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***Cutibacterium acnes* infection induces type I interferon synthesis through the cGAS-STING pathway**

1 **Katrin Fischer¹, Roland Tschismarov², Andreas Pilz¹, Susy Straubinger³, Sebastian**
2 **Carotta³, Andrew McDowell⁴ and Thomas Decker^{1*}**

3 ¹Max Perutz Labs, Department of Microbiology, Immunobiology and Genetics, University of
4 Vienna, Vienna Biocenter, Vienna, Austria

5 ²Themis Bioscience GmbH, Vienna, Austria

6 ³Boehringer Ingelheim RCV GmbH & Co KG, Vienna, Austria

7 ⁴School of Biomedical Sciences, Ulster University, Coleraine, United Kingdom

8 *** Correspondence:**

9 Thomas Decker

10 Thomas.decker@univie.ac.at

11 **Keywords: *Cutibacterium acnes*, Interferon, *Listeria monocytogenes*, cGAS, STING,**
12 **TRIF, STAT, NFκB**

13 **Abstract**

14 *Cutibacterium* (previously *Propionibacterium*) *acnes* is an anaerobic, Gram-positive
15 commensal of the human body. The bacterium has been associated with a variety of diseases,
16 including acne vulgaris, prosthetic joint infections, prostate cancer and sarcoidosis. The
17 accumulation of *C. acnes* in diseases such as acne and prostate cancer has been shown to
18 correlate with enhanced inflammation. While the *C. acnes*-induced proinflammatory axis, via
19 NF-κB and MAPK signaling and inflammasome activation, has been investigated over the last
20 few decades, the potential role of *C. acnes* in triggering the type I interferon (IFN-I) pathway
21 has not been addressed. Our results show that *C. acnes* induces the IFN-I signaling axis in
22 human macrophages by triggering the cGAS-STING pathway. In addition, IFN-I signaling
23 induced by *C. acnes* strongly depends on the adapter protein TRIF in a non-canonical manner;
24 these signaling events occurred in the absence of any detectable intracellular replication of the
25 bacterium. Collectively, our results provide important insight into *C. acnes*-induced
26 intracellular signaling cascades in human macrophages and suggest IFN-I as a factor in the
27 etiology of *C. acnes*-induced diseases. This knowledge may be valuable for developing novel
28 therapies targeting *C. acnes* in diseases where the accumulation of the bacterium leads to an
29 inflammatory pathology.

30 **Introduction**

31 *Cutibacterium acnes* (previously *Propionibacterium acnes*) is an anaerobic, Gram-positive
32 bacterium that preferentially colonizes the human skin, as well as mucosal surfaces (1,2). While
33 *C. acnes* has traditionally been considered a non-pathogenic resident of the human microbiota,
34 current literature challenges this notion. In particular, *C. acnes* has been shown to play a
35 morbidic role during the inflammatory skin disease acne vulgaris (3), as well as prostate disease
36 (2,4,5) and infections following implant surgeries (6–10). The bacterium produces a range of
37 pathogenic factors, including proteases, lipases and chemotactic factors for macrophages,
38 neutrophils and lymphocytes (11), and promotes innate immune cells such as macrophages to
39 secrete inflammatory cytokines, particularly tumor necrosis factor α (TNF-α), interleukin (IL)-
40 6, IL-8, IL-12 and IL-1 family members (12–15). Deciphering how *C. acnes* triggers the innate

41 immune response can be helpful for understanding diseases where the accumulation of *C. acnes*
42 plays a role, as well as for the development of host-directed novel therapies.

43 Type I Interferons (IFN-I) contribute to many aspects of immunity with a main focus on anti-
44 viral responses (16,17). IFN-I contribute to inflammatory responses by stimulating and
45 amplifying the secretion of chemokines and other immune mediators (18). Activation of the
46 IFN system in the defense of bacterial pathogens is not always beneficial, and may have
47 detrimental effects on the host during infection with certain pathogens (18). For instance,
48 enhanced IFN-I production during *Listeria monocytogenes* (*L.m.*) infections is associated with
49 decreased innate immunity and reduced host resistance (19). In general, there are several
50 possibilities for pathogens to stimulate the interferon pathway in host cells. For example,
51 conserved structures of bacterial cell surfaces can bind and activate membrane-bound Toll-like
52 receptors (TLR), with TLR4 as the main receptor for IFN-I induction. IFN stimulation via the
53 TLR4 axis requires the adapter molecule TIR-domain-containing adapter-inducing interferon-
54 β (TRIF) (20,21). As TLR4 recognizes lipopolysaccharides (LPS) derived from Gram-negative
55 bacteria, direct recognition of *C. acnes* by TLR4-TRIF appears unlikely. However, in some
56 macrophage populations, such as those residing in the mouse peritoneum, TRIF signaling
57 connects to TLR2, thus coupling the recognition of Gram-positive bacteria at the cell surface,
58 or in endosomes, to IFN-I synthesis (22). On the other hand, host cells can react to cytosolic
59 pathogenic intrusions by recognizing either foreign RNA (RIG-I-like receptors; RLR),
60 intracellular bacterial cell surface components (NOD-like-receptors; NLR) or cytoplasmic
61 DNA (cytosolic DNA-binding sensors). Cyclic GMP-AMP synthase (cGAS) is arguably the
62 most prominent DNA sensing receptor found in the cytoplasm with relevance during bacterial
63 infections (23,24). DNA recognition by the sensor protein cGAS causes the enzyme to produce
64 cyclic GMP-AMP (cGAMP), a cyclic di-nucleotide that associates with and activates stimulator
65 of interferon genes (STING), an essential scaffold for the activation of interferon regulatory
66 factors (IRF). As essential components of active IFN-I gene promoters, IRFs play a critical role
67 in the control of IFN-I production (25). Some intracellular bacteria, most prominently *L.m.*,
68 secrete cyclic-di-nucleotides that further stimulate the adapter STING in a cGAS-independent
69 manner (26,27). The potential role of *C. acnes* in triggering the interferon signaling axis, and
70 how it compares in this regard to intracellular *L.m.*, has not been considered yet and will be the
71 main focus of this study.

72 With our results we provide evidence that the Gram-positive bacterium *C. acnes* triggers the
73 interferon signaling axis in human macrophages. In accordance with published data
74 (12,21,28,29) we demonstrate a strong inflammatory cytokine response, as well as the
75 activation of the inflammasome. We further show that infection with *C. acnes* stimulates IFN-
76 I production via the cGAS-STING pathway with a strong dependency on the adapter molecule
77 TRIF. In contrast to *L.m.*, *C. acnes*-induced interferon production shows complete dependence
78 upon the cytoplasmic DNA sensor cGAS, suggesting DNA as the only trigger. While the pro-
79 inflammatory cytokine response shows little variation between *C. acnes* strains, not all strains
80 elicit a strong interferon response. However, for the tested strains the mechanism behind the
81 induction of interferon signaling in *C. acnes* infected macrophages, is the TRIF-dependent
82 activation of the cGAS-STING pathway.

