Supplementary Figure Legends

Supplementary Figure S1. A-B, mRNA expression of *AADC* and *MAOA* was detected by real-time PCR in human sourced normal colorectal epithelial cell line (NCM460) and four CRC cell lines (SW480, SW620, HCT116 and HT29). **C-D**, quantitative analysis of Western blotting for TPH1 expression in NCM460, SW480, SW620, HCT116, HT29 and THP-1 cells, as well as CEC, CT26 and iBMDM. **E, F,** quantitative analysis of Western blotting for cleaved-caspase-1 (C-casp1) and cleaved-IL1β (C-IL1β) expression in cell lysates from THP-1 cells after activated by LPS (100 ng/mL, 4 hours) and ATP (5 mM, 1 hour) with/without SW620 or HT29 conditional medium (CM) incubation for 24 hours. **G-H,** quantitative analysis of Western blotting for C-casp1 and C-IL1β expression in cell lysates from iBMDM cells after activated by LPS (100 ng/mL, 4 hours) and ATP (5 mM, 1 hour) with/without CT26 CM incubation for 24 hours. **I-J,** quantitative analysis of Western blotting for C-casp1 and C-IL1β expression in cell lysates from THP-1 cells after activated by LPS (100 ng/mL, 4 hours) and ATP (5 mM, 1 hour) with incubation of the CM from SW620/HT29 cells or LP-533401 (0.5 μM) treated SW620/HT29 cells for 24 hours. **K**, verification for TPH1 silence in SW620, HT29 cells after shRNA lentivirus transfection by Western blotting. **L**, quantitative analysis of Western blotting for C-casp1 expression in cell lysates from THP-1 cells after activated by LPS (100 ng/mL, 4 hours) and ATP (5 mM, 1 hour) with/without incubation of CM from TPH1 silenced (by anti-TPH1 shRNA) SW620 cells for 24 hours. Data represent mean±SD for at least three independent experiments; one-way ANOVA; N.D.: not detected. *$p<0.05$, **$p<0.01$.

Supplementary Figure S2. A-C, quantitative analysis of Western blotting for C-casp1 and C-IL1β expression in cell lysates from THP-1 cells after activated by LPS (100 ng/mL, 4 hours) and ATP (5 mM, 1 hour) with/without incubation of CM from TPH1 silenced (by anti-TPH1 shRNA) SW620 or HT29 cells for 24 hours. **D-E,** quantitative analysis of Western blotting for C-casp1 and C-IL1β expression in cell lysates from iBMDM cells after activated by LPS (100 ng/mL, 4 hours) and ATP (5 mM, 1 hour) with incubation of the CM from CT26 cells or LP-533401 (0.5 μM) treated CT26 cells for 24 hours. **F**, protein expression bands and **G-J**, quantitative analysis of C-casp1 and C-IL1β in cell lysates detected by Western blotting, as well as **K-L**, IL1β concentration in supernatants from THP-1 and iBMDM cells detected by ELISA after activated by LPS (100 ng/mL, 4 hours) and ATP (5 mM, 1 hour) with/without 5-HT treatment (10 μM, 5 hours). **M**, protein expression bands of TPH1, NLRP3, phospho-NLRP3 (Ser194), C-casp1 and C-IL1β in tumor tissues from each group of the CT26 and iBMDM co-implanted subcutaneous allograft CRC mouse model. For **A-E** and **G-L:** data represent mean±SD for three independent experiments; one-way ANOVA; Ctrl, control; WT: wild-type; sh3A: shHTR3A; shN3: shNLRP3; N.D.: not detected. *$p<0.05$, **$p<0.01$.

Supplementary Figure S3. A-B, quantitative analysis of Western blotting for C-casp1 and C-IL1β expression in tumor tissues from each group of the CT26 and iBMDM co-implanted subcutaneous allograft CRC mouse model. **C-F**, quantitative analysis of Western blotting for C-casp1 and C-IL1β in cell lysates from THP-1 and iBMDM cells after activated by LPS (100 ng/mL, 4 hours) and ATP (5 mM, 1 hour) with 5-HT (10 μM, 5 hours) and SGR (10 μM), or TPS (10 μM), or SB-269970 (10 μM) treatments for 5 hours. **G**, verification for HTR3A silence in THP-1 cells by Western blotting after shRNA lentivirus stable transfection. **H-K**, quantitative analysis of Western blotting for C-casp1 and C-IL1β in cell lysates from HTR3A silenced (by anti-HTR3A shRNA) THP-1 and iBMDM cells after activated by LPS (100 ng/mL, 4 hours) and ATP (5 mM, 1 hour) with 5-HT (10 μM, 5 hours)

treatment. **L**, quantitative analysis of Western blotting for C-casp1 in cell lysates from THP-1 cells after activated by LPS (100 ng/mL, 4 hours) and ATP (5 mM, 1 hour) with/without 10, 50, 100 nM 2Met5HT treatments for 5 hours. For **A-B:** data represent mean±SD for each group; for **C-F** and **H-L:** data represent mean±SD for three independent experiments; one-way ANOVA. WT: wild-type; sh3A: shHTR3A; shN3: shNLRP3; Ctrl, control; n.s.: no significant differences; N.D.: not detected. *$p<0.05$, **$p<0.01$.

Supplementary Figure S4. A, quantitative analysis of Western blotting for C-IL1β in cell lysates from THP-1 cells after activated by LPS (100 ng/mL, 4 hours) and ATP (5 mM, 1 hour) with/without 10, 50, 100 nM 2Met5HT treatments for 5 hours. **B-C**, quantitative analysis of Western blotting for C-casp1 and C-IL1β in cell lysates from THP-1 cells after activated by LPS (100 ng/mL, 4 hours) and ATP (5 mM, 1 hour) with/without 5-HT (10 μM) and 10, 50, 100 μM TPS treatments for 5 hours. **D,** protein expression bands and **E-H,** quantitative analysis of C-casp1 and C-IL1β in cell lysates detected by Western blotting, and **I-J**, IL1β concentration in supernatants from THP-1 cells detected by ELISA after activated by LPS (100 ng/mL, 4 hours) and MSU (500 μg/mL, 1 hour) or Nig (10 μM, 1 hour) and 5-HT (10 μM, 5 hours) with 10, 50, 100 μM TPS treatments for 5 hours. **K,** protein expression bands and **L-O,** quantitative analysis of C-casp1 and C-IL1β in cell lysates from THP-1 cells detected by Western blotting after activated by LPS (100 ng/mL, 4 hours) and MSU (500 μg/mL, 1 hour) or Nig (10 μM, 1 hour) with/without 10, 50, 100 nM 2Met5HT treatments for 5 hours. For **A-C, E-J** and **L-O:** data represent mean±SD for three independent experiments; one-way ANOVA; N.D.: not detected. *$p<0.05$, **$p<0.01$.

Supplementary Figure S5. A-B, IL1β concentration of supernatants was detected by ELISA from THP-1 cells after activated by LPS (100 ng/mL, 4 hous) and MSU (500 μg/mL, 1 hour) or Nig (10 μM, 1 hour) with/without 10, 50, 100 nM 2Met5HT treatments for 5 hours. **C**, protein expression bands and **E-F**, quantitative analysis of C-casp1 and C-IL1β in cell lysates detected by Western blotting, and **I**, IL1β concentration of supernatants from iBMDM cells detected by ELISA after activated by LPS (100 ng/mL, 4 hours) and ATP (5 mM, 1 hour) with/without 5-HT (10 μM) and TPS (100 μM) treatment for 5 hours. **D,** protein expression bands and **G-H**, quantitative analysis of C-casp1 and C-IL1β in cell lysates detected by Western blotting, and **J,** IL1β concentration of supernatants from iBMDM cells detected by ELISA after activated by LPS (100 ng/mL, 4 hours) and ATP (5 mM, 1 hour) with/without 2Met5HT (100 nM) treatment for 5 hours. **K-M**, concentrations of IL18, IL33 and IL1α in supernatants from THP-1 cells detected by ELISA after activated by LPS (100 ng/mL, 4 hours) and ATP (5 mM, 1 hour) with/without 5-HT (10 μM, 5 hours) and TPS (100 μM) treatment for 5 hours. **N**, expression bands and **O-R**, quantitative analysis of NLRP3, ASC, pro-caspase-1 (P-casp1), and pro-IL1β in cell lysates of THP-1 cells detected by Western blotting after activated by LPS (100 ng/mL, 4 hours) and ATP (5 mM, 1 hour) with/without TPS (100 μM) or 2Met5HT (100 nM) treatment for 5 hours. For **A-B, E-M** and **O-R:** data represent mean±SD for three independent experiments; one-way ANOVA; N.D.: not detected; n.s.: no significant differences. *$p<0.05$, **$p<0.01$.

