1	A toolbox for imaging RIPK1, RIPK3 and MLKL in mouse and human cells
2	
3	André L. Samson <sup>1,2*</sup> , Cheree Fitzgibbon <sup>1</sup> , Komal M. Patel <sup>1</sup> , Joanne M. Hildebrand <sup>1,2</sup> , Lachlan W.
4	Whitehead <sup>1,2</sup> , Joel S. Rimes <sup>1,2</sup> , Annette V. Jacobsen <sup>1,2</sup> , Christopher R. Horne <sup>1,2</sup> , Xavier J. Gavin <sup>1,2</sup> ,
5	Samuel N. Young <sup>1</sup> , Kelly L. Rogers <sup>1,2</sup> , Edwin D. Hawkins <sup>1,2</sup> , James M. Murphy <sup>1,2*</sup>
6	
7	<sup>1</sup> Walter and Eliza Hall Institute of Medical Research, 1G Royal Parade, Parkville, VIC 3052,
8	Australia
9	<sup>2</sup> Department of Medical Biology, University of Melbourne, Parkville 3052, Australia
10	
11	*Please address correspondence to samson.a@wehi.edu.au (ALS) or jamesm@wehi.edu.au (JMM)
12	
13	Running title: Imaging necroptosis in mouse and human cells
14	
15	Keywords: kinase, pseudokinase, cell death, programmed necrosis, fixative

#### 16 ABSTRACT

Necroptosis is a lytic, inflammatory cell death pathway that is dysregulated in many human 17 18 pathologies. The pathway is executed by a core machinery comprising the RIPK1 and RIPK3 kinases, 19 which assemble into necrosomes in the cytoplasm, and the terminal effector pseudokinase, MLKL. 20 RIPK3-mediated phosphorylation of MLKL induces oligomerization and translocation to the plasma 21 membrane where MLKL accumulates as hotspots and perturbs the lipid bilayer to cause death. The 22 precise choreography of events in the pathway, where they occur within cells, and pathway differences between species, are of immense interest. However, they have been poorly characterized 23 24 due to a dearth of validated antibodies for microscopy studies. Here, we describe a toolbox of 25 antibodies for immunofluorescent detection of the core necroptosis effectors, RIPK1, RIPK3 and MLKL, and their phosphorylated forms, in human and mouse cells. By comparing reactivity with 26 27 endogenous proteins in wild-type cells and knockout controls in basal and necroptosis-inducing 28 conditions, we characterise the specificity of frequently-used commercial and recently-developed 29 antibodies for detection of necroptosis signaling events. Importantly, our findings demonstrate that 30 not all frequently-used antibodies are suitable for monitoring necroptosis by immunofluorescence 31 microscopy, and methanol- is preferable to paraformaldehyde-fixation for robust detection of specific RIPK1, RIPK3 and MLKL signals. 32

#### **33 INTRODUCTION**

Cell death by necroptosis is thought to have originated as an ancestral host defence mechanism, which 34 is reflected in the breadth of pathogen-encoded proteins that inhibit the pathway<sup>1, 2, 3, 4, 5, 6</sup>. In addition 35 to reported innate immunity functions<sup>7, 8, 9</sup>, the dysregulation of necroptosis has been implicated in a 36 range of pathologies, including ischemic-reperfusion injuries, such as in the kidney<sup>10, 11</sup> and heart<sup>12</sup>, 37 and inflammatory diseases<sup>13, 14, 15, 16</sup>, including inflammatory bowel disease<sup>17</sup>. Accordingly, there is 38 39 widespread interest in therapeutically-targeting the pathway to counter human disease. Owing to the recent identification of the terminal effectors of the pathway, RIPK3 (in 2009)<sup>1, 18, 19</sup> and MLKL (in 40 2012)<sup>20, 21</sup>, however, the extent of indications attributable to necroptotic cell death is poorly 41 42 understood. Precisely defining pathologies impacted by necroptosis has posed a challenge owing to 43 the dearth of antibodies validated to specifically detect members of the pathway and their activated 44 (phosphorylated) forms in fixed cells and tissues. As a result, the contribution of necroptosis to many pathologies remains a subject of ongoing debate<sup>22, 23, 24, 25</sup>. 45

46 Necroptotic cell death signaling is initiated by ligation of death receptors, such as the TNF 47 receptor 1, or pathogen detectors, such as Toll-like receptors 3 and 4 and the ZBP1/DAI intracellular 48 viral RNA sensor protein. In cellular contexts where the activities of the Inhibitors of Apoptosis 49 proteins (IAPs) E3 Ubiquitin ligase family and the proteolytic apoptotic effector, Caspase-8, are depleted or compromised, necroptosis ensues. The precise choreography of necroptotic signaling is 50 still emerging, although recent studies have defined key events and checkpoints in the pathway<sup>26, 27,</sup> 51 52 <sup>28,29</sup>. Following pathway induction, RIPK1 autophosphorylation prompts hetero-oligomerization with RIPK3 via an amyloid-forming motif in the region C-terminal to their kinase domains termed the 53 RHIM (RIP Homotypic Interaction Motif) to form a cytoplasmic platform known as the necrosome<sup>30,</sup> 54 <sup>31, 32</sup>. Upon RIPK3 activation by autophosphorylation within necrosomes<sup>33, 34</sup>, RIPK3 is primed to 55 phosphorylate the activation loop of the MLKL pseudokinase domain to activate MLKL's killing 56 function<sup>14, 20, 27, 28, 35, 36, 37, 38, 39</sup>. In the case of human MLKL, dormant MLKL appears to be at least in 57

part pre-associated with RIPK3 in the cytoplasm<sup>20, 40</sup>, and stable recruitment to necrosomes appears 58 to be an essential checkpoint in MLKL activation<sup>28</sup>. In the case of mouse MLKL, a transient 59 interaction between RIPK3 and MLKL appears to be sufficient for MLKL activation in mouse cells<sup>35,</sup> 60 61 <sup>36, 37</sup>. Regardless of species, MLKL phosphorylation is thought to provoke a conformational change 62 in the pseudokinase domain that leads to oligomerization and unmasking of the killer N-terminal four-helix bundle (4HB) domain<sup>37, 40, 41, 42, 43</sup>. The human MLKL 4HB domain likely engages 63 64 chaperones to facilitate translocation to the plasma membrane via an actin-, Golgi- and microtubuledependent mechanism, where MLKL accumulates in hotpots. When a threshold is surpassed, the 4HB 65 domains of MLKL permeabilize the membrane to induce cell death<sup>26, 29</sup>. 66

While biochemical studies have defined these steps and checkpoints, visualizing the 67 spatiotemporal dynamics of endogenous proteins during in necroptosis using microscopy-based 68 69 approaches has proven challenging in the absence of antibodies that have been validated for target 70 specificity. Similarly, the lack of validated reagents poses a challenge to immunohistochemical 71 staining of patient tissue sections, and therefore attribution of a role for necroptosis in pathologies, 72 because knockout tissue controls are not available. Here, we have established procedures for staining 73 endogenous RIPK1, RIPK3 and MLKL, and their phosphorylated forms, in fixed mouse and human 74 cells. While several frequently-used antibodies were found to be suitable for selectively staining these 75 proteins, as validated by comparisons with cells deficient for each protein, many exhibited non-76 specific staining and are therefore unsuitable for immunofluorescence and immunohistochemistry. 77 Our studies also highlight the importance of validating antibody compatibility with fixation methods. 78 In most cases, paraformaldehyde fixation ablated epitopes, presumably because RIPK3 and MLKL 79 are lysine-rich and prone to modification by crosslinking, whereas methanol fixation enabled specific 80 detection of these proteins. Due to the sequence divergence between mouse and human RIPK3 and MLKL<sup>41, 43, 44, 45, 46</sup>, it was not possible to specifically-detect proteins across species using a single 81 82 reagent, which necessitated the development of a new antibody that specifically detected mouse

MLKL. Collectively, our studies present a toolbox of selective antibodies that will enable critical
 analysis of the chronology, checkpoints and kinetics of necroptotic signaling in mouse and human
 cells.

86

#### 87 **RESULTS**

#### 88 Immunofluorescent detection of human MLKL

89 We recently described a monoclonal antibody, clone 10C2 (source: WEHI Antibody Facility, inhouse), that recognises an epitope centred on residues 413-471 of human MLKL<sup>29</sup> (Fig. 1a). The 90 91 initial screen that identified this clone suggested it yielded specific immunosignals when cells were 92 fixed with methanol, but not when cells were fixed with paraformaldehyde. Organic solvents such as 93 methanol preserve cells by precipitating proteins, whereas aldehyde-based agents such as 94 paraformaldehyde fix cells by crosslinking lysines and other primary amines. Because human MLKL is lysine-rich (93<sup>rd</sup> percentile in the cytoplasmic and membrane-associated proteome), 95 paraformaldehyde likely causes widespread crosslinking of MLKL, which in turn masks epitopes and 96 97 reduces immunoreactivity. As several other necroptotic proteins are lysine-rich, we considered 98 whether the choice of fixative was a critical variable for robust immunodetection of MLKL, RIPK3 99 and RIPK1 in human and mouse cells. Accordingly, we compared the performance of 22 antibodies for immunofluorescent staining of human HT29 cells and mouse dermal fibroblasts (MDFs) - two 100 101 cellular models that are well-characterized to undergo necroptosis when treated with TNF, Smacmimetic and IDN-6556 (herein referred to as TSI)<sup>5, 28, 29, 44, 47</sup>. To quantitatively gauge the 102 performance of each antibody, their immunosignals were characterized in four ways: 1) A ratio of 103 the immunofluorescent signals between a positive and negative control. This produces a signal-to-104 105 noise curve that estimates 'specific signal abundance' (Fig. 1b). For testing phospho-specific antibodies, wild-type cells undergoing necroptosis were used as a positive control and untreated wild-106 107 type cells as a negative control (Fig. S1). For testing all other antibodies, untreated wild-type cells

108 were used as a positive control and relevant knockout cells as a negative control. 2) Micrographs 109 were gated so that the minimum/maximum immunosignals corresponded to the 5<sup>th</sup>/95<sup>th</sup> percentiles of 110 the signal-to-noise curve (Fig. 1b). 3) The percentage of total signals that fall within this gate were 111 determined to show how much signal from the positive control was considered specific (Fig. 1c). 4) 112 Antibodies were immunoblotted against positive and negative controls to independently assess their 113 specificity.

114 Using this approach, we confirmed that clone 10C2 specifically detects endogenous human MLKL in methanol-fixed, but not paraformaldehyde-fixed cells (Fig. 1d-f). The 10C2 clone produces 115 116 a favourable immunostaining profile, where the specific signals are abundant (Fig. 1e) and these specific signals represent the majority of all detectable signals (Fig.1d). We recently developed 117 another MLKL-specific antibody, clone 7G2 (source: in-house), that recognises an epitope centred 118 119 on  $\alpha$ F- $\alpha$ G loop the C-lobe of the human MLKL pseudokinase domain, which differs to the site recognised by the 10C2 clone<sup>29</sup>. Despite binding a distinct site in human MLKL to 10C2, the 7G2 120 clone shows similar specificity for human MLKL in immunoblot analyses and only yields specific 121 122 immunofluorescent signals on methanol-fixed cells (Fig. 1d-f). Notably, clone 7G2 is inferior to clone 123 10C2 for immunofluorescence studies, because specific signals were less abundant (Fig. 1e) and were 124 a minor fraction of all detectable signals (Fig.1d).