83 **Materials and Methods**

84 **Cell culture and differentiation**

85 Human monocytic THP-1 cells (ATCC #TIB-202 and Invivogen #thp-1sg) and U-937 cells
86 (ATCC #CRL-1593.2) were maintained in RPMI 1640 culture medium (Sigma-Aldrich)
87 supplemented with 10% (v/v) heat-inactivated fetal bovine serum (FBS) (Sigma-Aldrich) and
88 1% Penicillin/Streptomycin (both Sigma-Aldrich) (referred to as “complete medium”).

89 For the differentiation into macrophage-like cells, human monocytic THP-1 or U-937 cells were
90 seeded in complete medium supplemented with 100nM phorbol 12-myristate 13-acetate (PMA)
91 (Sigma-Aldrich #P1585). Cells were differentiated for 2 days at 37°C and 5% CO₂ atmosphere.
92 On the third day, media was exchanged to RPMI 1640 supplemented with 10% (v/v) FBS and
93 incubation at 37°C and 5% CO₂ was continued for an additional 24 hours.

94 HaCaT cells obtained from the German Cancer Research Center (DKFZ, Heidelberg, Germany)
95 were maintained in DMEM culture medium (Sigma-Aldrich) plus 10% (v/v) FBS and 1%
96 Pen/Strep and kept at 37°C in a 5% CO₂ atmosphere. Cells were split twice a week by washing
97 once with PBS, incubating for 10 minutes with 0.05% EDTA in PBS at 37°C followed by a 10
98 minutes incubation with Trypsin-EDTA at 37°C.

99 **Isolation of PBMCs and monocytes from human blood**

100 Peripheral blood mononuclear cells (PBMC) were isolated by density gradient centrifugation
101 with LymphoprepTM (StemCell Technologies, #07851) from fresh buffy coats of three healthy
102 donors received from the Austrian Red Cross. Erythrocytes were removed using ACK lysing
103 buffer (Gibco, #A10492-01). After 3 washing steps, cell viability was measured (viability above
104 95%). Next, monocytes were isolated from PBMCs by negative selection using EasySepTM
105 Human Monocyte Isolation Kit (StemCell Technologies, #19359) showing a viability above
106 91%. Monocytes were seeded on the same day in RPMI 1640 plus 10% (v/v) FBS and infected
107 the following day.

108 **Differentiation of primary monocytes into monocyte-derived macrophages**

109 Primary monocytes were seeded on the day of isolation in complete medium in 6-well plates.
110 For differentiation, cells were stimulated with 100ng/ml of recombinant human M-CSF (a kind
111 gift from L. Ziegler-Heitbrock, Helmholtz Center, Munich, Germany). At day 4, media were
112 refreshed (complete medium plus M-CSF). On day 6, media were exchanged to medium
113 containing only 10% (v/v) FBS. Infection experiments were performed with primary monocyte-
114 derived macrophages at day 7.

115

116 **Bacterial preparation and infection**

117 All *C. acnes* strains were cultured in brain-heart-infusion (BHI) media (BD Bioscience) at 37°C
118 under anaerobic conditions using BD GasPakTM (BD Bioscience). Bacteria were collected at
119 exponential growth phase (around 24 hours after inoculation), washed twice with 1x phosphate
120 buffered saline (PBS) and resuspended in RPMI 1640 supplemented with FBS. All
121 centrifugation steps were performed at 10,000xg for 5 minutes. The following strains were
122 used: NCTC737 (phylotype IA₁; ATCC6919); *P. acn*31 (phylotype IA₂); KPA171202
123 (phylotype IB; DSM16379); PV66 (phylotype IC); ATCC11828 (phylotype II); Asn12
124 (phylotype III) (see Table S1). Infection was performed with a multiplicity of infection (MOI)
125 of approximately 50. At different time-points, cells were washed twice with 1x PBS and lysed
126 for either RNA or protein isolation.

127 *L.m.* strain LO28 and the LLO-deficient strain LO28 Δ *hly* were grown overnight in BHI media
128 at 37°C with continuously shaking. After reaching stationary phase, bacteria were washed twice
129 with 1x PBS and resuspended in RPMI 1640 supplemented with 10% (v/v) FBS. Centrifugation
130 was performed at 10,000xg for 5 minutes. Cells were infected with a MOI of approximately 40
131 for 1 hour at 37°C. Media was exchanged to RPMI 1640 supplemented with 10% (v/v) FBS
132 and 50 μ g/ml gentamycin (MP Biomedicals, Santa Ana, US). After one more hour, media was
133 replaced with RPMI 1640 supplemented with 10% (v/v) FBS and 10 μ g/ml gentamycin. After
134 different time-points, cells were washed twice with 1x PBS and lysed for RNA or protein
135 isolation.

136 LPS (Sigma-Aldrich #L2637) was used at a final concentration of 0.4µg/ml.

137 **Colony-forming-unit (CFU) assay**

138 THP-1 and U-937 cells were seeded in 96-well plates and differentiated using PMA (see above).
139 Cells were infected with *C. acnes* strain NCTC737, P. acn31, KPA171202, PV66, ATCC11828
140 and Asn12 or *L.m.* strain LO28 or *L.m.* mutant strain LO28 Δ hly. After 1-hour post infection,
141 media of all wells was exchanged to RPMI 1640 supplemented with 10% (v/v) FBS and
142 50µg/ml gentamycin. After another hour, media was replaced by RPMI 1640 supplemented
143 with 10% (v/v) FBS and 10µg/ml gentamycin. After each timepoint, cells were washed twice
144 with 1x PBS. Subsequently, cells were burst open by adding sterile nuclease-free water.
145 Dilution series was made, and bacteria plated on either Brucella blood agar (*C. acnes*;
146 bioMérieux Austria GmbH) or BHI plates (*L.m.*). Brucella blood agar plates were incubated for
147 3 days at 37°C under anaerobic conditions. BHI plates with *L.m.* were kept for 1.5 days at 37°C.

148 **RNA isolation, cDNA synthesis and RT-qPCR**

149 Total RNA isolation was performed using the NucleoSpin RNA II kit (Macherey-Nagel,
150 Catalog #740955). For the synthesis of cDNA, Oligo (dT18) primer and RevertAid Reverse
151 Transcriptase (both Thermo-Fisher Scientific) were used. Real-time quantitative-PCR was run
152 on Eppendorf Mastercycler using SybrGreen (Promega Catalog # A6002). Primers for real-time
153 qPCR are listed in Table S2.

