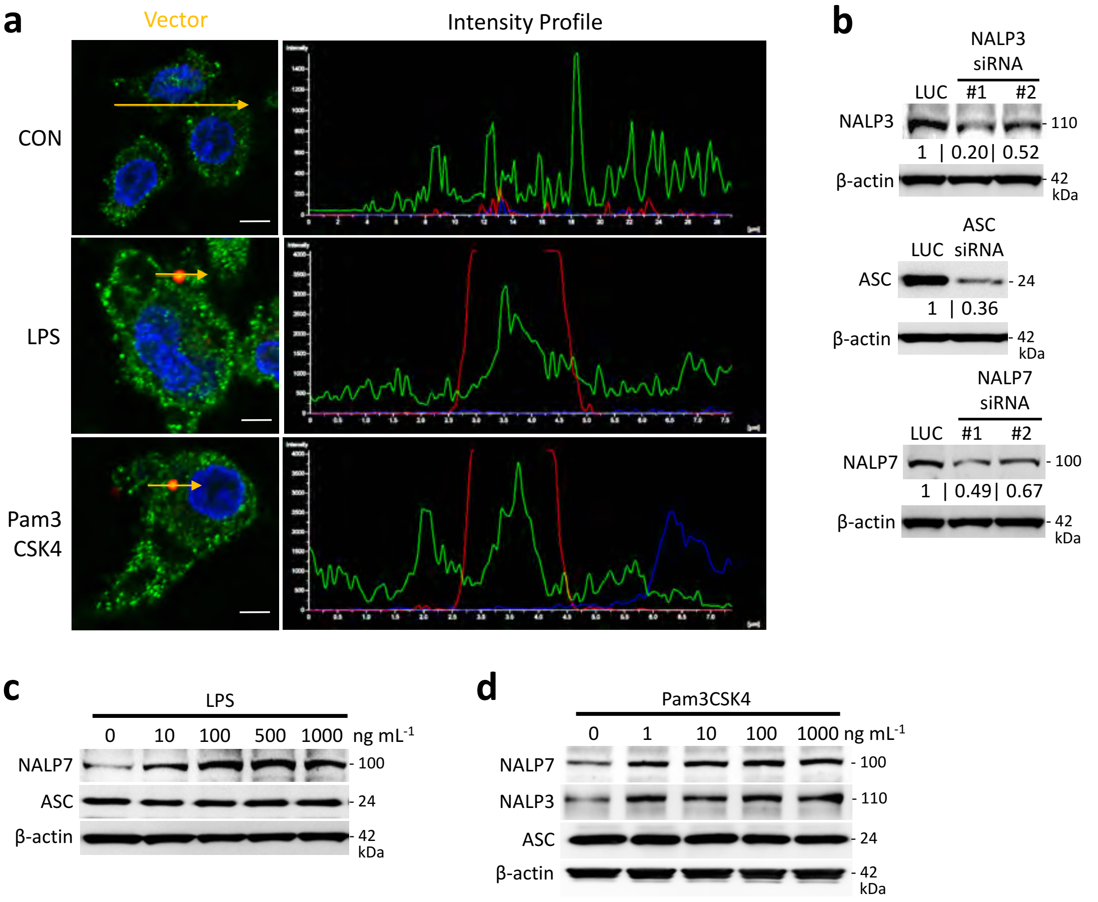
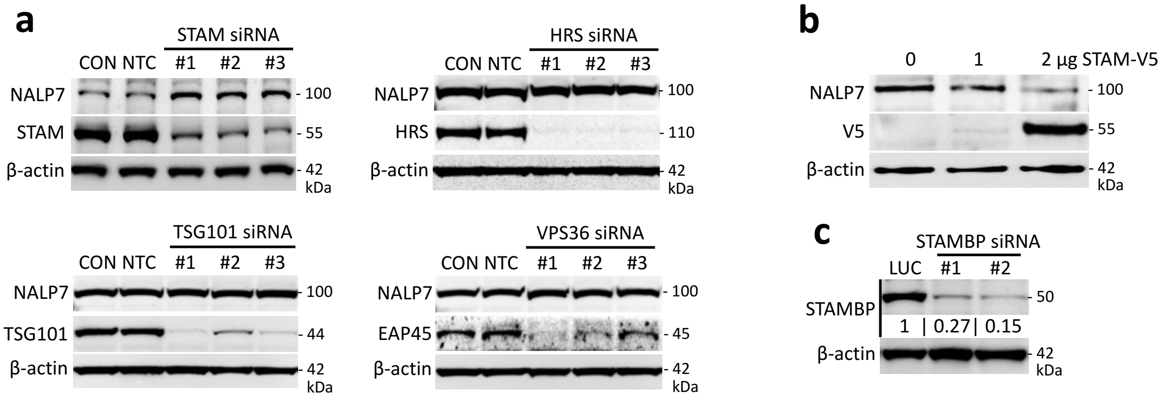
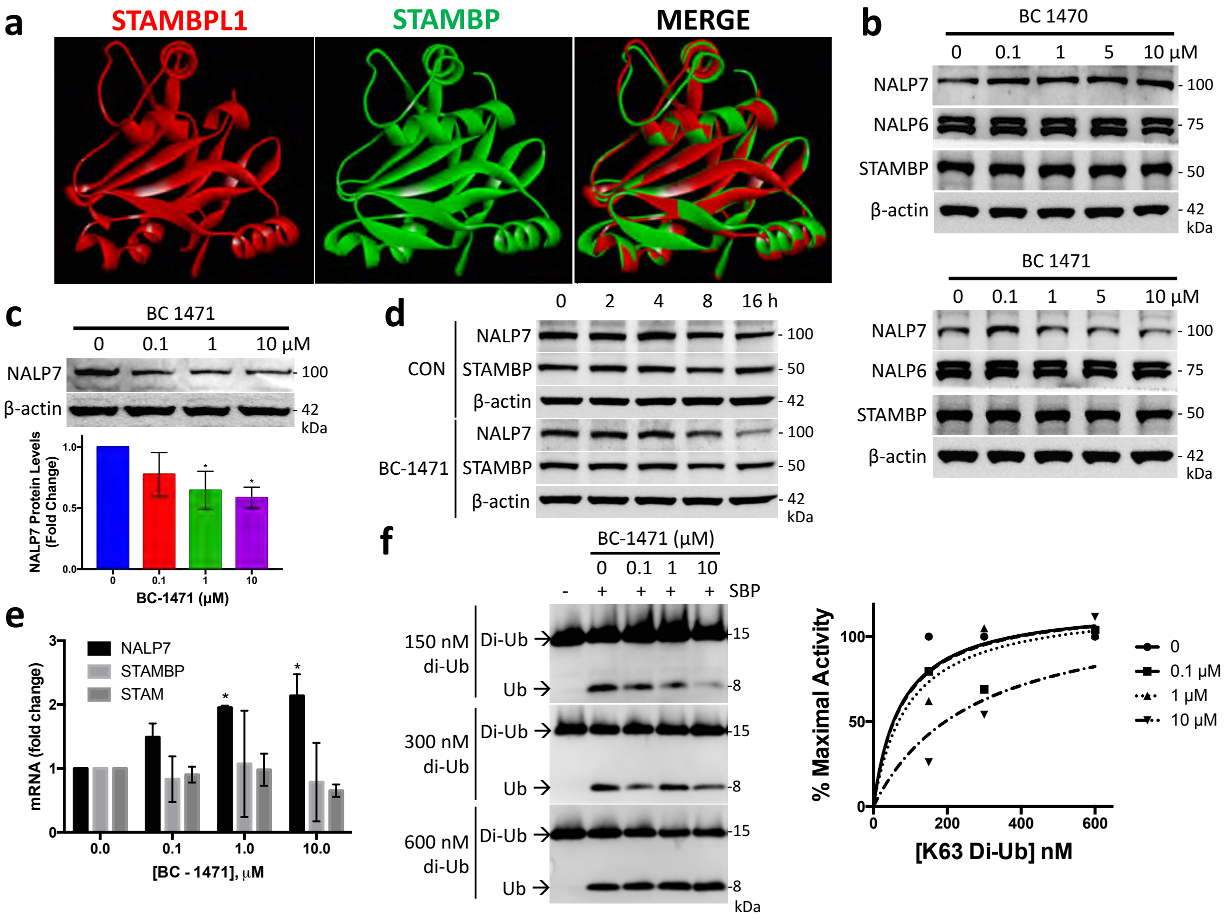