We observed that clone EPR9514 (source: Abcam), an antibody raised against phospho-S358 125 of human MLKL<sup>48</sup>, which is a hallmark of MLKL activation during necroptosis<sup>20</sup>, produced specific 126 127 and comparable immunofluorescent signals in both methanol- and paraformaldehyde-fixed cells undergoing necroptosis (Fig. 1e). As MLKL can be disulfide-crosslinked during necroptosis<sup>49, 50</sup> (Fig. 128 129 S2A-B), we tested whether fixation in the presence of *N*-ethylmaleimide (NEM) to prevent further 130 disulfide bonding, or post-fixative treatment with Tris(2-carboxyethyl)phosphine (TCEP) to reduce disulfide bonds, altered the immunofluorescent detection of phospho-MLKL by clone EPR9514. 131 However, neither preventing nor reducing disulfide bonds in fixed cells precluded the 132

immunodetection of MLKL by clone EPR9514 (Fig. S2C-D). Indeed, disulfide-crosslinking may be
a by-product of MLKL activation given that recombinant human MLKL oligomerizes in the absence
of disulfide bonds (Fig. S2E).

Two other anti-human MLKL antibodies were found to be non-specific (Novus Biological 136 clone 954702; and Sigma-Aldrich M6697, a polyclonal antibody raised against residues 58-70; Fig. 137 1a and 1e), with equivalent signal intensity and diffuse staining observed in wild-type and MLKL<sup>-/-</sup> 138 139 cells. Lastly, immunoblotting confirmed that clones 10C2, 7G2 (both in-house) and EPR9514 (Abcam) were highly-specific with bands corresponding to human MLKL's molecular weight of 140 54kDa observed in wild-type but not MLKL<sup>-/-</sup> HT29 cell lysates. In contrast, clone 954702 (Novus 141 Biological MAB9187) and the Sigma-Aldrich M6697 polyclonal antibody were non-specific, with 142 multiple bands not corresponding to the molecular weight of MLKL observed in both wild-type and 143 144 *MLKL*<sup>-/-</sup> HT29 cell lysates (Fig. 1g).

In summary, three of the five antibodies that were tested selectively recognised human MLKL in methanol-fixed cells (clones 10C2, 7G2 and EPR9514) and, accordingly, we recommend methanol fixation for detecting endogenous human MLKL by immunofluorescence. Under these conditions, cytoplasmic forms of MLKL could be detected using the 10C2 and 7G2 clones, and phospho-MLKL accumulating at the cell periphery with the EPR9514 clone (Fig. 1f). These data underscore the importance of careful consideration of fixation method when using MLKL as a histological marker of necroptosis.

152

# 153 Immunofluorescent detection of human RIPK3

We next assessed five anti-human RIPK3 antibodies (Fig. 2a). Two antibodies raised against the Cterminus (source: ProSci 2283, Novus Biological NBP2-24588) and one antibody raised against the N-terminus of RIPK3 (source: Novus Biological MAB7604, clone 780115) yielded non-specific signals via both immunofluorescence and immunoblotting (Fig. 2b-e). Our recently described

antibody, clone 1H2 (source: in-house)<sup>5</sup>, detected RIPK3 via immunofluorescence in methanol-fixed, 158 but not paraformaldehyde-fixed cells. However, most of the immunofluorescent signals produced by 159 160 1H2 were non-specific (Fig. 2b), and the remaining signals are specific but of very low abundance (Fig. 2c). Thus, although clone 1H2 is highly-selective when used as an immunoblotting reagent (Fig. 161 2d<sup>5</sup>), it should only be used for the immunofluorescent detection of human RIPK3 under carefully 162 controlled conditions. Our data also showed that clone D6W2T (source: Cell Signaling Technology), 163 164 an antibody raised against a mark of human RIPK3 activation in necroptosis, phospho-S227, produced specific immunofluorescent signals in paraformaldehyde-fixed cells undergoing 165 166 necroptosis, but not in methanol-fixed cells (Fig. 2d). Again, the low abundance of these specific immunosignals suggests that clone D6W2T should only be used for immunofluorescence under 167 carefully controlled conditions, such as where RIPK3<sup>-/-</sup> control cells are available for direct 168 169 comparison. Another caveat is that immunoblotting showed that clone D6W2T not only detected RIPK3 in cells undergoing necroptosis, but also in untreated cells when RIPK3 was presumably not 170 phosphorylated at S227 (Fig. 2d). Therefore, while two of the five antibodies that were tested 171 specifically recognised human RIPK3, the low abundance of their specific signals complicates use of 172 173 these antibodies for studying endogenous human RIPK3 via immunofluorescence. At present, more specific antibodies are needed to enable the immunofluorescent detection of human RIPK3. 174

175

#### 176 Immunofluorescent detection of human RIPK1

We next tested three monoclonal anti-RIPK1 antibodies: one against the N-terminal domain (source: Cell Signaling Technology clone D94C12), one against the C-terminal region (source: BD Transduction Laboratories clone 38/RIP) and one raised against phospho-S166 (source: Cell Signaling Technology clone D8I3A; Fig. 3a). All three clones yielded specific immunofluorescent signals in methanol- and paraformaldehyde-fixed cells, however, these signals were more abundant in methanol-fixed samples (Fig. 3b-d). All three clones were also specific via immunoblot (Fig. 3e).

Importantly, the immunosignals from clones D94C12 and 38/RIP were markedly lower in cells 183 undergoing necroptosis than in unstimulated wild-type cells (Fig. 3d-e). This observation is likely 184 185 due to RIPK1 undergoing widespread post-translational modification and/or proteasomal degradation 186 during TNF-induced cell death<sup>51, 52</sup>. Thus, despite clones D94C12 and 38/RIP exhibiting a favourable immunostaining profile in unstimulated cells, their decreased reactivity in cells undergoing 187 necroptosis indicates that they should be used judiciously for immunofluorescent labelling of samples 188 189 for accurate analysis of necroptosis. Conversely, while clone D813A preferentially stains RIPK1 in cells undergoing necroptosis, specific signals that were detected also had low intensity (Fig. 3b) and 190 191 low abundance (Fig. 3c). In summary, three highly-specific antibodies exist for human RIPK1. However, because their specific signals have very low intensity and abundance in necroptotic cells, 192 their use for the immunofluorescent detection of RIPK1 during necroptosis should be carefully 193 194 controlled, including side-by-side examination of wild-type and *RIPK1*<sup>-/-</sup> control cells.

195

#### 196 Immunofluorescent detection of mouse MLKL

To our knowledge, there are currently no validated monoclonal antibodies for the immunofluorescent 197 detection for mouse MLKL in unstimulated cells. Accordingly, we raised a monoclonal antibody, 198 clone 5A6 (source: in-house), against full-length mouse MLKL (Fig. 4a). The epitope for clone 5A6 199 resides in the C-terminal domain of mouse MLKL (Fig. S3). As shown in Fig. 4a-d, clone 5A6 200 201 produced specific and abundant signals for endogenous mouse MLKL in methanol-fixed, but not 202 paraformaldehyde-fixed cells. Immunoblotting confirmed that clone 5A6 was highly-specific (Fig. 203 4e). Notably, compared to human MLKL which translocates en masse into cytoplasmic clusters 204 during necroptosis, the relocation of mouse MLKL into cytoplasmic clusters during necroptosis was 205 more subtle. This observation may relate to the notion that human MLKL is recruited to the necrosome in a more stable manner than mouse MLKL<sup>28</sup>. 206

207 Phosphorylation of mouse MLKL at S345 is essential for necroptosis in murine cells<sup>37</sup>, and therefore many antibodies have been raised against this phosphosite. We tested three commonly-used 208 antibodies (Fig. 4a-e), namely clones: EPR9515(2) (source: Abcam), 7C6.1<sup>39</sup> (source: Millipore 209 210 MABC1158) and D6E3G (source: Cell Signaling Technology). All three clones yielded specific immunosignals in methanol-fixed cells (Fig. 4c), whereas only clone 7C6.1 was compatible with 211 paraformaldehyde fixation. However, the performance of clone D6E3G was superior to the other anti-212 213 phospho-MLKL antibodies, because specific signals were more abundant (Fig. 4c) and represented a higher percentage of the total detectable signal (Fig. 4b). This trend was also evident via immunoblot, 214 215 with clone 7C6.1 being largely non-specific, clone EPR9515(2) being moderately specific and clone 216 D6E3G exhibiting a high degree of specificity towards activated MLKL in necroptotic cells (Fig. 4e). In summary, clones 5A6 and D6E3G allow the immunofluorescent detection of mouse MLKL 217 218 under resting and necroptotic conditions, respectively. Moreover, as with human MLKL, methanol is 219 the fixative of choice for robust immunofluorescent detection of endogenous mouse MLKL.

220

#### 221 Immunofluorescent detection of mouse RIPK3

222 There are numerous well-validated antibodies raised against mouse RIPK3, including a polyclonal antibody against the C-terminus (source: ProSci 2283), and monoclonal antibodies recognising 223 phospho-T231/phospho-S232 (source: Genentech clone GEN135-35-953) and the extended kinase 224 225 domain (residues 2-353) of mouse RIPK3 (clone 8G7<sup>5</sup>, in-house; Fig. 5a). These antibodies yielded 226 specific signals via both immunofluorescence and immunoblot analyses (Fig. 5b-e). Interestingly, 227 while phospho-RIPK3 concentrates into cytoplasmic clusters during necroptosis, this relocation event was not detected by other, anti-total RIPK3 antibodies (Fig. 5d). This finding suggests that the 228 229 epitopes for RIPK3 detection are obscured via protein-protein interactions during the chronology of 230 necroptotic signaling events. To further probe the steps in the pathway, we generated another mouse RIPK3 antibody, clone 1H12 (source: in-house), which has a favourable staining profile (Fig. 5b-c) 231

and which recognises the translocation of mouse RIPK3 into cytoplasmic clusters during necroptosis 232 (Fig. 5d). Notably, monoclonal antibodies raised against the N-terminal kinase domain of RIPK3, 233 234 8G7 and 1H12, detected several species of lower molecular weight than full length RIPK3 by immunoblot. These signals are likely to be spliced isoforms of mouse RIPK3 of varying lengths, each 235 of which harbour the kinase domain antigen (residues 2-353), which are therefore not detected by 236 237 antibodies directed towards the C-terminus of the full-length mouse RIPK3 isoform, such as ProSci 238 2283. In summary, there are several excellent options for the immunofluorescent detection of 239 endogenous mouse RIPK3. Notably, unlike MLKL and RIPK1, the choice of fixative has no major 240 bearing on the ability to detect mouse RIPK3 by immunofluorescence (Fig. 5c).