154 **Western blot**

155 THP-1 cells were lysed in Laemmli buffer (120mM Tris-HCl, pH 8, 2% SDS and 10% glycerol)
156 and protein concentrations measured using Pierce™ BCA Protein Assay kit (Thermo-Fisher
157 Scientific). A total of 20µg of protein were resuspended with SDS-loading dye (50% β -
158 Mercaptoethanol, 0.02% Bromphenolblue), boiled and loaded on a 10% SDS polyacrylamide
159 gel. Proteins were transferred on a nitrocellulose or PVDF membrane for 16 hours at 200mA
160 and 2 hours at 400mA at 4°C using a carbonate transfer buffer (3mM Na₂CO₃, 10mM NaHCO₃
161 and 20% ethanol). Afterwards, membranes were blocked in 5% (w/v) milk powder in TBS-T
162 for 1-2 hours at room temperature. Membranes were incubated with the appropriate primary
163 antibody overnight at 4°C while shaking: α -Tubulin (Sigma Aldrich, Catalog # T9026, 1:5000);
164 GAPDH (Millipore, Catalog # ABS16, 1:3000); STAT1 (Santa Cruz, Catalog # SC346,
165 1:1000); Phospho-STAT1 (Tyr701; Cell signaling, Catalog # 9167, 1:1000); IRF9 (Santa Cruz,
166 Catalog # sc10793, 1:1000); I κ B- α (Cell signaling, Catalog #9242, 1:1000); MyD88 (Cell
167 signaling, Catalog # 4283, 1:1000); TRIF (Cell signaling, Catalog # 4596, 1:1000); STING
168 (Cell signaling, Catalog # 13647, 1:1000); cGAS (Cell signaling, Catalog # 15102, 1:1000).
169 The membrane was then washed three times with TBS-T before incubating for 1-2 hours at
170 room temperature with the appropriate secondary antibody (Jackson ImmunoResearch Inc.,
171 Catalog # 111-035-003, 1:6000 and Catalog # 115-035-144, 1:6000). After three washing steps
172 with 1x TBS-T, the membrane was incubated with SuperSignal West Pico Chemiluminescent
173 substrate (Thermo-Fisher Scientific) and developed using the ChemiDoc™ Imaging system
174 from Bio-Rad.

175 **Luminex assay**

176 ProcartaPlex Mix&Match human 8-plex from Affymetrix eBioscience was used for measuring
177 cytokine levels in the supernatant of *C. acnes* infected and uninfected cells. Protein levels were
178 measured at Affymetrix eBioscience, Campus Vienna Biocenter 2, 1030 Vienna. The kit was
179 used according to the manufacturer's specifications.

180 **THP1 ISG reporter activity**

181

182 Wildtype THP1-BlueTM ISG cells were differentiated in a 96-well plate (5x10⁴ cells/well) with
183 PMA as described above. Cells were infected with either *L.m.* strain LO28 or *C. acnes* strains
184 NCTC737 and Asn12 or stimulated with 0.4μg/ml LPS for either 24, 48 or 72 hours. After each
185 time-point, 20μl of the supernatant was added to 180μl of QUANTI-BlueTM solution
186 (Invivogen, Cat. # rep-qbs) in a flat-bottom 96-well plate and incubated at 37°C. Absorbance
187 at 620nm was measured using BioTek Synergy H1 Plate reader.
188

189 **Genome-editing via CRISPR-Cas9 system**

190 The guide RNAs of human *MYD88*, *TICAM1* (gene encoding human TRIF) and *IRF9* were
191 designed using Broad Institute GPP Web Portal
192 (<https://portals.broadinstitute.org/gpp/public/analysis-tools/sgrnadesign>). *LacZ* gRNA (non-
193 targeting control) (TGCGAATACGCCACGCGAT), *MYD88* gRNA
194 (TGTCTCTGTTCTTGAACGTG); *TICAM1* gRNA (GGAGAACCATGGCATGCAGG);
195 *IRF9* gRNA (ATACAGCTAAGACCATGTTC; published in Platanitis et al. (2019) (30)).
196 Oligos were ligated into the LentiCRISPRv2 plasmid. LentiCRISPRv2 was a gift from Feng
197 Zhang (Add gene plasmid # 52961; <http://n2t.net/addgene:52961>; RRID:Addgene_52961) (31).
198 THP-1 cells were transduced, and single cells selected.

199 Vector for the guide RNAs of human *TMEM173* (gene encoding human STING) and *CGAS*
200 were ordered from Sigma-Aldrich (U6gRNA-Cas9-2A-GFP-TMEM173 and U6gRNA-Cas9-
201 2A-GFP-MB21D1). *TMEM173* gRNA (GGGCCGACCGCATTTGGGAGGG); *CGAS* gRNA
202 (CGTCGGGCTGCTGAACACCGGG).

203 **Statistical information**

204 Data derived from RT-qPCR represent the mean values in a min/max box plot. Differences in
205 mRNA expression were compared using the two-tailed unpaired t-test of the log transformed
206 values. Differences in bacterial loads (CFU) were compared using the two-tailed unpaired t-
207 test. All statistical analysis was performed using GraphPad Prism. P-values: ns P > 0.05; *P ≤
208 0.05; **P ≤ 0.01; ***P ≤ 0.001. Number of biological replicates is stated in the corresponding
209 figure legend.

210 **Results**

211 ***C. acnes* intracellular degradation in human macrophages**

212 In order to analyze the ability of *C. acnes* to survive and/or replicate inside of its host cell, we
213 performed a CFU assay with *C. acnes*, as well as with the Gram-positive bacteria *L.m.* whose
214 intracellular fate is well studied (32–34). *L.m.* is an invasive bacterium that escapes the host
215 phagosome using the pore-forming toxin listeriolysin O (LLO). Recent literature suggests that
216 *C. acnes* may have developed strategies to neutralize phagosomes in order to survive or even
217 leave the phagosome without being targeted for degradation by bactericidal effector
218 mechanisms (35). For direct comparison, we included a mutant strain of *L.m.* (Δhly , lacking
219 LLO) that is rapidly degraded by the host cell. Indeed, while the load of wildtype *L.m.* increased
220 immensely over a period of 24 hours (Figure 1A, Supplementary Figure 1A), survival and/or
221 propagation of the Δhly strain was prevented by both THP-1 and U-937 cells in a similar time
222 period (Supplementary Figure 1B). *C. acnes* reference strain NCTC737 (phylotype IA₁) on the
223 other hand showed results comparable to the LLO mutant strain suggesting that THP-1 and U-
224 937 cells are indeed able to control *C. acnes* infections (Figure 1A, Supplementary Figure 1A).
225 A similar pattern could be observed after infection with strains representing each *C. acnes*
226 phylotype, suggesting a strain-independent host mechanism for *C. acnes* degradation in THP-1
227 cells (Figure 1B).

