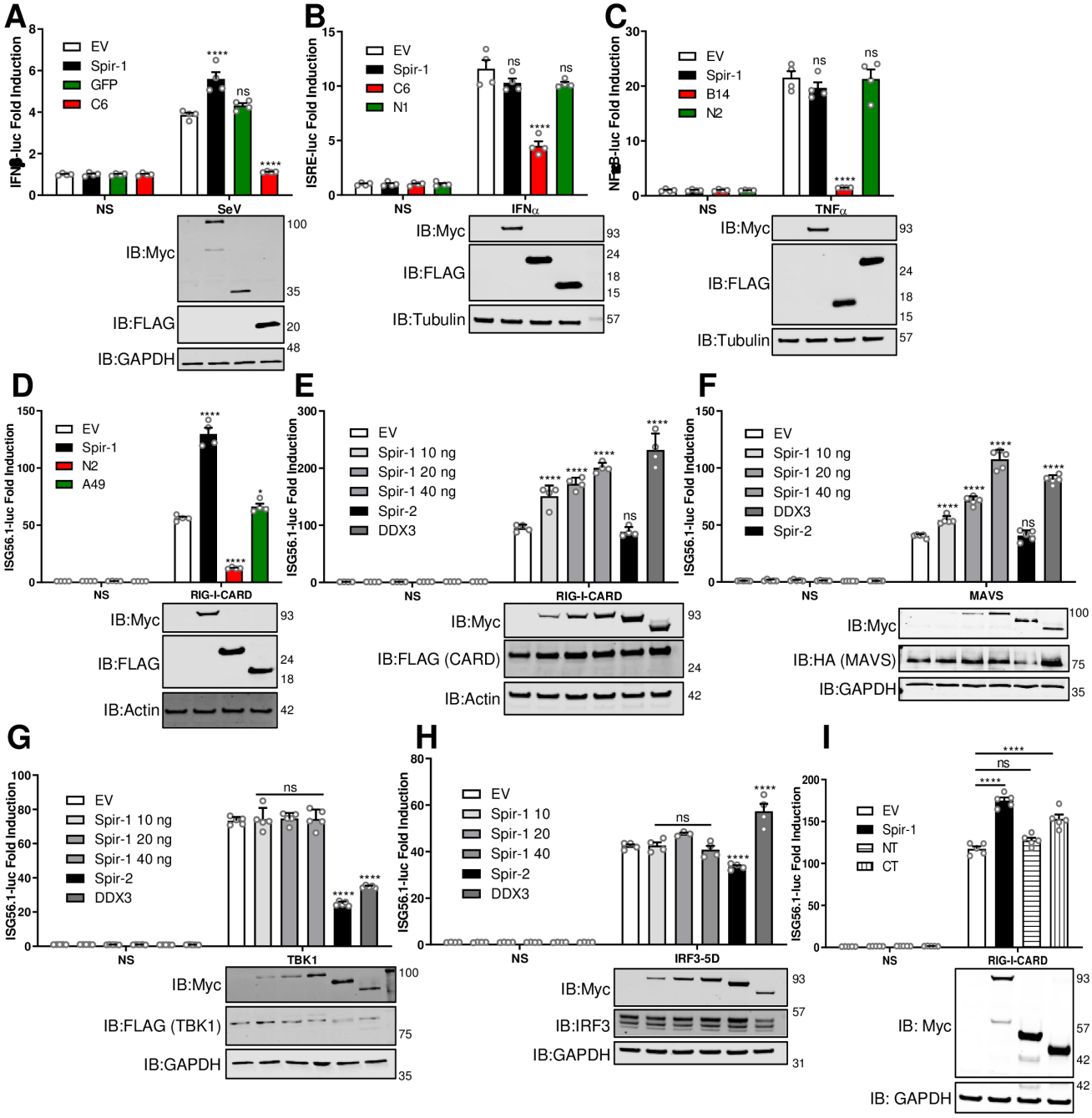
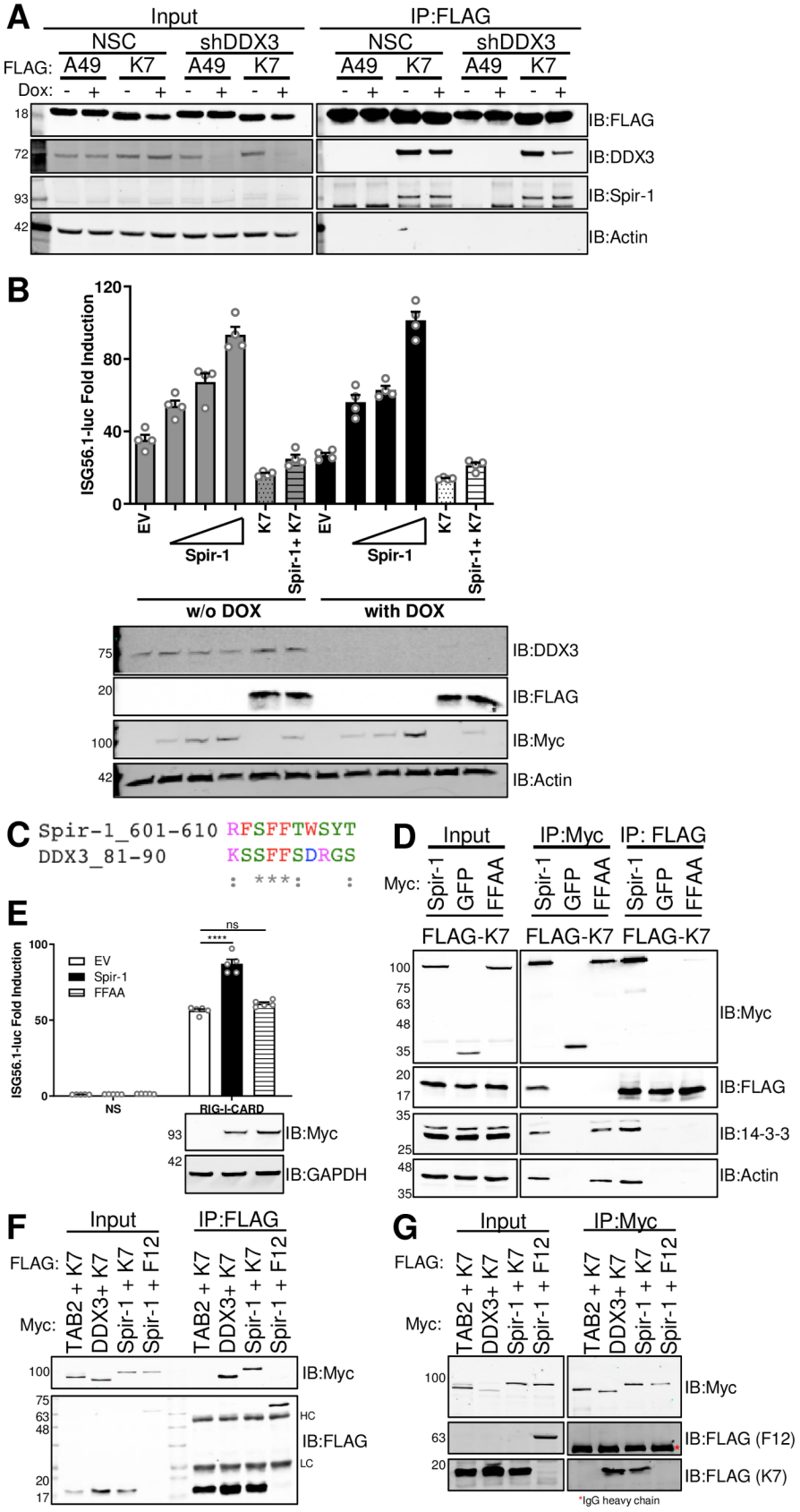
IP:HA
PFU/cell:
Mock
vHA-K7
vHA-B14
IB:Spir-1
IB:DDX3
IB:IKKβ
IB:HA
IB:C6
IB:Actin