241

## 242 Immunofluorescent detection of mouse RIPK1

RIPK1 exhibits greater sequence identity between mouse and human orthologs than either RIPK3 or
MLKL<sup>41</sup>. In keeping with this, both clone D94C12 (source: Cell Signaling Technology) and clone
38/RIP (source: BD Transduction Laboratories), which were raised against human RIPK1, also
specifically detected mouse RIPK1 via immunofluorescence and immunoblotting (Fig. 6a-e). A
polyclonal antibody raised against phospho-S166 of mouse RIPK1 (31122; source: Cell Signaling
Technology) was also found to specifically detect RIPK1 via immunoblot (Fig. 6e) and in methanolfixed, but not paraformaldehyde-fixed, cells undergoing necroptosis (Fig. 6b-d).

In summary, three highly-specific antibodies exist for mouse RIPK1. However, as was observed in human cells, necroptosis in mouse cells causes a marked reduction in RIPK1 levels (Fig. 6d-e). Thus, the specific immunosignals from the antibodies tested are of low intensity and abundance in necroptotic cells. Therefore, careful gating of signals is recommended for the study of mouse RIPK1 in necroptotic cells.

255

#### 256 Antibody cocktails for imaging endogenous necroptotic signaling

257 Having validated and compared the performance of numerous reagents, we now propose different antibody combinations that can be used to study endogenous necroptotic signaling (Fig. 7a-b). 258 259 Because these recommendations are made to facilitate the investigation of endogenous necroptotic 260 signaling in fixed cells, we also provide an ImageJ macro to generate signal-to-noise curves for the gating of specific immunosignals (Supplementary File 1). To exemplify the advantages of visualising 261 endogenous necroptotic events in situ, we co-stained MDFs for non-phosphorylated MLKL (clone 262 263 5A6; source: in-house) and phosphorylated MLKL (clone D6E3G; source: Cell Signaling Technology). Similar to what was described for human MLKL<sup>29</sup>, mouse MLKL was observed to 264 265 concentrate into cytoplasmic clusters during necroptosis. However, this compartmentalisation event 266 is less pronounced than those observed for human MLKL in necroptotic HT29 cells (arrowhead; Fig. 7c). Also similar to what was described for human MLKL<sup>29</sup>, phosphorylated MLKL was observed to 267 268 form focal structures at the plasma membrane, rather than docking uniformly with the cell periphery 269 (Fig. 7c). Remarkably, although smaller than the hotspots of phosphorylated human MLKL that form in necroptotic HT29 cells, junctional accumulations of phosphorylated mouse MLKL were also 270 271 apparent in necroptotic MDFs (Fig. 7d and Supplementary Video 1). These data suggest that the 272 assembly of both mouse and human MLKL into macromolecular structures at the plasma membrane, and preferentially at sites of intercellular contact, may be an intrinsic and penultimate feature of 273 274 necroptotic signaling.

275

#### 276 **DISCUSSION**

Here, we profiled the immunofluorescent staining of MLKL, RIPK3 and RIPK1 in fixed human and
mouse cells with a panel of 22 antibodies. While 17 of 22 antibodies were capable of detecting their
respective necroptotic protein target in fixed wild-type cells and not their knockout counterparts, only
14 of 22 antibodies exhibited favourable signal-to-noise for robust immunostaining (as summarized
in Fig. 7a).

The choice of fixative was a critical variable for the immunofluorescent detection of 282 necroptotic proteins. With the exception of phospho-S227 in human RIPK3 and pT231/pS232 in 283 284 mouse RIPK3, all other epitopes exhibited increased immunoreactivity in methanol-fixed samples. 285 Indeed, immunodetection of MLKL was often found to be entirely contingent upon the use of methanol as a fixative. This observation has ramifications for the experimental and clinical 286 287 immunohistological detection of cell death, which is almost exclusively performed on aldehyde-fixed 288 samples. Thus, stringent antigen retrieval steps to reverse crosslinks will likely be necessary for the development of a diagnostic assay for necroptosis in patient samples. High resolution microscopy is 289 290 also mostly performed on aldehyde-fixed cell monolayers. However, as these cell monolayers cannot typically withstand antigen retrieval, we recommend the use of methanol fixation for high resolution 291 immunofluorescence of necroptosis; even though methanol fixation can be sub-optimal for both the 292 293 retention of certain biomolecules<sup>54</sup> and the preservation of cellular architecture<sup>55, 56</sup>. Indeed, all but 294 one of the antibodies (source: Cell Signaling Technology clone D6W2T) in the suggested toolbox in 295 Fig. 7a are compatible with methanol fixation.

296 Our data underscore the importance of using controlled experimental conditions to maximise 297 the identification of specific immunosignals. To this end, we used wild-type cells that express high 298 levels of MLKL, RIPK3 and RIPK1, and which have a well-characterised response to necroptotic 299 stimuli. If possible, cell cultures should be fixed when low, but measurable, levels of necroptotic 300 death are occurring (Fig. S1). This is because end-stage dead cells are often lost during/after methanol fixation, and because the immunosignals for phospho-RIPK1, phospho-RIPK3 and phospho-MLKL 301 peak prior to cell death<sup>29</sup>. Notably, the use of knockout cells (for non-phospho-targets) or 302 303 unstimulated wild-type cells (for phospho-sites) as a negative control is critical, as it provides the information needed to define the signal-to-noise profile of an antibody (Fig. 1b). Additionally, it is 304 305 also helpful if different antibodies directed toward the same target yield concordant 306 immunofluorescent signals, and if accompanying immunoblot data confirm their specificity. This

307 combined approach was important for deducing that clone D6E3G (source: Cell Signaling
308 Technology) is the best option for detecting phospho-MLKL in mouse cells (Fig. 4).

309 It is concerning that the specificity of some antibodies could not be verified. For instance, while numerous studies use the ProSci 2283 antibody to detect human RIPK3<sup>57, 58, 59</sup>, we found that 310 it only recognised mouse RIPK3. Similarly, M6697 (source: Sigma-Aldrich) and clone 7C6.1 311 (source: Millipore) have been widely used to respectively detect human MLKL and mouse MLKL 312 phospho-S345 <sup>39, 60, 61, 62, 63, 64, 65</sup>, however these reagents exhibited a low degree of specificity in our 313 hands. Nonetheless, as we did not exhaustively test the performance of these antibodies for 314 315 immunofluorescence using a wide variety of fixatives, blocking agents, and detergents, we cannot categorically state that they are non-selective. Moreover, as ProSci 2283 (reported to detect mouse 316 and human RIPK3) and Sigma-Aldrich M6697 (reported to detect human MLKL) are polyclonal 317 318 antibodies, batch-to-batch variation may explain differences in their specificity between studies. It is also noteworthy that the majority of monoclonal antibodies that yielded the most abundant and 319 320 specific signals were raised against recombinant full-length protein or component domains, rather than unfolded partial domains or peptides. We reasoned that epitopes that are exposed in the cellular 321 322 forms of these proteins would be similarly presented within a folded protein for immune recognition 323 in the host. Phosphosite-specific antibodies differ in this regard; these were raised using linear 324 phosphopeptides and their specificity likely reflects the unstructured and solvent-exposed nature of 325 the sequences in which they reside.

Broadly, the specific immunosignals described in this study provide consensus about three key compartmentalisation events that underlie necroptotic signaling<sup>66</sup>. First, the core necroptotic proteins - MLKL, RIPK3 and RIPK1 - predominantly reside in the cytosol under basal conditions. Interestingly, rather than being diffusely distributed across the cytosol, this necroptotic machinery exists as small puncta that are below the resolution limit of conventional light microscopy. It may be that these necroptotic proteins are preassembled into a membrane-less organelle under basal

332 conditions. Second, RIPK1, RIPK3 and MLKL then coalesce into large cytoplasmic clusters. These clusters preferentially locate to the perinuclear space and are necrosome-related as they co-stain for 333 the presence of phospho-RIPK1, -RIPK3 and -MLKL (Fig. 1-7 and ref.<sup>29</sup>). It is important to note that 334 the formation of these necrosomal clusters in TSI-treated HT29 cells occurs subsequent to the 335 phosphorylation of MLKL<sup>29</sup>. While these clusters likely represent a higher-order form of the 336 necrosome, the mechanisms that govern cluster formation and limit their overall size are currently 337 338 unknown. Third, as necroptotic signaling continues, phospho-MLKL is actively trafficked away from the clusters towards the plasma membrane<sup>26</sup> where it accumulates into supramolecular assemblies 339 called "hotspots"<sup>29</sup>. Recent findings suggest the release of phospho-MLKL from clusters arises from 340 MLKL undergoing a conformational change that accompanies disengagement from necrosomal 341 RIPK3<sup>40</sup>. Our data support such a disengagement step because neither RIPK1 nor RIPK3 were 342 343 observed to accumulate at the plasma membrane during necroptosis in mouse or human cells (Fig. 2-344 3 and 5-6). This disengagement step, and formation of supramolecular assemblies by both mouse and human MLKL at the plasma membrane, are likely to be two additional checkpoints in necroptotic 345 346 signaling.

347

#### 348 METHODS

Materials - Primary antibodies and the dilutions used for immunoblotting/immunofluorescence 349 were: rat anti-human MLKL (clone 10C2; produced in-house<sup>29</sup>; 1:2000/1:400), rat anti-human 350 MLKL (clone 7G2; produced in-house<sup>29</sup>; 1:2000/1:400), rabbit anti-phospho-S358 human MLKL 351 (Abcam ab187091; clone EPR9514; 1:2000/1:200), rat anti-mouse, human, rat, horse MLKL (clone 352 3H1; produced in-house<sup>37</sup> and available as Millipore MABC604; 1:2000/ N/A), mouse anti-phospho-353 354 T357 human MLKL (Novus Biological MAB9187; clone 954702; 1:1000/1:200), rabbit anti-human MLKL (Sigma-Aldrich M6697; 1:1000/1:200), rabbit anti-RIPK3 (ProSci #2283; 1:1000/1:200), 355 356 rabbit anti-human RIPK3 (Novus Biological NBP2-24588; 1:1000/1:200), mouse anti-human RIPK3

357 (Novus Biological; clone 780115; 1:1000/1:200), rat anti-human RIPK3 (clone 1H2; produced inhouse<sup>5</sup> and available as Millipore MABC1640; 1:2000/1:400), rabbit anti-phospho-S227 human 358 359 RIPK3 (Cell Signaling Technology; clone D6W2T; 1:2000/1:200), rabbit anti-mouse or human 360 RIPK1 (Cell Signaling Technology; clone D94C12; 1:2000/1:200), mouse anti-mouse or human RIPK1 (BD Biosciences; clone 38/RIP; 1:1000/1:100), rabbit anti-phospho-S166 human RIPK1 (Cell 361 362 Signaling Technology; clone D8I3A; 1:2000/1:200), rat anti-mouse MLKL (clone 5A6; produced in-363 house), rabbit anti-phospho-S345 mouse MLKL (Abcam; clone EPR9515(2); 1:2000/1:200), mouse anti-phospho-S345 mouse MLKL (Millipore MABC158; clone 7C6.1; 1:2000/1:200), rabbit anti-364 365 phospho-S345 mouse MLKL (Cell Signaling Technology; clone D6E3G; 1:2000/1:200), rat antimouse RIPK3 (clone 8G7; produced in-house<sup>5</sup> and available from Millipore as MABC1595; 366 1:2000/1:400), rat anti-mouse RIPK3 (clone 1H12; produced in-house; 1:2000/1:400), rabbit anti-367 368 phospho-T231/S232 mouse RIPK3 (Genentech; clone GEN135-35-953; 1:2000/1:400), rabbit anti-369 phospho-S166 mouse RIPK1 (Cell Signaling Technology 31122; 1:2000/1:200), mouse anti-GAPDH (Millipore MAB374; 1:2000/N/A). Secondary antibodies for immunoblotting were: horseradish 370 peroxidase (HRP)-conjugated goat anti-rat IgG (Southern Biotech 3010-05), HRP-conjugated goat 371 372 anti-mouse IgG (Southern Biotech 1010-05), and HRP-conjugated goat anti-rabbit IgG (Southern 373 Biotech 4010-05). All secondary antibodies for immunoblotting were used at a dilution of 1:10000. 374 Secondary immunofluorescence detection reagents were: AlexaFluor647-conjugated donkey anti-375 rabbit IgG (ThermoFisher Scientific A31573), AlexaFluor568-conjugated donkey anti-rabbit IgG 376 (ThermoFisher Scientific A10042), AlexaFluor568-conjugated donkey anti-mouse IgG 377 (ThermoFisher Scientific A10037), AlexaFluor-594 donkey anti-rat IgG (ThermoFisher Scientific A-21209), AlexaFluor488-conjugated donkey anti-rat IgG (ThermoFisher Scientific A21208). All 378 379 secondary antibodies for immunofluorescence were used at a dilution of 1:1000. Bond-Breaker TCEP 380 solution (ThermoFisher Scientific 77720). N-Ethylmaleimide (Sigma-Aldrich E3876).