228 ***C. acnes* stimulates an IFN-I response in human macrophages**

229 We characterized the innate response to *C. acnes* infection by determining the production of
230 typical innate cytokines by PMA-differentiated human THP-1 macrophages (Figure 2). *C.*
231 *acnes* strain NCTC737 (phylotype IA₁) induced the expression of pro-inflammatory (TNF- α ,
232 IL-1 β , IL-1 α and IL-6) and anti-inflammatory (IL-10) cytokines (Figure 2A). Furthermore, *C.*
233 *acnes*-infected THP-1 cells showed an increased secretion of IL-1 β protein, confirming *C.*
234 *acnes*-induced inflammasome activation as published by Qin et al. (2014) (Figure 2B) (28). The
235 induction of inflammatory cytokines at the mRNA level correlated with the secreted protein
236 level in the supernatant of infected cells. Interestingly, alongside a strong pro-inflammatory
237 cytokine response, we observed an elevated expression of IFN- β as well as type I IFN-
238 stimulated genes (ISGs), such as Interferon-induced GTP-binding protein Mx1 (MX1) and
239 Interferon-induced protein with tetratricopeptide repeats 1 (IFIT1) in *C. acnes* infected THP-1
240 cells in the delayed phase of infection. This indicates that *C. acnes* not only activates an
241 inflammatory response in human macrophages, but in addition triggers a type I IFN signature.

242 Comparing the cytokine response caused by infection with different strains of *C. acnes* (one
243 strain of each phylotype) we did not observe any major differences in the amounts of
244 inflammatory cytokine mRNAs. In contrast, the IFN-I-induced genes *MX1* and *IFIT1* differed
245 vastly between strains (Figure 2C). Especially *C. acnes* strain Asn12 (phylotype III), which has
246 been recently associated with the skin disease macular hypomelanosis (36), was remarkably
247 potent in inducing ISG transcription. Thus, although *C. acnes* induced inflammatory cytokine
248 response seems to be strain independent, the induction of ISGs differs when comparing various
249 phlotypes.

250 Among the induced cytokines of figure 2B, IL-6 is controlled by both NF κ B and IFN-I
251 pathways (37), suggesting a potential contribution of IFN-I to cytokine secretion during *C.*
252 *acnes* infection. To determine whether IFN-I activity alone suffices for the detection of secreted
253 gene products we used THP1-BlueTM ISG cells that monitor the interferon signaling pathway
254 and its master transcription factor, the ISGF3 complex, through the stable integration of a
255 secreted embryonic alkaline phosphatase (SEAP) reporter. Specifically, the reporter gene is
256 under an ISG54 minimal promoter with five IFN-stimulated response elements (ISREs).
257 Secreted SEAP can be detected by QUANTI-BlueTM colorimetric enzyme assay. While
258 stimulation with LPS and infection with *L.m.* showed high IFN-induced SEAP levels in the
259 supernatant of cells infected for both 24 to 72 hours, absorbance increased over time with *C.*
260 *acnes* strain Asn12 (Figure 2D). In line with the mRNA expression of ISGs and IFN- β , cells
261 infected with *C. acnes* strain NCTC737 released significantly smaller quantities of SEAP.

262 To corroborate our findings with data from primary cells, we analyzed the expression of pro-
263 inflammatory cytokines and type-I IFN signaling in primary monocytes from three different
264 donors. While mRNA expression of the pro-inflammatory cytokine TNF- α and IL-1 β were
265 greatly induced upon infection with either *L.m.* or *C. acnes* strains NCTC737 or Asn12 as well
266 as upon stimulation with LPS, the induction of a type-I IFN response was only upregulated
267 upon LPS treatment which could neither be seen with *L.m.* nor with any of the two *C. acnes*
268 strains used (Supplementary Figure S2A). On the other hand, M-CSF-differentiated monocyte-
269 derived macrophages (MDMs) from the same donors strongly induced the expression of IFN-
270 β as well as MX1 in addition to a robust inflammatory cytokine response shown by elevated
271 mRNA expression of TNF- α and IL-1 β (Figure 3A). In addition, infection of primary MDMs
272 with *L.m.* induced the phosphorylation of STAT1 on Tyr701 at 6 and 24 hours post infection
273 (Figure 3B). In line with the mRNA expression of IFN- β as well as MX1, we observed a strong
274 phosphorylation of STAT1 at Tyr701 with *C. acnes* strain Asn12 and a much weaker signal
275 with NCTC737.

276 As *C. acnes* is a commensal of the human skin, we were interested in the inflammatory cytokine
277 response as well as the IFN-I signature in human keratinocytes. Thus, we infected the human
278 keratinocyte cell line HaCaT with either *L.m.*, *C. acnes* strain Asn12 or stimulated them with
279 LPS for 48 hours. Compared to macrophages, HaCaT cells showed only a minor induction of
280 cytokine expression upon infection, even with our positive controls *L.m.* and LPS
281 (Supplementary Figure S2B). Although *L.m.* as well as Asn12 induced mRNA expression of
282 TNF- α , IL-6, MX1 and IFIT1, the levels were only slightly above the basal state. Taken
283 together, differentiated THP-1 cells as well as primary human macrophages induce an IFN-I
284 signature as well as a strong inflammatory response upon infection with *C. acnes*.

285 **Multiple intracellular pathways contribute to cytokine production by *C. acnes*-infected** 286 **cells**

287 Cytokine expression in infected cells is initiated by signals from cell surface or endosomal
288 TLRs as well as cytoplasmic nucleic acid receptors and inflammasomes (21). We sought to
289 determine the signals targeting inflammatory cytokines and IFN-I in *C. acnes*-infected cells by
290 studying cells deficient for either myeloid differentiation primary response 88 (MyD88) or
291 TRIF (Figure 4A-C, Supplementary Figure S3A), the eponymous adapters for the major
292 pathways downstream of TLR. Recent experimental evidence shows that *C. acnes* is recognized
293 by a TLR2/6 heterodimer in human keratinocytes (29), which signals via the adapter molecule
294 MyD88 to stimulate the expression of inflammatory cytokines. Consistent with this, a knockout
295 of MyD88 in THP-1 cells completely abolished the expression of the inflammatory cytokines
296 TNF- α and IL-1 β upon infection with *C. acnes*, *L.m.*, or LPS (Figure 4A). In line with the
297 mRNA expression of inflammatory cytokines, cells lacking MyD88 were not able to degrade
298 I κ B- α , the inhibitor of the transcription factor nuclear factor 'kappa-light-chain-enhancer' of
299 activated B-cells (NF- κ B), upon infection with either *C. acnes* or *L.m.* (Figure 4B-C). Deletion
300 of TRIF slightly reduced TNF- α mRNA synthesis, but strongly increased that of IL-1 β . This
301 suggests a negative feed-back of the TRIF pathway on IL-1 β mRNA production through the
302 MyD88 pathway.

