



## 15 **Abstract**

16 Many viruses target signal transducers and activators of transcription (STAT) 1 and 2  
17 to antagonise antiviral interferon (IFN) signalling, but targeting of signalling by other  
18 STATs/cytokines, including STAT3/interleukin (IL-) 6 that regulate processes important to  
19 Ebola virus (EBOV) haemorrhagic fever, is poorly defined. We report that EBOV potently  
20 inhibits STAT3 responses to IL-6 family cytokines, and that this is mediated by the IFN-  
21 antagonist VP24. Mechanistic analysis indicates that VP24 effects a unique strategy combining  
22 distinct karyopherin-dependent and karyopherin-independent mechanisms to antagonise  
23 STAT3-STAT1 heterodimers and STAT3 homodimers, respectively. This appears to reflect  
24 distinct mechanisms of nuclear trafficking of the STAT3 complexes, revealed for the first time  
25 by our analysis of VP24 function. These findings are consistent with major roles for global  
26 inhibition of STAT3 signalling in EBOV infection, and provide new insights into the molecular  
27 mechanisms of STAT3 nuclear trafficking, significant to pathogen-host interactions, cell  
28 physiology and pathologies such as cancer.

29

## 30 **Author summary**

31 Ebola virus (EBOV) continues to pose a significant risk to human health globally,  
32 causing ongoing disease outbreaks with case-fatality rates between 40 and 60%. Suppression  
33 of immune responses is a critical component of EBOV haemorrhagic fever, but understanding  
34 of EBOV impact on signalling by cytokines other than interferon is limited. We find that  
35 infectious EBOV inhibits interleukin-6 cytokine signalling *via* antagonism of STAT3. The  
36 antagonistic strategy uniquely combines two distinct mechanisms, which appear to reflect  
37 differing nuclear trafficking mechanisms of critical STAT3 complexes. This provides  
38 fundamental insights into the mechanisms of pathogenesis of a lethal virus, and biology of  
39 STAT3, a critical player in immunity, development, growth and cancer.

## 40 **Key Words**

41 Ebola virus, VP24, STAT3, interleukin-6, oncostatin M, karyopherin, immune evasion,  
42 nuclear transport, STAT signalling

43

## 44 **Introduction**

45 Outbreaks of Zaire ebolavirus (EBOV, family *Filoviridae*, order *Mononegavirales*)  
46 cause severe haemorrhagic fever with fatality rates between 40 and 60% [1-4]. The 2014-2016  
47 West African outbreak (> 11,000 human deaths), and recent outbreak in the Democratic  
48 Republic of Congo (c. 2300 deaths in 2018-2020) highlight the ongoing danger to human health  
49 [3, 4].

50

51 The capacity of mammalian viruses to overcome the type-I IFN-mediated antiviral innate  
52 immune response is an important factor in virulence [5-7]. IFNs are induced in response to  
53 cellular detection of viral infection, and signal in autocrine and paracrine fashion to activate  
54 intracellular signalling, principally through STAT1 and STAT2. Following IFN-receptor  
55 binding, STAT1/2 are phosphorylated at conserved tyrosines, which results in the formation of  
56 phospho-(pY)-STAT1-STAT2 heterodimers and pY-STAT1 homodimers. Nuclear  
57 localisation signals (NLSs) formed within the dimers bind to nuclear import receptors of the  
58 NPI-1 karyopherin subfamily (which include karyopherin alpha-1 ( $K\alpha 1$ )) at a ‘non-classical’  
59 cargo-binding site, distinct from sites bound by most cellular cargoes [8-10]. The karyopherins  
60 mediate active nuclear accumulation of the STAT dimers, leading to antiviral IFN-stimulated  
61 gene (ISG) activation [11]. To evade IFN-dependent immune signalling, viruses encode IFN-  
62 antagonist proteins, many of which target STAT1/STAT2, including through interactions  
63 leading to sequestration, induction of degradation and inhibition of phosphorylation [5].  
64 Among IFN-antagonists, EBOV VP24 uses an unusual mechanism of competitive binding at

65 the non-classical STAT1-binding site in NPI-1 karyopherins, thereby preventing STAT1  
66 nuclear trafficking and ISG induction [12-15].

67

68 While IFN-STAT1/2 antagonism is reasonably well understood for many viruses, antagonism  
69 of other STATs including STAT3, the major mediator of signalling by IL-6 family cytokines  
70 (e.g. IL-6, oncostatin-M (OSM) [11]), is poorly defined, with only four mononegaviruses (three  
71 paramyxoviruses and one rhabdovirus) shown to express IFN-antagonist proteins that interact  
72 with STAT3 [16-19]. Nevertheless, STAT3-regulated processes are strongly  
73 implicated/dysregulated in EBOV disease, including the pro-inflammatory response,  
74 coagulation pathway and wound healing [6, 20-22]. Notably, despite critical roles in processes  
75 such as growth, development, apoptosis, infection and cancer, the precise mechanism(s)  
76 underlying cytokine-dependent STAT3 nuclear accumulation also remain poorly understood.  
77 Contrasting reports suggest three models whereby: (i) STAT3 undergoes constitutive  
78 nucleocytoplasmic shuttling with cytokines inducing intra-nuclear sequestration [23, 24], (ii)  
79 cytokine activation induces interaction of STAT3 with karyopherins including K $\alpha$ 1 resulting  
80 in nuclear import similar to STAT1 [25, 26], and (iii) STAT3 uses a combination of these  
81 mechanisms [27]. Notably, pY-STAT3 forms homodimers as well as heterodimers with pY-  
82 STAT1, which may regulate distinct gene subsets [28] and could use different trafficking  
83 mechanisms, possibly accounting for the contrasting models; this has not been directly  
84 examined.

85

86 Here, we aimed to examine the effect of EBOV on STAT3 responses, showing for the first  
87 time that EBOV VP24 antagonises STAT3 using a combination of mechanisms analogous to  
88 and distinct from that used for STAT1, to inhibit both STAT3 homodimers and heterodimers.

89 We further reveal that the STAT3 complexes use distinct mechanisms for nuclear  
90 accumulation, apparently necessitating VP24's multipronged strategy.

