

1 **Mitogen-activated protein kinases (MAPKs) regulate IL-6 over-**
2 **production during concomitant influenza virus and *Staphylococcus***
3 ***aureus* infection**

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5 Carolin Klemm¹, Christin Bruchhagen¹, Andre van Krüchten¹, Silke Niemann²,
6 Bettina Löffler³, Georg Peters^{2,4}, Stephan Ludwig^{1,4}, Christina Ehrhardt^{1,4*}

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8 ¹ Institute of Virology Muenster (IVM), Westfaelische Wilhelms-University
9 Muenster, Von Esmerch-Str. 56, D-48149 Muenster, Germany

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11 ² Institute of Medical Microbiology, University Hospital of Muenster,
12 Domagkstr. 10, D-48149 Muenster, Germany

13

14 ³ Institute of Medical Microbiology, University Hospital Jena, Erlanger Allee
15 101, D-07747 Jena, Germany

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17 ⁴ Cluster of Excellence Cells in Motion (CIM), University of Muenster,
18 Muenster, Germany

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20 * Corresponding author

21 PD Dr. rer. nat. Christina Ehrhardt

22 Phone: +49 (0)251-8353010

23 Fax: +49 (0)251-8357793

24 e-mail: ehrhardc@uni-muenster.de

25 **Supplementary**

26

27 **Methods**

28 **Additional cell lines and bacterial strain**

29 The human hepatic cell line HepG2 (a kind gift from Ute Albrecht, University
30 of Duesseldorf, Germany) was cultivated in DMEM/F-12 medium 1:1. The
31 human monocytic cell line THP-1 was cultivated in RPMI 1640 with 1%
32 glutamine. The murine lewis lung carcinoma (LLC) and mouse embryonic
33 fibroblast (MEF) cell lines were cultivated in DMEM. Each medium was
34 supplemented with 10% FBS. Primary human umbilical vein endothelial cells
35 (HUVEC) were cultivated in endothelial cell growth medium with supplement
36 mix (PromoCell, Heidelberg, Germany).

37 THP-1 cells (6-well: 2×10^6 , 12-well: 1×10^6) were stimulated with 10 ng ml^{-1}
38 phorbol-12-myristate-13-acetate (PMA, AppliChem, Darmstadt, Germany) for
39 differentiation into macrophages 16 h prior to infection. LLC (6-well: 0.3×10^6)
40 and MEF cells (6-well: 0.25×10^6) were seeded 16 h and HUVECs (6-well:
41 0.5×10^6) were seeded 48 h prior to infection. During infection culture medium
42 supplemented as indicated in the method section was used.

43 The mouse-adapted *S. aureus* strain LS1 was cultivated as described in the
44 method section.

45

46 **Plaque assay**

47 Standard plaque titration was performed as described earlier⁵⁰.

48

49 **Transfer of conditioned medium**

50 HepG2 cells (12-well: 0.3×10^6) were seeded in 1 ml culture medium 40 h prior
51 to stimulation. Calu-3 cells were infected as described in the method section.
52 Supernatants of three 6-wells were pooled and sterile filtrated with a 0.2 μm
53 filter to avoid transfer of living pathogens. HepG2 cells were washed and
54 stimulated with 800 μl conditioned medium for 20 h at 37°C, 5% CO₂.

55

56 **Actinomycin D treatment**

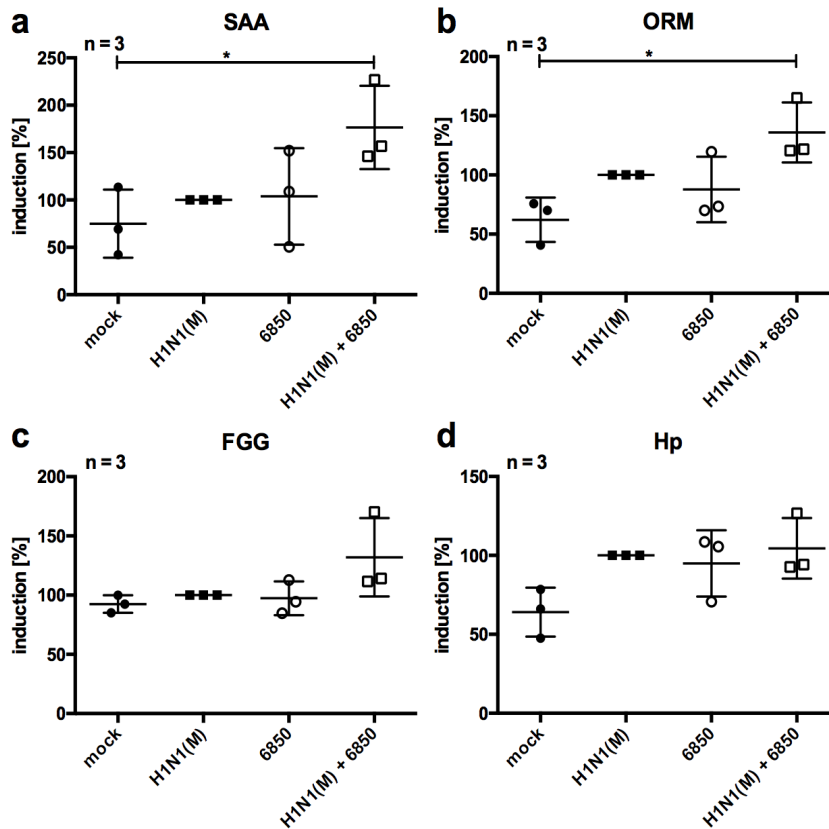
57 A549 cells were infected with IV H1N1(M) (MOI 5) and *S. aureus* 6850 (MOI
58 50) as described in the material and method section. At 6 h p.i. cells were
59 lysed, or washed and incubated in 1 ml of DMEM/BA supplemented with 1 μg
60 ml^{-1} actinomycin D (Santa Cruz Biotechnology, Dallas, USA) for further 0.5, 1
61 or 2 h at 37°C, 5% CO₂. Cells were lysed and total cellular RNA was isolated
62 as described in the method section. For investigation of *IL-6* mRNA stability,
63 the amount of *IL-6* mRNA was measured for each time point indicated by RT-
64 qPCR and *IL-6* levels were compared to untreated cells (0 h).

