The *Dictyostelium discoideum* E3 ubiquitin ligase TrafE coordinates endolysosomal damage response and cell-autonomous immunity to *Mycobacterium marinum*.

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ABSTRACT

Cells are perpetually challenged by pathogens, protein aggregates or chemicals, that induce plasma membrane or endolysosomal compartments damage. Endolysosomal perforations are recognised as severe stress, however the mechanisms of the cellular response that ensure quality control, repair and endolysosomal homeostasis are just beginning to be unravelled. The endosomal sorting complex required for transport (ESCRT) and the autophagy machinery are recruited to damaged membranes to either repair or to remove membrane remnants. Crucial element of the endolysosomal damage response (ELDR) are factors that sense damage, paralleled by extensive tagging of the damaged organelles with signals, such as ubiquitin, required for the recruitment of ELDR components. Unattended membrane damage leads to leakage of harmful components including protons and reactive oxygen species that cause cell death. To explore ELDR key factors responsible for detection and marking of damaged compartments we use the professional phagocyte *Dictyostelium discoideum*. We found an evolutionary conserved E3-ligase TrafE that is robustly recruited to intracellular compartments disrupted after infection with *Mycobacterium marinum* or after sterile damage caused by chemical components. Importantly, we show that the absence of TrafE severely compromises the xenophagy restriction of bacteria as well as autophagy-mediated and ESCRT-mediated ELDR, resulting in early cell death.

INTRODUCTION

After its internalisation by professional phagocytes, the first strategy of *Mycobacterium tuberculosis* and its close relative *Mycobacterium marinum* to escape the bactericidal phagosome is to impede its maturation and tailor the Mycobacterium-Containing Vacuole (MCV) as a permissive niche allowing the proliferation of the pathogen (Soldati and Neyrolles, 2012). From the very beginning, bacteria progressively gain access to the cytosol through the action of the ESX-1 secretion system, via the secretion of the membranolytic effector ESAT-6 and the mycobacterial branched apolar lipids phthiocerol dimycocerosates (PDIMs) (Pym et al., 2002; Lerner et al., 2018; Quigley et al., 2017; Augenstreich et al., 2019; Lienard et al., 2020; Osman et al., 2020). The ESX-1 secretion system plays a crucial role for *M. marinum* virulence and intracellular growth, and is primarily encoded by the genes within the "region of difference 1" (RD1) locus. Lessons from professional phagocytes such as the mammalian macrophages and the social amoeba *Dictyostelium discoideum* show that *M. marinum* mutants with non-functional ESX-1 inflict significantly less MCV membrane damage and fail to become exposed to or escape to the cytosol, hampering their detection by the host cell-autonomous defence machineries (Cardenal-Muñoz et al., 2017; Gao et al., 2004). Once in contact with the cytosol, the wild-type (WT) bacteria within damaged MCVs are detected and tagged with signals which trigger ELDR as well as selective anti-bacterial autophagy (López-Jiménez et al., 2019). To complete the infection cycle, the pathogen must

reach the cytosol and be released by host-cell lysis, exocytosis or ejection in order to disseminate to adjacent bystander cells (Hagedorn et al., 2009; Queval et al., 2017; Cardenal-Muñoz et al., 2017; López-Jiménez et al., 2019).

Eukaryotic cells target intracellular invaders towards the pathogen-specific autophagy pathway termed xenophagy (hereafter referred to as autophagy), a process which plays a fundamental role in cell-autonomous immunity (Sharma et al., 2018; Deretic et al., 2013). Upstream, autophagy requires the detection of the pathogen and its recruitment to the phagophore – a double membrane cup-like structure. Autophagy depends on the coordinated action of about 15 autophagy-related genes (ATG) and is initiated by the recruitment of the core-autophagy factors Atg1 (ULK1 in mammals) kinase complex and Atg9 (ATG9 in mammals) to the nascent phagophore. Its closure around the cargo depends on the atg16-atg12-atg5 E3-like complex, and the lipidation of Atg8 (LC3 in mammals), which marks the phagophore (Mesquita et al., 2017). The resulting autophagosome fuses with lysosomes allowing the degradation of their contents. The selectivity is achieved by the autophagy cargo receptors, which bring together the cargo and the autophagy machinery. Autophagy adaptors such as p62 (SQSTM1 in mammals) link ubiquitin-tagged bacteria and host components with Atg8 family proteins on the phagophore membranes, thereby enforcing proximity between the pathogen and the autophagosome (Boyle and Randow, 2013). We have shown previously that, upon infection, *M. marinum* does colocalize with ubiquitin (Ub) and the autophagy markers such as Atg8 and p62, and that autophagy deficiency results in drastic increase in bacteria proliferation, and that failure to repair or recycle damaged MCVs results in increased cell death (Cardenal-Muñoz et al., 2017; Eriksson et al., 2020; Wang et al., 2018). Autophagy is also involved in ELDR, and beside the elimination of extensively damaged compartments by a specific macroautophagy termed lysophagy, it cooperates with ESCRT to repair sterile- or pathogen-induced membrane damage (Skowyra et al., 2018; López-Jiménez et al., 2019; Papadopoulos et al., 2020). The ESCRT-III complex functions in membrane deformation away from the cytosol and plays a critical role in various membrane remodelling processes, including phagophore sealing, autophagosome-lysosome fusion, plasma membrane and lysosome membrane repair (Vietri et al., 2020; Schuck, 2020). One thoroughly studied ESCRT function is the coupling of cargo sorting and intralumenal vesicles formation required for degradation of receptors.

The endolysosomal and MCV membrane ruptures generate morphological and topological landscape for the detection machineries which deposit "repair-me" and "eat-me" signals (Boyle and Randow, 2013; Koerver et al., 2019; Papadopoulos et al., 2020). Ubiquitination is a well-studied, highly conserved and versatile post-translational modification used as a signalling platform in diverse catabolic processes and playing a role during infection with various intracellular bacteria. In mammalian cells, the RING domain E3 ligases LRSAM1 and TRAF6 have been shown to promote ubiquitination of vacuoles containing *Salmonella* Typhimurium and *Chlamydia trachomatis* bacteria, and the protozoan parasite *Toxoplasma gondii* (Coers and Haldar, 2015; Huett et al., 2012), and NEDD4 (Pei et al., 2017), Parkin (Manzanillo et al., 2013), Smurf1 (Franco et al., 2017) to mediate ubiquitination of mycobacteria and host proteins during infection. In addition, the mammalian cytosolic lectins, galectins, recognize damage by binding exposed glycans on the luminal membrane leaflets and components of bacteria cell wall, thereby serving as "eat-me" tags for autophagy. Moreover, complexes such as TRIM16-Galectin3 also mediate autophagy removal of damaged phagosomes and lysosomes during pathogen invasion (Chauhan et al., 2016; Randow and Youle, 2014). The human tumour necrosis factor receptor-associated factors (TRAF1-7) function in a number of biological processes such as innate and adaptive immunity and cell death as E3 ubiquitin ligases and scaffold proteins (Xie, 2013). TRAFs are composed of several domains: the N-terminal domain containing a RING motif (except TRAF1), a series of Zn-finger motifs that connect the N- and C-terminal regions and the C-terminal TRAF domain (except for TRAF7) subdivided in TRAF-N coiled-coil domain and TRAF-C domain comprised of seven to eight

antiparallel β-strands (Bradley and Pober, 2001; Park, 2018; Joazeiro and Weissman, 2000). The RING domain and the Zn-finger motifs of TRAF6 are required for the E3 ligase activity and together with the dimeric E2-conjugating enzyme complex Ubc13-UeV1A, TRAF6 catalyses the generation of poly-Ub chains linked via the lysin K63 of Ub, in a homo- or hetero-oligomerisation-dependent manner with other TRAF members (Middleton et al., 2017). The scaffolding function of TRAF proteins is conferred by the TRAF-N domain responsible for homo- and hetero-oligomerisation, which is also crucial for the E3 ligase activity, and the TRAF-C domain allows interaction with upstream receptors and adaptors (Yin et al., 2010). In recent years, the selective autophagy and maintenance of the endolysosomal homeostasis have been actively studied and linked to many aspects of human health. Endomembrane ruptures on one hand permit the pathogen to gain access to the cytosol, but on the other hand to be detected. Then, together with the vacuole membrane remnants, bacteria are targeted to the autophagy machinery. Defects in endomembrane repair and lysophagy correlate with weakened cellular defences against pathogens, ageing, cancer and neurodegeneration (Papadopoulos and Meyer, 2017). Even though the role of "eat-me" signals in autophagy is well understood, little is known about their implication in detection and repair of pathogen-induced or sterile membrane damage. Furthermore, how pathogen and membrane damages are detected, leading to the deposition of such "eat-me" signals, remains unknown.

Using the social amoeba *Dictyostelium discoideum – M. marinum* model system for host-pathogen interactions, we have unravelled a novel function of a TRAF-like family protein RING domain-containing E3 ligase. Among a dozen candidates explored, we found that TrafE is an evolutionary conserved E3-ligase, proximal to the bacteria detection machinery, which plays a key role in the preservation of endomembrane integrity during infection with *M. marinum* and upon sterile damage. Importantly, we provide evidence that in the absence of TrafE, the autophagy restriction of bacteria as well as the autophagy-mediated and ESCRT-mediated ELDR are severely compromised, leading to precocious cell death.

RESULTS

The E3-ligase TrafE is overexpressed early-on after infection and is recruited to MCVs

Using the sequence of the human TRAF6 as a reference we searched and identified bioinformatically a number of *D. discoideum* TRAF-like proteins, five of which, namely TrafA, TrafB, TrafC, TrafD and TrafE harbour all of the stereotypical TRAF protein family domains and are expressed during the vegetative cell cycle (Dunn et al., 2018; Stajdohar et al., 2017). In parallel, RNA-sequencing (RNA-seq) transcriptomic comparison between control and *M. marinum*-infected *D. discoideum* cells showed that out of the aforementioned candidates only *trafE* is overexpressed early after infection (S1 Fig) (Hanna et al., 2019) and enriched at the early MCV, as revealed by proteomics (Guého et al., 2019).

To validate a possible role in infection of the aforementioned TRAF-like proteins, we first sought to identify candidates that display remarkable relocalization during infection. To do so, we generated stably transformed cell lines ectopically expressing TrafA, TrafB, TrafC, TrafD and TrafE candidate proteins, N- or C-terminally fused to GFP, under a constitutive promoter. We monitored the subcellular localization of these GFP fusions by live confocal microscopy over a period of 24 hours in the context of an infection with *M. marinum*, compared to a mock-infected control. As early as 1 hour post infection (hpi), GFP-TrafE showed robust recruitment to MCVs, sustained over the infection time course, predominantly in the area of *M. marinum* bacteria poles (Fig 1A, 1B and 1C). GFP-TrafA and GFP-TrafB remained solely cytosolic or nuclear, respectively, in control and infection conditions at all time points (S2A and S2B Fig). We confirmed in silico that TrafB harbours a nuclear localization signal (NLS) similarly to human TRAF4, as predicted by both NLS Mapper and NLStradamus (Nguyen Ba et al., 2009; Kosugi et al., 2009). Interestingly, despite TrafC and TrafD being 98% similar in terms of amino acid sequence, they displayed different behaviour upon infection. GFP-TrafC like GFP-TrafE was recruited to MCV, which was not the case for GFP-TrafD (S3A and S3B Fig).

Real-Time quantitative-PCR (RT q-PCR) carried out to monitor the transcriptional profile in control and infected cells confirmed up to 4-fold upregulation of *trafE* already at 1 hpi (Fig 1D), consistent with the RNA-seq data (Hanna et al., 2019). We also evaluated a possible overexpression phenotype of TrafC , TrafD and TrafE during infection using an intracellular growth assay during infection with bioluminescent *M. marinum* (*M. marinum*-lux). In this assay the bioluminescence intensity is measured in relative light units (RLU) as a readout for bacterial growth (Sattler et al., 2007). Whilst the intracellular growth of *M. marinum* WT remained unaffected in cells overexpressing TrafC or TrafD, this growth was significantly hampered when TrafE was overexpressed (S4A Fig, Fig 1E). These results persuaded us to explore further the role of TrafE in infection as potentially the principal E3 ligase candidate.

In order to assess potential artefacts of overexpression, a TrafE-GFP chromosomal knock-in (TrafE-GFP KI) was generated and tested functionally by monitoring intracellular growth of *M. marinum*-lux. Importantly, bacteria growth in the TrafE-GFP KI strain was comparable to that in WT cells (S4B Fig), indicating that C-terminal GFP fusion of TrafE does not interfere with its function. In addition, the endogenous TrafE-GFP colocalized with MCVs already 1.5 hours after infection (Fig 1F) like the ectopically expressed GFP-TrafE (Fig 1A). Thus, our data suggests that TrafE is involved in the early MCV membrane damage detection and MCV or *M. marinum* ubiquitination, necessary for repair or degradation. We conclude that TrafE is a conserved E3-ligase upregulated and recruited to the *M. marinum* compartment upon infection and likely involved in *D. discoideum* cell-autonomous immunity.