303 Unlike the inflammatory cytokines, IFN-I-dependent STAT1 phosphorylation and ISG
304 induction by either *C. acnes* or *L.m.* remained largely unaffected by the absence of MyD88. In
305 stark contrast, the knockout of adapter molecule TRIF strongly reduced ISG induction and
306 STAT1 Tyr701 phosphorylation upon infection with *C. acnes* or *L.m.* (Figures 4A-C). This
307 finding was surprising given the complete independence of *L.m.*-induced IFN-I production in
308 mouse bone marrow-derived macrophages (38). To examine whether the involvement of TRIF
309 reflected signaling through a non-canonical, endosomal TLR2-TRIF pathway as recently
310 observed in mouse peritoneal macrophages infected with *L.m.* (22), we infected THP-1 cells
311 with the escape deficient *L.m.* strain Δhly . LLO-deficient *L.m.* were still capable of inducing
312 the pro-inflammatory response via the TLR2 axis (TNF- α and IL-1 β mRNA), however, they
313 were unable to stimulate IFN-I signaling as shown by the mRNA expression of MX1 and IFIT1
314 (Figure S3B). This result suggests that *L.m.*-induced ISG expression in THP-1 cells is
315 independent of TLR-TRIF signaling, however, dependent on the adapter TRIF in a different
316 signaling context.

317 IFN-I exert gene control via canonical and noncanonical mechanisms (39). The canonical mode
318 requires formation of the interferon-stimulated gene factor 3 (ISGF3) complex, a trimeric
319 protein complex consisting of STAT1, STAT2 and IRF9. We used IRF9 knockout THP-1 cells
320 to examine whether the expression of MX1 and IFIT1 was induced by the canonical IFN-I
321 signaling pathway in *C. acnes*-infected cells. Indeed, a knockout of IRF9 completely abolished
322 the expression of ISGs upon infection with *C. acnes* whereas it did not affect the
323 proinflammatory cytokine response (Figure 4D, Supplementary Figure S3C). Thus, *C. acnes*
324 induced IFN-I signaling occurs via the canonical type I IFN pathway.

325 ***C. acnes*-induced type I IFN signaling requires a cGAS-STING pathway**

326 To further interrogate the role of TRIF in IFN-I production, we investigated the role of STING
327 and its upstream regulator cGAS. These studies were in accordance with a recent report
328 demonstrating a TRIF requirement for STING signaling in cells infected with herpes simplex
329 virus (40).

330 Unlike wildtype cells, ISG induction in response to infection with either *C. acnes* or *L.m.* was
331 not detected in THP-1 cells lacking STING (Supplementary Figure S4A, Figure 5A). The
332 complete lack of a response to IFN-I confirms the absence of TLR2-TRIF signaling, which is
333 independent of STING. As expected, IFN signaling in LPS-stimulated cells was independent
334 of STING signaling as we observed a slight increase in ISG expression. These results were
335 corroborated by showing that the phosphorylation of STAT1 on tyrosine 701 is strongly
336 reduced in both *C. acnes* and *L.m.*-infected cells lacking the adapter STING (Figure 5B-C). In
337 contrast, the degradation of the NF- κ B inhibitor I κ B- α in wildtype and knockout cells was
338 similar. These results demonstrate that *C. acnes* induced type I IFN signaling is dependent on
339 the adapter STING, which is positively regulated by the adapter TRIF.

340 When infected with *C. acnes*, cGAS-deficient THP-1 cells revealed an essential function of the
341 DNA sensor for the induction of ISG expression, very similar to the STING knockouts (Figure
342 6A). *L.m.* on the other hand was capable of ISG induction in absence of cGAS. This is in
343 accordance with published data showing that *L.m.* is able to stimulate STING in a cGAS-
344 independent manner (26,27). Interestingly, cGAS independence was much less pronounced
345 when IFN- β synthesis was measured at earlier time points (41). This raises the possibility that
346 cyclic di-nucleotides produced by *L.m.* accumulate to generate cGAS-independence of STING
347 activation at delayed stages of infection.

348 In order to determine whether IFN signaling via the cGAS/STING pathway is generally
349 employed by *C. acnes* to stimulate an IFN-I response independently of the phylotype, we
350 performed infection experiments with *C. acnes* strain Asn12, the most potent IFN-I inducer
351 (Figure 2C), in cells lacking either cGAS or STING. As depicted in Figure 6B, *C. acnes* strain
352 Asn12 strongly induced ISG expression in wildtype cells. However, ISG expression was lost in
353 cells lacking either cGAS or STING. Taken together our results suggest TRIF-dependent
354 cGAS-STING signals in a default pathway of IFN synthesis in *C. acnes*-infected human
355 macrophages (Figure 7).

356 ***C. acnes* intracellular degradation is independent of inflammatory cytokine and type I**
357 **IFN response**

358 Cytokines shape the local inflammatory environment of a cell, but they can also influence the
359 establishment of cell-autonomous immunity. To determine whether pro-inflammatory cytokine
360 and/or interferon responses impact on effector mechanisms that influence bacterial growth we
361 performed CFU assays with wildtype cells or cells lacking either MyD88, TRIF, STING or the
362 ISGF3 subunit IRF9. As depicted in Figure 8A, *C. acnes* recovery from infected THP-1 cells
363 did not significantly differ when comparing wildtype versus any of the knockout cells. Contrary
364 to *C. acnes*, the intracellular growth of *L.m.* was curtailed by the MyD88-dependent
365 proinflammatory response (Figure 8B). This differs from results obtained in mouse bone
366 marrow-derived macrophages (42). Surprisingly, the knockout of TRIF reduced the growth of
367 *L.m.* whereas such an effect was not observed when IFN-I synthesis or response was abrogated
368 by the knockouts of STING or IRF9. This suggests that an IFN-independent activity of TRIF
369 blunts the ability of THP-1 cells to restrict *L.m.* growth. Taken together, our data show that
370 reduced proinflammatory cytokine or IFN-I synthesis fails to make macrophages permissive

371 for intracellular growth of *C. acnes*, and that the TLR adaptors MyD88 and TRIF impinge on
372 *L.m.* replication in opposing manners.

