

Supplemental Materials

Methods

Animal model

All procedures were approved by the Ethical Committee of Qilu Hospital of Shandong University (Approval No. DWLL-2018-018). A model of progressive atherosclerosis was generated in ApoE^{-/-} mice (Vital River Laboratory Animal Technology Co., Beijing, China) by high-fat diet (HFD) feeding for different durations (8, 12, 18, 24 and 38 weeks) to investigate the dynamic changes in LAMP-2A expression. Immunofluorescence analysis was used to examine two stages of atherosclerosis (“early” versus “advanced” lesions, as defined by the duration of HFD feeding, 8 weeks and 24 weeks, respectively) ^{47, 48}.

Macrophage-specific LAMP-2A (L2A)-deficient mice on a C57BL/6 background were generated using loxP insertion to selectively delete the exon region in the LAMP-2 gene that encodes the LAMP-2A variant (L2A^{fl/fl} mice, Viewsolid Biotech, Beijing, China) and crossed with Cre-recombinase transgenic mice under the control of the Lysosomal M promoter (Jackson Laboratory). L2A^{fl/fl} LysM-cre mice (L2A-mØKO mice) were further crossed with ApoE^{-/-} mice (C57BL/6 background) to generate L2A^{fl/fl}/LysM-Cre/ApoE^{-/-} mice (L2A-mØKO/ApoE^{-/-} mice). Eight-week-old L2A-mØKO/ApoE^{-/-} mice and their L2A^{fl/fl}/LysM-Cre (-)/ApoE^{-/-} littermates were fed a HFD (21% [wt/wt] fat, 1.0% cholesterol, 0.3% sodium cholate and 5% saccharose) for 16 weeks.

For *in vivo* LPS challenge, L2A-mØKO mice and their control littermates

1 were injected intraperitoneally with 1 mg/kg LPS (L2880, *Escherichia coli*,
2 055:B5, Sigma, USA). After 2 h, mice were euthanized and their serum was
3 collected for subsequent experiments. As previous studies reported that
4 estrogen may exert a protective effect on atherosclerosis ⁴⁶, we used only male
5 mice in this study to avoid potential conflicting results.

6 **Animal randomization and determination of group size**

7 A random number table was used for mouse randomization. Before grouping,
8 all mice were first ordered by their weight from 1 to n and each of them was
9 assigned one of the consecutive random numbers selected from the random
10 number table. Then, all the selected random numbers were ranged from small
11 to large and every consecutive 5 mice were chosen as one group. All data were
12 collected and analyzed by two observers who were not aware of group
13 assignment and treatment of mice. No samples or animals were excluded from
14 data analysis. According to our study ⁴⁹, after 16 weeks of high-fat feeding
15 (HFD), the proportion of aortic atherosclerotic lesions in ApoE^{-/-} mice was
16 approximately 10%, and a deletion of macroautophagy-related genes (eg, Atg5
17 or p62) resulted in a double increase in aortic plaque area relative to their
18 control groups ⁵⁰⁻⁵². Assuming type I error (α) and type II error (β) are 5% and
19 0.20, respectively, with a power >0.80, the sample size required is 4. By taking
20 into account of accidental mouse death, we set n=5 in each mouse group of
21 this study. Assuming type I error (α) and type II error (β) are 5% and 0.20,
22 respectively, with a power >0.80, the sample size required is 4. By taking

1 account of accidental mouse death, we set n=5 in each mouse group of this
2 study.

3 **Human coronary artery sampling**

4 Human coronary atherosclerotic plaques were obtained from autopsy
5 specimens of 5 male body donors with coronary heart disease after sudden
6 coronary death, and the bodies were provided by the Red Cross Society of
7 Shandong Province, China. The human study protocol was approved by the
8 Ethical Committee of Qilu Hospital of Shandong University (Approval No. KYLL-
9 2016-333). The coronary arteries were embedded with optimal cutting
10 temperature compound (OCT, Sakura, Japan) and cut into 7- μ m-thick cross
11 sections for histopathological staining.

12 **Atherosclerotic lesion analysis**

13 The atherosclerotic lesions in the aorta were quantified by *en face* analysis and
14 aortic root cross-sectional measurement. For *en face* analysis, mouse aortas
15 were placed in cold normal saline, cleaned of fatty tissue, and incised
16 longitudinally at the thoracic aorta and aortic arch. The aortas were stained with
17 0.5% oil red O (ORO, Yiyuan Biotechnology, Guangzhou, China) for 30 min
18 prior to visualization. Images were taken with a digital camera (70D, Canon,
19 Japan). The ORO-stained lesions were quantified as a percentage of the total
20 aortic area with SigmaScan Pro 5 (Systat Software, Inc.). For aortic root cross-
21 sectioning, the heart with attached aortic roots was embedded in OCT, and
22 serially sectioned at 7 μ m. Slides were fixed with 4% paraformaldehyde and

1 stained with ORO and hematoxylin-eosin (H&E; Solarbio, Beijing Solarbio
2 Science & Technology, China) following the manufacturer's protocol.
3 Measurement of the aortic atherosclerotic lesions was performed by
4 investigators blind to mouse genotype.

5 **Histopathological staining**

6 For immunohistochemical (IHC) staining, frozen cross-sections were incubated
7 with 3% H₂O₂ for 10 min at room temperature. Then, sections were blocked
8 with 5% normal goat serum in PBS for 1 hour at room temperature and
9 incubated with the corresponding primary antibodies at 4°C overnight: rat
10 monoclonal antibody against MOMA-2 (MCA519G; AbD, UK), rabbit polyclonal
11 antibody against LAMP-2A (AMC2, Invitrogen, USA) and rabbit monoclonal
12 antibody against α -smooth muscle actin (α -SMA, #19245, CST, USA). On the
13 next day, sections were incubated with horseradish peroxidase (HRP)-
14 conjugated goat anti-rabbit IgG (PV-9001, ZSJB-BIO, China) or goat anti-rat
15 IgG (PV-9004, ZSJB-BIO, China) for 30 min at room temperature. The positive
16 reactions of tissue sections were developed using an AEC Peroxidase
17 Substrate Kit (#A2010, Solarbio, China) displayed as red color. Sections
18 reacting with non-immune IgG as well as secondary antibodies were used as
19 negative controls. The proportion of positive staining area of LAMP-2A was
20 measured with the use of Image-Pro Plus software (Media Cybernetics, Inc.,
21 USA) by investigators blind to mouse genotype.

22 For immunofluorescent staining, frozen cross-sections were incubated with

1 3% H₂O₂ for 10 min and permeabilized with 0.4% Triton-X-100 in PBS for 15
2 min at room temperature. Then, sections were blocked with 5% normal donkey
3 serum in PBS for 1 hour at room temperature and incubated with the above
4 primary antibodies, as well as a mouse monoclonal antibody against CD68
5 (OM245833; OmnimABs, USA), rat monoclonal antibody against F4/80
6 (ab16911, Abcam, UK), rat monoclonal antibody against LAMP1(ab25245,
7 Abcam, UK), and mouse monoclonal antibody against NLRP3 (AG-20B-0014;
8 AdipoGen, USA). On the next day, sections were incubated with donkey anti-
9 mouse IgG H&L (Alexa Fluor® 594) (ab150112, Abcam, UK), donkey anti-rat
10 IgG H&L (Alexa Fluor® 594) (ab150156, Abcam, UK) or donkey anti-rabbit IgG
11 H&L (Alexa Fluor® 488) (ab150061, Abcam, UK) for 1 h at room temperature.
12 After washing, sections were stained with undiluted Fluoroshield Mounting
13 Medium with DAPI (ab104139, Abcam, UK). Sections reacting with non-
14 immune IgG as well as secondary antibodies were used as negative controls.
15 An electric upright microscope (DS-Ri2, Nikon, Japan) was used for imaging.