91

## 92 **Results and Discussion**

### 93 ***EBOV VP24 inhibits STAT3 responses***

94 Despite likely roles in EBOV infection for dysregulation of cytokines/STATs other  
95 than IFN/STAT1/2, antagonism of other STATs by EBOV remains unresolved. To determine  
96 whether EBOV affects STAT3, we infected COS7 cells with EBOV before treatment with  
97 OSM [18, 25] and analysis of STAT3 localisation by immunofluorescence staining and  
98 confocal laser scanning microscopy (CLSM; Figure 1A). In mock-infected cells, STAT3 was  
99 diffusely localised between the nucleus and cytoplasm of resting cells, with nuclear  
100 accumulation clearly observed following OSM treatment, as expected. In EBOV-infected cells,  
101 however, OSM-dependent STAT3 nuclear accumulation was inhibited, with quantitative  
102 image analysis confirming a significant decrease in nucleocytoplasmic localisation in EBOV-  
103 compared with mock-infected cells (Figure 1A,B). To exclude possible impact by virus-  
104 induced type-I IFN, we confirmed that EBOV also antagonises STAT3 responses in Vero cells,  
105 which do not produce IFN (Figure 1A,B). Notably, in infected cells, STAT3 accumulated into  
106 distinct cytoplasmic regions (zoom images, Figure 1A), which EBOV nucleoprotein  
107 immunolabelling indicated to be viral inclusion/replication bodies (Figure S1). The finding of  
108 STAT3 accumulation into cytoplasmic viral inclusions is, to our knowledge, the first such  
109 observation for any virus.

110

111 Since VP24 antagonises IFN/STAT1 responses [12], we tested its effects on STAT3 by  
112 analysing COS7 cells expressing GFP-VP24 or negative controls (GFP or GFP-rabies virus  
113 (RABV) N-protein, which does not affect STAT3 [18]), and co-transfected to express

114 mCherry-STAT3 (for live-cell analysis; Figure 2) or immunostained for endogenous STAT3  
115 (Figure 3A,B). OSM effected clear nuclear accumulation of STAT3 in GFP and N-protein-  
116 expressing cells, but this was strongly inhibited in VP24-expressing cells. Since OSM can  
117 induce pY-STAT3 homodimers and pY-STAT3-pY-STAT1 heterodimers [29] and VP24  
118 antagonises pY-STAT1 [12], we assessed the dependence of VP24-STAT3 antagonism on  
119 STAT1 using STAT1-deficient U3A cells [30, 31]. VP24 clearly antagonised STAT3 in U3A  
120 cells (Figure 3A,B) in which we confirmed a lack of STAT1 expression (Figure 3C), indicating  
121 that VP24 can inhibit STAT3 independently of STAT1 and thus antagonise STAT3  
122 homodimers.

123

124 Analysis of OSM-dependent signalling using a luciferase reporter gene assay [18, 32] in  
125 HEK293T and U3A cells indicated that VP24 effects significant suppression of OSM/STAT3  
126 signalling (Figure 3D; upper panel); RT-qPCR analysis confirmed that VP24 can inhibit OSM-  
127 induced expression of the STAT3-dependent *socs3* gene (Figure S2). Mumps virus V-protein  
128 (MUV-V, used as a positive control in our assays) induces STAT3 degradation to suppress IL-  
129 6 signalling [16]. We confirmed that MUV-V inhibits STAT3 responses and that this correlates  
130 with reduced levels of STAT3 expression in cell lysates. Since no similar effect was observed  
131 on STAT3 expression in VP24-expressing cells (Figure 3D; lower panel), it appeared that  
132 VP24 uses a different antagonistic mechanism.

133

#### 134 ***VP24 inhibits K $\alpha$ 1 interaction with STAT3, dependent on STAT1***

135 VP24 antagonises STAT1 responses by competitive binding to karyopherins [12, 13,  
136 15], including K $\alpha$ 1 that is also reported to mediate STAT3 nuclear import [25-27]. We thus  
137 examined whether VP24 can displace STAT3 from K $\alpha$ 1, by immunoprecipitation of FLAG-  
138 K $\alpha$ 1 from OSM-treated HEK293T cells (as previously used to analyse effects of VP24 on IFN-

139 activated pY-STAT1-karyopherin interactions [12, 13]) or U3A cells. Cells were co-  
140 transfected to express FLAG-K $\alpha$ 1 with GFP-VP24 or GFP, before OSM treatment and lysis  
141 for IP (Figure 4). pY-STAT1, pY-STAT3 and GFP-VP24 co-precipitated specifically with  
142 K $\alpha$ 1 as expected, consistent with reports that STAT1 and STAT3 are K $\alpha$ 1 cargoes [8, 25, 26],  
143 and VP24 can interact with K $\alpha$ 1 [12, 13]. Clearly, for both pY-STAT1 (as expected [12, 13])  
144 and pY-STAT3, the amount co-precipitated with K $\alpha$ 1 from HEK293T cells was reduced by  
145 VP24, consistent with competitive binding. Importantly, although a number of IFN-antagonists  
146 suppress STAT phosphorylation [5], VP24 did not affect levels of pY-STAT1 or pY-STAT3  
147 in lysates, indicating that reduced K $\alpha$ 1 interaction of STAT3 is not due to altered  
148 phosphorylation. Thus, it appears that VP24 can compete with STAT3-containing complexes  
149 for K $\alpha$ 1 interaction, similarly to its effect on STAT1.

150

151 Intriguingly, however, co-immunoprecipitation assays in U3A cells indicated that VP24 does  
152 not affect K $\alpha$ 1-pY-STAT3 interaction (Figure 4), despite clear impact on STAT3 responses in  
153 these cells (Figure 3). It has been suggested that karyopherin interactions of STAT homo- and  
154 heterodimers might differ [23, 24], and our data support this, providing evidence that STAT3  
155 homodimers may form interactions at a site in the karyopherin distinct to the non-classical  
156 STAT1/VP24-binding site, while STAT3-STAT1 heterodimers appear to bind at the  
157 STAT1/VP24 site and so can be displaced by VP24 (Figure 4). Since STAT1 homodimers and  
158 STAT1-STAT2 heterodimers also bind to this site [10], this might represent a common  
159 interface for STAT1-containing complexes, such that competitive binding by VP24 is likely to  
160 occur for heterodimers activated by other cytokines/mediators (e.g. STAT4-STAT1  
161 heterodimers). Since the data from U3A cells indicate that STAT3 homodimers bind to K $\alpha$ 1  
162 *via* a site not bound by VP24, it appears that an alternative mechanism must antagonise  
163 signalling by these complexes.

164

165 ***VP24 does not inhibit STAT3 binding to DNA***

166 Reports supporting constitutive nuclear trafficking of STAT3 suggest that STAT3  
167 accumulates in the nucleus in response to cytokine due to intra-nuclear  
168 interactions/sequestration, such as through induced DNA binding [24]. We therefore  
169 considered that VP24 may inhibit STAT3 nuclear accumulation in U3A cells by inhibiting the  
170 capacity of STAT3 to bind DNA, similar to the antagonistic mechanism of RABV P-protein  
171 for STAT1, where the P-protein binds proximal to or within the STAT1 DNA binding domain  
172 [33, 34]. To assess DNA binding by STAT3 directly, we performed electrophoretic mobility  
173 shift assay (EMSA) analysis of cell lysates using the m67 probe (Figure 5), which is a high  
174 affinity variant of the sis-inducible element from the *C-FOS* gene, commonly used to analyse  
175 STAT3-DNA binding [35-37]. OSM induced clear DNA binding of both endogenous and over-  
176 expressed STAT3 in the absence and presence of VP24, with VP24 having no evident  
177 inhibitory effect. Thus, the principal mechanism of antagonism does not appear to involve a  
178 direct hindrance of STAT3-DNA interaction.

