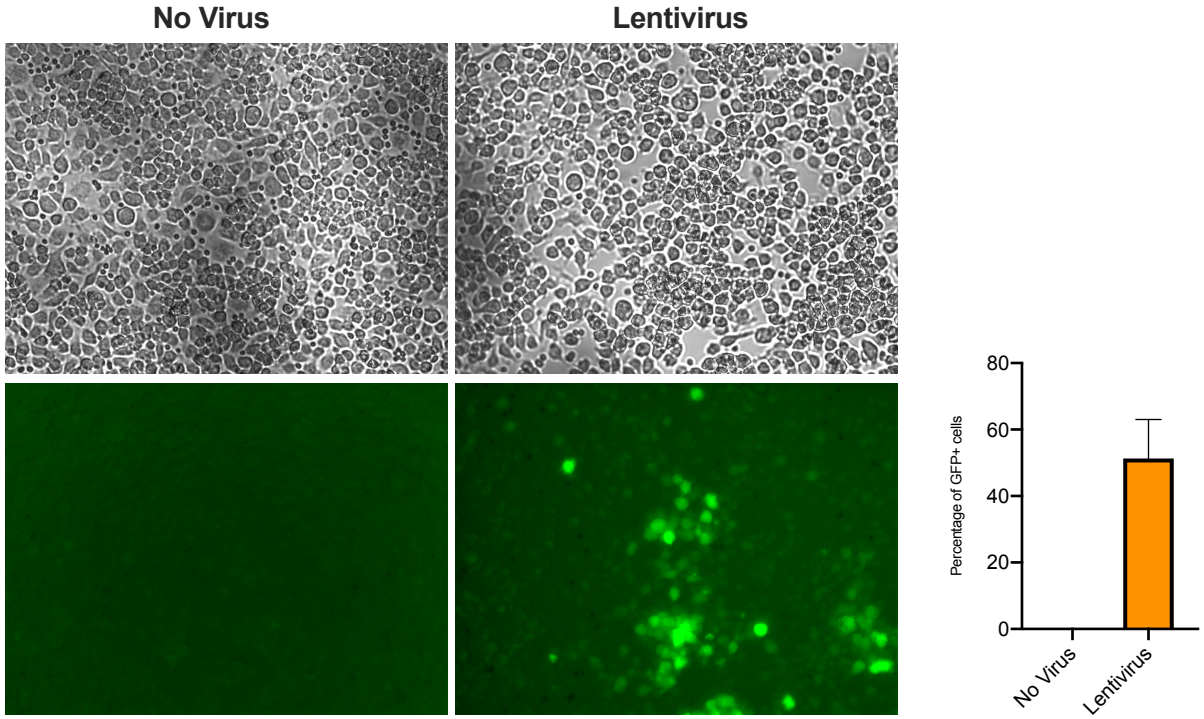


**Title: Modulation of the NLRP3 inflammasome by Sars-CoV-2 Envelope Protein**

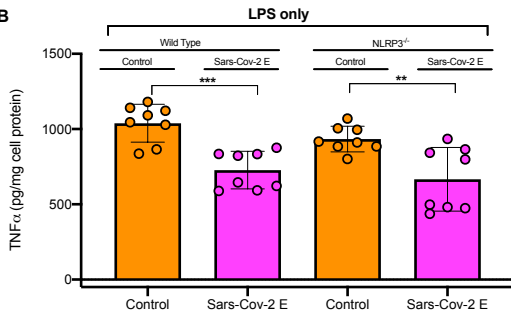
**Authors:** Mustafa Yalcinkaya<sup>1</sup>, Wenli Liu<sup>1</sup>, Mohammad N. Islam<sup>2</sup>, Andriana G. Kotini<sup>3-5</sup>, Galina A. Gusarova<sup>2</sup>, Trevor Fidler<sup>1</sup>, Eirini P. Papapetrou<sup>3-5</sup>, Jahar Bhattacharya<sup>2</sup>, Nan Wang<sup>1</sup>, Alan R. Tall<sup>1\*</sup>.

Supplementary Figure 1

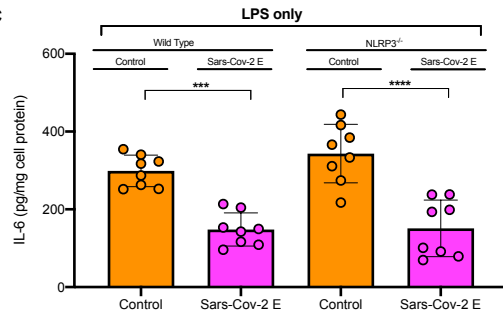
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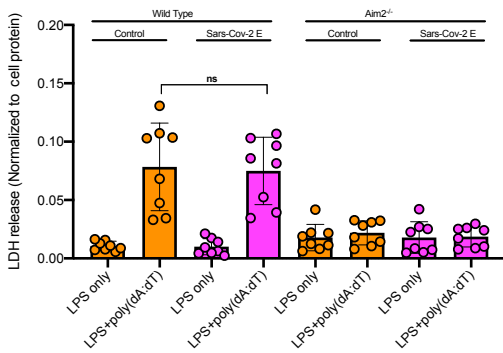
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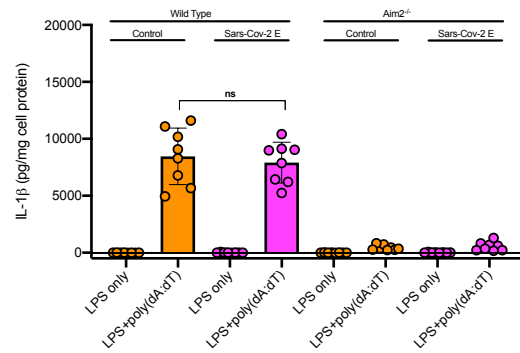
C



D



E



**Supplementary Figure 1: E-protein suppresses inflammasome priming but does not affect Aim2 inflammasome response to poly(dA:dT).**

(A) Bone marrow derived macrophages (BMDMs) were transduced with control and E-protein lentiviruses for 72h. Transduced cells (GFP positive) were analyzed by fluorescent microscope.

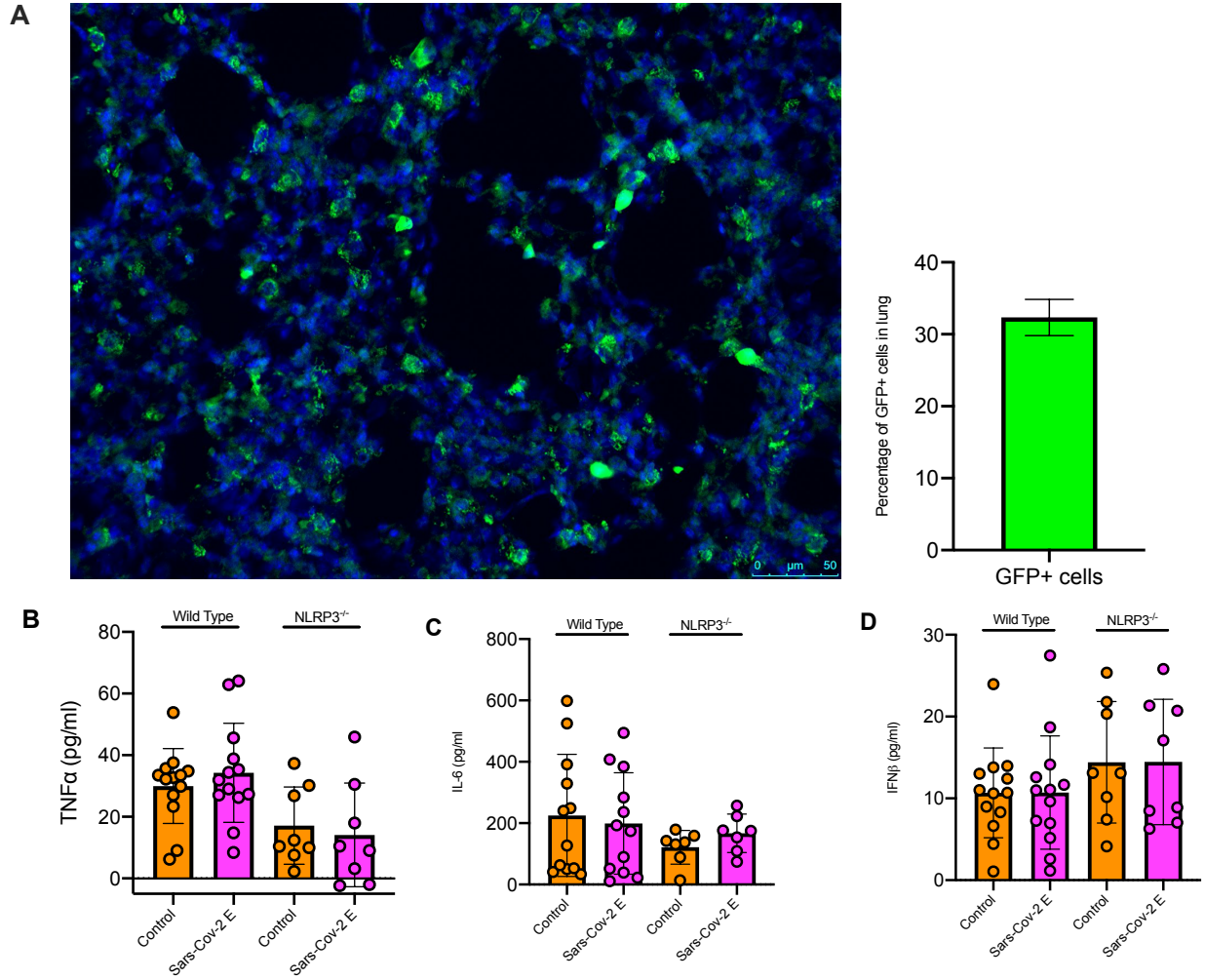
(B) Quantification of TNF- $\alpha$  secretion into cell media in Wild type (WT) and *Nlrp3*<sup>-/-</sup> BMDMs. BMDMs were transduced with control and E-protein lentiviruses for 72h and then primed with 20 ng/ml LPS for 4h. TNF- $\alpha$  secretion was assessed via TNF- $\alpha$  ELISA kit. Data are presented as mean  $\pm$  SD, which were analyzed by one-way ANOVA coupled with Tukey's test for multiple comparisons.