65

66 **Stimulation of cells with recombinant human IFN β**

67 A549 cells were incubated in 1 ml of DMEM/INV with *S. aureus* 6850 (MOI
68 50) for 3 h at 37°C, 5% CO₂. Extracellular bacteria were removed by
69 gentamicin treatment for 0.5 h at 37°C, 5% CO₂. Cells were incubated in 1 ml
70 of DMEM/BA supplemented with 100 U recombinant human IFN β (PBL Assay
71 Science, Piscataway, USA) or same volume of PBS for 4.5 h at 37°C, 5%
72 CO₂.

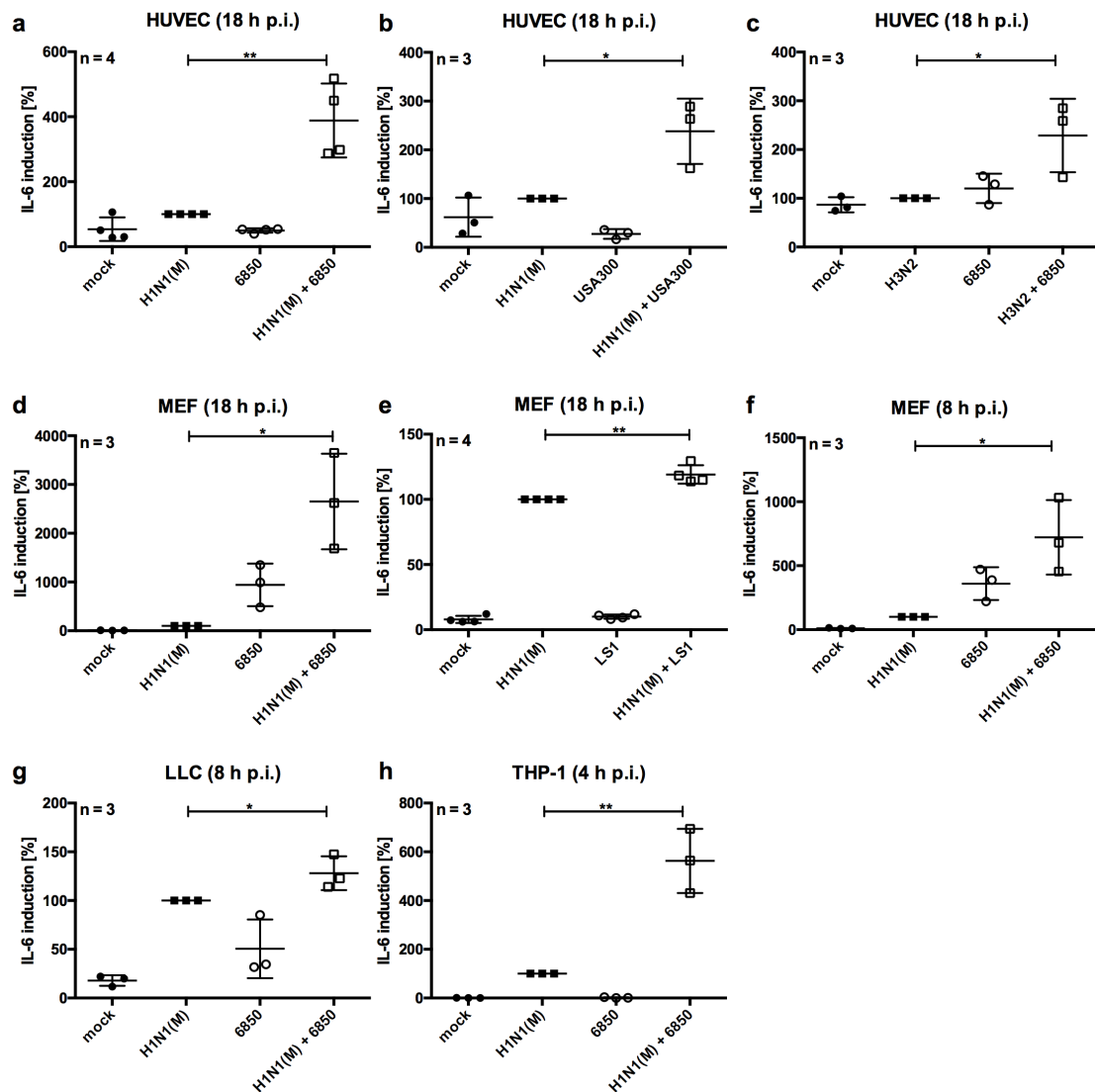
73 **Supplementary figures**



74

75 **Supplementary figure S1: Conditioned medium of IV and *S. aureus***
 76 **super-infected Calu-3 cells induces expression of APPs in HepG2 cells.**