16 **Macrophage culture and treatment**

17 Primary peritoneal macrophages were obtained from L2A-mØKO mice and
18 their control littermates as previously described³. Briefly, 1 mL of 3% sterile
19 starch was intraperitoneally injected into each mouse, and 3 days later, mice
20 were euthanized and sterilized in 75% ethanol for 10 s. The skin of the inferior
21 ventral abdomen was incised to expose peritoneum and 15 mL of cold PBS was
22 intraperitoneally injected. The cell suspension was aspirated from the peritoneal

1 cavity and centrifuged at 800 rpm at 4 °C for 5 min. The supernatant was
2 removed and the cell pellet was resuspended with DMEM supplemented with
3 10% FCS (Gibco) and 1% antibiotics (Gibco). The cells were counted and
4 incubated at 37 °C for 2 h. The non-adherent cells were removed using PBS
5 and the adherent macrophages were incubated in complete medium. The
6 macrophages were treated with the following reagents: LPS (L2880, *E. coli*,
7 055:B5, Sigma, USA), ATP (A7699, Sigma, USA) and cycloheximide (CHX,
8 2112, CST, USA).

9 **Western blotting**

10 Protein lysates were extracted from peritoneal macrophages on ice using RIPA
11 lysis buffer (R0020, Solarbio, China) supplemented with complete protease
12 inhibitor cocktail (P6730, Solarbio, China). Protein lysates of mouse whole aorta
13 were extracted using protein extraction kit (SD-001/SN-002, Invent, USA).
14 Samples were separated, transferred and incubated as previously described⁴⁵
15 with primary antibodies against the following: LAMP-2A (AMC2, Invitrogen,
16 USA), LAMP2 (ab13524, Abcam, UK), LAMP1 (#9091, CST, USA), NLRP3
17 (ab263899, Abcam, UK), pro-Caspase-1 + p10 + p12 (ab179515, Abcam, UK),
18 ASC (D2W8U, #67824, CST, USA), IL-1 β (p31) (ab234437, Abcam, UK), IL-1 β
19 (p17) (#63124, CST, USA), JNK (#9252, CST, USA), p-JNK (#9251, CST, USA),
20 p38 MAPK (#8690, CST, USA), p-p38 MAPK (#4511, CST, USA), p44/42 MAPK
21 (Erk1/2) (#4695, CST, USA), p-p44/42 MAPK (Erk1/2) (#4370, CST, USA), NF-
22 κ B p65 (#8242, CST, USA), p-NF- κ B p65 (Ser536) (#3033, CST, USA), I κ B α

1 (#4812, CST, USA), p-IkB α (Ser32) (#2859, CST, USA), histone H3 (#4499,
2 CST, USA), perilipin 2 (GP40, Progen Biotechnik, Germany), SQSTM1/p62
3 (#39749, CST, USA), LC3B (#43566, CST, USA), Atg7 (#8558, CST, USA),
4 Atg5 (#12994, CST, USA), Beclin-1 (#3495, CST, USA), Cathepsin B
5 (ab214428, Abcam, UK), Cathepsin D (ab75852, Abcam, UK), and β -actin
6 (#4970, CST, USA). On the second day, the membranes were incubated with
7 HRP-conjugated secondary antibodies (ZB-2301, ZB-2305, ZB-2307, ZSJB-
8 BIO, China) or at room temperature for 1.5 h. After washing, signals were
9 detected by adding immobilon ECL ultra western HRP substrate (WBULS0500,
10 Millipore, USA) and imaged by using a luminescent image analyzer (Amersham
11 Imager 600, GE, USA).

12 **Production of polyclonal antibodies against LAMP-2B and LAMP-2C**

13 Rabbit polyclonal antibodies against LAMP-2B and LAMP-2C were produced
14 by AtaGenix Laboratories (Wuhan, China). Synthetic peptides consisting of the
15 cytosolic tail of mouse LAMP-2B (aa 399 to 413, FISYMIGRRKSRTGY) or that
16 of LAMP-2C (aa 401 to the C-terminus, YLIGRRKTYAGYQTL) were used to
17 produce antibodies that recognize only LAMP-2B or LAMP-2C, respectively.

18 **Enrichment of active Caspase-1 and IL-1 β in the cellular supernatant**

19 Cleaved Caspase-1 (p10 + p12) and IL-1 β (p17) in the cellular supernatant
20 were enriched and assessed by Western blotting. Briefly, after macrophages
21 were treated with LPS/ATP, the cellular supernatant was mixed with 4 volumes
22 of cold acetone and placed in a refrigerator at -80°C overnight. The next day,

1 the mixture was centrifuged at 1,0000×g for 10 min. The supernatant was
2 carefully removed, and the tube was opened for 30 min to allow the acetone to
3 evaporate completely. To dissolve the pellets, 1× SDS loading buffer was added,
4 and the mixture was boiled at 100°C for 10 min.

5 **Transfections and adenovirus infection**

6 Adenovirus containing plasmids expressing LAMP-2A or tandem fluorescent
7 mRFP-GFP-LC3 were produced by BioSune Biotechnology (Shanghai, China)
8 and HANBIO (HB-AP2100001, China), respectively. For transfection of mRFP-
9 GFP-LC3 adenovirus, mouse peritoneal macrophages (5×10^5 cells/well) were
10 seeded in 12-well plates. For overexpression of LAMP-2A, mouse peritoneal
11 macrophages (5×10^5 cells/well) were seeded in 6-well plates. Transfection of
12 primary peritoneal macrophages was conducted with a MOI=300 in the
13 presence of 5 µg/mL polybrene for 12 h. After transfection for 12h, the
14 supernatant was removed and the cells were cultured in fresh medium for
15 another 48 h, according to the manufacturer's instructions.

16 **Plasmid construction and transfection**

17 Flag-tagged LAMP-2A (Flag-LAMP-2A), Flag-HSC70, Myc-tagged NLRP3
18 (Myc-NLRP3) or mutant Myc-NLRP3 (Myc-NLRP3 Mut), Myc-Caspase-1 and
19 Myc-ASC plasmids were provided by BioSune Biotechnology (Shanghai,
20 China). The plasmids were transiently transfected into HEK293T cells with
21 Lipofectamine 2000 (#11668019, Thermo Fisher) according to the
22 manufacturer's instructions.

1 **ELISA**

2 The concentrations of mouse IL-1 β (#MHSLB00 and #MLB00C, R&D
3 Systems,), IL-18 (#7625, R&D Systems) and TNF- α (#MHSTA50 and #MTA00B,
4 R&D Systems) in the serum and cellular supernatants were measured using
5 ELISA kits.

6 **RNA quantitation**

7 Total RNA was extracted from the primary macrophages of mice in the different
8 groups using an RNAfast2000 Total RNA Extraction Kit (Fastagen, China)
9 according to the manufacturer's instructions. cDNA was synthesized using a
10 PrimeScript RT Reagent Kit (Vazyme Biotech, China). Synthesis was
11 performed by subjecting each sample to 5 minutes at 25°C for annealing, 15
12 minutes at 55°C to allow for reverse transcription and 2 minutes at 85°C for
13 reverse transcriptase inactivation. The obtained cDNA was subjected to Q-PCR
14 using SYBR Green (Vazyme Biotech, China) for the relative quantification of IL-
15 1 β , IL-18 and TNF- α mRNA expression. The following PCR amplification
16 condition was used: 2 minutes at 50°C for Uracil-N-Glycosylase incubation, 10
17 minutes at 95°C for polymerase activation and 40 consecutive cycles for
18 amplification (15 seconds at 95°C for denaturation and 60 seconds at 58°C for
19 annealment/extension). β -actin was used to normalize mRNA levels and the 2-
20 $\Delta\Delta$ Ct method used for comparisons. The reverse transcription primer
21 sequences used for the target genes were shown in Online Table 1.