179

180 ***VP24 interacts with STAT3, independently of VP24-karyopherin binding***

181 Recombinant purified VP24 and STAT1 proteins were reported to interact *in vitro* [38],  
182 but no direct interaction has been detected for proteins expressed in mammalian cells, so there  
183 is currently no evidence that this is significant to STAT1 antagonist function [15, 39].  
184 Nevertheless, since STAT3 localizes into viral inclusion bodies (Figure 1A), of which VP24 is  
185 a component [40], and many IFN-antagonists inhibit STATs through physical interaction [5],  
186 we tested whether VP24 can bind to STAT3. Endogenous and transfected STAT3 co-  
187 precipitated with VP24 from U3A cells (Figure 6A,B), and reciprocal immunoprecipitation *via*  
188 STAT3 confirmed the interaction (Figure S3). Thus, VP24 interacts with STAT3



189 independently of STAT1, consistent with data for antagonism of OSM/STAT3 signalling  
190 (Figure 3). We also confirmed co-precipitation of STAT3 with VP24 from HEK293T and  
191 COS7 cells (Figure 6C, Figure S6).

192

193 To further investigate the antagonistic mechanism, we analysed a karyopherin-binding  
194 deficient VP24 protein, wherein mutations of key residues at the VP24:karyopherin interface  
195 (MUT; L201A/E203A/P204A/D205A/S207A) strongly impair karyopherin binding and  
196 STAT1/IFN antagonism [15]. The effect of the mutations in inhibiting STAT1-antagonist  
197 function was confirmed using a STAT1/2-IFN-dependent luciferase reporter assay (using  
198 pISRE-LUC plasmid), which indicated an almost nine fold increase in luciferase activity in  
199 IFN- $\alpha$ -treated HEK293T cells expressing mutated protein compared with wild-type (WT)  
200 protein (Figure 7A; left panel). Interestingly, analysis using the STAT3/OSM-dependent  
201 signalling assay (using m67-LUC plasmid) in U3A cells showed no significant impact of the  
202 mutations on VP24 inhibitory activity (Figure 7A; middle panel), indicating that specific  
203 antagonism of STAT3 by VP24 is independent of karyopherin-binding activity, consistent with  
204 the lack of an effect of VP24 on K $\alpha$ 1-STAT3 interaction in U3A cells. Assays of STAT3/OSM-  
205 dependent signalling in HEK293T cells, however, indicated some dependence on karyopherin-  
206 binding, probably reflecting a contribution to signalling by STAT3-STAT1 heterodimers  
207 (Figure 7A; right panel), and consistent with the capacity of VP24 to compete with STAT1 and  
208 STAT3 for K $\alpha$ 1 interaction in these cells. Thus, it appears that in contrast to STAT1 (and  
209 STAT3-STAT1 heterodimers), antagonism of signalling by STAT3 homodimers is  
210 independent of VP24-karyopherin binding. Consistent with this, the mutations had no evident  
211 effect on VP24-STAT3 interaction in U3A cells (Figure 7B). Taken together, these data  
212 indicate that the nuclear trafficking mechanisms of STAT1 and STAT3 are distinct, and,  
213 accordingly, antagonism by VP24 uses different mechanisms, likely including competition

214 with STAT1-containing complexes for karyopherin binding, as well as physical interaction  
215 with STAT3, which can cause localisation into cytoplasmic inclusions.

216

217 These findings indicate that VP24 uniquely uses two distinct mechanisms to inhibit different  
218 STAT3 complexes, consistent with important roles for global shutdown of STAT3 in EBOV  
219 infection, possibly relating to the dysregulation of inflammation, coagulation and mucosal  
220 wound healing observed during EBOV infection [6, 20-22, 41, 42]. Recent reports indicate that  
221 STAT3 antagonism by MUV is associated with neurovirulence *in vivo* [43], and suppression  
222 of IL-6 signalling by influenza A virus early in infection contributes to a cytokine storm  
223 implicated in disease severity [44]. Interestingly, although the IFN-antagonist VP40 of the  
224 filovirus Marburg virus does not specifically target STATs, it inhibits upstream kinases  
225 resulting in inhibition of activation of both STAT1 and STAT3 [45]. Together these data  
226 indicate that potent suppression of STAT3 responses by filoviruses may contribute to excessive  
227 inflammatory responses associated with severe haemorrhagic fever. The apparent importance  
228 of STAT3 targeting to filoviruses, and previous reports of roles in infection by  
229 paramyxoviruses and rhabdoviruses, also indicates that specific and direct antagonism of  
230 STAT3 is important to diverse pathogens in the order *Mononegavirales* [16-19]. Taken  
231 together, these data suggest that virus-STAT3 interactions could provide potential targets for  
232 antivirals for diverse pathogens. Beyond the implications for viral infection, the study also  
233 provides, to our knowledge, the first clear indication of distinct nuclear import strategies for  
234 STAT3 homodimers and heterodimers. This potentially accounts for the contrasting trafficking  
235 models previously proposed [23-27], and supports the idea that these complexes have distinct  
236 roles in signalling by STAT3, a pleiotropic molecule important to processes including cancer,  
237 development and immunity.

238

## 239 **Materials and Methods**

### 240 *Plasmids and Cell Culture*

241           Constructs to express EBOV-VP24 and MUV-V fused to GFP were generated by PCR  
242 amplification from pCAGGS-FLAG-VP24 (kindly provided by Christopher Basler, Georgia  
243 State University) and MUV V-FLAG (a gift from Curt Horvath [16], Addgene plasmid  
244 #44908), and cloning into the pEGFP-C1 vector C-terminal to GFP (Clontech). Constructs to  
245 express mCherry- or FLAG-tagged STAT3 were kind gifts from Marie Bogoyevitch  
246 (University of Melbourne), and the construct to express FLAG-tagged K $\alpha$ 1 was a kind gift  
247 from Christopher Basler (Georgia State University). Other constructs have been described  
248 elsewhere [18, 32]. U3A (a kind gift from George Stark, Lerner Research Institute, Cleveland  
249 Clinic), COS7, E6 Vero and HEK293T cells were maintained in DMEM supplemented with  
250 10 % FCS and GlutaMAX (Life Technologies), 5 % CO<sub>2</sub>, 37°C. Transfections used  
251 Lipofectamine 2000 (Invitrogen), Lipofectamine 3000 (Invitrogen), or FuGene HD (Promega),  
252 according to the manufacturer's instructions.