77 Calu-3 cells were infected with IV H1N1(M) (MOI 5) for 0.5 h and super-
 78 infected with *S. aureus* 6850 (MOI 50). Extracellular bacteria were removed
 79 by gentamicin treatment 3 h post bacterial infection. At 8 h p.i. cell
 80 supernatants were sterile filtrated and added to HepG2 cells for another
 81 incubation of 20 h. Levels of SAA (a), ORM (b), FGG (c) and Hp (d) were
 82 measured in duplicates. Means \pm SD of three independent experiments are
 83 shown. Samples, which were treated with conditioned medium of IV-infected
 84 Calu-3 cells, were arbitrarily set 100%. After normalisation, one-way ANOVA
 85 followed by Dunnett's multiple comparison tests were used to compare mock
 86 and IV and/or *S. aureus* infected samples (* $p < 0.05$).

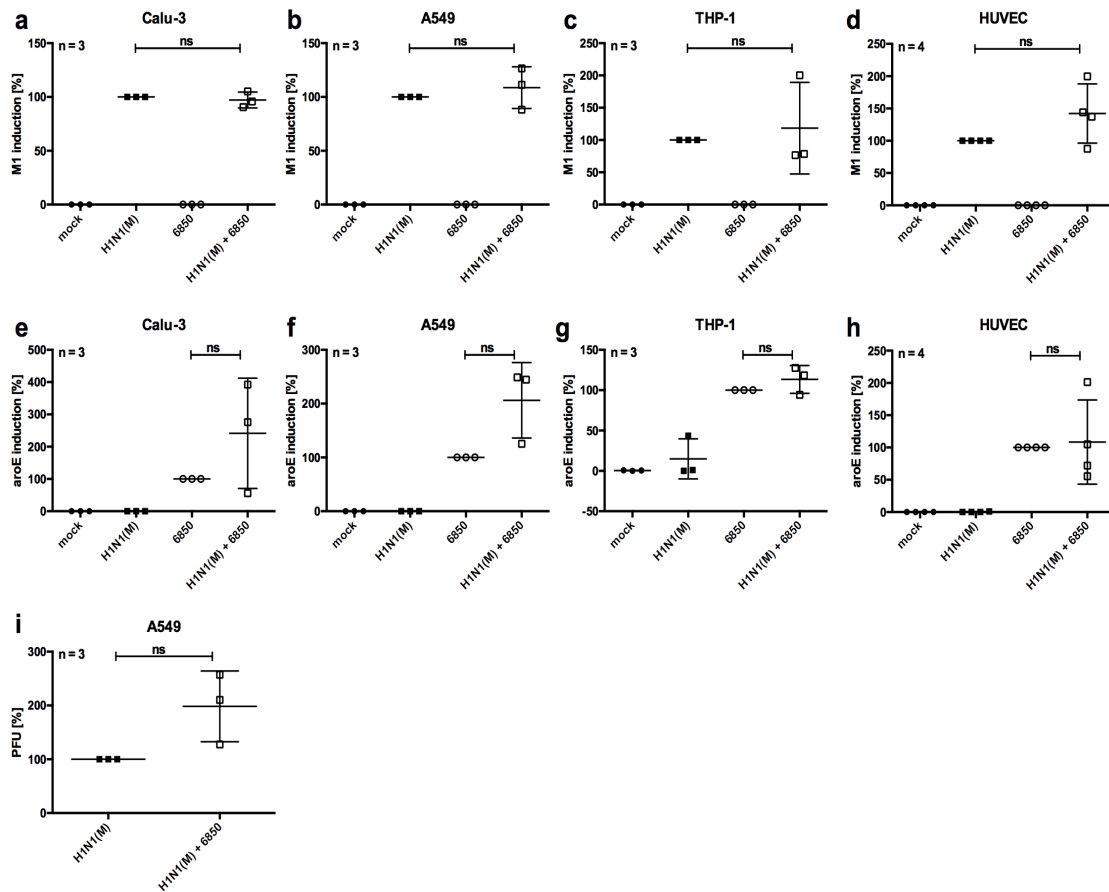


87

88 **Supplementary figure S2: Increased *IL-6* expression during super-**
 89 **infection is cell line independent.**

90 HUVEC (a – c), MEF (d – f), LLC (g) or THP-1 (h) cells were infected with
 91 H1N1(M) (MOI 0.5 (a, b, d, e), MOI 3 (f – h)) or H3N2 (MOI 0.5 (c)) for 0.5 h
 92 and super-infected with *S. aureus* 6850 (MOI 0.1 (a, c, d), MOI 10 (f, g), MOI
 93 1 (h)), MRSA USA300 (b) or LS1 (e) (MOI 0.01). Extracellular bacteria were
 94 removed by antibiotic treatment 3 h post bacterial infection. *IL-6* mRNA levels
 95 were measured at 18 h (a – e), 8 h (f, g) or 4 h p.i. (h). Means ± SD of at least
 96 three independent experiments are shown. Levels of IV-infected samples

97 were arbitrarily set as 100%. After normalisation, two-tailed unpaired t-tests
98 were performed for comparison between IV-infected and IV/*S. aureus* super-
99 infected samples (* $p < 0.05$, ** $p < 0.01$).