Loss of TrafE promotes *M. marinum* early release and replication, and is highly toxic for host cells

To explore further whether TrafE is either involved in the host defence response or is exploited by bacteria to favour their proliferation, we generated cell lines in which the *trafE* coding sequence (CDS) was ablated (*trafE* KO), and strains overexpressing TrafE. We observed that the load of *M. marinum*-lux was increased in *trafE* KO cells and, most interestingly, was comparable and phenocopied the growth of the pathogen in the autophagy-impaired *atg1* KO mutant cells (Fig 2A).

Previous studies indicated that in the absence of autophagy (e.g. *atg1* KO cells) or ESCRT-III-mediated membrane damage repair (e.g., *tsg101* KO cells), bacteria escape early to the cytosol (Cardenal-Muñoz et al., 2017; López-Jiménez et al., 2019). As a reporter for *M. marinum* escape to the cytosol, we monitored Plin, the *D. discoideum* homolog of the mammalian perilipins known to bind the hydrophobic cell wall of mycobacteria exposed to the cytosol (Barisch et al., 2015b). The proportion of mCherry-Plin-positive bacteria indicated that in *trafE* KO host cells *M. marinum* was exposed to the cytosol significantly earlier, compared to WT cells, but similar to *atg1* KO cells (Fig 2B). It has been shown that in the *atg1* KO and *tsg101* KO mutant cells *M. marinum* escapes earlier from the MCV to the cytosol due to a lack of both autophagic and ESCRT-III MCV membrane repair (Cardenal-Muñoz et al., 2017; López-Jiménez et al., 2019). However, in the context of these mutations *M. marinum* has distinct fates. In *atg1* KO cells, bacteria accumulate ubiquitin but proliferate significantly due to a lack of functional autophagy. In *tsg101* KO background *M. marinum* is ubiquitinated and recruited to the autophagy machinery, leading to restriction of bacterial growth. Interestingly, in *trafE* KO host cells *M. marinum* escapes earlier and displays high proliferation, suggesting that both MCV damage repair and xenophagy restriction of bacteria are impaired. Furthermore, we infected WT and *trafE* KO cells with mCherry-expressing bacteria and monitored the infection by high-content (HC) confocal microscopy. Surprisingly, after 30 hpi we observed a drastic decrease in the number of infected *trafE* KO cells compared to infected WT cells (Fig 2C). This was paralleled by a high number of extracellular *M. marinum* that had likely been released by lysis from host *trafE* mutant cells near 30 hpi (Fig 2D). In conclusion, we hypothesized that *M. marinum* escapes earlier to the cytosol of *trafE* KO cells and as a likely consequence, kills the host faster.

To validate this hypothesis, we employed a microfluidic device in which single infected cells are trapped in the InfectChip (Delincé et al., 2016). We confirmed that *M. marinum* is

highly toxic for *trafE* KO cells, a phenotype almost fully complemented by GFP-TrafE overexpression (Fig. 2E). Surprisingly, the survival probability of infected autophagy-deficient *atg1* KO host cells was not significantly affected under these conditions and time-frame (Fig 2E), even though *M. marinum* intracellular growth is drastically increased in these mutants compared to WT (Cardenal-Muñoz et al., 2017). Altogether, these results reveal that absence of Atg1 or TrafE facilitates *M. marinum* early escape from the MCVs to the cytosol, and strongly affects its targeting to the xenophagy machinery. As a consequence, the pathogen rapidly proliferates, suggesting that both Atg1 and TrafE work in the same pathway. Nevertheless, *M. marinum* is more toxic to *D. discoideum* in absence of TrafE than of Atg1, indicating that TrafE is more broadly involved in cell survival mechanisms.

TrafE action is triggered by *M. marinum*-induced MCV membrane damage

Taking into account that MCV membrane disruption prompts the recruitment of both the ESCRT and the autophagy machineries, we hypothesized that TrafE colocalization with *M. marinum* depends on membrane damage. Both, *M. tuberculosis* and *M. marinum* share the genomic locus Region of Difference 1 (RD1) encoding the ESX-I (type VII) secretion system required for the secretion of the membranolytic virulence factor ESAT-6 (Hagedorn et al., 2009). As previously shown (Cardenal-Muñoz et al., 2017), in *D. discoideum* cells infected with *M. marinum* ΔRD1, which induces less MCV damages, bacteria and their compartment ubiquitination is significantly decreased. In addition, nearly 80% of GFP-TrafE recruited to MCVs is in the vicinity of bacteria poles (Fig 1C), where ESX-1 is localized and active in both *M. tuberculosis* and *M. marinum* (Carlsson et al., 2009). Interestingly, upon infection with *M. marinum* ΔRD1, TrafE-GFP recruitment to MCV was severely reduced (Fig 3A and 3B). Previously, we showed that both intracellular growth of WT *M. marinum* as well as autophagosome formation depend on a functional ESX-1 system. Consequently, the bacteria load of *M. marinum* ΔRD1 was significantly and similarly reduced in both WT and *atg1* KO cells (Cardenal-Muñoz et al., 2017). Therefore, we measured the intracellular growth of WT and *M. marinum* ΔRD1 bacteria. Lack of the ESX-1 system drastically reduced bacterial proliferation in both WT and *trafE* KO cells (Fig 3C), indicating that the growth advantage of WT *M. marinum* in *trafE* KO cells is strictly dependent on MCV damage and escape to the cytosol. In addition, the survival probability of both *trafE* KO and *atg1* KO host cells was not affected during infection with the *M. marinum* ΔRD1 bacteria (Fig 3D). In conclusion, we propose that membrane damage is required for TrafE recruitment to MCVs and subsequent restriction of bacteria proliferation by xenophagy.

K63-ubiquitination levels are decreased in the absence of TrafE

A hallmark of damaged MCVs is ubiquitination that plays an essential role in pathways such as cell survival (e.g. autophagy), intracellular pathogen clearance (e.g. xenophagy) and cell death (e.g. apoptosis, necrosis) (Cardenal-Muñoz et al., 2017; Papadopoulos and Meyer, 2017; Yoshida et al., 2017; López-Jiménez et al., 2019; Gómez-Díaz and Ikeda, 2019; Papadopoulos et al., 2020). We carried out immunofluorescence assays using antibodies specific to K63-linkage polyubiquitin and determined that GFP-TrafE colocalized with K63-ubiquitinylated MCVs (Fig 4A). Next, we compared the total levels of polyubiquitin-positive MCVs or K63-linked polyubiquitinylated MCVs in infected WT or *trafE* KO cells, using a global anti-polyubiquitin antibody or the specific K63-linkage polyubiquitin antibody. Interestingly, at 6 hpi the global levels of polyubiquitination between *trafE* KO and WT cells remained comparable, while the fraction of K63-linkage positive MCVs was drastically reduced in *trafE* KO cells (Fig 4A and 4B). These results suggest that TrafE, as part of the ELDR, functions as a E3 ligase responsible for K63-linked polyubiquitination of MCVs and bacteria upon membrane damage.

TrafE recruitment to bacteria is mediated by its RING domain

It has been previously reported, that TRAF E3-ligase activity depends on the RING domain that mediates the interaction between the E2-conjugating enzymes and their substrates, and TRAF-N and RING domains-dependent homo- or hetero-oligomerizations with other members of the TRAF family (Das et al., 2021). Therefore, in order to dissect the functional

importance of the RING and the TRAF-N regions during *M. marinum* infection, we generated truncated versions of TrafE that were expressed in the *trafE* KO background. Absence of the N-terminal RING domain resulted in complete loss of TrafE recruitment to MCVs throughout the infection time-course, in contrast to the truncated TRAF-N domain version or the full-length protein (Fig 5A). Despite that, functional assays using *M. marinum*-lux indicated that both deleted protein domains fail to complement the *trafE* KO (Fig 5B). We reason that the absence of RING domain phenocopies the truncation of the TRAF-N region because both are required for the TrafE E3 ligase activity. Additionally, the RING domain determines substrate recognition (Jackson et al., 2000) and binding to E2-conjugating enzymes, which might explain why in its absence, TrafE is not recruited to damaged MCVs.

Sterile damage triggers TrafE recruitment on endolysosomes

Late endosomes and lysosomes are involved in the degradation of molecules endocytosed from the extracellular space or captured by the autophagy machinery in the cytosol (Huotari and Helenius, 2011). In *D. discoideum*, autophagy and ESCRT cooperate to promote membrane repair, however, extensively damaged endolysosomes are targeted to the autophagy machinery for removal (López-Jiménez et al., 2019). To address whether TrafE recruitment to bacteria is specific to infection-induced MCV damage or represents a general reaction to membrane damage, we employed the esterified dipeptide named L-leucyl-L-leucine methyl ester (LLOMe) which perforates endolysosomes, making them permeable to protons and small molecules of less than 10 kDa, resulting in endolysosomal pH increase and leading to apoptosis at concentrations above 4 mM in HeLa cells (Repnik et al., 2017). Surprisingly, minutes after treatment with 4.5 mM LLOMe, the homogenous cytosolic distribution of GFP-TrafE changed dramatically to dispersed puncta and rings (Fig 6A, S1 Movie). The cytosolic GFP-TrafE ΔTRAF-N was slowly recruited on the LLOMe-damaged compartments, but the cytosolic pattern of GFP-TrafE ΔRING remained unchanged until the end of the monitoring period (Fig 6B and 6C). A large fraction of TrafE was clearly recruited to Alexa Fluor 647-conjugated 10 kDa dextran-loaded endolysosomes (Fig 6D, S2 Movie). Our data suggest that the TrafE RING domain is essential for its response to membrane damage and importantly, considering the swiftness of TrafE reaction to LLOMe-induced damages, TrafE is likely an early sensor of damage and an upstream effector of the ELDR.

TrafE is essential for the maintenance of endolysosomal integrity

Previous results indicated that defects in the ESCRT and autophagy machineries, both known to contribute to membrane repair, lead to increased proton leakage upon LLOMe-induced sterile damage. To monitor how LLOMe affects the endolysosomal integrity and pH in the context of *trafE* KO, we used lysosensor DND-189 which is a fluorescent pH tracer that accumulates in acidic compartments, where protonation relieves quenching. The addition of 4.5 mM LLOMe was followed by a decrease of lysosensor fluorescence intensity in both WT and *trafE* KO cells, indicating proton leakage and pH increase within the endolysosomal compartments (Fig 7A). In WT cells, the lysosensor intensity first decreased but was restored to the initial level (Fig 7A and 7B), indicating that WT cells completed recovery in the course of the 25 minutes of LLOMe treatment. In contrast, the lysosensor fluorescence intensity remained low in the *trafE* mutant cells (Fig 7A and 7B), indicating a more pronounced and irreversible proton leakage. The results show that cells can fully repair damage to endolysosomes and restore their pH, while absence of TrafE has a strong negative impact on the integrity and the repair of damaged compartments.

TrafE is recruited to endolysosomes after hypertonic shock

LLOMe-induced membrane damage reduces membrane tension similarly to hyperosmotic conditions (Mercier et al., 2020). Indeed, water expulsion from the cytosol and from the endolysosomal compartments results in membrane tension decrease that is sufficient to trigger the recruitment of Alix and the ESCRT-III component CHMP4B and subsequent formation of intraluminal vesicles (ILVs). To reveal possible mechanisms of TrafE recruitment to endolysosomes, we asked whether a membrane tension decrease might be sufficient to trigger recruitment of TrafE to

endo-membranes. For this, we monitored *D. discoideum* cells expressing GFP-TrafE under hypertonic conditions. Strikingly, cytosolic TrafE relocated to endolysosomal compartments seconds after the addition of sorbitol. In addition, when cells adapted and regained their initial shape and motility, TrafE regained a cytosolic distribution (Figure 8A). The pH-tracer lysosensor was used again to address whether the hyperosmotic shock induced membrane perforations. Addition of high 5 mM LLOMe concentration resulted in a decrease of lysosensor fluorescence intensity indicative of proton leakage from damaged endolysosomes. In contrast, under hypertonic conditions, the lysosensor fluorescence intensity remained similar, indicating that the membrane integrity of acidic compartment was uncompromised (Fig 8B and 8C). Our data suggest that a decrease of membrane tension alone is enough to trigger TrafE recruitment to endolysosomal membranes.