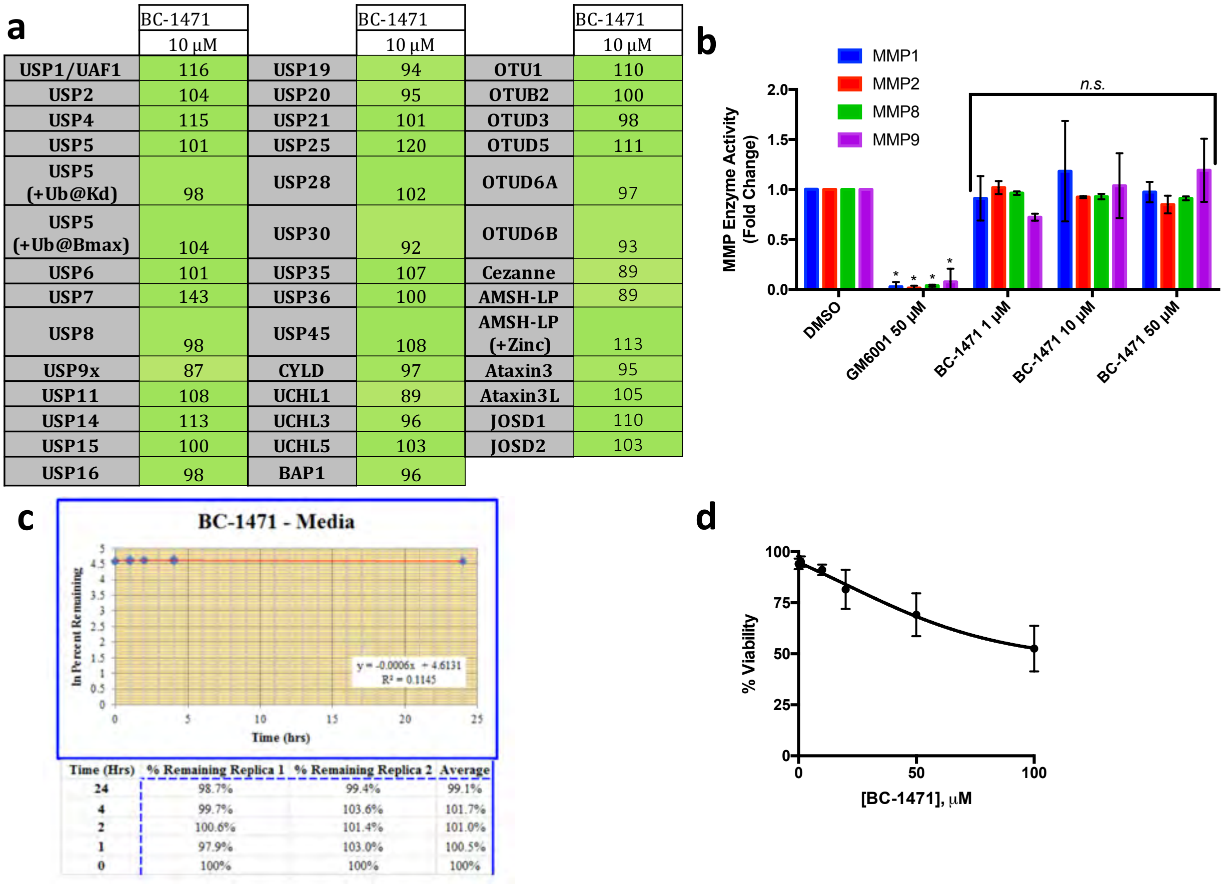
Supplementary Figure 1. Cellular expression of inflammasome components after stimuli. (a) THP-1 macrophages that formed an ASC-speck in Fig. 1b were further analyzed by immunofluorescence intensity profiling. Intensity was graphed as relative fluorescent units (RFUs) across the vector depicted by the yellow arrow. Cells exposed to LPS or Pam3CSK4 displayed formation of an ASC-speck (red) with co-localization of increased intensity NALP7 signal (green). Original magnification was 100x, scale bars = 10 µm. (b) Immunoblot analysis confirmed knockdown of NALP3, ASC, or NALP7 by siRNA or a control luciferase (LUC) in THP-1 cells assayed in Fig. 1c. Relative abundance compared to control noted below as determined by densitometry using ImageJ software. (c, d) Immunoblot analysis of NALP7, NALP3, and ASC in lysates of THP-1 cells after (c) LPS or (d) Pam3CSK4 exposure for 16 h.



Supplementary Figure 2. STAM modulates NALP7 abundance. (a) *STAM* knockdown with siRNA increases NALP7 protein abundance in Beas2B cells compared to untreated control (CON), or a nontargeting control (NTC) siRNA. *HRS, Tsg101,* and *VPS36* knockdown with siRNA did not impact NALP7 protein abundance. Note: EAP45 is the protein product of the VPS36 gene. (b) Overexpression of *STAM*-V5 plasmid in Beas2B cells decreased immunoreactive NALP7. (c) Immunoblot analysis confirmed knockdown of STAMBP by siRNA or a control luciferase (LUC) in THP-1 cells assayed in Fig. 4i. Relative abundance compared to control noted below as determined by densitometry using ImageJ software.