968

Fig 2

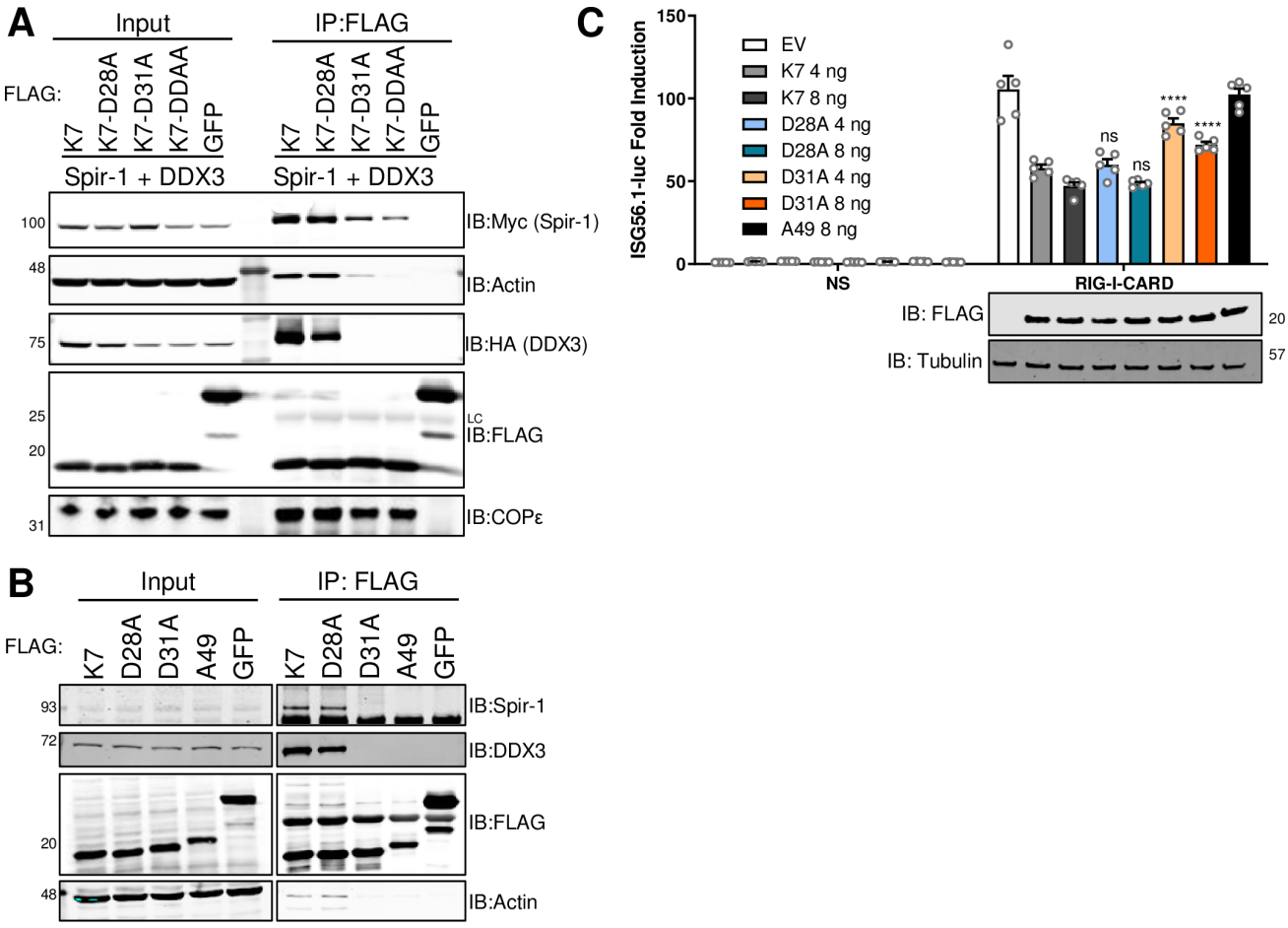

A
IFNβ-luc Fold Induction
EV
Spir-1
GFP
C6
NS
SeV
IB:Myc
IB:FLAG
IB:GAPDH
B
ISRE-luc Fold Induction
EV
Spir-1
C6
N1
NS
IFNα
IB:Myc
IB:FLAG
IB:Tubulin
C
NFκB-luc Fold Induction
EV
Spir-1
B14
N2
NS
TNFα
IB:Myc
IB:FLAG
IB:Tubulin
D
ISG56.1-luc Fold Induction
EV
Spir-1
N2
A49
NS
RIG-I-CARD
IB:Myc
IB:FLAG
IB:Actin
E
ISG56.1-luc Fold Induction
EV
Spir-1 10 ng
Spir-1 20 ng
Spir-1 40 ng
Spir-2
DDX3
NS
RIG-I-CARD
IB:Myc
IB:FLAG (CARD)
IB:Actin
F
ISG56.1-luc Fold Induction
EV
Spir-1 10 ng
Spir-1 20 ng
Spir-1 40 ng
DDX3
Spir-2
NS
MAVS
IB:Myc
IB:HA (MAVS)
IB:GAPDH
G
ISG56.1-luc Fold Induction
EV
Spir-1 10 ng
Spir-1 20 ng
Spir-1 40 ng
Spir-2
DDX3
NS
TBK1
IB:Myc
IB:FLAG (TBK1)
IB:GAPDH
H
ISG56.1-luc Fold Induction
EV
Spir-1 10
Spir-1 20
Spir-1 40
Spir-2
DDX3
NS
IRF3-5D
IB:Myc
IB:IRF3
IB:GAPDH
I
ISG56.1-luc Fold Induction
EV
Spir-1
NT
CT
NS
RIG-I-CARD
IB: Myc
IB: GAPDH

