#### **1** Supplemental Information to

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# Bacterial secretion system skews the fate of *Legionella*-containing vacuoles towards LC3-associated phagocytosis.

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- 25 Figure S1. The *L. dumoffii* replicates in ER-like vacuoles in a Dot/Icm type
- 26 IV secretion system dependent manner.



(A) Graph showing fold change in CFU/ml of *L. dumoffii* NY23 Str<sup>R</sup> and *L. dumoffii* $\Delta dotA$  NY23 Str<sup>R</sup> in THP-1 cells over 3 days. Data are from a single experiment and values shown are the average of three independent infections each performed with triplicate wells. Error bars are ± SEM. (B) Fluorescent image of a HeLa Fc $\gamma$ RII cell transfected with mtagRFP-KDEL (red) and infected with *L. dumoffii* constitutively expressing GFPmut3 (green). Clear localization

34 of the tagged-KDEL to the bacterial phagosome was observed at 90 min post-35 infection as indicated by white arrows and enlarged in inset. (C) Fluorescent 36 image of human THP-1 cells infected with *L. dumoffii* constitutively expressing mCherry (red). ER-association was assessed by indirect immunofluorescence 37 38 using a primary antibody raised against the C-terminal (ER luminal) region of 39 calnexin (Enzo#ADI-SPA-860). Image taken at 12 and 16 hours post-infection 40 show positive association of calnexin with *L. dumoffii*-containing phagosomes 41 as shown by white arrows.

- 43 Figure S2. Galectin-8 and adapters commonly involved in LC3-
- 44 recruitment are not associated with LdCVs.



HeLa cells stably expressing FcγRII receptor were co-transfected with pTLR2
(see Figure 6) and a single GFP-expression construct, as shown in fluorescent
micrographs; top to bottom: GFP-galectin-8, GFP-NDP52, Tecpr1-GFP, and
GFP-p62. Images shown are at 2 hours post-infection for opsonized *L. dumoffii*

- 50 (left) and S. Typhimurium (right), both organisms harbour plasmids for
  51 constitutive expression of mCherry (red).

54 Figure S3. *L. dumoffii*∆*flaA* replicates robustly in C57BL/6J (B6)-derived



55 macrophages.

57 (A). Graph showing fold change in CFU/ml of *L. dumoffii* NY23  $\Delta$ *flaA* over 2 58 days in bone marrow-derived macrophages from TLR2<sup>+/-</sup> and TLR2<sup>-/-</sup> C57BL/6J 59 (B6) mice. Data are average of three independent experiments, each performed 60 in triplicate. (B) Representative micrograph of TLR2<sup>+/-</sup> macrophage infected 61 with *L. dumoffii* $\Delta$ *flaA*. Nuclear and bacterial DNA is stained with Hoechst 33342. 62

#### 63 Figure S4. LC3-recruitment to LdCVs is independent of Ulk1.



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65 (A) qRT-PCR measuring Ulk1 mRNA levels in HEK293 cells 3 days posttransfection for scrambled (mock) and Ulk1 siRNA-treated cells. Data are 66 67 normalized to GAPDH and shown as fold expression level compared to mock-68 transfected cells. (B) Representative images of LC3-localization in HEK293 69 cells transfected with scrambled (control) or Ulk1-siRNA and infected with 70 mCherry-expressing L. dumoffii for 3 hours or treated with 100 nM of the 71 autophagy inducer rapamycin for 2 hours. (C) Quantification of LC3 recruitment 72 to L. dumoffii vacuoles at 3 hours post-infection in THP-1 cells treated with

DMSO (control) or Rapamycin. Data is the average of two independent
experiments performed in triplicate. Student's t-test was used to determine
significance.



#### 79 Figure S5. Live imaging shows degradation of an LC3-positive *L. dumoffii*.

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Micrographs show a time course of still images from 110 min to 245 min postinfection for RAW264.7 GFP-LC3 cells infected with mCherry-expressing *L. dumoffii*. Cells were incubated at 37°C on a heated stage and manually refocused during the course of infection. The boxed bacterium is LC3-positive at 110, 128, and 145 min post-infection (shown by white arrows). However, this bacterium is no longer visible >163 min post-infection (as shown by yellow arrows). In contrast, adjacent bacteria are still visible.

Figure S6. Live imaging shows acidification of a subset of *L. dumoffii* vacuoles at time-points 3-5 hours post-infection, which is temporally consistent with degradation of LC3-positive vacuoles.