22 **Immunofluorescence**

1 Primary peritoneal macrophages were seeded in 12-well dishes containing a
2 cover glass. Cells were washed in PBS and fixed with 4% PFA at room
3 temperature for 20 min followed by permeabilization with 0.3% Triton X-100 in
4 PBS for 5 min. The fixed cells were blocked with 5% normal goat or donkey
5 serum in PBS for 1 hour at room temperature and incubated with the
6 corresponding primary antibodies in PBS at 4°C overnight: the formation of
7 NLRP3/ASC specks was used to assess NLRP3 inflammasome activation by
8 double immunofluorescence for NLRP3 (AG-20B-0014, AdipoGen, USA) and
9 ASC (D2W8U, #67824, CST, USA). The colocalization of NLRP3 and LAMP-
10 2A or HSC70 (ab51052, Abcam, UK) was also investigated using double
11 immunofluorescence. Secondary donkey anti-mouse Alexa594 (ab150112,
12 Abcam, UK) or donkey anti-rabbit Alexa488 (ab150061, Abcam, UK) antibodies
13 were used. Slides reacting with non-immune IgG and secondary antibodies
14 were used as negative controls. Slides were imaged using an upright electric
15 fluorescence microscope (DS-Ri2, Nikon, Japan).

16 **Coimmunoprecipitation assay**

17 Coimmunoprecipitation (Co-IP) was performed using Immunoprecipitation Kits
18 (ab206996, Abcam, UK). Macrophages treated with or without LPS were used
19 to detect the endogenous interaction between NLRP3 and HSC70 or LAMP-2A.
20 These interactions were validated in HEK293T cells (ACS-4500, ATCC, USA)
21 transfected with exogenous plasmids expressing Flag-LAMP-2A, Flag-HSC70,
22 or Myc-NLRP3 or its mutants, Myc-Caspase-1 or Myc-ASC. For the analysis of

1 NLRP3 ubiquitination upon NLRP3 inflammasome activation in macrophages,
2 the following primary antibodies were used for immunoblot analysis: Ubiquitin
3 (#3933, CST, USA), K48-linkage Specific Polyubiquitin (#8081, CST, USA),
4 K63-linkage Specific Polyubiquitin (#5621, CST, USA). The general Co-IP
5 protocol consisted of sample preparation, antibody binding, and preparation of
6 protein A/G beads, bead capture and elution. Briefly, cells were cold lysed using
7 lysis buffer (nondenaturing) containing a protease inhibitor cocktail and mixed
8 on a rotary mixer for 30 min at 4°C. After centrifugation at 10,000 ×g at 4°C for
9 10 min, the supernatants were incubated with primary antibodies overnight at
10 4°C on a rotary mixer. The same amount of normal rabbit IgG (#2729, CST,
11 USA) was used as a control. The next day, the Protein A/G Sepharose was
12 washed twice with wash buffer and suspended as a 50% slurry in wash buffer.
13 Thirty microliters of protein A/G Sepharose beads were added to each tube and
14 incubated for 2 h at 4°C. The protein A/G Sepharose was collected, washed 3
15 times with wash buffer and centrifuged at 4°C, with the supernatant aspirated
16 between washes. Then, 40 µL of 2× SDS-PAGE loading buffer (P0015B,
17 Beyotime, China) was added to the beads, which were boiled for five mins and
18 analyzed by immunoblotting.

19 **Assessment of lysosomal function**

20 ***Measuring Physiological lysosomal pH Shifts***

21 One day before the experiment, cells were seeded into a 6 well plate at a
22 density of 1×10^6 /well, After treatment with PBS, NH₄CL or CHIR99021 (CHIR)

1 for 1 h, cells were incubated with LysoSensor™ Yellow/Blue DND-160 (2 μ M,
2 L7545, Thermo Fisher) for 5 min. Cells were washed three times with 1X PBS.
3 The microplate reader (Synergy HTX, BioTek, US) was set at excitation
4 wavelength 360nm and emission wavelength 450nm for reading of
5 LysoSensor™ Yellow/Blue DND-160 fluorescence. The average pH was
6 calculated according to the fluorescence intensity ratio.

7 ***Measuring β -galactosidase Activity***

8 The activity of β -galactosidase of lysosomes were measured using a micro β -
9 galactosidase assay kit (BC2585, Solarbio, China). One day before the
10 experiment, cells were seeded into a 6 well plate at a density of 1×10^6 /well.
11 After treatment with PBS, NH_4Cl or CHIR99021 (CHIR) for 1 h, cells were
12 collected into the centrifuge tubes. 1ml of extract per 5 million cells was added
13 and ultrasonic processor was used to break up cells (Ice bath, 20% power, 3 s
14 of ultrasound stimulation, 10 s interval, 30 repetitions). Then cells were
15 centrifuged at 15000 g for 15 min and the supernatant were obtained for
16 analysis. Sample, reagent 1, reagent 2 and reagent 3 were consecutively added
17 into the 96-well plate. The absorbance of the samples was determined with a
18 multi-mode microplate reader (Synergy HTX, BioTek, US) with a wavelength of
19 400 nm.

20 ***Measuring Active Lysosomal Cathepsin D***

21 One day before the experiment, cells were seeded into a 12 well plate at a
22 density of 5×10^5 /well. After treatment with PBS, NH_4Cl or CHIR99021 (CHIR)

1 for 1 h, cells were incubated with LysoTracker Red (1 μ M, CY-SC012,
2 Cytoskeleton) for 15 minutes at 37°. After washing of cells three times with
3 PBS, cells were stained with undiluted Fluoroshield Mounting Medium with
4 DAPI (ab104139, Abcam, UK). An electric upright microscope (DS-Ri2, Nikon,
5 Japan) was used for imaging.

6 **Lysosome isolation**

7 Lysosomes were isolated from primary peritoneal macrophages using a
8 Lysosome Isolation Kit (#LYSISO1, Sigma, USA). The method consisted of two
9 main parts: preparation of a crude lysosomal fraction (CLF) and further
10 purification of the CLF. Briefly, approximately 2×10^8 cells were trypsinized,
11 centrifuged, and resuspended in extraction buffer. The cells were broken in a
12 7-ml Dounce homogenizer and assessed using trypan blue staining solution to
13 ascertain the degree of breakage. After the sample had been centrifuged at
14 1,000 \times g for 10 min, the supernatant was collected and centrifuged at 20,000
15 \times g for 20 min. The supernatant was removed to collect the pellet, which was
16 suspended in a minimal volume of extraction buffer, and the resulting material
17 was the CLF. For further purification of the CLF, it was diluted in a solution
18 containing 19% OptiPrep density gradient medium, with the resulting sample
19 referred to as the diluted OptiPrep fraction (DOF). Calcium chloride was added
20 to a final concentration of 8 mM, and the DOF was incubated for 15 min to
21 remove contaminant mitochondria and endoplasmic reticulum, after which the
22 DOF was centrifuged at 5,000g, and the supernatant was collected. The

1 intactness of the lysosomes was assessed using the dye Neutral Red. All
2 procedures were carried out according to the manufacturer's instructions.

3 **Analysis of autophagic flux**

4 Macroautophagy activity was analyzed in two ways: LC3B-II flux and mRFP-
5 GFP-LC3 adenovirus transfection. For LC3B-II flux, macrophages were
6 cultured in serum-rich (Rest) or serum-free DMEM media (activated, Act) for 12
7 h, and cultured for the final 4 h in the presence (+) or absence (-) of bafilomycin
8 A1 (Baf A1, A8627, APExBIO, USA). Immunoblot analysis was used to detect
9 autophagosome membrane – associated form (LC3B-II). LC3B-II flux was
10 calculated as the ratio of treated lines to untreated lines after normalization to
11 β -actin. For fluorescence microscopy analysis of autophagic flux, macrophages
12 were transfected with adenovirus containing plasmids expressing tandem
13 fluorescent mRFP-GFP-LC3 (HB-AP2100001, HANBIO, China) for 36 h, and
14 cultured for the final 12 h in serum-rich (Rest) or serum-free DMEM media
15 (activated, Act). Yellow (merge of GFP signal and RFP signal) particles
16 represented early autophagosomes. Red fluorescent particles represent
17 autolysosomes.

