

# Ppm1b negatively regulates necroptosis through dephosphorylating Rip3

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**The auto-phosphorylation of murine receptor-interacting protein 3 (Rip3) on Thr 231 and Ser 232 in the necrosome is required to trigger necroptosis. However, how Rip3 phosphorylation is regulated is still largely unknown. Here we identified protein phosphatase 1B (Ppm1b) as a Rip3 phosphatase and found that Ppm1b restricts necroptosis in two settings: spontaneous necroptosis caused by Rip3 auto-phosphorylation in resting cells, and tumour necrosis factor- $\alpha$  (TNF)-induced necroptosis in cultured cells. We revealed that Ppm1b selectively suppresses necroptosis through the dephosphorylation of Rip3, which then prevents the recruitment of mixed lineage kinase domain-like protein (Mlkl) to the necrosome. We further showed that *Ppm1b* deficiency (*Ppm1b*<sup>d/d</sup>) in mice enhanced TNF-induced death in a Rip3-dependent manner, and the role of Ppm1b in inhibiting necroptosis was evidenced by elevated Rip3 phosphorylation and tissue damage in the caecum of TNF-treated *Ppm1b*<sup>d/d</sup> mice. These data indicate that Ppm1b negatively regulates necroptosis through dephosphorylating Rip3 *in vitro* and *in vivo*.**

Necroptosis is a kind of programmed necrosis that relies on the receptor-interacting serine/threonine kinase 1 (Rip1) and Rip3 (ref. 1), although Rip1 is dispensable in some conditions<sup>2–4</sup>. It has been found to be involved in many physiological and pathological processes, such as host defence against viruses, inflammation, tissue injury, eye diseases and cancers<sup>5,6</sup>. Although necroptosis can be triggered by various stimuli, our knowledge on the necroptotic pathway is mainly obtained through the study of that induced by TNF. Under TNF stimulation, a multiple protein complex (termed the necrosome) forms to initiate necroptosis<sup>1</sup>. Rip1 and Rip3 are the core components in the necrosome and interact through their RIP homotypic interaction motif<sup>7–11</sup> (RHIM). Rip3 in the necrosome recruits and phosphorylates the pseudokinase Mlkl (refs 12–14). The phosphorylated Mlkl translocates to the cytomembrane to execute necroptosis<sup>15–18</sup>. The phosphorylation of Rip3 (Thr 231 and Ser 232 in mouse Rip3; Ser 227 in human Rip3) is essential for the recruitment of Mlkl to the necrosome<sup>13,19</sup>. Here we identified Ppm1b as a Rip3 phosphatase and showed that Ppm1b suppressed necroptosis both in culture cells and *in vivo* by dephosphorylating Rip3.

## RESULTS

### Identification of Ppm1b as a Rip3 phosphatase

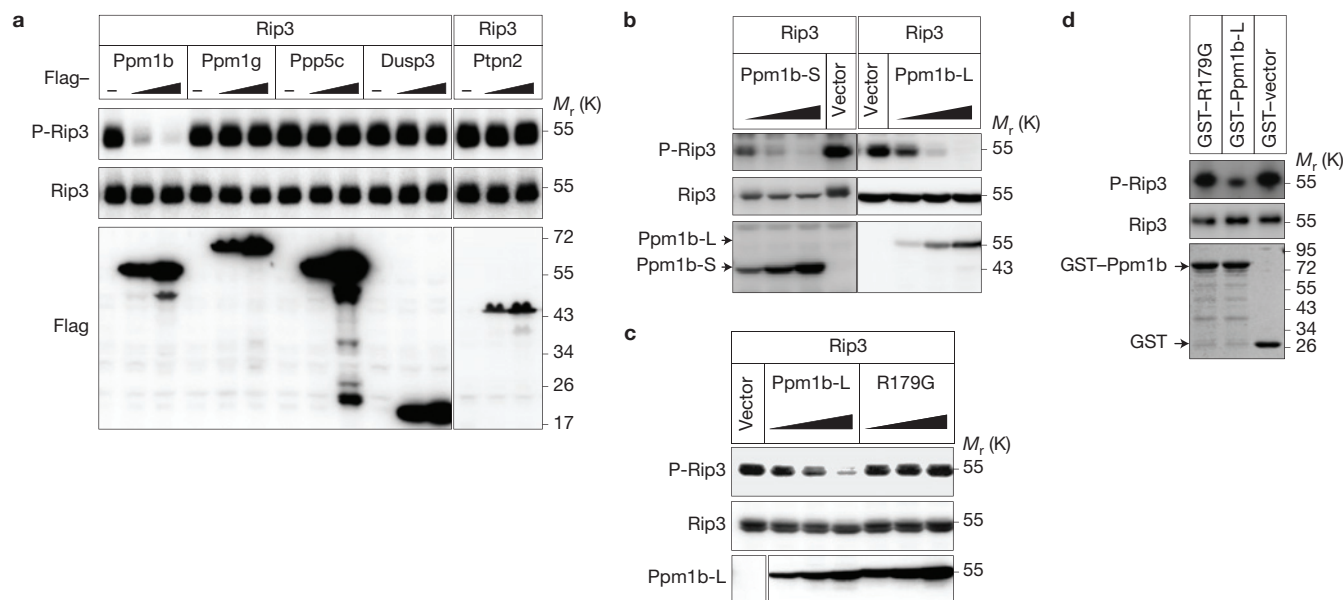
As a result of the requirement of Rip3 auto-phosphorylation in necroptosis<sup>13,19</sup>, we searched for Rip3 phosphatase(s) that regulate

Rip3 phosphorylation. By mass spectrometry analysis of murine Rip3 immunocomplexes, we identified five phosphatases, Ppm1b, protein phosphatase 1G (Ppm1g), serine/threonine-protein phosphatase 5 (Ppp5c), dual-specificity phosphatase 3 (Dusp3) and tyrosine-protein phosphatase non-receptor type 2 (Ptpn2; Supplementary Table 1). The three known proteins in the Rip3 complex including Rip1, FAS-associated death domain protein (Fadd) and Mlkl were found in the immunocomplexes, so these phosphatases could be Rip3-interacting proteins. As Rip3 underwent auto-phosphorylation when overexpressed in 293T cells<sup>19</sup>, we coexpressed each of these phosphatases with Rip3 in 293T cells to evaluate their phosphatase activity towards Rip3 and found that Ppm1b but not the other phosphatases reduced the phosphorylation of Rip3 (Fig. 1a).

There are seven splicing variants of murine Ppm1b encoding four proteins with different carboxy-terminal sequences. Splicing variants encoding isoform 1 (relative molecular mass 55,000 ( $M_r$ 55K), termed Ppm1b-L) and isoform 2 ( $M_r$ 43K, termed Ppm1b-S) are expressed ubiquitously<sup>20–22</sup>. The Ppm1b complementary DNA used in the above experiments encodes Ppm1b-L. Ppm1b-S is also capable of lowering Rip3 phosphorylation in a dose-dependent manner (Fig. 1b). The phosphatase dead mutant of Ppm1b (R179G, Arg 179 to glycine mutation<sup>23</sup>) failed to reduce the phosphorylation of Rip3, confirming that Ppm1b is a phosphatase of Rip3 (Fig. 1c). The data obtained by using bacterially expressed recombinant GST-Ppm1b-L

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**Figure 1** Identification of Ppm1b as a Rip3 phosphatase. **(a)** Ppm1b dephosphorylates Rip3 in 293T cells. Rip3 was coexpressed with or without increasing amounts of phosphatases in 293T cells. The cells were lysed and immunoblotted with the indicated antibodies 36 h post transfection. The vertical line represents a splice mark. The samples were obtained and processed in the same experiment, and the gels/blots were processed in parallel. **(b)** Both Ppm1b-L and Ppm1b-S dephosphorylate Rip3 in a dose-dependent manner. Rip3 was coexpressed with or without increasing amounts of Ppm1b-S and Ppm1b-L in 293T cells. The cells were lysed and immunoblotted with the indicated antibodies 36 h post transfection. **(c)** Ppm1b phosphatase activity is required for dephosphorylating Rip3.

Rip3 was coexpressed with or without increasing amounts of Ppm1b-L and its phosphatase-deficient mutant R179G in 293T cells. The cells were analysed as in **b**. The vertical line represents a splice mark. **(d)** Ppm1b dephosphorylates Rip3 *in vitro*. Flag-Rip3 (purified from 293T cells) was incubated with recombinant GST-Ppm1b-L, GST-R179G and GST-vector *in vitro*. The phosphorylated Rip3 and total Rip3 were detected by immunoblotting with the indicated antibodies. Recombinant Ppm1b and R179G were shown by Coomassie blue staining. Data shown are representative of two or more independent experiments. Uncropped images of blots are shown in Supplementary Fig. 7.

and GST-R179G mutant demonstrated that Ppm1b dephosphorylates Rip3 directly (Fig. 1d).

