

1 **Cullin1 represses systematic inflammasome activation by binding and catalyzing NLRP3**  
2 **ubiquitination**

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18 **Running title:** CUL1 inhibits inflammasome activation

19

20 **Keywords:** Cullin1/ Interleukin-1 $\beta$ / NLRP3 inflammasome complex/ Pro-inflammatory  
21 cytokines/ SCF E3 ubiquitin ligase complex

22

23 **Abstract**

24

25 Activation of the NLRP3 inflammasome is a key process of host immune response, the first line  
26 of defense against cellular stresses and pathogen infections. However, excessive inflammasome  
27 activation damages the hosts, and thus it must be precisely controlled. The mechanism  
28 underlying the repression of systematic inflammasome activation remains largely unknown.  
29 This study reveals that CUL1, a key component of the SCF E3 ligase, plays a critical role in  
30 regulation of the inflammasome. CUL1 suppresses the inflammasome activation in HEK293T  
31 cells, inhibits endogenous NLRP3 in macrophages, and represses inflammatory responses in  
32 C57BL/6 mice. Under normal physiological conditions, CUL1 interacts with NLRP3 to disrupt  
33 the inflammasome assembly, and catalyzes NLRP3 ubiquitination to repress the inflammasome  
34 activation. In response to inflammatory stimuli, CUL1 disassociates from NLRP3 to release the  
35 repression of NLRP3 inflammasome activation. This work reveals a distinct mechanism  
36 underlying the repression of inflammasome activation under physiological conditions and the  
37 induction of inflammasome activation in response to inflammatory stimuli, and thus provides  
38 insights into the prevention and treatment of infectious and inflammatory diseases.

39

## 40 **Introduction**

41

42 Innate immune response is the first line of defense against cellular stresses and pathogen

43 infections [1]. A key process of host immunity is the activation of inflammasomes [2,3]. The

44 NLRP3 inflammasome, a best characterized inflammasome, is crucial for acute and chronic

45 inflammatory responses. This inflammasome consists of three components, intracellular sensor

46 protein (NLRP3), adaptor protein (ASC), and effector protein (Casp-1), and regulates

47 maturation and secretion of pro-inflammatory cytokines IL-1 $\beta$  and IL-18, which initiate

48 multiple signaling pathways and drive inflammatory responses [4-7]. NLRP3 contains three

49 domains: PYRIN (PYD), NACHT (NBD), and leucine-rich repeat (LRR) [8]. ASC comprises

50 N-terminal PYD and C-terminal CARD [9,10]. Casp-1 harbors N-terminal caspase activation

51 and CARD, internal large domain (p20), and C-terminal domain (p10) [11-15]. During the

52 inflammasome activation, interaction between ASC PYD and NLRP3 PYD is necessary for

53 ASC oligomer assembly that provides a platform for pro-Casp-1 activation [16-19].

54 Inflammasome activation plays a key role in host immunity, but excessive and uncontrolled

55 activation damages host by causing infectious, inflammatory, and immune diseases [20-25], and

56 thereby it must be tightly controlled. Although negative regulations are employed by host and

57 pathogen to inhibit the NLRP3 inflammasome [26-28], the mechanisms underlying the

58 repression of systematic NLRP3 inflammasome activation remain largely unknown.

59 The ubiquitin-proteasome systems (UPS) play important roles in cell homeostasis, growth,

60 and differentiation [29,30]. Protein ubiquitination is managed by three enzymes: E1-ubiquitin

61 activating enzyme, E2-ubiquitin-conjugating enzyme, and E3-ubiquitin ligase [31]. Together

62 with E1 and E2, E3 ligase catalyzes ubiquitination of a variety of proteins [32]. E3 ligases are

63 grouped into three classes: really interesting new gene (RING), homologous to the E6-AP C  
64 terminus (HECTs), and RING between RING (RBR) [33]. Among them, Skp1-Cullin1-F-box  
65 (SCF) complex is responsible for turnover of many key proteins [34-36] and consists of three  
66 major components (CUL1, ROC1, and SKP1) along with one F-box protein [37,38]. CUL1 and  
67 ROC1 form the core of E3 ubiquitin ligase that associates with E2, whereas SKP1 links CUL1  
68 to F-box protein [39-41]. Loss of CUL1 results in early embryonic lethal and dysregulation of  
69 Cyclin E, whereas over-expression of CUL1 is associated with cancers [43-47]. However, the  
70 role of CUL1 in regulation of NLRP3 inflammasome has not been revealed.

71 This study elucidates the mechanism underlying repression of systematic NLRP3  
72 inflammasome activation. Results reveal that CUL1 interacts with NLRP3 to disrupt the  
73 inflammasome assembly and also catalyzes NLRP3 ubiquitination to repress the inflammasome  
74 activation under normal physiological conditions. Moreover, CUL1 disassociates from NLRP3  
75 to release the repression of inflammasome assembly and activation in response to inflammatory  
76 stimuli. Thus, we reveal a distinct mechanism by which CUL1 represses systematic NLRP3  
77 inflammasome activation.

## 78 **Results**

79

### 80 **CUL1 interacts with NLRP3 through its C-terminus**

81 To reveal the mechanism underlying NLRP3 inflammasome repression, we screened  
82 cellular proteins interacting with NLRP3 by yeast two-hybrid analyses (Fig EV1). Several  
83 proteins, including CUL1, PGM1, and ATP1b3, were identified to interact with NLRP3 PYD  
84 (Table 1). Co-IP analyses confirmed that NLRP3 and NLRP3 PYD interacted with CUL1 but  
85 not with ATP1b3 or PGM1 (Fig 1A), and CUL1 and NLRP3 interacted with each other (Fig  
86 1B). In macrophages, endogenous CUL1 interacted strongly with endogenous NLRP3 (Fig 1C).  
87 Immunofluorescence microscopy showed that CUL1 or NLRP3 alone diffusely distributed in  
88 the cytoplasm, whereas CUL1 and NLRP3 together were co-localized in the cells (Fig 1D).

89 To determine the region of CUL1 involved in interaction with NLRP3, a series truncated  
90 mutations of CUL1 lacking N terminus or C terminus were constructed (Fig 1E). NLRP3  
91 interacted with CUL1, CUL1-N1, CUL1-N2, CUL1-N3, CUL1-N4, CUL1-N5, and CUL1-N6,  
92 but not with CUL1-N7 (Fig 1F), suggesting that C-terminus is involved in the interaction.

93 NLRP3 interacted with CUL1, CUL1-C1, and CUL1-C2, but not with CUL1-C3, CUL1-C4,  
94 CUL1-C5, or CUL1-C6 (Fig 1G), demonstrating that C-terminus is required for the interaction.

95 A CUL1 mutant (CUL1C) carrying C-terminus (aa640–aa677) and lacking N-terminus (aa1–  
96 aa639) and a NLRP3 mutant (NLRP3PYD) containing PYD (aa1–aa93) and lacking the rest  
97 part of NLRP3 (aa94–aa991) were constructed (Fig 1H, upper). Yeast two-hybrid analyses

98 showed that CUL1C interacted with NLRP3PYD (Fig 1H, low), supporting that CUL1

99 C-terminus is required for interacting with NLRP3 PYD. Moreover, a CUL1 mutant (CUL1ΔC)

100 containing only N-terminus (aa1–aa640) and lacking C-terminus (aa641–aa677) was

101 constructed (Fig 1I, left). NLRP3 interacted with CUL1 but not with CUL1 $\Delta$ C (Fig 1I, right),  
102 suggesting that C-terminus is essential for CUL1 to interact with NLRP3. Taken together, we  
103 demonstrate that CUL1 interacts with NLRP3 through its C-terminus.

104

### 105 **NLRP3 interacts with CUL1 by competing with ROC1**

106 CUL1 is a scaffold protein of the SCF E3 ligase complex consisting of three components  
107 (CUL1, ROC1, and SKP-1) and one F-box protein [42], whereas NLRP3 is a sensor protein of  
108 the NLRP3 inflammasome complex consisting of three components (NLRP3, ASC, and  
109 pro-Casp-1) and the substrate (pro-IL-1 $\beta$ ) [7]. The mutual correlations among the two  
110 complexes were evaluated. In macrophages, endogenous CUL1 interacted with NLRP3 but not  
111 Casp-1 (Fig 2A). In HEK293T cells, NLRP3 interacted with CUL1 and ROC1 but not SKP1- $\alpha$   
112 or SKP1- $\beta$  (Fig 2B). CUL1 interacted with ROC1, SKP1, and NLRP3 (Fig 2C, left), whereas  
113 NLRP3 interacted with CUL1 and ROC1 but not SKP-1 (Fig 2C, right). Interaction of NLRP3  
114 with CUL1 was attenuated by ROC1, and interaction of NLRP3 with ROC1 was reduced by  
115 CUL1 (Fig 2D). Interestingly, interaction between CUL1 and NLRP3 was attenuated by ROC1  
116 but not by SKP-1 (Fig 2E and F). However, interaction between CUL1 and ROC1 was not  
117 affected by NLRP3 (Fig 2G).

118 Moreover, the effects of CUL1, ROC1, and SKP1 on interaction between CUL1 and  
119 NLRP3 were evaluated using short hairpin RNAs to *Cullin-1* (sh-Cullin-1#1 and sh-Cullin-1#2),  
120 *ROC1* (sh-ROC1#1 and sh-ROC1#2), or *SKP1* (sh-SKP1#1 and sh-SKP1#2) (Fig EV2A–C).  
121 Interaction between CUL1 and NLRP3 was up-regulated by sh-ROC1#2, but interaction  
122 between CUL1 and ROC1 was down-regulated by sh-ROC1#2 (Fig 2H), suggesting that ROC1  
123 plays an inhibitory role in interacting of CUL1 with NLRP3. Interaction between NLRP3 and

124 CUL1 was significantly attenuated by sh-Cullin-1#1, promoted by sh-ROC1#2, but not affected  
125 by sh-SKP1#1 (Fig 2I), indicating that ROC1 represses interaction of NLRP3 with CUL1.  
126 Considering the fact that CUL1 interacts with both NLRP3 and ROC1 through its C-terminus,  
127 we speculate that NLRP3 competes with ROC1 in interacting with CUL1.

128

### 129 **CUL1 represses NLRP3 inflammasome in HEK293T cells**

130 The role of CUL1 in regulation of NLRP3 inflammasome was determined in a  
131 reconstructed NLRP3 inflammasome system, in which HEK293T cells were co-transfected with  
132 plasmids encoding NLRP3 inflammasome components of (NLRP3, ASC, and pro-Casp1) and  
133 the substrate pro-IL-1 $\beta$  [48-51]. IL-1 $\beta$  secretion, IL-1 $\beta$  (p17) cleavage, and Casp-1 (p20)  
134 maturation were detected (Fig 3A), indicating that reconstructed NLRP3 inflammasome is  
135 active. IL-1 $\beta$  secretion was inhibited by CUL1 but not by ATP1b3, PGM1, or CUL1 $\Delta$ C (Fig 3B  
136 and C), and IL-1 $\beta$  secretion, IL-1 $\beta$  (p17) cleavage, and Casp-1 (p20) maturation were inhibited  
137 by CUL1 but not by CUL1 $\Delta$ C (Fig 3D), demonstrating that CUL1 specifically represses  
138 NLRP3 inflammasome and CUL1 C-terminus plays an essential role in the repression.

139 CUL1 is a member in the Cullin family [41]. We determined whether other family  
140 members also regulate NLRP3 inflammasome. NLRP3 strongly interacted with CUL1 but not  
141 with CUL2 or CUL3 (Fig 3E), and IL-1 $\beta$  secretion was inhibited by CUL1 but not by CUL2 or  
142 CUL3 (Fig 3F), revealing that only CUL1 represses NLRP3 inflammasome. The role CUL11 in  
143 repression of NLRP3 inflammasome was further evaluated using short hairpin RNAs to  
144 *Cullin-1* (sh-Cullin-1#1 and sh-Cullin-1#2) (Fig 3G). IL-1 $\beta$  secretion, IL-1 $\beta$  (p17) cleavage,  
145 and Casp-1 (p20) maturation were up-regulated by sh-Cullin-1#2, and attenuated by CUL1 (Fig.  
146 3H). Thus, we reveal that CUL1 represses NLRP3 inflammasome activation.

147

## 148 **CUL1 inhibits endogenous NLRP3 inflammasome in macrophages**

149 The role of CUL1 in repression of endogenous NLRP3 inflammasome was determined in  
150 THP-1 differentiated macrophages. Macrophages were infected with influenza A virus (IAV)  
151 H3N2 or treated with Z-YVAD-FMK (an inhibitor of Casp-1). *IL-1 $\beta$*  mRNA was induced by  
152 H3N2 but not by Z-YVAD-FMK (Fig EV3A), whereas IL-1 $\beta$  protein was induced by H3N2 but  
153 attenuated by Z-YVAD-FMK (Fig EV3B), indicating that Casp-1 is involved in IL-1 $\beta$  secretion  
154 but not *IL-1 $\beta$*  expression. THP-1 cell lines stably expressing sh-NC, sh-NLRP3, or sh-ASC  
155 were generated (Fig EV4C and D). In these cells, IL-1 $\beta$  secretion was induced by H3N2 but  
156 attenuated by sh-NLRP3 or sh-ASC (Fig EV4E), suggesting NLRP3 and ASC are required for  
157 H3N2-induced secretion of IL-1 $\beta$ . In macrophages, IL-1 $\beta$  (p17) cleavage and Casp-1 (p20)  
158 maturation were induced by IAV H3N2 and lipopolysaccharides (LPS) plus adenosine  
159 triphosphate (ATP) (Fig 4A), indicating H3N2 infection induces NLRP3 inflammasome  
160 activation.

