## The mitochondrial protease HtrA2 restricts the NLRP3 and AIM2 inflammasomes

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Supplemental information

## **Supplemental Methods**

## Reagents.

For immunoblotting: anti-mouse caspase-1 p20 (B4B, Genentech), anti-IL1 $\beta$  (AF401NA, R&D Systems), anti-NLRP3 (Cryo2, AdipoGen), anti-ASC (N-15R, Santa Cruz), anti- $\beta$ -actin (AC-15, Sigma) or anti-tubulin (H-235, Santa Cruz); anti-Beclin 1 (D40C5) and anti-LC3 (2775) (Cell Signaling Technology). The following DuoSet ELISA kits from R&D were used: anti-mouse IL-1 $\beta$  (DY401) and anti-human IL-1 $\beta$  (DY201). Ultrapure LPS (from *E. coli* strain 0111:B4) was from Invivogen. Brefeldin A, saponin, PMA, ionomycin, ATP, nigericin, rapamycin, Bcl-XL inhibitor Z36, Bafilomycin A1, chloroquine and cycloheximide were all from Sigma-Aldrich. Imject Alum adjuvant was from ThermoFischer Scientific. Inositol monophosphatase inhibitor L690-330 was from Tocris-Bioscience. The following plasmids were obtained directly from Addgene: pBabe mCherry-EGFP-LC3 (22418) and pCL-Eco (12371). The following antibodies or reagents were used for flow cytometry: anti-CD3-PerCPCy5.5 (145-2C11), anti-TCR $\beta$ -PerCPCy5.5 (H57-597), anti-CD69-PeCy7 (H1.2F3), anti-Ly49H (all from eBioscience); anti-NK1.1-APC (PK136), anti-IFN $\gamma$ -PECy7 (XM1.2) (all from BD Biosciences); Annexin V-CF405M, MitoView (Biotium); LysoTracker Deep Red, MitoTracker Red CMXRos (Life Technologies).

## **Supplemental Figure Legends**

Figure S1. Related to Figure 1. HtrA2 protease regulates the NLRP3 inflammasome.

(a) TNF $\alpha$  secretion in supernatants from LPS-primed *mnd2tg* and protease-sufficient littermate (+/+, +/*mnd2tg*) primary BMDMs treated with ATP (5 mM, 45 min), transfected with synthetic B-DNA analog (poly dA:dT, 1.8 µg ml<sup>-1</sup>; 18 h) or flagellin (1 µg ml<sup>-1</sup>, 18 h), or infected with SeV (500 HAU ml<sup>-1</sup>, 18 h).

(b) HtrA2 localization relative to ASC after ATP stimulation by confocal microscopy.

(c) Amounts of ROS by FACS in immortalized BMDMs treated as in Fig. 1i.

Data are representative of two experiments (a: mean  $\pm$  s.e.m.; n=3 mice per experiment) and one independent experiment performed once (b, c).

Figure S2. Related to Figure 2. *HtrA2 protease regulates the AIM2 but not NLRC4 inflammasome.* 

(a) Cleaved caspase-1 p20 and IL-1 $\beta$  p17 by immunoblot of culture supernatants of LPS-primed *mnd2* and +/+ immortalized BMDMs treated with ATP (5 mM, 45 min) or transfected with poly dA:dT (1.8 µg ml<sup>-1</sup>; 18 h) or flagellin (1 µg ml<sup>-1</sup>, 18 h).

(b) IL-1 $\beta$  secretion by LPS-primed immortalized +/+ and *mnd2* BMDMs treated with the indicated concentrations of polydA:dT (18 h).

Figure S3. Related to Figure 3. HtrA2 controls Autophagy flux.

(a) LC3 confocal imaging, (b) baseline number of GFP-LC3 puncta and (c) frequency of cells with greater than 3 strong GFP-LC3 puncta per cell in LC3-GFP transduced immortalized +/+ or *mnd2* BMDMs cultured in the absence or presence of chloroquine (50  $\mu$ M, CQ).

(d) IL-1 $\beta$  secretion in protease-sufficient BMDMs treated with rapamycin as in Fig. 3c.

(e) mCherry/GFP LC3 ratio following rapamycin stimulation in control, HtrA2- or ATG5depleted HEK-293T cells.

(f) ASC oligomerization in response to SeV infection in HEK-293T cells following inhibition of autophagic flux using BafA1 measured by FACS.

(g) Cycloheximide-chase analysis of formed ASC complexes in SeV infected control, HtrA2or ATG5-depleted cells.

Data are representative of two independent experiments (e: n>250,000 cells per condition; g: mean  $\pm$  s.d.; n=2 technical replicates per experiment), and independent experiments performed once (**a**,**b**,**c**: mean  $\pm$  s.e.m., n> 40 cells per condition; **d**: mean  $\pm$  s.e.m., n=3 mice; **f**: n>500,000 cells per condition). \*\*\*\* *p* < 0.0001 (Tukey one-way ANOVA post-test (**b**, **c**)).

Figure S4. Related to Figure 4. MCMV infection supporting data.

(a) Spleen weights 40 h post-infection with MCMV.

(b) PMA and ionomycin-induced IFN $\gamma$  in NK cells by intracellular FACS.

(c, d) Percentages of splenic CD69<sup>+</sup> NK cells and (d) CD69 MFI at 40 h post-infection with MCMV.

All data represent two independent MCMV infections pooled (mean  $\pm$  s.e.m., n=4-8 mice per genotype).