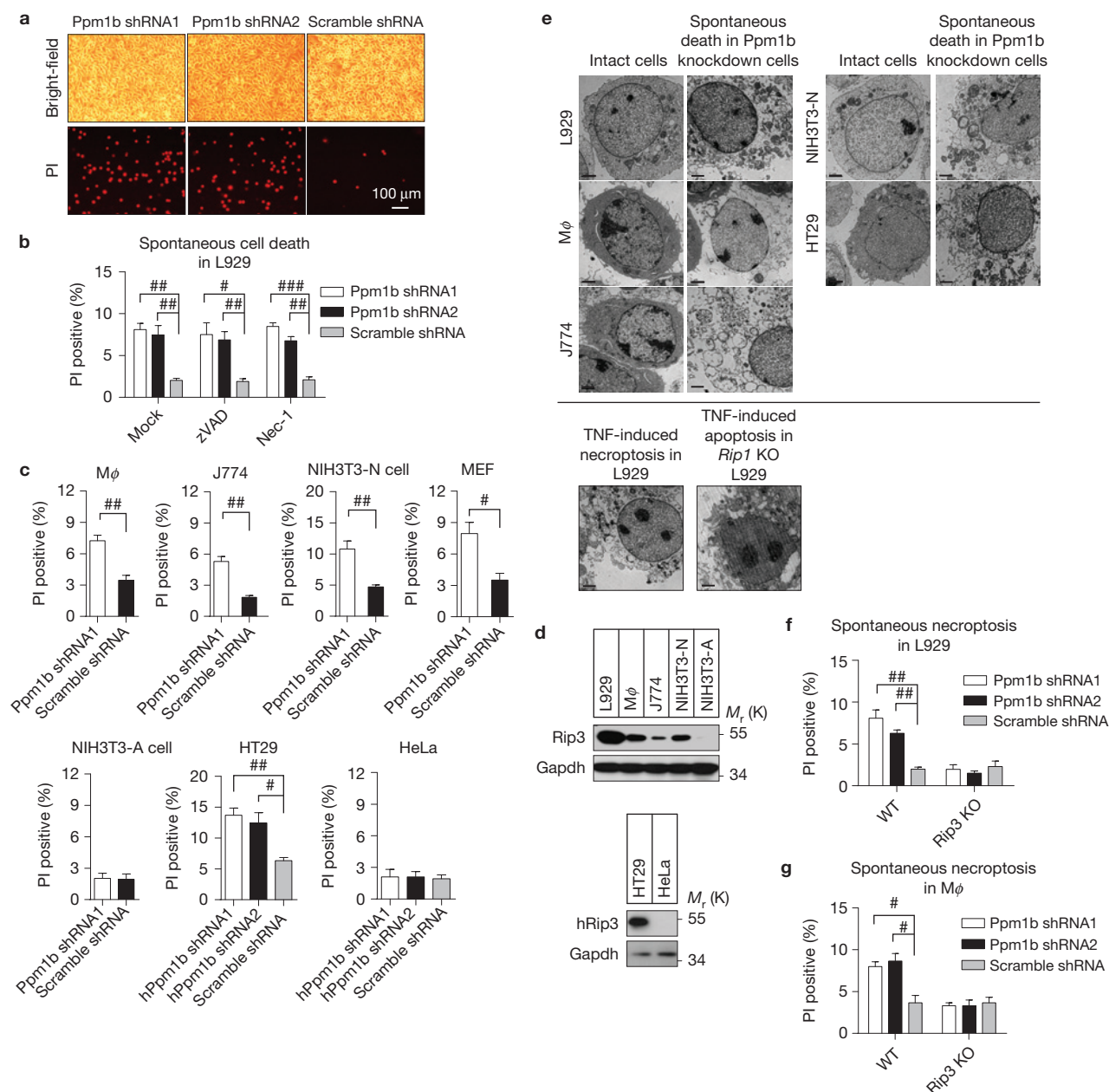
Ppm1b is likely to associate with Rip3 in resting cells because we can detect its interaction with Rip3 in L929 cells (Supplementary Fig. 1a) and when the two proteins were coexpressed in 293T cells (Supplementary Fig. 1b). The interaction is specific as Ppm1b interacts with Rip3 but not the other proteins involved in the necroptosis, such as Fadd, caspase-8, Mkl1 or Rip1 (Supplementary Fig. 1c). Ppm1b contains an amino-terminal phosphatase domain (PD) and a C-terminal domain (CD; Supplementary Fig. 1d). Whereas the CD was suggested to determine the substrate specificity of Ppm1b (ref. 23), we found that PD is responsible for the interaction with Rip3 (Supplementary Fig. 1e). We also found that the kinase domain (KD) of Rip3 is responsible for its interaction with Ppm1b (Supplementary Fig. 1f).

### Ppm1b protects cells from Rip3-dependent spontaneous necroptosis

Both Ppm1b-L and Ppm1b-S are expressed in L929, a cell line commonly used in studying TNF-induced necroptosis (Supplementary Fig. 2a). Knockdown of Ppm1b by short hairpin RNAs (shRNAs; targeting both L and S isoforms, Supplementary Fig. 2a) increased spontaneous cell death (Fig. 2a). Different L929 sublines vary in their sensitivity to zVAD-induced cell death<sup>24</sup>. To avoid zVAD-induced cell death, we used a L929 line that resists zVAD-induced death to determine whether the spontaneous cell death is caspase-dependent.

The spontaneous cell death is not dependent on caspase activity or Rip1 kinase activity, as neither general caspase inhibitor zVAD nor Rip1 kinase inhibitor necrostatin-1 (Nec-1; ref. 25) blocked the cell death (Fig. 2b). Ppm1b-L and Ppm1b-S seemed to have an additive effects because the spontaneous cell death became obvious only in Ppm1b-L and Ppm1b-S double-knockdown cells (Supplementary Fig. 2b). Unless specifically indicated, Ppm1b knockdown in the rest of our studies refers to knockdown of both Ppm1b-L and Ppm1b-S.

We next examined the effect of Ppm1b knockdown on cell viability in a panel of different types of cell. Knockdown of Ppm1b in primary peritoneal macrophages (M $\phi$ ), macrophage cell line J774, NIH3T3-N (ref. 8), mouse embryonic fibroblast (MEF) and HT29 cells (Supplementary Fig. 2c) increased spontaneous cell death (Fig. 2c), but had no effect on cell death in NIH3T3-A (ref. 8) and HeLa cells (Fig. 2c and Supplementary Fig. 2c). As NIH3T3-A and HeLa cells lack Rip3 expression, whereas all the others express Rip3 (ref. 8; Fig. 2d), the Ppm1b knockdown-mediated increase of spontaneous cell death seems to be dependent on the presence of Rip3. Meanwhile, using transmission electron microscopy, we found necrotic morphology in Ppm1b knockdown-induced death of L929, M $\phi$ , J774, NIH3T3-N and HT29 cells (Fig. 2e). Furthermore, Ppm1b knockdown (Supplementary Fig. 2d,e) increased spontaneous cell death in WT but not *Rip3* KO L929 and M $\phi$  cells (Fig. 2f,g), confirming that Ppm1b knockdown-mediated cell death is Rip3-dependent.