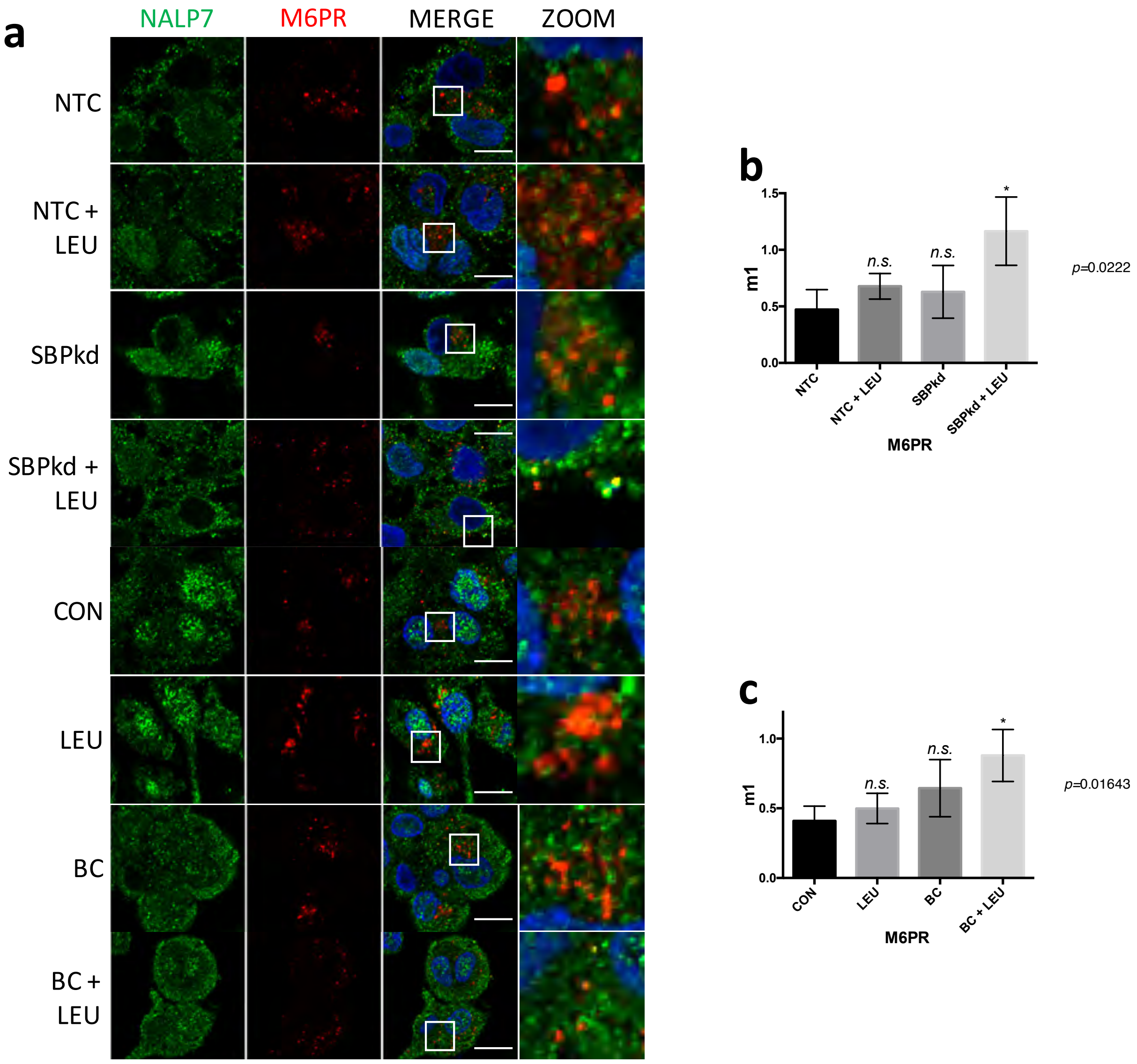
Supplementary Figure 3. Small molecule antagonism of NALP7. (a) STAMBPL1 (2ZNV.pdb) and STAMBP (3RZU.pdb) in a structural homology model (merge). (b) Phenotypic screening of NALP7 small molecule antagonists. (c) Endogenous NALP7 protein abundance is decreased in THP-1 cells exposed to BC-1471. *Below,* densitometric analysis of relative NALP7 protein abundance as determined by ImageJ software. Data shown as mean ± SD (n=3). *$P < 0.05$ compared to control. (d) Endogenous NALP7 half-life is decreased with BC-1471 pre-treatment (10μM for 2 h) compared to control in Beas2B cells. (e) NALP7, STAMBP and STAM mRNA with BC-1471 treatment for 16 h as analyzed by qPCR in THP-1 cells. Data shown as mean fold change ± SD by ΔΔCq analysis (n=3). (f) *In vitro* DUB assay as performed in Fig. 5d. Right: Relative mono-Ub was quantified by densitometry and fit to multiple inhibition models using GraphPad Prism software (n=2). (c) One-way and (e) two-way analysis of variance (ANOVA) with post-hoc Dunnett's multiple comparisons test.



	BC-1471		BC-1471		BC-1471
	10 μM		10 μM		10 μM
USP1/UAF1	116	**USP19**	94	**OTU1**	110
USP2	104	**USP20**	95	**OTUB2**	100
USP4	115	**USP21**	101	**OTUD3**	98
USP5	101	**USP25**	120	**OTUD5**	111
USP5 (+Ub@Kd)	98	**USP28**	102	**OTUD6A**	97
USP5 (+Ub@Bmax)	104	**USP30**	92	**OTUD6B**	93
USP6	101	**USP35**	107	**Cezanne**	89
USP7	143	**USP36**	100	**AMSH-LP**	89
USP8	98	**USP45**	108	**AMSH-LP (+Zinc)**	113
USP9x	87	**CYLD**	97	**Ataxin3**	95
USP11	108	**UCHL1**	89	**Ataxin3L**	105
USP14	113	**UCHL3**	96	**JOSD1**	110
USP15	100	**UCHL5**	103	**JOSD2**	103
USP16	98	**BAP1**	96		

Time (Hrs)	% Remaining Replica 1	% Remaining Replica 2	Average
24	98.7%	99.4%	99.1%
4	99.7%	103.6%	101.7%
2	100.6%	101.4%	101.0%
1	97.9%	103.0%	100.5%
0	100%	100%	100%

Supplementary Figure 4. Characterization of BC-1471. (a) BC-1471 treatment did not significantly inhibit the enzymatic activity of any of the tested DUBs in a high-throughput *in vitro* screen for off-target DUB inhibition. Data shown as mean percent of untreated control DUB activity (*n*=2). (b) BC-1471 treatment did not significantly inhibit the enzymatic activity of any of the tested MMPs in a fluorescent MMP activity assay. Data shown as MMP activity measured by relative fluorescence compared to the DMSO control (*n*=3). (c) BC-1471 was stable in RPMI media, as measured by mass spectrometry (*n*=2). (d) Percent viability of THP-1 cells treated with BC-1471 for 16 h as determined by trypan blue staining. Data represents mean ± SD with standard curve fit by nonlinear regression (*n*=3). (b) Two-way analysis of variance (ANOVA) with post-hoc Dunnett's multiple comparisons test.



Supplementary Figure 5. BC-1471 relocates NALP7 . (a) Representative images obtained by immunofluorescence co-staining of NALP7 (green), M6PR (red) and DAPI (blue) in PMA-differentiated THP-1 cells following STAMBP knockdown (SBP kd) with siRNA, nontargeting control plasmid (NTC), BC-1471 (BC) treatment (10 µM for 16 h), leupeptin (LEU) treatment (50 µM for 2 h), or a combination thereof. Original magnification was 100x, scale bars = 10 µm. (b,c) Colocalization analysis of images obtained as in Fig S5a. Data represents mean ± SD for the m1 colocalization coefficient of the red-green channel pair (*n*=3). (b, c) One-way analysis of variance (ANOVA) with post-hoc Dunnett's multiple comparisons test.

Supplementary Figure 6. Uncropped Western blots.