Supplementary Figure S6. A, mRNA expressipon of *NLRP3*, *IL1B*, and *IL18* in THP-1 cells after incubation with CM from SW620 or HT29 cells; **B,** mRNA expression of *Nlrp3, Il1b, and Il18* in iBMDM cells after incubation with CM from CT26 cells detected by real-time PCR analysis. **C,**

quantitative analysis for ASC oligomerization assay in THP-1 cells (with/without anti-HTR3A shRNA transfected) after activated by LPS (100 ng/mL, 4 hours) and ATP (5 mM, 1 hour) with 5-HT (10 μM, 5 hours) treatment. **D,** quantitative analysis for ASC oligomerization assay in THP-1 cells after activated by LPS (100 ng/mL, 4 hours) and ATP (5 mM, 1 hour) with/without 5-HT (10 μM) and TPS (100 μM) treatments for 5 hours. **E,** quantitative analysis for ASC oligomerization assay in THP-1 cells after activated by LPS (100 ng/mL, 4 hours) and ATP (5 mM, 1 hour) with/without 2Met5HT (100 nM) treatment for 5 hours. **F-I,** ASC oligomerization analysis for iBMDM cells after activated by LPS (100 ng/mL, 4 hours) and ATP (5 mM, 1 hour) and 5-HT (10 μM, 5 hours) with/without TPS (100 μM, 5 hours) treatment; and iBMDM cells after activated by LPS (100 ng/mL, 4 hours) and ATP (5 mM, 1 hour) with/without 2Met5HT (100 nM, 5 hours) treatment. **J-K,** CaMKIIα phosphorylation quantitative analysis of Western blotting in THP-1 and iBMDM cells after primed by LPS (100 ng/mL, 4 hours), and then treated with ATP (5 mM), 2Met5HT (100 nM) and TPS (100 μM) for 0, 30, 60 minutes. **L,** mRNA expression of *CAMK2A* in THP-1 cells was detected by real-time PCR after activated by LPS (100 ng/mL, 4 hours) and ATP (5 mM, 1 hour) with/without TPS (100 μM) or 2Met5HT (100 nM) treatment for 5 hours. **M,** protein expression bands and **N-Q,** quantitative analysis of C-casp1 and C-IL1β in cell lysates of THP-1 and iBMDM cells detected by Western blotting after activated by LPS (100 ng/mL, 4 hours) and ATP (5 mM, 1 hour) with/without 2Met5HT (100 nM) or KN-62 (1 μM) treatments for 5 hours. **R-S,** quantitative analysis for ASC oligomerization assay in THP-1 and iBMDM cells after activated by LPS (100 ng/mL, 4 hours) and ATP (5 mM, 1 hour) with/without 2Met5HT (100 nM) or KN-62 (1 μM) treatments for 5 hours. **T,** protein expression bands of NLRP3, ASC, P-casp1 and pro-IL1β, and **U,** quantitative analysis of NLRP3 and ASC in cell lysates of THP-1 cells detected by Western blotting after activated by LPS (100 ng/mL, 4 hours) and ATP (5 mM, 1 hour) with/without 2Met5HT (100 nM) or KN-62 (1 μM) treatments for 5 hours. For **A-E, H-L, N-S** and **U:** data represent mean±SD for at least three independent experiments; one-way ANOVA. Ctrl, control; n.s.: no significant differences; N.D.: not detected. *$p<0.05$, **$p<0.01$.

Supplementary Figure S7. A, quantitative analysis of Western blotting for P-casp1 and pro-IL1β in cell lysates from THP-1 cells after activated by LPS (100 ng/mL, 4 hours) and ATP (5 mM, 1 hour) with/without 2Met5HT (100 nM) or KN-62 (1 μM) treatments for 5 hours. **B,** protein expression bands and **C-F,** quantitative analysis of NLRP3, ASC, P-casp1, and pro-IL1β in cell lysates from iBMDM cells detected by Western blotting after activated by LPS (100 ng/mL, 4 hours) and ATP (5 mM, 1 hour) with/without 2Met5HT (100 nM) or KN-62 (1 μM) treatments for 5 hours. **G,** quantitative analysis of Western blotting for NLRP3 phosphorylation levels in tumor tissues from each group of the CT26 and iBMDM co-implanted subcutaneous allograft CRC mouse model. **H,** representative immunohistochemical photos for NLRP3, phospho-NLRP3 (Ser194) in tumor tissues from the CT26 and iBMDM co-implanted subcutaneous allograft CRC mouse model. Scale bar: 50 μm. **I,** quantitative analysis of Western blotting for TPH1 in cell lysates from SW620, HT29 and CT26 cells after incubation with CM from activated macrophages (A-Φ CM, THP-1 for SW620/HT29, and iBMDM for CT26) with/without Dia (10 μM) treatment. **J,** protein expression bands and **K-L,** quantitative analysis of TPH1 in SW620, HT29, and CT26 cells detected by Western blotting after incubation with CM from activated (A-THP-1, A-iBMDM) or inactivated THP-1, iBMDM cells for 24 hours (THP-1 and iBMDM cells activation were induced by 100 ng/mL LPS for 4 hours and 5 mM ATP for 1 hour). **M,** protein expression bands and **N,** quantitative analysis of TPH1 in cell lysates (SW620) after SW620 and HT29 cells were treated with/without rhIL1β (10 μg/mL) and TLR1 (100

μM) for 24 hours. For **A, C-F, I, K-L** and **N:** data represent mean±SD for three independent experiments; for **G:** data represent mean±SD for each group; one-way ANOVA. WT, wild-type; sh3A, shHTR3A; shN3, shNLRP3; n.s.: no significant differences. *$p<0.05$, **$p<0.01$.