971 Fig 3

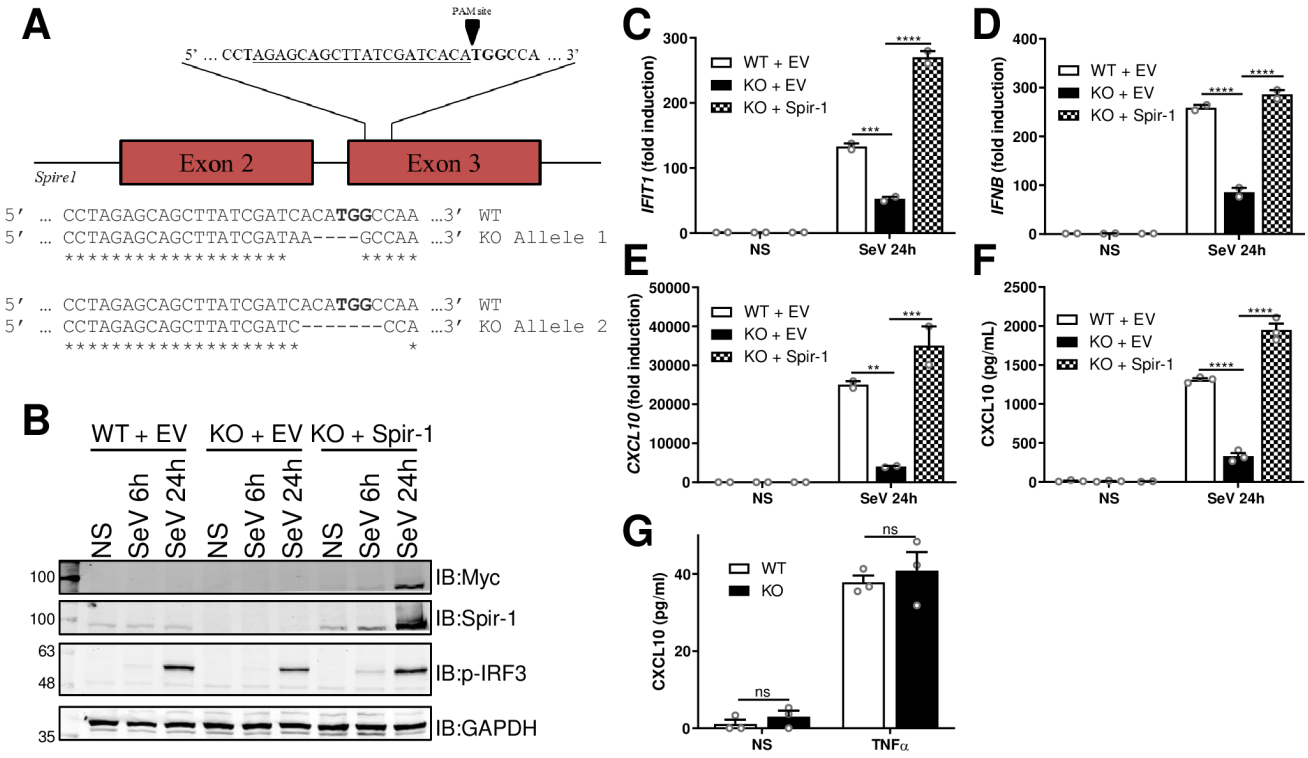

A
Input
IP:FLAG
NSC
shDDX3
FLAG: A49 K7 A49 K7
Dox: - + - + - + - +
IB:FLAG
IB:DDX3
IB:Spir-1
IB:Actin
B
ISG56.1-luc Fold Induction
EV
Spir-1
K7
Spir-1+ K7
w/o DOX
with DOX
IB:DDX3
IB:FLAG
IB:Myc
IB:Actin
C
Spir-1_601-610 RFSFFTWSYT
DDX3_81-90 KSSFFSDRGS
D
Input
IP:Myc
IP: FLAG
Myc: Spir-1 GFP FFAA
FLAG-K7
IB:Myc
IB:FLAG
IB:14-3-3
IB:Actin
E
ISG56.1-luc Fold Induction
EV
Spir-1
FFAA
ns
****
NS
RIG-I-CARD
IB:Myc
IB:GAPDH
F
Input
IP:FLAG
FLAG:
Myc: TAB2 + K7 DDX3+ K7 Spir-1 + K7 Spir-1 + F12
IB:Myc
HC
IB:FLAG
LC
G
Input
IP:Myc
FLAG:
Myc: TAB2 + K7 DDX3+ K7 Spir-1 + K7 Spir-1 + F12
IB:Myc
IB:FLAG (F12)
IB:FLAG (K7)
*IgG heavy chain