253

### 254 *Virus infection*

255 All infectious work was conducted at Physical Containment Level 4 (PC4) at the Australian  
256 Centre for Disease Preparedness (ACDP, formerly AAHL). EBOV infections used Mayinga  
257 1976 isolate (MOI of 10), which was originally received from NIH Rocky Mountain  
258 Laboratories and passaged three times in Vero cells at ACDP after receipt.

259

### 260 *CLSM*

261           For analysis of STAT3 localisation, cells growing on coverslips transfected with  
262 plasmids or infected with EBOV were incubated in serum-free-(SF)-DMEM for 1 h and treated  
263 without or with 10 ng/mL recombinant human OSM (BioVision) for 15 min (analysis of

264 fixed/immunostained cells) or 30 min (analysis of STAT3-mCherry in living cells) before  
265 fixation using 3.7 % formaldehyde (10 min, room temperature (RT) for transfected cells) or 4  
266 % paraformaldehyde (48 h, 4°C for infected cells), followed by 90 % methanol (5 min, RT)  
267 and immunostaining. Antibodies used for were: anti-STAT3 (Santa Cruz, sc-482; or Cell  
268 Signaling Technology, 9139), anti-EBOV nucleoprotein (rabbit clone #691, final bleed  
269 1410069), anti-mouse Alexa Fluor 488 (ThermoFisher Scientific, A11001) and anti-rabbit  
270 Alexa Fluor 568 (ThermoFisher Scientific, A11036). Imaging used a Leica SP5 or Nikon C1  
271 inverted confocal microscope with 63 X objective. For live cell analysis, cells were imaged in  
272 phenol-free DMEM using a heated chamber. Digitized confocal images were processed using  
273 Fiji software (NIH). To quantify nucleocytoplasmic localisation, the ratio of nuclear to  
274 cytoplasmic fluorescence, corrected for background fluorescence (Fn/c), was calculated for  
275 individual cells expressing transfected protein [18, 32]; mean Fn/c was calculated for  $n \geq 35$   
276 cells for each condition in each assay.

277

### 278 *Co-immunoprecipitation*

279 Transfected cells were incubated in SF-DMEM (3 h) before treatment with or without  
280 OSM (10 ng/ml, 15 min), lysis and immunoprecipitation using GFP-Trap Agarose beads  
281 (Chromotek) or Anti-FLAG M2 Magnetic beads (Sigma-Aldrich), according to the  
282 manufacturer's instructions. Lysis and wash buffers were supplemented with PhosSTOP  
283 (Roche), cOmplete Protease Inhibitor Cocktail (Roche) and 10 mM NaF. Lysates and  
284 immunoprecipitates were analysed by SDS-PAGE and immunoblotting (IB) using antibodies  
285 against STAT3 (above), pY-STAT3 (Cell Signaling Technology, 9145), STAT1 (Cell  
286 Signaling Technology, 14994), pY-STAT1 (Tyr701, Cell Signaling Technology, 9167), FLAG  
287 (Sigma-Aldrich, F1804), GFP (Roche Applied Science, 11814460001), mCherry (Abcam,  
288 ab167453),  $\text{K}\alpha 1$  (Abcam, ab154399) and  $\beta$ -tubulin (Sigma-Aldrich, T8328), and HRP-

289 conjugated secondary antibodies (Merck). Visualisation of bands used Western Lightning  
290 chemiluminescence reagents (PerkinElmer).

291

### 292 ***Luciferase Reporter Gene Assays***

293 Cells were co-transfected with m67-LUC or pISRE-LUC (in which Firefly luciferase  
294 expression is under the control of a STAT3 or STAT1/2-dependent promoter, respectively) and  
295 pRL-TK (transfection control, from which *Renilla* luciferase is constitutively expressed), as  
296 previously described [18, 46], together with protein expression constructs. Cells were treated  
297 16 h (OSM) or 8 h (IFN- $\alpha$ ) post-transfection with or without OSM (10 ng/mL for 8 h) or IFN-  
298  $\alpha$  (1,000 U/ml for 16 hours) before lysis using Passive Lysis Buffer (Promega). Firefly and  
299 *Renilla* luciferase activity was then determined in a dual luciferase assay, as previously  
300 described [18, 46]. The ratio of Firefly to *Renilla* luciferase activity was determined for each  
301 condition, and then calculated relative to that determined for GFP-N-protein-expressing cells  
302 treated with OSM (relative luciferase activity). Data from  $\geq 3$  independent assays were  
303 combined, where each assay result is the mean of three replicate samples.

304

### 305 ***EMSA***

306 Transfected cells were incubated in SF-DMEM (2 h) before treatment with or without  
307 OSM (10 ng/ml, 15 min) and lysis in 20 mM Hepes (pH 7.0), 300 mM NaCl, 20 % (v/v)  
308 glycerol, 10 mM KCl, 1 mM MgCl<sub>2</sub>, 0.5 mM DTT, 0.1 % (v/v) Triton X-100, as previously  
309 [47], supplemented with PhosSTOP (Roche), cOmplete Protease Inhibitor Cocktail (Roche)  
310 and 10 mM NaF. 10 ng of clarified cell lysate (calculated using Pierce Microplate BCA Protein  
311 Assay Kit - Reducing Agent Compatible, ThermoFisher Scientific) was incubated with 1 ng of  
312 digoxigenin-labelled m67 probe (double-stranded; 5'-  
313 AGCTTCATTTCCCGTAAATCCCTA-3')

314 30 mM KCL, 10 mM (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub>, 1 mM DTT, 1 mM EDTA, 0.2 % (w/v) Tween-20, 1 μg  
315 poly[d(I-C)] and 0.1 μg poly-Lysine (based on DIG Gel Shift Kit, 2<sup>nd</sup> Generation, Roche) for  
316 15 min at RT. DNA-protein complexes were resolved on a 4.5 % polyacrylamide gel in 0.5 x  
317 TBE running buffer (4°C), before electrophoretic transfer to a nylon membrane and IB using  
318 anti-Digoxigenin-AP Fab fragments (Roche). Visualisation of bands used CDP-Star  
319 chemiluminescence reagents (Roche).