161 To evaluate the role of CUL1 in regulation of NLRP3 inflammasome, we generated a  
162 THP-1 cell line stably expressing *Cullin1* mRNA and CUL1 protein (Fig EV3F). Cyclin E1 was  
163 down-regulated by CUL1 (Fig 4B), which is consistent with previous reports [52,53]. The  
164 stable cells were differentiated into macrophages and then stimulated with ATP. ATP-induced  
165 IL-1 $\beta$  secretion, IL-1 $\beta$  (p17) cleavage, and Casp-1 (p20) maturation were attenuated by CUL1  
166 (Fig 4C). A THP-1 cell line stably expressing CUL1 $\Delta$ C was also established (Fig EV3G). The  
167 cells were differentiated into macrophages and then treated with ATP or infected with H3N2.  
168 IL-1 $\beta$  secretion was induced by ATP or H3N2 but not by CUL1 $\Delta$ C (Fig 4D). These results  
169 demonstrate that CUL1 specifically represses NLRP3 inflammasome activation. The role of



170 CUL1 in regulation of NLRP3 inflammasome was further evaluated in THP-1 cells stably  
171 expressing sh-Cullin-1#1 or sh-Cullin-1#2 (Fig EV3H). Cyclin E1 was up-regulated by  
172 sh-Cullin-1#2 (Fig EV3I), indicating that they are effective. The cells were differentiated into  
173 macrophages and then stimulated with LPS, LPS+ATP, or LPS+Nigericin. IL-1 $\beta$  (p17) cleavage  
174 and Casp-1 (p20) maturation were induced by LPS, LPS+ATP, or LPS+Nigericin, and further  
175 enhanced by sh-Cullin-1#2 (Fig 4E), indicating that knock-down of *Cullin-1* facilitates NLRP3  
176 inflammasome activation.

177 NLRP3 inflammasome activation is triggered by diverse stimuli or agonists [54,55]. IL-1 $\beta$   
178 secretion, IL-1 $\beta$  (p17) cleavage, and Casp-1 (p20) maturation were induced by ATP, Nigericin,  
179 Alum, and H3N2, and such inductions were further up-regulated by sh-Cullin-1#2 in  
180 macrophages (Fig 4F–I), suggesting that knock-down of Cullin-1 up-regulates NLRP3  
181 inflammasome. However, IL-1 $\beta$  secretion, IL-1 $\beta$  (p17) cleavage, and Casp-1 (p20) maturation  
182 were induced by poly(dAdT) but such induction was not affected by sh-Cullin-1#2 (Fig 4J),  
183 indicating that CUL1 has no effect on AIM2 inflammasome. Taken together, we demonstrate  
184 that CUL1 specifically represses NLRP3 inflammasome activation in macrophages.

185

### 186 **CUL1 interacts with NLRP3 to repress inflammasome assembly**

187 The mechanism by which CUL1 represses NLRP3 inflammasome was elucidated. NLRP3  
188 inflammasome is a multi-protein platform that comprises NLRP3, ASC, and Casp-1 [55]. We  
189 revealed that ASC strongly interacted with NLRP3 PYD in 293T cells (Fig EV4). Interestingly,  
190 CUL1 interacted with NLRP3 and its three domains (PYD, NBD, and LRR) (Fig 5A) but not  
191 with ASC or Casp-1 (Fig 5B), suggesting that CUL1 is specifically and tightly associated with  
192 NLRP3.

193 The effect of CUL1 on interaction between NLRP3 and ASC was evaluated. ASC  
194 interacted with NLRP3 in the absence of CUL1 but failed to interact with NLRP3 in the  
195 presence of CUL1 (Fig 5C), and interaction of ASC with NLRP3 was attenuated by CUL1 (Fig  
196 5D). Because CUL1 interacts with NLRP3 PYD [16-19], it is possible that CUL1 may compete  
197 with ASC PYD in interacting with NLRP3 PYD, and thus disrupt NLRP3-ASC complex  
198 assembly. Interestingly, interaction between NLRP3 and CUL1 was attenuated by ASC (Fig 5E),  
199 interaction between NLRP3 and ASC was stimulated by ATP or Nigericin, and interaction  
200 between NLRP3 and CUL1 was inhibited by ATP or Nigericin (Fig 5F). These results reveal  
201 that CUL1 inhibits NLRP3 inflammasome through competing with ASC, leading to disruption  
202 of inflammasome assembly.

203 Moreover, in THP-1 differentiated macrophages, interaction between endogenous CUL1  
204 and NLRP3 was significantly attenuated by ATP, Nigericin, or H3N2 (Fig 5G), indicating that  
205 CUL1 disassociates from NLRP3 in response to stimuli. Confocal microscopy analyses showed  
206 that in the absence of stimuli, endogenous NLRP3 and CUL1 were co-localized and mainly  
207 distributed in the cytoplasm of macrophages, however, in the presence of ATP and Nigericin,  
208 endogenous NLRP3 formed spots in the cytoplasm and CUL1 was mainly located in the  
209 nucleus (Fig 5H), confirming that CUL1 is disassociated for NLRP3 during induction of  
210 inflammasome activation. IL-1 $\beta$  secretion was induced by ATP and significantly stimulated by  
211 Nigericin (Fig 5I), suggesting that NLRP3 inflammasome is activated. Taken together, we  
212 reveal that CUL1 interacts with NLRP3 to block the binding of ASC to NLRP3 and thereby  
213 repress NLRP3 inflammasome assembly in resting macrophages, whereas CUL1 disassociates  
214 from NLRP3 to allow ASC to bind NLRP3 and thereby release the repression of NLRP3  
215 inflammasome assembly in response to stimuli.

216

## 217 **CUL1 promotes NLRP3 ubiquitination but not protein degradation**

218 Ubiquitination of NLRP3 is essential for NLRP3 inflammasome repression [57], whereas  
219 deubiquitination of NLRP3 is critical for inflammasome activation [58,59]. CUL1 is a  
220 component of the SCF E3 ubiquitin ligase that catalyzes ubiquitination of a variety of proteins  
221 [32]. Thus, we investigated that the role of CUL1 in regulation of NLRP3 ubiquitination.  
222 NLRP3 ubiquitination increased as the concentration of ubiquitin increased (Fig 6A), indicating  
223 that NLRP3 is ubiquitinated under these conditions. NLRP3 ubiquitination was significantly  
224 promoted by CUL1 but not by ROC1 (Fig 6B and C), demonstrating that CUL1 catalyzes  
225 NLRP3 ubiquitination. By using UbPred software [60] to predicate potential ubiquitination sites  
226 in NLRP3, we revealed that one Lys (Lys689) is high confidence and six Lys (Lys93, Lys192,  
227 Lys194, Lys324, Lys430, and Lys696) are medium confidence. Thus, we constructed seven  
228 mutations of CUL1, in which the K residues were replaced by R residues (Fig 6D). Like CUL1,  
229 the mutants K93R, K192R, K194R, K324R, K430R, and K696R facilitated NLRP3  
230 ubiquitination, but K689R failed to act (Fig 6E), confirming that Lys689 is a significant NLRP3  
231 ubiquitination acceptor site.

232 NLRP3 is ubiquitinated with both K48 and K63 linkages in macrophages [57]. NLRP3  
233 ubiquitination was detected in the presence of Ub and significantly facilitated by CUL1, and  
234 CUL1 promoted NLRP3 ubiquitination in the presence of K63 but not in the presence of K48  
235 (Fig 6F), indicating that CUL1 catalyzes K68-linked ubiquitination of NLRP3. THP-1  
236 differentiated macrophages stably expressing sh-NC or sh-Cullin-1#2 were infected with H3N2.  
237 K63-linked ubiquitination of endogenous NLRP3 was down-regulated by sh-Cullin-1#2 and  
238 H3N2, and H3N2-mediated reduction of NLRP3 ubiquitination was further attenuated by

239 sh-Cullin-1#2 (Fig 6G), confirming that CUL1 promotes K68-linked ubiquitination of  
240 endogenous NLRP3.

241 For our surprise, the levels of NLRP3, ASC, pro-Casp-1, and pro-IL-1 $\beta$  proteins were not  
242 affected by CUL1 (Fig 6H and Fig EV5), suggesting that CUL1 regulates NLRP3  
243 inflammasome independent of protein degradation. NLRP3 level was not affected by CUL1 or  
244 ROC1 or both proteins (Fig 6I), demonstrating that CUL1 and ROC1 have no effect on NLRP3  
245 stability. We noticed that this result is different from previous reports showing that dopamine  
246 and TRIM31 inhibit NLRP3 inflammasome by promoting proteasomal degradation of NLRP3  
247 [27].

248

#### 249 **CUL1 suppresses IL-1 $\beta$ activation and inflammatory response in mice**

250 The effect of CUL1 on peritoneal inflammation was determined in a mouse peritonitis  
251 model described previously [61]. Three siRNAs targeting to mouse *Cullin-1* (siR-Cullin1#1,  
252 siR-Cullin1#2, and siR-Cullin1#3) were generated. In mice L929 cells, *Cullin-1* mRNA and  
253 CUL1 protein were significantly down-regulated by siR-Cullin1#1, reduced by siR-Cullin1#2,  
254 and relatively unaffected by siR-Cullin1#3 (Fig 7A). C57BL/6 mice were injected with  
255 siR-Cullin1#1 and then stimulated with Alum to trigger peritonitis. Endogenous CUL1 in mice  
256 peritoneal exudates cells (PECs) was down-regulated by siR-Cullin1#1, and secreted IL-1 $\beta$   
257 protein in mice sera was significantly up-regulated by siR-Cullin1#1 (Fig 7B). Secreted IL-1 $\beta$   
258 in mice peritoneal lavage fluid was induced by Alum and further enhanced by siR-Cullin1#1  
259 (Fig 7C), however, secreted IL-6 was induced by Alum but relatively unaffected by  
260 siR-Cullin1#1 (Fig 7D). The total numbers of PECs (Fig 7E) and Neutrophils (Fig 7F) in  
261 peritoneal cavity were stimulated by Alum and further enhanced by siR-Cullin1#1. Moreover,

262 inflammatory response in mice spleen was slightly induced by Alum, but significantly  
263 facilitated by siR-Cullin1#1 (Fig 7G). The findings demonstrate that CUL1 suppress NLRP3  
264 inflammasome activation and represses inflammatory response in mice. Taken together, we  
265 reveal a distinct mechanism by which CUL1 represses systemic NLRP3 inflammasome  
266 activation (Fig 8).

267

## 268 **Discussion**

269

270 The NLRP3 inflammasome is activated in response to pathogen-associated molecular patterns  
271 (PAMP) and danger-associated molecular patterns (DAMP) to induce inflammatory responses  
272 [62,63]. Precise and tight control of NLRP3 inflammasome is critical to adequate immune  
273 protection and limit detrimental responses. Although significant attempts have been made and  
274 negative regulations are employed by hosts and pathogens to inhibit NLRP3 inflammasome  
275 activation [64], the mechanisms underlying repression of systematic NLRP3 inflammasome  
276 activation remain largely unknown.

277 This study initially reveals that CUL1 interacts with NLRP3 PYD through its C-terminus,  
278 which is required for nuclear localization and SCF ubiquitin ligase assembly [65]. CUL1  
279 interacts with all three domains (PYD, NACHT, and LRR) of NLRP3, and endogenous NLRP3  
280 and CUL1 co-localized and distributed in the cytoplasm of macrophages. Thus, we demonstrate  
281 that CUL1 strongly associates with NLRP3. CUL1, a scaffold protein of SCF E3 ligase  
282 complex that consists three major components (CUL1, ROC1, and SKP-1) [42], and NLRP3, is  
283 a sensor protein of the NLRP3 inflammasome complex that also contains three major  
284 components (NLRP3, ASC, and pro-Casp-1) [7,56]. The mutual correlations among the two  
285 complexes are revealed: CUL1 interacts with NLRP3 but not pro-Casp-1 or ASC, whereas  
286 NLRP3 interacts with CUL1 and ROC1 but not SKP-1. Interaction of NLRP3 with CUL1 is  
287 attenuated by ROC1, interaction of NLRP3 with ROC1 is reduced by CUL1, and interaction  
288 between CUL1 and ROC1 is not affected by NLRP3. Considering the fact that CUL1 interacts  
289 with both NLRP3 and ROC1, we propose that NLRP3 competes with ROC1 in interacting with  
290 CUL1. NLRP3 binds MAVS, which is critical for activating NLRP3 inflammasome [66,67]. We

291 speculate that binding between CUL1 and NLRP3 may play a role in regulating MAVS,  
292 although it needs to be further investigated. Nevertheless, the results suggest that SCF E3 ligase  
293 and NLRP3 inflammasome are highly associated, which may play roles in controlling important  
294 cellular functions.