(C) Quantification of IL-6 secretion into cell media in WT and *Nlrp3*<sup>-/-</sup> BMDMs. BMDMs were transduced with control and E-protein lentiviruses for 72h and then primed with 20 ng/ml LPS for 4h.

(D) Quantification of LDH release into cell media in BMDMs, transduced with control and E-protein lentiviruses for 72h and then primed with 20 ng/ml LPS for 3h and treated with poly(dA:dT) for 6h.

(E) Quantification of IL-1 $\beta$  secretion into cell media in BMDMs, transduced with control and E-protein lentiviruses for 72h and then primed with 20 ng/ml LPS for 3h and treated with poly(dA:dT) for 6h. \*\*\*P $\leq$  0.001, \*\*P $\leq$  0.01, \*P $\leq$  0.05

Supplementary Figure 2



**Supplementary Figure 2: E-protein did not have an effect on other cytokines in bronchoalveolar lavage fluid (BALF).**

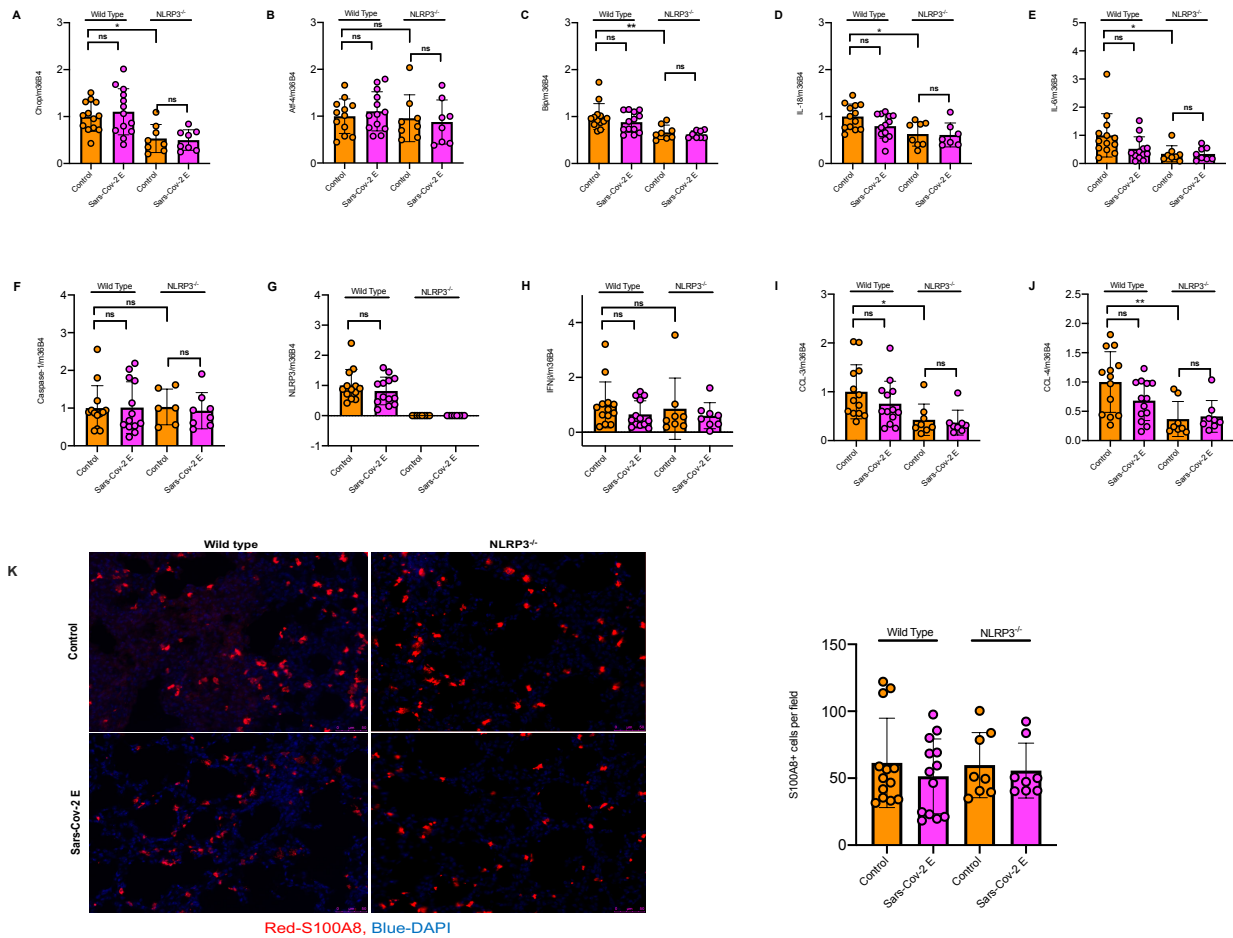
**(A)** Quantification of GFP<sup>+</sup> cells in lung sections. Transduced cells (GFP positive) were analyzed by fluorescent microscope.

**(B)** Quantification of TNF- $\alpha$  secretion into BALF. TNF- $\alpha$  secretion was assessed via TNF- $\alpha$  ELISA. Data are presented as mean  $\pm$  SD, which were analyzed by one-way ANOVA coupled with Tukey's test for multiple comparisons. \*\*\*\*P $\leq$  0.0001, \*\*\*P $\leq$  0.001, \*\*P $\leq$  0.01, \*P $\leq$  0.05

**(C)** Quantification of IL-6 secretion into BALF. IL-6 secretion was assessed via IL-6 ELISA. Data are presented as mean  $\pm$  SD, which were analyzed by one-way ANOVA coupled with Tukey's test for multiple comparisons. \*\*\*\*P $\leq$  0.0001, \*\*\*P $\leq$  0.001, \*\*P $\leq$  0.01, \*P $\leq$  0.05

**(D)** Quantification of IFN- $\beta$  secretion into BALF. IFN- $\beta$  secretion was assessed via IFN- $\beta$  ELISA. Data are presented as mean  $\pm$  SD, which were analyzed by one-way ANOVA coupled with Tukey's test for multiple comparisons. \*\*\*\*P $\leq$  0.0001, \*\*\*P $\leq$  0.001, \*\*P $\leq$  0.01, \*P $\leq$  0.05

### Supplementary Figure 3

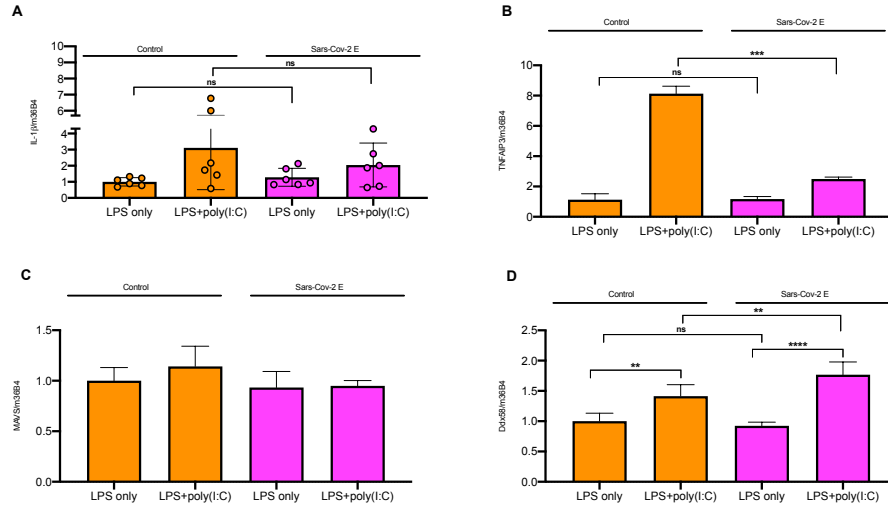


### Supplementary Figure 3: E-protein did not affect neutrophil recruitment.

- (A) Quantitative real-time PCR analysis of spliced *Chop* in whole lung of Wt and *Nlrp3*<sup>-/-</sup> mice.
- (B) Quantitative real-time PCR analysis of *Atf4* in whole lung of Wt and *Nlrp3*<sup>-/-</sup> mice.
- (C) Quantitative real-time PCR analysis of *Bip* in whole lung of Wt and *Nlrp3*<sup>-/-</sup> mice.
- (D) Quantitative real-time PCR analysis of *Il18* in whole lung of Wt and *Nlrp3*<sup>-/-</sup> mice.
- (E) Quantitative real-time PCR analysis of *Il6* in whole lung of Wt and *Nlrp3*<sup>-/-</sup> mice.
- (F) Quantitative real-time PCR analysis of *Caspase1* in whole lung of Wt and *Nlrp3*<sup>-/-</sup> mice.
- (G) Quantitative real-time PCR analysis of *Nlrp3* in whole lung of Wt and *Nlrp3*<sup>-/-</sup> mice.
- (H) Quantitative real-time PCR analysis of *Ifnb* in whole lung of Wt and *Nlrp3*<sup>-/-</sup> mice.
- (I) Quantitative real-time PCR analysis of *Ccl3* in whole lung of Wt and *Nlrp3*<sup>-/-</sup> mice.
- (J) Quantitative real-time PCR analysis of *Ccl4* in whole lung of Wt and *Nlrp3*<sup>-/-</sup> mice.

**(K)** Quantification of S100A8+ cells via immunostaining in whole lung of WT and *Nlrp3*<sup>-/-</sup> mice, injected intranasally with control and E-protein lentiviruses for 10 days and challenged intranasally with poly (I:C) for 24h. Data are presented as mean ± SD, which were analyzed by one-way ANOVA coupled with Tukey's test for multiple comparisons. \*\*\*\*P ≤ 0.0001, \*\*\*P ≤ 0.001, \*\*P ≤ 0.01, \*P ≤ 0.05

### Supplementary Figure 4



### Supplementary Figure 4: E-protein decreases *Tnfai3* (A20) and increases *Ddx58* (RIG-1) expression response to poly(I:C), respectively.