320

### 321 ***RT-qPCR***

322 Transfected HEK293T cells were incubated in SF-DMEM (3 h) before treatment  
323 without or with OSM (10 ng/ml, 45 min) and RNA extraction (ReliaPrep RNA Cell Miniprep  
324 System, Promega). cDNA was generated using oligo(dT)<sub>20</sub> primer (GoScript Reverse  
325 Transcription System, Promega), before RT-qPCR using primers for *socs3* and *gapdh*, and  
326 iTaq Universal SYBR Green Supermix (Bio-Rad). Standard curves were generated for each  
327 primer pair using serial dilutions of the reference cDNA (samples from GFP-N-protein-  
328 expressing cells treated with OSM). *Socs3* expression was normalized to *gapdh* [46], and then  
329 calculated relative to that for GFP-N-expressing cells treated with OSM. Data from 2  
330 independent assays were combined, where each assay result is the mean of replicate samples.  
331 Primer sequences were: 5'-GGAGTTCCTGGACCAGTACG-3' and 5'-  
332 TTCTTGTGCTTGTGCCATGT-3' for *socs3*; 5'-GAAGGTGAAGGTCGGAGTC-3' and 5'-  
333 GGTCATGAGTCCTTCCACGAT-3' for *gapdh*.

334

### 335 ***Statistical Analysis***

336 Unpaired two-tailed Student's *t*-test was performed using Prism software (version 7,  
337 GraphPad).

338

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352

353 **Author Contributions**

354 A.R.H. and G.W.M. designed experiments, analysed data and wrote the manuscript.  
355 A.R.H performed the experiments, except EBOV infection experiments, which were  
356 performed by S.T. and G.A.M, and preparation/imaging of infected samples, which was  
357 performed by M.D. and D.G.

358

359 **Conflict of Interest**

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

361

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- 493
- 494

495 **Figure Legends**

496 **Figure 1. EBOV infection inhibits STAT3 responses to OSM.** (A) COS7 (upper panel) or  
497 E6 Vero (lower panel) cells infected with EBOV (MOI 10, which results in infection of c. 100  
498 % of cells, see Figure S1) or mock-infected were treated 72 h post-infection with or without  
499 OSM (10 ng/ml, 15 min) before fixation, immunofluorescent staining for STAT3 (green), and  
500 analysis by CLSM. DAPI (blue) was used to localise nuclei. Representative images are shown.  
501 Arrowheads indicate accumulation of STAT3 in cytoplasmic regions corresponding to viral  
502 inclusions (see Figure S1); indicated regions in merged images are expanded in panels below  
503 (Zoom). (B) Images such as those shown in A were analysed to calculate the nuclear to  
504 cytoplasmic fluorescence ratio (Fn/c) for STAT3 (mean  $\pm$  SEM,  $n \geq 70$  cells for each  
505 condition). Statistical analysis (Student's *t*-test) was performed using GraphPad Prism  
506 software; \*\*\*\*,  $p < 0.0001$ ; No add., no addition.

507

508 **Figure 2. EBOV VP24 protein expression inhibits STAT3 responses to OSM.** COS7 cells  
509 co-transfected to express the indicated proteins were treated 24 h post-transfection with or  
510 without OSM (10 ng/ml, 30 min) before live-cell CLSM analysis (A) to determine the Fn/c for  
511 STAT3-mCherry (B; mean  $\pm$  SEM;  $n \geq 35$  cells for each condition; results are from a single  
512 assay representative of two independent assays; GFP-N, GFP-RABV-N-protein). Statistical  
513 analysis used Student's *t*-test; \*\*\*\*,  $p < 0.0001$ .

514

515 **Figure 3. EBOV VP24 antagonises STAT3 independently of STAT1.** (A,B) COS7 (upper  
516 panel) or U3A (lower panel) cells transfected to express the indicated proteins were treated 24  
517 h post-transfection with or without OSM (10 ng/ml, 15 min) before fixation,  
518 immunofluorescent staining for STAT3 (red) and CLSM (A) to determine the Fn/c for STAT3  
519 (B; mean  $\pm$  SEM,  $n \geq 35$  cells for each condition; results are from a single assay representative

520 of two independent assays). Filled and unfilled arrowheads indicate cells with or without,  
521 respectively, detectable expression of the transfected protein. MUV V, Mumps virus V protein.  
522 (C) Lysates of COS7 and U3A cells were analysed by immunoblotting (IB) for STAT1 and  
523 STAT3. (D) *upper panel*: HEK293T or U3A cells co-transfected with m67-LUC and pRL-TK  
524 plasmids, and plasmids to express the indicated proteins, were treated 16 h post-transfection  
525 with or without OSM (10 ng/ml, 8 h) before determination of relative luciferase activity (mean  
526  $\pm$  SEM; n = 3 independent assays); *lower panel*: cell lysates used in a representative assay were  
527 analysed by IB using antibodies against the indicated proteins. Statistical analysis used  
528 Student's *t*-test; \*\*, p<0.01; \*\*\*, p < 0.001; \*\*\*\*, p < 0.0001.

529

530 **Figure 4. EBOV VP24 inhibits K $\alpha$ 1-STAT3 interaction, dependent on STAT1.** HEK293T  
531 or U3A cells co-transfected to express the indicated proteins were treated 24 h post-transfection  
532 with or without OSM (10 ng/ml, 15 min) before lysis and immunoprecipitation for FLAG.  
533 Lysates (input) and immunoprecipitates (IP) were analysed by IB using antibodies against the  
534 indicated proteins. Results are representative of  $\geq$  2 independent assays. Expanded images of  
535 all membranes are shown in Figure S4.

536

537 **Figure 5. EBOV VP24 does not prevent interaction of STAT3 with target DNA.** *Upper*  
538 *panel*: U3A cells co-transfected to express the indicated proteins were treated 24 h post-  
539 transfection with or without OSM (10 ng/ml, 15 min) before lysis and incubation of equal  
540 amounts of cell lysate protein or no lysate control (no protein) with digoxigenin-labelled m67  
541 probe. EMSA reactions were resolved on 4.5 % polyacrylamide gel in 0.5 x TBE, before  
542 transfer to a nylon membrane and IB for digoxigenin. Results are representative of 3  
543 independent assays. Filled and unfilled arrowheads indicate bands consistent with DNA  
544 complexes with STAT3-mCherry and endogenous STAT3, respectively. *Lower panel*: Cell

545 lysates were also analysed by SDS-PAGE and IB (input) using antibodies against the indicated  
546 proteins.

547

548 **Figure 6. EBOV VP24 interacts with STAT3.** (A) U3A cells co-transfected to express  
549 FLAG-STAT3 and GFP or GFP-VP24 as indicated were treated 24 h post-transfection with or  
550 without OSM (10 ng/ml, 30 min) before lysis, immunoprecipitation for GFP, and IB, as  
551 described in the legend to Figure 4. (B,C) U3A (B) or HEK293T (C) transfected to express the  
552 indicated proteins were treated with or without OSM (10 ng/ml, 15 min) before  
553 immunoprecipitation for GFP and IB for endogenous STAT3. Results are representative of 2  
554 independent assays and show data from a single blot with intervening and marker lanes  
555 removed. Expanded images of all membranes are shown in Figures S5-S6.