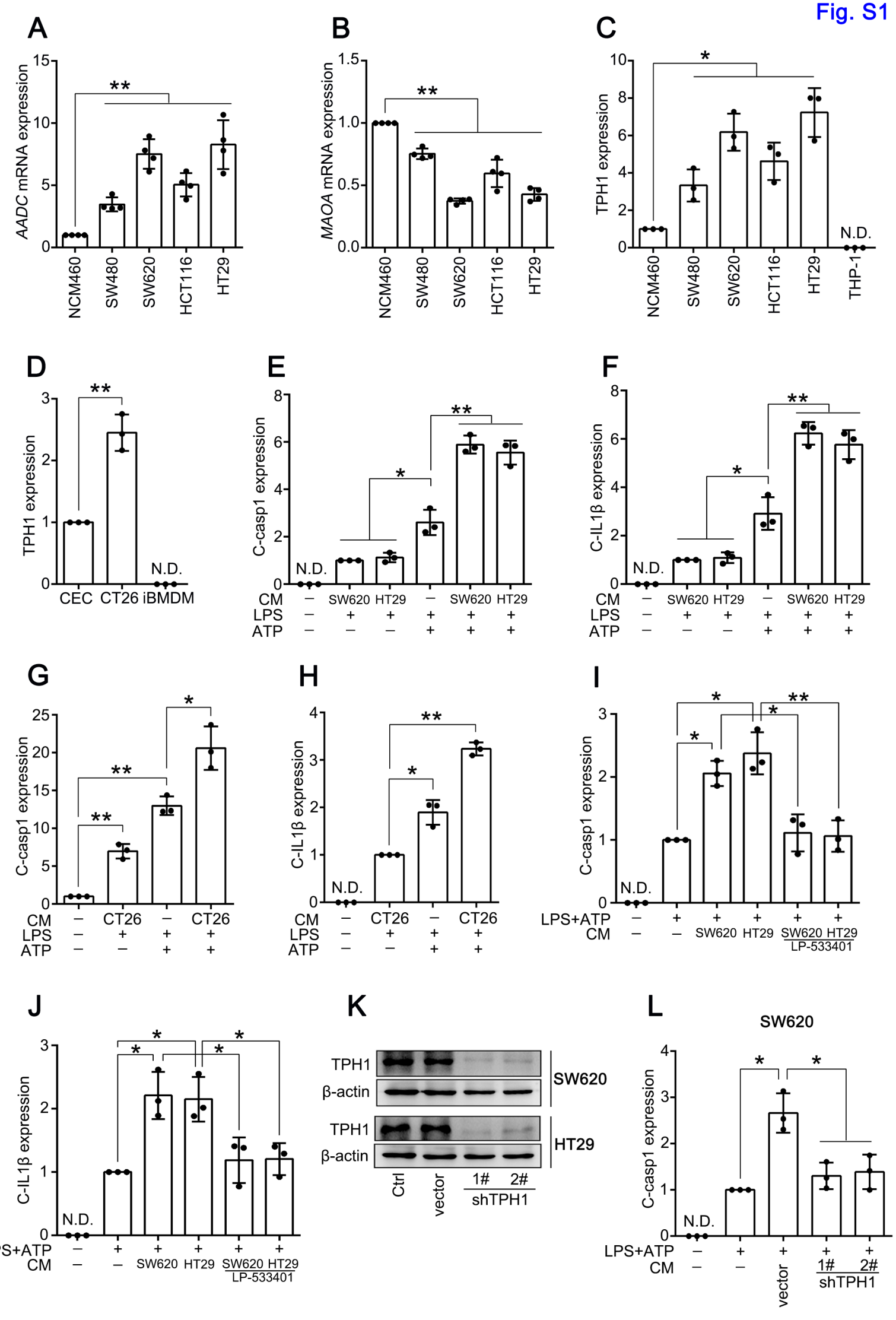
Supplementary Figure S8. A, quantitative analysis of TPH1 in cell lysates (HT29) detected by Western blotting, **B-C,** 5-HT concentration in supernatants detected by ELISA from SW620 and HT29 cells after treated with/without rhIL1β (10 μg/mL) and TLR1 (100 μM) for 24 hours. **D-F,** quantitative analysis of IKKβ (Tyr 188) and NF-κB p65 (Ser 536) phosphorylation levels in cell lysates from SW620, HT29 and CT26 cells after incubation with CM from activated macrophages (A-Φ CM: THP-1 for SW620/HT29, and iBMDM for CT26) with/without Dia (10 μM) treatment. **G**, protein expression bands and **H,** quantitative analysis of TPH1 in cell lysates of SW620, and HT29 cells detected by Western blotting after incubation with CM from activated THP-1 cells (A-THP-1), and treated with/without IL1RA (0.1 μg/mL) or TLR1 (100 μM) or BMS-345541 (4 μM) for 24 hours. **I**, protein expression bands and **J,** quantitative analysis of TPH1 expression in cell lysates from CT26 cells detected by Western blotting after incubation with CM from activated iBMDM cells (A-iBMDM), and treated with/without TLR1 (100 μM) or BMS-345541 (4 μM) for 24 hours. **K,** quantitative analysis of Western blotting for TPH1, **L,** mRNA expression of *Tph1* detected by real-time PCR, **M,** 5-HT concentrations detected by ELISA in tumor tissues from each group of the CT26 and iBMDM co-implanted subcutaneous allograft CRC mouse model. **N,** verification for TPH1 and NLRP3 silence in CT26 cells after shRNA lentivirus transfection by Western blotting. **O,** verification for HTR3A and NLRP3 silence in iBMDM cells by Western blotting after shRNA lentivirus stable transfection. Since both shRNA sequences 1# and 2# had similar silence rates on expression of TPH1, NLRP3 in CT26 cells, as well as expression of HTR3A, NLRP3 in iBMDM cells, shRNA 1# for each gene was selected as stable transfected CT26, iBMDM cells for further co-implanted subcutaneous allograft experiment. For **A-F, H,** and **J:** data represent mean±SD for three independent experiments, for **K-M:** data represent mean±SD for each group; one-way ANOVA. WT, wild-type; sh3A, shHTR3A; shN3, shNLRP3; n.s.: no significantly differences. *$p<0.05$, **$p<0.01$.

Supplementary Figure S9. A, representative immunohistochemical photos for Ki67, F4/80, and GP70 in tumor tissues from each group of the CT26 and iBMDM co-implanted subcutaneous allograft CRC mouse model. Scale bar: 50 μm. **B,** protein expression bands and **C-D,** quantitative analysis of NLRP3 detected by Western blotting in human sourced cell lines (NCM460, SW480, SW620, HCT116, HT29, and THP-1) and mouse sourced cell lines (CT26 and iBMDM). **E,** protein expression bands of TPH1, NLRP3, phospho-NLRP3 (Ser194), C-casp1 and C-IL1β and **F-I,** quantitative analysis of TPH1, C-casp1 and C-IL1β, as well as phosphorylation levels of NLRP3 in colorectal tumor or normal tissues (in Ctrl group) detected by Western blotting. **J,** 5-HT concentrations of colorectal tumor and normal tissues detected by ELISA from each group of AOM/DSS induced CRC mouse model. For **C-D:** data represent mean±SD for three independent experiments, for **F-J:** data represent mean±SD for each group; one-way ANOVA for **C, F-J,** and unpaired student's t test for **D**. WT, wild-type; sh3A, shHTR3A; shN3, shNLRP3; Ctrl, control; n.s.: no significantly differences. *$p<0.05$, **$p<0.01$.

Supplementary Figure S10. 5-HT-NLRP3 positive feedback loop in CRC microenvironment. In CRC microenvironment, CRC cell-secreted 5-HT binds to HTR3A receptor on macrophages, which

induces Ca^{2+} influx, and follows with phosphorylation and activation of CaMKIIα. Activated CaMKIIα induces NLRP3 phosphorylation (human: Ser198, and mouse: Ser194), an essential step for NLRP3 activation, which enhances NLRP3 inflammasome assembling and activation under DAMPs or PAMPs challenges, resulted in excessive IL1β maturation and secretion into CRC microenvironment. On the other hand, IL1β activates NF-κB signaling via IL1R in CRC cells, which induces transcription of *TPH1*, resulted in excessive 5-HT biosynthesis and secretion from CRC cells.