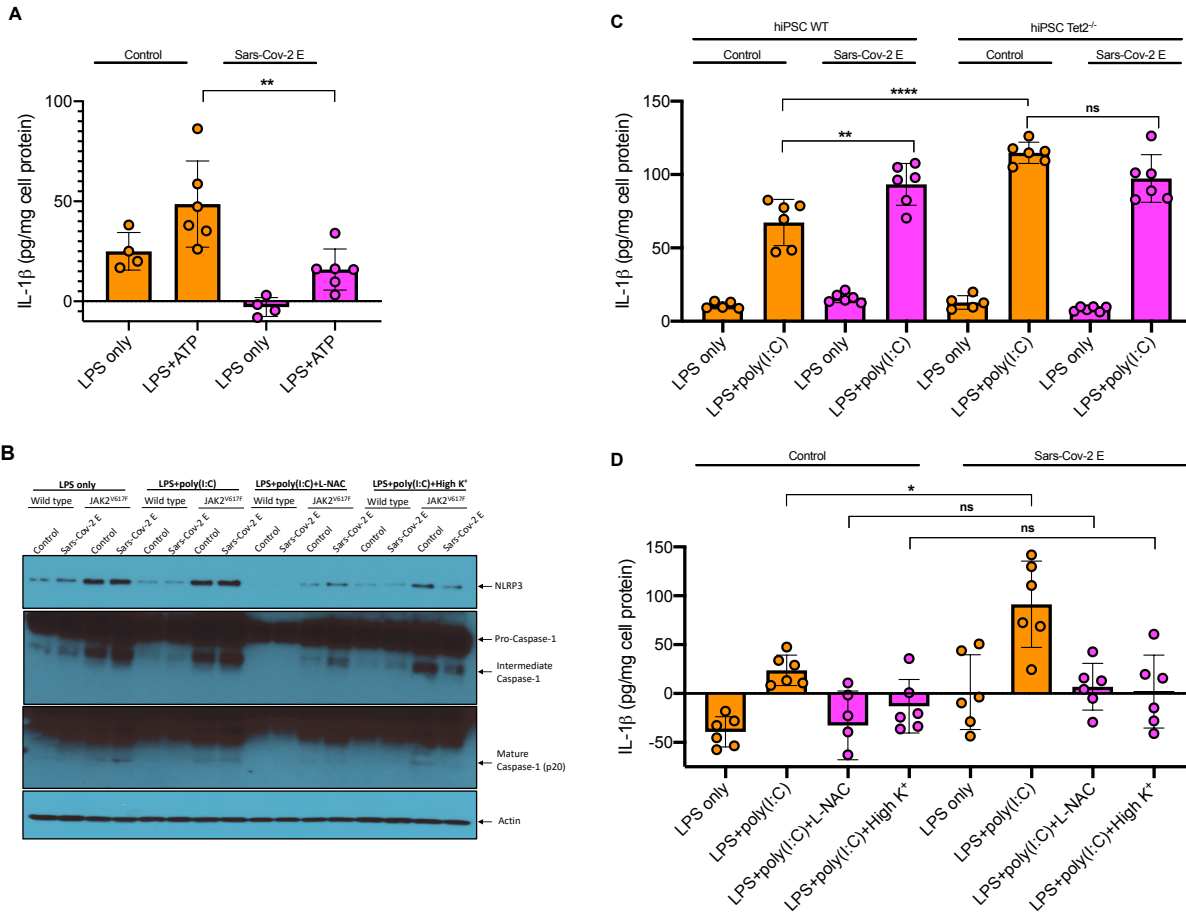
**(A)** Quantitative real-time PCR analysis of *Il1b* gene expression in BMDMs, primed with 20 ng/ml LPS and treated with poly(I:C) for 16h. Data are presented as mean ± SD, which were analyzed by unpaired t-test. \*\*\*P ≤ 0.001, \*\*P ≤ 0.01, \*P ≤ 0.05

**(B)** Quantitative real-time PCR analysis of *Tnfai3* (A20) gene expression in BMDMs, primed with 20 ng/ml LPS and treated with poly(I:C) for 16h. Data are presented as mean ± SD, which were analyzed by unpaired t-test. \*\*\*P ≤ 0.001, \*\*P ≤ 0.01, \*P ≤ 0.05

**(C)** Quantitative real-time PCR analysis of *Mavs* gene expression in BMDMs, primed with 20 ng/ml LPS and treated with poly(I:C) for 16h. Data are presented as mean ± SD, which were analyzed by unpaired t-test. \*\*\*P ≤ 0.001, \*\*P ≤ 0.01, \*P ≤ 0.05

**(D)** Quantitative real-time PCR analysis of *Ddx58* gene expression in BMDMs, primed with 20 ng/ml LPS and treated with poly(I:C) for 16h. Data are presented as mean ± SD, which were analyzed by unpaired t-test. \*\*\*P ≤ 0.001, \*\*P ≤ 0.01, \*P ≤ 0.05

## Supplementary Figure 5



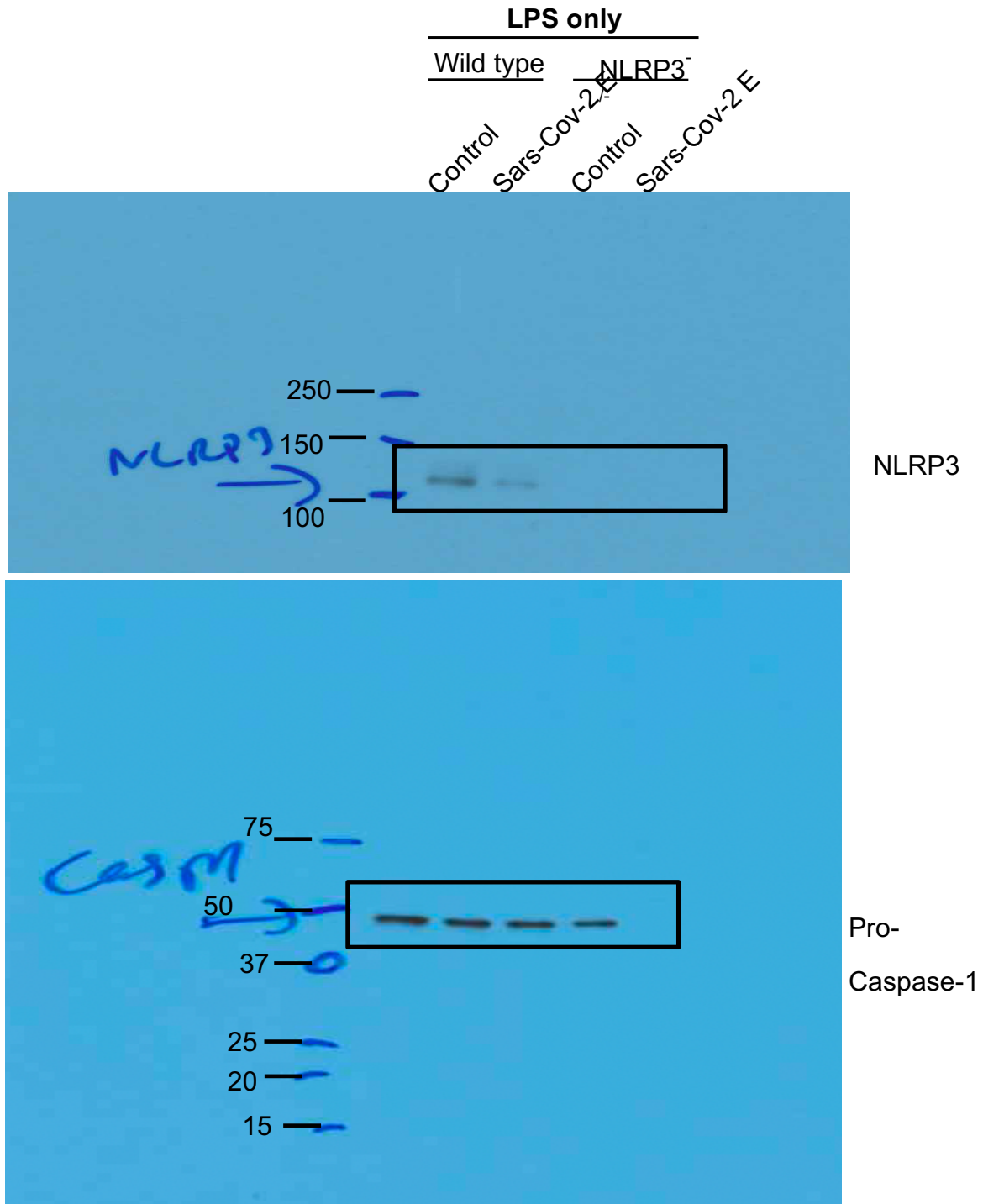
### Supplementary Figure 5: E-protein mediated inflammasome regulation is more pronounced in JAK<sup>V617F</sup> human but not TET2<sup>-/-</sup> hPSC-derived macrophages.

(A) Quantification of IL-1 $\beta$  secretion into cell media in WT hPSC-derived macrophages, transduced with control and E-protein lentiviruses for 72h and then primed with 20 ng/ml LPS for 3h and treated with ATP for 1h. IL-1 $\beta$  secretion was assessed via IL-1 $\beta$  ELISA. Data are presented as mean  $\pm$  SD, which were analyzed by one-way ANOVA coupled with Tukey's test for multiple comparisons. \*\*\*P $\leq$  0.001, \*\*P $\leq$  0.01, \*P $\leq$  0.05

(B) Western blot analysis of inflammasome proteins in cellular lysates of WT and JAK2<sup>V617F</sup> hPSC-derived macrophages, transduced with control and E-protein lentiviruses for 72h and then primed with 20 ng/ml LPS for 3h and treated with poly(I:C) for 16h.