18 **Statistical analyses**

19 Statistical analysis was performed with SPSS version 23.0 (SPSS Inc., Chicago,
20 IL, USA). Continuous data with Gaussian distribution were expressed as mean
21 and standard error of the mean (SEM). Continuous data with a non-Gaussian
22 distribution were expressed as medians and quartiles. Categorical data were

1 expressed as number (%). Tests for assessing significance were detailed in
2 each figure legend and precise p values of significant changes were indicated
3 in each figure. The number of biological and technical replicates in each
4 experimental group was indicated in each figure legend. Shapiro-Wilk test was
5 first used to assess Gaussian distribution. As the sample size in the present
6 study was relatively small (n=5), Mann-Whitney U test was used for between-
7 group comparison, and Kruskal-Wallis test followed by Nemenyi post-hoc test
8 used for multiple group comparisons. Multiple linear mixed effects modelling
9 was used for two-group comparison of repeated measures with the treatment
10 group variable being the fixed effect and the biological replicates the random
11 effect. No experiment-wide/across-test multiple test correction was applied in
12 this study. Difference was considered significant if $p < 0.05$. Representative
13 images reflecting the average results of each experiment were chosen in
14 relevant figures of this study.

15

1 **Online Table I**

2 **The reverse transcription primer sequences used for the target genes**

Genes	Primer type	Sequence 5'-3'
IL-1 β	Forward	ACCTTCCAGGATGAGGACATGA
	Reverse	AACGTCACACACCAGCAGGTTA
IL-18	Forward	CGGCCAAAGTTGTCTGATTCC
	Reverse	ACTCTTGCGTCAACTTCAAGG
TNF- α	Forward	GCCACCACGCTCTTCTGTCT
	Reverse	TGAGGGTCTGGGCCATAGAAC
NLRP3	Forward	TGAGGGTCTGGGCCATAGAAC
	Reverse	CTGCGTGTAGCGACTGTTGAG
β -actin	Forward	TGTTACCAACTGGGACGACA
	Reverse	CTGGGTCATCTTTTCACGGT

3

4

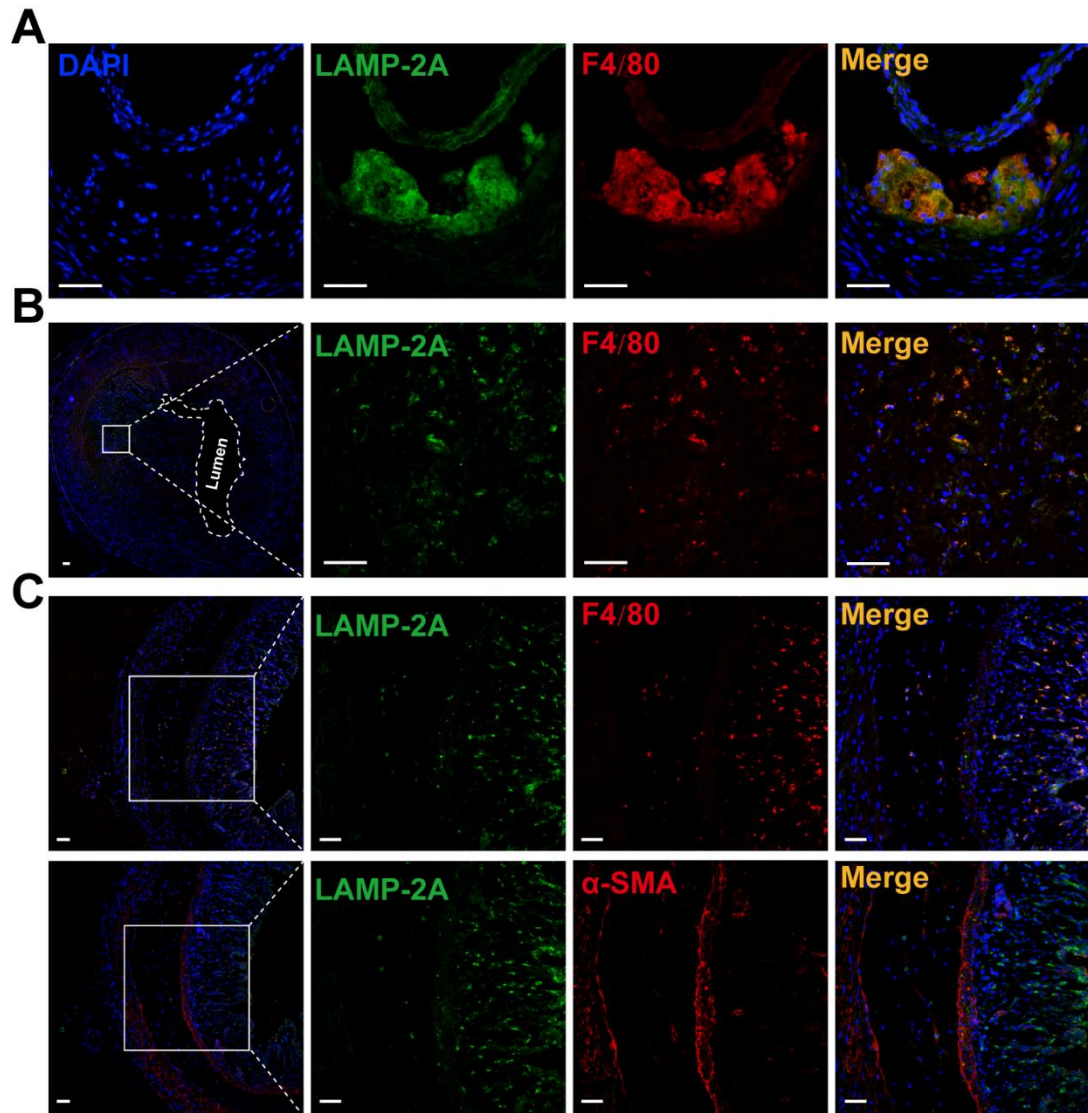
1 **Online Table II**

2 **Metabolic profile in control ApoE^{-/-} mice and L2A-m \emptyset KO/ApoE^{-/-} Mice**

Characteristics	ApoE^{-/-} (n=7)	L2A-m\emptysetKO/ApoE^{-/-} (n=7)	p values
BW (g)	27.30 (26.80, 28.10)	25.60 (24.10, 26.60)	0.053
Glucose (mmol/L)	8.00 (7.20, 9.00)	7.50 (7.00, 9.10)	0.710
TC (mmol/L)	35.11 (31.05, 48.97)	36.50 (28.02, 42.71)	0.535
TG (mmol/L)	2.29 (1.81, 2.91)	2.31 (1.68, 2.65)	0.710
HDL-C (mmol/L)	1.40 (1.28, 1.75)	1.55 (1.36, 1.73)	0.805
LDL-C (mmol/L)	13.87 (13.57, 22.65)	18.47 (11.77, 18.83)	0.710

3 BW, body weight; TC, total cholesterol; TG, triglycerides; HDL-C, high-density
 4 lipoprotein cholesterol; LDL-C, low-density lipoprotein cholesterol. n=7 per
 5 group. Mann-Whitney Test was used for statistical comparisons. Data were
 6 presented as medians and quartiles (25th and 75th percentiles). There was no
 7 statistically significant difference in these parameters between two groups of
 8 mice.