382 5A6 and 1H12 antibody production - Antibodies were generated at the Walter and Eliza Hall Institute Monoclonal Antibody Facility by immunizing Wistar rats with recombinant full-length 383 mouse MLKL<sup>37</sup> for clone 5A6 or recombinant mouse RIPK3 residues 2-353 for clone 1H12 and the 384 previously-reported clone 8G7<sup>5</sup> that was expressed and purified from Sf21 insect cells using the 385 baculovirus expression system, before splenocytes were fused with SP2/O mouse myeloid cells and 386 arising hybridoma lines cloned. The specificity of clone 5A6 for mouse MLKL was validated via 387 388 immunoblot analyses as exemplified in Fig. 4e and Fig. S3. The specificity of clone 1H12 for mouse RIPK3 was validated via immunoblot analyses as exemplified in Fig. 5e. 389

390

Cell lines – HT29 cells were provided by Mark Hampton (University of Otago). RIPK1<sup>-/-</sup>, RIPK3<sup>-/-</sup> 391 and MLKL<sup>-/-</sup> HT29 cells have been previously reported<sup>28, 29, 67</sup>. MDF lines were generated in-house 392 from the tails of wild-type C57BL/6J, Mlkl-/-37 and Ripk3-/-68 mice and immortalized by SV40 large T 393 antigen as reported previously<sup>35, 37</sup>. The sex and precise age of these animals were not recorded, 394 although our MDFs are routinely derived from tails from 8-week-old mice. *Mlkl<sup>-/-</sup>Ripk1<sup>-/-</sup>* MDFs were 395 derived from the belly/back dermis of Mlkl-/-Ripk1-/- E19.5 mice16 and immortalized as described 396 397 above. MDF lines were generated in accordance with protocols approved by the Walter and Eliza Hall Institute of Medical Research Animal Ethics Committee. Cell line identities were not further 398 399 validated, although their morphologies and responses to necroptotic stimuli were consistent with their 400 stated origins. Cell lines were routinely monitored to confirm they were mycoplasma-free.

401

402 *Cell culture* – HT29 cells were maintained in Dulbecco's Modified Eagle Medium (DMEM; Life 403 Technologies) containing 8% v/v heat-inactivated fetal calf serum (FCS), 2 mM L-Glutamine/-404 GlutaMAX (ThermoFisher Scientific 35050061), 50 U ml<sup>-1</sup> penicillin and 50 U ml<sup>-1</sup> streptomycin 405 (G/P/S) under humidified 10% CO<sub>2</sub> at 37°C.

407	Cell Treatment – Cells were seeded into Ibi-treated 8-well µ-slides (Ibidi 80826) in media containing
408	8% v/v FCS and G/P/S at $3.0 \times 10^4$ cells per well for HT29 and 0.25 x $10^4$ cells per well for MDFs.
409	Cells were left to adhere overnight then treated in media containing 1% v/v FCS and G/P/S and
410	supplemented with the following stimuli: 100ng/mL recombinant human TNF- $\alpha$ -Fc (produced in-
411	house as in ref. <sup>69</sup> ), 500nM Smac mimetic/Compound A (provided by Tetralogic Pharmaceuticals; as
412	in ref. <sup>70</sup> ), 5µM IDN-6556 (provided by Tetralogic Pharmaceuticals). Unless stipulated, HT29 cells
413	were stimulated for 7.5 h with TSI and MDF cells were stimulated for 90 min with TSI.

*LDH release* – Colorimetric LDH release assay kit (Promega G1780) was performed according to
416 manufacturer's instructions.

Whole cell lysate, SDS-PAGE, immunoblot & quantification - Cells were lysed in ice-cold RIPA buffer (10mM Tris-HCl pH 8.0, 1mM EGTA, 2mM MgCl<sub>2</sub>, 0.5% v/v Triton X100, 0.1% w/v Na deoxycholate, 0.5% w/v SDS and 90mM NaCl) supplemented with 1x Protease & Phosphatase Inhibitor Cocktail (Cell Signaling Technology 5872S) and 100U/mL Benzonase (Sigma-Aldrich E1014). Whole cell lysates were boiled for 10 minutes in 1× SDS Laemmli sample buffer (126 mM Tris-HCl, pH 8, 20% v/v glycerol, 4% w/v SDS, 0.02% w/v bromophenol blue, 5% v/v 2mercaptoethanol), and resolved on 1.5mm NuPAGE 4-12% Bis-Tris gels (ThermoFisher Scientific NP0335BOX) using MES Running buffer (ThermoFisher Scientific NP000202) or Bio-Rad Criterion TGX 4-15% gels (Bio-Rad 5678085) using 1x TGS buffer (Bio-Rad 1610772). After transfer onto nitrocellulose, membranes were blocked in 5% w/v skim milk powder in TBS-T, probed with primary antibodies (see Materials above) then the appropriate HRP-conjugated secondary antibody (see Materials above) and signals revealed by enhanced chemiluminescence (Merck P90720) on a ChemiDoc Touch Imaging System (Bio-Rad). Between each probe, membranes were incubated in 

431 stripping buffer (200mM glycine pH 2.9, 1% w/v SDS, 0.5mM TCEP) for 30 minutes at room
432 temperature then re-blocked.

433

Subcellular fractionation, BN-PAGE & immunoblot – HT29 cells or MDFs were seeded into 6-well 434 plates ( $1.0 \times 10^6$  cells per well) in media containing 8% v/v FCS and G/P/S and equilibrated overnight 435 under humidified 10% CO<sub>2</sub> at 37 °C conditions. Cells were then treated in media containing 1% FCS 436 437 and G/P/S supplemented with the agonists (as indicated above). Cells were fractionated into cytoplasmic and membrane fractions<sup>35</sup>. Cells were permeabilized in MELB buffer (20 mM HEPES 438 439 pH 7.5, 100 mM KCl, 2.5 mM MgCl<sub>2</sub> and 100 mM sucrose, 0.025% v/v digitonin, 2 µM N-ethyl maleimide, phosphatase and protease inhibitors). Crude membrane and cytoplasmic fractions were 440 separated by centrifugation (5 minutes 11,000g), and fractions prepared in buffers to a final 441 442 concentration of 1% w/v digitonin. The samples were resolved on a 4-16% Bis-Tris Native PAGE 443 gel (ThermoFisher), transferred to polyvinylidene difluoride (Merck IPVH00010). After transfer, membranes were destained (in 50% (v/v) methanol, 25% (v/v) acetic acid), denatured (in 6M 444 445 Guanidine hydrochloride, 10 mM Tris pH6.8, 5 mM β-mercaptoethanol), blocked in 5% skim milk 446 (Diploma), and probed in the same manner as above.

447

**Protein production and purification** – Full-length human and mouse MLKL and the C-terminal, 448 449 pseudokinase domain of mouse and human MLKL were expressed in Sf21 insect cells using the Bacto-Bac system (ThermoFisher Scientific) and purified using established procedures<sup>28, 37, 42</sup>. Briefly, 450 proteins were expressed with an N-terminal, TEV protease-cleavable GST (full length human MLKL) 451 452 or His<sub>6</sub> (full length mouse MLKL and pseudokinase domains) tags and captured from lysates using 453 glutathione resin (UBP Bio) or HisTag Ni-NTA resin (Roche) respectively. Proteins were cleaved 454 on-resin from the GST tag or off-resin for His<sub>6</sub> tags using His-tagged TEV protease, before protease 455 was removed by Ni-NTA chromatography (HisTag resin, Roche). Protein was concentrated by

456 centrifugal ultrafiltration and applied to a Superdex-200 (GE Healthcare) size exclusion 457 chromatography column; protein was eluted in 20 mM HEPES pH 7.5, 200 mM NaCl, 5% v/v 458 glycerol. Protein containing fractions were spin concentrated to 5-10 mg/mL, aliquoted, snap frozen 459 in liquid N<sub>2</sub> and stored at  $-80^{\circ}$ C until required.

460

461 Immunofluorescence – Cells in 8-well µ-Slides (Ibidi 80826) were ice-chilled for 3 minutes, then washed in ice-cold Dulbecco's PBS (dPBS; ThermoFisher Scientific 14190144), then fixed for 30 462 463 minutes in either ice-cold methanol or ice-cold 4% w/v PFA. Cells were washed twice in ice-cold 464 dPBS, then blocked in ice-cold Tris-balanced salt solution with 0.05% v/v Triton-X100 (TBS-T) 465 supplemented with 10% v/v donkey serum (Sigma-Aldrich D9663) for >1 hour. Cells were incubated in primary antibodies (see *Materials* above) overnight at 4 °C in TBS-T with 10% v/v donkey serum. 466 467 Cells were washed twice in TBS-T then incubated in the appropriate secondary antibodies 468 supplemented with 0.1µg/mL Hoechst 33342 (ThermoFisher Scientific H3570) for 3 hours at room temperature with gentle rocking. Cells were washed four times in ice-cold TBS-T then stored at 4 °C 469 until imaged. Where indicated, to demarcate the plasma membrane, 2µL of biotinylated wheat germ 470 agglutinin (Sigma-Aldrich L5142) was added to each well 10 minutes before fixation. The fixed 471 472 wheat germ agglutinin was then detected via the addition of 1:1000 dilution of DyLight650-473 conjugated streptavidin (ThermoFisher Scientific 84547) during the secondary antibody incubation 474 step.