556

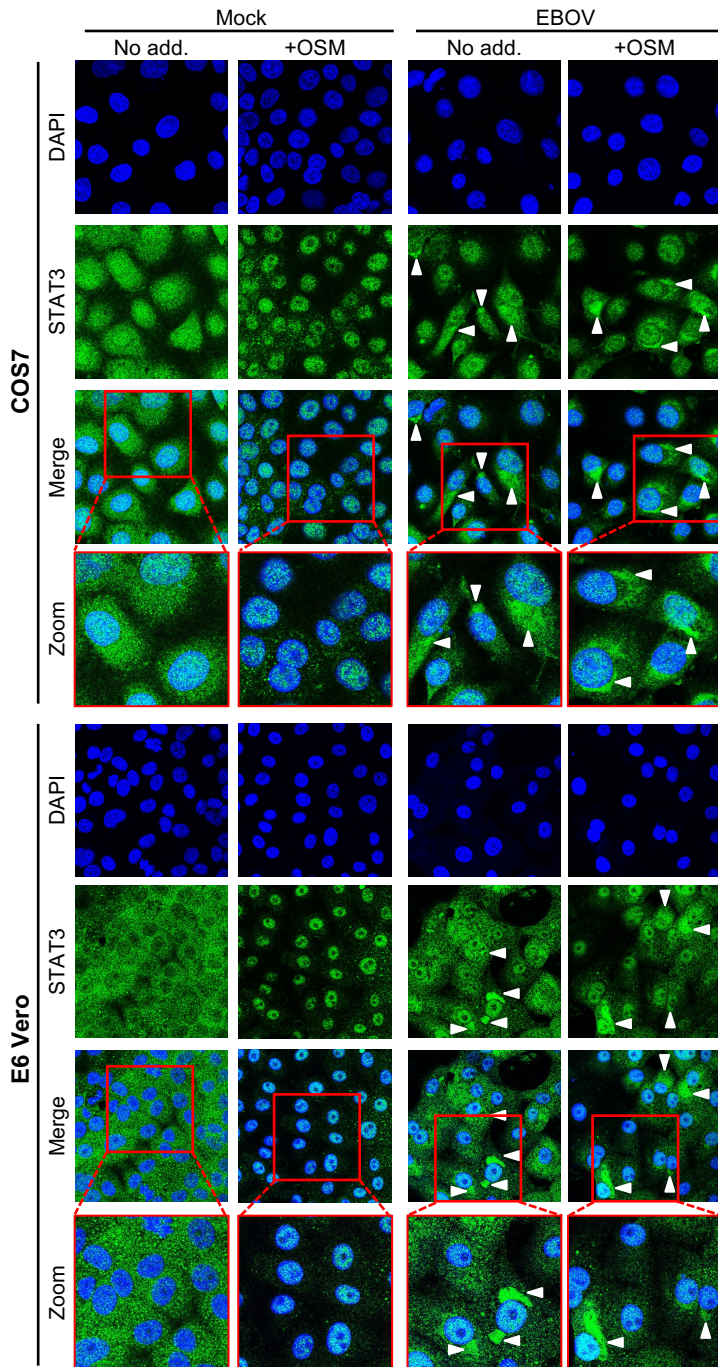
557 **Figure 7. Antagonism of STAT3 by EBOV VP24 in U3A cells is independent of VP24-**  
558 **karyopherin interaction.** (A) *upper panel:* HEK293T or U3A cells co-transfected with  
559 pISRE-LUC or m67-LUC plasmid, pRL-TK plasmid, and plasmids to express the indicated  
560 proteins, were treated 8 h (IFN- $\alpha$ ) or 16 h (OSM) post-transfection with or without IFN- $\alpha$   
561 (1,000 U/ml for 16 hours) or OSM (10 ng/ml for 8 h) before determination of relative luciferase  
562 activity (mean  $\pm$  SEM;  $n \geq 3$  independent assays); *lower panel:* cell lysates used in  
563 representative assays were analysed by IB for GFP and  $\beta$ -tubulin. Statistical analysis used  
564 Student's *t*-test; \*\*,  $p < 0.01$ ; \*\*\*,  $p < 0.001$ ; \*\*\*\*,  $p < 0.0001$ ; NS, not significant. (B) U3A  
565 cells transfected to express the indicated proteins were treated with OSM before  
566 immunoprecipitation for GFP and IB, as described in the legend to Figure 6. Results are  
567 representative of 2 independent assays and show data from a single blot with intervening and  
568 marker lanes removed. Expanded images of membranes are shown in Figure S7.