9
 10

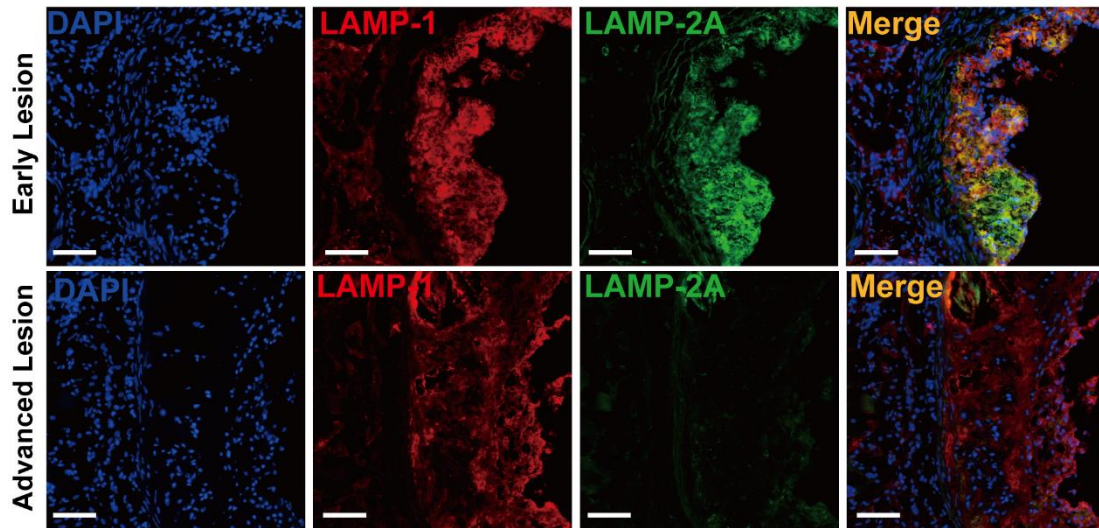


1

2 **Online Figure I. Detection of CMA marker LAMP-2A *in vivo*.**

3 (A) Representative immunofluorescence analysis to detect colocalization
 4 (yellow particles) of LAMP-2A (green particles) and F4/80 (red particles) in
 5 frozen sections from the aortic root of ApoE^{-/-} mice (n=5, male) fed a HFD for
 6 12 weeks. Scale bar=100 μ m. (B) Representative immunofluorescence analysis
 7 to detect colocalization (yellow particles) of LAMP-2A (green particles) and
 8 F4/80 (red particles) in frozen sections from human coronary atherosclerotic
 9 plaques. Scale bar=100 μ m. (C) Representative immunofluorescence analysis

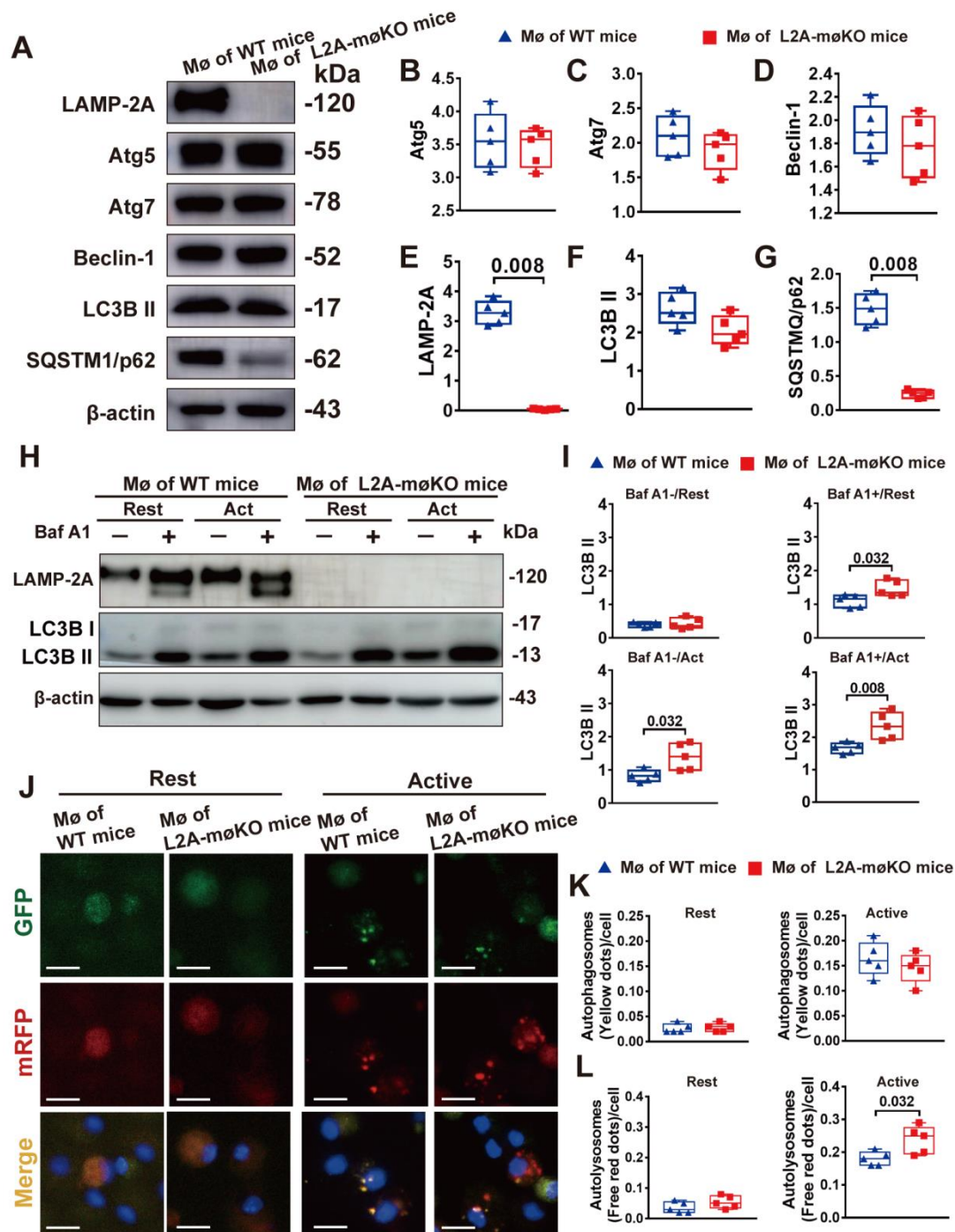
1 to detect colocalization (yellow particles) of LAMP-2A (green particles), F4/80
2 (red particles) and α -SMA (red particles) in frozen sections from the colitis
3 tissues of mice (n=5, male). Scale bar=100 μ m.



4

5 **Online Figure II. Alterations of LAMP-1 and LAMP-2A in progressive**
6 **atherosclerosis**

7 Representative double immunofluorescence images for LAMP-1 (red particles)
8 and LAMP-2A (green particles) in “early lesions” (fed a HFD for 8 weeks) and
9 “advanced lesions” (fed a HFD for 24 weeks). n = 5 in each group. Scale
10 bar=100 μ m.