Fig. S1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SW620
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HT29
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MAOA mRNA expression
C
TPH1 expression
N.D.
THP-1
D
TPH1 expression
CEC
CT26
iBMDM
E
C-casp1 expression
CM
LPS
ATP
F
C-IL1β expression
G
C-casp1 expression
H
C-IL1β expression
I
C-casp1 expression
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CM
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J
C-IL1β expression
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SW620
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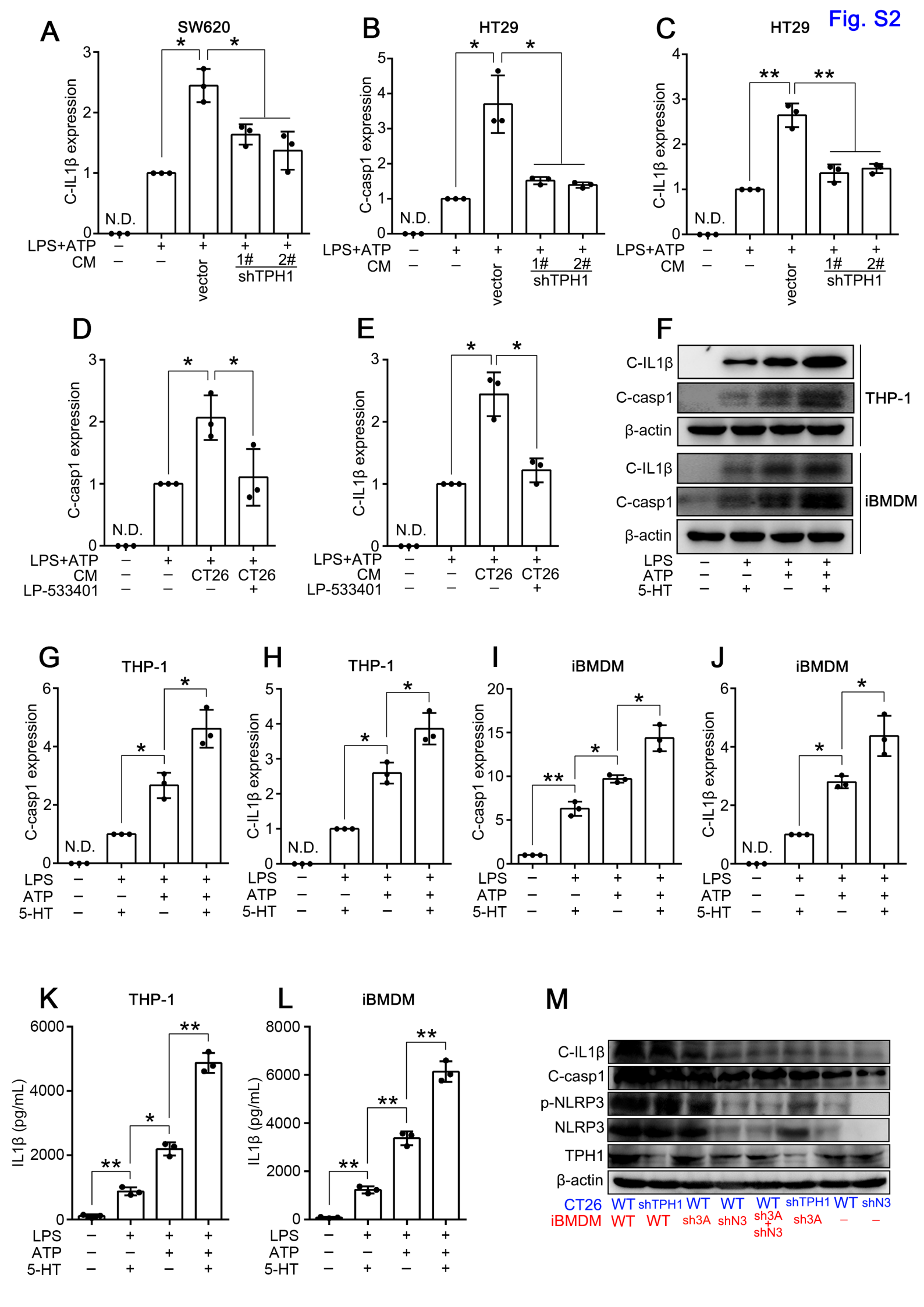
Fig. S2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C
HT29
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D
C-casp1 expression
CT26
LP-533401
E
C-IL1β expression
F
C-IL1β
C-casp1
β-actin
THP-1
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LPS
ATP
5-HT
G
THP-1
C-casp1 expression
H
THP-1
C-IL1β expression
I
iBMDM
C-casp1 expression
J
iBMDM
C-IL1β expression
K
THP-1
IL1β (pg/mL)
L
iBMDM
IL1β (pg/mL)
M
C-IL1β
C-casp1
p-NLRP3
NLRP3
TPH1
β-actin
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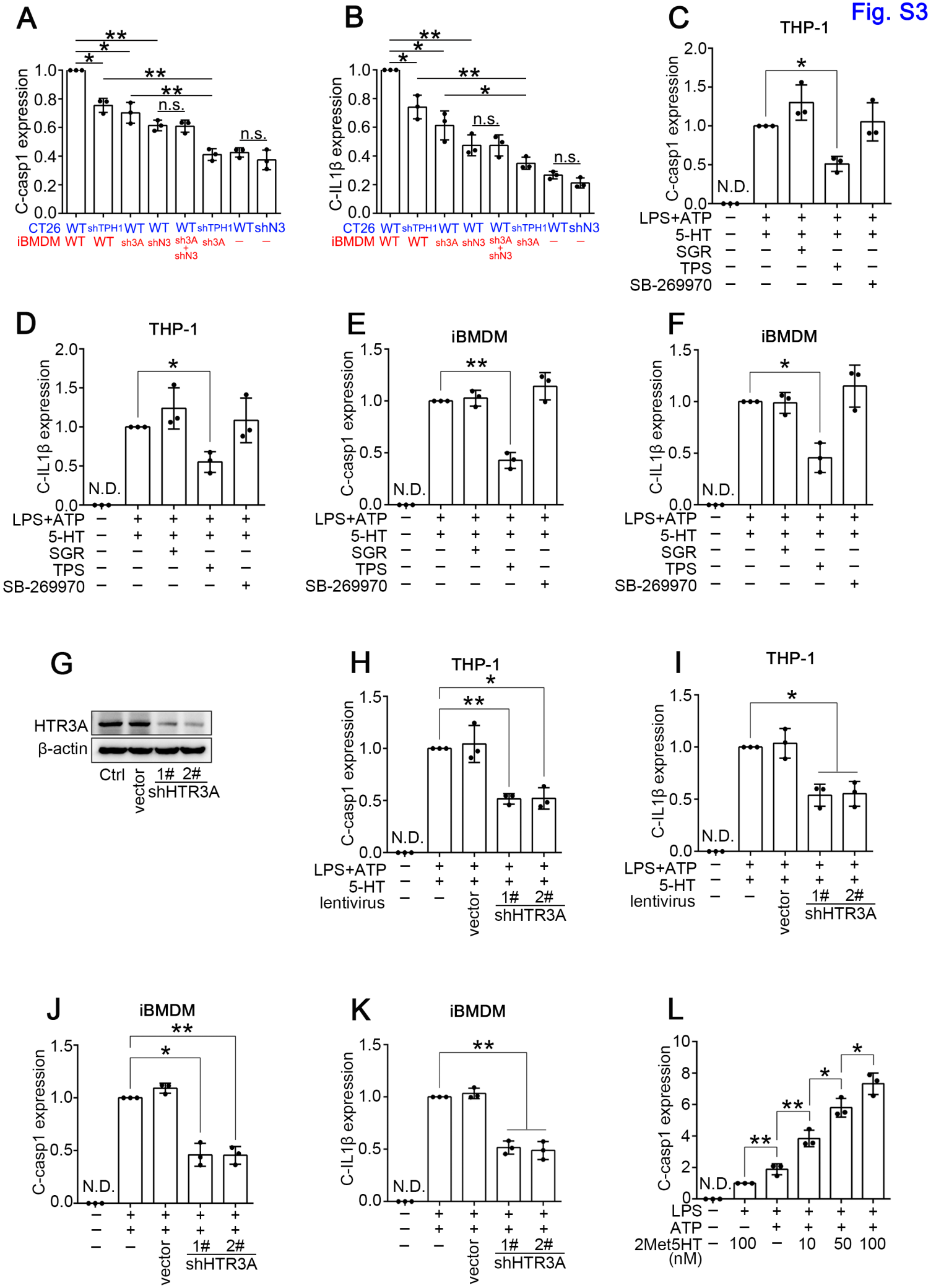
iBMDM WT WT sh3A shN3 sh3A + shN3 sh3A – –