295 Interaction between NLRP3 and ASC is necessary for inflammasome assembly, which  
296 provides a platform for pro-Casp-1 activation [16,18,19]. Interaction between NLRP3 and ASC  
297 is repressed by CUL1, indicating CUL1 disrupts inflammasome assembly. NLRP3  
298 inflammasome is activated by LPS, ATP, Nigericin, Alum, and H3N2, but such induction is  
299 attenuated by CUL1 and enhanced by sh-Cullin-1, revealing that CUL1 represses NLRP3  
300 inflammasome activation. Moreover, by using a mouse peritonitis mode, we further reveal that  
301 knock-down of Cullin-1 up-regulates IL-1 $\beta$  secretion in mice sera and peritoneal lavage fluid,  
302 increases PECs and Neutrophils in peritoneal cavity, and induces inflammatory responses in  
303 mice spleen, demonstrating that CUL1 suppress NLRP3 inflammasome and inflammatory  
304 response. Taken together, we demonstrate that CUL1 represses NLRP3 inflammasome  
305 assembly and activation.

306 Ubiquitination of NLRP3 is essential for NLRP3 inflammasome repression [57,68],  
307 whereas deubiquitination of NLRP3 is critical for the inflammasome activation [23,58]. This  
308 study demonstrates that CUL1 catalyzes K68-linked ubiquitination of NLRP3, and CUL1  
309 represses NLRP3 inflammasome activation through catalyzing ubiquitination. However, the  
310 levels of NLRP3, ASC, and pro-Casp-1 are not affected by CUL1, indicating that CUL1  
311 represses NLRP3 inflammasome independent of protein degradation. This result is different  
312 from previous reports showing that TRIM31 inhibits NLRP3 inflammasome by promoting  
313 proteasomal degradation of NLRP3 [27,57], and FBXL3 interacts with NLRP3 to facilitate

314 SCFFBXL2-mediated degradation of NLRP3 [68]. Thus, CUL1, as an important component of  
315 the SCF E3 ubiquitin ligase, represses NLRP3 inflammasome through a distinct mechanism:  
316 catalyzes NLRP3 ubiquitination and has no effect on protein stability. This unique mechanism  
317 ensures to keep NLRP3 in check by restricting its function without destroying the protein.

318 Interestingly, interaction between NLRP3 and CUL1 is inhibited by ATP or Nigericin and  
319 attenuated by ASC. Because CUL1 interacts with NLRP3 PYD, and thus we propose that CUL1  
320 inhibits NLRP3 inflammasome through competing with ASC in interacting with NLRP3 to  
321 disrupt inflammasome assembly. In addition, interaction between endogenous CUL1 and  
322 NLRP3 in macrophages is attenuated by ATP, Nigericin, and H3N2. Moreover, in the presence  
323 of ATP or Nigericin, endogenous NLRP3 forms small spot in cytoplasm and CUL1 mainly  
324 distributes in the nucleus. Taken together, these results demonstrate that CUL1 disassociates for  
325 NLRP3 to release NLRP3 inflammasome repression in response to inflammatory stimuli and  
326 pathogen infections.

327 In conclusion, we reveal a distinct mechanism by which CUL1 represses systemic NLRP3  
328 inflammasome activation. In resting cells and under normal physiological conditions, CUL1  
329 interacts with NLRP3 to disrupt the inflammasome assembly, and catalyzes NLRP3  
330 ubiquitination to repress the inflammasome activation (Fig. 8A). However, in response to  
331 inflammatory stimuli, CUL1 disassociates from NLRP3 to release the repression of  
332 inflammasome assembly and activation (Fig. 8B).

333



## 334 **Materials and Methods**

335

### 336 **Animal study**

337 Female C57BL/6 mice (6 weeks) were obtained from Hubei Provincial Center for Disease  
338 Control and Prevention (Wuhan, China). All animal experiments were undertaken in accordance  
339 with the National Institutes of Health Guide for the Care and Use of Laboratory Animals, with  
340 the approval of the Wuhan University animal care and use committee guidelines.

341 Mice peritoneal exudates cells (PECs) were harvested and Red Blood Cell (RBC) Lyses  
342 Buffer was added to PECs. The cells were washed twice with PBS buffer supplemented with 2%  
343 BSA. For PECs, the cells were directly analyzed by flow cytometry (Beckman Coulter).

344 For neutrophils, PECs were Fc-blocked by TruStain fcX<sup>TM</sup> anti-mouse CD16/32 Antibody  
345 for 10 minutes prior to staining, then PECs in PBS buffer supplemented with 2% BSA are  
346 incubated with Anti-FITC-CD11b and Anti-APC-Ly-6G on ice for 1h in the dark. Cells were  
347 washed twice with PBS buffer supplemented with 2% BSA, and analyzed by flow cytometry  
348 (Beckman Coulter).

349 All spleen tissues were fixed in 4% paraformaldehyde and Histopathological changes in  
350 the spleen tissue were examined by H&E staining.

351 For induction of peritonitis, mice were injected with 700 µg Alum (Thermo scientific).

352 For analysis of inflammatory cell subsets and cytokines in the peritoneal cavity, mice were  
353 killed 8h after alum injection and peritoneal cavities were washed with 5 ml of PBS. PECs and  
354 neutrophils were collected and analyzed by flow cytometry and the peritoneal fluids were  
355 concentrated for ELISA analysis.

356 All mouse siRNAs were synthesized as following: siR-Cullin1#1:

357 5'-GCTTGTGGTCGCTTCATAA-3'; siR-Cullin1#2: 5'-GGTTGTATCAACTGTCCAA-3';  
358 siR-Cullin1#3: 5'-GGTCGCTTCATAACAACA-3'. Mice were intraperitoneally injected with  
359 siCullin1-1 and negative control for 60–72 h and all these siRNAs were specially modified by 5'  
360 Cho1 and 2' OMe. All siRNA were synthesized by RiboBio (Guangzhou, China).

361

## 362 **Cell lines and cultures**

363 Human embryonic kidney cell line (HEK293T) was purchased from American Type  
364 Culture Collection (ATCC) (Manassas, VA, USA). Human monocytic cell line (THP-1) was a  
365 gift from Dr. Bing Sun of Institute of Biochemistry and Cell Biology, Shanghai Institute for  
366 Biological Sciences. HEK293T cells were maintained in DMEM purchased from Gibco (Grand  
367 Island, NY, USA) supplemented with 10% fetal bovine serum (FBS), 100 U/ml penicillin, and  
368 100 µg/ml streptomycin sulfate. THP-1 cells were maintained in RPMI 1640 medium  
369 supplemented with 10% FBS, 100 U/ml penicillin, and 100 µg/ml streptomycin sulfate. THP-1  
370 cells were differentiated for 12 h with 100 ng phorbol-12-myristate-13-acetate (PMA).

371

## 372 **Reagents**

373 Lipopolysaccharide (LPS) (Cat# L2630), adenosine triphosphate (ATP) (Cat# A7699),  
374 and phorbol-12-myristate-13-acetate (TPA) (Cat# P8139), were purchased from Sigma-Aldrich  
375 (St. Louis, MO, USA). Nigericin (Cat# tlrl-nig), Alum (Cat# tlrl-alk), Poly(dA:dT)/LyoVec  
376 (Cat# tlrl-patc), Lipofectamine 2000 (Cat# 11668019) were purchased from InvivoGene  
377 Biotech Co., Ltd. (San Diego, CA, USA).

378 X-α-Gal (Cat# XA250) was purchased from Gold Biotechnology (St. Louis, MO, USA).

379 Aureobasidin A (Cat# 630499) was obtained from Clontech (Mountain View, CA, USA).

380 Z-YVAD-FMK (Cat# 1012-100) was obtained from BioVision (Heinrichstr, Zürich). cOmplete,  
381 EDTA-free Protease Inhibitor Cocktail Tablets provided in EASYpacks (Cat# 04 693 132 001)  
382 was purchased from Roche (Indianapolis, IN, USA).

383 Anti-Human IL-1 $\beta$  (D3U3E) (Cat# 12703), Anti-Human Caspase-1 (D7F10) (Cat# 3866),  
384 Anti-Human/Mouse NLRP3 (D4D8T) (Cat# 15101), Anti-Human/Mouse/Rat Cyclin E1  
385 (D7T3U) (Cat# 20808), Anti-Human/Mouse/Rat Skp1 (Cat# 2156), and Anti-Human/Mouse  
386 K63-linkage Specific Polyubiquitin (Cat# 5621) antibodies were purchased from Cell Signaling  
387 Technology (Beverly, MA, USA). Anti-Human/Mouse/Rat ASC(F-9) (Cat# sc-271054),  
388 Anti-Human/Mouse/Rat Cullin1 (D-5) (Cat# sc-17775), and Anti-Human/Mouse/Rat Cullin1  
389 (H-213) (Cat# sc-11384) antibodies were purchased from Santa Cruz Biotechnology (Santa  
390 Cruz, CA, USA). Anti-Flag (Cat# F3165), Anti-HA (Cat# H6908), and Anti-GAPDH (Cat#  
391 G9295) antibodies were purchased from Sigma-Aldrich. Anti-Human/Mouse/Rat ROC1 (Cat#  
392 14895-1-AP) antibody was obtained from Proteintech (Rosemont, IL, USA).

393 Anti-Human/Mouse NLRP3 (Cryo-2) (Cat# AG-20B-0014-C100) antibody was purchased from  
394 Adipogen (San Diego, CA, USA). Anti-Mouse IgG Dylight 649 (Cat# A23610), Anti-Mouse  
395 IgG Dylight 488 (Cat# A23210), Anti-Rabbit IgG Dylight 649 (Cat# A23620), and Anti-Rabbit  
396 IgG FITC (Cat# A22120) antibodies were purchased from Abbkine (California, USA). Human  
397 IL-1 $\beta$  ELISA Kit II (Cat# 557966) was purchased from BD Biosciences (Franklin Lakes, NJ,  
398 USA). Human IL-1 $\beta$ /IL-1F2 Quantikine ELISA Kit (Cat# DLB50) was purchased from R&D  
399 Systems (Minnesota, USA).

400

#### 401 **Yeast two-hybrid screening**

402 Mate & Plate Library-Universal Human (Normalized), *Saccharomyces cerevisiae* strain

403 Y2HGold and Y187, control vectors pGBKT7, pGADT7, pGBKT7-p53, pGADT7-T and  
404 pGBKT7-lam, and some reagents were purchased from Clontech (Mountain View, CA, USA).  
405 All experimental procedures were following the Matchmaker® Gold Yeast Two-Hybrid System  
406 User Manual.

407

#### 408 **Western blot analysis**

409 For western blot analysis, cells were lysed in lyses buffer (50 mM Tris-HCl, pH7.4, 150  
410 mM NaCl, 1% (vol/vol) Triton X-100, 5 mM EDTA, and 10% (vol/vol) glycerol). Protein  
411 concentration was determined by Bradford assay (Bio-Rad, Hercules, CA, USA). Cell lysates  
412 were separated by 10–12% SDS-PAGE and then transferred onto a nitrocellulose membrane  
413 (Millipore). The membranes were blocked in phosphate buffered saline with 0.1% Tween 20  
414 (PBST) containing 5% nonfat dried milk before incubation with specific antibodies. Blots were  
415 detected with the Clarity Western ECL substrate (Bio-Rad, Hercules, CA, USA) and protein  
416 band were detected using a Luminescent image Analyzer (Fujifilm LAS-4000).

417

#### 418 **Co-immunoprecipitation and immunoblot assays**

419 Cells were washed with cold PBS and lysed in Nonidet P-40 lyses buffer (50 mM  
420 Tris-HCl, pH7.4, 150 mM NaCl, 1% (vol/vol) NP-40, 1 mM EDTA, and 5% (vol/vol) glycerol)  
421 containing protease inhibitors. A proportion of the lysates were saved for immunoblot analysis  
422 to detect the expression of target proteins. For immunoprecipitation, the rest of lysates were  
423 incubated with a control IgG or the indicated primary antibodies at 4°C for 12–16 h, and were  
424 further incubated with protein A/G-agarose (GE Healthcare, Milwaukee, WI, USA) for 3–4 h.  
425 The beads were washed for five times by 1ml washing buffer [50 mM Tris-HCl, pH7.4, 300

426 mM NaCl, 1% (vol/vol) NP-40, 1 mM EDTA, and 5% (vol/vol) glycerol] and reconstituted in  
427 50  $\mu$ l 2 x SDS loading buffer before immunoblot analysis.