Full uncropped scans of Western blots for Figures 1, 2, 3a – 3c

Figure 1d – NALP7: Lanes 1 – 5

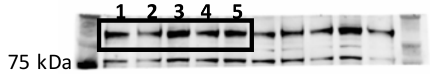


Figure 1d – NALP3: Lanes 1 – 5

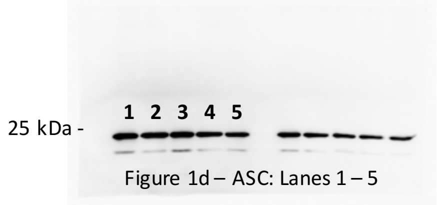


Figure 1d – ASC: Lanes 1 – 5

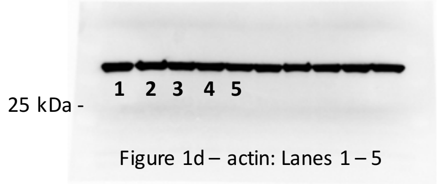


Figure 1d – actin: Lanes 1 – 5

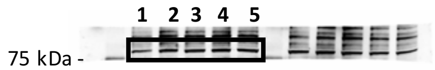


Figure 1e – NALP7: Lanes 1 – 5

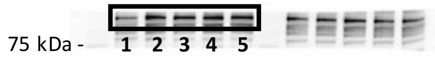


Figure 1e – NALP3: Lanes 1 – 5

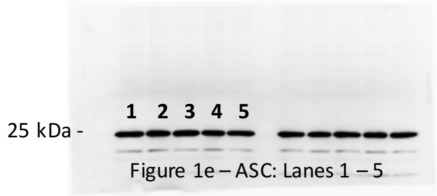


Figure 1e – ASC: Lanes 1 – 5

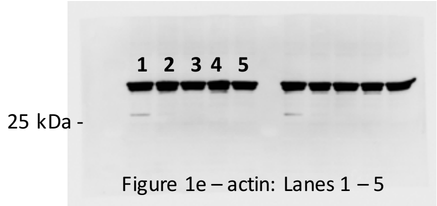


Figure 1e – actin: Lanes 1 – 5

Figure 2b (CHX) – NALP7: Lanes 1 – 5

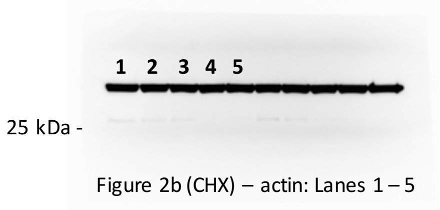


Figure 2b (CHX) – actin: Lanes 1 – 5

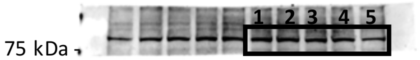


Figure 2b (CHX + LPS) – NALP7: Lanes 1 – 5

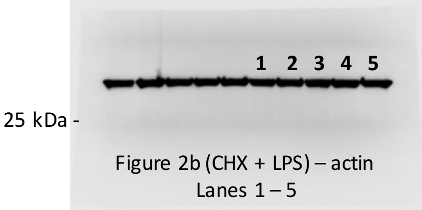


Figure 2b (CHX + LPS) – actin
Lanes 1 – 5

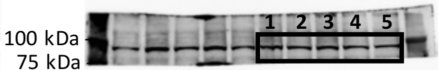


Figure 2b (CHX + Pam3CSK4) – NALP7
Lanes 1 – 5

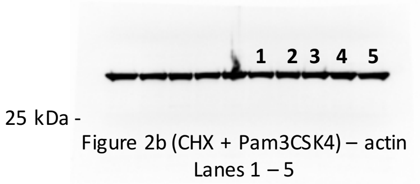


Figure 2b (CHX + Pam3CSK4) – actin
Lanes 1 – 5

Figure 2c (Leupeptin) – NALP7
Lanes 1 – 5

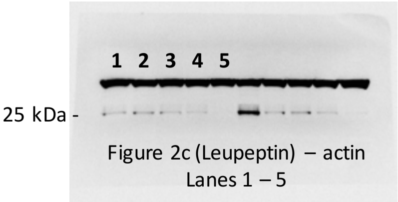


Figure 2c (Leupeptin) – actin
Lanes 1 – 5

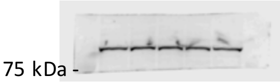


Figure 2c (MG-132) – NALP7

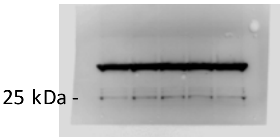


Figure 2c (MG-132) – actin

Figure 2c (Bafilomycin) – NALP7
Lanes 1 – 5

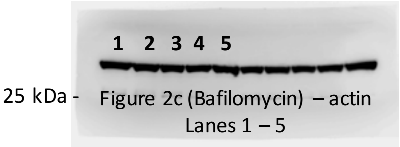


Figure 2c (Bafilomycin) – actin
Lanes 1 – 5

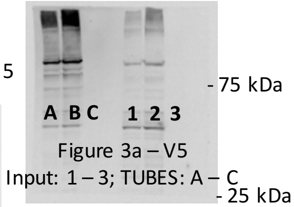


Figure 3a – V5
Input: 1 – 3; TUBES: A – C

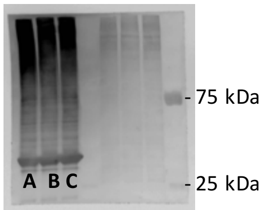


Figure 3a – Ubi
TUBES: A – C

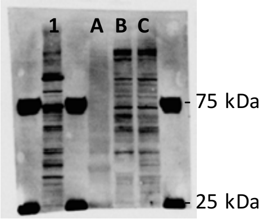


Figure 3b – V5
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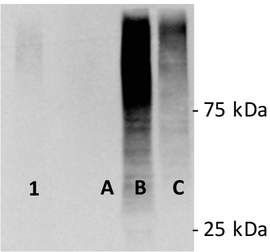

Figure 3b – Ubi
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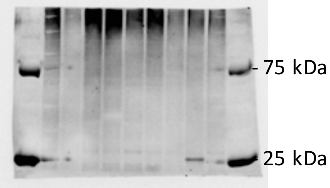


Figure 3c – Ubi

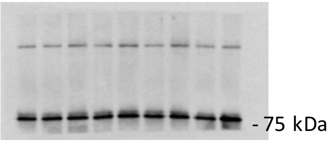


Figure 3c – V5

Supplementary Figure 6 (cont). Uncropped Western blots.

Full uncropped scans of Western blots for Figures 3e & 3f

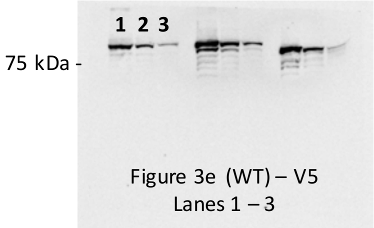


Figure 3e (WT) – V5
Lanes 1 – 3

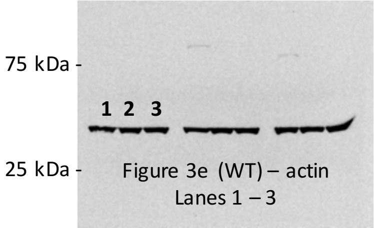


Figure 3e (WT) – actin
Lanes 1 – 3

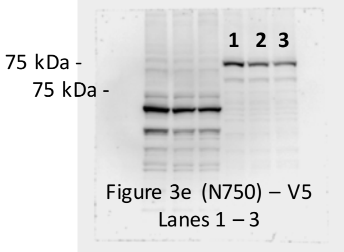


Figure 3e (N750) – V5
Lanes 1 – 3

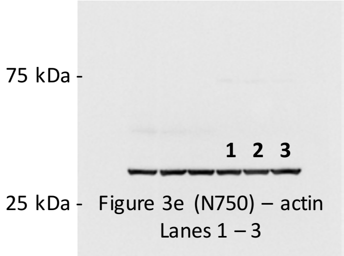


Figure 3e (N750) – actin
Lanes 1 – 3

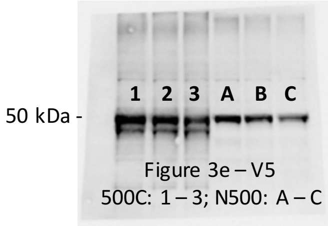


Figure 3e – V5
500C: 1 – 3; N500: A – C

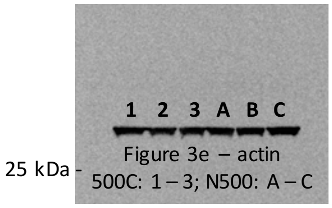


Figure 3e – actin
500C: 1 – 3; N500: A – C

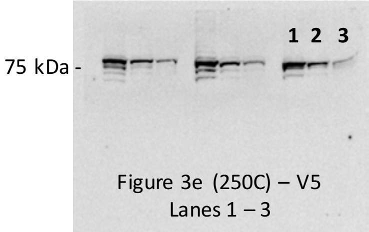


Figure 3e (250C) – V5
Lanes 1 – 3

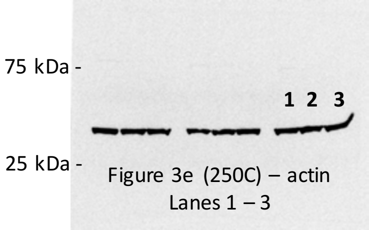


Figure 3e (250C) – actin
Lanes 1 – 3

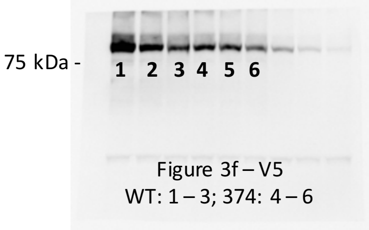


Figure 3f – V5
WT: 1 – 3; 374: 4 – 6

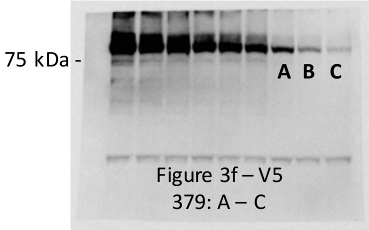
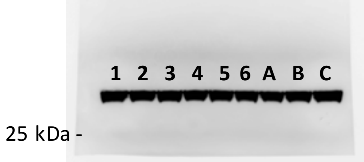