475

476 *Two-dimensional epifluorescence microscopy* - Samples in TBS-T were imaged on an Inverted Axio 477 Observer.Z1 microscope (Zeiss) with the following specifications: C-Apochromat 40x/1.20 W 478 autocorr UV VIS IR lens, HXP 120V excitation source, AlexaFluor647 and DyLight650 imaged with 479 a  $\lambda_{\text{Excitation}}$ =625-655nm;  $\lambda_{\text{beamsplitter}}$ =660nm;  $\lambda_{\text{Emission}}$ =665-715nm filter, AlexaFluor568 imaged with a 480  $\lambda_{\text{Excitation}}$ =532-544nm;  $\lambda_{\text{beamsplitter}}$ =560nm;  $\lambda_{\text{Emission}}$ =573-613nm, AlexaFluor488 imaged with a 481  $\lambda_{\text{Excitation}}=450-490$ nm;  $\lambda_{\text{beamsplitter}}=495$ nm;  $\lambda_{\text{Emission}}=500-550$ nm, Hoechst 33342 imaged with a 482  $\lambda_{\text{Excitation}}=359-371$ nm;  $\lambda_{\text{beamsplitter}}=395$ nm;  $\lambda_{\text{Emission}}=397-\infty$  nm, a sCMOS PCO.edge 4.2 camera, ZEN 483 blue 2.5 pro capture software and ImageJ 1.53c post-acquisition processing software<sup>71</sup>. Typically, for 484 each independent experiment, 5-10 randomly selected fields were captured per treatment group, 485 whereby only the Hoechst 33342 signal was visualised prior to multi-channel acquisition. To ensure 486 consistent signal intensities across independent experiments, the same excitation, emission and 487 camera settings were used throughout this study.

488

Airyscan microscopy - Fixed immunostained cells in 8-well µ-Slides (Ibidi 80827) were subjected 489 490 to super-resolution 3-dimensional Airyscan microscopy on an Inverted LSM 880 platform (Zeiss) 491 equipped with the following specifications: a 63x/1.4 N.A. PlanApo DIC M27 oil immersion objective (Zeiss), 405-, 488-, 568- and 640-nm laser lines, and radially-stacked Airyscan GaASP 492 493 detectors set to SR-mode, 405-, 488-, 561-, 633-nm laser lines and ZEN black 2.3 SP1 FP3 v14.0 494 capture software. Image stacks were acquired with a z-step size of 159nm. Super-resolution 495 deconvolution was performed using the automated '3D AiryScan Processing' function of ZEN blue 496 software.

497

*Hotspot quantitation* – Micrographs (captured as in *two-dimensional epifluorescence microscopy*) 498 499 were opened in ImageJ 1.53c<sup>71</sup>. A rolling ball filter of 7 was applied and phospho-S358 MLKL 500 immunosignals thresholded (≥7000 units) and objects segmented using the 'Analyze>Analyze 501 Particles' tool. Segmented objects with size 0.5-100µm<sup>2</sup> and feret diameter>2 (i.e. elliptical objects) were considered hotspots. The number of segmented objects per 100 cells was taken as an index of 502 503 hotspot occurrence. The mean size of the segmented objects was taken as an index of hotspot size. 504 The fluorescence intensity of each segmented object divided by its size was taken as an index of 505 hotspot intensity.

506

#### 507 ACKNOWLEDGEMENTS

# We thank the Walter and Eliza Hall Institute Monoclonal Antibody Facility for their assistance generating clones 3H1, 10C2, 7G2, 1H2, 5A6, 8G7 and 1H12; and Cathrine Hall for assistance generating *Mlkl*<sup>-/-</sup> *Ripk1*<sup>-/-</sup> MDF lines. We are grateful to the Australian National Health and Medical

- 511 Research Council for fellowship (J.M.H., 1142669; E.D.H., 1159488; J.M.M., 1172929), grant
- 512 (1124735, 1124737, and 1105023), and infrastructure (IRIISS 9000587) support, with additional
- 513 support from the CASS Foundation (A.L.S.) and the Victorian Government Operational
- 514 Infrastructure Support scheme. We acknowledge the support for A.V.J. from an Australian Research
- 515 Training Program Scholarship.
- 516

### 517 AUTHOR CONTRIBUTIONS

- 518 Investigation: A.L.S., K.P., C.F., J.M.H., L.W., J.R., A.V.J., C.R.H., X.G., S.N.Y. Supervision and
- 519 Methodology: A.L.S., J.M.H., K.L.R., E.D.H. and J.M.M.; Conceptualization: A.L.S., E.D.H. and
- 520 J.M.M.; Writing Original Draft: A.L.S. and J.M.M.; Writing Review & Editing: all authors.
- 521

# 522 COMPETING INTERESTS

- 523 A.L.S., K.P. C.F., J.M.H., S.N.Y. and J.M.M. contribute to a project developing necroptosis inhibitors
- 524 in collaboration with Anaxis Pharma. The other authors declare no competing interests.
- 525

# 526 MATERIALS REQUESTS

- All materials will be provided under Materials Transfer Agreement upon request to James Murphy
  (jamesm@wehi.edu.au).
- 529

```
530 REFERENCES
```

532	1.	Cho YS, Challa S, Moquin D, Genga R, Ray TD, Guildford M, et al. Phosphorylation-driven
533		assembly of the RIP1-RIP3 complex regulates programmed necrosis and virus-induced
534		inflammation. Cell 2009, 137(6): 1112-1123.
535		
536	2.	Guo H, Omoto S, Harris PA, Finger JN, Bertin J, Gough PJ, et al. Herpes simplex virus
537		suppresses necroptosis in human cells. Cell Host Microbe 2015, 17(2): 243-251.
538		
539	3.	Pearson JS, Giogha C, Muhlen S, Nachbur U, Pham CL, Zhang Y, et al. EspL is a bacterial
540		cysteine protease effector that cleaves RHIM proteins to block necroptosis and inflammation.
541		<i>Nat Microbiol</i> 2017, <b>2:</b> 16258.
542		
543	4.	Pearson JS, Murphy JM. Down the rabbit hole: Is necroptosis truly an innate response to
544		infection? Cell Microbiol 2017, 19(8): e12750.
545		
546	5.	Petrie EJ, Sandow JJ, Lehmann WIL, Liang LY, Coursier D, Young SN, et al. Viral MLKL
547		Homologs Subvert Necroptotic Cell Death by Sequestering Cellular RIPK3. Cell reports
548		2019, <b>28</b> (13): 3309-3319 e3305.
549		
550	6.	Fletcher-Etherington A, Nobre L, Nightingale K, Antrobus R, Nichols J, Davison AJ, et al.
551		Human cytomegalovirus protein pUL36: A dual cell death pathway inhibitor. Proc Natl Acad
552		<i>Sci U S A</i> 2020, <b>117</b> (31): 18771-18779.
553		
554	7.	Kitur K, Wachtel S, Brown A, Wickersham M, Paulino F, Penaloza HF, et al. Necroptosis
555		Promotes Staphylococcus aureus Clearance by Inhibiting Excessive Inflammatory Signaling.
556		<i>Cell reports</i> 2016, <b>16</b> (8): 2219-2230.
557		
558	8.	Shubina M, Tummers B, Boyd DF, Zhang T, Yin C, Gautam A, et al. Necroptosis restricts
559		influenza A virus as a stand-alone cell death mechanism. <i>J Exp Med</i> 2020, <b>217</b> (11).
560		
561	9.	Simpson J, Loh Z, Ullah MA, Lynch JP, Werder RB, Collinson N, et al. Respiratory Syncytial
562		Virus Infection Promotes Necroptosis and HMGB1 Release by Airway Epithelial Cells. Am
563		J Respir Crit Care Med 2020, <b>201</b> (11): 1358-1371.
564		

565	10.	Muller T, Dewitz C, Schmitz J, Schroder AS, Brasen JH, Stockwell BR, et al. Necroptosis
566		and ferroptosis are alternative cell death pathways that operate in acute kidney failure. Cell
567		Mol Life Sci 2017, 74(19): 3631-3645.

- 568
- 569 11. Pefanis A, Ierino FL, Murphy JM, Cowan PJ. Regulated necrosis in kidney ischemia570 reperfusion injury. *Kidney Int* 2019, 96(2): 291-301.
- 571
- 572 12. Luedde M, Lutz M, Carter N, Sosna J, Jacoby C, Vucur M, *et al.* RIP3, a kinase promoting
  573 necroptotic cell death, mediates adverse remodelling after myocardial infarction. *Cardiovasc*574 *Res* 2014, **103**(2): 206-216.
- 575
- 576 13. Hildebrand JM, Kauppi M, Majewski IJ, Liu Z, Cox AJ, Miyake S, *et al.* A missense mutation
  577 in the MLKL brace region promotes lethal neonatal inflammation and hematopoietic
  578 dysfunction. *Nat Commun* 2020, **11**(1): 3150.
- Wang H, Sun L, Su L, Rizo J, Liu L, Wang LF, *et al.* Mixed Lineage Kinase Domain-like
  Protein MLKL Causes Necrotic Membrane Disruption upon Phosphorylation by RIP3. *Mol Cell* 2014, 54(1): 133-146.
- 583

579

# 15. Rickard JA, Anderton H, Etemadi N, Nachbur U, Darding M, Peltzer N, *et al.* TNFR1dependent cell death drives inflammation in Sharpin-deficient mice. *Elife* 2014, 3: e03464.

- 586
- 16. Rickard JA, O'Donnell JA, Evans JM, Lalaoui N, Poh AR, Rogers TW, *et al.* RIPK1 regulates
  RIPK3-MLKL driven systemic inflammation and emergency hematopoiesis. *Cell* 2014,
  157(2): 1175-1188.
- 590

591 17. Pierdomenico M, Negroni A, Stronati L, Vitali R, Prete E, Bertin J, *et al.* Necroptosis is active
592 in children with inflammatory bowel disease and contributes to heighten intestinal
593 inflammation. *Am J Gastroenterol* 2014, **109**(2): 279-287.