428

## 429 **Quantitative PCR**

430 Total RNA was extracted with TRIzol reagent (Invitrogen, CA, USA), following the  
431 manufacturer's instructions. Real-time quantitative RT-PCR was performed using the Roche  
432 LC480 and SYBR RT-PCR kits (DBI Bio-science, Ludwigshafen, Germany) in a reaction  
433 mixture of 10  $\mu$ l SYBR Green PCR master mix, 1  $\mu$ l DNA diluted template, 2  $\mu$ l Real-time  
434 PCR primers and RNase-free water to complete the 20  $\mu$ l volume. All Real-time PCR primers  
435 were designed in Nucleotide of National Center for Biotechnology Information (USA). All  
436 primers were as follows: GAPDH forward, 5'-AAGGCTGTGGGCAAGG-3', GAPDH reverse,  
437 5'-TGGAGGAGTGGGTGTCG-3', IL-1 $\beta$  forward, 5'-CACGATGCACCTGTACGATCA-3',  
438 IL-1 $\beta$  reverse, 5'-GTTGCTCCATATCCTGTCCCT-3', Cullin1 forward,  
439 5'-TTGCAAAGGGCCCTACGTT-3', Cullin1 reverse 5'-CGTTGTTCTCAAGCAGACG-3',  
440 NLRP3 forward, 5'-AAGGGCCATGGACTATTTCC-3', NLRP3 reverse,  
441 5'-GACTCCACCCGATGACAGTT-3', ASC forward,  
442 5'-AACCCAAGCAAGATGCGGAAG-3, ASC reverse, 5-TTAGGGCCTGGAGGAGCAAG-3.

443

## 444 **Lentiviral production and infection**

445 A pLKO.1-encoding shRNA vector for a scrambled (Sigma-Aldrich, St. Louis, MO, USA)  
446 or a specific-target molecule (Sigma-Aldrich, St. Louis, MO, USA) was transfected along with  
447 pMD2.G (an envelope plasmid) and psPAX2 (a packaging plasmid) into HEK293T cells.  
448 HEK293T culture supernatants were harvested at 36 and 48 h after transfection. Filtering the

449 culture supernatants through a 0.45  $\mu\text{m}$  filter to remove the cells. THP-1 cells and HEK293T  
450 cells were infected with collected culture supernatants plus 8  $\mu\text{g}/\text{ml}$  Polybrene (Sigma-Aldrich,  
451 St. Louis, MO, USA) for 24 h. After 24 h, 1.5  $\mu\text{g}/\text{ml}$  puromycin (InvivoGen, San Diego, CA,  
452 USA) was added into lentiviral-infected THP-1 cells for selection. 2  $\mu\text{g}/\text{ml}$  puromycin  
453 (InvivoGen, San Diego, CA, USA) was added into lentiviral-infected HEK293T cells for  
454 selection. Knock down efficiency of each shRNA-targeted molecule was identified by RT-PCR  
455 and immunoblot analysis. The targeting sequences of shRNA for human Cullin1 are as follows:  
456 sh-Cullin1#1: 5'-GCACACAAGATGAATTAGCAA-3', sh-Cullin1#2:  
457 5'-GCCAGCATGATCTCCAAGTTA-3'. The targeting sequences of shRNA for human NLRP3  
458 and ASC are as follows: sh-NLRP3: 5'-CAGGTTTGACTATCTGTTCT-3', sh-ASC:  
459 5'-GATGCGGAAGCTCTTCAGTTTCA-3'

460

#### 461 **Reconstitution of the NLRP3 inflammasome in HEK293T cells**

462 HEK293T cells at 70% confluence were seeded into 6cm plates overnight and then  
463 transfected with plasmids encoding NLRP3 inflammasome component proteins and pro-IL-1 $\beta$ ,  
464 including 1  $\mu\text{g}$  pcDNA3.1-NLRP3, 100 ng pcDNA3.1-ASC, 400 ng pcDNA3.1-procaspase-1  
465 and 1  $\mu\text{g}$  pcDNA3.1-pro-IL-1 $\beta$ . The cells were washed with culture medium 24 h after  
466 transfection and were further incubated for 6 h. Cell pellets were collected and lysed in cell  
467 lyses buffer for immunoblot analysis and Cell culture medium was collected for ELISA to  
468 detect IL-1 $\beta$  (BD Biosciences).

469

#### 470 **Immunofluorescence microscopy**

471 All Cells were washed three times with PBS, and cells were fixed with 4%

472 paraformaldehyde for 15 min, washed three times with PBS, permeabilized with PBS  
473 containing 0.5% Triton X-100 for 5 min, washed three times with PBS, and finally blocked with  
474 PBS containing 5% bovine serum albumin (BSA) for 1 h at room temperature. The cells were  
475 then incubated with the primary antibody at 4°C, followed by incubation with FITC-conjugate  
476 donkey anti-mouse IgG (Abbkine) and Dylight 649-conjugate donkey anti-rabbit IgG (Abbkine)  
477 or FITC-conjugate donkey anti-rabbit IgG (Abbkine) and Dylight 649-conjugate donkey  
478 anti-mouse IgG (Abbkine) for 1 h, After cells washed three times with PBS, cells were  
479 incubated with DAPI (Vector Laboratories, Burlingame, CA) for 5 min in 37°C. Finally, the  
480 cells were analyzed using a confocal laser scanning microscope (FluoView FV 1000; Olympus,  
481 Tokyo, Japan).

482

### 483 **Cytokine measurements**

484 The concentrations of human IL-1 $\beta$  in culture supernatants were measured by  
485 commercially available enzyme linked immunosorbent assay (ELISA) kits (BD Biosciences,  
486 San Jose, CA, USA). The concentrations of mouse IL-1 $\beta$  in peritoneal fluids or mouse IL-1 $\beta$  in  
487 the serum were measured by ELISA kits (R&D Systems, Minneapolis, USA). The  
488 concentrations of mouse IL-6 in peritoneal fluids were measured by ELISA kits (BioLegend,  
489 San Diego, USA).

490

### 491 **Measurement of activated Casp-1 and mature IL-1 $\beta$**

492 1 ml medium from each well was mixed with 0.5 ml methanol and 0.125 ml chloroform,  
493 vortexed, and centrifuged for 5 min at 13000 rpm in a microcentrifuge (Thermo scientific). The  
494 upper phase of each sample was removed and 0.5 ml methanol was added. Samples were

495 centrifuged for 5 min at 13000 rpm. Next, the supernatants were removed and pellets were  
496 dried for 5 min at 50°C in the water bath. Then, 50 µl 2 x SDS loading buffer was added to each  
497 sample, followed by boiling for 10 min.

498

#### 499 ***In vivo* ubiquitination assay**

500 Cells were lysed in 100 µl SDS lyses buffer (50 mM Tris-HCl, pH7.4, 150 mM NaCl, 1%  
501 (vol/vol) NP-40, 1 mM EDTA, and 5% (vol/vol) glycerol, 1% SDS). After boiling for 5 min,  
502 lysates were diluted 10-fold with dilution buffer (50 mM Tris-HCl, pH7.4, 150 mM NaCl, 1%  
503 (vol/vol) NP-40, 1 mM EDTA, and 5% (vol/vol) glycerol) containing protease inhibitors. A  
504 proportion of the lysates (100 µl) were saved for immunoblot analysis to detect the expression  
505 of target proteins, the rest of the lysates were immunoprecipitated with specific antibodies. Rest  
506 of experiment procedures were following the co-immunoprecipitation and immunoblot assays.

507

#### 508 **Statistics**

509 All experiments were repeated at least three times with similar results. All results were  
510 expressed as the mean ± the standard deviation (SD). Statistical analysis was carried out using  
511 the t-test for two groups and one-way ANOVA for multiple groups (GraphPad Prism5). The  
512 date was considered statistically significant when  $P \leq 0.05$  (\*),  $P \leq 0.01$  (\*\*),  $P \leq 0.001$  (\*\*\*)).

513



514 **Acknowledgments**

515 This work was supported by National Natural Science Foundation of China (81730061,  
516 31230005, 81471942, 31200134, and 31270206), and the National Health and Family Planning  
517 Commission of China (National Mega Project on Major Infectious Disease Prevention)  
518 (2017ZX10103005 and 2017ZX10202201).

519 We thank Dr. Jiahuai Han of State Key Laboratory of Cellular Stress Biology, School of  
520 Life Sciences, Xiamen University, Fujian, China, for kindly providing the cDNA of genes  
521 Cullin1 and NLRP3.

522

523 **Author Contributions**

524 P.W., Q.Z., Y.L., K.W., Y.L., and J.W. conceived the project and designed the experiments;  
525 P.W. performed experiments with help from Q.Z., W.L., Y.J., T.W., W.W., P.P., G.Y., Q.X., S.H.,  
526 Q.Y., and W.Z.; W.L., and F.L., contributed to the reagents; P.W., Q.Z., W.L., W.W., K.W., F.L.,  
527 Y.L., and J.W. performed data analyses; P.W., and J.W. wrote the manuscript; P.W., K.W., Y.L.,  
528 and J.W. edited the manuscript.

529

530 **Conflict of Interest:** The authors disclose no conflicts or competing financial interests.

531

532

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706

707

708

709 **Figure legends**

710

711 **Figure 1 – CUL1 interacts with NLRP3 through its C-terminus.**

712 **A** HEK293T cells were transfected with pCAGGS-HA-PYD or pCAGGS-HA-NLRP3 and

713 pcDNA3.1(+)-3XFlag-ATP1β3, pcDNA3.1(+)-3XFlag-PGM1, or

714 pcDNA3.1(+)-3XFlag-Cullin1, respectively.

715 **B** HEK293T cells were transfected with pcDNA3.1(+)-3XFlag and pCAGGS-HA,

716 pcDNA3.1(+)-3XFlag and pCAGGS-HA-NLRP3, or pcDNA3.1(+)-3XFlag and

717 pCAGGS-HA-NLRP3, respectively.

718 **C** THP-1 cells were differentiated into macrophages with PMA.

719 **D** HEK293T cells were transfected with pcDNA3.1(+)-3XFlag-Cullin1 and

720 pCAGGS-HA-NLRP3. The cells were immunostained with anti-Flag and anti-HA antibodies.

721 The sub-cellular localizations of HA-NLRP3 (green), Flag-Cullin1 (Red), and nucleus marker

722 DAPI (blue) were analyzed under confocal microscopy.

723 **E** N terminal mutants and C terminal mutants of CUL1 were constructed and indicated.

724 **F** HEK293T cells were transfected with pCAGGS-HA-NLRP3 and

725 pcDNA3.1(+)-3XFlag-Cullin1 or the N terminal mutants, respectively.

726 **G** HEK293T cells were transfected with pCAGGS-HA-NLRP3 and

727 pcDNA3.1(+)-3XFlag-Cullin1 or the C terminal mutants, respectively.

728 **H** Yeast strain Y2HGold was co-transformed with the combination of BD and AD plasmid, as

729 indicated. Transfected yeast cells were grown on SD-minus Trp/Leu (DDO) plates, and colonies

730 were replicated onto SD-minus Trp/Leu/Ade/His Plates containing Aureobasidin A and X-β-gal

731 (QDO/A/X) to check for the expression of reporter genes.

732 **I** HEK293T cells were transfected with pCAGGS-HA-PYD and  
733 pcDNA3.1(+)-3XFlag-Cullin1 or pcDNA3.1(+)-3XFlag-Cullin1 $\Delta$ C.  
734 Data information: In (**A–C**, **F**, **G**, and **I**), the cell lysates were immunoprecipitated with  
735 anti-Flag, anti-HA, or anti-Cullin1 antibodies and then immunoblotted with indicated  
736 antibodies.

737

738 **Figure 2 – NLRP3 interacts with CUL1 by competing with ROC1.**

739 **A** The lysates of PMA-differentiated THP-1 macrophages were immunoprecipitated with  
740 anti-Cullin1 antibody and then immunoblotted with indicated antibodies.

741 **B** HEK293T cells were transfected with pCAGGS-HA-NLRP3 and  
742 pcDNA3.1(+)-3xFlag-Cullin1, pcDNA3.1(+)-3xFlag-ROC1, pcDNA3.1(+)-3xFlag-SKP1- $\alpha$   
743 and pcDNA3.1(+)-3xFlag-SKP1- $\beta$ , respectively.

744 **C** HEK293T cells were transfected with pcDNA3.1(+)-NLRP3 and  
745 pcDNA3.1(+)-3XFlag-Cullin1.

746 **D** HEK293T cells were transfected with pCAGGS-HA-NLRP3 and  
747 pcDNA3.1(+)-3xFlag-Cullin1, pcDNA3.1(+)-3xFlag-ROC1, pcDNA3.1(+)-3xFlag-Cullin1,  
748 and pcDNA3.1(+)-3xFlag-ROC1.

749 **E** HEK293T cells were transfected with pcDNA3.1(+)-3xFlag-Cullin1 and  
750 pCAGGS-HA-NLRP3, pcDNA3.1(+)-3xFlag-ROC1 and pcDNA3.1(+)-3xFlag-SKP1,  
751 pcDNA3.1(+)-3XFlag-SKP1 and pCAGGS-HA-NLRP3, or pcDNA3.1(+)-3xFlag-ROC1 and  
752 pCAGGS-HA-NLRP3, respectively.

753 **F** HEK293T cells were transfected with pCAGGS-HA-NLRP3 and  
754 pcDNA3.1(+)-3xFlag-Cullin1 and pcDNA3.1(+)-3xFlag-ROC1 at different concentrations.