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93 (A) Micrographs show representative images of RAW264.7 GFPLC3 cells
94 infected with Hoescht 3342-stained *L. dumoffii*∆*dotA* (top) or *L. dumoffii*

95 (bottom) at 1 hour post-infection. Cells were incubated with 75 nM 96 LysoTracker® Red DND-99 (Life Technologies#L7528) for 1 hour prior to 97 infection and maintained in media throughout assay. Accumulation of the probe 98 in compartments with a low pH is shown by a red signal. (B) Micrographs show 99 representative images of RAW264.7 GFPLC3 cells infected with Hoescht 3342-100 stained L. dumoffii (bottom) at 3, 4 and 5 hours post-infection. Co-localization 101 of LC3 and lysotracker signals was not readily observed. However, the 102 appearance of lysotracker positive signals associating with L. dumoffii was 103 more frequently observed at >3 hours post-infection, after the peak of LC3 104 association.

- 107 Tables S1-S3 list the bacterial strains, plasmids and primers used in this study,
- 108 respectively.

## **Table S1. Bacterial strains**

Strain	Genotype (name in study)	Reference	
Legionella pneumophila			
Lp01	Legionella pneumophila serogroup 1,	1	
	Lp01 <i>rpsL</i>		
Lp01∆ <i>dotA</i>	Lp01∆ <i>dotA rpsL</i>	2	
Lp01∆ <i>ravZ</i>	Lp01∆ <i>ravZ rpsL</i>	This study	
Lp01 pmCherry	Legionella pneumophila serogroup 1,	This study	
	Lp01 <i>rpsL</i> + pMMB207::mCherry		
Lp01∆ <i>dotA</i>	Lp01∆ <i>dotA rpsL</i> + pMMB207::mCherry,	This study	
pmCherry			
Legionella dumoffii			
Ld00	Legionella dumoffii NY23 (ATCC33279)	3	
Ld01	Ld00, Str <sup>R</sup>	This study	
Ld01 ∆ <i>dotA</i>	<i>L dumoffii ∆dotA,</i> Str <sup>R</sup>	This study	
Ld01 ∆ <i>flaA</i>	<i>L dumoffii ∆flaA,</i> Str <sup>R</sup>	This study	
Ld01 ∆ <i>dotA</i>	<i>L dumoffii</i> ∆ <i>dot</i> A + pMMB207::mCherry	This study	
pmCherry	Str <sup>R</sup> ,		
Ld01 ∆ <i>flaA</i>	<i>L dumoffii∆flaA</i> + pMMB207::mCherry	This study	
pmCherry	Str <sup>R</sup> ,		

Salmonella enterica serover Typhimurium		
SR-11 χ3181	Prototoroph, mouse-passaged $\chi 3041$	4
SR-11 pmCherry	SR-11 + pMMB207::mCherry	This study
E.coli		
DH5a	endA1 hsdR17 supE44 thi-1 recA1 gyrA	Invitrogen
	relA1 Δ(laclZYA-argF)U169, deoR	
	(φ80dlacΔ(lacZ)M15)	
DH5α (λpir)	DH5 $\alpha$ $\lambda$ pir phage lysogen	2
MT607 pRK600	MT607 <i>E. coli</i> containing plasmid	5
	pRK600; ColE1 replicon with RK2	
	transfer genes	

# **Table S2. Plasmids used**.

Plasmid Name	Provided by	Reference
pEGFP-LC3	M. Ogawa	6
pLEXEF.pur.GFP-	Kenji Matsuzawa	This study
LC3		
pEGFP-galectin-3	M. Ogawa	7
pEGFP-galectin-8	M. Ogawa	This study
pTecpr1-EGFP	M. Ogawa	7
pEGFP-p62	M. Ogawa	8
pEGFP-NDP52	M. Ogawa	This study
pTLR2	K. Kobiyama/F. Takeshita	9
pTLR4	K. Kobiyama/F. Takeshita	
pSR47S	R6K suicide vector, Km <sup>R</sup> , sacB	10
pSR47SLd∆ <i>flaA</i>	pSR47S containing 5' and 3' flanking	This study
	genomic regions of <i>L. dumoffii flaA</i> (for	
	gene deletion)	
pSR47SLd∆ <i>dotA</i>	pSR47S containing 5' and 3' flanking	This study
	genomic regions of <i>L. dumoffii dotA</i> (for	
	gene deletion)	
pSR47SLp∆ <i>ravZ</i>	pSR47S containing 5' and 3' flanking	This study
	genomic regions of <i>L. pneumophila ravZ</i>	
	(for gene deletion)	
pMMB207	Cloning vector derived from RSF1010	11

pAM239	pMMB207 containing <i>gfp</i> mut3	12
pMMB207::	pMMB207 containing <i>mCherry</i>	This study
mCherry		
pMMB207- <i>ravZ</i>	pMMB207 encoding <i>L. pneumophila</i>	This study
	ravZ	
pMMB207- <i>ravZ</i>	pMMB207 encoding <i>L. pneumophila</i>	This study
C258A	ravZ C258A	