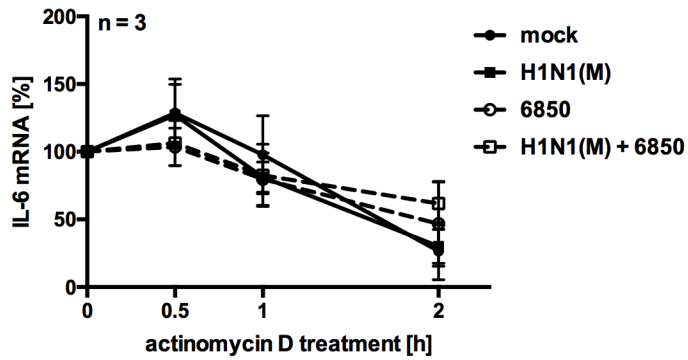
100

101 **Supplementary figure S3: Levels of viral *M1* and bacterial *aroE* are not**
 102 **significantly changed upon super-infection with IV and *S. aureus*.**

103 Calu-3 (a, e), A549 (b, f, i), THP-1 (c, g) or HUVEC (d, h) cells were infected
 104 with H1N1(M) (MOI 5 (a, b, e, f, i), MOI 3 (c, g), MOI 0.5 (d, h)) and super-
 105 infected with *S. aureus* 6850 (MOI 50 (a, b, e, f, i), MOI 1 (c, g), MOI 0.1 (d,
 106 h)). Extracellular bacteria were removed by antibiotic treatment 3 h post
 107 bacterial infection. *M1* (a – d) and *aroE* (e – h) levels were measured at 8 h
 108 (a, b, e, f), 4 h (c, g) or 18 h p.i. (d, h). Infectious virus titres were determined
 109 by standard plaque assay at 8 h p.i. (i). Means \pm SD of at least three
 110 independent experiments are shown. Levels of IV (a – d, i) or *S. aureus* (e –
 111 h) infected samples were arbitrarily set as 100%. After normalisation, two-

112 tailed unpaired t-tests were performed for comparison between single and
113 super-infected samples (ns not significant).

114

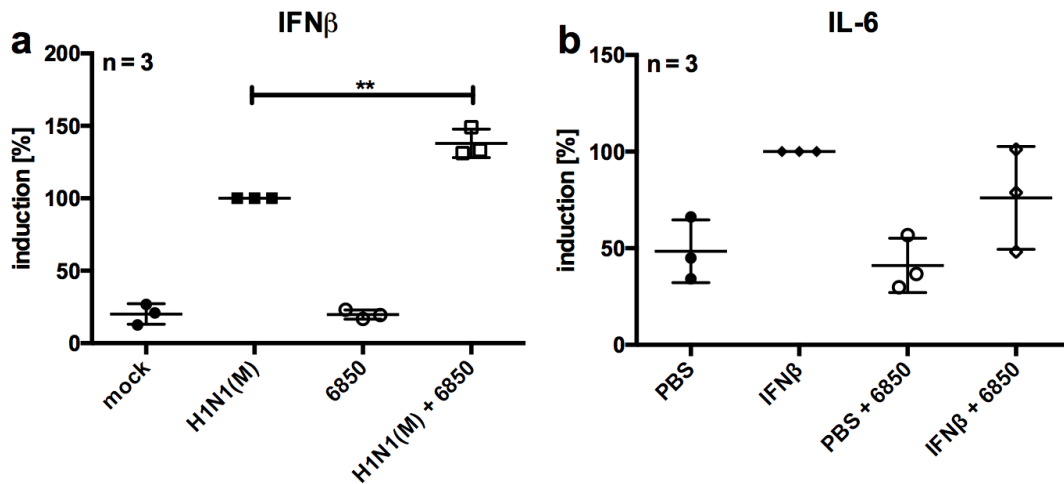


115

116 **Supplementary figure S4: *IL-6* mRNA stability is not altered by infection**
 117 **or super-infection with IV H1N1(M) and/or *S. aureus* 6850.**

118 A549 cells were infected with IV H1N1(M) (MOI 5) for 0.5 h and super-
 119 infected with *S. aureus* 6850 (MOI 50). Extracellular bacteria were removed
 120 by gentamicin treatment 3 h post bacterial infection. At 6 h p.i. cells were
 121 lysed or treated with 1 $\mu\text{g ml}^{-1}$ actinomycin D for 0.5, 1 or 2 h. *IL-6* mRNA
 122 levels were measured in duplicates by RT-qPCR. Means \pm SD of three
 123 independent experiments are shown. Untreated samples (0 h) were arbitrarily
 124 set as 100%.