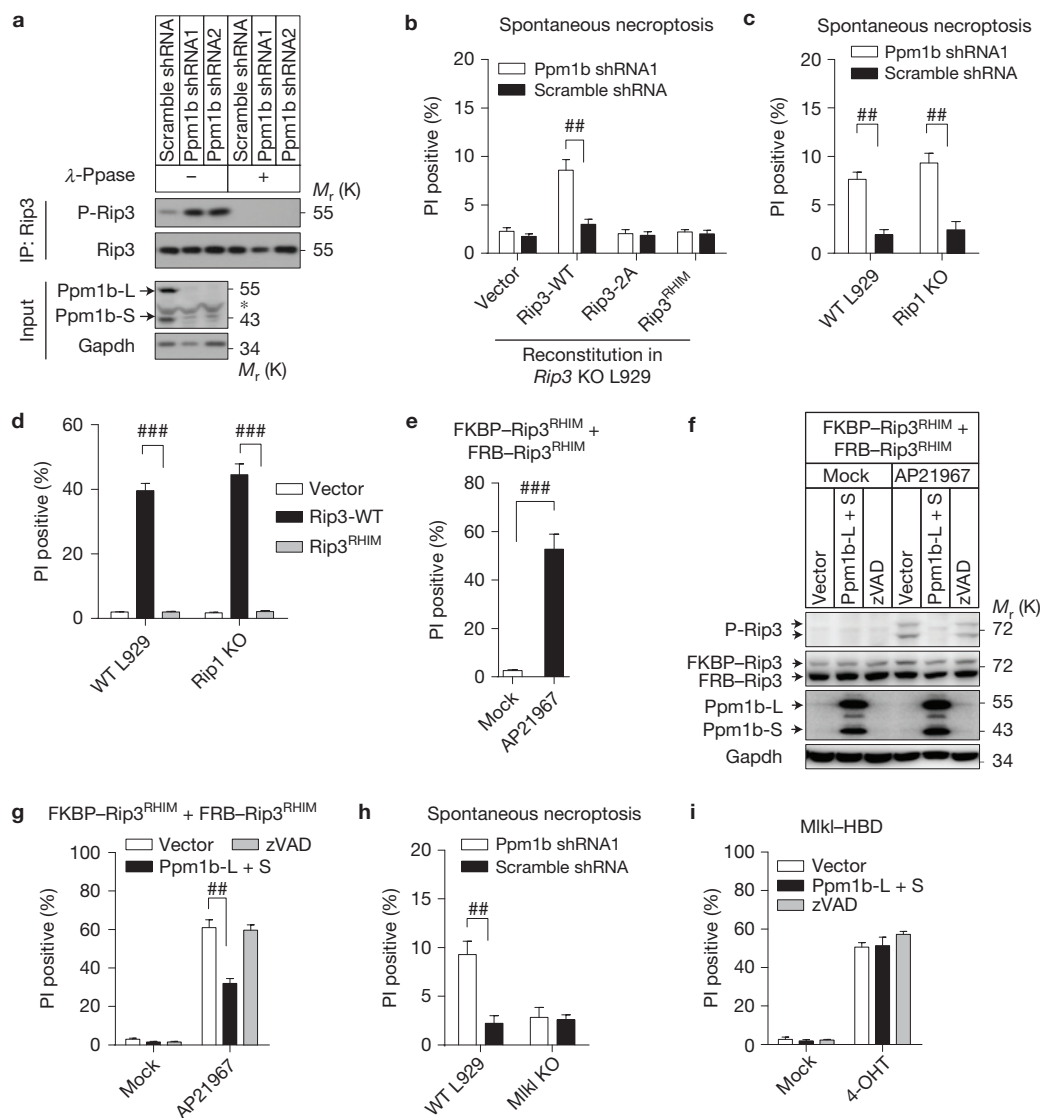
**Figure 2** Ppm1b protects cells from Rip3-dependent spontaneous necroptosis. **(a)** Ppm1b was knocked down by lentivirus-delivered shRNAs targeting both the Ppm1b-L and Ppm1b-S isoforms in L929 cells. Forty-eight hours after infection, the cells were stained with propidium iodide (PI) and analysed under a microscope. Dead cells were PI positive. Scale bar, 100  $\mu$ m. shScramble: non-target control shRNA. The protein expression levels are shown in Supplementary Fig. 2a. **(b)** Ppm1b was knocked down by lentivirus-delivered shRNA in L929 cells. Six hours after infection, these cells were treated with DMSO, zVAD (20  $\mu$ M) and Nec-1 (30  $\mu$ M). Spontaneous cell death was analysed by PI staining under a microscope 48 h later.  $n=3,000$  cells pooled from three independent experiments. **(c)** Ppm1b was knocked down in different mouse and human cell lines. Spontaneous cell death was counted by PI staining under a microscope 48 h (72 h for Mφ and J774) later. Mφ: mouse peritoneal macrophage. The protein expression levels are shown

in Supplementary Fig. 2c.  $n=3,000$  cells pooled from three independent experiments. **(d)** The Rip3 expression level correlates with the cell death caused by Ppm1b knockdown in the cells analysed in **c**. **(e)** The morphology of Ppm1b knockdown-induced spontaneous dead cells was analysed by transmission electron microscopy. Scale bar, 2  $\mu$ m. TNF-induced necroptosis in L929 cells and TNF-induced apoptosis in *Rip1* KO L929 cells were included as a control. **(f,g)** Ppm1b was knocked down in WT, *Rip3* KO L929 cells **(f)** and WT, *Rip3* KO Mφ **(g)**. Then, spontaneous cell death was analysed.  $n=3,000$  cells pooled from three independent experiments. The protein expression levels are shown in Supplementary Fig. 2d,e. For **b,c,f,g**, results shown are mean  $\pm$  s.e.m.; \* $P<0.05$ , \*\* $P<0.01$ , \*\*\* $P<0.001$ . For **a,d,e** data shown are representative of two or more independent experiments. Statistics source data for this figure can be found in Supplementary Table 2. Uncropped images of blots are shown in Supplementary Fig. 7.

### Ppm1b prevents Rip3 auto-activation in resting cells

We addressed whether knockdown of Ppm1b would increase the basal phosphorylation level of Rip3. Rip3 was immunoprecipitated

from WT and Ppm1b knockdown L929 cells, and its phosphorylation level was measured by immunoblotting with anti-phospho-Rip3 antibody. Rip3 phosphorylation was indeed increased in Ppm1b



**Figure 3** Ppm1b prevents Rip3 auto-activation and it mediated spontaneous necroptosis. **(a)** Endogenous Rip3 was immunoprecipitated with anti-Rip3 antibody in Ppm1b knockdown and control cells. The immunoprecipitates were treated with or without  $\lambda$ -Ppase and subsequently immunoblotted with the indicated antibodies. **(b)** *Rip3* KO L929 cells reconstituted with Rip3-WT, Rip3-2A and Rip3<sup>RHIM</sup> mutants were infected with Ppm1b or control shRNA. Spontaneous necroptosis was analysed. Protein expression levels are shown in Supplementary Fig. 3a. **(c)** Ppm1b knockdown-induced spontaneous cell death in WT and *Rip1* KO L929 cells was analysed. Protein expression levels are shown in Supplementary Fig. 3b. **(d)** WT Rip3, Rip3<sup>RHIM</sup> and empty vector were introduced into WT and *Rip1* KO L929 by lentiviral vectors. Necroptosis was analysed 24 h later. Protein expression levels are shown in Supplementary Fig. 3c. **(e)** FKBP-Rip3<sup>RHIM</sup> and FRB-Rip3<sup>RHIM</sup> mutants were introduced into *Rip1*-*Rip3* DKO L929 and forced to interact with each other by treatment of dimerizer AP21967; subsequent cell death was analysed

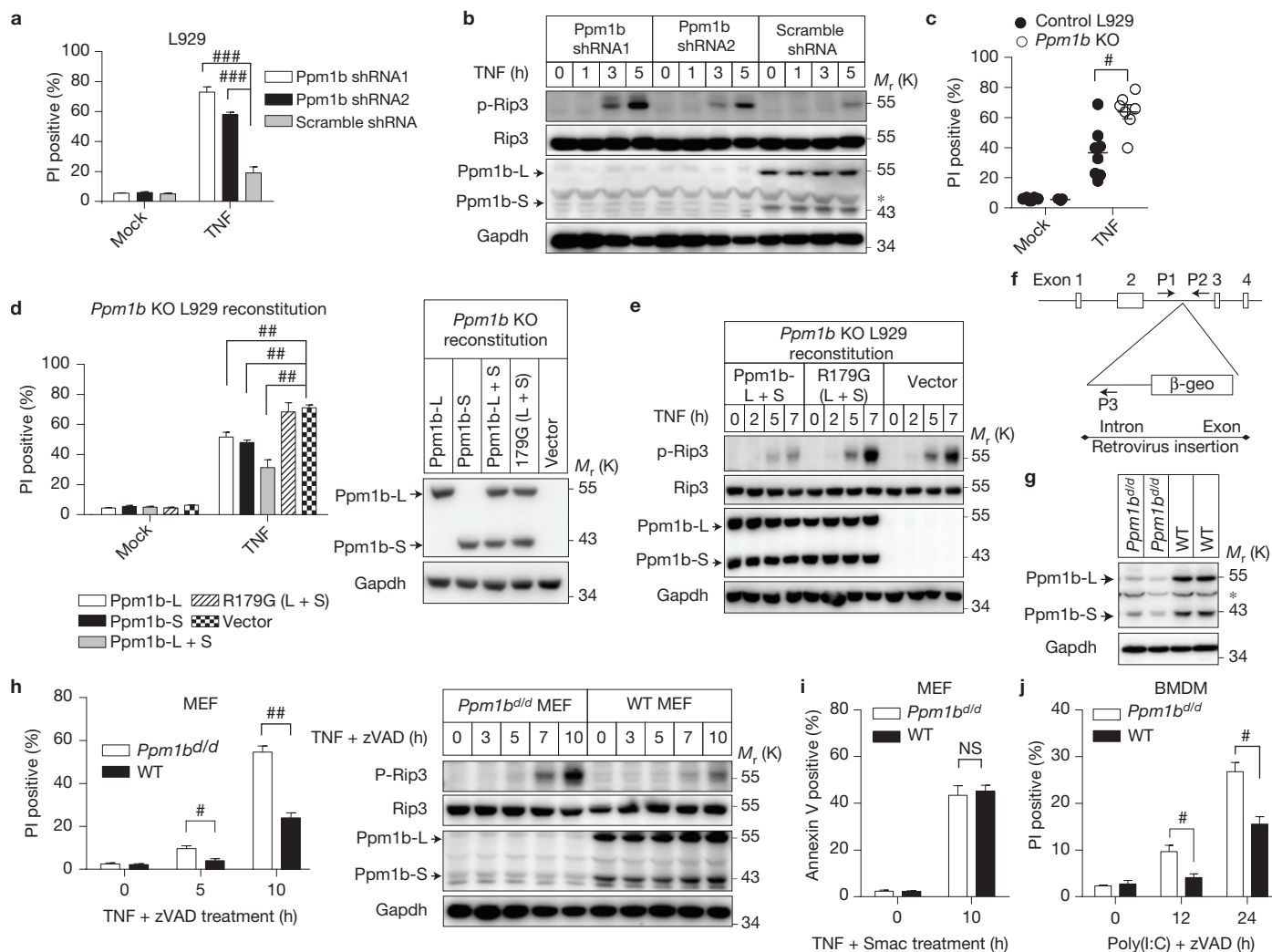
(see Methods). **(f,g)** Cells expressing FKBP–Rip3<sup>RHIM</sup> and FRB–Rip3<sup>RHIM</sup> were infected with lentiviral vector encoding Ppm1b (co-infection of Ppm1b-L and Ppm1b-S) or with empty vector, or treated with zVAD (20  $\mu$ M). Twenty-four hours later, cells were treated with or without AP21967 (250 nM) for 2 h. **(f)** cells were then lysed and immunoblotted; **(g)** cell death was analysed. **(h)** Ppm1b knockdown-induced spontaneous cell death in WT and *Mkl1* KO L929 cells was analysed. Protein expression levels are shown in Supplementary Fig. 3d. **(i)** *Mkl1* KO L929 cells expressing Mkl1–HBD were analysed as in **g**, except that 4-OHT (1  $\mu$ M) rather than AP21967 was used to induce Mkl1 oligomerization-mediated cell death. For **b–e,g–i**, results shown are mean  $\pm$  s.e.m.;  $n=3,000$  cells pooled from three independent experiments; \*\*\* $P<0.01$ , \*\*\*\* $P<0.001$ . For **a,f**, data shown are representative of two or more independent experiments. The asterisk denotes a nonspecific band. Statistics source data for this figure can be found in Supplementary Table 2. Uncropped images of blots are shown in Supplementary Fig. 7.