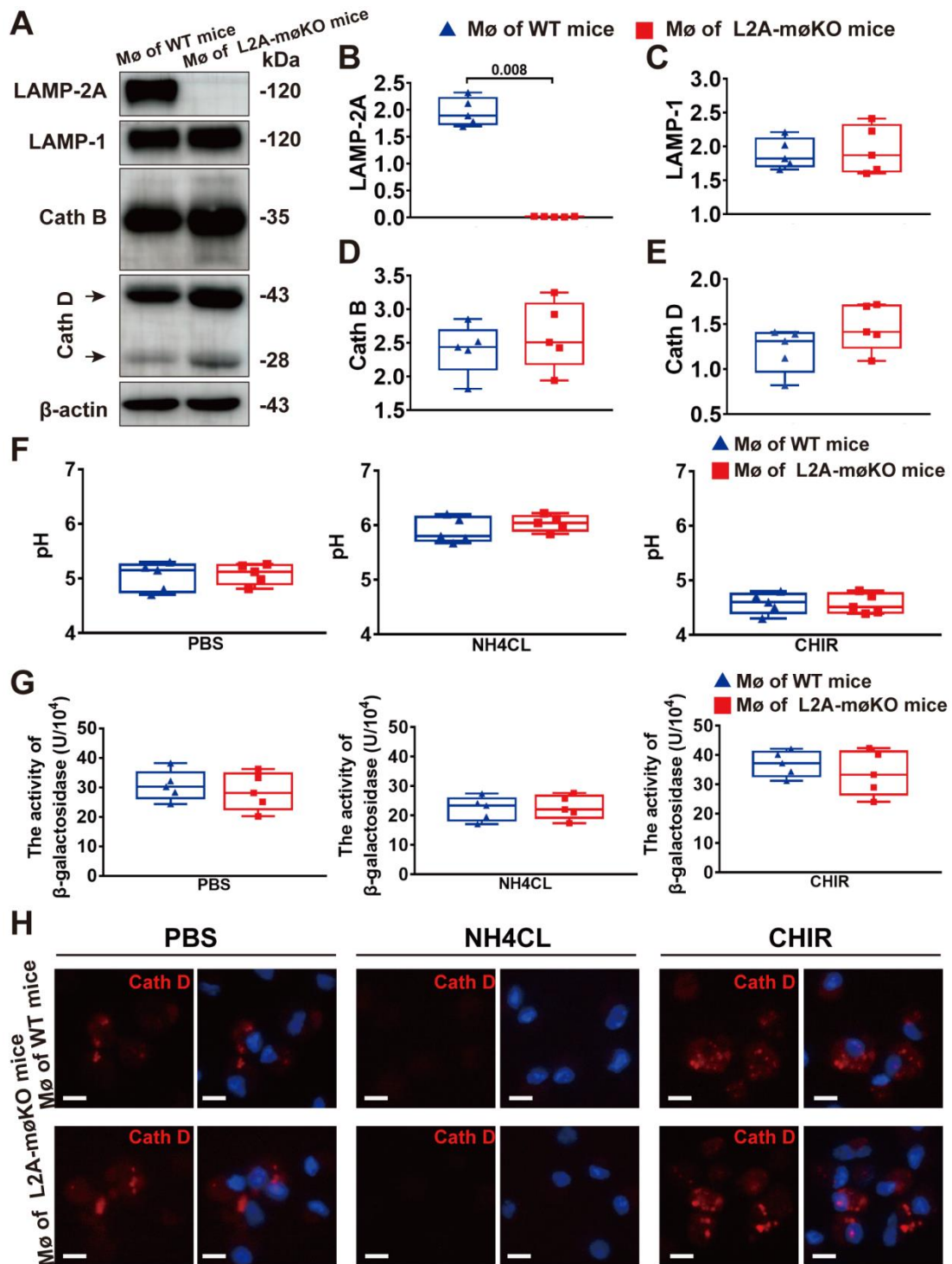


1

2 **Online Figure III. Effect of LAMP-2A deficiency on macroautophagy.**

3 **(A)** Representative immunoblot images and **(B-G)** quantitative analysis of the
 4 indicated macroautophagy-related protein expression in primary peritoneal
 5 macrophages from wild-type (WT, C57 background, male) and macrophage-
 6 specific L2A-knockout (L2A-mØKO, C57 background, male) mice. Five

1 independent experiments were performed. Statistical analysis was performed
2 using Mann-Whitney Test. Data were presented as medians and quartiles. Atg5,
3 autophagy protein 5; Atg7, autophagy protein 7; LC3B, microtubule-associated
4 proteins 1A/1B light chain 3B. **(H)** Representative immunoblot images and **(I)**
5 quantitative analysis to detect the autophagy-related protein LC3 in its cytosolic
6 form (LC3-I) and autophagosome membrane – associated form (LC3-II) in
7 primary peritoneal macrophages from wild-type (WT, C57 background, male)
8 and macrophage-specific L2A-knockout (L2A-mØKO, C57 background, male)
9 mice. Macrophages were cultured in serum-rich (Rest) or serum-free DMEM
10 media (activated, Act) for 12 h, and cultured for the final 4 h in the presence (+)
11 or absence (–) of bafilomycin A1 (Baf A1). Five independent experiments were
12 performed. Data were presented as medians and quartiles. Comparison was
13 made only between WT and L2A-mØKO groups. Statistical analysis was
14 conducted using Mann-Whitney Test. **(J)** Representative images and **(K-L)**
15 statistical analysis of autophagic flux in primary peritoneal macrophages from
16 wild-type (WT, C57 background) and macrophage-specific L2A-knockout (L2A-
17 mØKO, C57 background) mice by using mRFP-GFP-LC3 adenovirus
18 transfection. Five independent experiments were performed. Data were
19 presented as medians and quartiles. Statistical analysis was made using Mann-
20 Whitney Test. Comparison was made only between WT and L2A-mØKO groups.
21 Scale bar=10µm.



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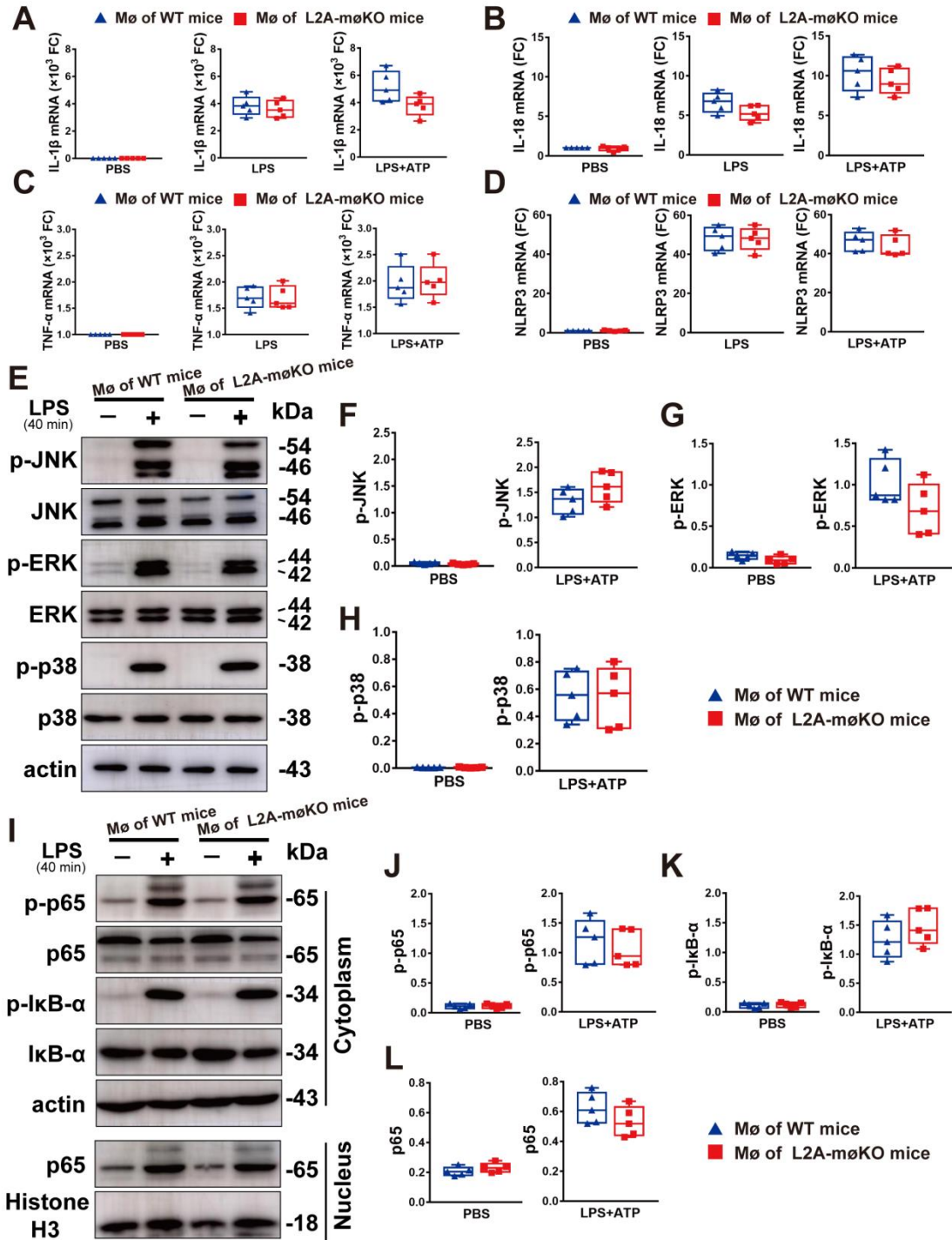
2 **Online Figure IV. Effect of LAMP-2A deficiency on lysosomal function.**

3 (A) Representative western blot images and (B-E) quantitative analysis of
 4 protein expression of LAMP-2A, LAMP-1, Cathepsin B (Cath B) and Cathepsin
 5 D (Cath D) in primary peritoneal macrophages from wild-type (WT, C57

1 background, male) and macrophage-specific L2A-knockout (L2A-mØKO, C57
2 background, male) mice. Five independent experiments were performed. Data
3 were presented as medians and quartiles. Statistical analysis was conducted
4 using Mann-Whitney Test. **(F)** LysoSensor pH quantitation to detect the pH
5 values of lysosomes in primary peritoneal macrophages from WT and L2A-
6 mØKO mice (male). Macrophages were treated with PBS, NH₄CL and
7 CHIR99021 (CHIR) for 1 h, respectively. Five independent experiments were
8 performed. Data were presented as medians and quartiles. Comparison was
9 made only between WT and L2A-mØKO groups. Statistical analysis was
10 performed using Mann-Whitney Test. **(G)** Quantitation of the activity of β-
11 galactosidase in primary peritoneal macrophages from WT and L2A-mØKO
12 mice. Macrophages were treated with PBS, NH₄CL and CHIR99021 (CHIR) for
13 1 h, respectively. Five independent experiments were performed. Data were
14 presented as medians and quartiles. Comparison was made only between WT
15 and L2A-mØKO groups. Statistical analysis was done using Mann-Whitney Test.
16 **(H)** Representative immunofluorescence images of SiR-Lysosome assay for
17 measuring active lysosomal cathepsin D in primary peritoneal macrophages
18 from WT and L2A-mØKO mice. Macrophages were treated with PBS, NH₄CL
19 and CHIR99021 (CHIR) for 1 h, respectively. Five independent experiments
20 were performed. Scale bar=10µm.