373 Discussion

374 Infection with *C. acnes* is associated with a variety of diseases ranging from inflammatory acne
375 lesions of the skin to prostate disease, soft-tissue infections and sarcoidosis. The latter disease,
376 characterized by bouts of inflammation in a variety of different organs, has been genetically
377 correlated with single-nucleotide polymorphism (SNPs) in the nucleotide binding domains of
378 the genes encoding the intracellular pattern recognition receptor NOD1 (43). The deposition
379 and survival of *C. acnes* in internal organs was proposed to result from its ability to survive in
380 circulating monocytes and epithelial cells [reviewed in (44)]. The pathogenesis of the human
381 skin disorder acne vulgaris is believed to occur from altered keratinization (45), as well as
382 elevated sebum production (46), leading to proliferation of *C. acnes* in the human hair follicle
383 (15,47). While the association of *C. acnes* with acne (3) and post-surgical implant infection (6–
384 10) is well-described, its intracellular fate and means of inducing innate immune signaling
385 pathways is still not fully understood.

386 It has previously been shown that *C. acnes* induces a strong inflammatory response *in vitro*
387 from THP-1, as well as U937 monocytes (12), which is consistent with data showing that
388 inflammatory acne lesions have an elevated expression of cytokines such as IL-1 β , TNF- α and
389 IL-10 compared to uninvolved adjacent skin (48). We now extend these studies to primary
390 human monocytes as well as monocyte-derived macrophages. The data clearly show that the
391 ability to induce IFN-I synthesis is a property of differentiated macrophages much more than
392 of their monocyte progenitors. As *C. acnes* is a Gram-positive bacterium, several studies have
393 focused on the recognition of the *C. acnes*' peptidoglycan (PG) layer by intracellular NOD
394 receptors (43) and membrane-bound Toll-like receptors, particularly TLR2, 1 and 6 (29,49,50).
395 While there is a clear understanding that *C. acnes* triggers inflammatory cytokine expression
396 via heterodimers of TLR2 with TLR1 or 6, followed by the activation of the NF- κ B as well as
397 mitogen-activated protein kinase (MAPK) signaling cascade (51,52), it has not been known if,
398 and indeed, how *C. acnes* may induce the interferon signaling pathway. In our studies, *C. acnes*
399 infection of THP-1 cells lacking the TLR adapter MyD88 clearly showed that production of
400 inflammatory cytokines, but not that of IFN-I, was driven by a MyD88 pathway. This is
401 perfectly in line with current literature suggesting a TLR2, 1 and 6 dependency.

402 To our surprise, we observed that the interferon response in a *C. acnes* infection strongly relied
403 on the adapter TRIF. This contradicts the notion that TRIF pathways are downstream of TLRs
404 3 and 4, but not those recognizing ligands of Gram-positive bacteria (53). Infection of
405 differentiated THP-1 cells with the Gram-positive bacterium *L.m.* showed similar dependency
406 on TRIF for IFN-I synthesis. The recognition of *L.m.* seems to strongly depend on the
407 macrophage population, as the IFN-I production in mouse bone marrow-derived macrophages
408 shows complete independence of TRIF (38) while macrophages residing the mouse peritoneum
409 show IFN-I synthesis via a TLR2-TRIF pathway upon *L.m.* infection (22). Therefore, one
410 possible interpretation of our results would be the wiring of a TLR2-TRIF pathway in human
411 macrophages. As for *L.m.* infections in THP-1 cells, a TLR2-TRIF pathway for IFN-I synthesis
412 can be ruled out due to the lack of ISG expression upon the infection with the escape-deficient
413 *hly* mutant strain which has been shown in this study. However, owing to our finding of a drastic
414 reduction of the response to IFN-I in either TRIF, cGAS and STING knockout cells, we posit
415 an association between the cGAS-STING pathway and TRIF as proposed by Wang et. al. (40).
416 These authors provide data showing that TRIF is needed for STING dimerization and is,
417 therefore, required for STING-mediated transcriptional activation of IRF3 homodimers. Thus,
418 our data would be the first to extend this signaling mechanism to a bacterial pathogen. Whereas

419 direct interaction between TRIF and STING was demonstrated, an involvement of TLR in this
420 interaction was not formally ruled out.

421 We noted an enhanced expression of pro-inflammatory cytokine mRNAs, especially those for
422 TNF- α , in knockouts of either STING or cGAS. This increase was not observed in cells
423 deficient for the ISGF3 subunit IRF9, suggesting it is not result of a transcription-based
424 cooperativity between IRF and STAT transcription factor families. A possible explanation is
425 provided by a report from Clark *et al.* (54) showing crosstalk between the canonical I κ B kinase
426 (IKK) complex (IKK α -IKK β) and the TANK-binding kinase 1 (TBK1)-IKK ϵ kinases which
427 negatively regulates the canonical IKKs. Consequently, by blocking the TBK1-IKK ϵ axis
428 downstream of STING activation one would lose the negative regulation of the canonical IKKs
429 and would, therefore, enhance the inflammatory response.

430 Our data showed that different *C. acnes* phylotypes differ significantly in their ability to
431 produce a response to IFN-I, however they show similar patterns in expression of pro-
432 inflammatory cytokines. This can be explained by the variations in morphological
433 characteristics such as cell wall composition, production of different virulence factors and other
434 immunologically relevant properties of the different *C. acnes* phylotypes (2). This raises the
435 possibility that inflammatory diseases associated with these phylotypes are more prone to the
436 proinflammatory effects, such as the synthesis of chemokines or the enhanced synthesis of some
437 inflammatory mediators such as nitric oxide (NO) (18).

438 We did not find any evidence of prolonged *C. acnes* survival in infected THP-1 or U937 cells
439 (Figure 1 and Supplementary Figure S1). In fact, the loss of viable bacteria corresponded well
440 to that of the escape-deficient *hly* mutant of *L.m.* This suggests that unlike wildtype *L.m.*, *C.*
441 *acnes* is not endowed with a widely applicable mechanism for intracellular survival. Our data
442 do not rule out, however, that some primary cell types might present niches for intracellular
443 survival and organismic spread. In contrast to our data, Fischer *et al.* showed a persistence of
444 *C. acnes* in THP-1 cells over a period of 3 days (35). They suggested that *C. acnes* can either
445 neutralize the phagosomal acidic pH or escape the phagosome in order to prevent its
446 degradation, the latter being in line with our data showing *C. acnes*-induced cGAS-STING
447 signaling. However, while using the same host cell, Fischer *et al.* used a very low infection rate,
448 different bacterial strains, as well as different antibiotic treatments to kill extracellular bacteria,
449 which could explain the contrasting results. On the other hand, Nakamura *et al.* discovered that
450 *C. acnes* can be taken up by autophagic vacuoles, especially when using high infection rates
451 (56). While *C. acnes* could persist in those vacuoles in HeLa cells after 3 days of infection, the
452 loss of bacteria over time in either the murine macrophage cell line RAW264.7 or mouse
453 embryonic fibroblasts (MEFs) suggests a cell type specificity for *C. acnes* intracellular
454 degradation. Interestingly, type-I IFN signaling does not restrict *C. acnes* intracellular growth
455 and/or host-induced bacterial killing as seen in Figure 1B. Not even the most potent strain in
456 inducing an IFN-I axis, Asn12, showed differences in bacterial numbers counted by CFU.