knockdown cells (Fig. 3a). The specificity of the phospho-Rip3 antibody was confirmed by immunoblotting with the samples treated with  $\lambda$ -phosphatase ( $\lambda$ -Ppase). Reintroducing Rip3 WT but not the Rip3 phosphorylation-deficient mutant (Thr 231 and Ser 232 mutated to alanine, termed Rip3-2A) into *Rip3* KO L929 cells restored the sensitivity of L929 cells to Ppm1b depletion-induced necroptosis

(Fig. 3b and Supplementary Fig. 3a), indicating that the upregulation of Rip3 phosphorylation corresponds to spontaneous necroptosis.

Reintroducing the Rip3 RHIM domain mutant (QIG449-451AAA mutation in RHIM, termed Rip3<sup>RHIM</sup>) to *Rip3* KO L929 cells cannot rescue the spontaneous necroptosis (Fig. 3b and Supplementary Fig. 3a), suggesting that the RHIM-mediated Rip3 interaction



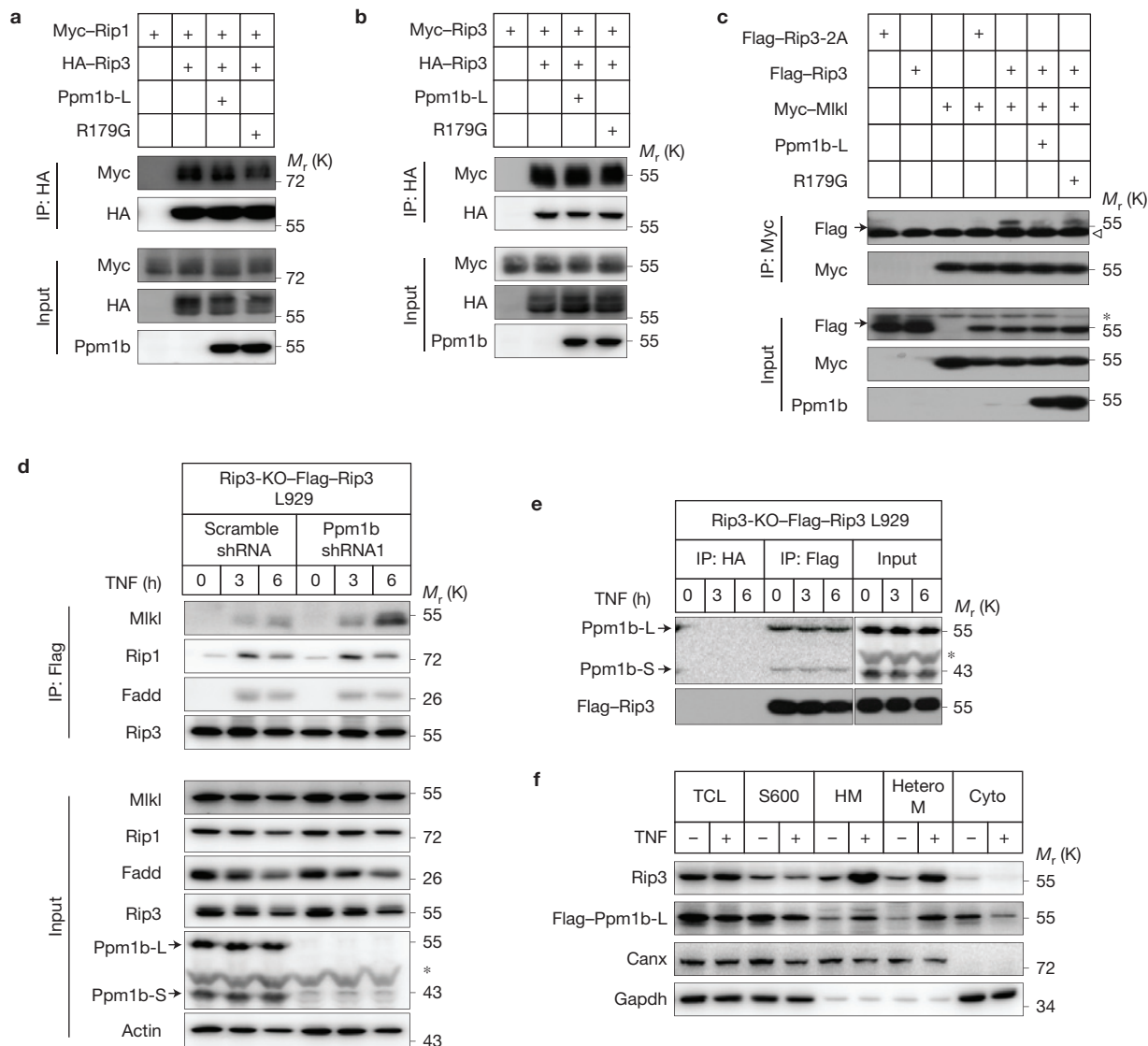


**Figure 4** Ppm1b negatively regulates TNF-induced necroptosis. **(a,b)** L929 cells were infected with Ppm1b or control shRNA. Forty-eight hours later, spontaneous dead cells were removed by re-plating the cells. **(a)** These cells were then treated with or without TNF (10 ng ml<sup>-1</sup>) for 5 h. Cell death was analysed by flow cytometer;  $n=3$  independent experiments. **(b)** These cells were treated with TNF for the indicated time and then analysed by immunoblotting. **(c)** TNF-induced necroptosis was analysed in Ppm1b KO (n=7 clones) and WT (n=8 clones) L929 cells.  $n$  is representative of a single experiment where two independent experiments were performed to assess reproducibility. **(d)** Ppm1b KO L929 cells were reconstituted with Ppm1b-L, Ppm1b-S, both isoforms or the R179G mutants. Left, TNF-induced necroptosis was analysed.  $n=3$  independent experiments. R179G (L + S): Ppm1b-L R179G and Ppm1b-S R179G mutants. Right, cell lysates were immunoblotted. **(e)** Ppm1b KO L929 cells reconstituted with Ppm1b or its mutants were treated with TNF for the indicated time. Then cell lysates were immunoblotted. **(f)** Ppm1b<sup>d/d</sup> mice with a gene-trap vector inserted in the

second intron of Ppm1b genomic locus. **(g)** Cell lysates of primary Ppm1b<sup>d/d</sup> and WT MEF cells were immunoblotted. **(h)** The immortalized Ppm1b<sup>d/d</sup> and WT MEF cells were treated with TNF (30 ng ml<sup>-1</sup>) plus zVAD (20 μM) for the indicated time. Left, cell death was analysed.  $n=3$  independent experiments. Right, cell lysates were immunoblotted. **(i)** Ppm1b<sup>d/d</sup> and WT MEF cells were treated with TNF (30 ng ml<sup>-1</sup>) plus Smac mimetic (Smac; 100 nM) for the indicated time. Then apoptosis was measured by Annexin V staining.  $n=3$  independent experiments. **(j)** BMDMs from Ppm1b<sup>d/d</sup> and WT mice were treated with poly(I:C) (100 μg ml<sup>-1</sup>) plus zVAD (20 μM) for the indicated time, and then cell death was analysed.  $n=3$  independent experiments. For **a,c,d,h-j**, results shown are mean ± s.e.m.; NS: no significant difference, \* $P < 0.05$ , \*\* $P < 0.01$ , \*\*\* $P < 0.001$ . For **b,e,g,h**, data shown are representative of two independent experiments. The asterisk denotes a nonspecific band. Statistics source data can be found in Supplementary Table 2. Uncropped images of blots are shown in Supplementary Fig. 7.