125



126

127 **Supplementary figure S5: Increased IFN β synthesis after super-infection**
 128 **does not induce hyper-transcription of *IL-6*.**

129 A549 cells were infected with IV H1N1(M) (MOI 5) for 0.5 h and super-
 130 infected with *S. aureus* 6850 (MOI 50) (a) or cells were directly incubated with
 131 *S. aureus* 6850 (MOI 50) (b). Extracellular bacteria were removed by
 132 gentamicin treatment 3 h post bacterial infection. Subsequently cells were left
 133 untreated (a) or were stimulated with 100 U of recombinant human IFN β or
 134 PBS as control (b). IFN β (A) and *IL-6* (b) mRNA levels were measured in
 135 duplicates at 8 h p.i.. Means \pm SD of three independent experiments are
 136 shown. IV-infected (a) or IFN β -stimulated (b) samples were arbitrarily set as
 137 100%. After normalisation, two-tailed unpaired t-test was performed for
 138 comparison of IV H1N1(M)-infected and IV H1N1(M)/*S. aureus* 6850 super-
 139 infected samples (** p < 0.01).

140

141 **Supplemental table S6: Primer sequences for RT-qPCR**

142 The tables list the sequences of used RT-qPCR primers.

143 human

Gene	Forward (5' – 3')	Reverse (5' – 3')
CCL3	AGTTCTCTGCATCACTTGCTG	CGGCTTCGCTTGGTTAGGAA
CCL5	CGGCACGCCTCGCTGTCATC	GCAAGCAGAAACAGGCAAAT
CXCL8	ACTGAGAGTGATTGAGAGAGTGGAC	AACCCTCTGCACCCAGTTTTTC
FGG	GACGCTGCTACTTTGAAGTCC	TGGATTTGCACCGTGTCTTTG
GAPDH	GCCAATTCCATGGCACCGT	GCCCCACTTGATTTTGGAGG
Hp	CAGCACAGTCCCCGAAAAGAA	CAGTCGCATACCAGGTGTCC
IL-1 β	CAGCTACGAATCTCCGACCAC	GGCAGGGAACCAGCATCTTC
IL-6	AACCTGAACCTTCCAAAGATGG	TCTGGCTTGTTCCCTCACTAGT
IFN β	TCTGGCACAACAGGTAGTAGGC	GAGAAGCACAACAGGAGAGCAA
SAA	CAAATACTTCCATGCTCGGGG	CGCAGCCTCTAACTTCTCCAC
ORM	GCTGTTCCCTTAGGGACACCAA	TGACATCTGACCTGGGAATGC
TNF α	ATGAGCACTGAAAGCATGATC	GAGGGCTGATTAGAGAGAGGT

144

145 murine

Gene	Forward (5' – 3')	Reverse (5' – 3')
GAPDH	TGACCACAGTCCATGCCATC	GACGGACACATTGGGGGTAG
Hp	GCTATGTGGAGCACTTGGTTC	CACCCATTGCTTCTCGTCGTT
IL-1 β	GCAACTGTTCCCTGAACTCAACT	ATCTTTTGGGGTCCGTCAACT
IL-6	TAGTCCTTCCTACCCCAATTT	TTGGTCCTTAGCCACTCCTTC
ORM	CGAGTACAGGCAGGCAATTCA	ACCTATTGTTTGAGACTCCCGA
SAA	TGGCTGGAAAGATGGAGACAA	AAAGCTCTCTCTTGCATCACTG
TNF α	CCCTCACACTCAGATCATCTTCT	GCTACGACGTGGGCTACAG

146

147

148 pathogenic

Gene	Forward (5' – 3')	Reverse (5' – 3')
aroE	CTATCCACTTGCCATCTTTAT	ATGGCTTTAATATCACAATTCC
M1	TGCAAAAACATCTTCAAGTCTCTG	AGATGAGTCTTCTAACCGAGGTCCG

149

150

151 **Supplemental table S7: Raw Ct values of *IL-6* in different cell lines upon**
 152 **infection**

153 Analyses of *IL-6* mRNA were determined with Brilliant SYBR Green
 154 Mastermix (Agilent, Waldbronn, Germany) by RT-qPCR on a Stratagene
 155 Cycler (Agilent Technologies, Santa Clara, USA). Means and SD of at least
 156 three independent experiments with at least two biological replicates are
 157 shown. Ct values <35 were considered as specific.