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2 **Online Figure V Effect of LAMP-2A deficiency on transcription of IL-1 β , IL-**

3 **18, TNF- α and NLRP3**

4 **(A-C)** RT-PCR analysis of IL-1 β , IL-18 and TNF- α mRNA expression in mouse

5 peritoneal macrophages from wild-type (WT) and macrophage-specific L2A-

6 knockout (L2A-m ϕ KO) mice. Macrophages were primed with LPS (100 ng/ml)

1 for 8 h, followed by stimulation with ATP (5 mM) for 30 min. Five independent
2 experiments were performed. Data were presented as medians and quartiles.
3 Comparison was made only between WT and L2A-mØKO groups. Statistical
4 analysis was made using Mann-Whitney Test. **(D)** RT-PCR analysis of NLRP3
5 mRNA expression in mouse peritoneal macrophages from wild-type and
6 macrophage-specific L2A-knockout (L2A-mØKO) mice. Macrophages were
7 primed with LPS (100 ng/ml) for 8 h, followed by stimulation with ATP (5 mM)
8 for 30 min. Five independent experiments were performed. Data were
9 presented as medians and quartiles. Comparison was made only between WT
10 and L2A-mØKO groups. Statistical analysis was carried out using Mann-
11 Whitney Test. **(E-H)** Representative immunoblot images and quantitative
12 analysis of protein expression of MAPK pathways in mouse peritoneal
13 macrophages from wild-type and macrophage-specific L2A-knockout (L2A-
14 mØKO) mice. Macrophages were treated with LPS (100 ng/ml) for 40 min. Five
15 independent experiments were performed. Data were presented as medians
16 and quartiles. Comparison was made only between WT and L2A-mØKO groups.
17 Statistical analysis was conducted using Mann-Whitney Test. **(I-L)**
18 Representative immunoblot images and quantitative analysis of protein
19 expression of IκBα/NF-κB pathways from mouse peritoneal macrophages of
20 wild-type and macrophage-specific L2A-knockout (L2A-mØKO) mice.
21 Macrophages were treated with LPS (100 ng/ml) for 40 min. Five independent
22 experiments were performed. Data were presented as medians and quartiles.

1 Comparison was made only between WT and L2A-møKO groups. Statistical
2 analysis was done using Mann-Whitney Test. There was no significant
3 difference in these parameters between two groups of mice.

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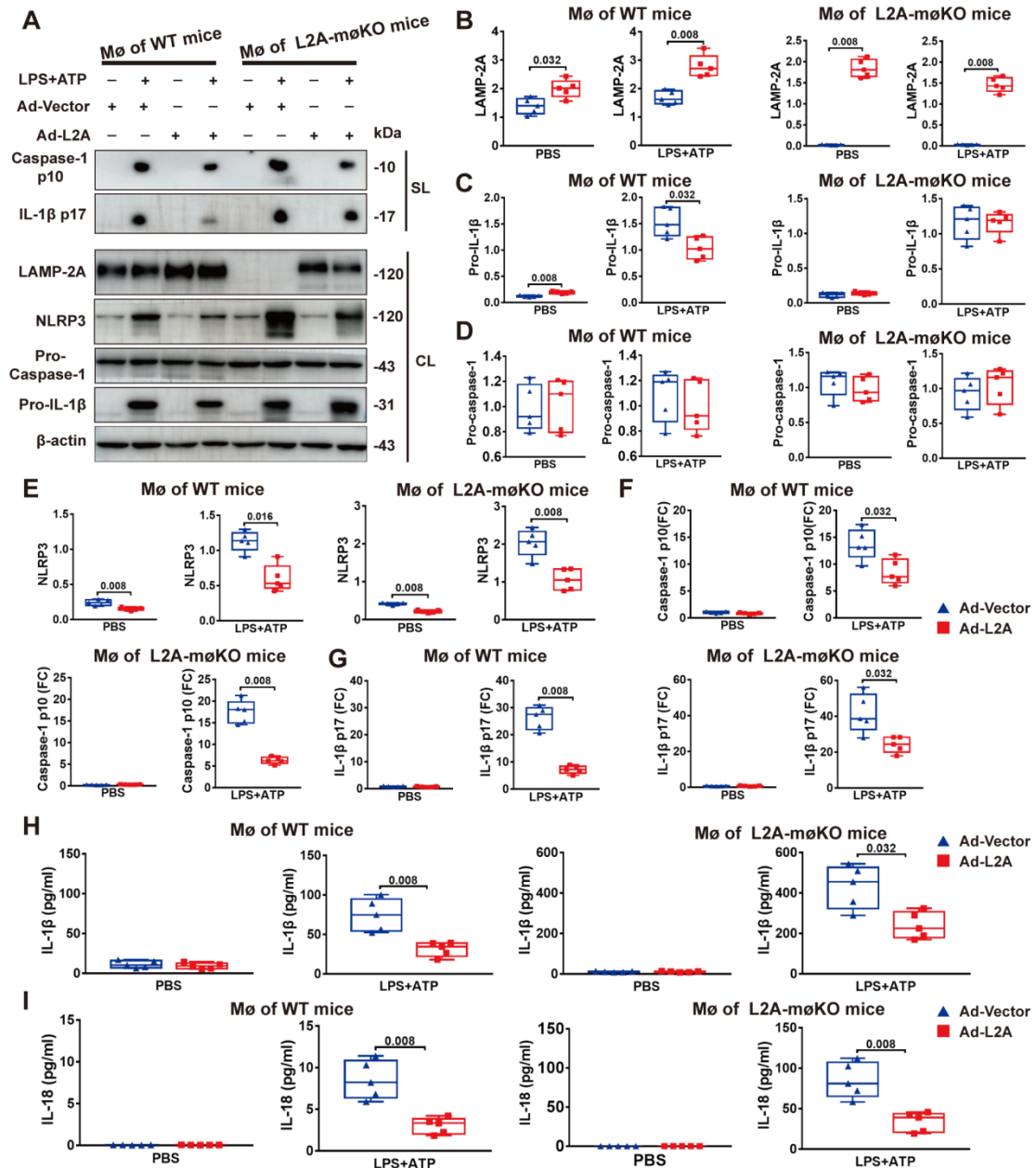
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2 **Online Figure VI Gain-of Function experiments investigating the effect of**
 3 **LAMP2A rescue on NLRP3 inflammasome activation**

4 (A) Representative western blot images and (B-G) quantitative analysis of
 5 protein expression in cellular supernatants (SNs) and cell lysates (CLs) of
 6 mouse peritoneal macrophages from WT and L2A-møKO mice infected with
 7 adenovirus vector or adenovirus expressing LAMP-2A (L2A). Macrophages
 8 were stimulated with LPS (100 ng/ml) for 8 h with or without subsequent

1 stimulation with ATP (5 mM) for 30 min. Five independent experiments were
2 performed. Data were presented as medians and quartiles. Comparison was
3 made only between Ad-Vector and Ad-L2A groups. Statistical analysis was
4 performed using Mann-Whitney Test. **(H-I)** ELISA was used to detect IL-1 β and
5 IL-18 levels in the supernatants of mouse peritoneal macrophages from WT
6 and L2A-m \emptyset KO mice. Macrophages were infected with adenovirus vector or
7 adenovirus expressing LAMP-2A, and stimulated with LPS (100 ng/ml) for 8 h
8 with or without subsequent stimulation with ATP (5 mM) for 30 min. Five
9 independent experiments were performed. Data were presented as medians
10 and quartiles. Comparison was made only between Ad-Vector and Ad-L2A
11 groups. Statistical analysis was made using Mann-Whitney Test.