Absence of TrafE confers acute susceptibility to sterile damage

In the absence of TrafE, the probability of survival of *M. marinum*-infected *D. discoideum* cells was drastically decreased compared to infected WT cells (Fig 2A). In addition, recent studies showed that disruption of lysosomal membrane leads to increase of cytosol acidity and necrosis or lysosome-dependent cell death (Wang et al., 2018). We hypothesized that the observed failure to repair damaged MCVs would correlate with an increased susceptibility of *trafE* KO cells to severe sterile endolysosomal damage caused by LLOMe. To test this, the fluorescent DNA stain propidium iodide (PI), which penetrates dead or dying cells and intercalates and stains their DNA, but is excluded from live cells, was used as a reporter for lytic cell death. *In vivo* time-lapse confocal microscopy was carried out to compare viability of WT, *atg1* KO and *trafE* KO cells after 55 min of high 5 mM LLOMe concentration treatment. Paralleling the results on infected cells (Fig 2E), cells lacking TrafE showed the highest susceptibility to LLOMe-induced sterile perforations (Fig 8D, S3 Movie). These results suggest that the severity of the phenotypes caused by the absence of TrafE are a cumulative consequence of non-functional autophagy- and ESCRT-dependent membrane repair.

Loss of TrafE affects the transcription of autophagy and ESCRT gene sets

To investigate possible explanation of the rapid infection- or LLOMe-induced death of *trafE* null cells, as well as to identify genes and pathways underlying TrafE-mediated *M. marinum* restriction and endolysosomal homeostasis, we performed a genome-wide transcriptional analysis. RNA of *trafE* KO mutant cells was collected, sequenced and compared to RNA of WT cells, revealing 283 genes with significantly differential expression (DE) (Fig. 9A, Table S4). Importantly, the steady-state levels of all of the ATGs, including *atg1*, *atg9*, *atg8a* and the autophagy cargo adaptors *p62* and *cnrD*, were clearly upregulated (Fig. 9B). They also listed under the KEGG term “autophagy-other”, which is significantly enriched by gene set enrichment analysis (GSEA) (Fig. 9C, Table S4 and S5). Earlier studies have demonstrated that high, uncontrolled autophagy activity could be harmful for cells and may lead to accelerated cell death or promote replication and spread of intracellular pathogens or cancer cells (Levine and Yuan, 2005; Ravikumar et al., 2010). In addition, despite that the read counts of the ESCRT genes do not show a clear pattern (Fig. 9B, Table S4), our data showed an overexpression of ALG-2 interacting protein X (*ALIX*) and downregulation of its putative interacting partner *Alg2A* (homolog of the human Apoptosis-linked-gene-2). Importantly, it has been demonstrated in human cells, that ALIX overexpression is sufficient to induce cell death, thus establishing a link between the endolysosomal system and the cell death machinery (Mahul-Mellier et al., 2006; Kaul and Chakrabarti, 2017), and that increased association of ALG-2 with ALIX permits increased association of ALIX with membranes (Sun et al., 2015). Enrichment pathway analysis previously performed in our lab following RNA-seq transcriptomic comparison of non-infected or *M. marinum*-infected *D. discoideum* cells showed that most of the Biological Processes (BP) of genes upregulated during infection comprise such involved in damage response and cellular defence, particularly in the specific pathways involved in membrane repair (ESCRT) and bacteria elimination (autophagy) (Hanna et al., 2019). Taken together, our data indicates that lack of TrafE alone is sufficient to affect the expression of

genes belonging to the autophagy and the ESCRT machineries, possibly leading to non-functional or severely compromised ESCRT-III and autophagic MCV/endolysosome membrane repair, resulting in drastic reduction of *M. marinum* intracellular growth restriction and precocious cell death.

TrafE is required for optimal ESCRT and autophagy response to membrane damage

In mammalian and *D. discoideum* cells, LLOMe-induced sterile membrane damage prompts accumulation of LC3/Atg8 puncta and vigorous recruitment of ALIX and CHMP4B/Vps32 to damaged endolysosomal compartments (López-Jiménez et al., 2019; Mercier et al., 2020). In view of our findings, we asked how the absence of TrafE could impact both the autophagy and the ESCRT machinery responses to sterile endolysosomal damage. To address this question, we generated *D. discoideum* WT or *trafE* KO cell lines ectopically expressing GFP-fusions of Atg8a, p62, ALIX or Vps32. We monitored by time-lapse HC confocal microscopy the behaviour of the aforementioned reporter constructs during LLOMe-induced sterile damages. Remarkably, the absence of TrafE impacted the behaviour of all four proteins tested. As expected, the autophagy machinery was recruited to damaged endolysosomes, revealed by as increase in the number of GFP-Atg8a puncta in WT cells but not in *trafE* KO cells where the number of GFP-Atg8a structures remained similar throughout the 40 min period of LLOMe treatment (Fig 10A). In contrast, compared to WT cells, sterile damage in *trafE* KO cells resulted in higher levels of GFP-p62 accumulation (Fig 10B), possibly due to inhibition of its degradation (Wu et al., 2020). In WT *D. discoideum* cells LLOMe treatment caused rapid increase of GFP-Vps32 structures by nearly 10-fold and unusually high, possibly deleterious increase of GFP-Vps32 structures in *trafE* KO mutant cells of up to 80-fold (Fig. 10C). Whilst Vps32 was recruited to endolysosomes in a possibly uncontrolled manner, compared to WT, ALIX-GFP reacted weakly to LLOMe-induced endolysosomal damage (Fig. 10D). These data provide supportive evidence that TrafE is likely upstream of autophagic and ESCRT-III ELDR. Absence of TrafE leads to non-functional ELDR and drastic reduction of intracellular pathogen restriction.

DISCUSSION

In recent years, studies in mammals have revealed some of the components of the ELDR signalling pathway that detects, repairs and / or removes intracellular compartments disrupted by invading pathogens or by mechanical damage. Cells have developed molecular sensors that determine the size and the extent of membrane damage, repaired by default by the ESCRT machinery, however extensive and prolonged damage triggers the autophagy machinery. Despite intense research, we still need to extend our insight in the molecular factors involved in membrane damage detection and how it is translated into a vigorous and specific ubiquitynation response. *D. discoideum* is a powerful model system to address the aforementioned questions thanks to its experimental versatility and the high evolutionary conservation of the ESCRT and the autophagy pathways with their mammalian counterparts.

It was previously shown that in *D. discoideum, M. marinum* infection or LLOMe-induced sterile damage leads to an increase of Ub and Atg8-positive structures and to recruitment of the ESCRT subunits Tsg101, Vps32 and Vps4, reportedly ahead of the recruitment of autophagy markers p62 and Atg8 at the MCV and endolysosomes (Cardenal-Muñoz et al., 2017; López-Jiménez et al., 2019). In this study, we demonstrate that early after infection the *D. discoideum* E3 ubiquitin ligase TrafE is recruited to MCVs in a membrane damage-dependent manner (Fig 1A, 1B, 1E, 3A and 3B). This recruitment was significantly attenuated upon infection with *M. marinum* ΔRD1 (Fig 3A and 3B) that produces PDIMs but lacks a functional ESX-1 secretion system. We also demonstrate that the intracellular growth of *M. marinum*-lux is significantly increased in *atg1* KO and *trafE* KO cells compared to WT cells (Fig 2A), suggesting that autophagy is the main *M. marinum* cell-autonomous restriction pathway. In addition, cells lacking the E3 ligase TrafE show exceptionally high and early susceptibility to infection with WT *M. marinum* which is not the case in the autophagy-deficient *atg1* KO cells (Fig 2E). Upon starvation, *atg1* KO cells that are fully defective in autophagy, display severe developmental phenotypes and do not proceed beyond aggregation (Otto et al., 2004). In contrast, *trafE* KO cells successfully complete

their developmental cycle and form spores (Fig. S5), emphasizing on the functional specificity of TrafE to ELDR. Altogether, our data indicate that *trafE* KO phenocopies the autophagy-deficient *atg1* mutants in terms of unrestricted *M. marinum* intracellular growth, however the higher cytotoxicity exerted by bacteria in *trafE* KO cells compared to WT and *atg1* KO cells (Fig 7A and 7B) leads to the speculation that TrafE might be upstream of both ESCRT- and autophagy-mediated membrane repair. Following that hypothesis, the particularly rapid death of infected *trafE* KO cells likely results from inefficient MCV repair, and leads to early bacteria escape and release by host cell lysis (Fig 2B and 2D).

Ubiquitin is required for various aspects of autophagy, such as removal of protein aggregates (aggrephagy), recycling of mitochondria (mitophagy) and bacteria (xenophagy), or endolysosomal homeostasis (lysophagy). Xenophagy depends on decoration of intracellular pathogens with K63-linked Ub chains that bring bacteria to the phagophore membrane via autophagy cargo receptors such as p62 and NDP52. We demonstrated that although the levels of polyubiquitin-positive MCVs remain unaffected in *M. marinum*-infected *trafE* KO cells, the levels of K63-linked polyUb-positive MCVs are significantly decreased but not abolished compared to wt *D. discoideum* cells (Fig 4A and 4B), possibly due to the presence of other E3-ligases, such as for instance TrafC, which is also recruited to MCVs during infection and might have partially redundant functions (S1B Fig). It has been shown that human TRAF6 forms heterodimers with TRAF2, TRAF3 and TRAF5 through their RING domains and that the resulting heterodimers are more stable than the TRAF6 homodimers (Das et al., 2021). Therefore, the severity of the *trafE* KO phenotypes during infection may be due to the instability or non-functionality of a potential heterodimerization redundant partner(s), such as other DdTRAFs. Furthermore, we found that the recruitment of TrafE to MCVs is abolished in the absence of its RING domain and not when the TRAF domain is deleted (Fig 5A), likely because RING domains-mediated dimerization confers the specificity to the substrate via TrafE interaction with the E2-conjugating enzyme (Middleton et al., 2017; Kiss et al., 2021). Nevertheless, both domains are equally important for the restriction of *M. marinum* intracellular growth (Fig 5B).

Similar to xenophagy, lysophagy also depends on Ub and it has been shown that ubiquitination of Lysosome-Associated Membrane Protein 2 (LAMP2) in damaged lysosomes leads to their autophagic degradation (Papadopoulos et al., 2017). In addition, recent studies in mammalian cells have demonstrated that disrupted lysosomes leak protons and reactive oxygen species that lead to pyroptotic cell death (Papadopoulos et al., 2020). Repair of damaged lysosomes is vital for the cells and depends both on the ESCRT machinery and lysophagy, which repair and / or remove extensively damaged compartments (López-Jiménez et al., 2019; Daussy and Wodrich, 2020). Studies in HeLa Kyoto cells have demonstrated that membrane tension plays a role in endosomal membrane remodelling and that both hyperosmotic shock and LLOMe induced perforations, result in a decrease of membrane tension sufficient to trigger the recruitment of the ESCRT-III subunit CHMP4B (Mercier et al., 2020). Remarkably, we found that TrafE is recruited to endolysosomes minutes after LLOMe treatment or hyperosmotic shock (Fig 6A and 8A), suggesting its involvement in endolysosomal membrane remodelling and repair signalling pathways. We also demonstrate that, unlike WT *D. discoideum* cells, TrafE mutants fail to restore their endolysosomal pH after LLOMe-induced sterile damage (Fig 7A and 7B). Furthermore, as observed during *M. marinum* infection, *trafE* KO mutant cells are extremely susceptible to LLOMe compared to *atg1* KO or WT cells (Fig 8D), in agreement with our hypothesis that TrafE is upstream of ESCRT and autophagic ELDR pathways. Comparison of total RNA extracted from WT and *trafE* KO cells under basal conditions indicated overexpression of nearly all genes belonging to the autophagy pathway (Fig. 9B, Table S4), which in human cells is essential for reactive oxygen species, DNA damage, organelle damage or intracellular pathogen related stress response (Kroemer et al., 2010). The transcriptomic analysis of *trafE* KO cells also revealed upregulation (Table S4) of a number of *D. discoideum* homologs of the human heat shock 70 kDa protein (HSP70) involved in various cellular stress responses and protection against stress-induced cell death. Furthermore, despite

an upregulation of the ESCRT-III adapter *ALIX*, our RNA-seq data indicated downregulation of *pefA* which is *D. discoideum* homolog of the human *Alg2A* (Fig. 9A), required for recruitment of ALIX to plasma membrane perforations (Scheffer et al., 2014). To investigate further our working model that TrafE is upstream of ESCRT and autophagic ELDR pathways, we monitored the behaviour of the ESCRT-III adapter Alix, the ESCRT-III subunit Vps32 or the autophagy proteins Atg8a and p62 in *trafE* KO cells compared to WT cells after LLOMe treatment and found that the recruitment of GFP-Atg8a, GFP-p62, GFP-Vps32 and Alix-GFP is deregulated (Fig 10A - 10D). Taken together, our results suggest that TrafE plays a master role upstream of both autophagy- and ESCRT-III-coordinated membrane damage repair. As a consequence, absence of TrafE leads to non-functional ELDR, rapid infection- or sterile damage-related cell death and unrestricted *M. marinum* proliferation.