Figure 3f – V5
379: A – C

Figure 3f (WT, 374, 379) – actin
WT: 1 – 3; 374: 4 – 6; 379: A – C



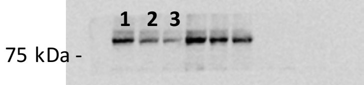


Figure 3f (275) – V5: Lanes 1 – 3

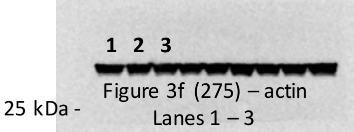


Figure 3f (275) – actin
Lanes 1 – 3

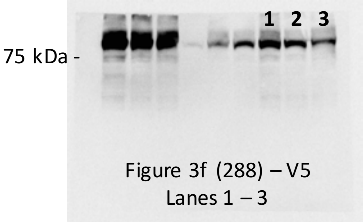


Figure 3f (288) – V5
Lanes 1 – 3

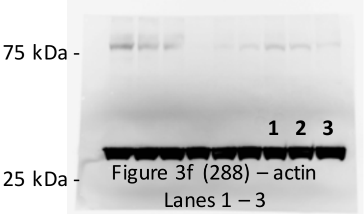


Figure 3f (288) – actin
Lanes 1 – 3

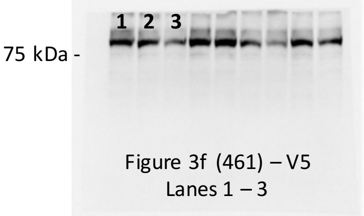


Figure 3f (461) – V5
Lanes 1 – 3

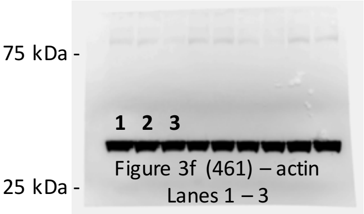


Figure 3f (461) – actin
Lanes 1 – 3

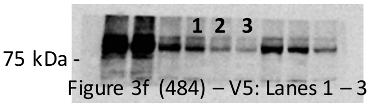


Figure 3f (484) – V5: Lanes 1 – 3

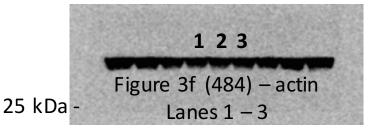


Figure 3f (484) – actin
Lanes 1 – 3

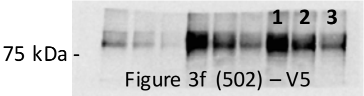


Figure 3f (502) – V5
Lanes 1 – 3

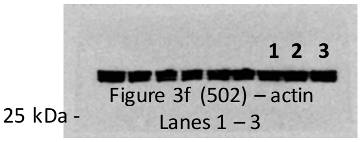


Figure 3f (502) – actin
Lanes 1 – 3

Supplementary Figure 6 (cont). Uncropped Western blots.

Full uncropped scans of Western blots for Figures 3f (cont.), 3i, 4a & 4c

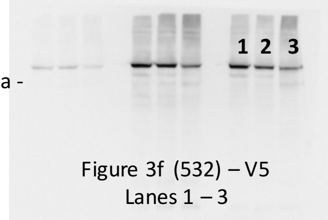


Figure 3f (532) – V5
Lanes 1 – 3

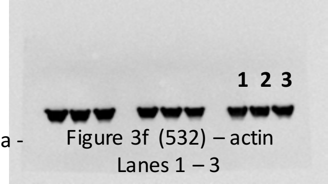


Figure 3f (532) – actin
Lanes 1 – 3

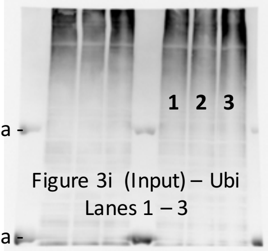


Figure 3i (Input) – Ubi
Lanes 1 – 3

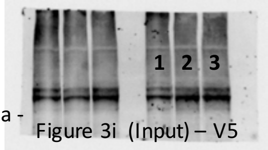


Figure 3i (Input) – V5
Lanes 1 – 3

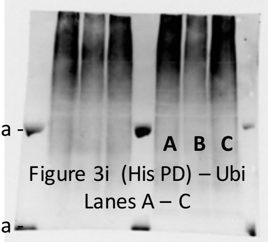


Figure 3i (His PD) – Ubi
Lanes A – C

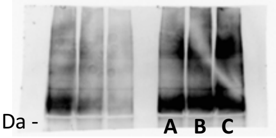


Figure 3i (His PD) – V5
Lanes A – C

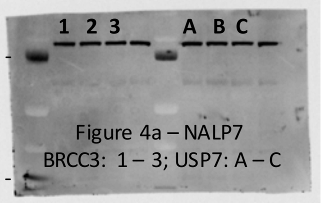


Figure 4a – NALP7
BRCC3: 1 – 3; USP7: A – C

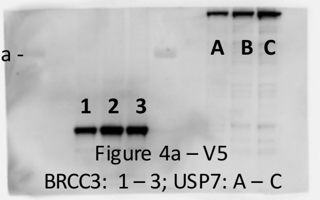


Figure 4a – V5
BRCC3: 1 – 3; USP7: A – C

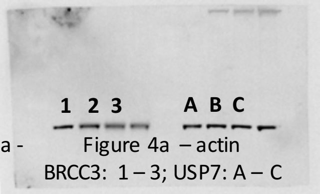


Figure 4a – actin
BRCC3: 1 – 3; USP7: A – C

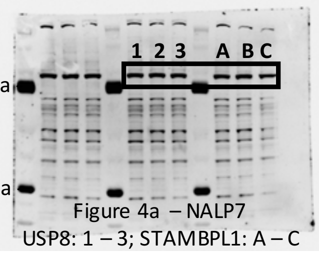


Figure 4a – NALP7
USP8: 1 – 3; STAMBPL1: A – C

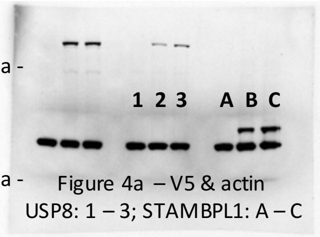


Figure 4a – V5 & actin
USP8: 1 – 3; STAMBPL1: A – C

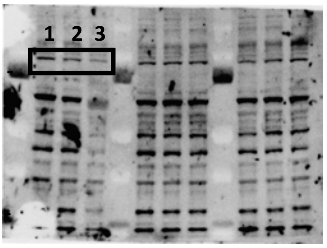


Figure 4a – NALP7
COPS5: 1 – 3

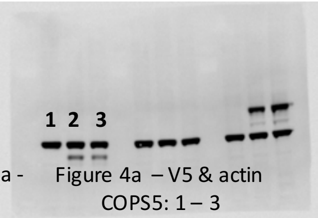


Figure 4a – V5 & actin
COPS5: 1 – 3

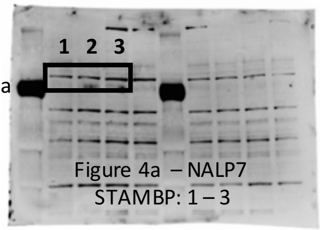


Figure 4a – NALP7
STAMBP: 1 – 3

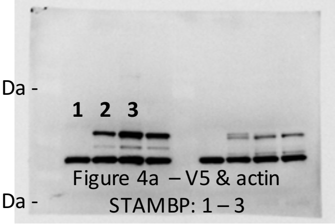


Figure 4a – V5 & actin
STAMBP: 1 – 3

Figure 4c – NALP7: Lanes 1 – 3

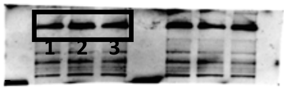


Figure 4c – NALP3: Lanes 1 – 3

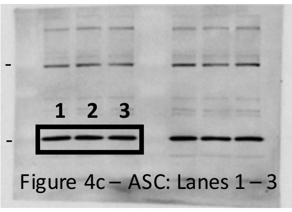


Figure 4c – ASC: Lanes 1 – 3

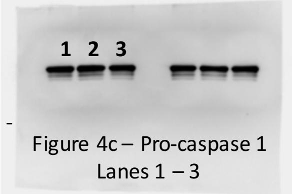


Figure 4c – Pro-caspase 1
Lanes 1 – 3

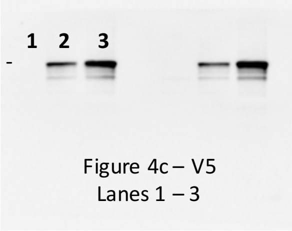


Figure 4c – V5
Lanes 1 – 3

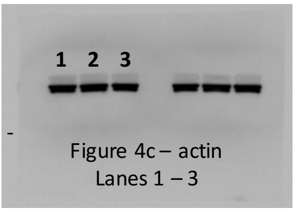


Figure 4c – actin
Lanes 1 – 3

Supplementary Figure 6 (cont). Uncropped Western blots.