755 **G** HEK293T cells were transfected with pcDNA3.1(+)-3XFlag-Cullin1 or  
756 pcDNA3.1(+)-3XFlag-ROC1 and pCAGGS-HA-NLRP3 at different concentrations.  
757 **H** HEK293T cells were transfected with pcDNA3.1(+)-3xFlag-Cullin1 and  
758 pSilencer2.1-U6-sh-Cullin1#1 or pSilencer2.1-U6-sh-Cullin1#2.  
759 **I** HEK293T cells were transfected with pcDNA3.1(+)-3xFlag-Cullin1 or  
760 pcDNA3.1(+)-3xFlag-NLRP3 and pSilencer2.1-U6-shROC1#2.  
761 Data information: In (**B–I**), the cell lysates were immunoprecipitated with anti-Flag antibody  
762 (B), anti-NLRP3 antibody (C, E), anti-HA antibody (D, F), anti-Cullin1 antibody (G–I) and  
763 then immunoblotted with indicated antibodies.

764

765 **Figure 3 – CUL1 represses NLRP3 inflammasome in HEK293T cells.**

766 **A** HEK293T cells were transfected or co-transfected with pcDNA3.1(+)-NLRP3,  
767 pcDNA3.1(+)-pro-IL-1 $\beta$ , pcDNA3.1(+)-pro-caspase-1, and pcDNA3.1(+)-ASC, as indicated.  
768 **B** HEK293T cells were co-transfected with pcDNA3.1(+)-NLRP3, pcDNA3.1(+)-pro-IL-1 $\beta$ ,  
769 pcDNA3.1(+)-pro-caspase-1, and pcDNA3.1(+)-ASC, along with pcDNA3.1(+)-3Flag-ATP1 $\beta$ 3,  
770 pcDNA3.1(+)-3Flag-PGM1, or pcDNA3.1(+)-3Flag-Cullin1, as indicated. Secreted IL-1 $\beta$  in  
771 the supernatants were analyzed by ELISA.  
772 **C** Diagrams of Cullin1 and Cullin1 $\Delta$ C (upper). HEK293T cells were co-transfected with  
773 pcDNA3.1(+)-NLRP3, pcDNA3.1(+)-pro-IL-1 $\beta$ , pcDNA3.1(+)-pro-caspase-1, and  
774 pcDNA3.1(+)-ASC along with pcDNA3.1(+)-3XFlag-Cullin1 or  
775 pcDNA3.1(+)-3XFlag-Cullin1 $\Delta$ C, as indicated. Secreted IL-1 $\beta$  in the supernatants were  
776 analyzed by ELISA.  
777 **D** HEK293T cells were co-transfected with pcDNA3.1(+)-NLRP3, pcDNA3.1(+)-pro-IL-1 $\beta$ ,

778 pcDNA3.1(+)-pro-caspase-1, and pcDNA3.1(+)-ASC along with

779 pcDNA3.1(+)-3XFlag-Cullin1 or pcDNA3.1(+)-3XFlag-Cullin1 $\Delta$ C.

780 **E** HEK293T cells were co-transfected with pCAGGS-HA-NLRP3 and

781 pcDNA3.1(+)-3XFlag-Cullin1, pcDNA3.1(+)-3XFlag-Cullin2, or

782 pcDNA3.1(+)-3XFlag-Cullin3, respectively. The cell lysates were immunoprecipitated with

783 anti-HA antibody and then immunoblotted with indicated antibodies.

784 **F** HEK293T cells were co-transfected with pcDNA3.1(+)-NLRP3, pcDNA3.1(+)-ASC,

785 pcDNA3.1(+)-pro-caspase-1, and pcDNA3.1(+)-pro-IL-1 $\beta$  along with

786 pcDNA3.1(+)-3XFlag-Cullin1, pcDNA3.1(+)-3XFlag-Cullin2, or

787 pcDNA3.1(+)-3XFlag-Cullin3, respectively.

788 **G** HEK293T cells were transduced with lentiviruses stably expressing shRNA (sh-NC) and

789 shRNA against Cullin1 (sh-Cullin1#1 and sh-Cullin1#2) and selected with puromycin for 2

790 weeks. Cullin1 and GAPDH mRNAs were determined by qRT-PCR (upper) and Cullin1 and

791 GAPDH proteins were detected Western blot analyses (low).

792 **H** HEK293T cells stably expressing sh-NC or sh-Cullin1#2 were co-transfected with

793 pcDNA3.1(+)-NLRP3, pcDNA3.1(+)-pro-IL-1 $\beta$ , pcDNA3.1(+)-pro-caspase-1, and

794 pcDNA3.1(+)-ASC, along with pcDNA3.1(+)-3XFlag-Cullin1.

795 Data information: In (**A**, **D**, **F**, and **H**), secreted IL-1 $\beta$  in the supernatants were analyzed by

796 ELISA (upper). Matured IL-1 $\beta$  (p17) and matured Casp-1 (p20) in the cell lysates were

797 determined by immunoblot analyses with indicated antibodies (low).

798 Data information: In (**A–D**, **G–H**), data shown are means  $\pm$  SEM, \*P<0.05, \*\*P<0.01,

799 \*\*\*P<0.0001.

800

801 **Figure 4 – CUL1 inhibits endogenous NLRP3 inflammasome in macrophages.**

802 **A** PMA-differentiated THP-1 macrophages were infected with H3N2 for 24 h or treated with  
803 LPS and ATP for 30 min. The cell lysates were immunoblotted with indicated antibodies.

804 **B** CUL1, Cyclin E1, and GAPDH proteins were examined by Western blot analysis in THP-1  
805 cells stably expressing CUL1.

806 **C** Macrophages stably expressing CUL1 were treated with ATP for 30 min.

807 **D** Macrophages stably expressing CUL1 $\Delta$ C were treated with ATP or infected with H3N2.  
808 Secreted IL-1 $\beta$  in the supernatants were analyzed by ELISA.

809 **E** Macrophages stably expressing sh-Cullin1#2 were treated with LPS for 6 h, LPS for 6 h  
810 and ATP for 30 min, or LPS for 6 h and Nigericin for 1 h, respectively. Matured IL-1 $\beta$  (p17) in  
811 the cell lysates was determined by immunoblot analysis with indicated antibodies.

812 **F** Macrophages stably expressing sh-Cullin1#2 were treated with ATP for 30 min.

813 **G** Macrophages stably expressing sh-Cullin1#2 were treated with Nigericin for 1 h.

814 **H** Macrophages stably expressing sh-Cullin1#2 were treated with Alum for 6 h

815 **I** Macrophages stably expressing sh-Cullin1#2 were infected with IAV H3N2 for 24 h

816 **J** Macrophages stably expressing sh-Cullin1#2 were treated with Poly(dA:dT)/LyoVec<sup>TM</sup> for  
817 12 h.

818 Data information: In (**C**, **F–J**), secreted IL-1 $\beta$  in the supernatants were analyzed by ELISA  
819 (upper). Matured IL-1 $\beta$  (p17) and matured Casp-1 (p20) in the cell lysates were determined by  
820 immunoblot analysis with indicated antibodies (low).

821 Data information: In (**C**, **D**, **F–J**), data shown are means  $\pm$  SEM, \*P<0.05, \*\*P<0.01,

822 \*\*\*P<0.0001.

823

824 **Figure 5 – CUL1 interacts with NLRP3 to repress inflammasome assembly.**

825 **A** HEK293T cells were transfected with pcDNA3.1(+)-3XFlag-Cullin1 and  
826 pCAGGS-HA-NLRP3, pCAGGS-HA-PYD, pCAGGS-HA-NBD, pCAGGS-HA-LLR,  
827 respectively.

828 **B** HEK293T cells were transfected with pCAGGS-HA-Cullin1 and  
829 pcDNA3.1(+)-3XFlag-NLRP3, pcDNA3.1(+)-3XFlag-ASC, or  
830 pcDNA3.1(+)-3XFlag-pro-caspase-1, respectively.

831 **C** HEK293T cells were transfected with pcDNA3.1(+)-NLRP3 and pcDNA3.1(+)-ASC along  
832 with pcDNA3.1(+)-3XFlag-Cullin1.

833 **D** HEK293T cells were transfected with pCAGGS-HA-NLRP3 and pCAGGS-HA-ASC along  
834 with pcDNA3.1(+)-3XFlag-Cullin1 at different concentrations.

835 **E** HEK293T cells were co-transfected with pcDNA3.1(+)-NLRP3 and/or pcDNA3.1(+)-ASC  
836 along with pcDNA3.1(+)-3XFlag-Cullin1, as indicated.

837 **F** HEK293T cells were co-transfected with pcDNA3.1(+)-NLRP3, pcDNA3.1(+)-ASC,  
838 pcDNA3.1(+)-3XFlag-Cullin1 and then treated with 5 mM ATP for 30 min and 10  $\mu$ M  
839 Nigericin for 1 h.

840 **G** PMA-differentiated THP-1 macrophages were stimulated with ATP or Nigericin, and  
841 infected with H3N2.

842 **H** PMA-differentiated THP-1 macrophages were stimulated with ATP or Nigericin. The cells  
843 were immunostained with anti-NLRP3 and anti-Cullin1 antibodies. The sub-cellular  
844 localizations of endogenous NLRP3 (green), endogenous Cullin1 (Red), and nucleus marker  
845 DAPI (blue) were analyzed under confocal microscopy.

846 **I** PMA-differentiated THP-1 macrophages were stimulated with ATP or Nigericin. The cells

847 were immunostained with anti-NLRP3 and anti-Cullin1 antibodies. The supernatants were  
848 analyzed by ELISA for IL-1 $\beta$  secretion. Data shown are means  $\pm$  SEM, \*p<0.05, \*\*p<0.01,  
849 \*\*\*p<0.0001.

850 Data information: In (A–G), the cell lysates were immunoprecipitated with anti-HA antibody  
851 (A), anti-Flag antibody (B, C), anti-NLRP3 antibody (D, F), or anti-Cullin1 antibody (E, G) and  
852 then immunoblotted with indicated antibodies.

853

854 **Figure 6 – CUL1 promotes NLRP3 ubiquitination but not protein degradation.**

855 **A** HEK293T cells were transfected with pcDNA3.1(+)-NLRP3 and pCAGGS-HA-Ub at  
856 different concentrations.

857 **B** HEK293T cells were transfected with pcDNA3.1(+)-NLRP3, pcDNA3.1(+)-HA-Ub, and/or  
858 pcDNA3.1(+)-3Flag-Cullin1, respectively.

859 **C** HEK293T cells were transfected with pcDNA3.1(+)-NLRP3, pcDNA3.1(+)-HA-Ub,  
860 pcDNA3.1(+)-3Flag-Cullin1 or pcDNA3.1(+)-3Flag-ROC1, as indicated.

861 **D** Daigrams of full-length NLRP3 and its point mutants. The potential ubiquitination sites in  
862 NLRP3 among the Lys residues were predicated by using UbPred software. One Lys (Lys689)  
863 is high confidence and six Lys (Lys93, Lys192, Lys194, Lys324, Lys430, and Lys696) are  
864 medium confidence. Seven mutations of CUL1 (K93R, K192R, K194R, K324R, K430R,  
865 K689R, and K696R), in which the K residues were replaced by R residues.

866 **E** HEK293T cells were co-transfected with pcDNA3.1(+)-HA-Ub and pcDNA3.1(+)-Cullin1,  
867 along with pcDNA3.1(+)-3xFlag -NLRP3 or its mutants, respectively.



868 **F** HEK293T cells were co-transfected with pcDNA3.1(+)-NLRP3 and/or  
869 pcDNA3.1(+)-HA-Ub, pcDNA3.1(+)-3Flag-Cullin1, pcDNA3.1(+)-HA-K48 or  
870 pcDNA3.1(+)-HA-K63, as indicated.

871 **G** PMA-differentiated THP-1 macrophages stably expressing sh-NC and sh-Cullin1#2 were  
872 infected with IAV H3N2.

873 **H** HEK293T cells were transfected with pcDNA3.1(+)-3XFlag-NLRP3,  
874 pcDNA3.1(+)-3XFlag-ASC, pcDNA3.1(+)-3XFlag-pro-caspase-1,  
875 pcDNA3.1(+)-3XFlag-pro-IL-1 $\beta$ , or pcDNA3.1(+)-3xFlag-Cullin1, as indicated.

876 **I** HEK293T cells were transfected with pCAGGS-HA-NLRP3 and/or  
877 pcDNA3.1(+)-3XFlag-Cullin1, or pcDNA3.1(+)-3XFlag-ROC1.

878 Data information: In (**A–C**), the lysates were immunoprecipitated with anti-NLRP3 antibody  
879 and immunoblotted with indicated antibodies. In (**E–I**), the lysates were immunoprecipitated  
880 with anti-Flag antibody (E) or anti-NLRP3 antibody (F, G) and then immunoblotted with  
881 indicated antibodies. The lysates were immunoblotted with the indicated antibodies (H, I).