MATERIALS AND METHODS

***Dictyostelium discoideum* strains, culture and plasmids.** *D. discoideum* Ax2(Ka) WT and mutant strains, listed in Table S1A, were grown in axenic conditions at 22°C in HL5c medium (Formedium) supplemented with 100 U/mL penicillin and 100 µg/mL streptomycin (Invitrogen) to avoid contamination. Cell lines expressing fluorescent reporters and KO cell lines were cultured in the presence of the appropriate antibiotics, hygromycin (50 µg/mL), blasticidin (5 µg/mL) or Geneticin G418 (5 µg/mL). *D. discoideum* WT, *trafE* knock-out (*trafE* KO) or *atg1* KO cell lines were stably transformed with GFP-TrafA, GFP-TrafB, GFP-TrafC, GFP-TrafD, GFP-TrafE, GFP-Atg8a, GFP-p62, GFP-Vps32, mCherry-Plin constructs (Table S1A). The *trafE* KO was generated in Ax2(Ka) background by homologous recombination following a one-step cloning in pKOSG-IBA-dicty1 (Table S1A) as previously described (Wiegand et al., 2011). The *trafE* GFP knock-in (TrafE-GFP KI) was generated in Ax2(Ka) background by homologous recombination following two-step cloning in pPI183 (Table S1A) (Paschke et al., 2018).

***Mycobacterium marinum* strains, culture and plasmids.** *M. marinum* WT and ΔRD1 strains (Table S1B) expressing GFP, mCherry or a bacterial luciferase operon (Carroll et al., 2010; Andreu et al., 2010; Cardenal-Muñoz et al., 2017) were cultured in shaking at 150 rpm at 32°C in Middlebrook 7H9 (Difco) supplemented with 10% oleic acid-albumin-dextrose-catalase (OADC), 0.2% glycerol, and 0.05% Tween 80. Bacterial clumping was minimized by adding 5-mm glass beads during cultivation. Mutants and plasmid carriers were grown in medium supplemented with hygromycin (100 µg/ml) or kanamycin (25 µg/ml), as appropriate.

Infection assay. Infections were performed as previously described (Hagedorn and Soldati, 2007; Arafah et al., 2013; Barisch et al., 2015a). *M. marinum* bacteria were spinoculated onto adherent *D. discoideum* cells and extracellular bacteria were rinsed off. The infected cells were resuspended in HL5c containing 5 U mL^{-1} of penicillin and 5 µg mL^{-1} of streptomycin (Invitrogen) to prevent extracellular bacterial growth. Infections were performed at a multiplicity of infection (MOI) of 10 for *M. marinum* WT in *D. discoideum* WT. MOI used for *M. marinum* ΔRD1 mutant cells was double the MOI of *M. marinum* WT. Infected cells for time points analysis were incubated at 25°C.

Intracellular bacteria growth assay. Measurements of luciferase-expressing *M. marinum* intracellular growth were carried out as previously described (Arafah et al., 2013). In this assay, three different dilutions of infected cells (0.5 – 2 x 10^5 cells/well) were plated on non-treated, white F96 MicroWell plates (Nunc) with a gas permeable moisture barrier seal (Bioconcept). Luminescence was measured at 1-hour intervals for 30 to 72 hours at a constant temperature of 25°C using a Synergy Mx microplate reader (Biotek).

Live fluorescence microscopy. Live microscopy was performed using inverted 3i Marianas or Nikon Ti CSU-W1 spinning disk microscopes with a 63x glycerol / air or 100x oil objectives. 7-10 slices 0.5 µm apart were taken for z-stacks. For time-lapse experiments, images were acquired from non-infected or infected cells at intervals of 1 min, 5 min or at the indicated time points (hpi). Image analysis was performed using Fiji (ImageJ). *D. discoideum* cells were plated at 10^6/ml in 35

mm Glass Bottom Dishes (MatTek) or in 4-wells µ-slides (Ibidi). Sterile damage in *D. discoideum* was induced using 4.5–5 mM of LLOMe (Bachem) from a 10-fold concentrated solution that was added 5 min after the start of imaging. To induce a hyperosmotic shock, 2 M sorbitol was added to a final concentration of 200 mM, as described previously (Na et al., 2007). The lumen of endolysosomal compartments was visualized using 10-15 µg/mL of 10 kDa Fluor 647 Dextran (Invitrogen) added 3 h prior to microscopy and washed 10-20 min before visualization of the sample. To detect neutralization of endolysosomes, 1 µM Lysosensor Green DND-189 (Invitrogen) was added 3 h prior to microscopy and washed away 10-20 min before visualization of the sample. To distinguish live from dead cells 1 µg/mL of propidium iodide (PI) was added directly to the cell culture immediately prior to time-lapse imaging. For high-content live microscopy, *M. marinum*-infected WT and *trafE* KO *D. discoideum* cells (as described above) were deposited in 96-well black, glass-bottom plates (Perkin Elmer, MA, USA) and left to adhere for 30 min at room temperature. Images were recorded every 1 min for 30-60 min using a 10x objective with the ImageXpress Micro XL high-content microscope (Molecular Devices). The number of infected cells and extracellular bacteria or GFP-p62-, GFP-atg8a- and GFP-vps32-positive structures were counted using the MetaXpress software (Molecular Devices, CA, USA), and analysed using GraphPad Prism® software.

Antibodies and immunofluorescence. *D. discoideum* cells on coverslips were rapidly fixed by immersion in -85°C ultracold methanol as described previously (Hagedorn et al., 2006). The GFP fluorescent signal was enhanced using anti-GFP rabbit polyclonal antibody (MBL), anti-Ub (FK2) mouse monoclonal antibody (Enzo Life Sciences), anti-K63-linkage-specific mouse monoclonal antibody (Enzo Life Sciences). Nuclei were stained with 1 µM DAPI (Invitrogen). Cells were embedded using ProlongGold antifade (Invitrogen). As secondary antibodies we used goat anti-rabbit and anti-mouse coupled to Alexa 488 or Alexa 594 (Invitrogen). Images were acquired with a LSM700 or LSM800 microscope (Zeiss) using an oil 63x objective. Image analysis was performed using ImageJ.

qRT-PCR sample collection and analysis. To monitor *trafE* mRNA levels, mock- or *M. marinum*-infected WT *D. discoideum* cells were harvested, RNA was extracted, and cDNA was synthesized using the Bio-Rad iScript kit. The mean calculated threshold cycles (CT) were averaged and normalized to the CT of a reference gene with constant expression (GAPDH). The normalized CT was used to calculate the fold change using the ΔΔCT method. Relative levels of target mRNA, normalized with respect to an endogenous control (GAPDH), were expressed as 2-ΔΔCT (fold), where ΔCT = CT target gene - CT reference gene (GAPDH), and ΔΔCT = ΔCT studied sample - ΔCT calibrator conditions.

RNA extraction. RNA was extracted from cells using the directzol RNA extraction kit (Zymo research) following the manufacturer's instructions for total RNA isolation. To remove contaminating genomic DNA, samples were treated with 0.25 U of DNase I (Zymo) per 1µg of RNA for 15 min at 25 °C. RNA was quantified using Qubit 4.0 (Invitrogen) and its quality was checked on the Agilent 2100 Bioanalyzer (Agilent Technologies).

Sequencing. Total RNAs were subjected to cDNA synthesis and NGS library construction using the Ovation Universal System (NuGEN Technologies, San Carlos, California, USA). 100 ng of total DNAse I-treated RNA was used for first- and then second-strand cDNA synthesis following the manufacturer's protocol. In order to obtain comparable library size, a double bead cut strategy was applied using the 10X genomics protocol. cDNA was recovered using magnetic beads with two ethanol washing steps, followed by enzymatic end repair of the fragments. Next, barcoded adapters were ligated to each sample, followed by an enzymatic strand selection step and magnetic bead recovery, as above. rRNAs were targeted for depletion by the addition of custom designed oligonucleotides specific for *D. discoideum* (5S,18S, 28S). To amplify the libraries, 18 cycles of PCR were performed based on QC experiments carried out using RT-PCR. The quality of the libraries was monitored by TapeStation (Agilent, High Sensitivity D1000 ScreenTape, # 5067–5584). Eight-plexed samples were pooled in approximately equimolar amounts and run in 50 bp single read

flow cells (Illumina, # 15022187) and run on a Hiseq 4000 (Illumina).

Alignment. RNA-seq libraries from infected and mock-treated cells taken at the indicated time points were analyzed in pairwise comparisons. 50 nt single-end reads were mapped to the *D. discoideum* genome (downloaded from dictybase) (Fey et al., 2008) using tophat (version 2.0.13) and bowtie2 (version 2.2.4) softwares. Multi hits were not allowed, by using option --max-multi hits 1. The other parameters were set to default. The read counts per gene were generated using HTSeq software (version 0.6.1) and the GFF annotation downloaded from dictybase (February 2019). Options for htseq-count were -t exon --stranded = yes -m union.

Analysis of differentially expressed genes. Gene counts were imported to R (version 4.0.3) filtered for remaining ribosomal gene counts (DDB_G0295651, DDB_G0295641, DDB_G0295653, DDB_G0295655, DDB_G0295647, DDB_G0295643, DDB_G0295645, DDB_G0295649, DDB_G0294034) and subsequently analyzed using DESeq2 (version 1.30.1) (Love et al., 2014) employing the HTS filter (Rau et al., 2013). A binary comparison *trafE* KO versus WT was performed, fold change was calculated using the ashr method (Stephens, 2016) in DESeq2, the *p*-value was corrected using the Benjamini-Hochberg (Benjamini and Hochberg, 1995).

Correction. The resulting false discovery rate (FDR) was used for downstream analysis. Hard thresholds for differentially expressed genes (DE genes) were set at the absolute log2 fold change ≥ 0.585 (equals to a fold change of 1.5) and FDR ≤ 0.05.

Pathway analysis of DE genes. Pathway analysis was performed using the R package clusterProfiler (Yu, 2012) and GO (downloaded from QuickGo, 2021-02-16) and KEGG (22.6.2021) annotations. For GSEA genes were ranked by false discovery rate, a group was considered significant at p-value $\leq$ 0.05, q-value $\leq$ 0.1, group size between 2 and 200, using 10000 permutations.

Heatmap of normalized counts. Gene counts were filtered for remaining ribosomal genes (DDB_G0295651, DDB_G0295641, DDB_G0295653, DDB_G0295655, DDB_G0295647, DDB_G0295643, DDB_G0295645, DDB_G0295649, DDB_G0294034) and subsequently for low expressed genes with the function filterByExpr from the edgeR package (Robinson et al., 2009), then normalized using the vst function from the limma package (Ritchie et al., 2015) and batch corrected for the effect of the experimental date using the removeBatchEffect function from the limma package. Normalized counts were subjected to the heatmap.2 function from the package gplots (3.1.1), scaling and centering the data for each gene.

Single-cell experiments. Single-cell experiment were performed using the InfectChip device (Delincé et al., 2016) as described (Mottet et al, 2021). Briefly, the device is composed of a microfluidic chip in PDMS with a micropatterned serpentine channel, two holders (one in PMMA and one in aluminium), plastic screws and a micropatterned coverslip. Cells were infected as described above and seeded onto the coverslip. The microfluidic chip was placed onto the PMMA holder and covered with an agarose sheet prepared as explained elsewhere (Mottet et al, 2021). Then, the coverslip was placed onto the aluminium holder and the device was mounted and closed with the screws. A 60 mL syringe was filled with 35 mL of HL5c supplemented with 5 µg/mL of streptomycin and 5 U/mL of penicillin, and connected to the tubing of the microfluidic chip. Imaging was performed with a spinning disk confocal microscope (Intelligent Imaging Innovations Marianas SDC mounted on an inverted microscope (Leica DMIRE2)) with the following parameters: 63X glycerol objective, transmitted light, excitation with laser lines 488 nm and 594 nm and temperature controlled at 25°C. The loaded InfectChip device was placed on the stage and the syringe placed into a syringe pump (WPI, NE-1000) with a flow rate of 10 µL/min. Z stacks of 8 slices of 1.5 µm each were acquired every 15 min using phase contrast and every 1 h for fluorescence for 20 hours total. Image analysis for the single-cell experiments was performed as follows. Briefly, using the ImageJ software (https://imagej.net/Fiji/Downloads), cells were

manually tracked, and their time of death was recorded, and the results were presented in the form of a survival curves using the GraphPad Prism® software.