Full uncropped scans of Western blots for Figures 4d – 4h & 5

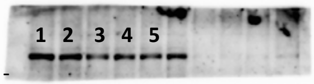


Figure 4d – NALP7: Lanes 1 – 5

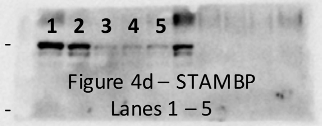


Figure 4d – STAMBP
Lanes 1 – 5

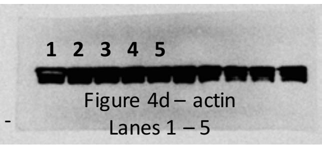


Figure 4d – actin
Lanes 1 – 5

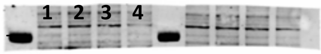


Figure 4e – NALP7: Lanes 1 – 4

Figure 4e – STAMBP: Lanes 1 – 4

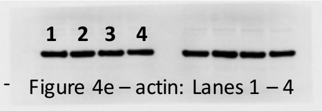


Figure 4e – actin: Lanes 1 – 4

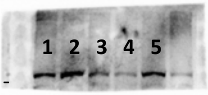


Figure 4f – NALP7: Lanes 1 – 5

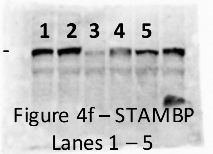


Figure 4f – STAMBP
Lanes 1 – 5

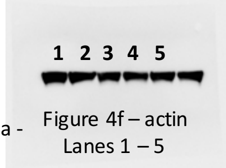


Figure 4f – actin
Lanes 1 – 5

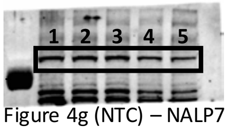


Figure 4g (NTC) – NALP7
Lanes 1 – 5

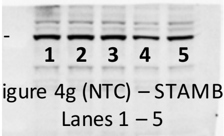


Figure 4g (NTC) – STAMBP
Lanes 1 – 5

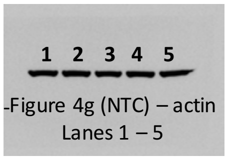


Figure 4g (NTC) – actin
Lanes 1 – 5

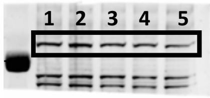


Figure 4g (STAMBP) – NALP7
Lanes 1 – 5

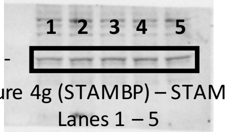


Figure 4g (STAMBP) – STAMBP
Lanes 1 – 5

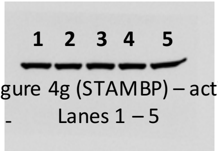


Figure 4g (STAMBP) – actin
Lanes 1 – 5

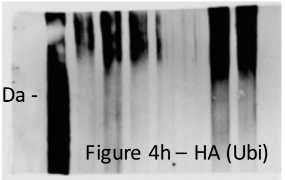


Figure 4h – HA (Ubi)

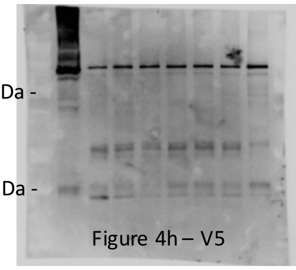


Figure 4h – V5

Figure 5b – NALP7: Lanes 1 – 5

Figure 5b – NALP3: Lanes 1 – 5

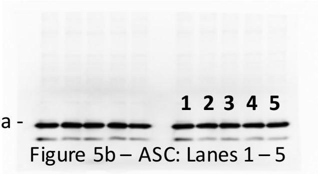


Figure 5b – ASC: Lanes 1 – 5

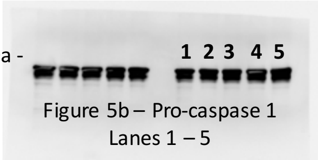


Figure 5b – Pro-caspase 1
Lanes 1 – 5

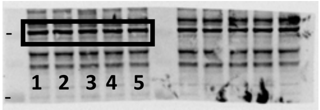


Figure 5b – STAMBP: Lanes 1 – 5

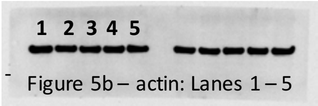


Figure 5b – actin: Lanes 1 – 5

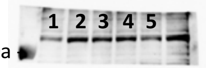


Figure 5c – NALP7: Lanes 1 – 5

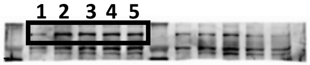


Figure 5c – NALP3: Lanes 1 – 5

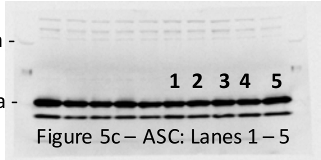


Figure 5c – ASC: Lanes 1 – 5

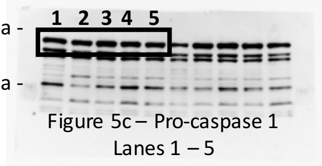


Figure 5c – Pro-caspase 1
Lanes 1 – 5

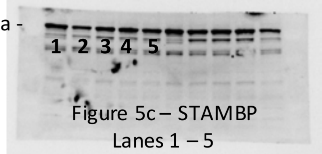


Figure 5c – STAMBP
Lanes 1 – 5

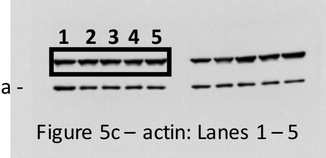


Figure 5c – actin: Lanes 1 – 5

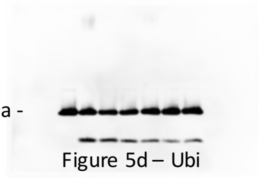


Figure 5d – Ubi

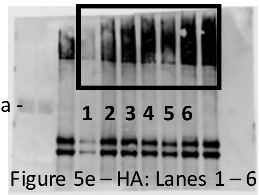


Figure 5e – HA: Lanes 1 – 6

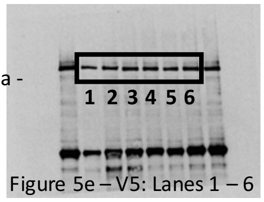


Figure 5e – V5: Lanes 1 – 6

Supplementary Figure 6 (cont). Uncropped Western blots.