882

883 **Figure 7 – CUL1 suppresses IL-1 $\beta$  secretion and inflammatory response in mice.**

884 **A** L929 cells were transfected with siR-NC (25 nM), siR-Cullin1#1 (25 nM), siR-Cullin1#2  
885 (25 nM), or siR-Cullin1#3 (25 nM). *Cullin1* and *GAPDH* mRNAs were determined by  
886 qRT-PCR (left) and CUL1 and GAPDH proteins were detected Western blot analyses (right).

887 **B** C57BL/6 mice were injected with siR-NC (5 nM), siR-Cullin1#1 (5 nM), or siR-Cullin1#1  
888 (10 nM) for 60 h, and the peritonitis of treated mice were then injected with Alum for 12 h. The  
889 endogenous mCUL1, mNLRP3, and mGAPDH proteins in the mice peritoneal exudates cells

890 (PECs) were detected by Western blot analyses (left). Secreted IL-1 $\beta$  in the mice sera were  
891 analyzed by ELISA (right).

892 **C** C57BL/6 mice (six mice per group) were injected with siR-NC or siR-Cullin1#1 for 60 h,  
893 and the peritonitis of treated mice were then injected with Alum. Secreted IL-1 $\beta$  in mice  
894 peritoneal lavage fluid were analyzed by ELISA.

895 **D** C57BL/6 mice (six mice per group) were injected with siR-NC or siR-Cullin1#1 for 60 h,  
896 and the peritonitis of treated mice were then injected with Alum. Secreted IL-6 in mice  
897 peritoneal lavage fluid was analyzed by ELISA.

898 **E** C57BL/6 mice (six mice per group) were injected with siR-NC or siR-Cullin1#1 for 60 h,  
899 and the peritonitis of treated mice were then injected with Alum. The total numbers of PECs in  
900 peritoneal cavity were stimulated.

901 **F** C57BL/6 mice (six mice per group) were injected with siR-NC or siR-Cullin1#1 for 60 h,  
902 and the peritonitis of treated mice were then injected with Alum. The total numbers of  
903 Neutrophils (F) in peritoneal cavity were stimulated.

904 **G** C57BL/6 mice (six mice per group) were injected with siR-NC or siR-Cullin1#1 for 60 h,  
905 and the peritonitis of treated mice were then injected with Alum. Histopathological changes in  
906 the mice spleen tissues were examined by H&E staining.

907 Data information: In (**A–F**), data shown are means  $\pm$  SEM, \*P<0.05, \*\*P<0.01, \*\*\*P<0.0001.

908

909 **Figure 8 – A proposed mechanism underlying CUL1-mediated repression of systematic**  
910 **NLRP3 inflammasome activation.**

911 **A** In resting cells and under normal physiological conditions, CUL1 interacts with NLRP3 to  
912 disrupt the NLRP3 inflammasome assembly, and catalyzes NLRP3 ubiquitination to repress the  
913 NLRP3 inflammasome activation.

914 **B** In response to and inflammasome stimuli and pathogen infection, CUL1 disassociates from  
915 NLRP3 to release the repression of NLRP3 inflammasome assembly and activation. ASC binds  
916 NLRP3 to form ASC oligomers, which provides a platform for activation of pro-Casp-1 that  
917 regulates the maturation and secretion of IL-1 $\beta$  and IL-18, which in turn initiate multiple  
918 signaling pathways and drive inflammatory responses.

919

920

921 **Tables and their legends**

922

923 **Table 1 – The proteins interacted with NLRP3 as identified by yeast two-hybrid screening.**

<b>Clone number</b>	<b>Comparison results after sequencing</b>	<b>Gene identified</b>
19-1	Correct	Cullin1 (CUL1)
22-3/51-4	Correct	Phosphoglucomutase 1 (PGM1)
43-3/44-1	Correct	ATPase Na <sup>+</sup> /K <sup>+</sup> transporting subunit beta 3 (ATP1β3)
10-5	Frameshift mutation	PNN-interacting serine/arginine-rich protein (PNISR)
25-1	Frameshift mutation	Peptidylprolyl isomerase A (PPIA)
51-1	Frameshift mutation (not in CDS)	Zinc finger protein 146 (ZNF146)
55-2	Frameshift mutation	Oxysterol binding protein-like 1A (OSBPL1A)
11-6/22-5/44-6/5 1-3/52-3	No significant similarity found	None

924 The cellular proteins interacting with NLRP3 were identified through yeast two-hybrid  
925 screening using PYD of NLRP3 as the bait. Several cellular proteins, including Cullin1 (CUL1),  
926 phosphoglucomutase 1 (PGM1), and ATPase transporting subunit beta 3 (ATP1b3), were  
927 identified to interact with NLRP3 PYD.

928 **Expanded View Figure Legends**

929

930 **Figure EV1 – Two-hybrid library screening using yeast mating.**

931 The entire Matchmaker screening process consists of the following steps: Step 1, Clone the  
932 targeted gene into pGBKT7 Vector; Step 2, Test bait for autoactivation and toxicity; Step3,  
933 Screen Mate & Plate library; Step 4, confirm and interpret results.

934

935 **Figure EV2 – Analyses of the efficiency of short hairpin RNAs (shRNA) in HEK293T cells.**

936 **A** HEK293T cells were transfected with pcDNA3.1(+)-3XFlag-Cullin1 along with control,  
937 plasmid pSilencer2.1-U6-shCullin1#1 and shCullin1#2. The levels of Flag-Cullin1 protein were  
938 detected Western blot analyses.

939 **B** HEK293T cells were transfected with pcDNA3.1(+)-3XFlag-Cullin1 along with control,  
940 plasmid pSilencer2.1-U6-shCullin1#1 and shCullin1#2. The levels of ROC1 protein were  
941 detected Western blot analyses.

942 **C** HEK293T cells were transfected with pcDNA3.1(+)-3XFlag-Cullin1 along with control,  
943 plasmid pSilencer2.1-U6-shCullin1#1 and shCullin1#2. The levels of SKP1 protein were  
944 detected Western blot analyses.

945 The method of verifying knockdown its gene of pSilencer2.1-U6-shROC1 or  
946 pSilencer2.1-U6-shSKP1 was similar to that above.

947

948 **Figure EV3 – The effect of IAV H3N2 on the activation of IL-1 $\beta$  and the role of Cullin1 in**  
949 **regulating the components of NLRP3 inflammasome.**

950 **A** PMA-differentiated THP-1 macrophage cells were treated by H3N2 for 24 h and different

951 concentration of Z-YVAD-FMK (inhibitor of Caspase-1) for 6 h. Supernatants were analyzed  
952 by ELISA for IL-1 $\beta$  secretion.

953 **B** PMA-differentiated THP-1 macrophage cells were treated by H3N2 for 24 h and different  
954 concentration of Z-YVAD-FMK (inhibitor of Caspase-1) for 6 h. The level of IL-1 $\beta$  mRNA was  
955 determined by qRT-PCR.

956 **C** THP-1 cells were transduced with lentiviruses stably expressing shRNA(shNC) and shRNA  
957 against NLRP3 (sh-NLRP3) and ASC (sh-ASC) and selected with puromycin for 2 weeks. The  
958 levels of NLRP3 mRNA were determined by qRT-PCR.

959 **D** THP-1 cells were transduced with lentiviruses stably expressing shRNA(shNC) and shRNA  
960 against NLRP3 (sh-NLRP3) and ASC (sh-ASC) and selected with puromycin for 2 weeks. The  
961 levels of ASC mRNA were determined by qRT-PCR.

962 **E** TPA-differentiated THP-1 cells with shRNA mediated knockdown of gene expression were  
963 infected by influenza A virus H3N2, the supernatants were analyzed by ELISA for IL-1 $\beta$   
964 secretion.

965 **F** The level of IL-1 $\beta$  mRNA was determined by qRT-PCR in THP-1 cells and  
966 PMA-differentiated THP-1 cells.

967 **G** THP-1 cells were transduced with lentiviruses stably expressing Cullin1 and selected with  
968 puromycin for 2 weeks. The level of Cullin1 and GAPDH proteins were detected by RT PCR  
969 and Western blot analyses.

970 **H** THP-1 cells were transduced with lentiviruses stably expressing shRNA(sh-NC) and  
971 shRNA against Cullin1 (sh-Cullin1#1 and sh-Cullin1#2) and selected with puromycin for 2  
972 weeks. The level of Cullin1 and GAPDH mRNA was determined by qRT-PCR(upper panel) and  
973 the level of Cullin1 and GAPDH proteins were detected Western blot analyses (lower panel).

974 **I** Proteins level of Cullin1, Cyclin E1 and GAPDH were examined by Western blot analysis in  
975 THP-1 cells stably expressing sh-NC and shCullin#2.

976

977 **Figure EV4 – Identification of interaction between ASC and the PYD of NLRP3.**

978 HEK293T cells were transfected with HA-ASC plasmid in combination with plasmids encoding  
979 Flag-PYD, Flag-NBD and Flag-LRR. The cell lysates were immunoprecipitated with control  
980 IgG or an anti-Flag antibody and then immunoblotted with the indicated antibodies.

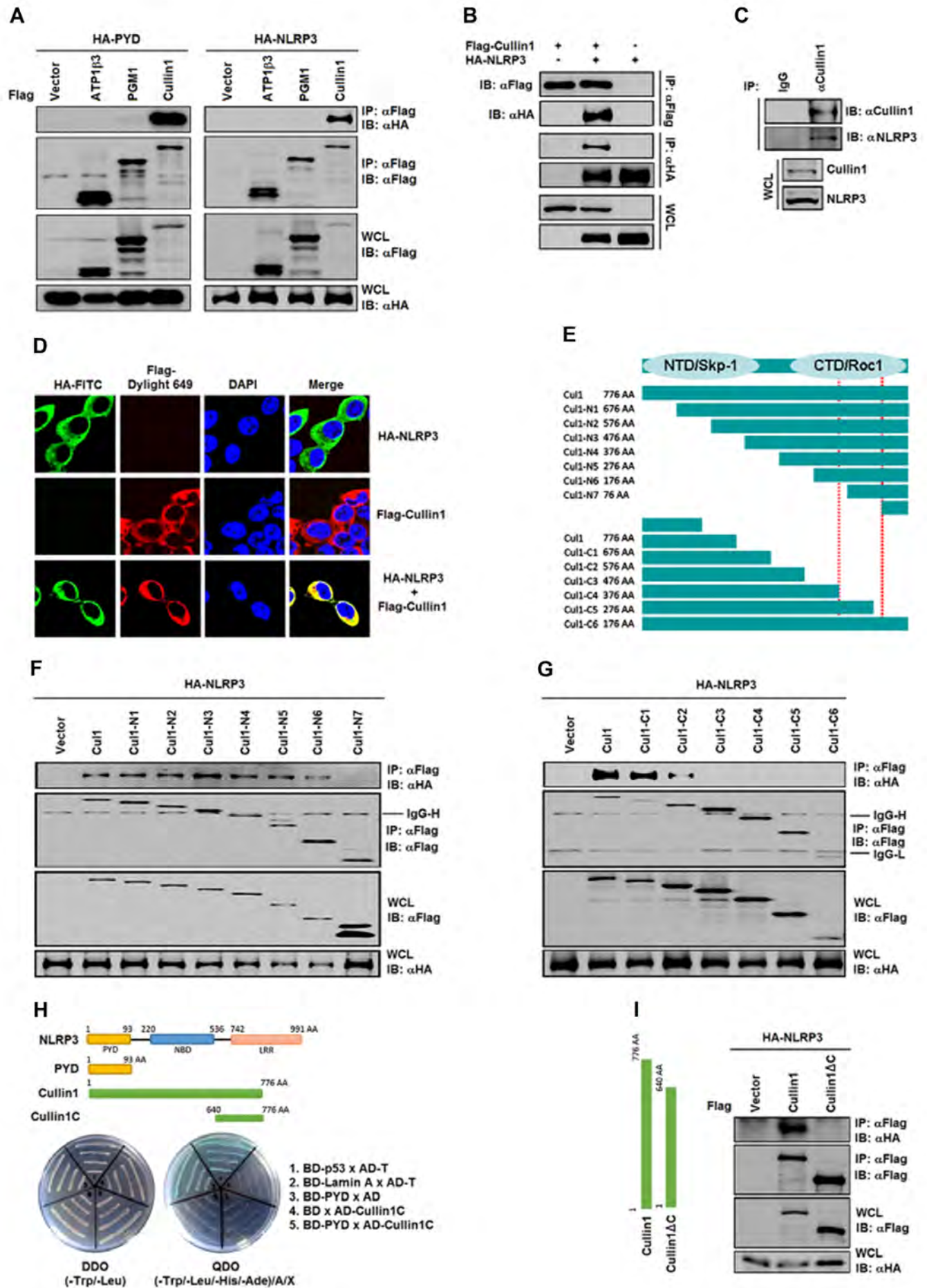
981

982 **Figure EV5 – Cullin1 can't promote degradation of NLRP3.**

983 HEK293T cells were transfected with pCAGGS-HA-NLRP3 along with control and three  
984 different quantities of pcDNA3.1(+)-3XFlag-Cullin. Lysates were immunoblotted with the  
985 indicated antibodies.