457 Our data provide convincing evidence that *C. acnes* activates the cGAS-STING pathway and
458 that, unlike *L.m.*, does not secrete cyclic di-nucleotides capable of STING activation. An
459 important open question to be addressed in future research is how *C. acnes* DNA acquires
460 access to the intracellular sensor cGAS. This could occur either through phagosome leakage or
461 through a cytoplasmic escape mechanism that is not necessarily associated with intracellular
462 growth. Another open question concerns the consequences of an IFN response during *C. acnes*
463 infection, both for local and systemic inflammation. Taken together, studying the innate
464 immune signaling cascades activated downstream of *C. acnes* recognition is an important step
465 in order to fully understand pathogenic characteristics. This information can further be used for
466 pathogen-specific novel therapies against diseases where bacterial accumulation plays an
467 essential role.

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470 strains used in this study. We gratefully acknowledge help and suggestions from Gijs Versteeg
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474 **Figure legend**

475 **Figure 1. Intracellular degradation of *C. acnes* by human macrophages.** A CFU assay was
476 performed using PMA-differentiated THP-1 cells. **(A)** THP-1 cells were either infected with *C.*
477 *acnes* strain NCTC737 or *L.m.* for indicated timepoints. Graphs show the standard deviation
478 and mean of five independent experiments. **(B)** Differentiated THP-1 cells were infected with
479 one strain of each *C. acnes* phylotype: NCTC737 (phylotype IA₁), P. acn31 (phylotype IA₂),
480 KPA171202 (phylotype IB), PV66 (phylotype IC), ATCC11828 (phylotype II) and Asn12
481 (phylotype III) for indicated timepoints. Graphs show the standard deviation and mean of three
482 independent experiments. **(A-B)** Unpaired t-test of log transformed values compared to the 2-
483 hour timepoint was calculated for each timepoint. P-values (*P ≤ 0.05; **P ≤ 0.01; ***P ≤
484 0.001).

485 **Figure 2. Cytokine expression and secretion in response to *C. acnes*.** **(A)** Differentiated
486 THP-1 cells were infected with *C. acnes* strain NCTC737 for indicated timepoints. HPRT-
487 normalized gene expression was measured using RT-qPCR and shown as log transformed fold-
488 change to the uninfected sample. **(B)** Cytokine levels in the supernatant of **(A)** were measured
489 using the Luminex assay. **(C)** Differentiated THP-1 cells were infected with one strain of each
490 *C. acnes* phylotype: NCTC737 (phylotype IA₁), P. acn31 (phylotype IA₂), KPA171202
491 (phylotype IB), PV66 (phylotype IC), ATCC11828 (phylotype II) and Asn12 (phylotype III).
492 HPRT-normalized gene expression was measured using RT-qPCR and shown as log
493 transformed fold change to the uninfected sample. TNF-α, IL-1β, IL-1α, IL6 and IL-10 mRNA
494 expression was measured after 6 hours post infection (pi). IFN-β, MX1 and IFIT1 mRNA
495 expression was measured 24 hours pi. **(D)** THP1-Blue™ ISG cells (see text) were infected
496 with *L.m.*, *C. acnes* strain NCTC737 and Asn12 or stimulated with 0.4μg/ml LPS. After 24, 48
497 and 72 hours, supernatant was analyzed by measuring the absorbance at 620nm with QUANTI-
498 Blue™ solution. **(A-D)** Data represent the mean values of three independent experiments. P.
499 values were calculated using the unpaired t-test of log transformed values compared to the
500 uninfected sample (*P≤0.05; **P≤0.01; ***P≤0.001).

501 **Figure 3. Cytokine expression and type-I IFN signaling in primary monocyte-derived**
502 **macrophages.** Monocyte-derived macrophages were infected with either *C. acnes* strain
503 NCTC737 and Asn12, *L.m.* or stimulated with LPS for either 6 or 24 hours. **(A)** HPRT-
504 normalized gene expression of TNF-α, IL-1β, MX1 and IFN-β was measured using RT-qPCR
505 and shown as log transformed fold change to the uninfected sample. Data represent the mean
506 values of three independent experiments. P. values were calculated using the unpaired t-test of
507 log transformed values (*P≤0.05; **P≤0.01; ***P≤0.001). **(B)** Protein expression of total
508 STAT1, Phospho-Y701 STAT1 and GAPDH (housekeeping gene) was measured by Western
509 blot.

510 **Figure 4. Induction of innate immune signaling pathways in response to *C. acnes* infection**
511 **in TRIF, MyD88 and IRF9 deficient human macrophages.** **(A)** Differentiated wildtype,

512 MYD88-deficient and TRIF-deficient THP-1 cells were infected with either *C. acnes* strain
513 NCTC737, *L.m.* or stimulated with lipopolysaccharide (LPS) for either 6 (TNF- α , IL-1 β) or 24
514 hours (MX1, IFIT1). HPRT-normalized gene expression was measured using RT-qPCR and
515 shown as log transformed fold change to the uninfected sample. (B) Differentiated wildtype,
516 MYD88-deficient and TRIF THP-1 cells were infected with either *C. acnes* strain NCTC737
517 or *L.m.* for indicated timepoints. Protein expression of I κ B- α , total STAT1, Phospho-Y701
518 STAT1 and tubulin (housekeeping gene) was measured by Western blot. (C) The representative
519 blots in (B) were quantified using Image Lab. Relative intensities of the bands were normalized
520 to their corresponding tubulin levels. Data represent relative intensities in percent to the
521 corresponding uninfected control (equals 100%). (D) Differentiated wildtype and *IRF9*^{-/-} THP-
522 1 cells were infected with either *C. acnes* strain NCTC737, *L.m.* or stimulated with
523 lipopolysaccharide (LPS) for either 6 (TNF- α , IL-1 β) or 24 hours (MX1, IFIT1). HPRT-
524 normalized gene expression was measured using RT-qPCR and shown as log transformed fold
525 change to the uninfected sample. (A, D) Data represent the mean values of three independent
526 experiments. P. values were calculated using the unpaired t-test of log transformed values
527 (*P \leq 0.05; **P \leq 0.01; ***P \leq 0.001).