Full uncropped scans of Western blots for Figure S1 & S2

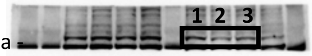


Figure S1b (NALP3) – NALP3: Lanes 1 – 3

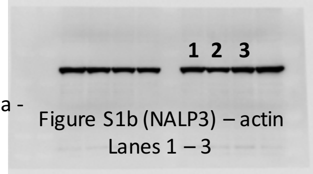


Figure S1b (NALP3) – actin
Lanes 1 – 3

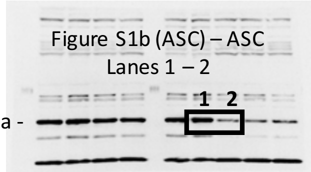


Figure S1b (ASC) – ASC
Lanes 1 – 2

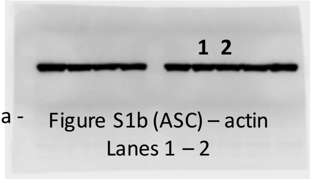


Figure S1b (ASC) – actin
Lanes 1 – 2

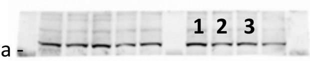


Figure S1b (NALP7) – NALP7: Lanes 1 – 3

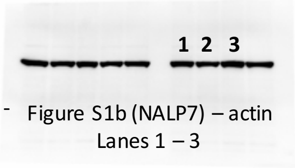


Figure S1b (NALP7) – actin
Lanes 1 – 3

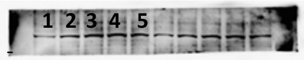


Figure S1c – NALP7: Lanes 1 – 5

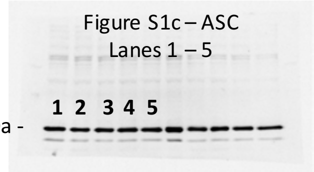


Figure S1c – ASC
Lanes 1 – 5

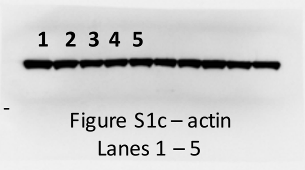


Figure S1c – actin
Lanes 1 – 5

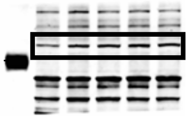


Figure S1d – NALP7

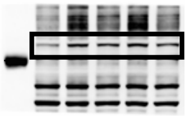


Figure S1d – NALP3

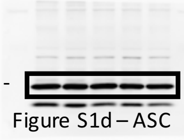


Figure S1d – ASC

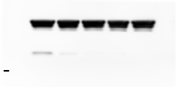


Figure S1d – actin

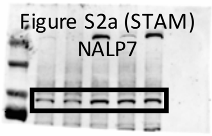


Figure S2a (STAM)
NALP7

Figure S2a (STAM) – STAM

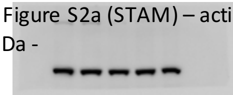


Figure S2a (STAM) – actin

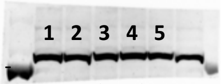


Figure S2a (HRS) – NALP7
Lanes 1 – 5

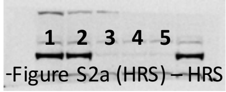


Figure S2a (HRS) – HRS
Lanes 1 – 5

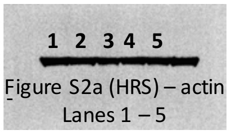


Figure S2a (HRS) – actin
Lanes 1 – 5

Figure S2a (TSG101) – NALP7
Lanes 1 – 5

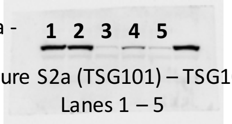


Figure S2a (TSG101) – TSG101
Lanes 1 – 5

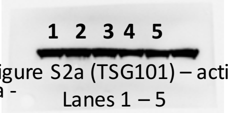


Figure S2a (TSG101) – actin
Lanes 1 – 5

Figure S2a (VPS36) – NALP7
Lanes 1 – 5

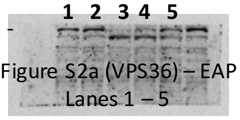


Figure S2a (VPS36) – EAP
Lanes 1 – 5

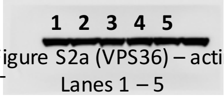


Figure S2a (VPS36) – actin
Lanes 1 – 5

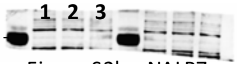


Figure S2b – NALP7
Lanes 1 – 3

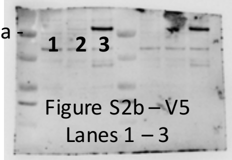


Figure S2b – V5
Lanes 1 – 3

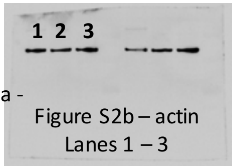


Figure S2b – actin
Lanes 1 – 3

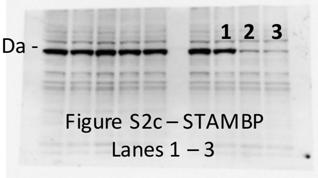


Figure S2c – STAMBP
Lanes 1 – 3

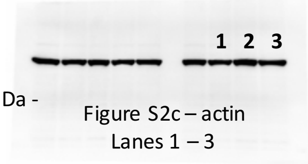


Figure S2c – actin
Lanes 1 – 3

Supplementary Figure 6 (cont). Uncropped Western blots.

Full uncropped scans of Western blots for Figure S3

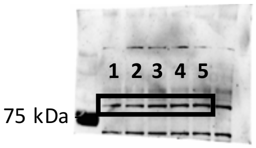


Figure S3b (1470) – NALP7
Lanes 1 – 5

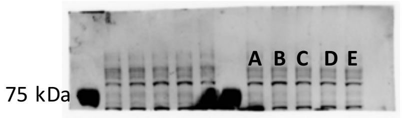


Figure S3b (1471) – NALP7
Lanes A – E

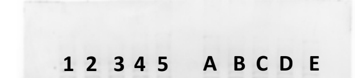


Figure S3b – NALP6
BC1470: 1 – 5; BC1471: A – E

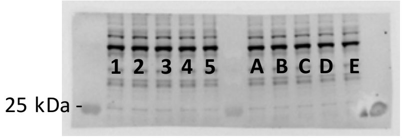


Figure S3b – STAMBP
BC1470: 1 – 5; BC1471: A – E

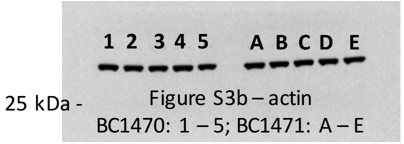


Figure S3b – actin
BC1470: 1 – 5; BC1471: A – E

Figure S3c – NALP7: Lanes 1 – 4

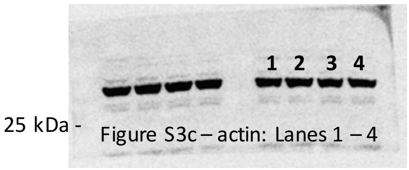


Figure S3c – actin: Lanes 1 – 4

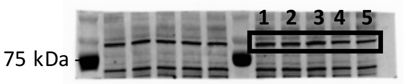


Figure S3d (CON) – NALP7
Lanes 1 – 5

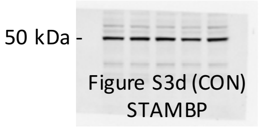


Figure S3d (CON)
STAMBP

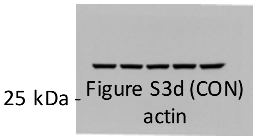


Figure S3d (CON)
actin

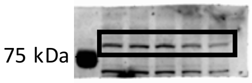


Figure S3d (BC-1471) – NALP7

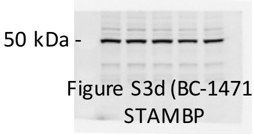


Figure S3d (BC-1471)
STAMBP

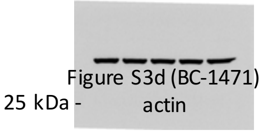


Figure S3d (BC-1471)
actin

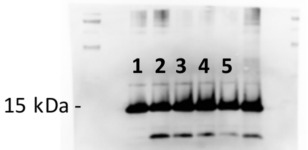


Figure S3f (150 nM) – Ubi
Lanes 1 – 5

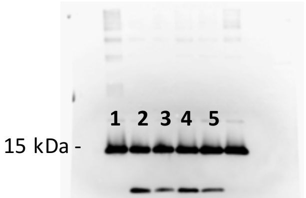


Figure S3f (300 nM) – Ubi
Lanes 1 – 5

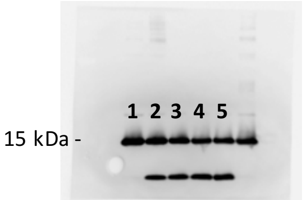


Figure S3f (600 nM) – Ubi
Lanes 1 – 5

Supplementary Table 1. List of primer sequences.