is essential for the spontaneous necroptosis. Rip3 also interacts with Rip1 through its RHIM (ref. 26), but Ppm1b knockdown increased spontaneous death in Rip1 KO L929 cells to a level similar to that observed in WT L929 cells (Fig. 3c and Supplementary Fig. 3b), indicating that Ppm1b depletion-induced spontaneous necroptosis is not Rip1-dependent. This is consistent with the data of Nec-1 treatment (Fig. 2b). As RHIM is essential for Rip3

overexpression-induced Rip1-independent cell death process (Fig. 3d and Supplementary Fig. 3c), we examined whether RHIM is directly required for targeting Rip3 by Ppm1b. We expressed FK506 binding protein (FKBP)-fused Rip3<sup>RHIM</sup> (FKBP-Rip3<sup>RHIM</sup>) and FKBP-rapamycin binding domain (FRB)-fused Rip3<sup>RHIM</sup> (FRB-Rip3<sup>RHIM</sup>) in Rip1-Rip3 double knockout cells by lentiviral vectors<sup>27</sup> and created RHIM-independent Rip3 homo-interaction



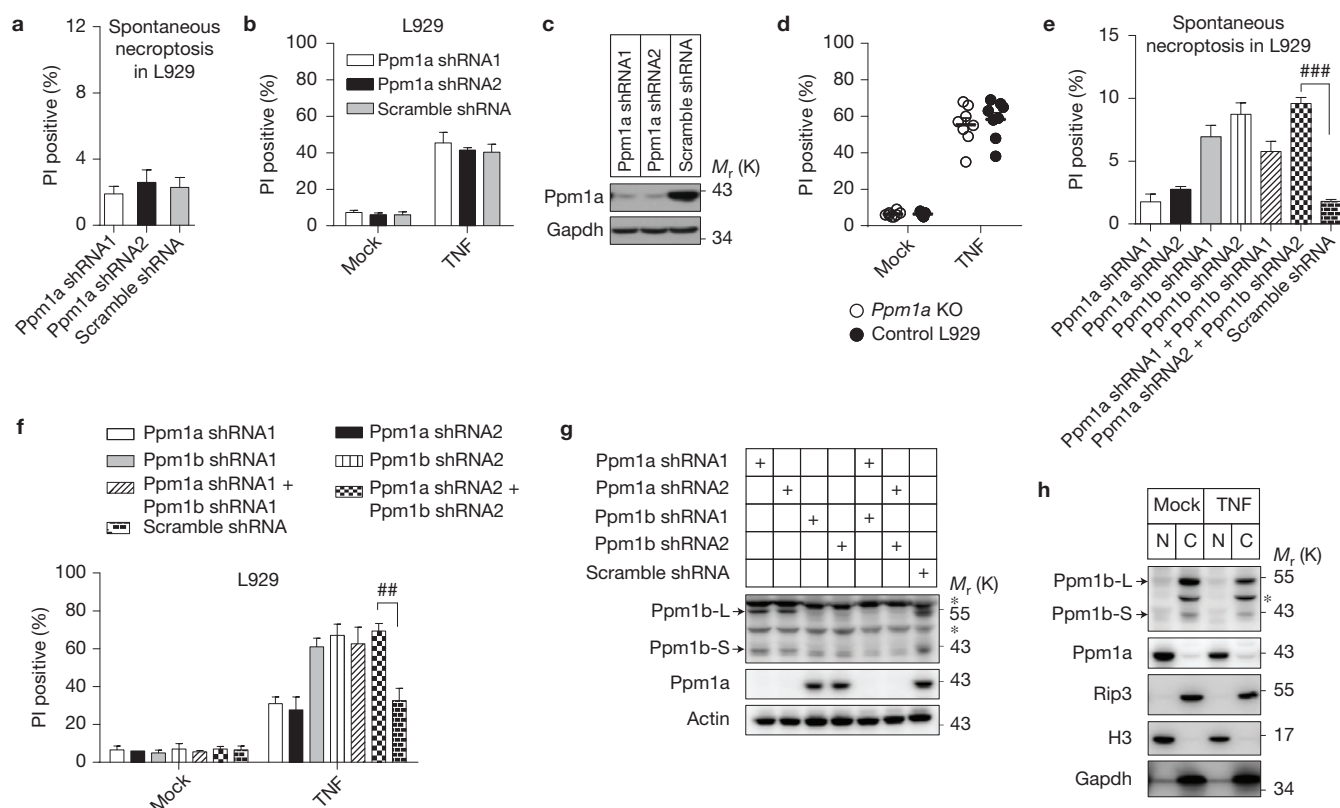
**Figure 5** Ppm1b suppresses Mkl1 recruitment to the necrosome under TNF stimulation. **(a–c)** 293T cells were transfected with the plasmids as indicated. Cell lysates were immunoprecipitated with anti-HA antibody (IP: HA) or anti-Myc antibody (IP: Myc). The lysates (Input) and immunoprecipitates were immunoblotted. **(d)** Ppm1b was knocked down in Rip3-KO-Flag-Rip3 L929 cells, and then the cells were treated with TNF (10 ng ml<sup>-1</sup>) for the indicated time. The necrosome was analysed by immunoprecipitation with anti-Flag antibody (IP: Flag). The cell lysates (Input) and immunocomplexes were analysed by immunoblotting with the indicated antibodies. **(e)** Rip3-KO-Flag-Rip3 L929 cells were treated with TNF for the indicated time. The cell lysates were immunoprecipitated with anti-HA (IP: HA) and anti-Flag (IP: Flag) antibodies and analysed by immunoblotting with the indicated antibodies.

The vertical line represents a splice mark. The samples were obtained and processed in the same experiment, and the gels/blots were processed in parallel, except that the exposure time of Ppm1b for the immunoprecipitates is ten times that for the input. **(f)** L929 cells expressing Flag-Ppm1b-L were treated with or without TNF for 6 h. Then cells were subjected to subcellular fractionation (see Methods). Each fraction was subjected to immunoblotting with the indicated antibodies. TCL: total cell lysate; S600: supernatant fraction after centrifugation at 600g; HM: heavy membrane fraction; HeteroM: heterotypic membrane fraction. Canx: ER marker. Data shown are representative of two or more independent experiments. The arrowhead denotes the heavy chain and the asterisk denotes a nonspecific band. Uncropped images of blots are shown in Supplementary Fig. 7.

by the addition of AP21967 to induce interaction of FKBP and FRB (Fig. 3e). This RHIM-independent Rip3–Rip3 interaction drove the auto-phosphorylation of Rip3 (Fig. 3f), and Ppm1b still attenuated the phosphorylation level (Fig. 3f) and blocked the cell death (Fig. 3g).

Mkl1 is a downstream effector of Rip3 in the necroptosis pathway<sup>12–15,17,18,28</sup> and we confirmed that Ppm1b knockdown did not increase spontaneous cell death in *Mkl1* KO cells (Fig. 3h and Supplementary Fig. 3d). Consistently, the cell death caused by the

hormone binding domain of oestrogen receptor (HBD)-mediated oligomerization of the Mkl1–HBD fusion protein<sup>17</sup> cannot be affected by Ppm1b (Fig. 3i). We also excluded a role of TNF autocrine<sup>29</sup> in Ppm1b depletion-induced spontaneous necroptosis by using *TNFR1* KO L929 (ref. 30; Supplementary Fig. 3e). Collectively, our data suggest that the spontaneous cell death is initiated by Rip3 RHIM-mediated auto-activation and its downstream mechanism is most likely the same as TNF-induced necroptosis.