(C) Quantification of IL-1 $\beta$  secretion into cell media in WT and TET2<sup>-/-</sup> hPSC-derived macrophages, transduced with control and E-protein lentiviruses for 72h and then primed with 20 ng/ml LPS for 3h and treated with poly(I:C) for 16h. IL-1 $\beta$  secretion was assessed via IL-1 $\beta$  ELISA.

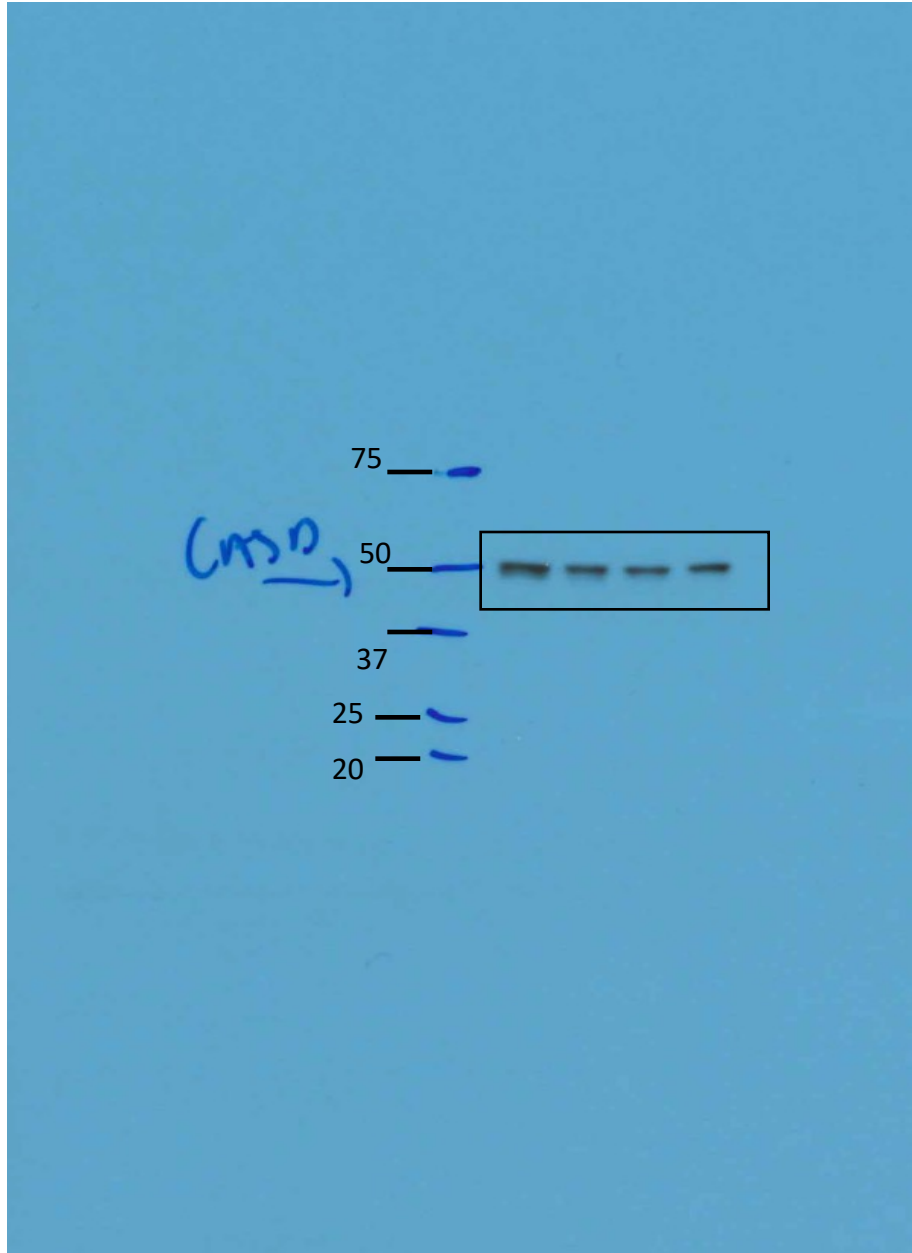
(D) Quantification of IL-1 $\beta$  secretion into cell media in hPSC-derived macrophages, transduced with control and E-protein lentiviruses for 72h and then primed with 20 ng/ml LPS for 3h and treated with poly(I:C) for 16h. For inhibitor experiments, LPS-primed hPSC-derived macrophages were preincubated with L-NAC (30 mM) 1h prior to stimulation with poly(I:C). High K<sup>+</sup> was supplied by adding 70 mM of K<sup>+</sup> to extracellular media during stimulation with poly(I:C). IL-1 $\beta$  secretion was assessed via IL-1 $\beta$  ELISA. Data are presented as mean  $\pm$  SD, which were analyzed by one-way ANOVA coupled with Tukey's test for multiple comparisons. \*\*\*P $\leq$  0.001, \*\*P $\leq$  0.01, \*P $\leq$  0.05





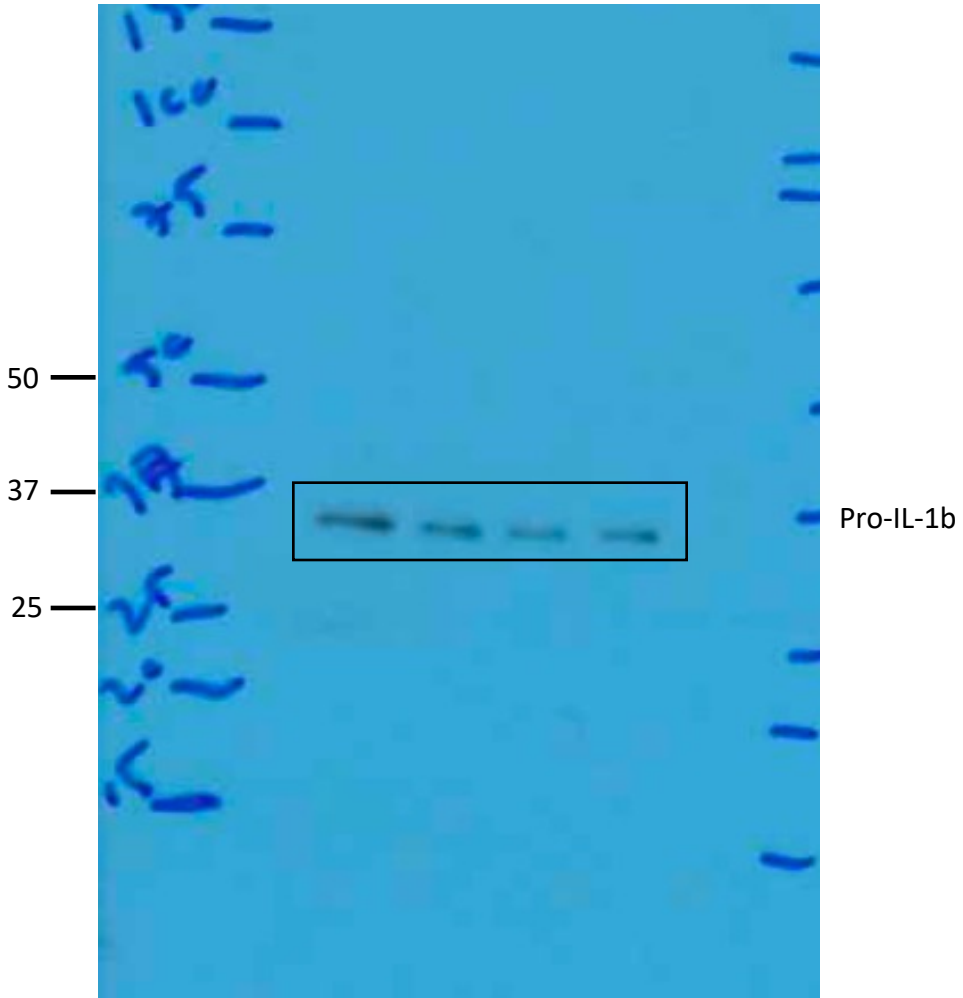
**LPS only**

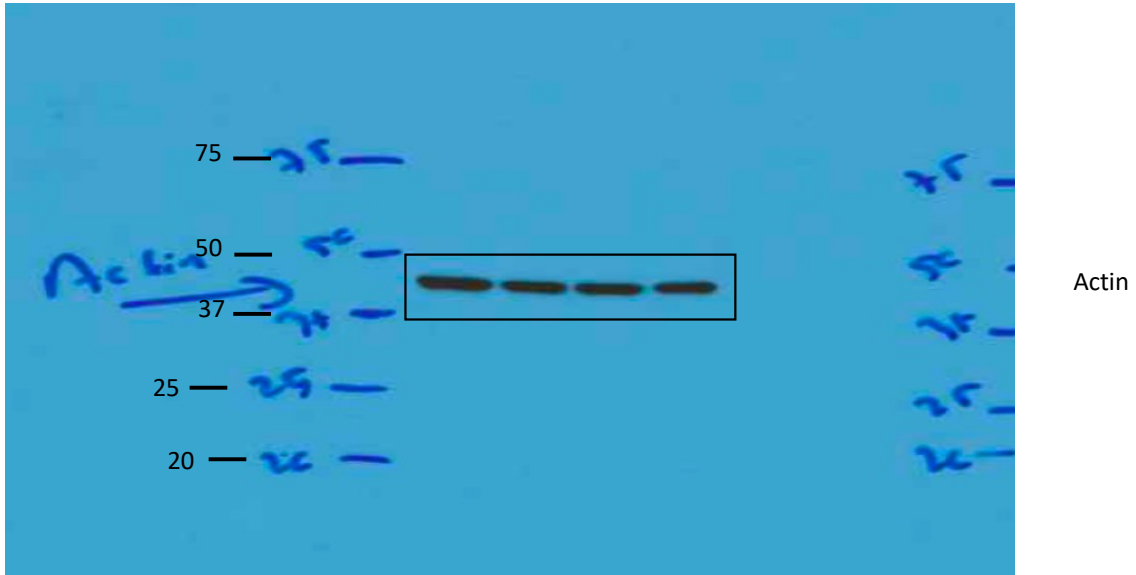
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Control	Sars-Cov-2 E	Control	Sars-Cov-2 E