569



Figure 1

A



B

□ No add. ■ + OSM

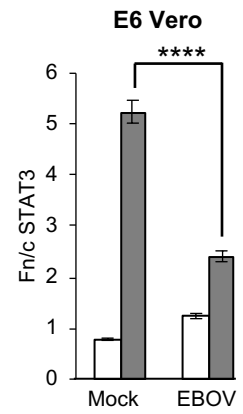
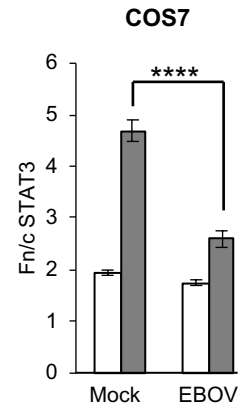
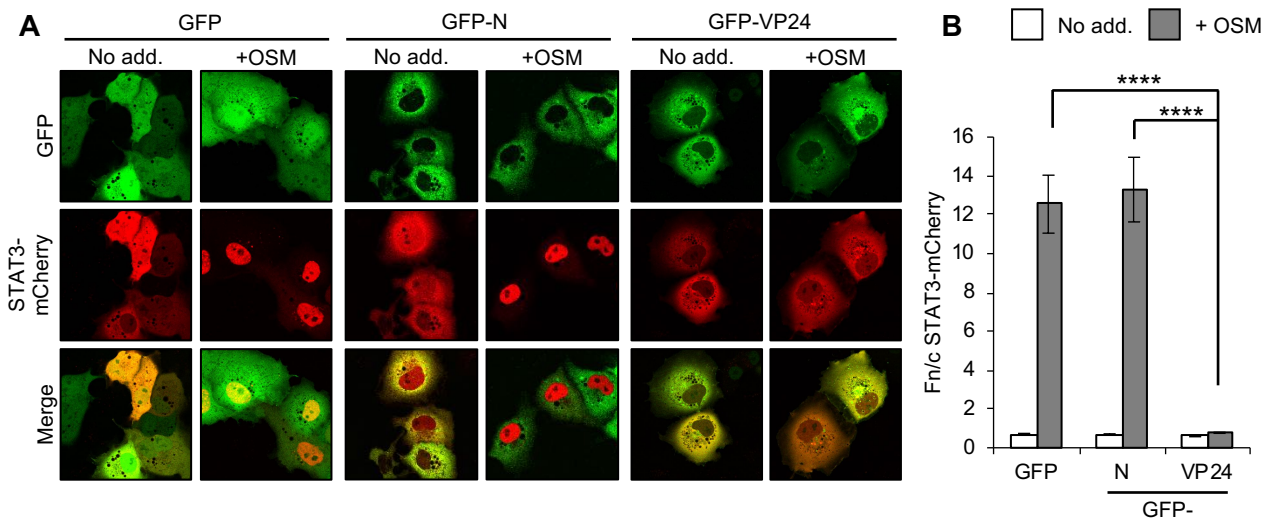
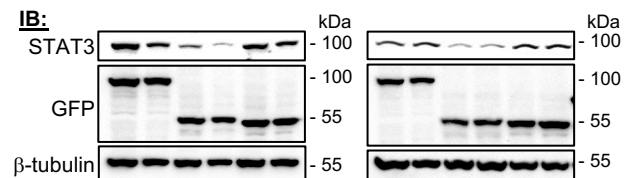
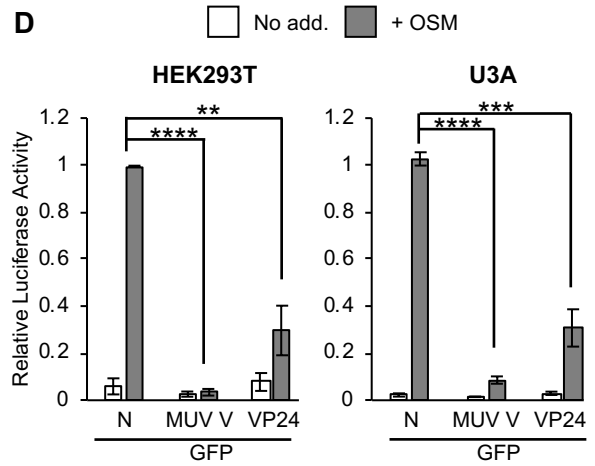
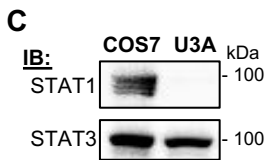
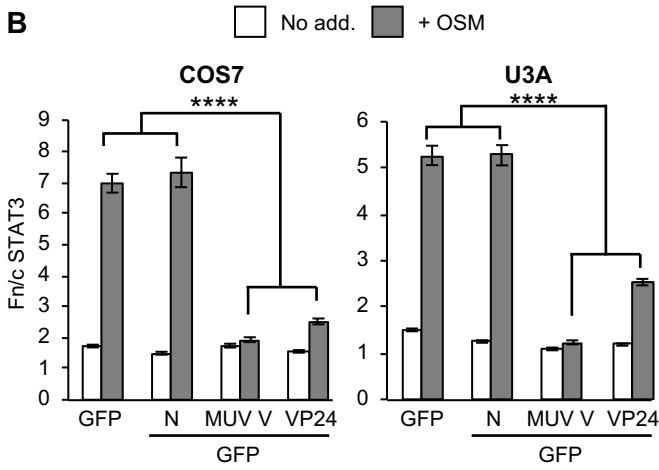
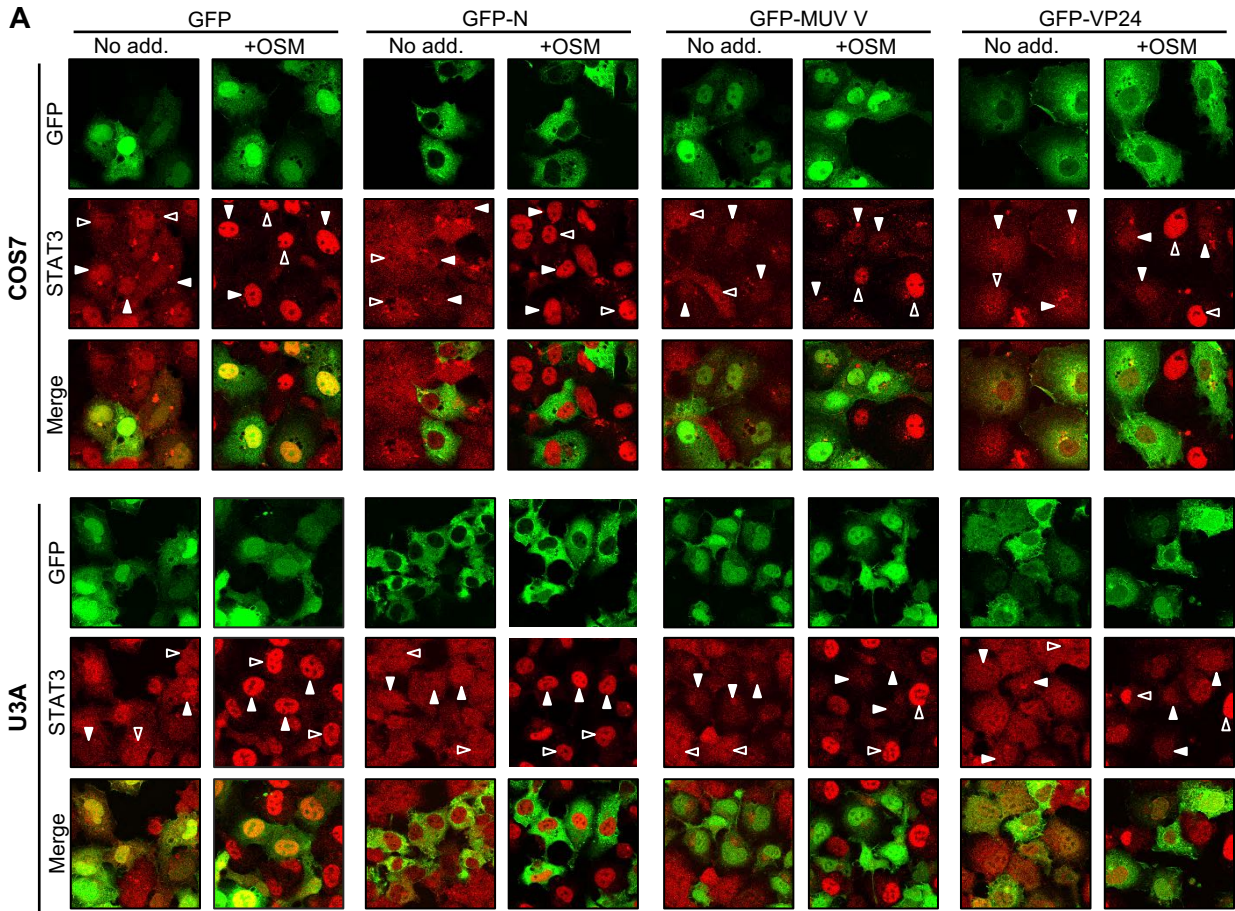