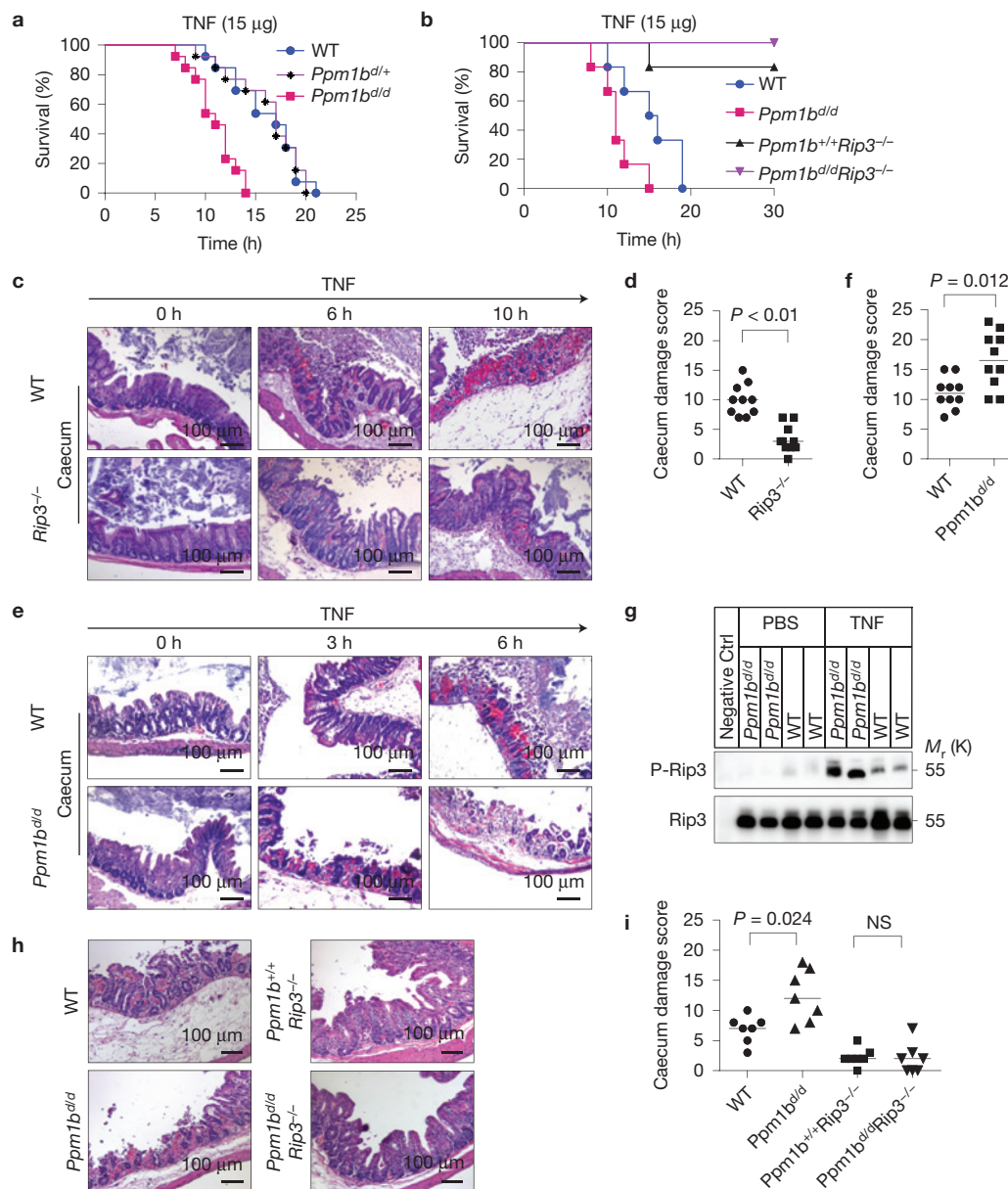
**Figure 6** Ppm1a does not negatively regulate necroptosis. (**a–c**) Ppm1a was knocked down in L929 cells. (**a**) Forty-eight hours later, spontaneous cell death was measured;  $n=3,000$  cells pooled from three independent experiments. (**b**) The cells were treated with or without TNF ( $10 \text{ ng ml}^{-1}$ ) for 6 h and cell death was analysed by flow cytometer;  $n=3$  independent experiments. (**c**) The cell lysates were immunoblotted with the indicated antibodies. (**d**) *Ppm1a* KO L929 cells were generated by CRISPR/Cas9 technology. *Ppm1a* KO ( $n=8$  clones) and WT ( $n=8$  clones) L929 were treated with or without TNF. Then cell death was analysed.  $n$  is representative of a single experiment where two independent experiments were performed to assess reproducibility. (**e–g**) Ppm1a does not compensate for Ppm1b in restricting necroptosis. Ppm1a and Ppm1b were knocked down respectively or together. (**e**) Forty-eight hours later, spontaneous cell

death was recorded; (**f**) the cells were treated with or without TNF and then cell death was analysed; (**g**) the cell lysates were immunoblotted with the indicated antibodies.  $n=3$  independent experiments. (**h**) Different subcellular localization of Ppm1a and Ppm1b. L929 cells were treated with or without TNF for 6 h. Then nucleus and cytosol fractions of the cells were isolated by subcellular fractionation. These fractions were analysed by immunoblotting with the indicated antibodies. N: nucleus fraction; C: cytosol fraction; H3: Histone H3, a nucleus marker; Gapdh: a cytosol marker. For **a,b,d–f**, results shown are mean  $\pm$  s.e.m.;  $^{*}P < 0.01$ ;  $^{***}P < 0.001$ . For **c,g,h**, data shown are representative of two or more independent experiments. The asterisk denotes a nonspecific band. Statistics source data can be found in Supplementary Table 2. Uncropped images of blots are shown in Supplementary Fig. 7.

### Ppm1b negatively regulates TNF-induced necroptosis

As Rip3 phosphorylation is required for TNF-induced necroptosis<sup>13,19</sup>, we next investigated whether Ppm1b affects TNF-induced necroptosis. The dead cells caused by spontaneous death in culture were removed before the analyses (see Methods). Compared with the control, knockdown of Ppm1b enhanced TNF-induced necroptosis in L929 cells (Fig. 4a and Supplementary Fig. 4a,b). This enhanced necroptosis correlates with the increase of Rip3 phosphorylation in L929 cells (Fig. 4b). In contrast, knockdown of Ppm1b in NIH3T3-A cells did not affect TNF-induced apoptosis (Supplementary Fig. 4c). Both Ppm1b-L and Ppm1b-S are important in this process as knockdown of either of them exhibited a less enhancing effect than double knockdown (Supplementary Fig. 4d). We knocked out the *Ppm1b* gene in L929 cells and selected a number of *Ppm1b* knockout lines. As controls, we also isolated several Ppm1b-expressing colonies during the process of knocking out *Ppm1b*. Perhaps owing to the growth selection in culture, none

of the *Ppm1b* KO lines showed a higher level of spontaneous cell death than control L929 cells. However, *Ppm1b* knockout cells were more sensitive to TNF-induced cell death (Fig. 4c). Reconstitution of either Ppm1b-L or Ppm1b-S expression in *Ppm1b* KO cells attenuated TNF-induced cell death, and re-expression of both of them led to a severe inhibitory effect on TNF-induced cell death, but re-expression of R179G mutants showed no difference from the control (Fig. 4d). It seemed that these two Ppm1b isoforms exhibited no functional difference in inhibiting necroptosis and the inhibitory effect was decided by their overall expression level. We observed that the infection of L929 cells with 10 moi virus encoding Ppm1b-L (L) + 10 moi virus encoding Ppm1b-S (S) (20 moi in total) had a similar effect to the infection with 20 moi L or 20 moi S alone (Supplementary Fig. 4e); and the infection of L929 cells with 20 moi L + 20 moi S had a stronger effect than that with 20 moi L or S alone (Supplementary Fig. 4e). The level of TNF-induced Rip3 phosphorylation in Ppm1b-reconstituted L929



**Figure 7** *Ppm1b* protects mice from TNF-induced SIRS through dephosphorylating Rip3. (a) *Ppm1b<sup>d/d</sup>*, *Ppm1b<sup>d/+</sup>* and WT mice raised as littermates were injected with 15  $\mu$ g TNF through the tail vein. Mouse survival is presented as a Kaplan–Meyer plot and log-rank test was performed.  $n=13$  mice for each group pooled from three independent experiments. *Ppm1b<sup>d/d</sup>* versus WT,  $P<0.001$ . (b) WT, *Ppm1b<sup>d/d</sup>*, *Ppm1b<sup>+/+</sup>* *Rip3<sup>-/-</sup>* and *Ppm1b<sup>d/d</sup>* *Rip3<sup>-/-</sup>* mice were analysed as in a.  $n=6$  mice of a single experiment where two independent experiments were performed to assess reproducibility. (c,d) Caecum of WT and *Rip3<sup>-/-</sup>* mice injected with TNF for the indicated time was sectioned and stained with H&E. The representative images are shown in c. At the 6 h time point,  $n=10$  mice for each group. At other time points,  $n=4$  mice. Original magnification:  $\times 200$ ; scale bar, 100  $\mu$ m. The TNF-induced caecum damage at the 6 h time point was scored (see Methods) and is shown in d.  $n$  is representative of a single experiment

where two independent experiments were performed to assess reproducibility. Wilcoxon signed-rank test,  $P<0.01$ . (e,f) Sections of the caecum of WT and *Ppm1b<sup>d/d</sup>* mice were analysed as in c,d. Wilcoxon signed-rank test,  $P=0.012$ . (g) WT and *Ppm1b<sup>d/d</sup>* mice were injected with PBS or TNF (15  $\mu$ g) for 6 h. Then the caecum was collected and lysed. Rip3 protein was enriched from the lysate through immunoprecipitation and subsequently subjected to immunoblotting with p-Rip3 and Rip3 antibodies. A *Rip3<sup>-/-</sup>* mouse was used as a negative control (negative CTRL). (h,i) WT, *Ppm1b<sup>d/d</sup>*, *Ppm1b<sup>+/+</sup>* *Rip3<sup>-/-</sup>* and *Ppm1b<sup>d/d</sup>* *Rip3<sup>-/-</sup>* mice were injected with TNF for 6 h and subsequently analysed as in c,d, except that  $n=7$  mice for each group of a single experiment where two independent experiments were performed to assess reproducibility; Wilcoxon signed-rank test; NS: no significant difference. Statistics source data for this figure can be found in Supplementary Table 2. Uncropped images of blots are shown in Supplementary Fig. 7.

cells was lower than in control cells (Fig. 4e), but the level in *Ppm1b* R179G mutant-expressing cells was not (Fig. 4e), supporting the role of *Ppm1b* in dephosphorylating Rip3. Importantly, *Ppm1b* is specific for TNF-induced phospho-Rip3 dephosphorylation in L929

cells, as *Ppm1b* knockdown had no effect on TNF-induced p65 and p38 phosphorylation (Supplementary Fig. 4f). Together, these data demonstrate that *Ppm1b* dephosphorylates Rip3 and thus negatively regulates TNF-induced necroptosis in L929 cells.