- 594
- He S, Wang L, Miao L, Wang T, Du F, Zhao L, *et al.* Receptor interacting protein kinase-3
  determines cellular necrotic response to TNF-alpha. *Cell* 2009, **137**(6): 1100-1111.
- 597

598	19.	Zhang DW, Shao J, Lin J, Zhang N, Lu BJ, Lin SC, et al. RIP3, an energy metabolism
599		regulator that switches TNF-induced cell death from apoptosis to necrosis. Science 2009,
600		<b>325</b> (5938): 332-336.
601		
602	20.	Sun L, Wang H, Wang Z, He S, Chen S, Liao D, et al. Mixed lineage kinase domain-like
603		protein mediates necrosis signaling downstream of RIP3 kinase. Cell 2012, 148(1-2): 213-
604		227.
605		
606	21.	Zhao J, Jitkaew S, Cai Z, Choksi S, Li Q, Luo J, et al. Mixed lineage kinase domain-like is a
607		key receptor interacting protein 3 downstream component of TNF-induced necrosis. Proc
608		Natl Acad Sci US A 2012, 109(14): 5322-5327.
609		
610	22.	Wang T, Perera ND, Chiam MDF, Cuic B, Wanniarachchillage N, Tomas D, et al.
611		Necroptosis is dispensable for motor neuron degeneration in a mouse model of ALS. Cell
612		Death Differ 2019.
613		
614	23.	Dermentzaki G, Politi KA, Lu L, Mishra V, Perez-Torres EJ, Sosunov AA, et al. Deletion of
615		Ripk3 Prevents Motor Neuron Death In Vitro but not In Vivo. eNeuro 2019, 6(1).
616		
617	24.	Dominguez S, Varfolomeev E, Brendza R, Stark K, Tea J, Imperio J, et al. Genetic
618		inactivation of RIP1 kinase does not ameliorate disease in a mouse model of ALS. Cell Death
619		<i>Differ</i> 2020.
620		
621	25.	Dara L, Johnson H, Suda J, Win S, Gaarde W, Han D, et al. Receptor interacting protein
622		kinase 1 mediates murine acetaminophen toxicity independent of the necrosome and not
623		through necroptosis. <i>Hepatology</i> 2015, <b>62</b> (6): 1847-1857.
624		
625	26.	Petrie EJ, Birkinshaw RW, Koide A, Denbaum E, Hildebrand JM, Garnish SE, et al.
626		Identification of MLKL membrane translocation as a checkpoint in necroptotic cell death
627		using Monobodies. Proc Natl Acad Sci USA 2020, 117(15): 8468-8475.
628		
629	27.	Petrie EJ, Czabotar PE, Murphy JM. The Structural Basis of Necroptotic Cell Death
630		Signaling. Trends Biochem Sci 2019, 44(1): 53-63.
631		

632	28.	Petrie EJ, Sandow JJ, Jacobsen AV, Smith BJ, Griffin MDW, Lucet IS, <i>et al.</i> Conformational
633		switching of the pseudokinase domain promotes human MLKL tetramerization and cell death
634		by necroptosis. <i>Nat Commun</i> 2018, <b>9</b> (1): 2422.
635 635	20	Samaan AL Zhang V. Caashagan ND. Cavin VI. Davias KA. Mladrianashi MI. at al MI.KI
636	29.	Samson AL, Zhang Y, Geoghegan ND, Gavin XJ, Davies KA, Mlodzianoski MJ, et al. MLKL
637 638		trafficking and accumulation at the plasma membrane control the kinetics and threshold for
638		necroptosis. <i>Nat Commun</i> 2020, <b>11</b> (1): 3151.
639	20	
640	30.	Li J, McQuade T, Siemer AB, Napetschnig J, Moriwaki K, Hsiao YS, et al. The RIP1/RIP3
641		necrosome forms a functional amyloid signaling complex required for programmed necrosis.
642		<i>Cell</i> 2012, <b>150</b> (2): 339-350.
643	21	
644	31.	Mompean M, Li W, Li J, Laage S, Siemer AB, Bozkurt G, et al. The Structure of the
645		Necrosome RIPK1-RIPK3 Core, a Human Hetero-Amyloid Signaling Complex. <i>Cell</i> 2018,
646		<b>173</b> (5): 1244-1253 e1210.
647	22	
648	32.	Sun X, Yin J, Starovasnik MA, Fairbrother WJ, Dixit VM. Identification of a novel homotypic
649		interaction motif required for the phosphorylation of receptor-interacting protein (RIP) by
650		RIP3. J Biol Chem 2002, 277(11): 9505-9511.
651	22	
652	33.	Cook WD, Moujalled DM, Ralph TJ, Lock P, Young SN, Murphy JM, et al. RIPK1- and
653		RIPK3-induced cell death mode is determined by target availability. <i>Cell Death Differ</i> 2014,
654		<b>21</b> (10): 1600-1612.
655		
656	34.	Orozco S, Yatim N, Werner MR, Tran H, Gunja SY, Tait SW, et al. RIPK1 both positively
657		and negatively regulates RIPK3 oligomerization and necroptosis. Cell Death Differ 2014,
658		<b>21</b> (10): 1511-1521.
659		
660	35.	Hildebrand JM, Tanzer MC, Lucet IS, Young SN, Spall SK, Sharma P, et al. Activation of
661		the pseudokinase MLKL unleashes the four-helix bundle domain to induce membrane
662		localization and necroptotic cell death. Proc Natl Acad Sci U S A 2014, 111(42): 15072-
663		15077.
664		

665 36. Murphy JM. The Killer Pseudokinase Mixed Lineage Kinase Domain-Like Protein (MLKL).
666 *Cold Spring Harb Perspect Biol* 2020, 12(8).

- 667
- Murphy JM, Czabotar PE, Hildebrand JM, Lucet IS, Zhang JG, Alvarez-Diaz S, *et al.* The
  pseudokinase MLKL mediates necroptosis via a molecular switch mechanism. *Immunity*2013, 39(3): 443-453.
- 671

- Tanzer MC, Tripaydonis A, Webb AI, Young SN, Varghese LN, Hall C, *et al.* Necroptosis
  signalling is tuned by phosphorylation of MLKL residues outside the pseudokinase domain
  activation loop. *The Biochemical journal* 2015, **471**(2): 255-265.
- 876 39. Rodriguez DA, Weinlich R, Brown S, Guy C, Fitzgerald P, Dillon CP, *et al.* Characterization
  877 of RIPK3-mediated phosphorylation of the activation loop of MLKL during necroptosis. *Cell*878 *Death Differ* 2016, 23(1): 76-88.
- 679
- Garnish SE, Meng Y, Koide A, Sandow JJ, Denbaum E, Jacobsen AV, *et al.* Conformational
  interconversion of MLKL and disengagement from RIPK3 precedes cell death by necroptosis.
  Under review.
- 683
- 41. Davies KA, Fitzgibbon C, Young SN, Garnish SE, Yeung W, Coursier D, *et al.* Distinct
  pseudokinase domain conformations underlie divergent activation mechanisms among
  vertebrate MLKL orthologues. *Nat Commun* 2020, **11**(1): 3060.
- 687
- Murphy JM, Lucet IS, Hildebrand JM, Tanzer MC, Young SN, Sharma P, *et al.* Insights into
  the evolution of divergent nucleotide-binding mechanisms among pseudokinases revealed by
  crystal structures of human and mouse MLKL. *The Biochemical journal* 2014, **457**(3): 369377.
- 692
- 43. Tanzer MC, Matti I, Hildebrand JM, Young SN, Wardak A, Tripaydonis A, *et al.*Evolutionary divergence of the necroptosis effector MLKL. *Cell Death Differ* 2016, 23(7):
  1185-1197.
- 696

697	44.	Davies KA, Tanzer MC, Griffin MDW, Mok YF, Young SN, Qin R, et al. The brace helices
698		of MLKL mediate interdomain communication and oligomerisation to regulate cell death by
699		necroptosis. Cell Death Differ 2018, 25(9): 1567-1580.
700		
701	45.	Dondelinger Y, Hulpiau P, Saeys Y, Bertrand MJM, Vandenabeele P. An evolutionary
702		perspective on the necroptotic pathway. Trends Cell Biol 2016, 26(10): 721-732.
703		
704	46.	Newton K, Manning G. Necroptosis and Inflammation. Annu Rev Biochem 2016, 85: 743-
705		763.
706		
707	47.	Petrie EJ, Birkinshaw RW, Koide A, Denbaum E, Hildebrand JM, Garnish SE, et al.
708		Identification of MLKL membrane translocation as a checkpoint in necroptotic cell death
709		using Monobodies. Proc Natl Acad Sci USA 2020.
710		
711	48.	Wang H, Sun L, Su L, Rizo J, Liu L, Wang LF, et al. Mixed lineage kinase domain-like
712		protein MLKL causes necrotic membrane disruption upon phosphorylation by RIP3. Mol Cell
713		2014, <b>54</b> (1): 133-146.
714		
715	49.	Cai Z, Jitkaew S, Zhao J, Chiang HC, Choksi S, Liu J, et al. Plasma membrane translocation
716		of trimerized MLKL protein is required for TNF-induced necroptosis. Nature cell biology
717		2014, <b>16</b> (1): 55-65.
718		
719	50.	Chen X, Li W, Ren J, Huang D, He WT, Song Y, et al. Translocation of mixed lineage kinase
720		domain-like protein to plasma membrane leads to necrotic cell death. Cell research 2014,
721		<b>24</b> (1): 105-121.
722		
723	51.	Alturki NA, McComb S, Ariana A, Rijal D, Korneluk RG, Sun SC, et al. Triad3a induces the
724		degradation of early necrosome to limit RipK1-dependent cytokine production and
725		necroptosis. Cell Death Dis 2018, 9(6): 592.
726		
727	52.	Simpson DS, Gabrielyan A, Feltham R. RIPK1 ubiquitination: Evidence, correlations and the
728		undefined. Semin Cell Dev Biol 2020.
729		

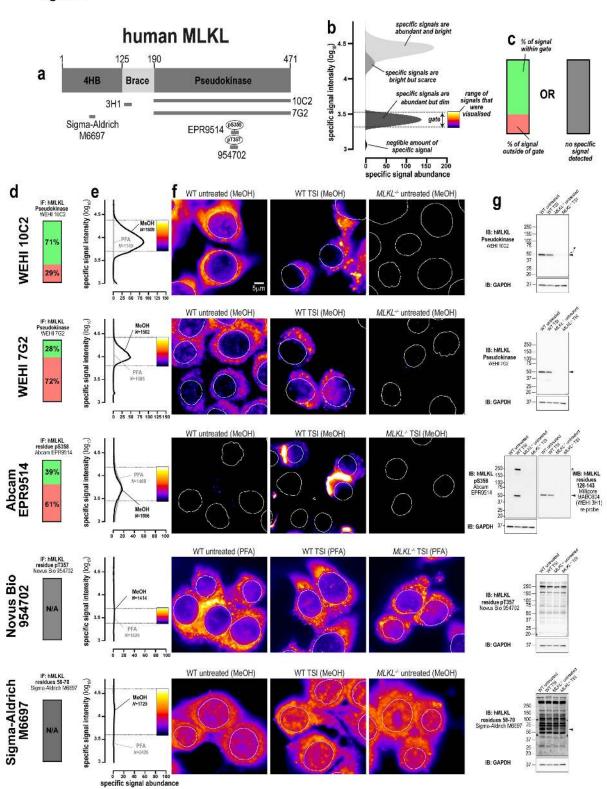
- 730 53. Newton K, Wickliffe KE, Maltzman A, Dugger DL, Strasser A, Pham VC, *et al.* RIPK1
  731 inhibits ZBP1-driven necroptosis during development. *Nature* 2016, **540**(7631): 129-133.
- 732
- 54. Hoetelmans RW, Prins FA, Cornelese-ten Velde I, van der Meer J, van de Velde CJ, van
  Dierendonck JH. Effects of acetone, methanol, or paraformaldehyde on cellular structure,
  visualized by reflection contrast microscopy and transmission and scanning electron
  microscopy. *Appl Immunohistochem Mol Morphol* 2001, 9(4): 346-351.
- 737
- Moloney M, McDonnell L, O'Shea H. Atomic force microscopy of BHK-21 cells: an
  investigation of cell fixation techniques. *Ultramicroscopy* 2004, **100**(3-4): 153-161.
- 740
- 56. Whelan DR, Bell TD. Correlative Synchrotron Fourier Transform Infrared Spectroscopy and
  Single Molecule Super Resolution Microscopy for the Detection of Composition and
  Ultrastructure Alterations in Single Cells. *ACS Chem Biol* 2015, **10**(12): 2874-2883.
- 744
- 745 57. Xu X, Kalac M, Markson M, Chan M, Brody JD, Bhagat G, *et al.* Reversal of CYLD
  746 phosphorylation as a novel therapeutic approach for adult T-cell leukemia/lymphoma
  747 (ATLL). *Cell Death Dis* 2020, 11(2): 94.
- 748
- Yang C, Li J, Yu L, Zhang Z, Xu F, Jiang L, *et al.* Regulation of RIP3 by the transcription
  factor Sp1 and the epigenetic regulator UHRF1 modulates cancer cell necroptosis. *Cell Death Dis* 2017, 8(10): e3084.
- 752
- 59. Wang S, Ni HM, Dorko K, Kumer SC, Schmitt TM, Nawabi A, *et al.* Increased hepatic
  receptor interacting protein kinase 3 expression due to impaired proteasomal functions
  contributes to alcohol-induced steatosis and liver injury. *Oncotarget* 2016, 7(14): 1768117698.
- 757
- 758 60. Zhang S, Che L, He C, Huang J, Guo N, Shi J, *et al.* Drp1 and RB interaction to mediate
  759 mitochondria-dependent necroptosis induced by cadmium in hepatocytes. *Cell Death Dis*760 2019, 10(7): 523.
- 761
- Ali M, Mocarski ES. Proteasome inhibition blocks necroptosis by attenuating death complex
  aggregation. *Cell Death Dis* 2018, 9(3): 346.