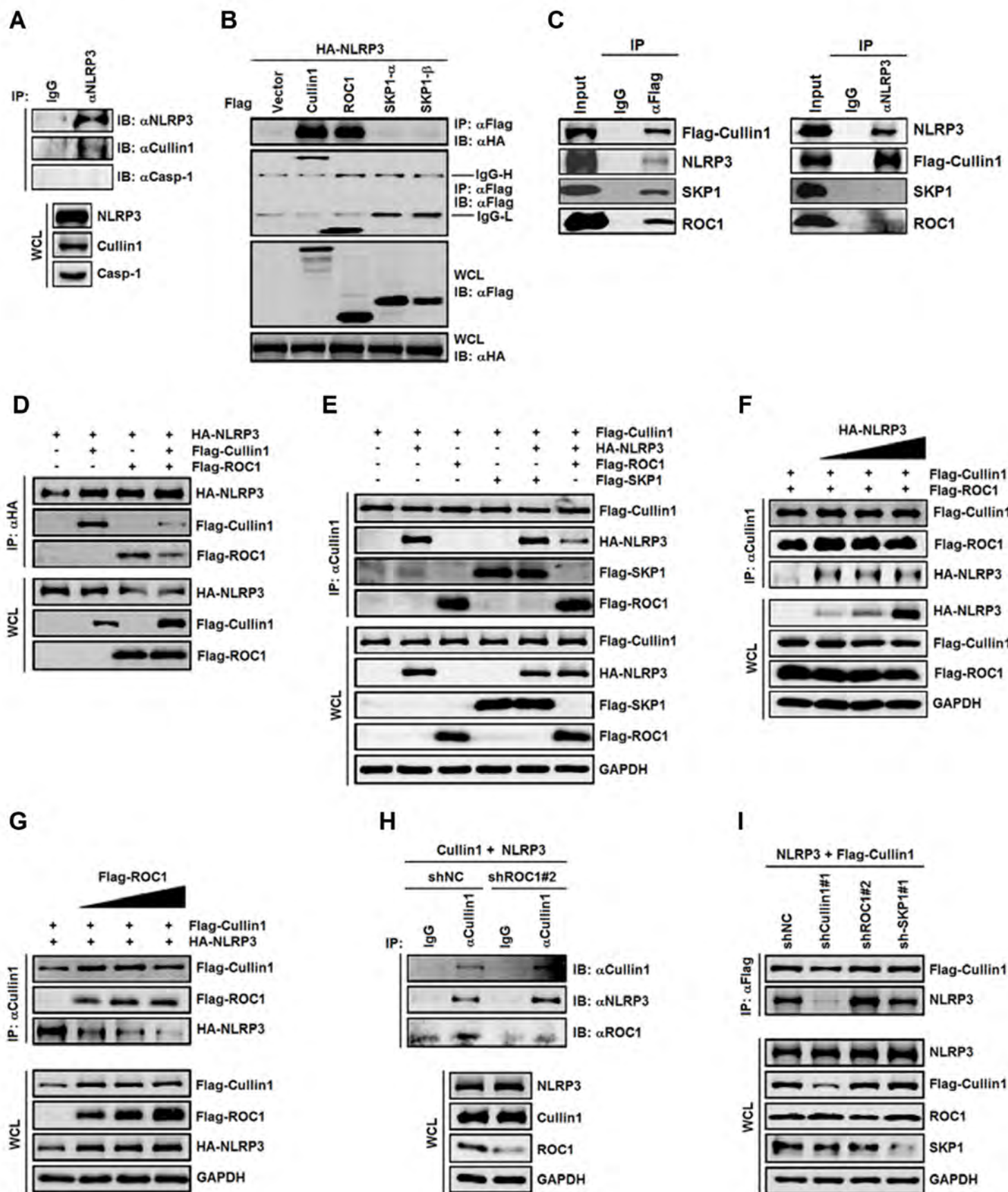
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# Figure 1