As *Ppm1b* KO mouse is pre-implantation lethal<sup>31</sup>, we generated a *Ppm1b* gene-trap mouse line (*Ppm1b*<sup>+/d</sup>) using embryonic stem cells containing a retroviral gene trap in the second intron of the *Ppm1b* locus (Fig. 4f). The insertion resulted in the expression of a *Ppm1b*- $\beta$ -galactosidase-neomycin ( $\beta$ -geo) fusion protein containing 1–282 amino acids of *Ppm1b*, which lacks a functional phosphatase domain (1–300 amino acids; Supplementary Fig. 4g) and thus is a loss-of-function mutant. The *Ppm1b*<sup>d/d</sup> mice are viable and born with a normal Mendelian distribution. The normal development of *Ppm1b*<sup>d/d</sup> mice is due to the expression of a small amount of wild-type *Ppm1b* because we detected *Ppm1b*-L and *Ppm1b*-S protein in MEF cells isolated from *Ppm1b*<sup>d/d</sup> mice (Fig. 4g). The expression of *Ppm1b* most probably resulted from the splicing out of the intron in which the retroviral vector inserts. Similar to what was observed in L929 cells, *Ppm1b*<sup>d/d</sup> MEF cells are more sensitive to TNF + zVAD-induced Rip3 phosphorylation and necroptosis (Fig. 4h). It was reported that kinase dead Rip3 promotes Rip1-dependent apoptosis in mice and MEF cells<sup>32</sup>. We questioned whether *Ppm1b* regulates Rip1-dependent apoptosis and found that TNF plus Smac mimetic (Smac)-induced apoptosis<sup>33,34</sup> in *Ppm1b*<sup>d/d</sup> and WT MEF cells were comparable (Fig. 4i). It should be mentioned that the dephosphorylation of Rip3 should not affect the kinase activity of Rip3 because mutation of the phosphorylation sites (Thr 231 and Ser 232 to alanine) did not affect the kinase activity of Rip3 (ref. 19). We also found that *Ppm1b* knockdown enhanced poly(I:C)+zVAD-induced necroptosis of bone marrow-derived macrophages (BMDMs; Fig. 4j).

### The regulation of necroptosis by *Ppm1b* is independent of the NF- $\kappa$ B pathway

*Ppm1b* can dephosphorylate inhibitor of nuclear factor  $\kappa$ -B kinase subunit  $\beta$  (IKK $\beta$ ) and negatively regulate NF- $\kappa$ B activation in HeLa cells<sup>35</sup> (Supplementary Fig. 5a). However, the knockdown of *Ppm1b* in L929 cells (Supplementary Fig. 4f) and HT29 cells (Supplementary Fig. 5b) did not affect NF- $\kappa$ B p65 phosphorylation. TNF-induced interleukin 6 (IL-6) production was also not influenced by *Ppm1b* knockdown in L929 cells (Supplementary Fig. 5c). Thus, *Ppm1b* regulates NF- $\kappa$ B in some but not all types of cell. Using the IKK $\beta$  inhibitors TPCA-1 (ref. 36) and IMD 0354 (ref. 37), and an IKK $\beta$  knockout L929 line, we showed that the role of *Ppm1b* in necroptosis has no linkage to IKK $\beta$  (Supplementary Fig. 5d,e,f). TGF- $\beta$  activated kinase 1 (TAK1) was also reported to be dephosphorylated by *Ppm1b* (ref. 38). However, *Ppm1b* knockdown still enhanced TNF-induced necroptosis in the presence of the TAK1 inhibitor 5Z-7-oxozeaenol (5z-7; ref. 39; Supplementary Fig. 5g). NF- $\kappa$ B activation is known to play a pro-survival role in TNF-stimulated cells, which was also the result we saw here in that the IKK $\beta$  and TAK1 inhibition or depletion increased cell death in TNF-treated cells (Supplementary Fig. 5e,g). However, our data demonstrate that the regulation of necroptosis by *Ppm1b* is independent of the NF- $\kappa$ B pathway.

As *Ppm1b* inhibits IKK $\beta$  in HeLa but not in L929 and HT-29 cells, and Rip3 is expressed in L929 and HT-29 but not in HeLa (Fig. 2d), one would ask whether the presence of Rip3 makes *Ppm1b* unable to target IKK $\beta$ . We used HeLa-hRip3 (HeLa cells stably expressing human Rip3) to address this question. Similar to that in control HeLa cells (Supplementary Fig. 5a), the knockdown of *Ppm1b* enhanced the NF- $\kappa$ B p65 phosphorylation in HeLa-hRip3 cells (Supplementary

Fig. 5h). Besides, spontaneous and TNF (TNF plus Smac mimetic plus zVAD (TSZ; ref. 13))-induced necroptosis in HeLa-hRip3 cells was also enhanced by *Ppm1b* knockdown (Supplementary Fig. 5i). The effects of IKK $\beta$  inhibitors were the same as what was observed in L929 cells (Supplementary Fig. 5i). These data again indicate that the effects of *Ppm1b* on Rip3 and IKK $\beta$  are independent of each other. Different from L929 and HT-29 cells, the two functions of *Ppm1b* in HeLa-hRip3 cells coexist. As *Ppm1b* depletion promotes necroptosis, the *Ppm1b*-Rip3 pathway seems to be more dominant than the *Ppm1b*-IKK $\beta$  pathway in HeLa-hRip3 cells. We also measured the serum IL-6 levels and found that they were comparable in TNF-treated *Ppm1b*<sup>d/d</sup> and WT mice (Supplementary Fig. 5j), which suggested that the *Ppm1b*-Rip3 pathway might be the predominant one *in vivo*.

### *Ppm1b* suppresses Mlkl recruitment to the necrosome on TNF stimulation

As Rip3 phosphorylation is essential for the Rip3-Mlkl interaction but not the Rip1-Rip3 interaction<sup>13,19,40</sup>, we tested whether *Ppm1b* affects the interaction of Rip1-Rip3, Rip3-Rip3 and Rip3-Mlkl by co-immunoprecipitation in 293T cells and found that *Ppm1b*-L attenuated the interaction between Rip3 and Mlkl, but not the interaction between Rip1 and Rip3 or Rip3 and Rip3 (Fig. 5a–c). To analyse the recruitment of Mlkl to the necrosome in TNF-stimulated cells, we used *Rip3* KO L929 cells reconstituted with Flag-Rip3 (*Rip3*-KO-Flag-Rip3) because *Rip3*-KO-Flag-Rip3 cells behave similarly to WT L929 cells in necroptosis and the Flag tag facilitates immunoprecipitation with the advantage of specific anti-Flag monoclonal antibody. Whereas knockdown of *Ppm1b* did not affect the assembly of the necrosome, as we were able to detect similar levels of Rip1 and Fadd proteins in the immunoprecipitates of Flag-Rip3 in control and *Ppm1b* knockdown cells after TNF stimulation (Fig. 5d), the recruitment of Mlkl to Flag-Rip3-containing necrosome was significantly increased in *Ppm1b* knockdown compared with control cell. It is unclear how *Ppm1b* is regulated, as we observed consistent association of *Ppm1b* with Rip3 before and after TNF stimulation in L929 cells (Fig. 5e) and translocation of both *Ppm1b* and Rip3 to a heterotypic membrane fraction on TNF treatment<sup>41</sup> (Fig. 5f). Nonetheless, these data demonstrate that *Ppm1b*-mediated dephosphorylation of Rip3 impairs Rip3-mediated recruitment of Mlkl to the necrosome.

### *Ppm1a* does not regulate necroptosis

Protein phosphatase 1A (*Ppm1a*) is the closest homologue of *Ppm1b*. However, knockdown of *Ppm1a* neither caused spontaneous cell death nor changed the sensitivity of L929 cells to TNF-induced cell death (Fig. 6a–c). Knockout of *Ppm1a* by CRISPR-Cas9 technology also did not sensitize L929 cells to TNF killing (Fig. 6d). Double knockdown of *Ppm1a* and *Ppm1b* did not exhibit an additive effect on spontaneous necroptosis or TNF-induced cell death compared with *Ppm1b* single knockdown (Fig. 6e–g). The lack of effect on necroptosis could be due to the nuclear localization of *Ppm1a* (ref. 42), because *Ppm1b* and Rip3 were found in the cytosol fraction (Fig. 6h).