528 **Figure 5. Induction of innate immune signaling pathways in response to *C. acnes* infection**
529 **in STING-deficient human macrophages.** (A) Differentiated wildtype and STING-deficient
530 THP-1 cells were infected with either *C. acnes* strain NCTC737, *L.m.* or stimulated with
531 lipopolysaccharide (LPS; 0.4 μ g/ml) for either 6 (TNF- α , IL-1 β) or 24 hours (MX1, IFIT1).
532 HPRT-normalized gene expression was measured using RT-qPCR and shown as log
533 transformed fold change to the uninfected sample. Data represent the mean values of seven
534 independent experiments. P values were calculated using the unpaired t-test of log transformed
535 values (*P \leq 0.05; **P \leq 0.01; ***P \leq 0.001). (B) Differentiated wildtype and STING-deficient
536 THP-1 cells were infected with either *C. acnes* strain NCTC737 or *L.m.* for indicated
537 timepoints. Protein expression of I κ B- α , total STAT1, Phospho-Y701 STAT1 and tubulin
538 (housekeeping gene) was measured by western blot. (C) The representative blots in (B) were
539 quantified using Image Lab. Relative intensities of the bands were normalized to their
540 corresponding tubulin levels. Data represent relative intensities in percent to the corresponding
541 uninfected control (equals 100%).

542 **Figure 6. Induction of innate immune signaling pathways in response to *C. acnes* infection**
543 **in cGAS-deficient human macrophages.** (A) Differentiated wildtype, STING-deficient and
544 cGAS-deficient THP-1 cells were infected with either *C. acnes* strain NCTC737, *L.m.* or
545 stimulated with lipopolysaccharide (LPS; 0.4 μ g/ml) for either 6 (TNF- α , IL-1 β) or 24 hours
546 (MX1, IFIT1). (B) Differentiated wildtype, STING-deficient and cGAS-deficient THP-1 cells
547 were infected with either *C. acnes* strain Asn12, *L.m.* or stimulated with lipopolysaccharide
548 (LPS; 0.4 μ g/ml) for either 6 (TNF- α , IL-1 β) or 24 hours (MX1, IFIT1). (A-B) HPRT-
549 normalized gene expression was measured using RT-qPCR and shown as log transformed fold
550 change to the uninfected sample. Data represent the mean values of four independent
551 experiments. P values were calculated using the unpaired t-test of log transformed values
552 (*P \leq 0.05; **P \leq 0.01; ***P \leq 0.001).

553 **Figure 7. Model of the *C. acnes*-induced intracellular signaling pathways.** *C. acnes*
554 recognition in human macrophages is carried out by membrane bound toll-like receptors with
555 its adapter MyD88. This further leads to the activation of the NF- κ B pathway and the
556 subsequent expression of inflammatory cytokines. The TLR adapter TRIF shows importance
557 during *C. acnes*-induced IFN-signaling. TRIF can be activated by specific TLR activation on

558 the cell membrane or in the endosome and has also been shown to positively regulate the
559 cGAS/STING pathway. Whether *C. acnes* is recognized by membrane-bound or endosomal
560 TLR-TRIF or simply boosts the cGAS/STING pathway in a TRIF-dependent manner is not
561 known.

562 **Figure 8. Intracellular survival of *C. acnes* and *L.m.* in human macrophages deficient for**
563 **either MyD88, TRIF, IRF9 or STING.** Colony-forming-unit (CFU) assay was performed
564 using PMA-differentiated THP-1 cells deficient for either MyD88, TRIF, IRF9 or STING.
565 THP-1 cells were either infected with *C. acnes* strain NCTC737 (A) or *L.m.* (B) for indicated
566 timepoints. Graphs show the standard deviation and mean of three independent experiments.
567 Unpaired t-test of log transformed values was calculated. P-values (*P ≤ 0.05; **P ≤ 0.01; ***P
568 ≤ 0.001).

569 **Figure S1. (A)** CFU assay was performed using PMA-differentiated U-937 cells. U-937 cells
570 were infected with either *C. acnes* strain NCTC737 (left; grey) or wildtype *L.m.* (right; black)
571 for indicated timepoints. **(B)** CFU assay was performed using PMA-differentiated THP-1
572 (black squares) and U-937 (grey triangles) cells. Cells were infected with the *L.m.* mutant strain
573 Δhly for indicated timepoints. **(A-B)** Representative of two independent experiments.

574 **Figure S2. (A)** Primary monocytes were infected with either *C. acnes* strain NCTC737 and
575 Asn12, *L.m.* or stimulated with LPS for either 6 or 24 hours. HPRT-normalized gene expression
576 of TNF- α , IL-1 β , MX1 and IFIT1 was measured using RT-qPCR and shown as log transformed
577 fold change to the uninfected sample. **(B)** HaCaT cells were infected with either *C. acnes* strain
578 Asn12, *L.m.* or stimulated with LPS for 48 hours. HPRT-normalized gene expression of TNF-
579 α , MX1, IFIT1 and IL-6 was measured using RT-qPCR and shown as log transformed fold
580 change to the uninfected sample. **(A-B)** Data represent the mean values of three independent
581 experiments. P. values were calculated using the unpaired t-test of log transformed values
582 (*P ≤ 0.05; **P ≤ 0.01; ***P ≤ 0.001).

583 **Figure S3. (A)** Confirmation of CRISPR/Cas9 generated MyD88 and TRIF knockout THP-1
584 cells. MyD88, TRIF and tubulin protein levels of wildtype, MyD88 and TRIF knockout THP-
585 1 cells was analyzed by western blot. **(B)** Differentiated THP-1 cells were infected with either
586 *C. acnes* strain NCTC737, wildtype *L.m.* or LLO-deficient *L.m.* strain Δhly for either 6 (TNF-
587 α , IL-1 β) or 24 hours (MX1, IFIT1). HPRT-normalized gene expression was measured using
588 RT-qPCR and shown as log transformed fold change to the uninfected sample. Data represent
589 the mean values of three independent experiments. P. values were calculated using the unpaired
590 t-test of log transformed values (*P ≤ 0.05; **P ≤ 0.01; P*** ≤ 0.001). **(C)** Confirmation of
591 CRISPR/Cas9 generated IRF9 knockout THP-1 cells. IRF9 protein level of wildtype and IRF9
592 knockout THP-1 cells was analyzed by western blot.

593 **Figure S5. (A)** Confirmation of STING knockout THP-1 cells. STING and tubulin protein
594 levels of wildtype and STING knockout THP-1 cells was analyzed by western blot. **(B)**
595 Confirmation of cGAS knockout THP-1 cells. STING, cGAS and tubulin protein levels of
596 wildtype, cGAS and STING knockout THP-1 cells was analyzed by western blot.

597 **Table S1.** *C. acnes* strains

598 **Table S2.** RT-qPCR primer

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