Fig. S3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B
C
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C-IL1β expression
n.s.
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iBMDM WT WT sh3A shN3 sh3A + shN3 sh3A – –
N.D.
LPS+ATP
5-HT
SGR
TPS
SB-269970
D
THP-1
E
iBMDM
F
iBMDM
G
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β-actin
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vector
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THP-1
I
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2Met5HT (nM)
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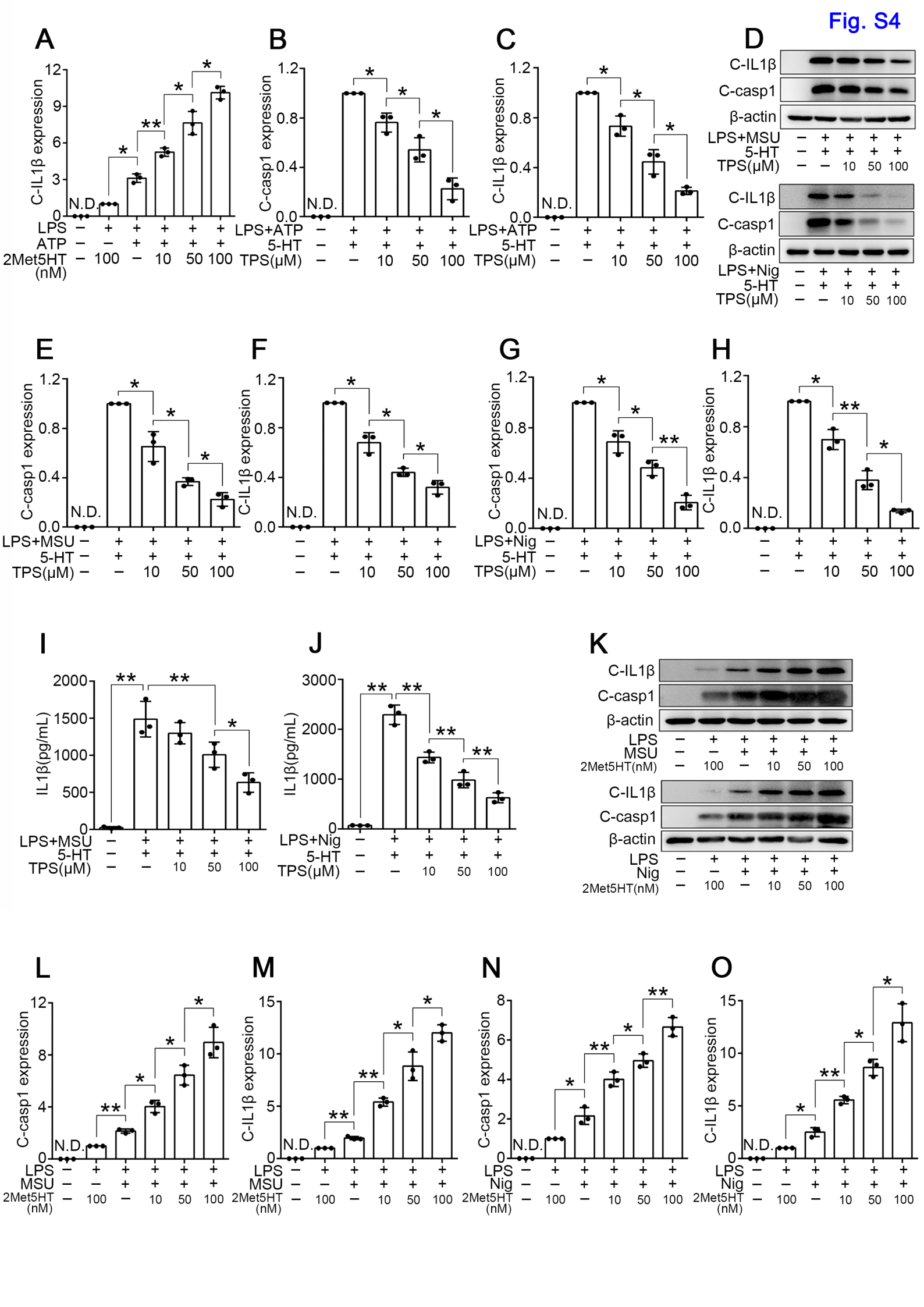
Fig. S4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C-IL1β expression
D
C-IL1β
C-casp1
β-actin
LPS+MSU
LPS+Nig
E
C-casp1 expression
F
C-IL1β expression
G
C-casp1 expression
H
C-IL1β expression
I
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J
IL1β(pg/mL)
K
LPS
MSU
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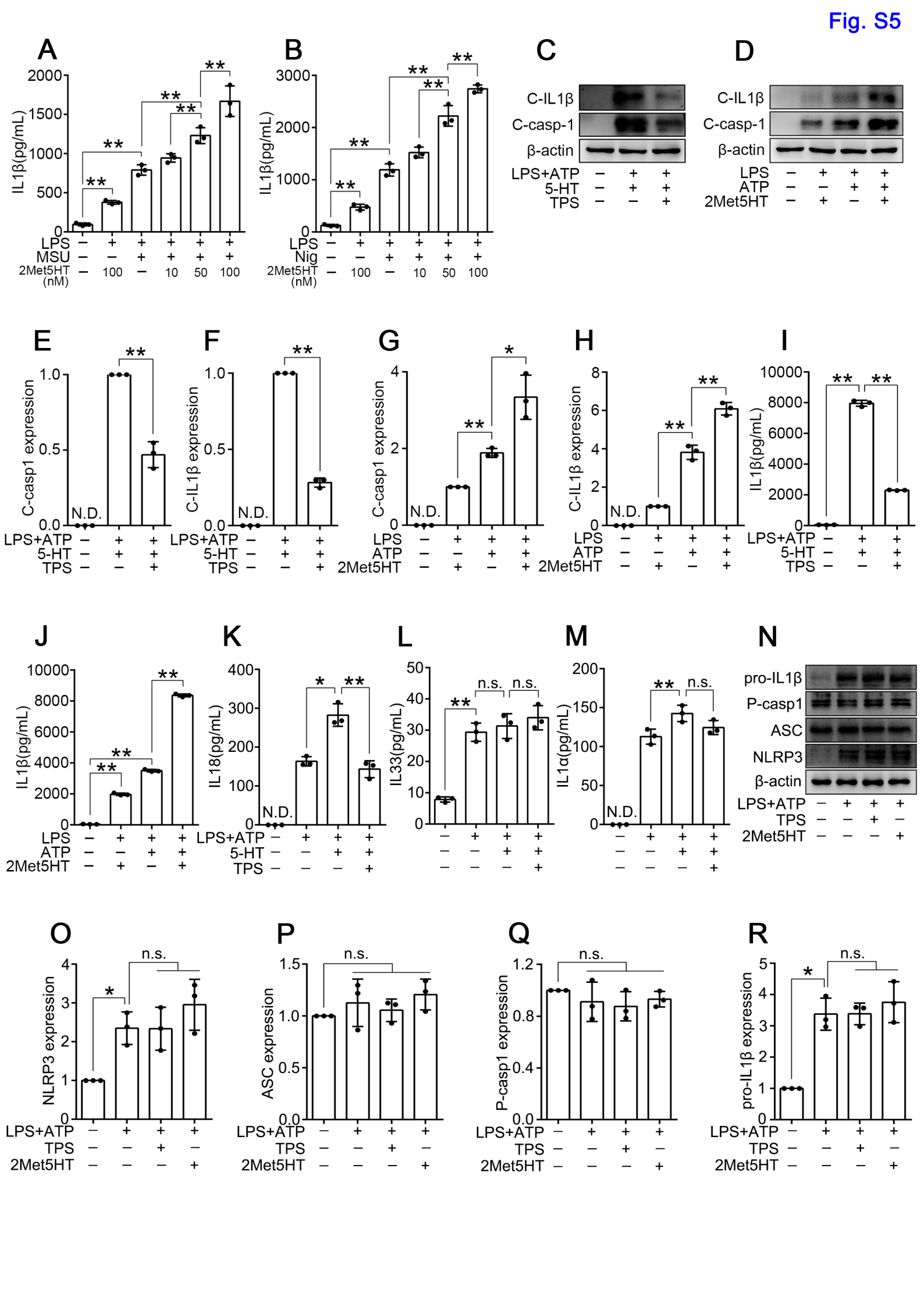
C-IL1β expression