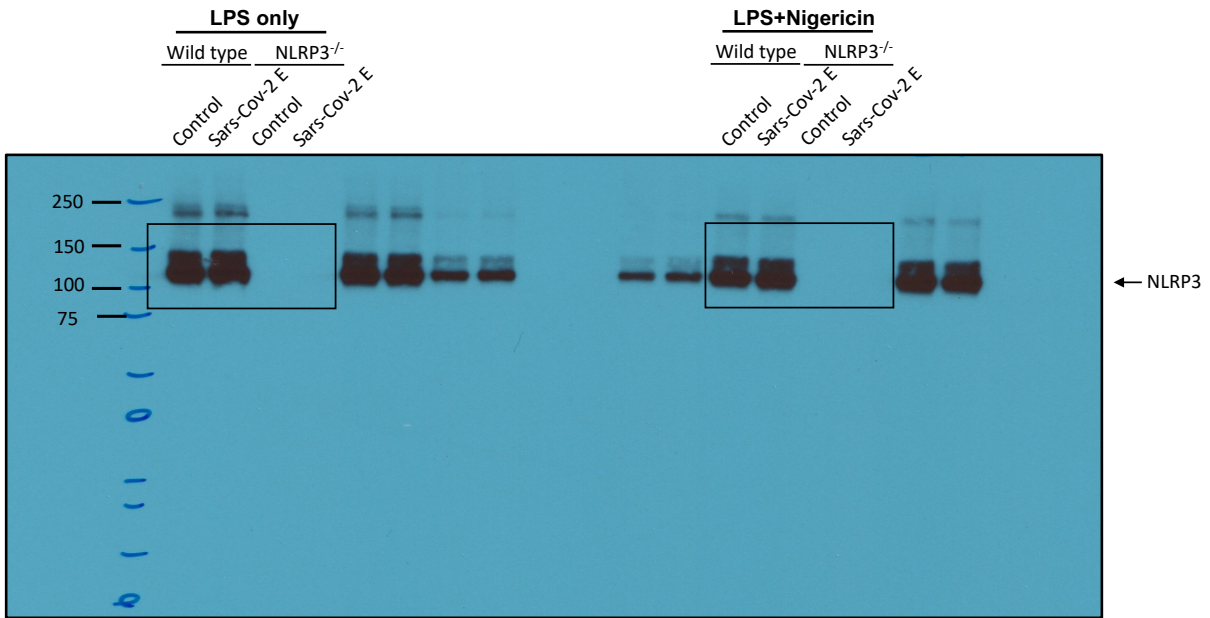
**LPS only**

Wild type		NLRP3 <sup>-/-</sup>	
Control	Sars-Cov-2 E	Control	Sars-Cov-2 E



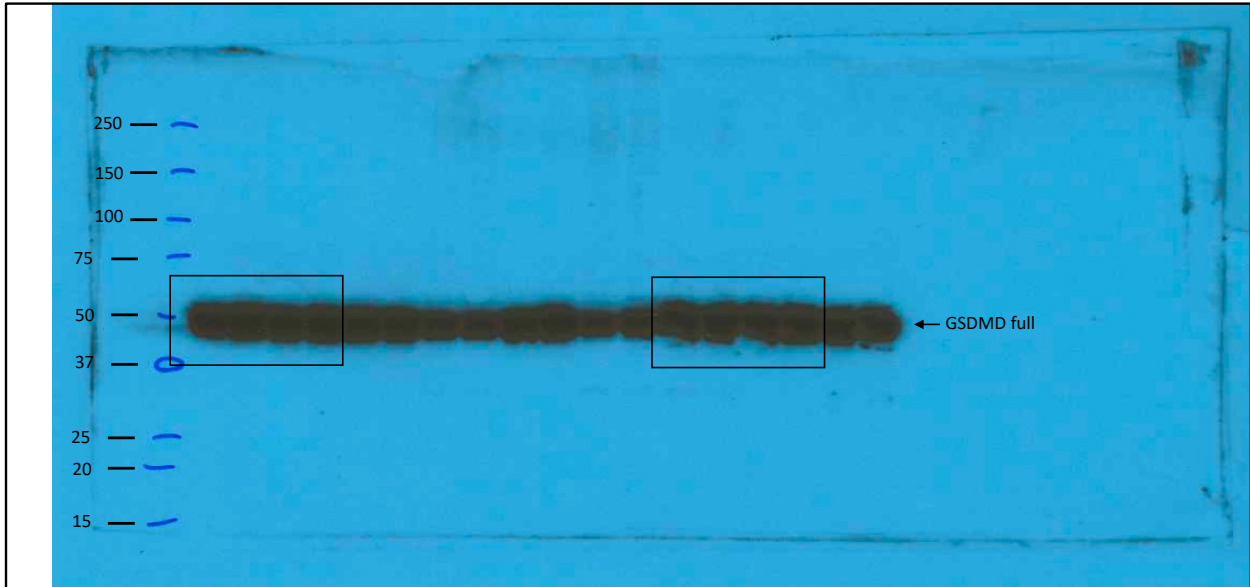


Source Data 1D



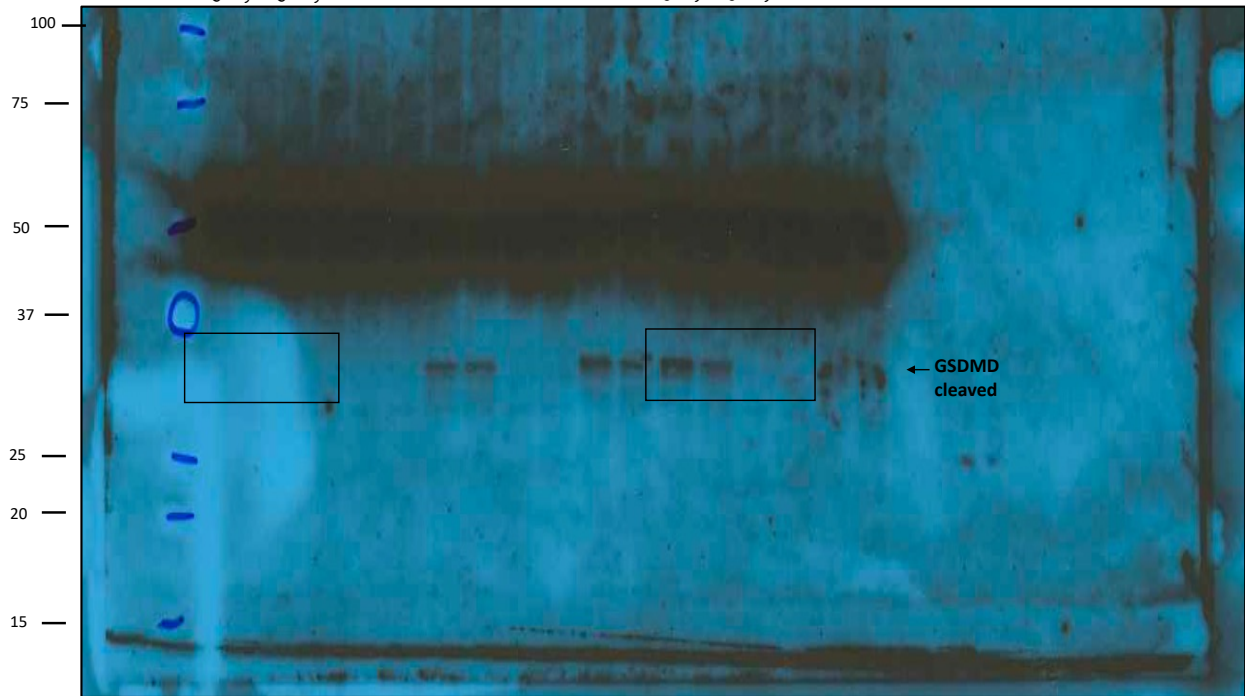
**LPS only**  
 Wild type    NLRP3<sup>-/-</sup>  
 Control    Sars-Cov-2 E  
             Control    Sars-Cov-2 E