Statistics. Microscopy images were analysed using Fiji ImageJ. Experiments in Figs 1B, 1C, 2B, 3B, 4C and 4E were quantified manually. Experiments in Figs 7B and 8C were quantified automatically using Fiji ImageJ Time Series Analizer V3. Experiments in Figs 2C, 2D, 9B, 9C and 9D were quantified using MetaXpress. Plots and statistical tests were performed using GraphPad Prism® software. In all plots, standard error of the mean are shown, unless explicitly mentioned. Two-tailed t-test, ANOVA or Two-way ANOVA were used. Post hoc Fisher's LSD and Tukey's multiple comparison tests were performed when necessary (n.s. : non-significant, * : p-value $\leq$ 0.05, ** : p-value $\leq$ 0.01, *** : p-value $\leq$ 0.001, **** : p-value $\leq$ 0.0001).

ACKNOWLEDGMENTS:

We would like to acknowledge the members of the Bioimaging and ACCESS Platforms of the Faculty of Sciences. We thank Dr. Dimitri Moreau for his help with MetaX-press and Dr. Nabil Hanna for his contribution to the conception and practical realization of the RNA-seq experiment.

AUTHOR CONTRIBUTIONS:

L.R. conceived and designed experiments and analyses, constructed plasmids, generated GFP-fusion, knock-out, knock-in constructs and strains, performed and analyzed the experiments, wrote the paper.

M.M. performed the long-term single-cell experiments in microfluidic jails.

L.R. and **M.M.** created and **L.R.** analyzed data for Fig. 2E and 3D.

J.N. analyzed RNA-seq data and designed Fig. 9A, 9B and 9C.

T.S. acquired funding, conceived and supervised the project, reviewed and edited the paper.

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LEGENDS OF FIGURES AND SUPPLEMENTARY FIGURES

Figure 1. Upon infection TrafE is overexpressed and recruited to MCVs. (A) GFP-TrafE-expressing *D. discoideum* cells (green) were mock-infected or infected for 1.5, 3, 6 or 24 h with mCherry-expressing or DsRed-expressing *M. marinum* (red). Representative maximum projections of live images with arrowheads pointing at GFP-TrafE recruitment to MCVs/bacteria. Scale bars correspond to 10 µm. Images are representative of at least 3 independent experiments. (B) Quantification of the percentage of intracellular MCVs/bacteria positive for GFP-TrafE during the infection time-course. Bars represent SEM from 3 independent experiments. (C) Quantification of GFP-TrafE in the vicinity of *M. marinum* poles from random images in 3 independent experiments. (D) Normalized mRNA levels of *trafE* in mock-infected or *M. marinum*-infected *D. discoideum* cells at 1.5, 6 or 24 hours. Shown are mean and SEM from 3 independent experiments. Statistical differences were calculated with an unpaired t test (n.s. : non-significant, * : $p \leq 0.05$). (E) The intracellular growth of *M. marinum*-lux was monitored every hour inside WT and TrafE overexpressing cells. Error bars represent SEM. Statistical difference from 2 independent experiments were calculated using Bonferroni multiple comparison test after ANOVA (*** : $p \leq 0.001$). (F) Recruitment of the endogenous TrafE-GFP (green) to MCV/bacteria (red) after 1.5 hpi. Scale bars correspond to 10 µm. Images are representative of at least 3 independent experiments.

Figure 2. Loss of TrafE is detrimental for *D. discoideum* cells after infection with *M. marinum*. (A) The intracellular growth of *M. marinum*-lux was monitored every 1 hour inside WT, *atg1* KO, *trafE* KO or GFP-TrafE complemented *trafE* KO cells. Error bars represent SEM. Statistical difference from 2-4 independent experiments were calculated using Bonferroni multiple comparison test after ANOVA *** : $p \leq 0.001$). (B) WT, *atg1* KO or *trafE* KO cells expressing mCherry-Plin were infected with GFP-expressing *M. marinum*. The percentage of cells with intracellular bacteria colocalizing with GFP/RFP Plin was assessed manually at 6 and 24 hpi. Error bars indicate the SEM from 3 independent experiments. Statistical differences are indicated with an asterisk and were calculated with an unpaired *t* test (n.s. : non-significant, * : $p \leq 0.05$, ** : p-value ≤ 0.01, *** : $p \leq 0.001$). (C-D) WT or *trafE* KO cells infected with DsRed-expressing *M. marinum* imaged by high-content microscopy every 1 h. Number of infected cells (C) or number of extracellular bacteria (D) were monitored and the average of 3 replicates n≥200 cells per time point was plotted. Error bars represent SEM. Statistical differences were calculated using Bonferroni multiple comparison test after two-way ANOVA (*** : $p \leq 0.001$). (E) WT, *atg1* KO, *trafE* KO or GFP-TrafE-complemented *trafE* KO cells infected with mCherry-expressing *M. marinum* in microfluidic chip single-cell experiment were monitored every 1 h. The number of live cells was counted at each time point for 20 h and the counts from 3 independent experiments were plotted as Kaplan-Meier survival curves. Statistical differences were calculated using Bonferroni multiple comparison test after two-way ANOVA (n.s. : non-significant, *** : $p \leq 0.001$).

Figure 3. TrafE recruitment to MCVs/bacteria is membrane damage-dependent. (A) *D. discoideum* cells expressing TrafE-GFP (green) were infected for 1.5, 3 or 24 h with *M. marinum* WT (red) or *M. marinum* ΔRD1 (red). Representative maximum projections of live images with arrowheads pointing at TrafE-GFP recruitment to MCVs/bacteria. Scale bars correspond to 10 µm. Images are representative of 3 independent experiments. (B) Quantification of the percentage of intracellular MCV/bacteria positive for TrafE-GFP during the infection time-course. SEM from 2-4 independent experiments. Statistical differences were calculated with an unpaired t test (**** : p-value ≤ 0.0001). (C)) The intracellular growth of *M. marinum*-lux WT or *M. marinum* ΔRD1

was monitored every hour inside WT or *trafE* KO cells. Error bars represent SEM. Statistical differences from 2 independent experiments were calculated using Bonferroni multiple comparison test after one-way ANOVA (*** : $p \leq 0.001$). (D) WT, *atg1* KO, *trafE* KO or GFP-TrafE-complemented *trafE* KO cells infected with *M. marinum*-lux ΔRD1 in microfluidic chip single-cell experiment were monitored every 1 h. The number of live cells was counted at each time point for 20 h and the counts from 3 independent experiments were plotted as Kaplan-Meier survival curves. Statistical difference were calculated using Bonferroni multiple comparison test after ANOVA (n.s. : non-significant).

Figure 4. K-63-linked polyubiquitination decrease in *D. discoideum trafE* KO cells. (A) Maximum projections showing colocalization (white arrowheads) of *M. marinum* (blue), K63-linked polyubiquitin chains (grey) and GFP-TrafE (green). Maximum projections showing (B) polyubiquitin (grey) or (D) K63-linked polyubiquitin (grey) colocalization (white arrowheads) with *M. marinum.* Scale bars correspond to 10 µm. Quantification of the percentage of (C) FK2-positive or (E) K63-positive intracellular MCV/bacteria at 6 hpi was carried out manually from 10-15 images per experiment $n \geq 200$ cells. Error bars indicate SEM. Statistical differences were calculated with an unpaired t test (n.s. : non-significant, ** : $p \leq 0.01$).

Figure 5. TrafE recruitment to MCV is RING domain-dependent. (A) *D. discoideum trafE* KO cells expressing GFP-TrafE, GFP-TrafE with truncated RING domain or GFP-TrafE with truncated N-terminal TRAF domain (green) were infected for 1.5, 3, 6 or 24 h with mCherry-expressing *M. marinum* (red). Representative maximum projections of live images with arrow heads pointing at GFP-TrafE recruitment to MCVs/bacteria. Scale bars correspond to 10 µm. Images are representative of 3 independent experiments. (B) The intracellular growth of *M. marinum*-lux was monitored every hour inside WT, *trafE* KO or *D. discoideum* cells expressing GFP-TrafE with truncated RING domain or GFP-TrafE with truncated N-terminal TRAF domain. Error bars represent SEM. Statistical differences from 2-4 independent experiments were calculated using Bonferroni multiple comparison test after ANOVA (n.s. : non-significant, *** : $p \leq 0.001$).

Figure 6. LLOMe-induced damage triggers TrafE recruitment to endolysosomes. *D. discoideum trafE* KO cells expressing (A) GFP-TrafE, (B) GFP-TrafE with truncated RING domain or (C) GFP-TrafE with truncated N-terminal TRAF domain (green) were treated with 4.5 mM LLOMe 5 min (t=0) after 25 min live microscopy time-course. Images were taken every 1 min. White rectangles indicate zoom of selected areas. Images are representative of at least 3 independent experiments. Scale bars correspond to 10 µm. (D) Colocalization of GFP-TrafE (green) with Alexa Fluor 647 10 kDa dextran (red) 10 min after LLOMe treatment. Images are representative of at least 3 independent experiments. Scale bars correspond to 10 µm.

Figure 7. Absence of TrafE impacts the repair of damaged compartments. (A) Maximum projection confocal images of live *D. discoideum* WT or *trafE* KO cells incubated with Lysosensor Green DND-189 (green), imaged every 1 min, 5 min before and 30 min after addition of 4.5 mM LLOMe. Images are representative of 3 independent experiments. Scale bars correspond to 10 µm. (B) Quantification of pH tracer Lysosensor Green DND-189 (green) fluorescence average intensity using ImageJ Time Series Analyzer V3. Error bars represent SEM. Statistical differences were calculated using Bonferroni multiple comparison test after two-way ANOVA (*** : $p \leq 0.001$).

Figure 8. TrafE is relocalized to endolysosomes following hypertonic shock. (A) Maximum projection of confocal images of *D. discoideum* cells expressing GFP-TrafE (green) imaged every 1 min, 5 min before and 55 min after addition of 200 mM sorbitol Images are representative of at least 3 three experiments. Scale bars correspond to 10 µm. (B) Maximum projection of confocal images of live *D. discoideum* WT cells incubated with Lysosensor Green DND-189 (green) and imaged every 1 min, 5 min before and 30 min after addition of 4.5 mM LLOMe or 200 mM sorbitol. Images are representative of 3 independent experiments. Scale bars correspond to 10 µm. (C) Quantification of fluorescence average intensity of pH tracer

Lysosensor Green DND-189 (green), before and after LLOMe or Lysosensor addition, using ImageJ Time Series Analyzer V3. Error bars represent SEM. Statistical difference were calculated using Bonferroni multiple comparison test after two-way ANOVA (*** : $p \leq 0.001$). (D) WT, *atg1* KO or *trafE* KO cells were incubated in propidium iodide (PI) and monitored by live confocal time-lapse microscopy every 1 min 5 min before and 55 min after addition of 5 mM LLOMe. Number of PI-positive cells at min 55 were counted from 4 independent experiments. Error bars represent SEM. Statistical differences were calculated with an unpaired t test (n.s. : non-significant, * : $p \leq 0.05$, ** : $p \leq 0.01$)

Figure 9. RNA-seq results. (A) Volcano plot of Differential Expression (DE) genes comparing *trafE* KO to WT. After filtering for remaining ribosomal gene reads and low expressed genes, 8744 genes were left for the DE genes analysis, of which 283 were DE (absolute log2fc $\geq$ 0.585, FDR $\leq$ 0.05). From these, 144 were upregulated (red) and 139 were downregulated (blue). For illustrational purposes, *trafE* was included, which is DE and downregulated (blue dot on the far left), which is a confirmation of the *trafE* clean KO on transcriptional level. (B) Heatmap of normalized read counts. Filtered and normalized read counts were interrogated for a previously defined list of genes of interest. This included a set associated with autophagy (upper segment) and a set associated with the ESCRT machinery (lower segment). Biological replicates are depicted as three columns per condition (WT and *trafE* KO). A clear pattern of upregulation is visible in autophagy-related genes, whereas no clear overall pattern is visible for ESCRT-related genes. However, key players in the ESCRT machinery such as *alxA* show a striking pattern and most notably, Ca^{2+} dependent regulators *pefA* and *pefB* are regulated inversely. None of the genes depicted are DE by the statistical criteria defined previously. (C) Gene set enrichment analysis (GSEA) of log2 fold change of filtered genes. For GSEA, genes were ranked by log2 fold change, resulting groups were restricted by minimum and maximum group size of respectively 2 and 200 and considered significant at a *p*-value $\leq$ 0.05 and a *q*-value $\leq$ 0.1. Depicted are the log2 fold change density distributions for enriched core genes in each respective term. The significant signature included several metabolic terms including Proteasome, Endocytosis and most notably Autophagy as being upregulated.