Fig. S5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C-IL1β
C-casp-1
β-actin
LPS+ATP
5-HT
TPS
D
C-IL1β
C-casp-1
β-actin
LPS
ATP
2Met5HT
E
C-casp1 expression
N.D.
LPS+ATP
5-HT
TPS
F
C-IL1β expression
N.D.
LPS+ATP
5-HT
TPS
G
C-casp1 expression
N.D.
LPS
ATP
2Met5HT
H
C-IL1β expression
N.D.
LPS
ATP
2Met5HT
I
IL1β(pg/mL)
LPS+ATP
5-HT
TPS
J
IL1β(pg/mL)
LPS
ATP
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K
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LPS+ATP
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TPS
L
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n.s.
M
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N.D.
n.s.
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pro-IL1β
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ASC
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NLRP3 expression
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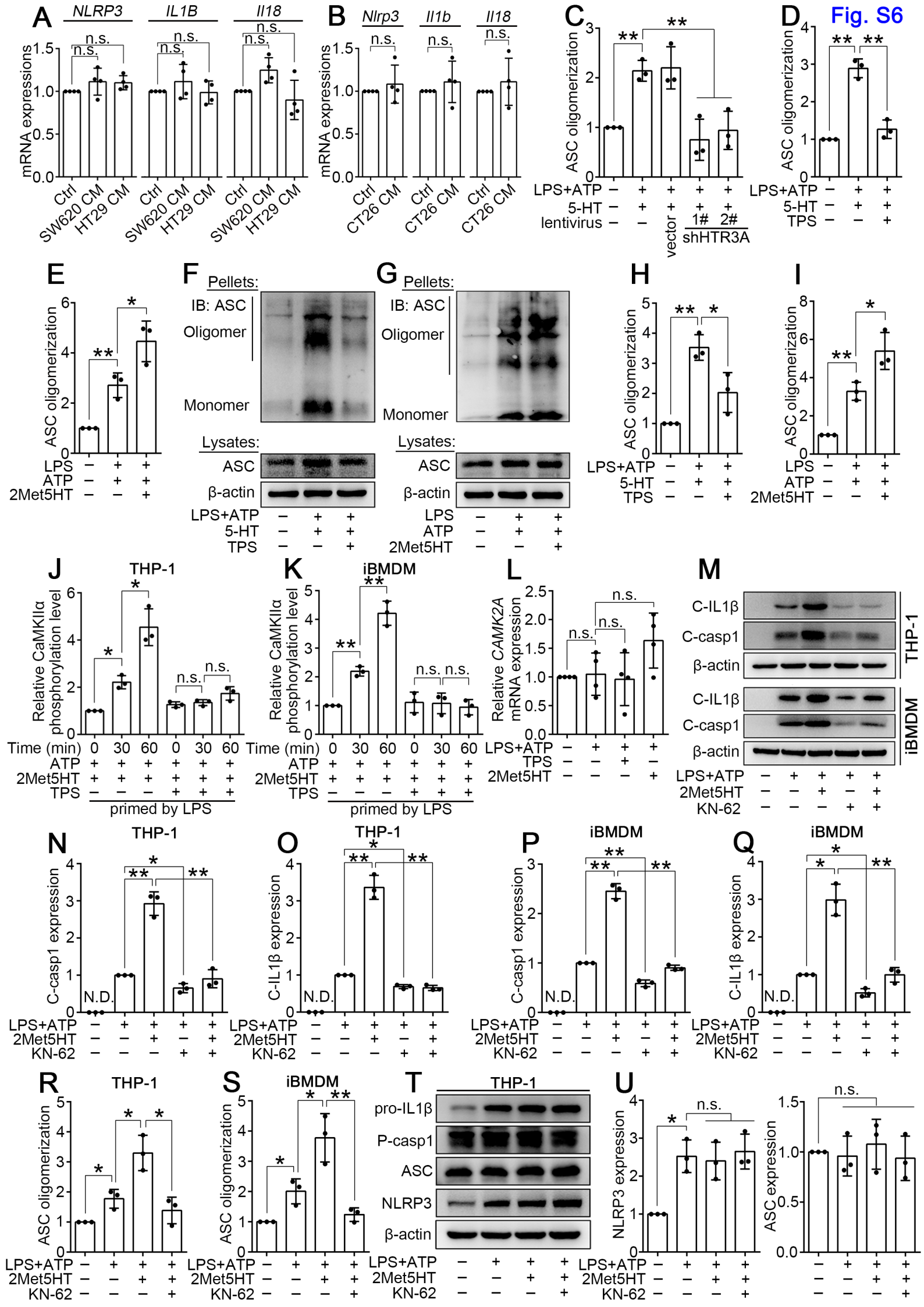
Fig. S6
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Il18
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HT29 CM
B
Nlrp3
Il1b
Il18
Ctrl
CT26 CM
C
ASC oligomerization
LPS+ATP
5-HT
lentivirus
vector
1#
2#
shHTR3A
D
TPS
E
LPS
ATP
2Met5HT
F
Pellets:
IB: ASC
Oligomer
Monomer
Lysates:
ASC
β-actin
G
H
I
J
THP-1
Relative CaMKIIα phosphorylation level
Time (min)
primed by LPS
K
iBMDM
L
Relative CAMK2A mRNA expression
M
C-IL1β
C-casp1
KN-62
N
C-casp1 expression
N.D.
O
C-IL1β expression
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Q
R
S
T
pro-IL1β
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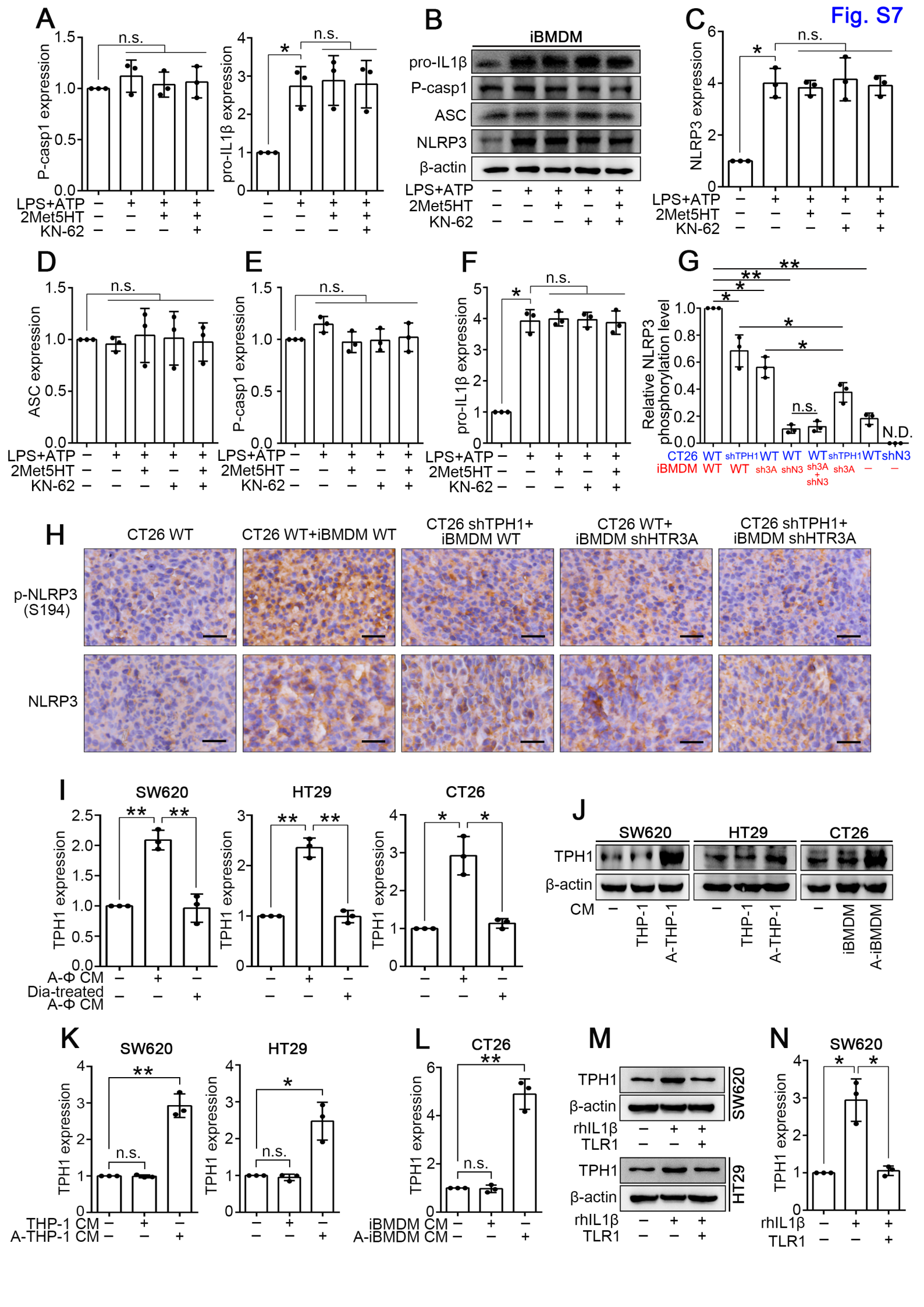
U
NLRP3 expression
ASC expression