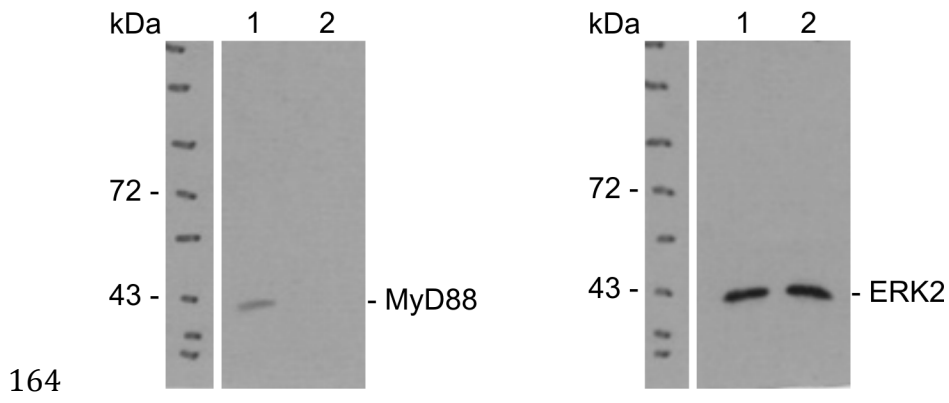
cell line	n	sample							
		mock		H1N1(M)		6850		H1N1(M) + 6850	
		mean	SD	mean	SD	mean	SD	mean	SD
Calu-3 (8 h p.i.)	16	22.34	0.73	17.44	0.69	19.98	0.93	15.86	1.20
A549 (8 h p.i.)	24	30.38	0.89	23.71	0.53	28.62	1.30	22.00	0.49
THP-1 (4 h p.i.)	12	32.93	1.52	25.08	0.81	30.87	1.75	22.52	0.87
HUVEC (18 h p.i.)	16	22.34	1.40	21.68	1.86	22.26	1.55	20.04	0.91

158

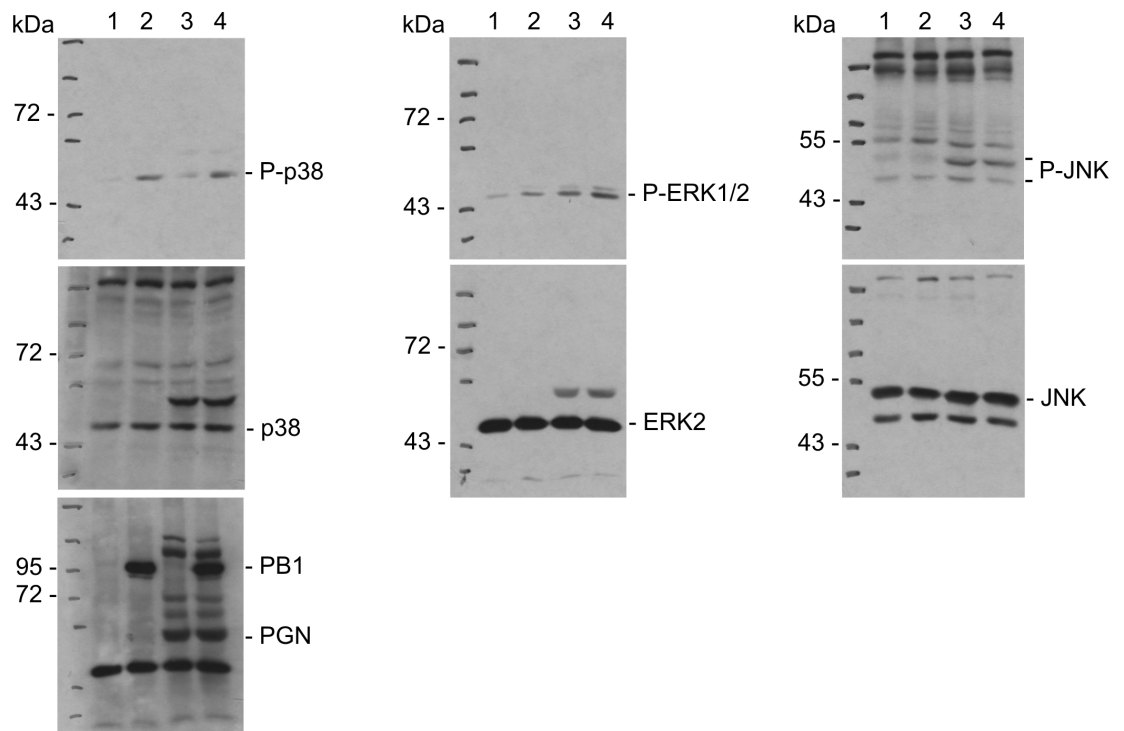
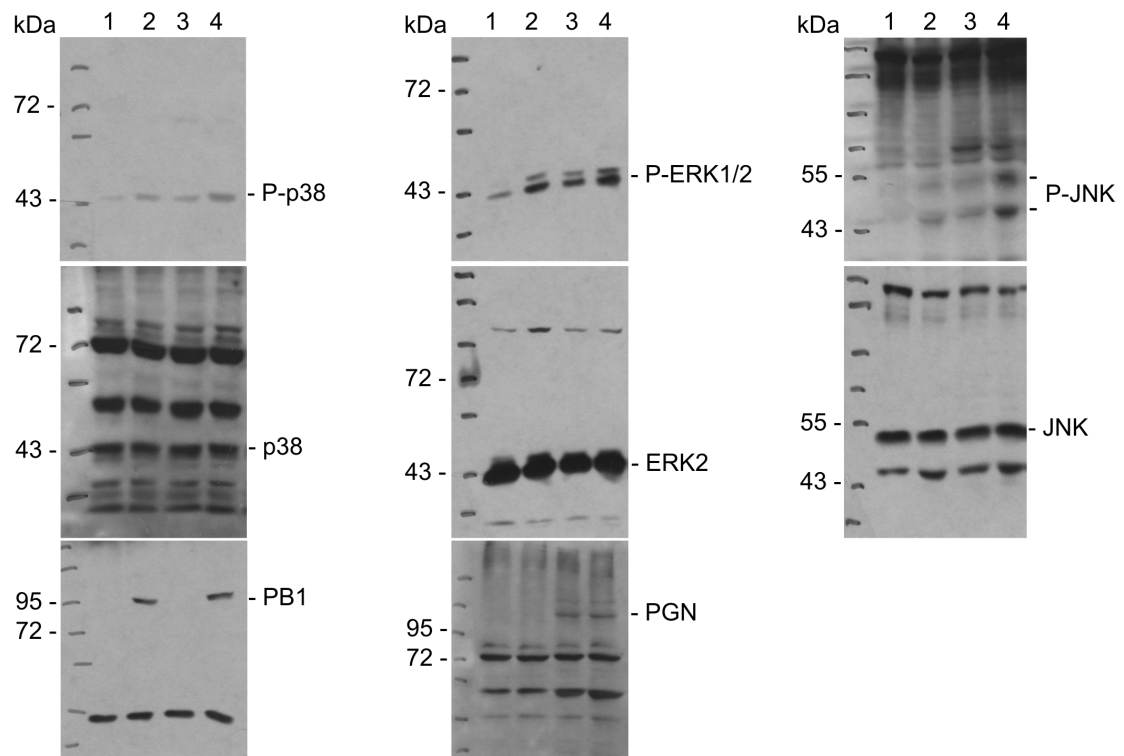
159 A 2-fold dilution series of cDNA from Calu-3 cells was used for PCR efficiency
 160 (E) calculation⁶¹. Both primer pairs for *IL-6* and *GAPDH* show high
 161 amplification efficiency, with an estimated E of 98.5% (\pm 1.8%) and 106.2% (\pm
 162 6.1%), respectively.