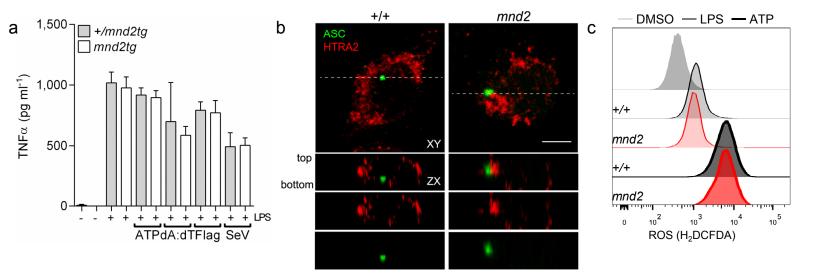
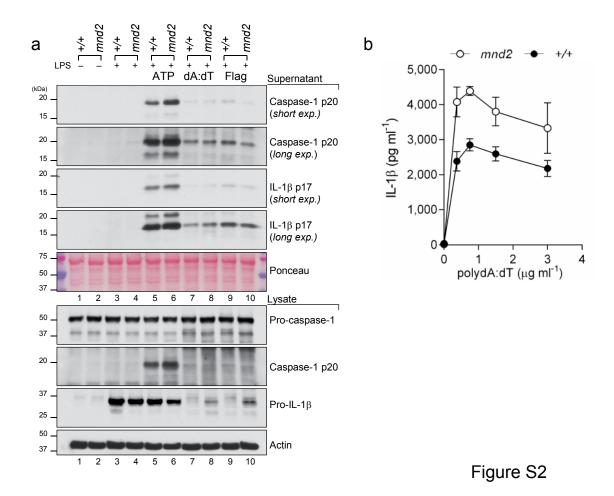


Figure S1



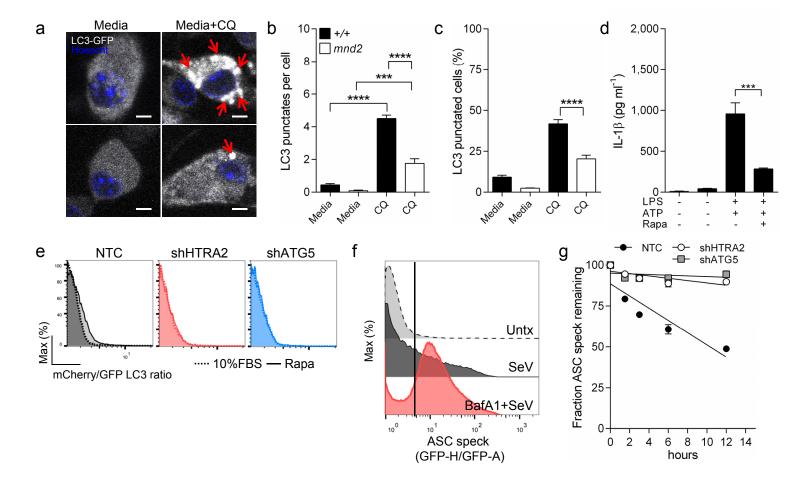


Figure S3

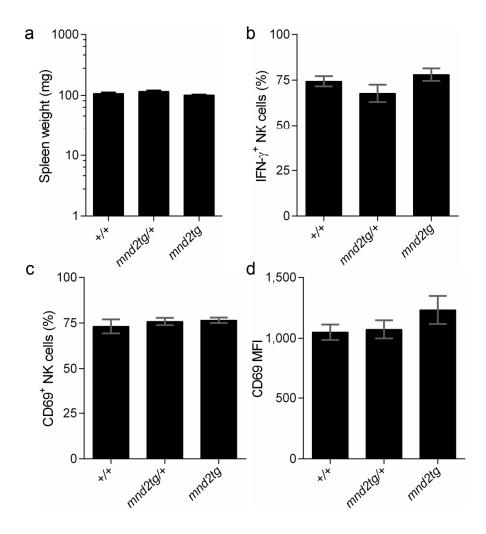


Figure S4

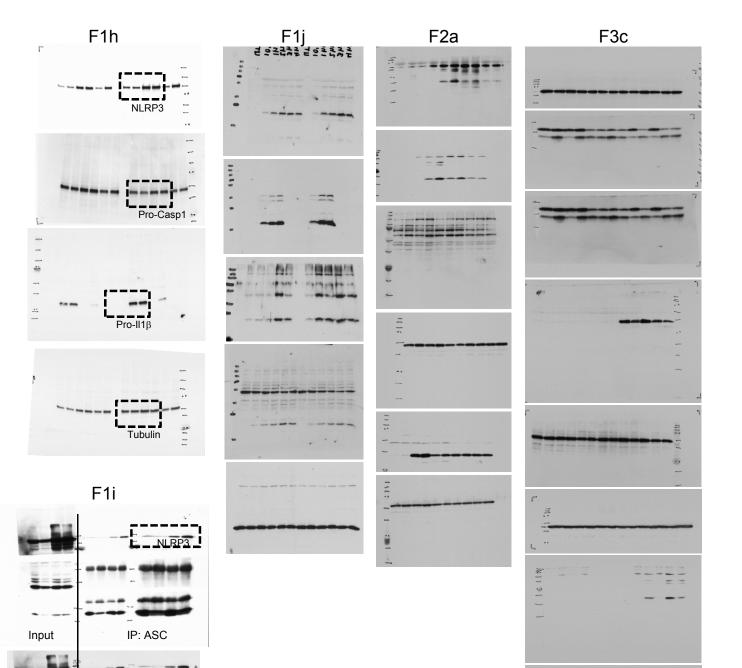


Figure Westernblots

HTRA2

NLRP3

8.P.

C

5

L

ASC

I. TKA2 5 LM 3 nnd

1:11:11

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