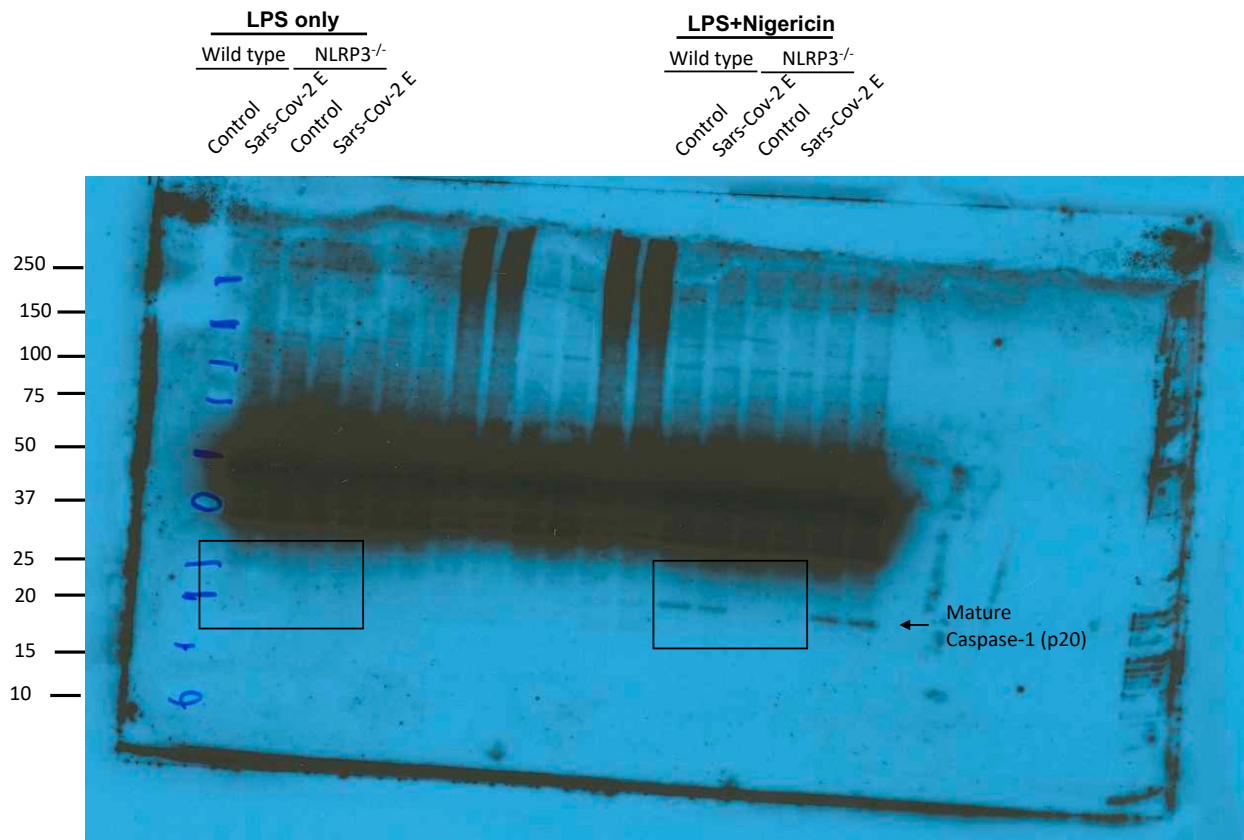
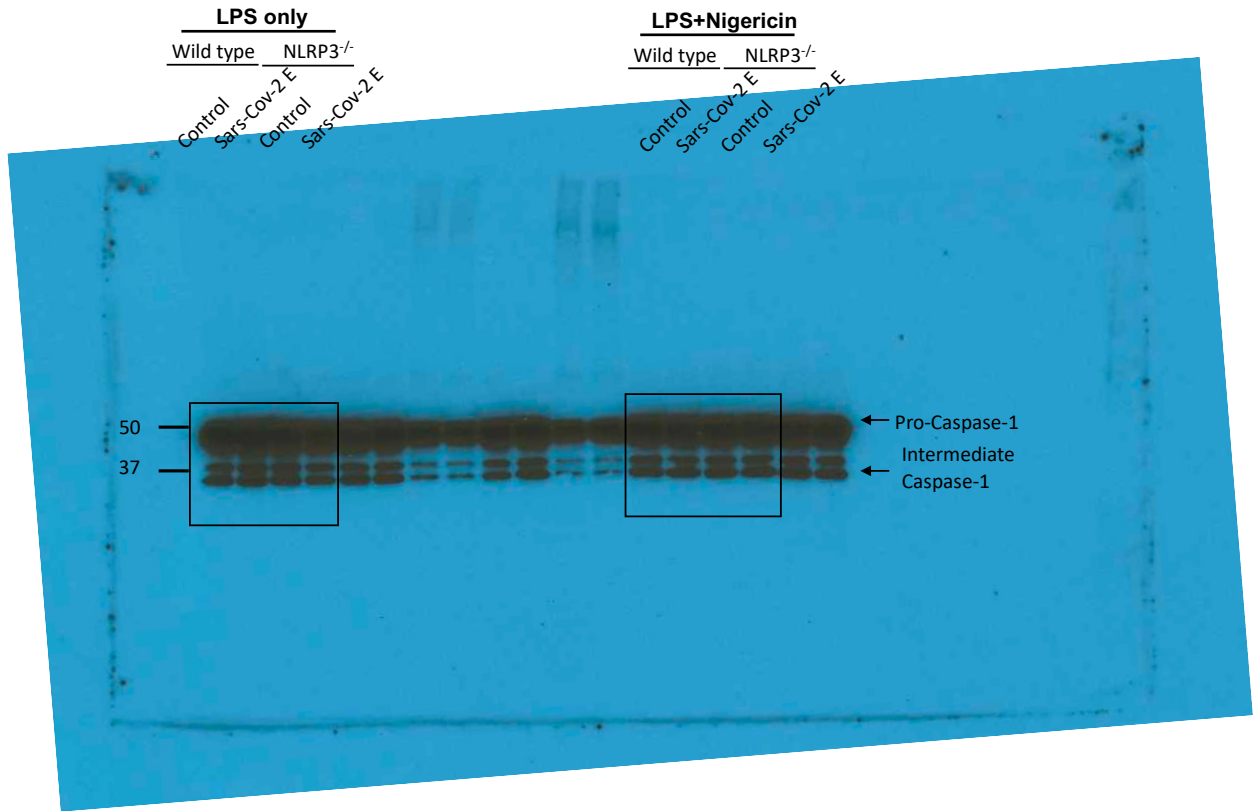
**LPS+Nigericin**  
 Wild type    NLRP3<sup>-/-</sup>  
 Control    Sars-Cov-2 E  
             Control    Sars-Cov-2 E



**LPS only**  
 Wild type    NLRP3<sup>-/-</sup>  
 Control    Sars-Cov-2 E  
             Control    Sars-Cov-2 E

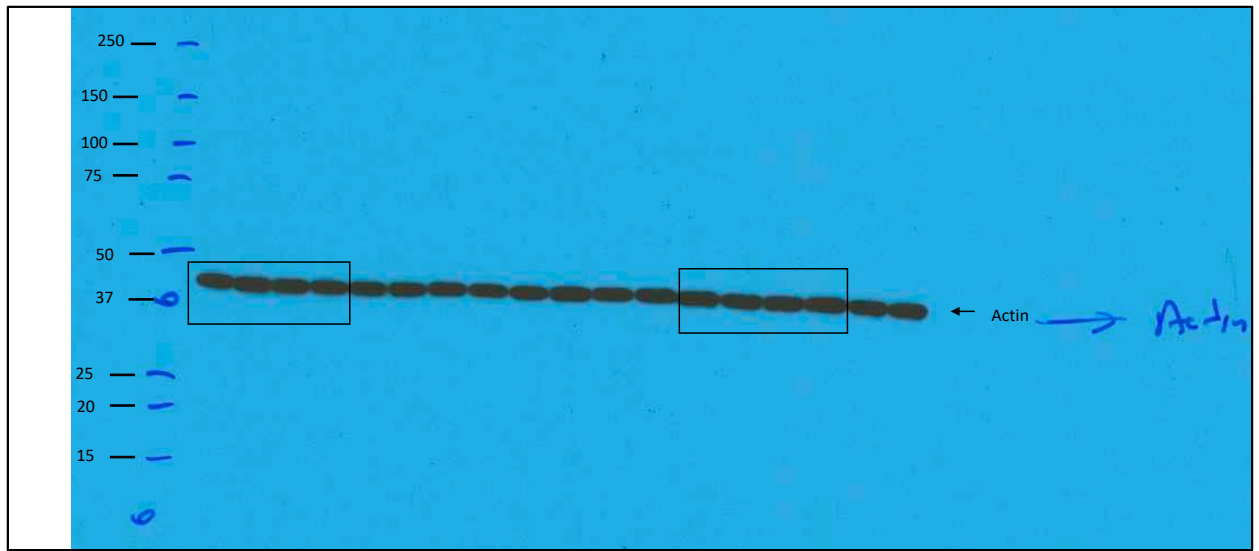
**LPS+Nigericin**  
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 Control    Sars-Cov-2 E  
             Control    Sars-Cov-2 E