163

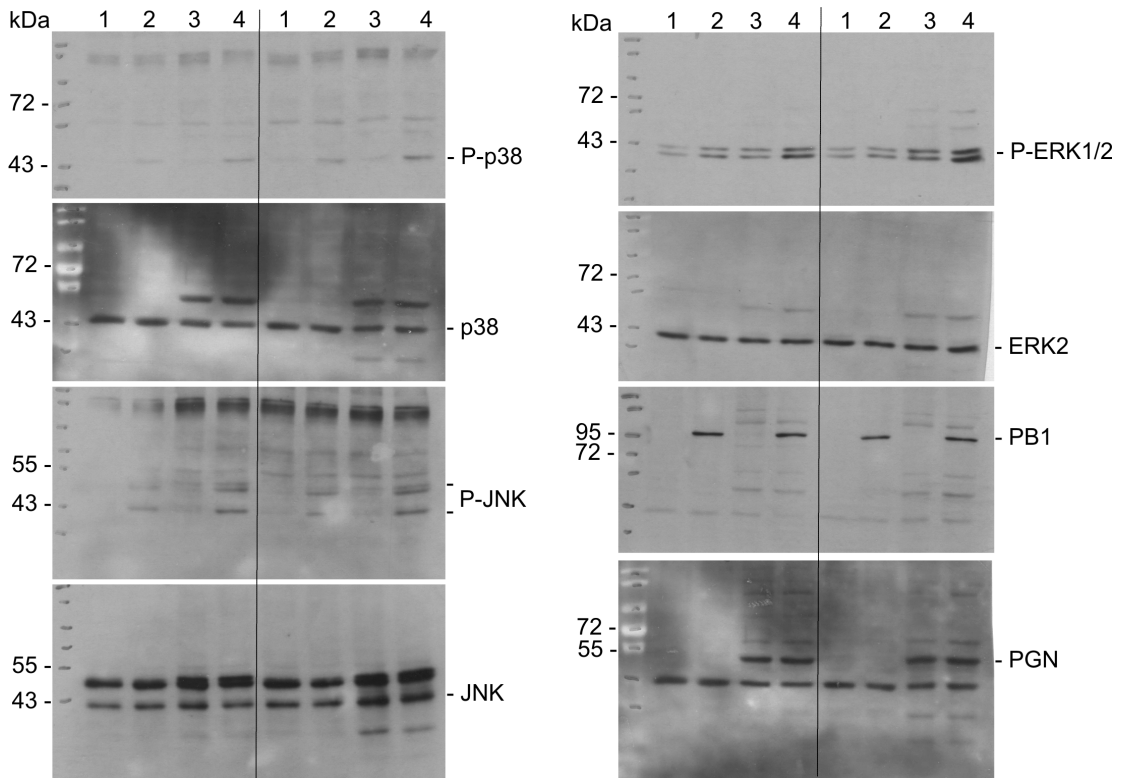
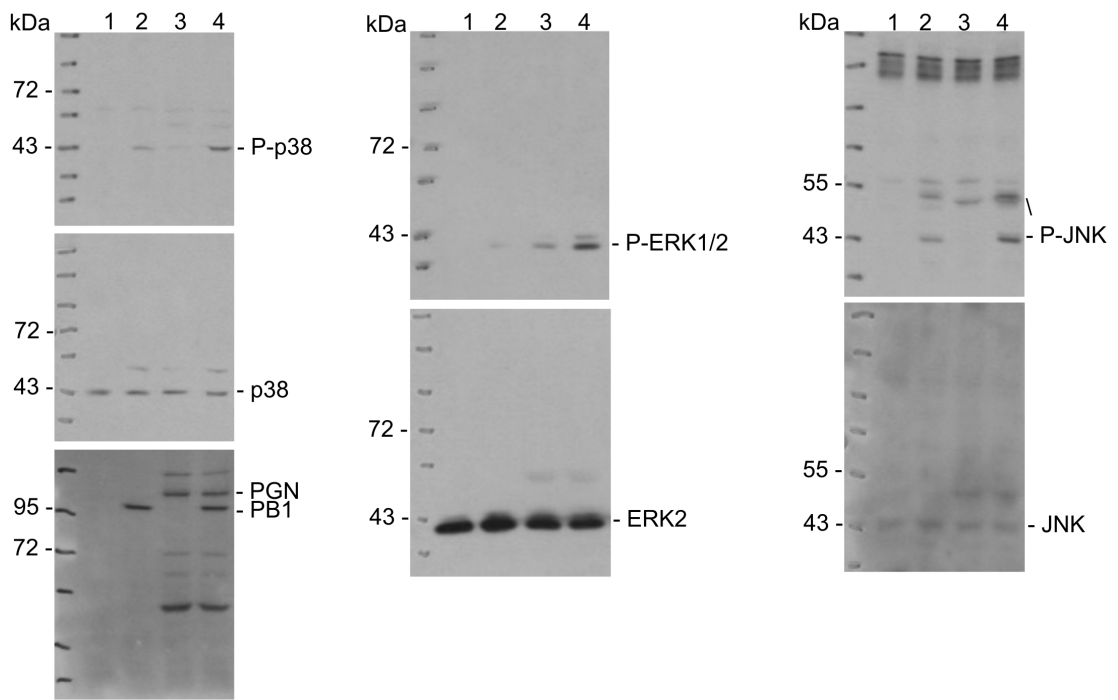
a