972

Fig 4

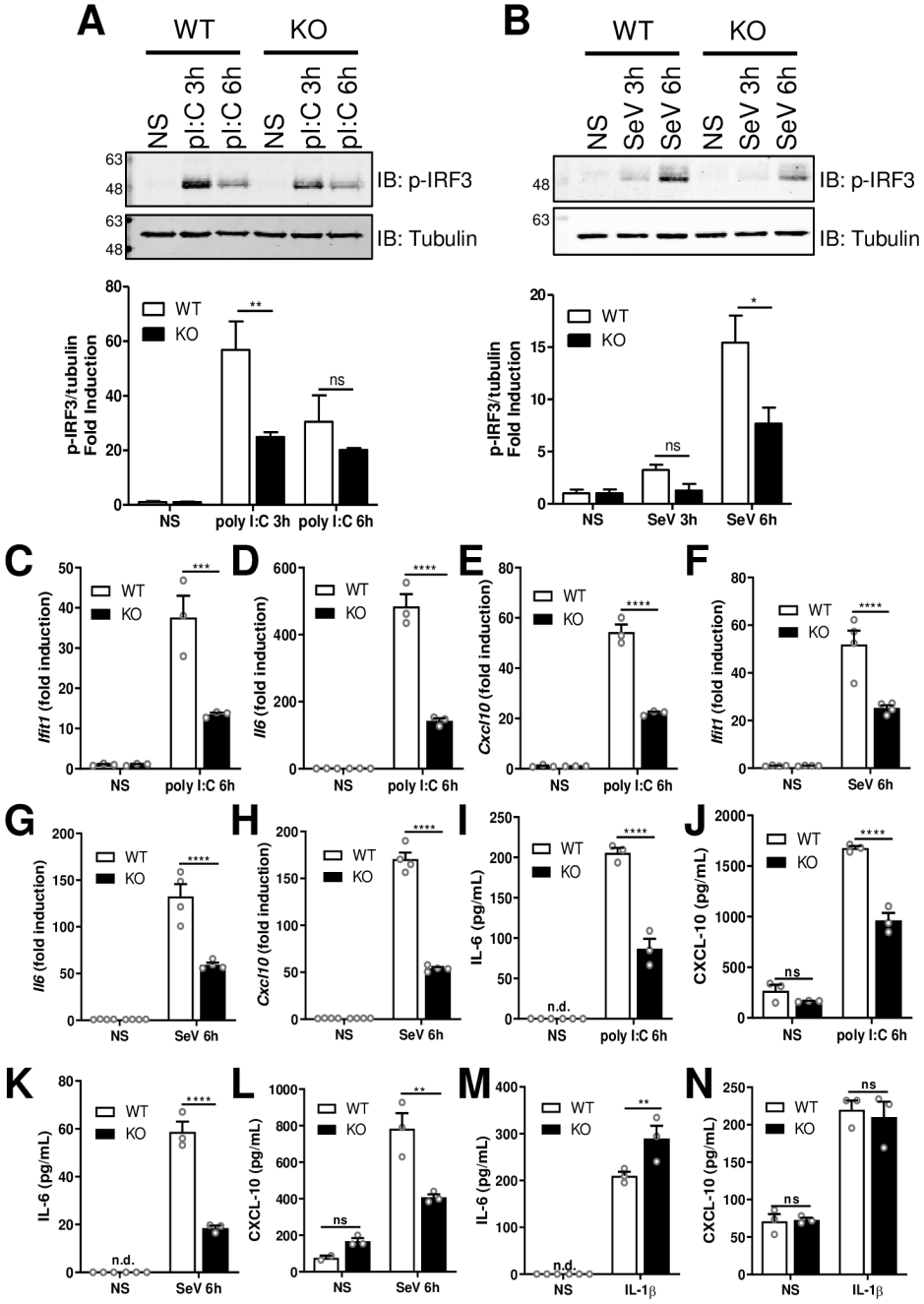

A
Input
IP:FLAG
FLAG:
K7
K7-D28A
K7-D31A
K7-DDAA
GFP
Spir-1 + DDX3
100
48
75
25
20
31
IB:Myc (Spir-1)
IB:Actin
IB:HA (DDX3)
LC
IB:FLAG
IB:COPε
B
Input
IP: FLAG
FLAG:
K7
D28A
D31A
A49
GFP
93
72
20
48
IB:Spir-1
IB:DDX3
IB:FLAG
IB:Actin
C
ISG56.1-luc Fold Induction
150
100
50
0
EV
K7 4 ng
K7 8 ng
D28A 4 ng
D28A 8 ng
D31A 4 ng
D31A 8 ng
A49 8 ng
ns
ns
****
****
NS
RIG-I-CARD
IB: FLAG
IB: Tubulin
20
57

975 Fig 5


A
PAM site
5' ... CCTAGAGCAGCTTATCGATCACATGGCCA ... 3'
Spire1
Exon 2
Exon 3
5′ … CCTAGAGCAGCTTATCGATCACATGGCCAA …3′ WT
5′ … CCTAGAGCAGCTTATCGATAA----GCCAA …3′ KO Allele 1
5′ … CCTAGAGCAGCTTATCGATCACATGGCCAA …3′ WT
5′ … CCTAGAGCAGCTTATCGATC-------CCA …3′ KO Allele 2
B
WT + EV
KO + EV
KO + Spir-1
NS
SeV 6h
SeV 24h
IB:Myc
IB:Spir-1
IB:p-IRF3
IB:GAPDH
C
IFIT1 (fold induction)
D
IFNB (fold induction)
E
CXCL10 (fold induction)
F
CXCL10 (pg/mL)
G
CXCL10 (pg/ml)
WT
KO
NS
SeV 24h
TNFα
ns