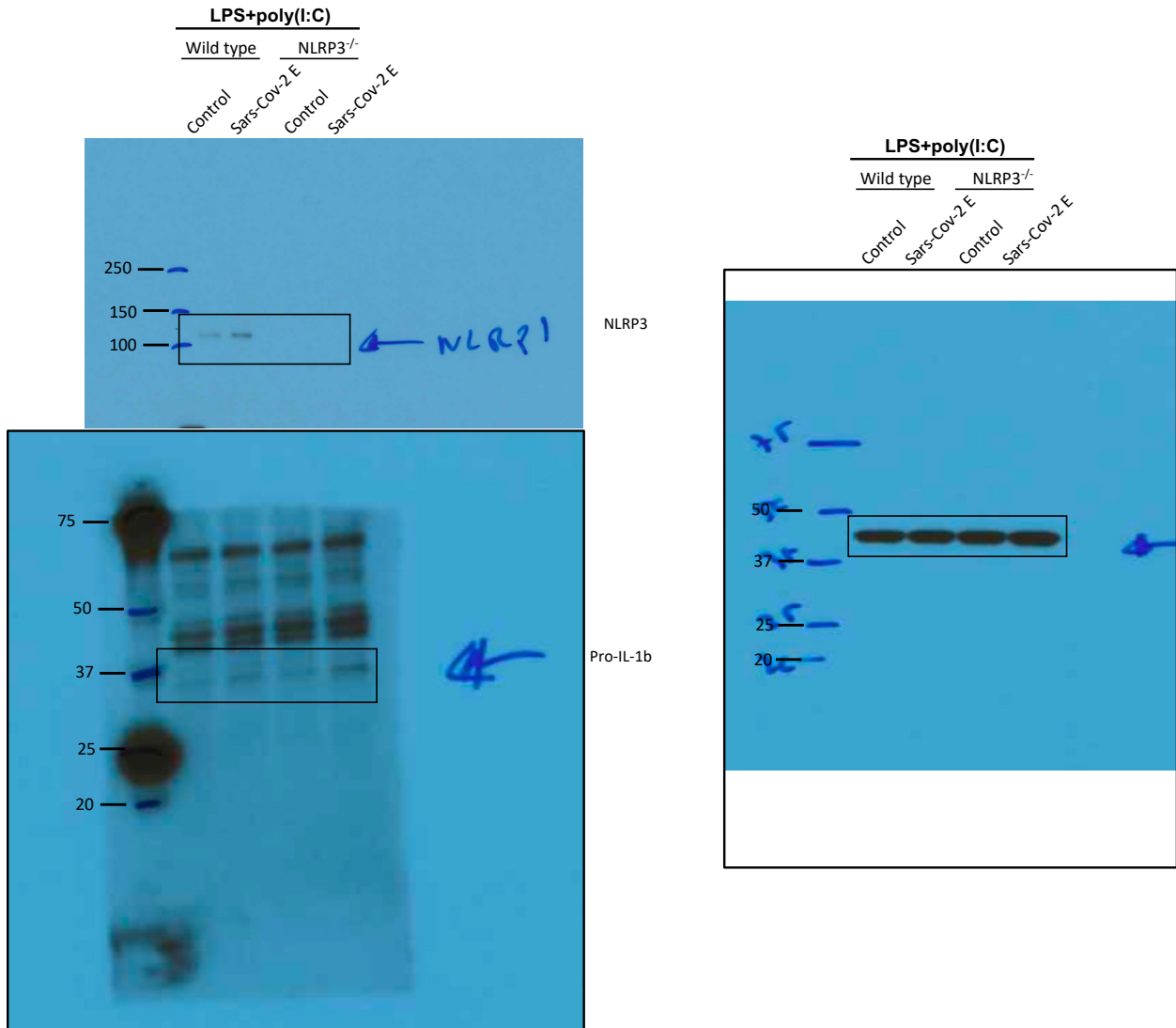


**LPS only**  
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 Control    Sars-Cov-2 E  
 Control    Sars-Cov-2 E

**LPS+Nigericin**  
 Wild type    NLRP3<sup>-/-</sup>  
 Control    Sars-Cov-2 E  
 Control    Sars-Cov-2 E

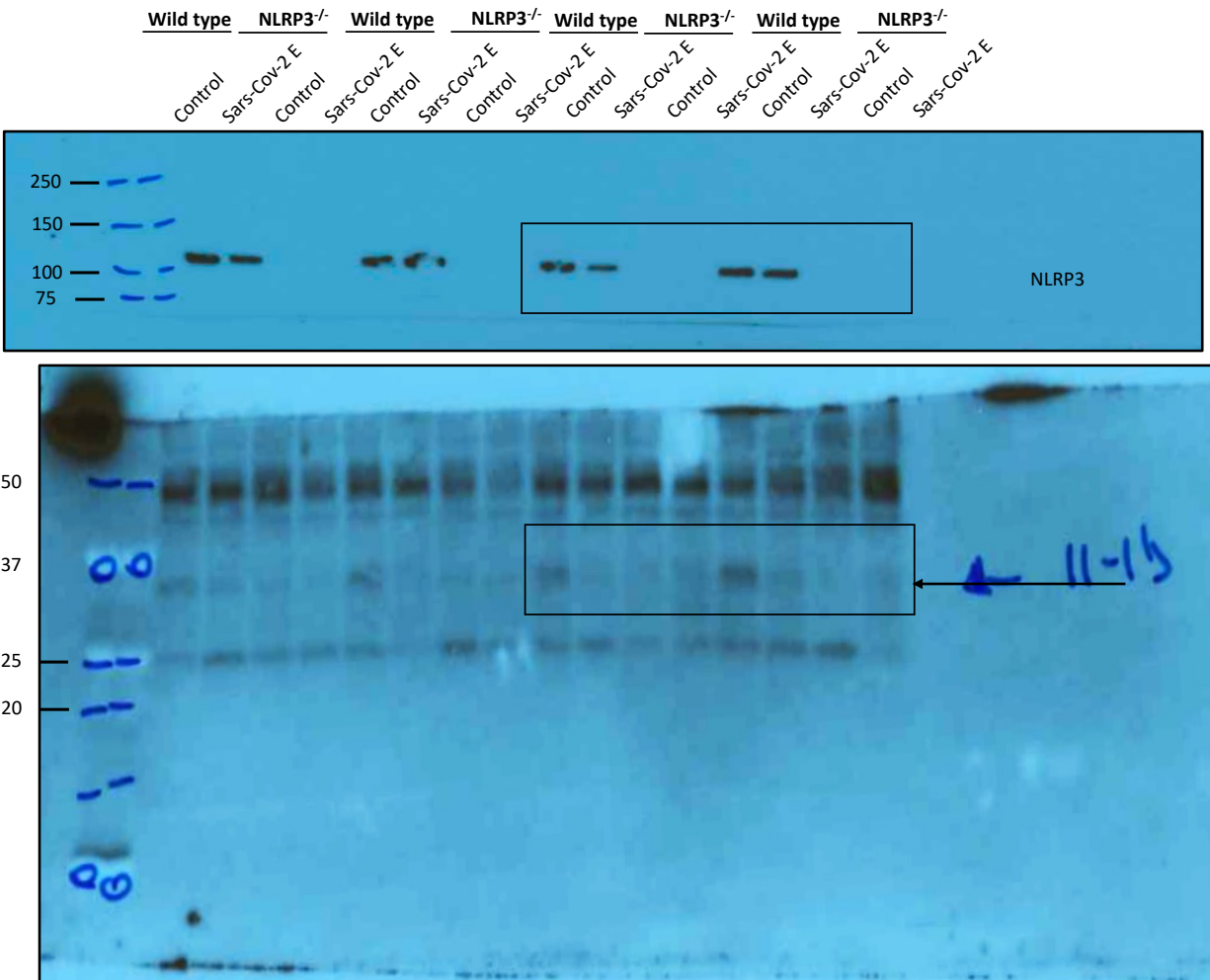


Source Data 4A



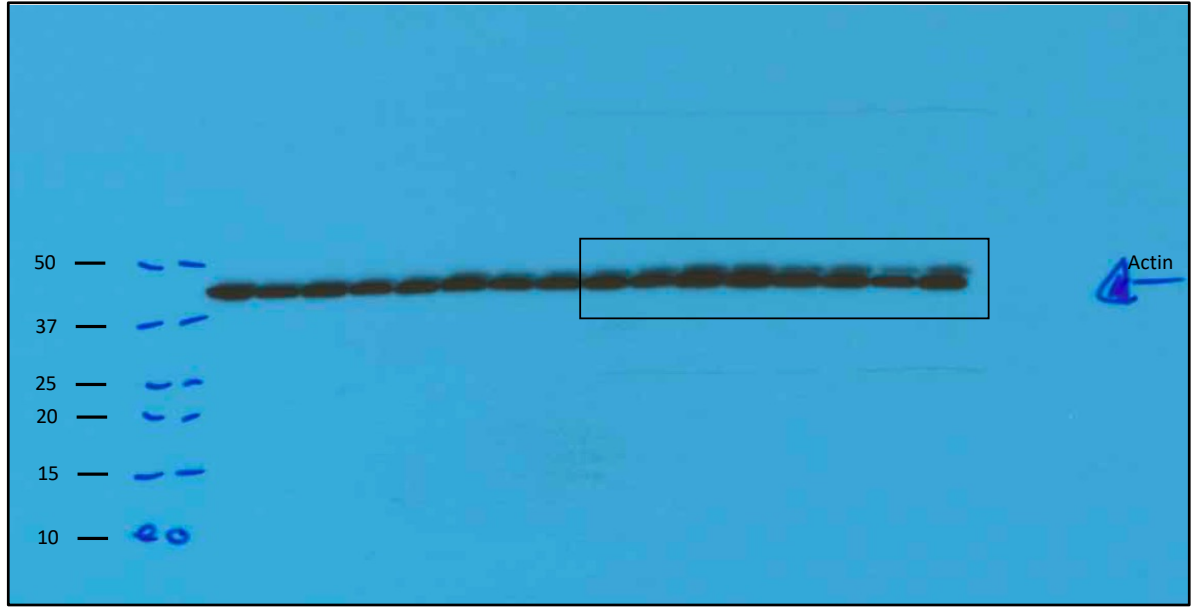
Source Data 2F

Blot 1

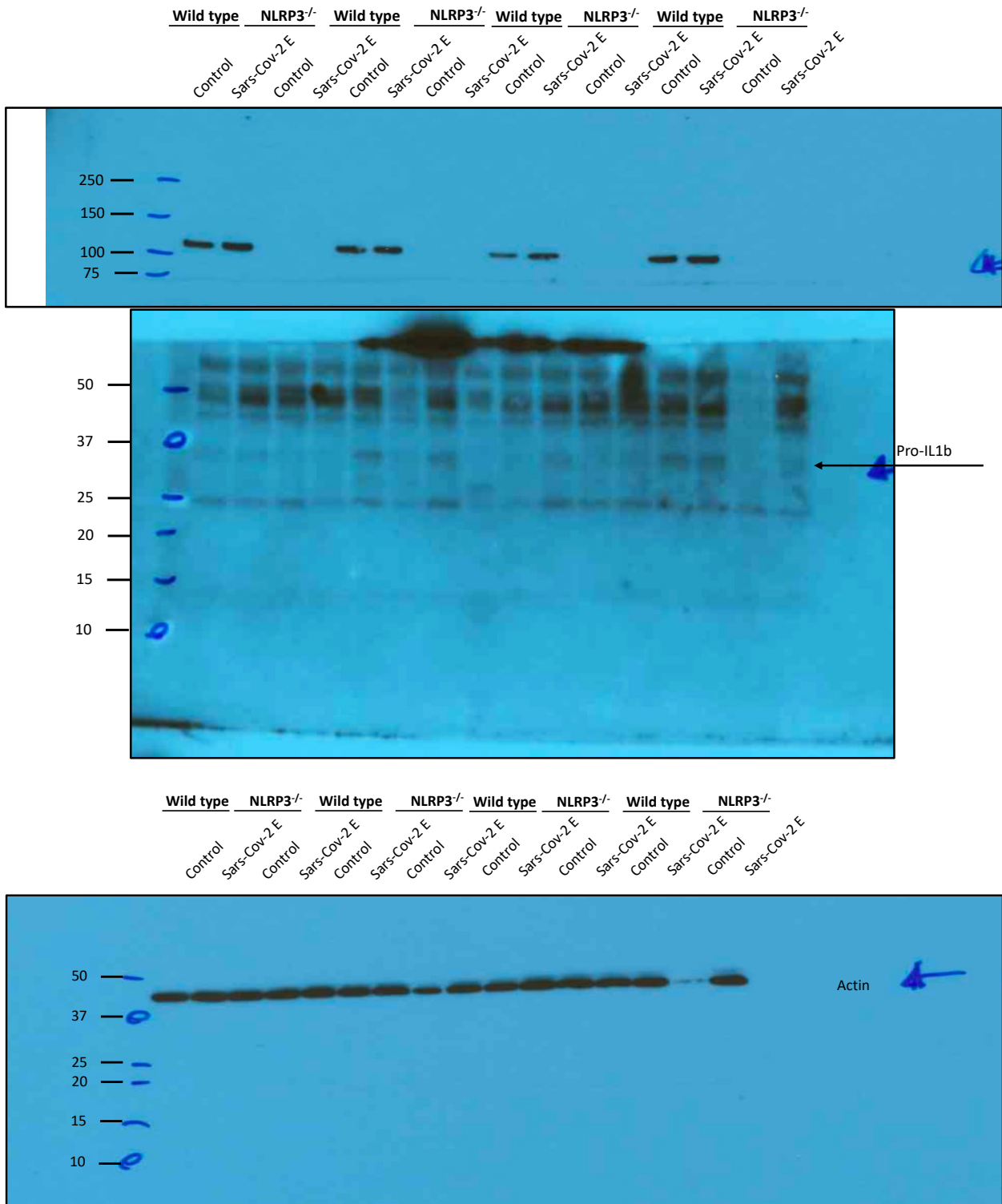




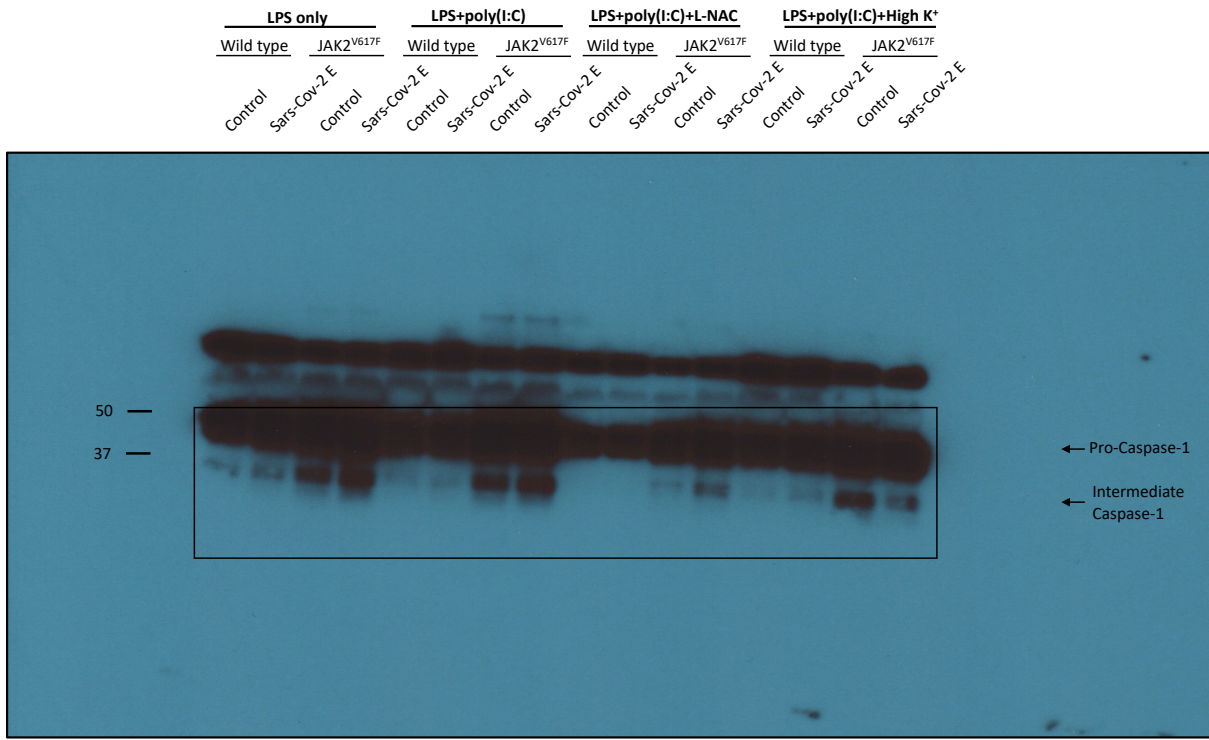
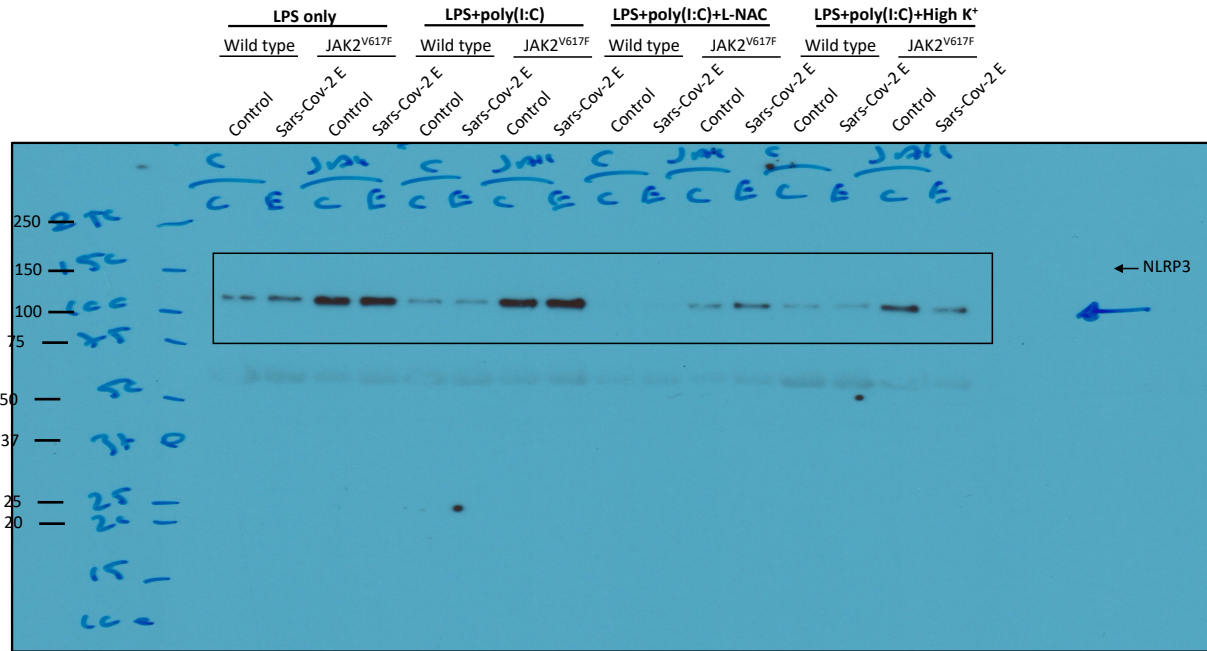
Wild type	NLRP3 <sup>-/-</sup>	Wild type	NLRP3 <sup>-/-</sup>	Wild type	NLRP3 <sup>-/-</sup>	Wild type	NLRP3 <sup>-/-</sup>
Control	Sars-Cov-2 E	Control	Sars-Cov-2 E	Control	Sars-Cov-2 E	Control	Sars-Cov-2 E