#### Table S3. List of primers used in this study

5'-	$\Delta$ mutants
cggagctcATCAATACTACTCCCATTA-	
3'	
5'-	
AAAGAAATGAAAGTAGAATTGGTCGT	
GTTA-3'	
5'-	
ΑΑΤΤΟΤΑΟΤΤΤΟΑΤΤΤΟΤΤΤΤΟΤΟΟΤΑ	
ACA-3'	
5'-	-
gc <b>tctaga</b> CCACTACTTACTACTATAGT-	
3'	
	5'- cggagctcATCAATACTACTCTCCATTA- 3' 5'- AAAGAAATGAAAGTAGAATTGGTCGT GTTA-3' 5'- AATTCTACTTTCATTTCTTTTCTCCTA ACA-3' 5'- gctctagaCCACTACTTACTACTATAGT- 3'

pSR47SLd∆ <i>flaA</i>	5'-	
	cg <b>gagctc</b> ACGAGCCGATATCCTGTGA	
	Т-3'	
	5'-	
	TTTTCTATAAATTTTAGTCTCCTCAGA	
	CCT-3'	
	5'-	
	AGACTAAAATTTATAGAAAAAGATGT	
	AAGA-3'	
	5'-	•
	gc <b>tctaga</b> AAAGCAGACAATTCCATAG	
	-3'	
pSR47SLp∆ <i>ravZ</i>	5'-	
	cgc <b>gagctc</b> CTCAACCCCTTTATTTAG	
	-3'	
	5'-	
	CAATTCACACTATTTGACCTCTAAAC	
	TG -3'	
	5'-	
	AGAGGTCAAATAGTGTGAATTGAATT	
	C -3'	
	5'-	
	gc <b>tctaga</b> GGCTGACTGCAAAAGAGAG	
	C -3'	
pSR47Sac1	5'-TAGCTCACTCATTAGGCACC-3'	Sequencing

pSR47SXba1	5'-CTGTTTCTTTTCATTCTCTG-3'	
GFPLC3 f	5'-	Cloning
	AAAAAGCAGGCTATGGTGAGCAAGG	
	GCGAG-3'	
GFPLC3 r	5'-	
	AGAAAGCTGGGTGTGGTATGGCTGA	
	TTATGATC-3'	
Ulk1 f_2	5'-GCAAGGACTCTTCCTGTGACAC-3'	RT-PCR
Ulk1 r_2	5'-CCACTGCACATCAGGCTGTCTG-3'	
Ulk1 f	5'-AAGAACCTCGCCAAGTCTCA-3'	
Ulk1 r	5'-CCGTTGCAGTACTCCATAACC-3'	
GAPDH_f	5'-ACAGTCAGCCGCATCTTCTT-3'	
GAPDH_r	5'-ACGACCAAATCCGTTGACTC-3'	
GFP-Galectin8 f	5'-	Cloning
(BgIII)	ga <b>agatct</b> ATGATGTTGTCCTTAAACAA	(pEGFP-C1)
	CCTAC-3'	
GFP-Galectin8 r	5'-	
(Sall)	ggccgac <b>gtcgac</b> CTACCAGCTCCTTACT	
	TCCAGTAAG-3'	
GFP-NDP52 f	5'-	Cloning
(EcoRI)	ccggaattcATGGAGGAGACCATCAAAG	(pEGFP-C2)
	ATCCC-3'	
GFP-NDP52 r (Sall)	5'-	
	ggccgac <b>gtcgac</b> GAGAGAGTGGCAGAA	
	CACGTGGTC-3'	

<i>ravZ</i> f (BamHI)	5'-	Cloning
	gc <b>ggatcc</b> AGAAAGGCAAGTTAACAGG-	(pMMB207)
	3'	
<i>ravZ</i> r (Xbal)	5'-	
	gc <b>tctaga</b> CTATTTTACCTTAATGCCAC	
	C-3'	
<i>ravZ</i> C258A f	5'-	Site-directed
	GAAGGCAATGCCGGGTCTTATACC-3'	mutagenesis
<i>ravZ</i> C258A r	5'-	
	GGTATAAGACCCGGCATTGCCTTC-3'	

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