Fig. S7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pro-IL1β expression
n.s.
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KN-62
B
iBMDM
pro-IL1β
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ASC
NLRP3
β-actin
C
NLRP3 expression
D
ASC expression
E
P-casp1 expression
F
pro-IL1β expression
G
**
Relative NLRP3 phosphorylation level
N.D.
CT26 WT
shTPH1
WT
shN3
sh3A
sh3A + shN3
iBMDM WT
H
CT26 WT
CT26 WT+iBMDM WT
CT26 shTPH1+ iBMDM WT
CT26 WT+ iBMDM shHTR3A
CT26 shTPH1+ iBMDM shHTR3A
p-NLRP3 (S194)
NLRP3
I
SW620
HT29
CT26
TPH1 expression
A-Φ CM
Dia-treated A-Φ CM
J
TPH1
β-actin
CM
THP-1
A-THP-1
iBMDM
A-iBMDM
K
THP-1 CM
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L
iBMDM CM
A-iBMDM CM
M
rhIL1β
TLR1
N

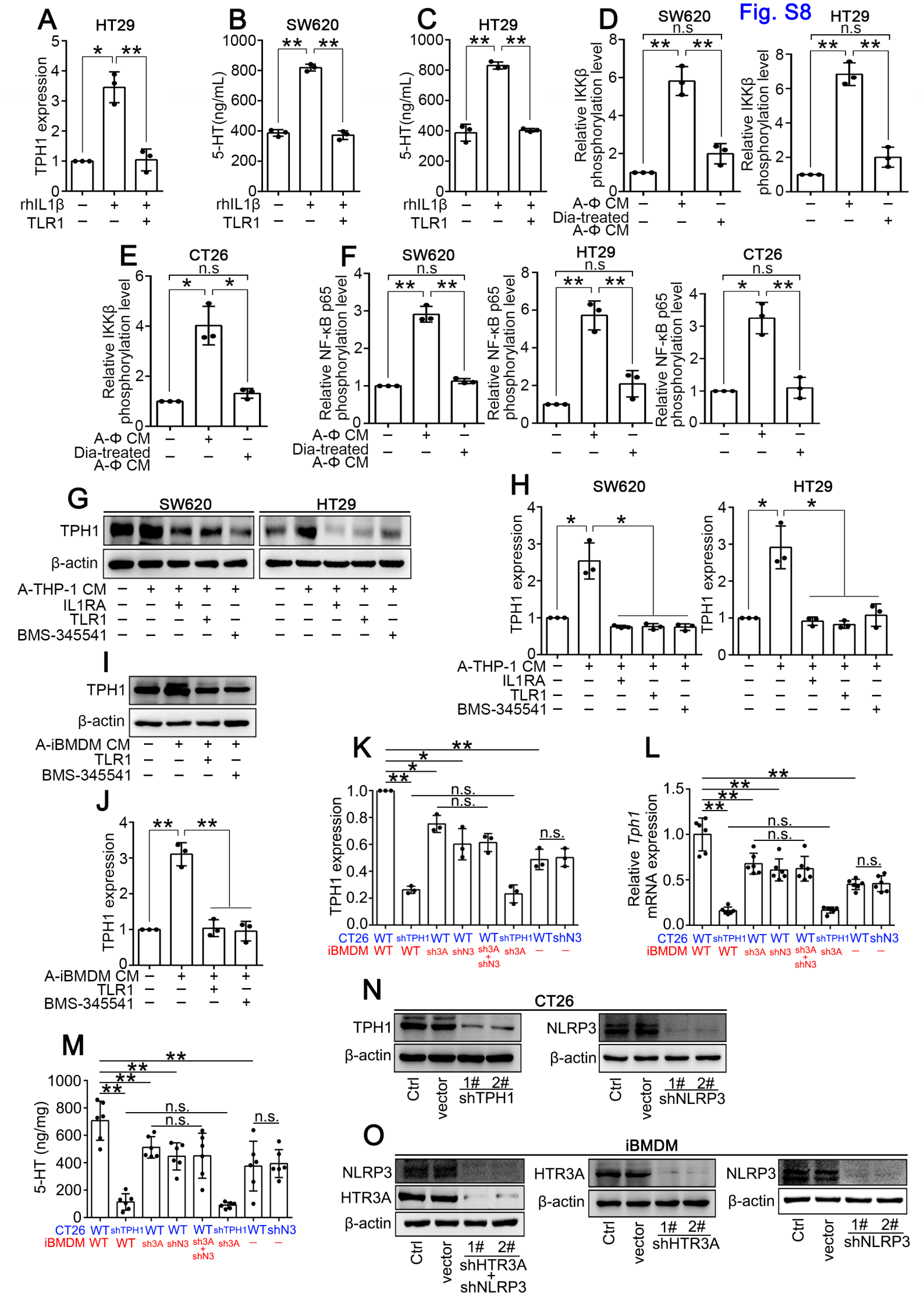
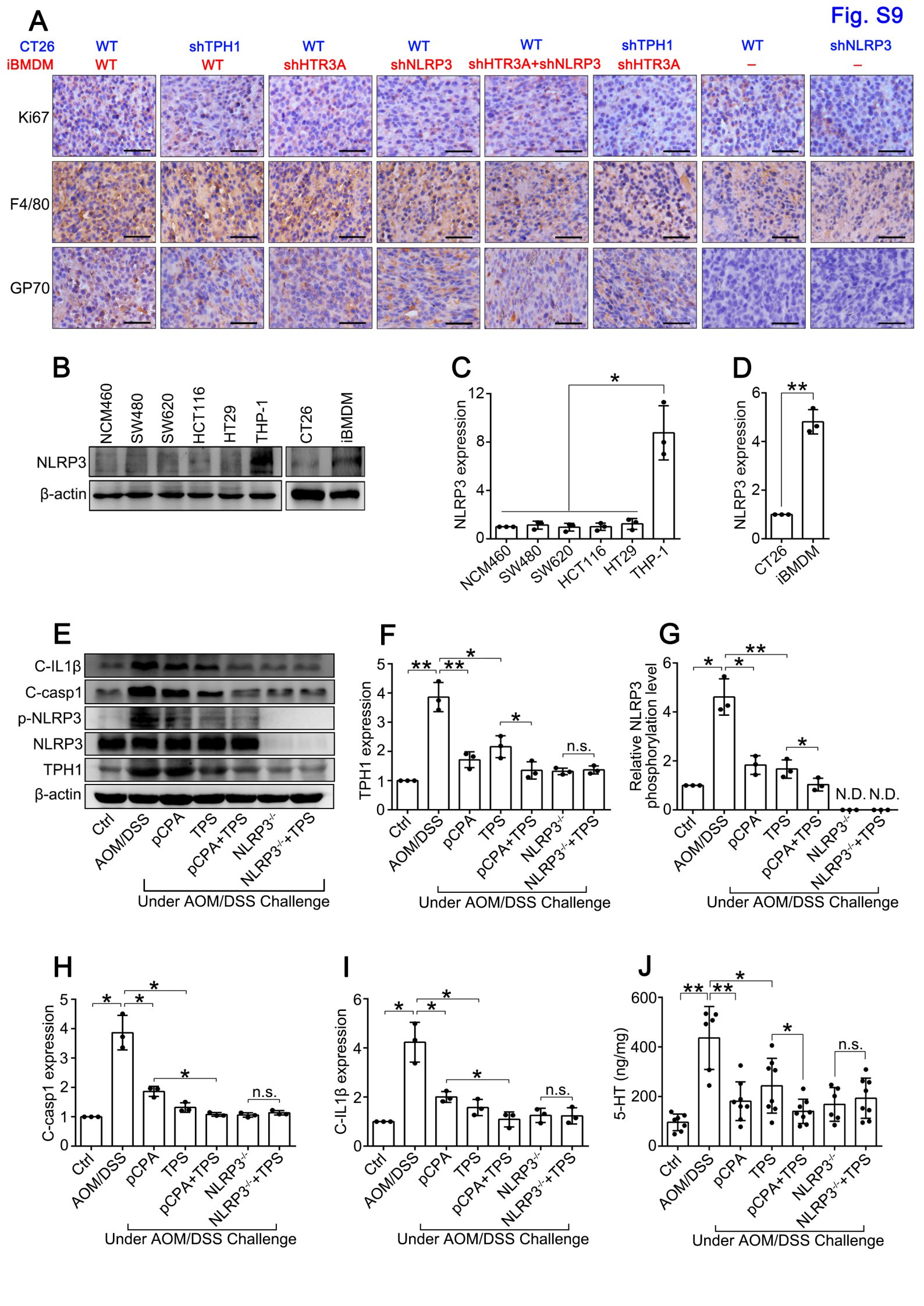