764		
765	62.	Gong YN, Guy C, Olauson H, Becker JU, Yang M, Fitzgerald P, et al. ESCRT-III Acts
766		Downstream of MLKL to Regulate Necroptotic Cell Death and Its Consequences. Cell 2017,
767		<b>169</b> (2): 286-300 e216.
768		
769	63.	Yoon S, Bogdanov K, Kovalenko A, Wallach D. Necroptosis is preceded by nuclear
770		translocation of the signaling proteins that induce it. Cell Death Differ 2016, 23(2): 253-260.
771		
772	64.	Wang Z, Jiang H, Chen S, Du F, Wang X. The mitochondrial phosphatase PGAM5 functions
773		at the convergence point of multiple necrotic death pathways. Cell 2012, 148(1-2): 228-243.
774		
775	65.	Mizumura K, Cloonan SM, Nakahira K, Bhashyam AR, Cervo M, Kitada T, et al. Mitophagy-
776		dependent necroptosis contributes to the pathogenesis of COPD. J Clin Invest 2014, 124(9):
777		3987-4003.
778		
779	66.	Samson AL, Garnish SE, Hildebrand JM, Murphy JM. Location, location, location: a
780		compartmentalized view of necroptotic signaling. Under review.
781		
782	67.	Tanzer MC, Khan N, Rickard JA, Etemadi N, Lalaoui N, Spall SK, et al. Combination of IAP
783		antagonist and IFNgamma activates novel caspase-10- and RIPK1-dependent cell death
784		pathways. Cell Death Differ 2017, 24(3): 481-491.
785		
786	68.	Newton K, Sun X, Dixit VM. Kinase RIP3 is dispensable for normal NF-kappa Bs, signaling
787		by the B-cell and T-cell receptors, tumor necrosis factor receptor 1, and Toll-like receptors 2
788		and 4. Mol Cell Biol 2004, 24(4): 1464-1469.
789		
790	69.	Bossen C, Ingold K, Tardivel A, Bodmer JL, Gaide O, Hertig S, et al. Interactions of tumor
791		necrosis factor (TNF) and TNF receptor family members in the mouse and human. J Biol
792		Chem 2006, <b>281</b> (20): 13964-13971.
793		
794	70.	Vince JE, Wong WW, Khan N, Feltham R, Chau D, Ahmed AU, et al. IAP antagonists target
795		cIAP1 to induce TNFalpha-dependent apoptosis. Cell 2007, 131(4): 682-693.
796		

- 797 71. Schneider CA, Rasband WS, Eliceiri KW. NIH Image to ImageJ: 25 years of image analysis.
  798 *Nat Methods* 2012, 9(7): 671-675.
- 799

#### 801 FIGURES LEGENDS

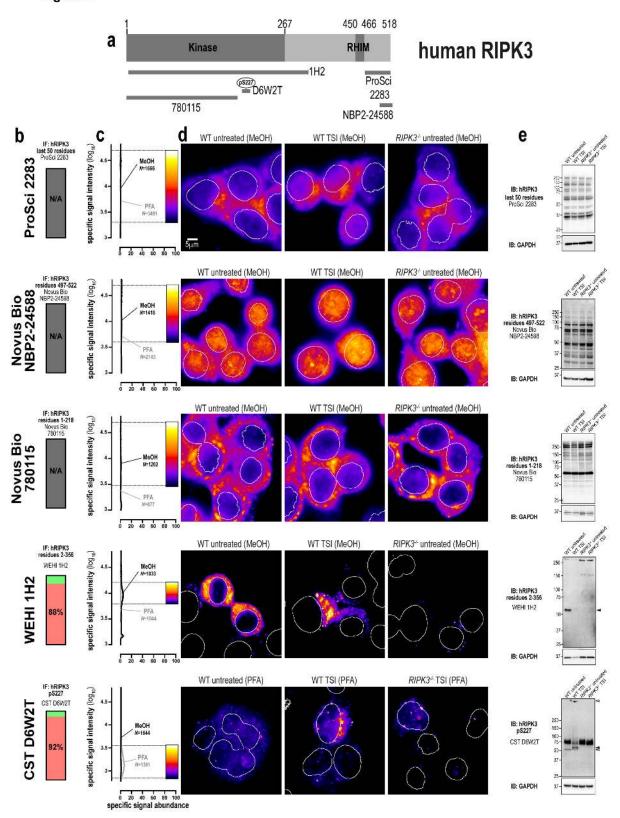




#### 803 Figure 1: Methanol fixation is optimal for the immunofluorescent detection of human MLKL

804 a Human MLKL domain architecture showing the immunogens used to raise the tested anti-MLKL 805 antibodies. **b** Demonstration of how signal-to-noise ratios were used to quantify the abundance and brightness of specific immunofluorescent signals generated by different antibodies. The 5th and 95th 806 807 percentile of each signal-to-noise curve defines the gate where specific immunosignals were observed. As indicated by the pseudocolour look-up-table, only immunosignals within this gate were 808 809 visualised. c Chart exemplifying how the amount of signal within the gate, relative to the total amount of detectable signal, provides another gauge of antibody specificity for immunofluorescence. d 810 811 Quantitation of the percentage of gated signals for the tested MLKL antibodies. e Quantitation of specific signal abundance produced by the tested MLKL antibodies on methanol-fixed (MeOH) or 812 paraformaldehyde-fixed (PFA) HT29 cells. The number of cells imaged (N) to generate each signal-813 814 to-noise curve is shown. f Micrographs of immunofluorescent signals for the tested MLKL antibodies 815 on HT29 cells. As indicated by each pseudocolour look-up-table, only immunosignals within the respective gate in panel e were visualised. Data are representative of n=3 (clones 10C2, 7G2) and 816 817 n=2 (Abcam clone EPR9514, Novus Biological MAB9187/clone 954702 and Sigma-Aldrich M6697) 818 independent experiments. Nuclei were detected by Hoechst 33342 staining and are demarked by white outlines in micrographs. g Immunoblot using the tested MLKL antibodies against wild-type 819 and MLKL<sup>-/-</sup> HT29 cell lysates. Closed arrowheads indicate the main specific band. Asterisks indicate 820 821 non-specific bands that could otherwise confound data interpretation. Immunoblots were re-probed 822 for GAPDH as loading control.

Figure 2

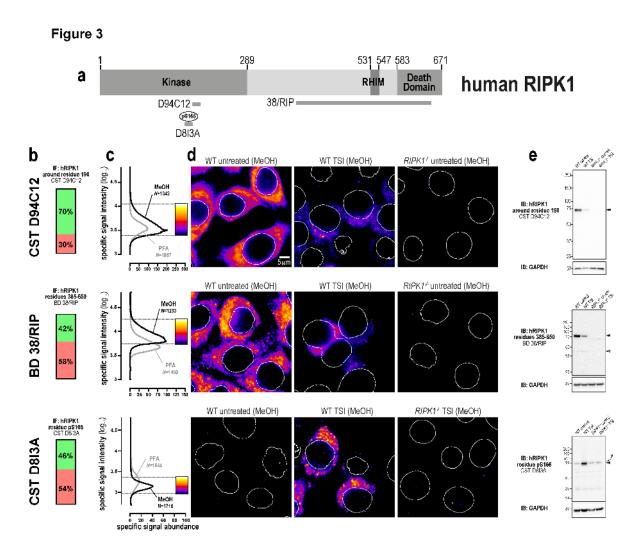


824

#### Figure 2: Better antibodies are needed for imaging human RIPK3.

a Human RIPK3 domain architecture showing the immunogens or epitopes for the tested anti-RIPK3 827 antibodies. b Quantitation of the percentage of gated signals for the tested RIPK3 antibodies. c 828 829 Quantitation of specific signal abundance produced by the tested RIPK3 antibodies on methanol-830 fixed (MeOH) or paraformaldehyde-fixed (PFA) HT29 cells. The number of cells imaged (N) to generate each signal-to-noise curve is shown. d Micrographs of immunofluorescent signals for the 831 832 tested RIPK3 antibodies on HT29 cells. As indicated by each pseudocolour look-up-table, only immunosignals within the respective gate in panel c were visualised. Data are representative of n=3 833 834 (Cell Signaling Technology clone D6W2T and in-house clone 1H2) and n=2 (ProSci 2283, Novus Biological NBP2-24588 and MAB7604/clone 780115) independent experiments. Nuclei were 835 detected by Hoechst 33342 staining and are demarked by white outlines in micrographs. e 836 837 Immunoblot using the tested RIPK3 antibodies against wild-type and RIPK3<sup>-/-</sup> HT29 cell lysates. 838 Closed arrowheads indicate the main specific band. Open arrowheads indicate other specific bands of interest. Immunoblots were re-probed for GAPDH as loading control. 839