Figure 10. TrafE directs ESCRT and autophagy ELDR. (A-D) WT or *trafE* KO cells expressing GFP-fusions of Atg8a, p62, Vps32 or Alix were monitored by time-lapse high-content confocal microscopy, imaged every 1 min 5 min before and 40 min after treatment with 4.5 mM LLOMe. Number of (A) Atg8a, (B) p62, (C) Vps32 or (D) Alix structures were quantified from the average of 3 independent experiments n$\geq$200 cells per time point and experiment are plotted. Bars represent SEM. Statistical differences were calculated using Bonferroni multiple comparison test after two-way ANOVA (*** : $p \leq 0.001$).

Supplementary Table 1. *D. discoideum* material used in this study. The table includes the *D. discoideum* strains used in this study, the overexpression plasmids and the plasmids used for generation of *trafE* knock-out and GFP knock-in.

Supplementary Table 2. *M. marinum* material used in this study. The table includes all *M. marinum* strains and *M. marinum* plasmids used in this study.

Supplementary Table 3. Primers used in this study. The table includes all primers used to amplify *trafA*, *trafB*, *trafC* and *trafE* CDSs, primers used for knock-out, GFP knock-in generation and primers for screens.

Supplementary Table 4. Differential Expression (DE) genes results for the *D. discoideum* WT and *trafE* KO cells transcriptome analyzis.

Supplementary Table 5. Gene set enrichment analysis (GSEA) on log2 fold change of filtered genes and statistics output.

Supplementary Figure 1. *trafE* is upregulated early after infection. RNA-sequencing of non-infected and *M. marinum*-infected *D. discoideum* cells. RNA levels were compared and the fold change (FC) was plotted.

Supplementary Figure 2. TrafA and TrafB do nor relocalize after infection with *M.*

***marinum*.** (A) GFP-TrafA-or (B) GFP-TrafB expressing *D. discoideum* cells (green) were mock-infected or infected for 1.5, 3, 6 or 24 h with mCherry-expressing or DsRed-expressing *M. marinum* (red). Representative maximum projections of live images of at least 3 independent experiments. Scale bars correspond to 10 µm.

Supplementary Figure 3. Despite their similarity TrafC and TrafD display different behaviour after infection with *M. marinum*. (A) GFP-TrafC-or (B) GFP-TrafD expressing *D. discoideum* cells (green) were mock-infected or infected for 1.5, 3, 6 or 24 h with mCherry-expressing or DsRed-expressing *M. marinum* (red). Representative maximum projections of live images of at least 3 independent experiments. Scale bars correspond to 10 µm.

Supplementary Figure 4. *M. marinum* growth is not affected by TrafC, TrafD overexpression and TrafE C-terminal GFP tagging. (A) The intracellular growth of *M. marinum*-lux was monitored every hour inside WT, TrafC or TrafD overexpressing cells. Error bars represent SEM. Statistical differences from 3 independent experiments were calculated using Bonferroni multiple comparison test after ANOVA (n.s. : non-significant). (B) The intracellular growth of *M. marinum*-lux was monitored every hour inside WT or TrafE-GFP KI cells. Error bars represent SEM. Statistical differences from 3 independent experiments were calculated using Bonferroni multiple comparison test after ANOVA (n.s. : non-significant).

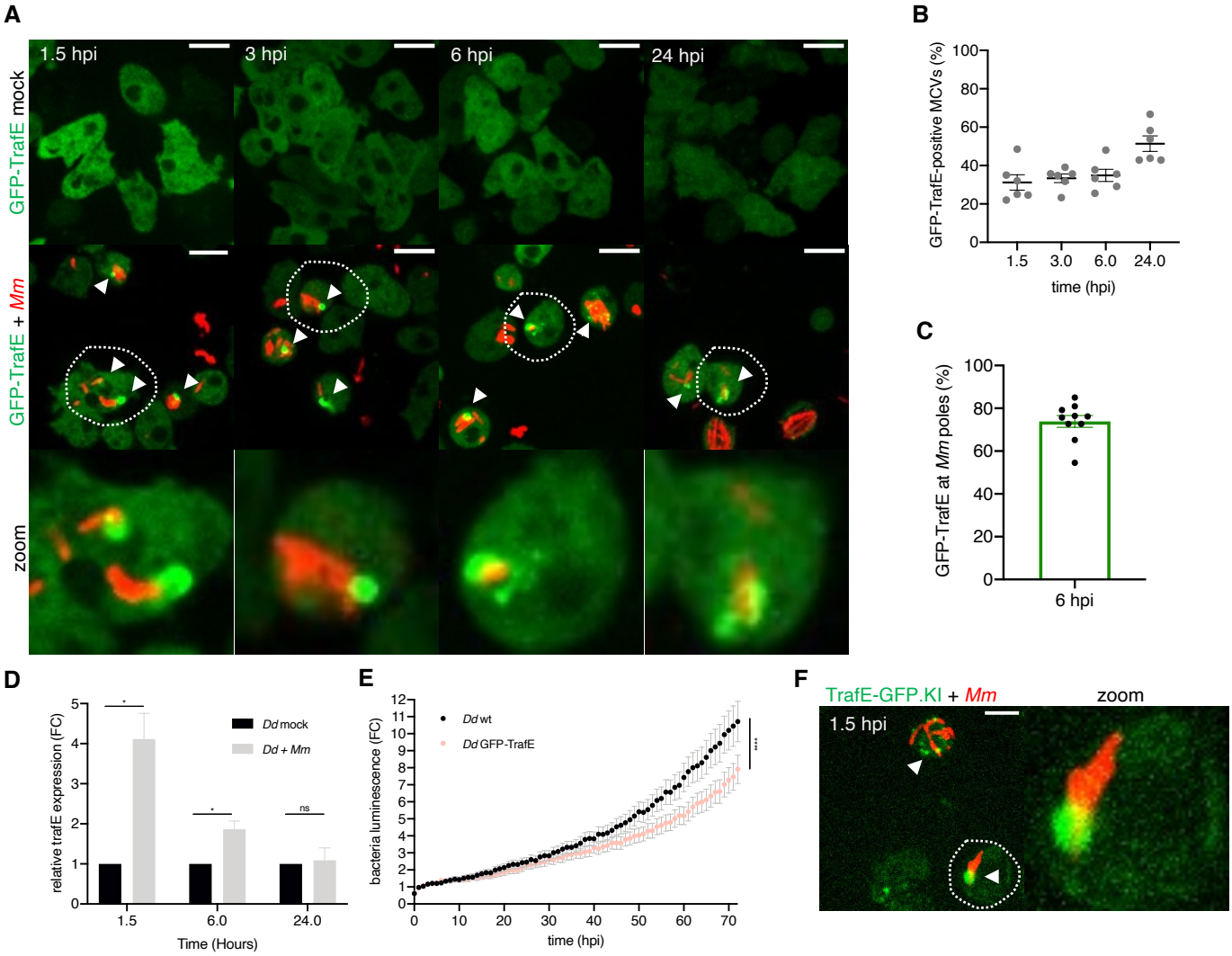
Supplementary Figure 5. Development of *D. discoideum*. WT, *atg1* KO and *trafE* KO cells were deposited on Soerensen-agar plates and visualized by microscopy after 24 h of starvation. WT and *trafE* KO cells aggregate and form fruiting bodies, whereas *atg1* KO cells do not aggregate and do not progress to the formation of fruiting bodies.

Movie S1. TrafE relocalization to endolysosomal compartments upon LLOMe treatment. Live microscopy time-course of *D. discoideum trafE* KO cells expressing GFP-TrafE, treated with 4.5 mM LLOMe. Images were taken every 1 min, 5 min before (t=0) and 55 min after LLOMe treatment. Images are representative of at least 3 independent experiments. Scale bars correspond to 10 µm.

Movie S2. TrafE colocalizes with 10 kDa dextran upon LLOMe treatment. Colocalization of GFP-TrafE (green) with Alexa Fluor 647 10 kDa dextran (red) 10 min after LLOMe treatment. Images were taken every 5 min, 5 min before (t=0) and 55 min after LLOMe treatment. Scale bars correspond to 10 µm.

Movie S3. TrafE is required for optimal mebrane damage response. WT, *atg1* KO or *trafE* KO cells were stained with propidium iodide (PI) and monitored by live confocal time-lapse microscopy every 1 min, 5 min before and 55 min after addition of 5 mM LLOMe. No LLOMe control to assess the effect of the fluorescent excitation on the cell fitness.

Fig 1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GFP-TrafE mock
GFP-TrafE + Mm
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B
GFP-TrafE-positive MCVs (%)
time (hpi)
C
GFP-TrafE at Mm poles (%)
6 hpi
D
relative trafE expression (FC)
Dd mock
Dd + Mm
Time (Hours)
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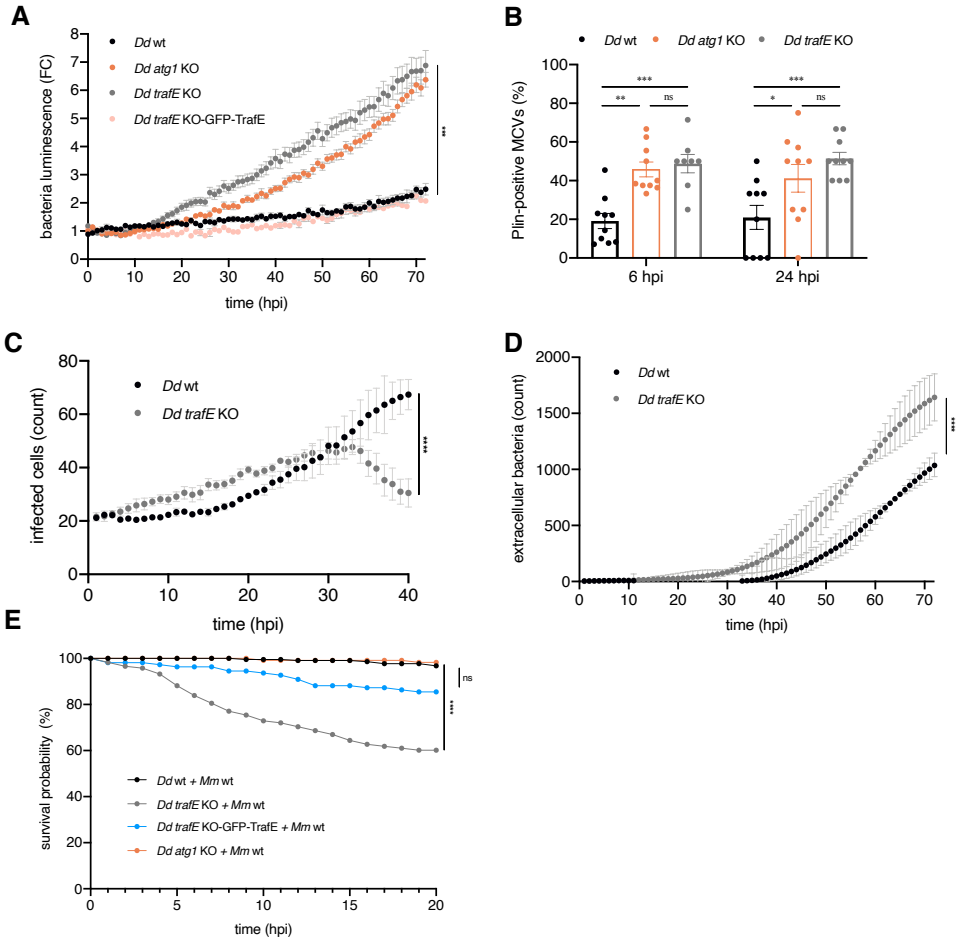
F
TrafE-GFP.KI + Mm
zoom
1.5 hpi

Fig 2


A
bacteria luminescence (FC)
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B
Plin-positive MCVs (%)
Dd wt
Dd atg1 KO
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24 hpi
C
infected cells (count)
time (hpi)
Dd wt
Dd trafE KO
****
D
extracellular bacteria (count)
time (hpi)
Dd wt
Dd trafE KO
****
E
survival probability (%)
time (hpi)
Dd wt + Mm wt
Dd trafE KO + Mm wt
Dd trafE KO-GFP-TrafE + Mm wt
Dd atg1 KO + Mm wt
ns
***