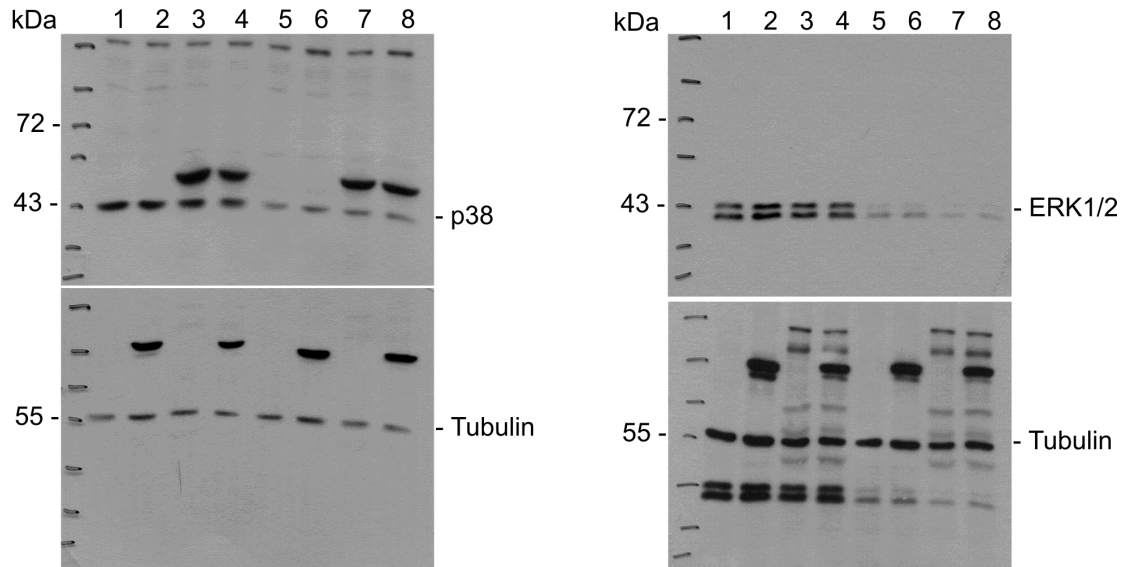
b



C



d



167

168 **Supplementary figure S8: Original blots of figures 4g, 5a, e, i and 6d, e.**

169 Lane 1: mock-infected, lane 2: IV infection, lane 3: bacteria infection, lane 4:
170 super-infection (a-d). In figure S8d lanes 5 - 8 represent the same infection
171 scheme as described above, but in a siRNA scenario.

172 Figure S8a represents the original blots of figure 4g. Within figure S8b the
173 upper panel shows the original blots of figure 5a, the lower panel represents
174 the original blots of figure 5e. The upper panel of figure S8c corresponds to
175 figure 5i (experiments performed with *S. aureus* 6850). On the left-hand side
176 of the lower panel original blots of figure 5i (experiments performed with *S.*
177 *aureus* SH1000) are shown. Blots on the right-hand side stand for figure 5i
178 (experiments performed with *S. aureus* USA300).

179