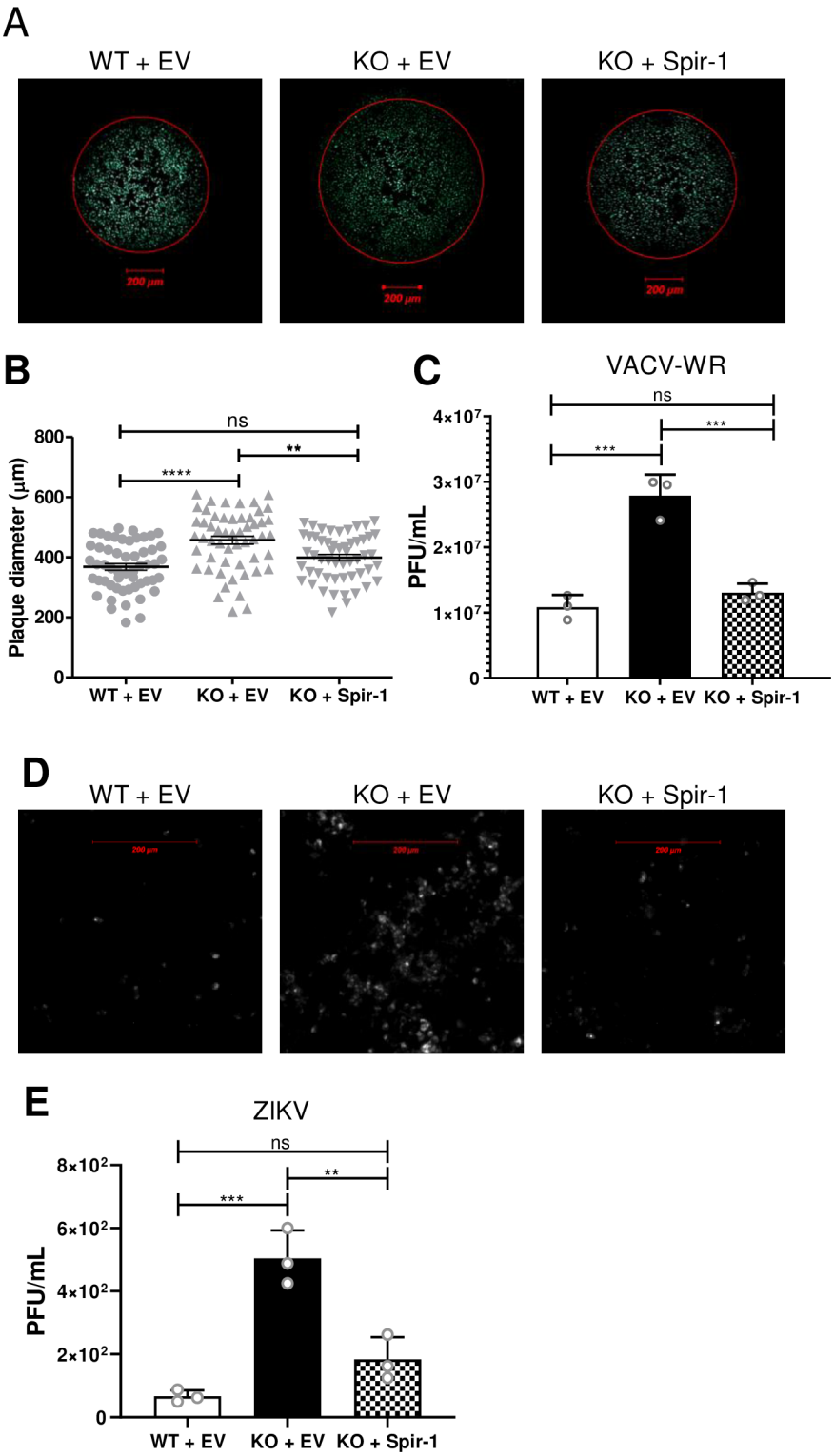
976

977 Fig 6


A
WT
KO
NS
pI:C 3h
pI:C 6h
IB: p-IRF3
IB: Tubulin
p-IRF3/tubulin Fold Induction
poly I:C 3h
poly I:C 6h
B
SeV 3h
SeV 6h
C
D
E
F
G
H
I
J
K
L
M
N
Ifit1 (fold induction)
Il6 (fold induction)
Cxcl10 (fold induction)
IL-6 (pg/mL)
CXCL-10 (pg/mL)
n.d.
ns
IL-1β

978

979 Fig 7

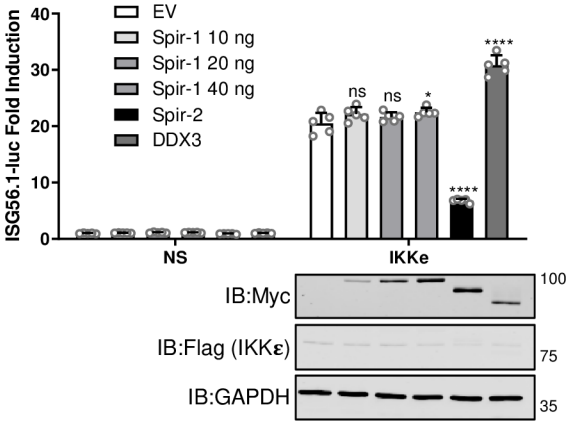


980

981

982

S1 Fig


ISG56.1-luc Fold Induction
40
30
20
10
0
EV
Spir-1 10 ng
Spir-1 20 ng
Spir-1 40 ng
Spir-2
DDX3
ns
ns
*
****
****
NS
IKKe
IB:Myc
IB:Flag (IKKε)
IB:GAPDH
100
75
35