Fig 3

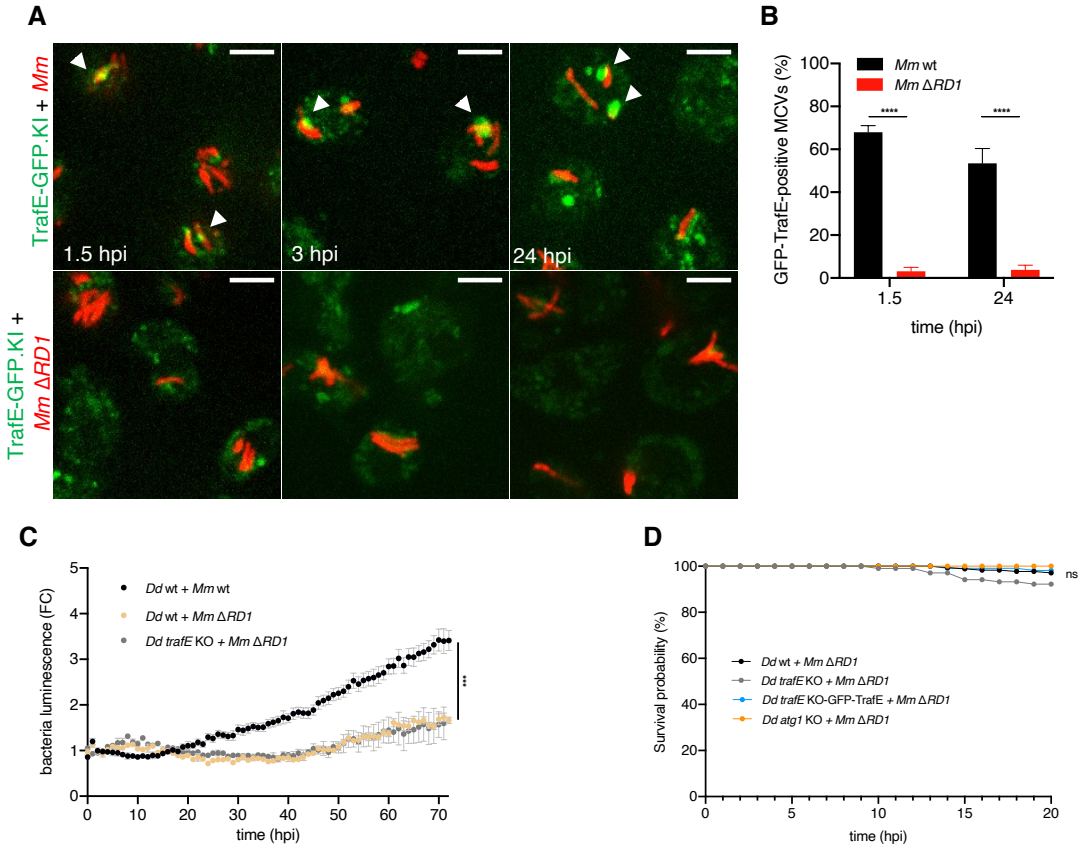

A
TrafE-GFP.KI + Mm
TrafE-GFP.KI + Mm ΔRD1
1.5 hpi
3 hpi
24 hpi
B
Mm wt
Mm ΔRD1
GFP-TrafE-positive MCVs (%)
100
80
60
40
20
0
****
****
1.5
24
time (hpi)
C
Dd wt + Mm wt
Dd wt + Mm ΔRD1
Dd trafE KO + Mm ΔRD1
bacteria luminescence (FC)
5
4
3
2
1
0
***
0
10
20
30
40
50
60
70
time (hpi)
D
Survival probability (%)
100
80
60
40
20
0
ns
Dd wt + Mm ΔRD1
Dd trafE KO + Mm ΔRD1
Dd trafE KO-GFP-TrafE + Mm ΔRD1
Dd atg1 KO + Mm ΔRD1
0
5
10
15
20
time (hpi)

Fig 4

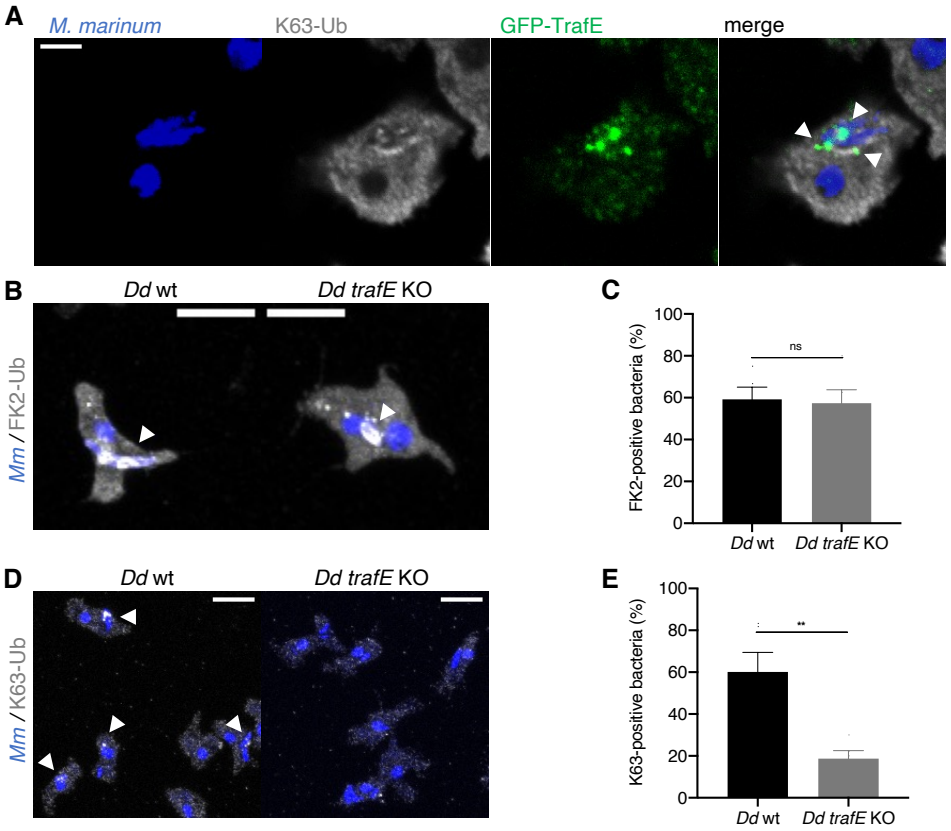

A
M. marinum
K63-Ub
GFP-TrafE
merge
B
Dd wt
Dd trafE KO
Mm / FK2-Ub
C
FK2-positive bacteria (%)
ns
Dd wt
Dd trafE KO
D
Dd wt
Dd trafE KO
Mm / K63-Ub
E
K63-positive bacteria (%)
**
Dd wt
Dd trafE KO

Fig 5

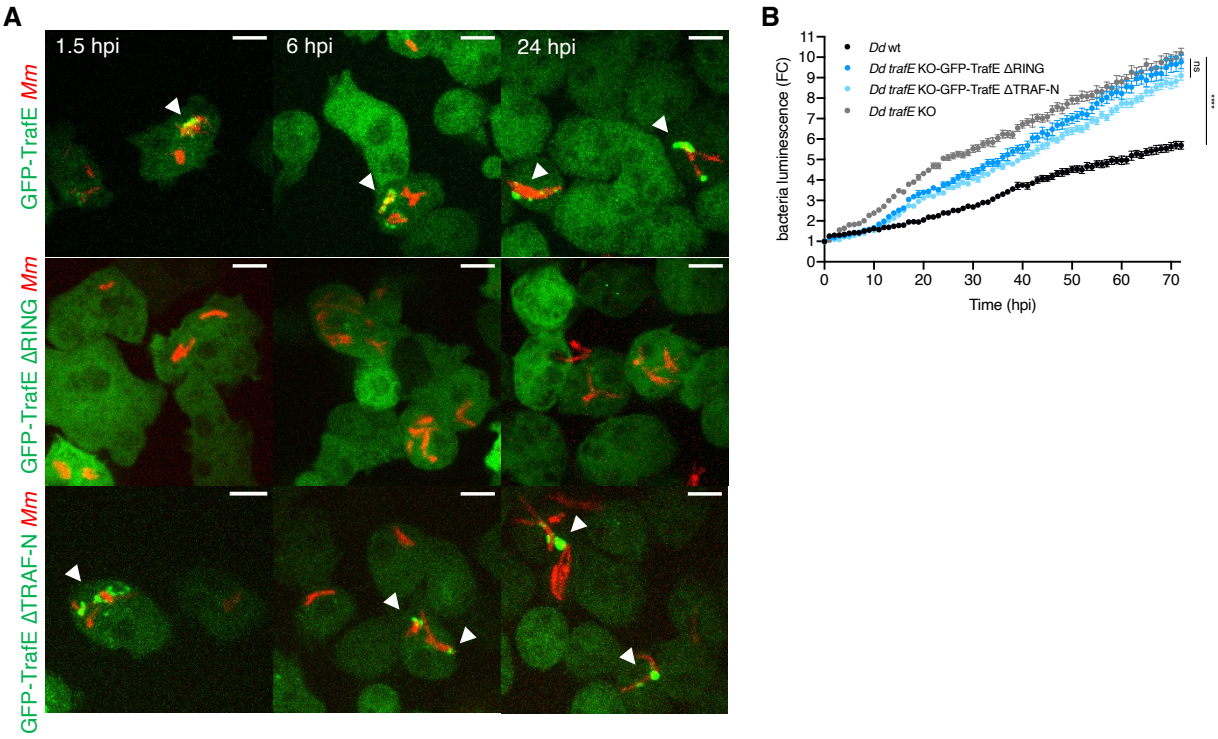

A
1.5 hpi
6 hpi
24 hpi
GFP-TrafE Mm
GFP-TrafE ΔRING Mm
GFP-TrafE ΔTRAF-N Mm
B
Dd wt
Dd trafE KO-GFP-TrafE ΔRING
Dd trafE KO-GFP-TrafE ΔTRAF-N
Dd trafE KO
bacteria luminescence (FC)
Time (hpi)
ns
***

Fig 6

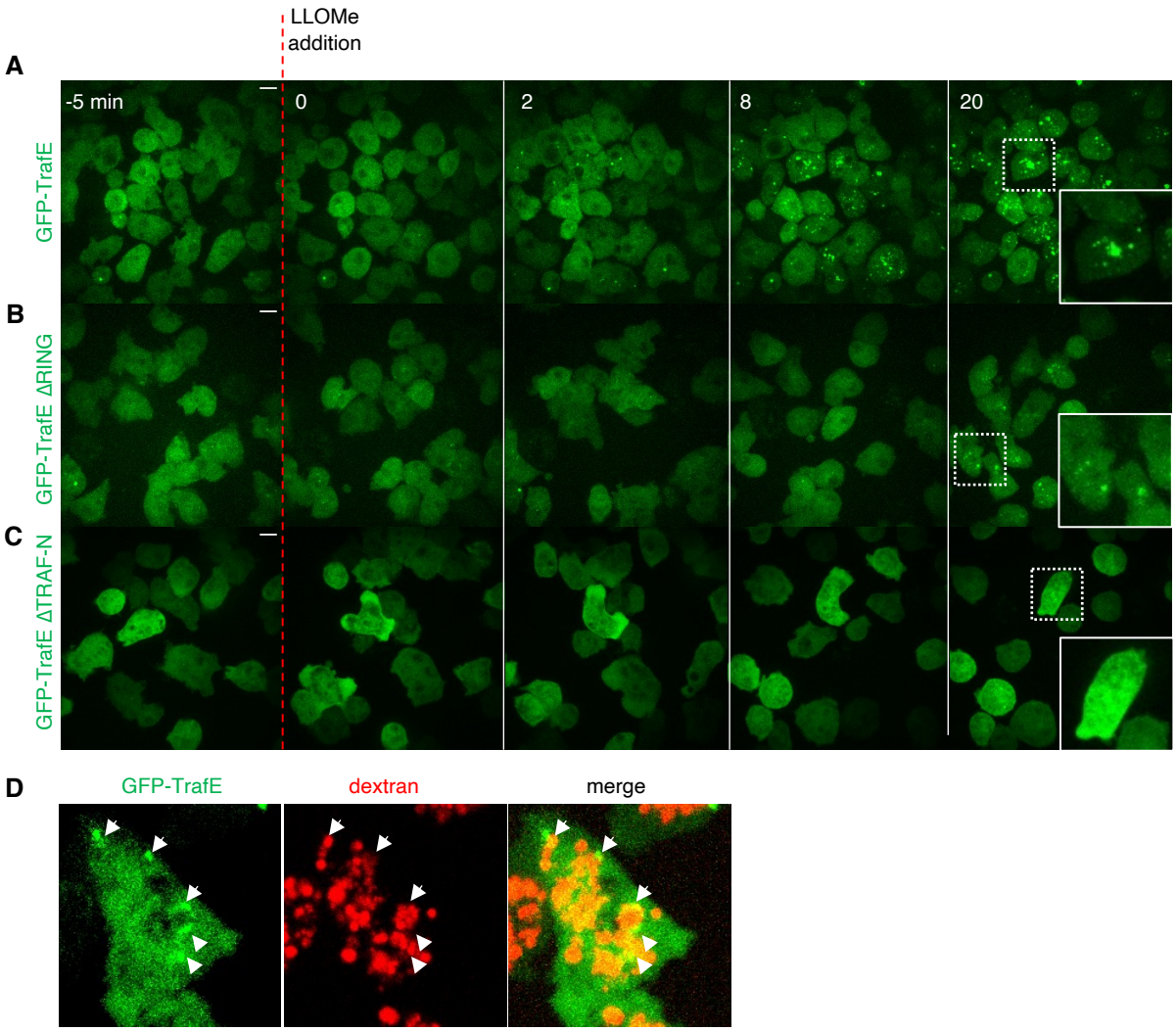

LLOMe
addition
A
-5 min
0
2
8
20
GFP-TrafE
B
GFP-TrafE ΔRING
C
GFP-TrafE ΔTRAF-N
D
GFP-TrafE
dextran
merge