PLASMID CLONING		
Target	Forward	Reverse
NALP7 for topo	CAC CAT GTC TGA CCA TGG AGA TGT GAG	GCA AAA AAA GTC ACA GCA CGG AGG
STAMBP for topo	CAC CAT GTC TGA CCA TGG AGA TGT GAG	TCG AAG GTC TGT GAT GGT CAC TGC
qPCR PRIMERS		
Target	Forward primer	Reverse primer
NALP7	CTG CAG ATG TTG TCG TTG G	CTT GCT GAC AAC CAA GAC AG
Pro-IL-1beta	CTC GCC AGT GAA ATG ATG G	TGG AAG GAG CAC TTC ATC TG
STAMBP	CCT CTA TAA CAA GTA TAT CAC GCT C	CTT TGG GAA ATG CAA TCT CCT
STAM	ACT TTG AAG CTG CTG AAG AC	TCC ACC AGT TAG GAT CAC TG
GAPDH	GCA TCC TGG GCT ACA CTG AG	AAG TGG TCG TTG AGG GCA AT
TRUNCATION MUTANT PRIMERS		
WT NALP7 forward	CAC CAT GTC TGA CCA TGG AGA TGT GAG	
WT NALP7 reverse	GCA AAA AAA GTC ACA GCA CGG AGG	
N500 (reverse)	TAC GTC CCC GAT GTC CCA GG	
N750 (reverse)	CAG CAT CAT CGT GCG TTC CCA	
250C (forward)	CAC CAT GGT GGT CGA TGG CC	
500C (forward)	CAC CAT GCA GAA GCT GCT TTC CG	
SITE-DIRECTED MUTAGENESIS PRIMERS		
Target	Forward	Reverse
KKK275RRR	GCG GGG ACT GGG AGA GAA GAA GAC CGG TGC CCG TCC TC	GAG GAC GGG CAC CGG TCT TCT TCT CTC CCA GTC CCC GC
KRK288RRR	GGG GAG TTT GCT GAG AAG ACG GAT GTT ACC CAG GG	CCC TGG GTA ACA TCC GTC TTC TCA GCA AAC TCC CC
K374R	GTG CAC GAC TCT GAG ACT GCA GAT GGA GAA G	CTT CTC CAT CTG CAG TCT CAG AGT CGT GCA C
K379R	GCA GAT GGA GAG AGG GGA GGA CCC G	CGG GTC CTC CCC TCT CTC CAT CTG C
K461R	GAC AGA GTC TCC AGA GGC TGC TAC TC	GAG TAG CAG CCT CTG GAG ACT CTG TC
K484R	CTA CGC CCT GGA GAG AGA GGA GGG GGA GG	CCT CCC CCT CCT CTC TCT CCA GGG CGT AG
K502R	GGG ACG TAC AGA GAC TGC TTT CCG G	CCG GAA AGC AGT CTC TGT ACG TCC C
K532R	GAG AAG AGA GCC AGA GAG TTG GAG GCC AC	GTG GCC TCC AAC TCT CTG GCT CTC TTC TC

Supplementary Table 2. List of DsiRNA sequences.

Target		Sequence (Sense)	Sequence (Antisense)
NLRP3	1	rGrGrA rArGrA rCrArC rCrArG rGrArC rArArU rGrArC rArGC A	rUrGrC rUrGrU rCrArU rUrGrU rCrCrU rGrGrU rGrUrC rUrUrC rCrUrC
	2	rGrGrU rGrUrU rGrGrA rArUrU rArGrA rCrArA rCrUrG rCrAA C	rGrUrU rGrCrA rGrUrU rGrUrC rUrArA rUrUrC rCrArA rCrArC rCrUrG
ASC	1	rGrCrG rArGrG rGrUrC rArCrA rArArC rGrUrU rGrArG rUrGG C	rGrCrC rArCrU rCrArA rCrGrU rUrUrG rUrGrA rCrCrC rUrCrG rCrGrA
NLRP7	1	rGrGrU rGrCrA rArGrA rArArU rArGrA rUrArA rUrCrC rUrGA G	rCrUrC rArGrG rArUrU rArUrC rUrArU rUrUrC rUrUrG rCrArC rCrUrG
	2	rGrGrA rUrArA rUrArA rArGrU rUrArG rArGrC rArCrU rCrUC G	rCrGrA rGrArG rUrGrC rUrCrU rArArC rUrUrU rArUrU rArUrC rCrCrU
STAMBP	1	rGrUrA rGrCrU rCrArG rArArA rUrUrA rArGrA rArArG rArAT G	rCrArU rUrCrU rUrUrC rUrUrA rArUrU rUrCrU rGrArG rCrUrA rCrUrU
	2	rGrGrA rGrUrU rGrArG rArUrU rArUrC rCrGrA rArUrG rGrCA T	rArUrG rCrCrA rUrUrC rGrGrA rUrArA rUrCrU rCrArA rCrUrC rCrArG
	3	rGrCrU rCrUrU rArCrC rArGrA rUrGrA rUrGrU rUrGrC rCrAG A	rUrCrU rGrGrC rArArC rArUrC rArUrC rUrGrG rUrArA rGrArG rCrArG
STAM	1	rArGrA rArUrU rGrArU rArCrA rArGrG rCrUrA rUrUrU rGrUC T	rArGrA rCrArA rArUrA rGrCrC rUrUrG rUrArU rCrArA rUrUrC rUrUrU
	2	rArGrA rGrUrG rArArC rCrArC rArArA rGrArU rCrCrU rCrAC G	rCrGrU rGrArG rGrArU rCrUrU rUrGrU rGrGrU rUrCrA rCrUrC rUrUrC
	3	rArGrA rArUrG rArUrC rCrArC rArGrC rUrUrA rGrUrC rUrAA T	rArUrU rArGrA rCrUrA rArGrC rUrGrU rGrGrA rUrCrA rUrUrC rUrUrA
HRS	1	rGrCrC rUrUrA rCrArA rCrArU rGrCrA rGrArA rUrCrU rCrAT G	rCrArU rGrArG rArUrU rCrUrG rCrArU rGrUrU rGrUrA rArGrG rCrUrG
	2	rArGrA rArUrU rCrArA rArGrA rGrArG rCrGrA rUrGrC rCrAT G	rCrArU rGrGrC rArUrC rGrCrU rCrUrC rUrUrU rGrArA rUrUrC rUrGrG
	3	rGrGrA rGrUrA rArCrA rCrUrA rCrArU rArCrA rGrUrU rCrAC C	rGrGrU rGrArA rCrUrG rUrArU rGrUrA rGrUrG rUrUrA rCrUrC rCrGrG
TSG101	1	rGrCrC rUrUrG rArArA rCrGrA rArCrA rGrArA rGrArA rGrAC C	rGrGrU rCrUrU rCrUrU rCrUrG rUrUrC rGrUrU rUrCrA rArGrG rCrArU
	2	rUrGrG rUrGrU rCrCrA rArGrU rArCrA rArArU rArCrA rGrAG A	rUrCrU rCrUrG rUrArU rUrUrG rUrArC rUrUrG rGrArC rArCrC rArUrU
	3	rArGrA rUrCrA rArGrA rArGrU rArGrC rCrGrA rGrGrU rUrGA T	rArUrC rArArC rCrUrC rGrGrC rUrArC rUrUrC rUrUrG rArUrC rUrArA
Vps36	1	rGrGrA rArUrA rGrCrU rArArC rCrCrA rGrUrU rArCrC rArGA G	rCrUrC rUrGrG rUrArA rCrUrG rGrGrU rUrArG rCrUrA rUrUrC rCrCrA
	2	rCrCrU rArGrC rCrArA rArGrA rArArG rGrUrU rGrCrU rGrCT T	rArArG rCrArG rCrArA rCrCrU rUrUrC rUrUrU rGrGrC rUrArG rGrArG
	3	rGrGrC rUrArA rUrArC rUrGrC rArUrG rUrArG rArUrU rGrCT T	rArArG rCrArA rUrCrU rArCrA rUrGrC rArGrU rArUrU rArGrC rCrArG