Fig. S8
A
HT29
TPH1 expression
rhIL1β
TLR1
B
SW620
5-HT(ng/mL)
C
HT29
D
SW620
HT29
n.s
Relative IKKβ phosphorylation level
A-Φ CM
Dia-treated A-Φ CM
E
CT26
F
SW620
HT29
CT26
Relative NF-κB p65 phosphorylation level
G
SW620
HT29
TPH1
β-actin
A-THP-1 CM
IL1RA
TLR1
BMS-345541
H
SW620
HT29
I
A-iBMDM CM
J
K
L
Relative Tph1 mRNA expression
CT26 WT shTPH1 WT WT WT shTPH1 WT shN3
iBMDM WT WT sh3A shN3 sh3A + shN3 sh3A
M
5-HT (ng/mg)
N
CT26
NLRP3
Ctrl
vector
1# 2# shTPH1
1# 2# shNLRP3
O
iBMDM
HTR3A
1# 2# shHTR3A + shNLRP3
1# 2# shHTR3A
1# 2# shNLRP3

Fig. S9


A
CT26
iBMDM
WT
WT
shTPH1
WT
WT
shHTR3A
WT
shNLRP3
WT
shHTR3A+shNLRP3
shTPH1
shHTR3A
WT
–
shNLRP3
–
Ki67
F4/80
GP70
B
NCM460
SW480
SW620
HCT116
HT29
THP-1
CT26
iBMDM
NLRP3
β-actin
C
NLRP3 expression
NCM460
SW480
SW620
HCT116
HT29
THP-1
D
NLRP3 expression
CT26
iBMDM
E
C-IL1β
C-casp1
p-NLRP3
NLRP3
TPH1
β-actin
Ctrl
AOM/DSS
pCPA
TPS
pCPA+TPS
NLRP3-/-
NLRP3-/-+TPS
Under AOM/DSS Challenge
F
TPH1 expression
n.s.
Under AOM/DSS Challenge
G
Relative NLRP3 phosphorylation level
N.D.
N.D.
Under AOM/DSS Challenge
H
C-casp1 expression
n.s.
Under AOM/DSS Challenge
I
C-IL1β expression
n.s.
Under AOM/DSS Challenge
J
5-HT (ng/mg)
n.s.
Under AOM/DSS Challenge

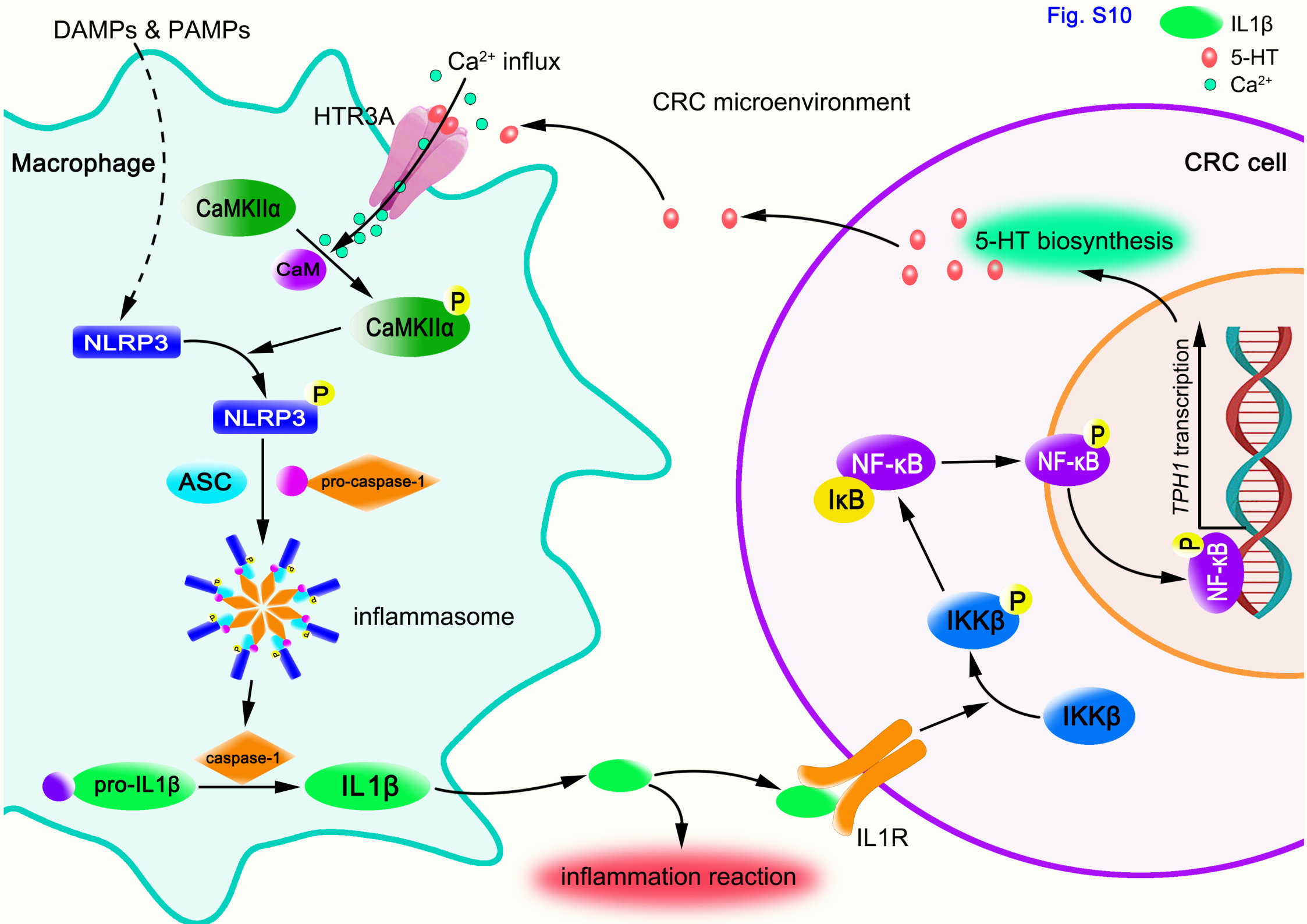


Fig. S10
IL1β
5-HT
Ca2+
DAMPs & PAMPs
Ca2+ influx
HTR3A
CRC microenvironment
Macrophage
CRC cell
CaMKIIα
CaM
P
CaMKIIα
NLRP3
P
NLRP3
5-HT biosynthesis
ASC
pro-caspase-1
TPH1 transcription
NF-κB
IκB
P
NF-κB
P
NF-κB
inflammasome
IKKβ
P
IKKβ
caspase-1
pro-IL1β
IL1β
IL1R
inflammation reaction