Fig 7

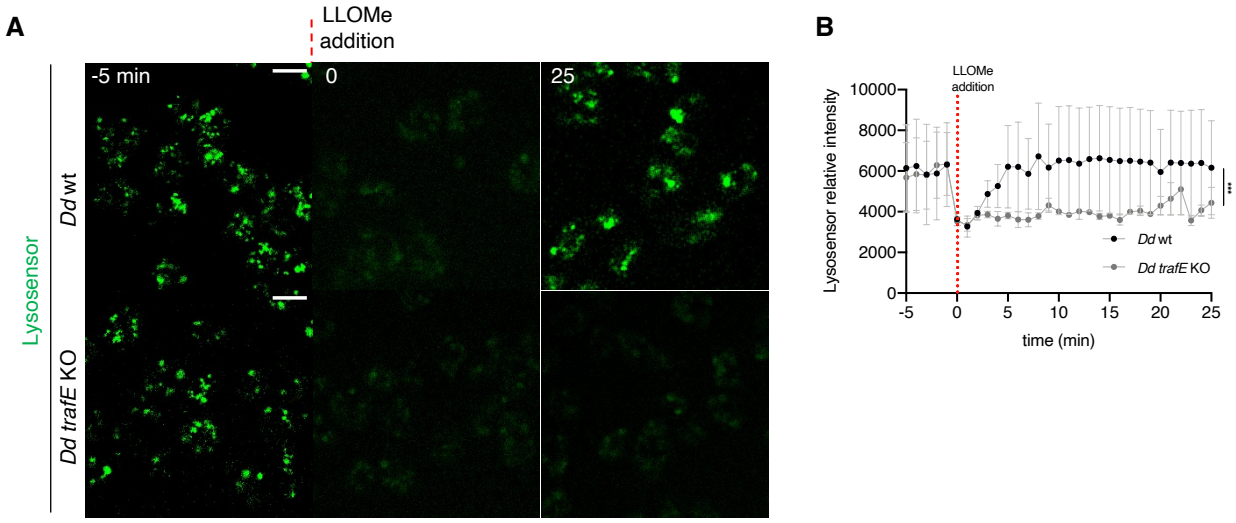

A
LLOMe
addition
-5 min
0
25
Lysosensor
Dd wt
Dd trafE KO
B
LLOMe
addition
Lysosensor relative intensity
10000
8000
6000
4000
2000
0
-5
0
5
10
15
20
25
time (min)
Dd wt
Dd trafE KO
***

Fig 8

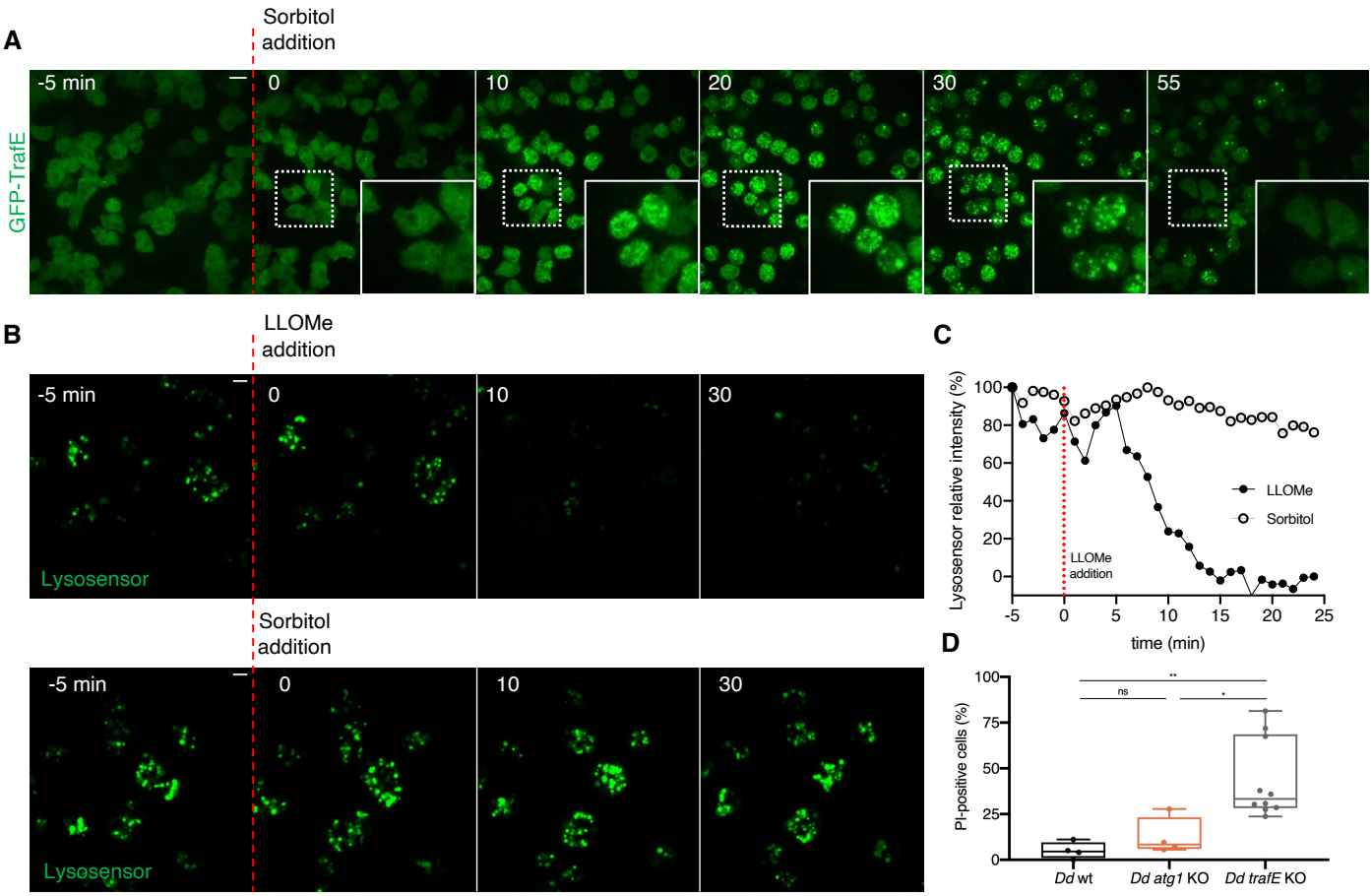

A
Sorbitol addition
GFP-TrafE
-5 min
0
10
20
30
55
B
LLOMe addition
Lysosensor
-5 min
0
10
30
Sorbitol addition
Lysosensor
C
Lysosensor relative intensity (%)
LLOMe addition
LLOMe
Sorbitol
time (min)
D
Pi-positive cells (%)
ns
**
*
Dd wt
Dd atg1 KO
Dd trafE KO

Fig 9

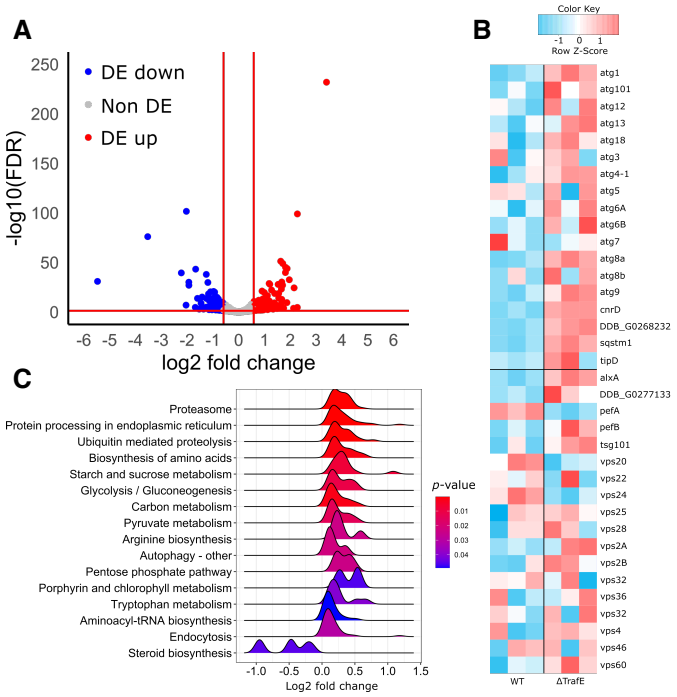
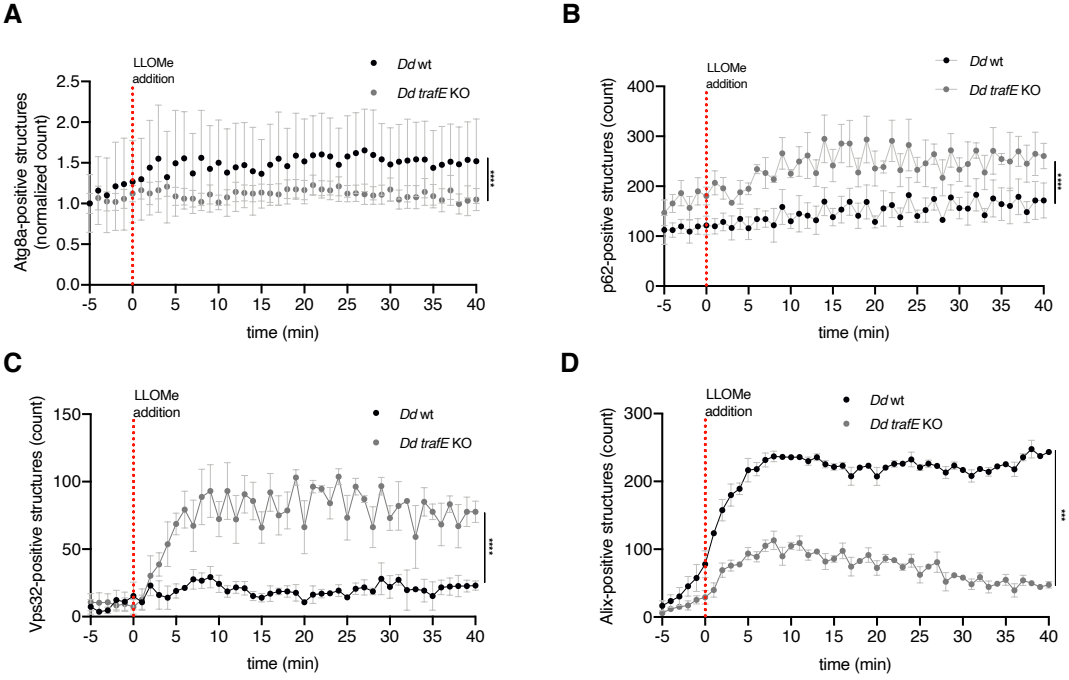

A
DE down
Non DE
DE up
-log10(FDR)
log2 fold change
B
Color Key
Row Z-Score
atg1
atg101
atg12
atg13
atg18
atg3
atg4-1
atg5
atg6A
atg6B
atg7
atg8a
atg8b
atg9
cnrD
DDB_G0268232
sqstm1
tipD
alxA
DDB_G0277133
pefA
pefB
tsg101
vps20
vps22
vps24
vps25
vps28
vps2A
vps2B
vps32
vps36
vps32
vps4
vps46
vps60
WT
ΔTrafE
C
Proteasome
Protein processing in endoplasmic reticulum
Ubiquitin mediated proteolysis
Biosynthesis of amino acids
Starch and sucrose metabolism
Glycolysis / Gluconeogenesis
Carbon metabolism
Pyruvate metabolism
Arginine biosynthesis
Autophagy - other
Pentose phosphate pathway
Porphyrin and chlorophyll metabolism
Tryptophan metabolism
Aminoacyl-tRNA biosynthesis
Endocytosis
Steroid biosynthesis
p-value
Log2 fold change

Fig 10


A
LLOMe addition
Dd wt
Dd trafE KO
Atg8a-positive structures (normalized count)
time (min)
B
LLOMe addition
Dd wt
Dd trafE KO
p62-positive structures (count)
time (min)
C
LLOMe addition
Dd wt
Dd trafE KO
Vps32-positive structures (count)
time (min)
D
LLOMe addition
Dd wt
Dd trafE KO
Alix-positive structures (count)
time (min)