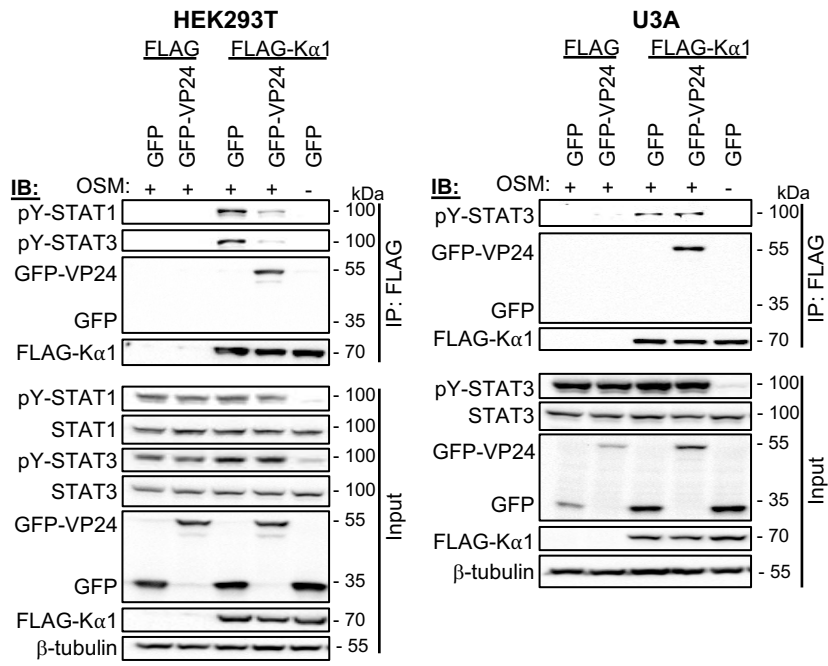
Figure 2



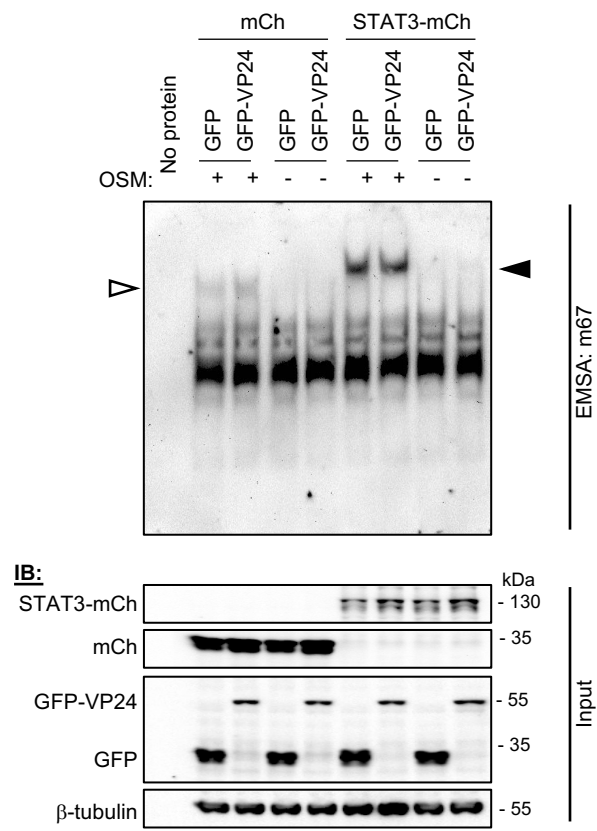
**Figure 3**



**Figure 4**



**Figure 5**



**Figure 6**

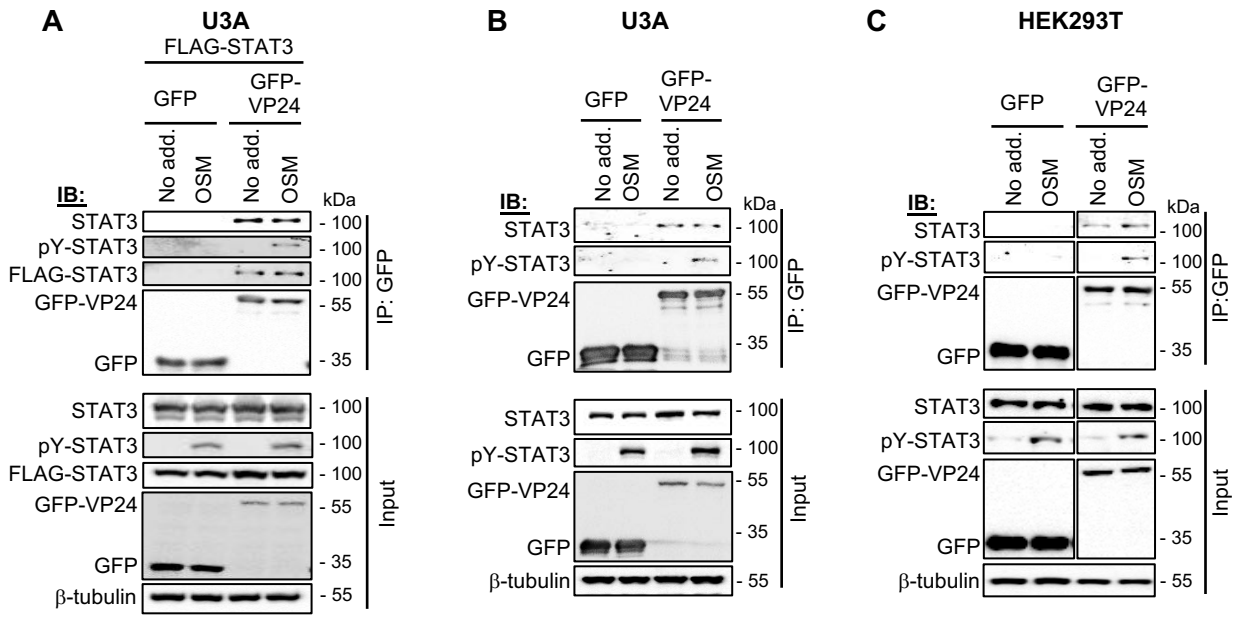


Figure 7