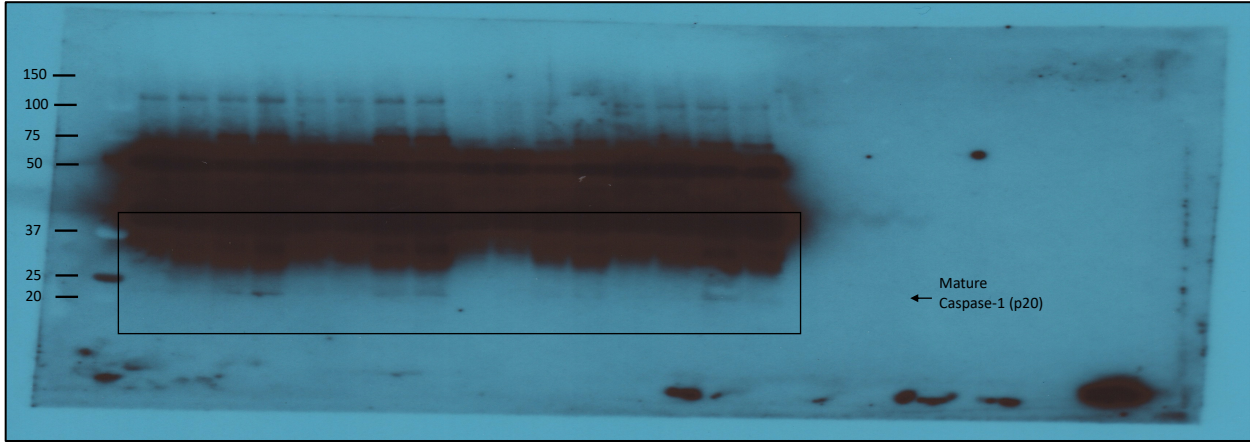
**Blot 2**



Source Data Supplementary Figure 5B



LPS only		LPS+poly(I:C)		LPS+poly(I:C)+L-NAC		LPS+poly(I:C)+High K <sup>+</sup>	
Wild type	JAK2 <sup>V617F</sup>	Wild type	JAK2 <sup>V617F</sup>	Wild type	JAK2 <sup>V617F</sup>	Wild type	JAK2 <sup>V617F</sup>
Control	Sars-Cov-2 E	Control	Sars-Cov-2 E	Control	Sars-Cov-2 E	Control	Sars-Cov-2 E



LPS only		LPS+poly(I:C)		LPS+poly(I:C)+L-NAC		LPS+poly(I:C)+High K <sup>+</sup>	
Wild type	JAK2 <sup>V617F</sup>	Wild type	JAK2 <sup>V617F</sup>	Wild type	JAK2 <sup>V617F</sup>	Wild type	JAK2 <sup>V617F</sup>
Control	Sars-Cov-2 E	Control	Sars-Cov-2 E	Control	Sars-Cov-2 E	Control	Sars-Cov-2 E