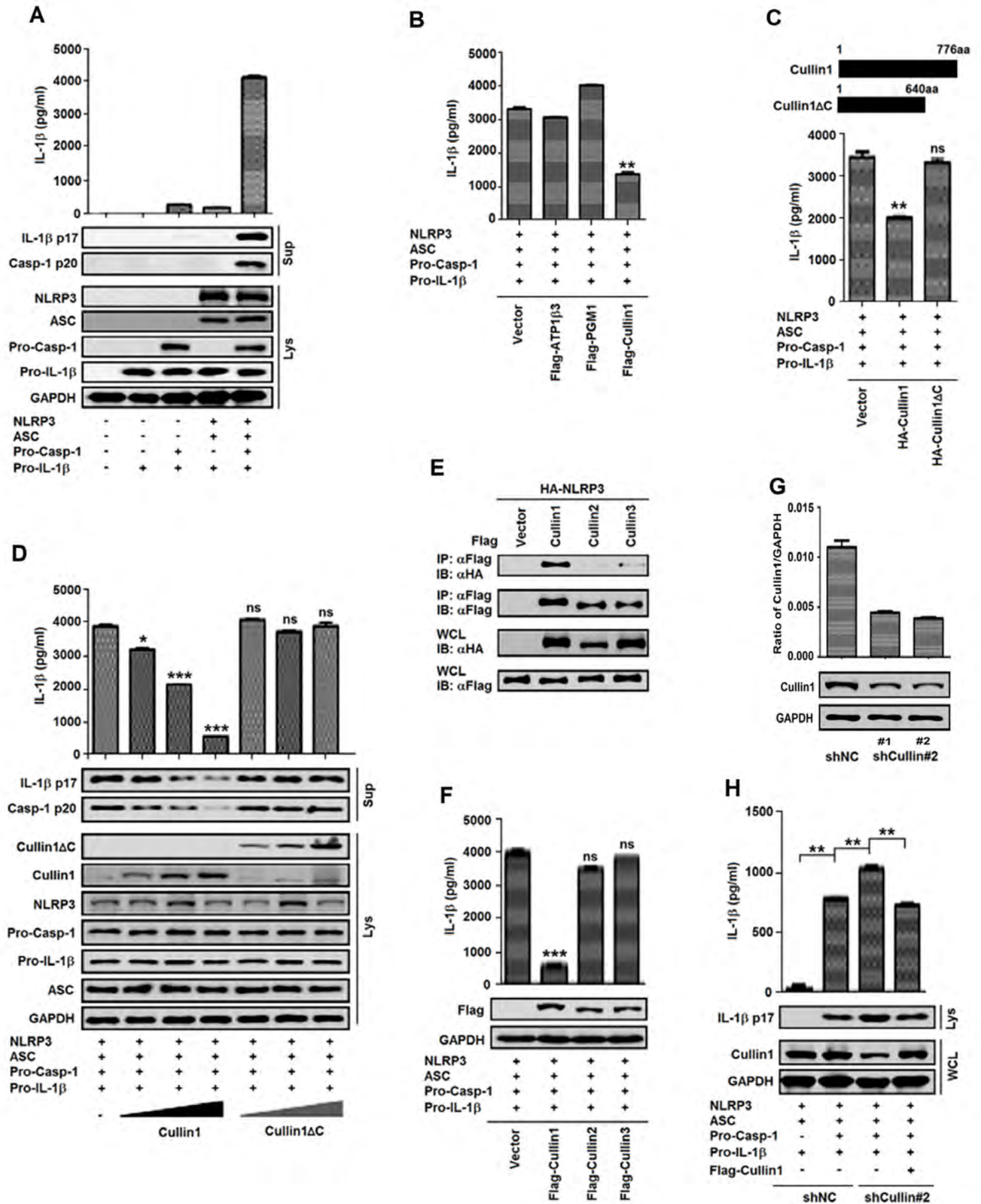




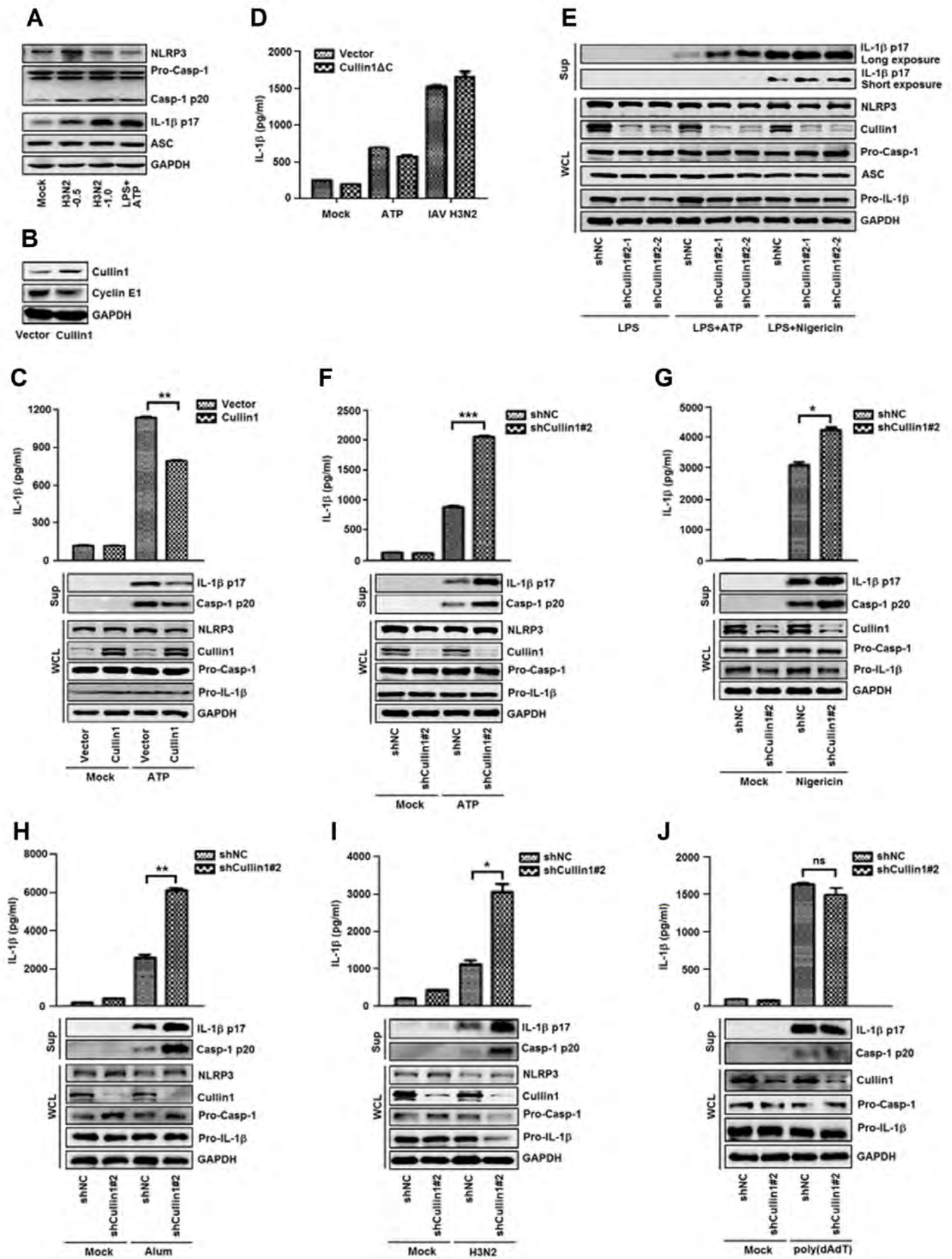
**Figure 2**



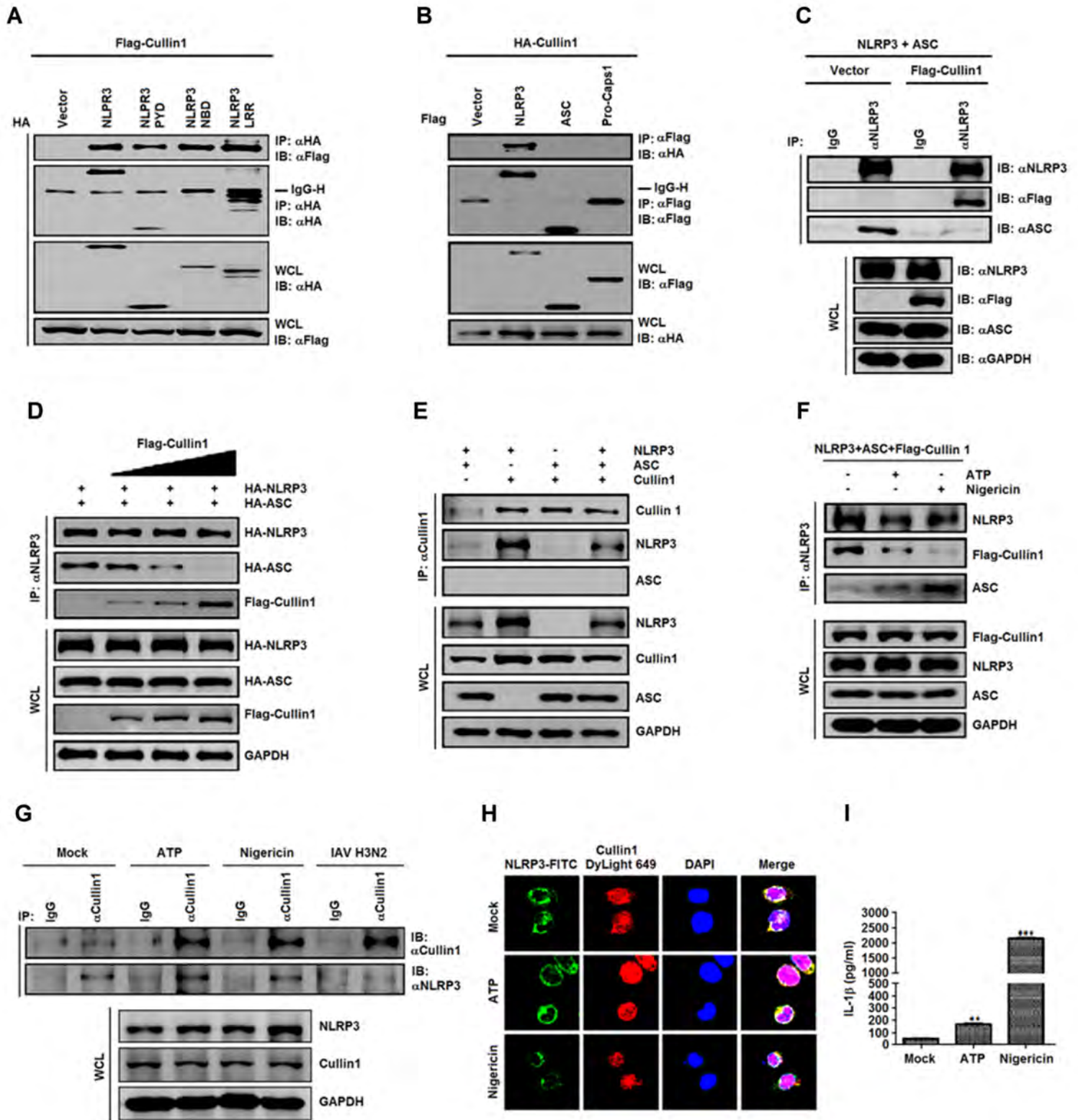
# Figure 3



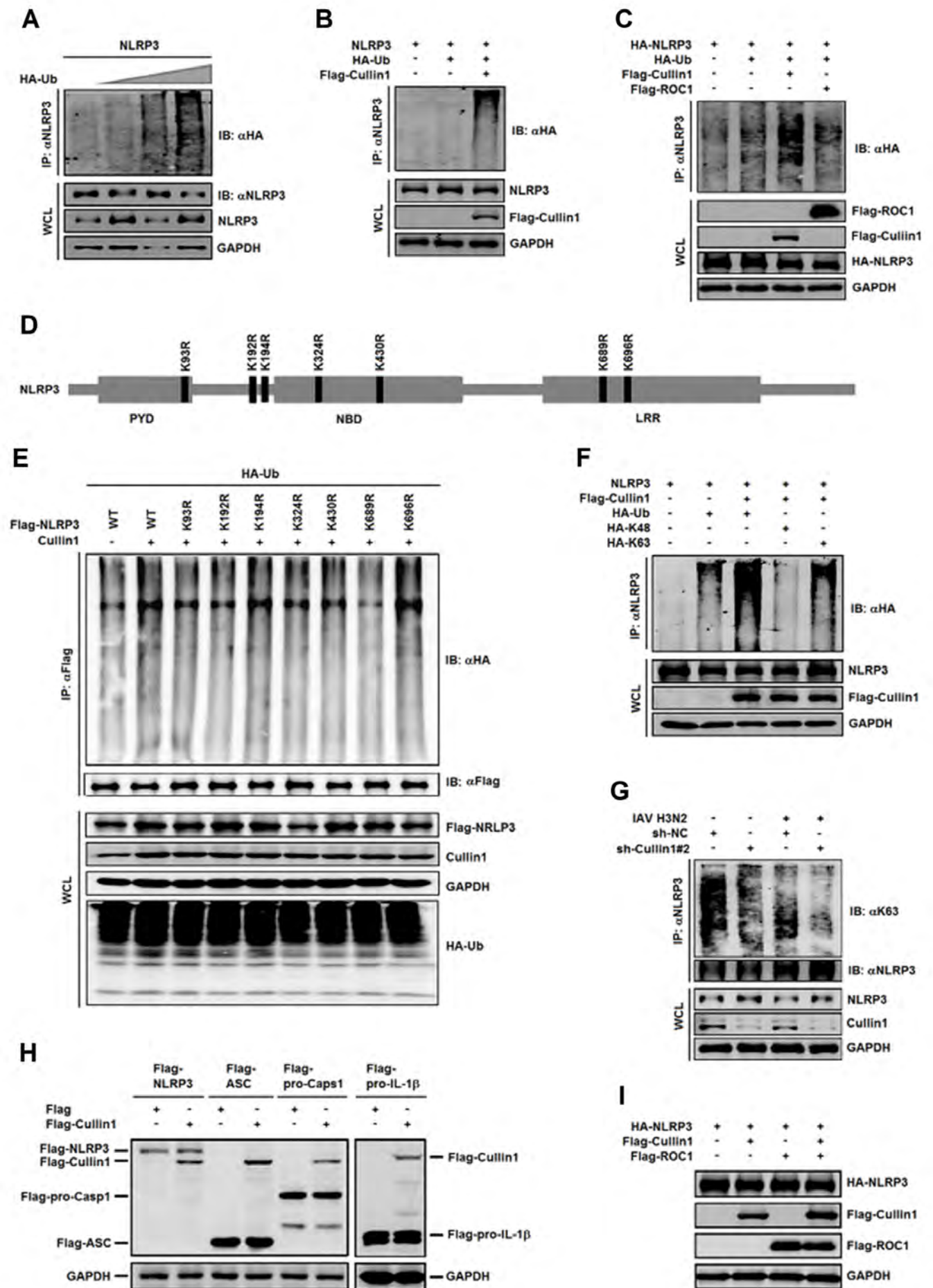
# Figure 4



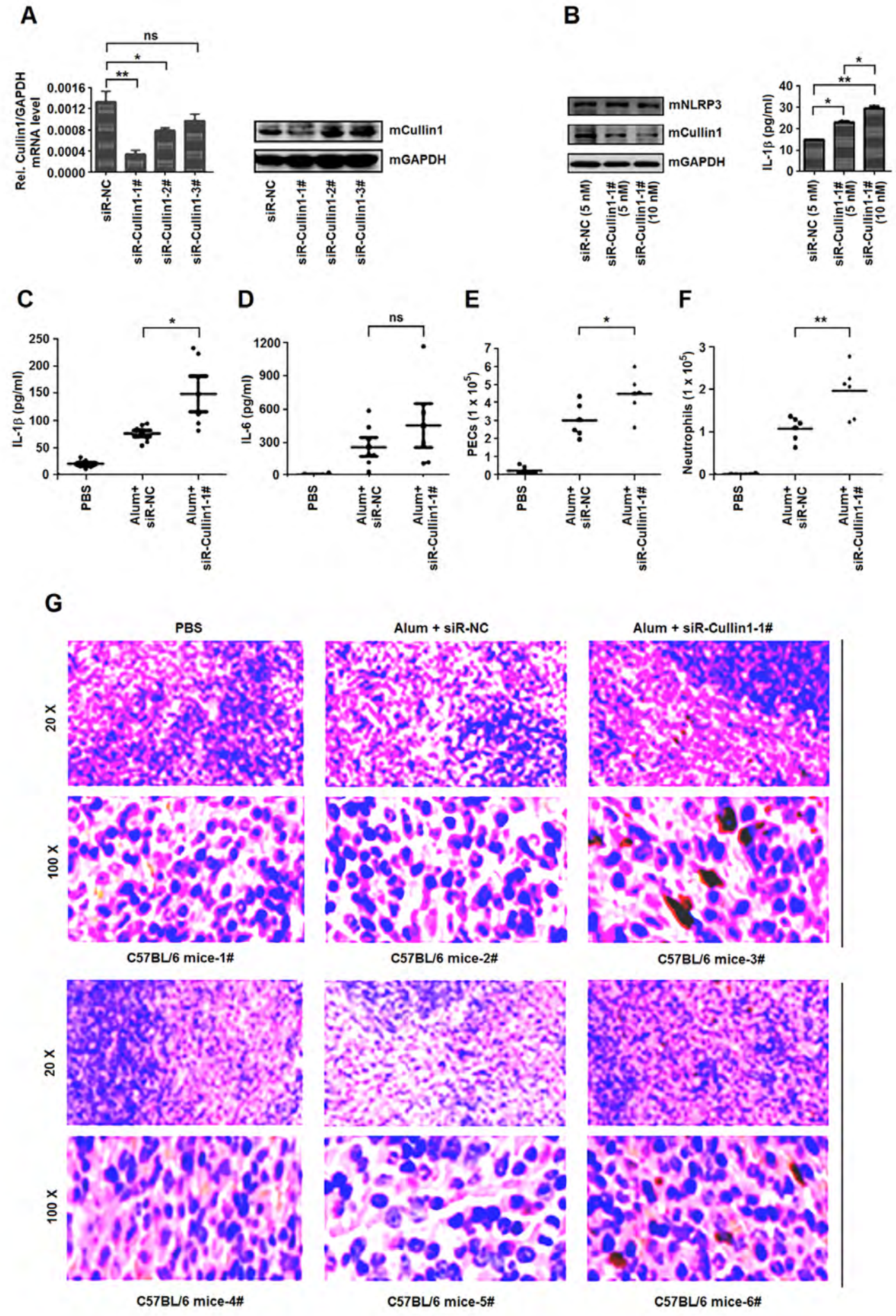
**Figure 5**



# Figure 6



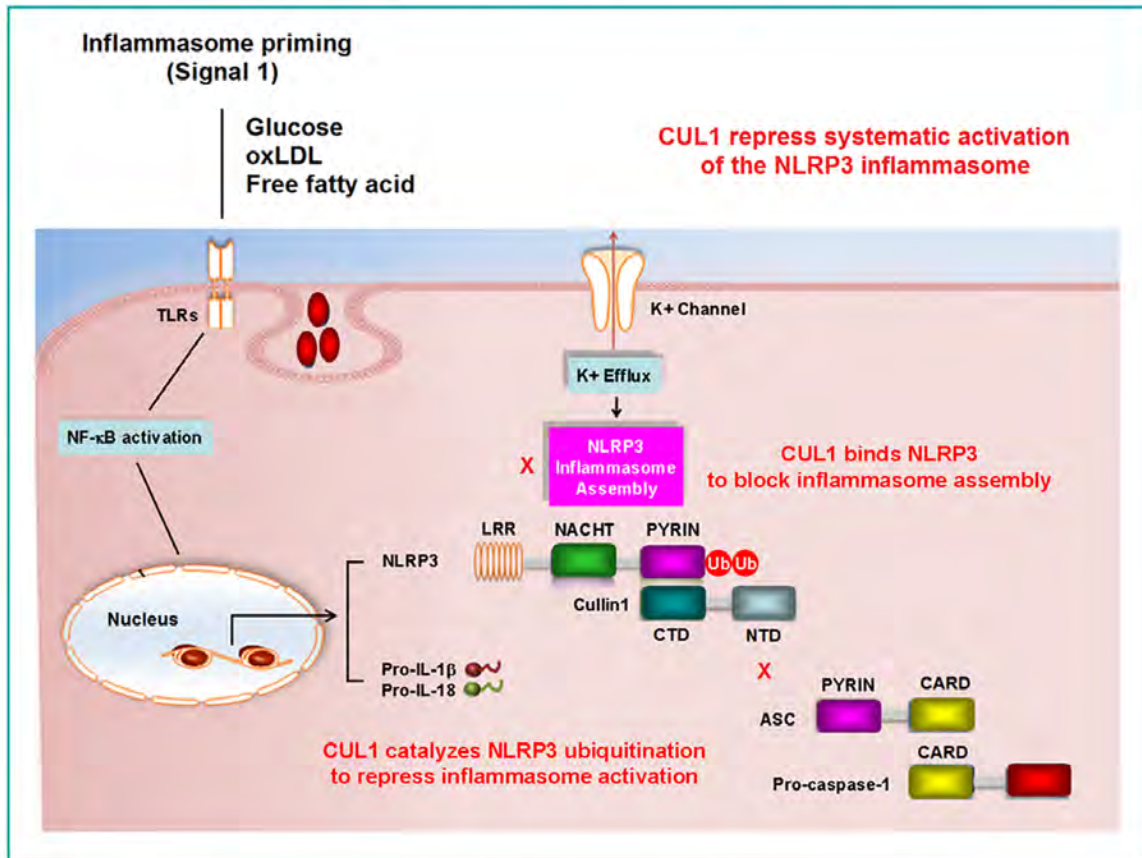
**Figure 7**



**Figure 8**

**A**

**In resting cells or under normal physiological conditions**



**B**

**In response to viral infection or inflammation stimuli**