A CLUSTAL 0(1.2.0) multiple alignment of human Caspase-1

ASC	MADKVLKEKRKLFIRSMGEGTINGLLDELLQTRVLNKEEMKVKRENATVM
KFERQ	-----
ASC	DKTRALIDSVIPKGA-----
KFERQ	-----
ASC	-----PEHKTS DSTFLVFM SHGIREGICGKKHSEQVPDILQLNAIFNMKK
KFERQ	-----
ASC	AHIEKDFIAFCSSTPDNVSWRHPTMGSVFIGRLIEHMQEYACSCDVEEIFRK
KFERQ	-----
ASC	VRFSFEQPDGRAQMPPTTERTVLTTRCFYLFPGH
KFERQ	-----

CLUSTAL 0(1.2.0) multiple alignment of mouse Caspase-1

ASC	MADKILRAKRKQFINSV SIGTINGLLDELLEKRVLNQEEMDKIKLANITAMDKA
KFERQ	-----
ASC	RDLCDHVSKKGPQASQ-----
KFERQ	-----
ASC	TEFQHLSPRVGA ¹⁸² QVDL ¹⁸⁶ REM KLLLEDLG YTVKVKENLT ALEMVKE-----
KFERQ	-----KFERQ-----
ASC	-----SWRHPVRGSLFIESLIKHMKEYAWSCDLEDIFRKVRFSF
KFERQ	-----
ASC	³⁷⁹ EQPE ³⁸³ FRLQMP TADRVLT LKRFYLFPGH
KFERQ	-----KFERQ-----

B CLUSTAL 0(1.2.0) multiple alignment of human ASC

ASC	MGRARDAILDALENLTAEELKKFKL KLLSVPLREGYGRIPRGALLSMDALDLT
KFERQ	-----
ASC	DKLVSFYLETYGAELTANVLRDMGLQEMAGQLQAATHQGSGAAPAGIQAPP
KFERQ	-----
ASC	QSAAKPGLHFIDQHRAALIARVTNVEWLLDALYGKVLTD EQYQAVRAEPTNP
KFERQ	-----
ASC	SKMRKLSFPTAWNWTC KDLLLQALRESQSYLVEDLERS
KFERQ	-----

CLUSTAL 0(1.2.0) multiple alignment of mouse ASC

ASC	MGRARDAILDALENLSGDELKKFKM KLLTVQLREGYGRIPRGALLQMDAIDL
KFERQ	-----
ASC	TDKLVSYYLESYGLELTMTVLRDMGLQELAEQLQT TKEESGAVAAAASVPAQ
KFERQ	-----
ASC	STARTGHFVDQHRQALIARVTEVDGVL DALHG SVLTEGQYQAVRAETTSQD
KFERQ	-----
ASC	KMRKLSFVPSWNLTC KDSLLQALKEIHPYLVMDLEQS
KFERQ	-----

1 **Online Figure VII. Alignment of the amino acid sequences of mouse and**
2 **human Caspase-1 and ASC with the KFERQ motif**

3 (A) The amino acid sequence of human and mouse Caspase-1. In the KFERQ
4 motifs, Q (in red) and the other four amino acids (in purple) were marked.

5 (B)The amino acid sequence of human and mice ASC.

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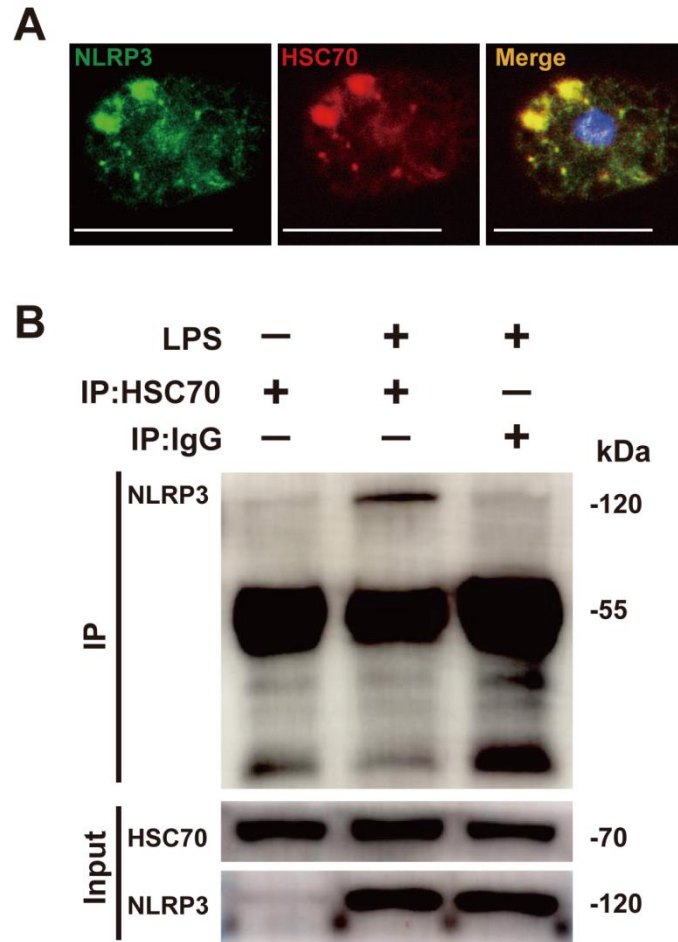
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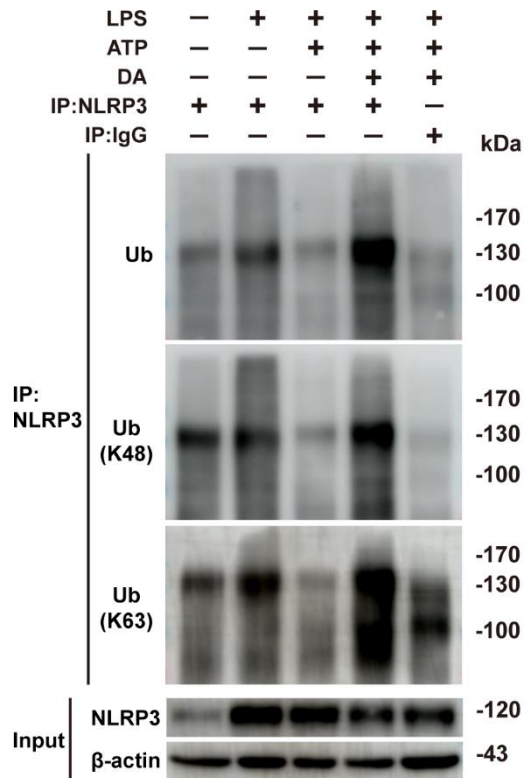


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2 **Online Figure VIII. NLRP3 interacts with HSC70**

3 (A) Colocalization (yellow particles) of NLRP3 (green particles) with HSC70
 4 (red particles) in peritoneal macrophages treated with LPS and ATP. Bar=20 μ m.

5 (B) Co-IP of endogenous NLRP3 with HSC70 from LPS-primed mouse
 6 peritoneal macrophages. Five independent experiments were performed. Scale
 7 bar=10 μ m.



1

2 **Online Figure IX. NLRP3 protein undergoes de-ubiquitination during**
3 **NLRP3 inflammasome activation**

4 Immunoblot analysis of lysates from WT peritoneal macrophages treated with
5 LPS, ATP or dopamine (DA), followed by IP with anti-NLRP3, probed with anti-
6 Ub, anti-K48-Ub or anti-K63-Ub. DA, a compound proved to promote NLRP3
7 ubiquitination, was used as a positive control. Five independent experiments
8 were performed.

9