840



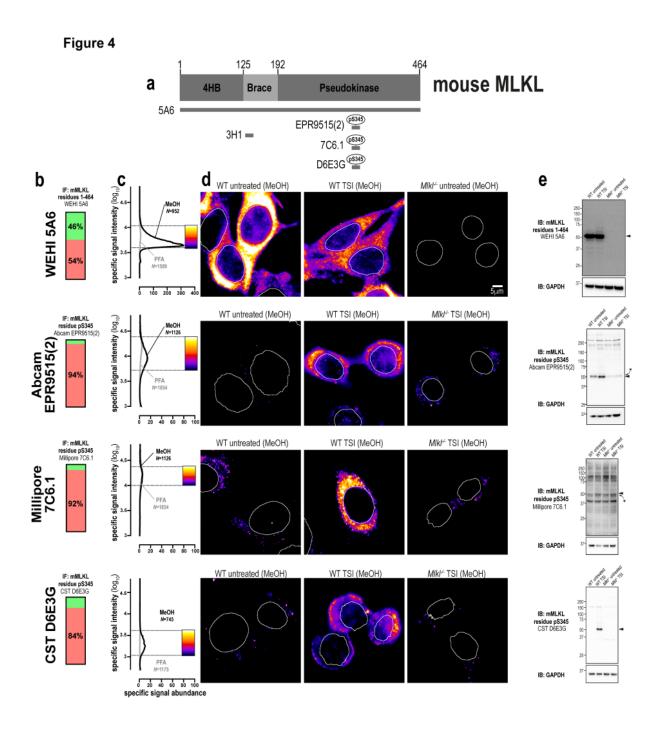
842

#### 843 Figure 3: Three specific antibodies for imaging endogenous human RIPK1.

844 a Human RIPK1 domain architecture showing the immunogens or epitopes for the tested anti-RIPK1 845 antibodies. b Quantitation of the percentage of gated signals for the tested RIPK1 antibodies. c Quantitation of specific signal abundance produced by the tested RIPK1 antibodies on methanol-846 847 fixed (MeOH) or paraformaldehyde-fixed (PFA) HT29 cells. The number of cells imaged (N) to generate each signal-to-noise curve is shown. d Micrographs of immunofluorescent signals for the 848 849 tested RIPK1 antibodies on HT29 cells. As indicated by each pseudocolour look-up-table, only 850 immunosignals within the respective gate in panel c were visualised. Data are representative of n=2 (Cell Signaling Technology clones D94C12 and D8I3A, BD Transduction laboratories clone 38/RIP) 851 852 independent experiments. Nuclei were detected by Hoechst 33342 staining and are demarked by

- 853 white outlines in micrographs. e Immunoblot using the tested RIPK1 antibodies against wild-type
- and *RIPK1<sup>-/-</sup>* HT29 cell lysates. Closed arrowheads indicate the main specific band. Open arrowheads
- 855 indicate other specific bands of interest. Asterisks indicate non-specific bands that could otherwise
- 856 confound data interpretation. Immunoblots were re-probed for GAPDH as loading control.

857



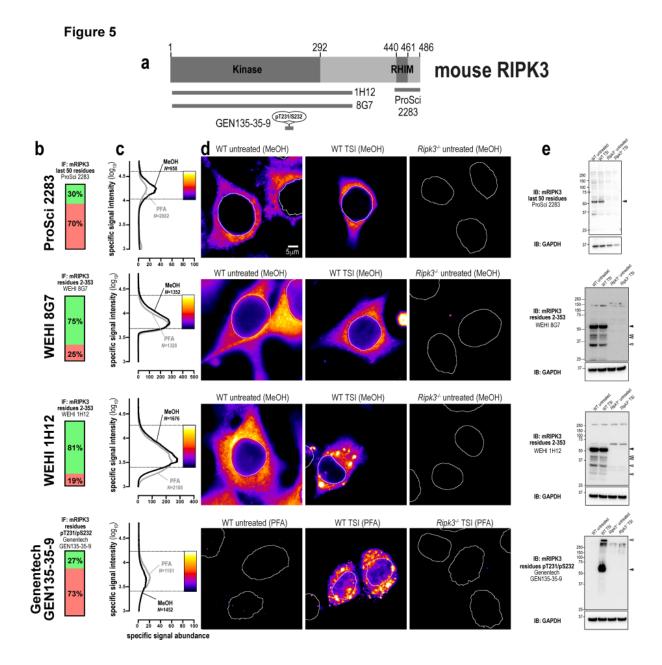




a Mouse MLKL domain architecture showing the immunogens or epitopes for the tested anti-MLKL
antibodies. b Quantitation of the percentage of gated signals for the tested MLKL antibodies. c
Quantitation of specific signal abundance produced by the tested MLKL antibodies on methanolfixed (MeOH) or paraformaldehyde-fixed (PFA) MDFs. The number of cells imaged (N) to generate
each signal-to-noise curve is shown. d Micrographs of immunofluorescent signals for the tested

866 MLKL antibodies on MDFs. As indicated by each pseudocolour look-up-table, only immunosignals 867 within the respective gate in panel c were visualised. Data are representative of n=3 (in-house clone 5A6) and n=2 (Abcam clone EPR9515(2), Millipore MABC1158/clone 7C6.1 and Cell Signaling 868 869 Technology clone D6E3G) independent experiments. Nuclei were detected by Hoechst 33342 870 staining and are demarked by white outlines in micrographs. e Immunoblot using the tested MLKL antibodies against lysates from wild-type and Mlkl-/- MDFs. Closed arrowheads indicate the main 871 specific band. Asterisks indicate non-specific bands that could otherwise confound data 872 873 interpretation. Immunoblots were re-probed for GAPDH as loading control.

874

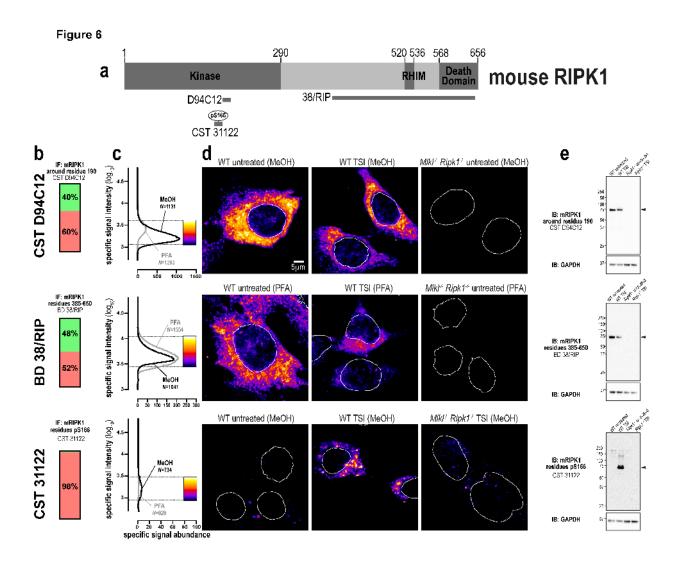


876

877 Figure 5: Unlike human RIPK3, mouse RIPK3 is highly amenable to detection by
878 immunofluorescence and immunoblotting.

a Mouse RIPK3 domain architecture showing the immunogens or epitopes for the tested anti-RIPK3
antibodies. b Quantitation of the percentage of gated signals for the tested RIPK3 antibodies. c
Quantitation of specific signal abundance produced by the tested RIPK3 antibodies on methanolfixed (MeOH) or paraformaldehyde-fixed (PFA) MDFs. The number of cells imaged (N) to generate
each signal-to-noise curve is shown. d Micrographs of immunofluorescent signals for the tested

884	RIPK3 antibodies on MDFs. As indicated by each pseudocolour look-up-table, only immunosignals
885	within the respective gate in panel $c$ were visualised. Data are representative of n=3 (in-house clone
886	8G7 and Genentech clone GEN135-35-9) and n=2 (ProSci 2283, in-house clone 1H12) independent
887	experiments. Nuclei were detected by Hoechst 33342 staining and are demarked by white outlines in
888	micrographs. e Immunoblot using the tested RIPK3 antibodies against lysates from wild-type and
889	Ripk3-/- MDFs. Closed arrowheads indicate the main specific band. Open arrowheads indicate other
890	specific bands of interest. Immunoblots were re-probed for GAPDH as loading control.



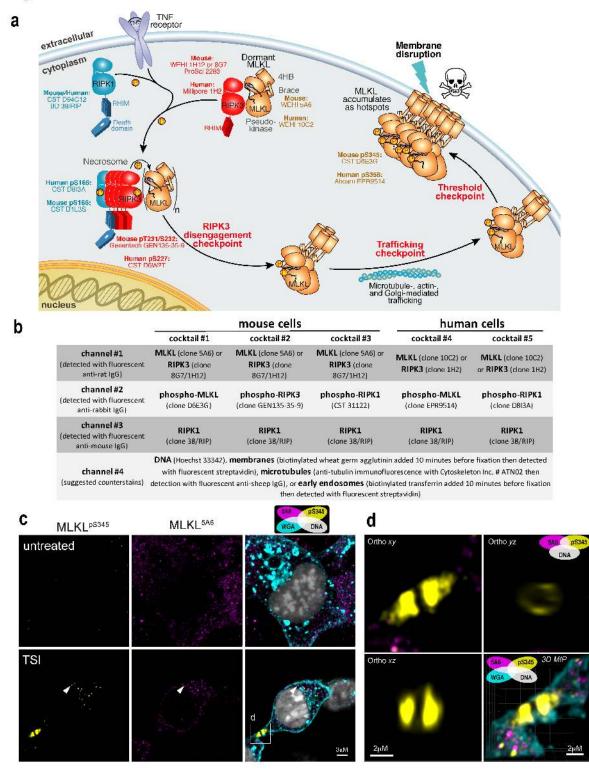
893



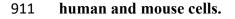
a Mouse RIPK1 domain architecture showing the immunogens or epitopes for the tested anti-RIPK1 895 antibodies. b Quantitation of the percentage of gated signals for the tested RIPK1 antibodies. c 896 897 Quantitation of specific signal abundance produced by the tested RIPK1 antibodies on methanolfixed (MeOH) or paraformaldehyde-fixed (PFA) MDFs. The number of cells imaged (N) to generate 898 899 each signal-to-noise curve is shown. d Micrographs of immunofluorescent signals for the tested RIPK1 antibodies on MDFs. As indicated by each pseudocolour look-up-table, only immunosignals 900 901 within the respective gate in panel c were visualised. Data are representative of n=2 (Cell Signaling Technology clones D94C12 and 31122, and BD Transduction Laboratories clone 38/RIP) 902 903 independent experiments. Nuclei were detected by Hoechst 33342 staining and are demarked by

white outlines in micrographs. e Immunoblot using the tested RIPK1 antibodies against lysates from
wild-type and *Ripk1-/-* MDFs. Closed arrowheads indicate the main specific band. Open arrowheads
indicate other specific bands of interest. Immunoblots were re-probed for GAPDH as loading control.





910 Figure 7: Optimised antibody cocktails for visualising endogenous necroptotic signaling in fixed



912 a Cartoon summary of the currently-understood chronology of TNF-induced necroptosis. 913 Recommendations of validated antibodies for immunostaining various steps in the necroptotic 914 pathway are provided. **b** Summary of validated antibody cocktails and counterstains that can be multiplexed to examine endogenous necroptotic signaling in fixed human and mouse cells. Successful 915 916 detection of specific signals relies on fixation in methanol, rather than crosslinking fixatives such as paraformaldehyde. c Two-dimensional Airyscan micrographs of Wheat Germ Agglutinin (WGA)-917 918 stained membranes, Hoechst-stained DNA and anti-MLKL immunosignals from clone 5A6 and clone 919 D6E3G on methanol-fixed wild-type MDFs that had been left untreated or TSI-treated for 60min. 920 Arrowhead exemplifies the small clusters of MLKL that form during necroptosis. The box indicates 921 the junctional accumulation of phospho-MLKL. d Three-dimensional orthogonal projections and maximum intensity projection (MIP) of the boxed region from panel **c** showing a ring-like structure 922 923 adopted by phospho-MLKL at the WGA-stained plasma membrane. Accompanied by Supplementary 924 Video 1.