### *Ppm1b* protects mice from TNF-induced caecum damage through dephosphorylating Rip3

TNF-induced necroptosis is essential for TNF-induced systemic inflammatory response syndrome (SIRS) as *Rip3* KO mice are resistant

to TNF-induced death<sup>32,43,44</sup>. Littermates of WT and *Ppm1b*<sup>d/d</sup> mice were injected intravenously with mouse TNF, with *Ppm1b*<sup>d/d</sup> mice being more sensitive to TNF-induced death than WT mice (Fig. 7a). An underlying mechanism of this *in vivo* result is likely to be that Ppm1b suppresses TNF-induced necroptosis in this mouse model. However, Ppm1b has been reported to negatively regulate the NF- $\kappa$ B pathway<sup>35</sup>, which might also affect TNF-induced SIRS. We examined *Ppm1b*<sup>d/d</sup> *Rip3*<sup>-/-</sup> mice and found that the effect of Ppm1b deficiency on TNF-induced mouse death was completely prevented by *Rip3* knockout (Fig. 7b). Thus, the dephosphorylation of Rip3 should be the *in vivo* function of Ppm1b in TNF-treated mice.

To better understand the role of Ppm1b *in vivo*, we first analysed necroptosis-mediated tissue injury in TNF-treated mice. Unlike in previous reports<sup>43,44</sup>, we did not find that *Rip3* deletion affects TNF-induced injuries in liver and kidney (Supplementary Fig. 6). Among spleen, thymus, small intestine, liver, kidney, heart, lung, pancreas and caecum, caecum was the only organ whose injury was attenuated by *Rip3* knockout (Fig. 7c,d and Supplementary Fig. 6). It is worth noting that caecum was described as particularly sensitive to TNF-induced injury in the report of the first TNF-SIRS model<sup>45</sup>. We then analysed the effect of Ppm1b and found that TNF-induced caecum damage was enhanced in *Ppm1b*<sup>d/d</sup> mice (Fig. 7e,f). Analysis of the caecum lysate showed that TNF-induced phosphorylation of Rip3 in *Ppm1b*<sup>d/d</sup> was higher than that in WT mice (Fig. 7g). Moreover, the enhanced caecum damage in TNF-treated *Ppm1b*<sup>d/d</sup> mice was completely prevented by *Rip3* knockout (Fig. 7h,i). These data further support that Ppm1b functions in restricting necroptosis by dephosphorylating Rip3 *in vivo*.

## DISCUSSION

In this study we identified a Rip3 phosphatase that negatively regulates Rip3-dependent spontaneous and TNF-induced necroptosis. Although the interaction of Ppm1b with Rip3 in the resting stage explains the role of Ppm1b in preventing spontaneous necroptosis, how Ppm1b is regulated during TNF-induced necroptosis is unclear. The expression level and the cytosolic localization of Ppm1b did not change during the course of TNF stimulation. Protein kinase A (PKA) was shown to regulate protein stability of Ppm1b (ref. 46), but activation of PKA by forskolin treatment did not change the protein abundance of Ppm1b in L929. As Ppm1b can be activated by fatty acids *in vitro*<sup>47</sup> and Ppm1b translocated to the heterotypic membrane fraction on TNF treatment, whether Ppm1b activity was increased in the lipid-enriched fraction is interesting to know but technically inaccessible at this moment. Consistent association with its substrates has been observed in many phosphatases, including protein phosphatase 1D (also termed as Wip1), which interacts with ataxia-telangiectasia mutated kinase (ATM) before and after ionizing radiation and regulates the ATM-dependent signalling pathways<sup>48</sup>.

It was shown that gene deletion of *Ppm1b* led to early pre-implantation lethality in mice<sup>31</sup>. Although *Rip3* knockout can rescue spontaneous necroptosis in Ppm1b knockdown cells, *Rip3* KO cannot rescue the lethality of *Ppm1b* gene deletion. A *Rip3*-independent function of Ppm1b should be responsible for the normal development through the period of pre-implantation. The identification of Ppm1b as a Rip3 phosphatase is encouraging because it not only advances our understanding of the necroptosis pathway but also provides a

tool to manipulate necroptosis *in vitro* and *in vivo*. The information presented in this report could be useful in exploring the contribution of necroptosis to various physiopathological conditions. □

## METHODS

Methods and any associated references are available in the [online version of the paper](#).

*Note: Supplementary Information is available in the online version of the paper*

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## AUTHOR CONTRIBUTIONS

W.C., J.W., L.L., Zhengmo Z., J.R., Y.L., X.-H.F. and J.H. carried out the experiments. F.C., C.Y., Zhenru Z., S.S.S., X.Z., Zhirong Z., C.-Q.Z., H.W., M.X. and X.L. helped to prepare cell lines, generated the *ppm1b* gene-trap line, provided reagents and mass spectrum analysis. J.H. contributed to the overall design of the project. W.C. and J.H. interpreted the data and wrote the manuscript.

## COMPETING FINANCIAL INTERESTS

The authors declare no competing financial interests.

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## METHODS

**Antibodies and reagents.** Anti-mRip3, p-Rip3, Fadd and Mkl1 antibodies were described previously<sup>19</sup>. Anti-Ppm1b antibody was raised in rabbit using GST-tagged full-length human Ppm1b-L as the antigen. Anti-human Rip3 (ab72106, dilution 1:1,000) and anti-Ppm1a (ab14824, dilution 1:1,000) antibodies were from Abcam. Anti-Flag (F7425, dilution 1:500), Myc (A7470, agarose affinity gel) and HA (A2095, agarose affinity gel) antibodies were obtained from Sigma. Anti-Myc (sc-40, dilution 1:500), HA (sc-805, dilution 1:500) and anti- $\beta$ -actin (sc-47778, dilution 1:10,000) antibodies were obtained from Santa Cruz Biotechnology. Anti-Rip1 (610459, dilution 1:1,000) antibody was obtained from BD Biosciences. Anti-Gapdh (60004-1-Ig, dilution 1:2,000) and anti-Canx (10427-2-AP, dilution 1:500) antibodies were from Proteintech. Anti-p-p65 (3033s, dilution 1:1,000), p65 (8242s, dilution 1:200), p-p38 (9216S, dilution 1:1,000), p38 (9212s, dilution 1:200) and H3 (9715, 1:5,000) antibodies were obtained from Cell Signaling Technology. Mouse TNF $\alpha$  was purchased from eBioscience. zVAD was obtained from Calbiochem. Propidium iodide (PI), 4-hydroxytamoxifen (4-OHT) and Protease Inhibitor Mix were from Sigma.  $\lambda$ -phosphatase ( $\lambda$ -Ppase) was from NEB. AP21967 (A/C Heterodimerizer) was obtained from ARIAD Pharmaceuticals.

**Plasmids.** Ppm1b-L and S (NM\_001159496 and NM\_011151) were amplified from mouse cDNA and cloned into pBOBI or pLV lentivirus vector with no tag or C-terminally tagged by the Exo III-assisted ligase-free cloning method. Deletion mutants and point mutations of Ppm1b and Rip3 were introduced using standard PCR or two rounds of PCR.

**RNA interference.** All lentiviral-shRNAs were constructed into pLV-H1-EF1 $\alpha$ -puro vector following the manufacturer's instruction (Biosettia). The indicated shRNA target sequences are: Ppm1b no. 1: 5'-ACAAGTGTGTGGATGGCAA-3'; Ppm1b no. 2: 5'-GGAGAGTAGAAATGGAAGA-3'; Ppm1b-L no. 1: 5'-GGCTAG AGCTGGCCTATAA-3'; Ppm1b-L no. 2: 5'-GAGGAGTGCTGAAAATATA-3'; Ppm1b-S no. 1: 5'-CTAAGGAAATACAGAGATA-3'; Ppm1b-S no. 2: 5'-TGCTGA ACATGAAGAGTAA-3'; hPpm1b no. 1: 5'-CAGTGGGAGTTATGATTTC-3'; hPpm1b no. 2: 5'-GGTGATTACGCTGCTGTTC-3'; Ppm1a no. 1: 5'-CCAAAGATGGAAGCATA-3'; Ppm1a no. 2: 5'-GAAGAAACATGGTGCGAGAT-3'.

**Lentivirus infection.** For lentivirus production, 293T cells were transfected with lentiviral vectors carrying cDNAs or shRNAs of interest (or its mutants) and lentivirus-packing plasmids (PMDL/REV/VSVG) by the calcium phosphate precipitation method. Twelve hours later, cell culture medium was changed and the virus-containing medium was collected 36 h later. For infection, 1 ml virus-containing medium and 1.5 ml fresh medium containing 10  $\mu$ g ml<sup>-1</sup> Polybrene were added to cells plated in 6-well plates. The plates were centrifuged at 1,500g for 30 min and returned to the cell incubator. The infectious medium was changed 12 h later.

**KO cell lines and cell culture.** *Rip1* KO, *Rip3* KO and *Mkl1* KO L929 were described previously<sup>17,19</sup>. *Ppm1b*, *Ppm1a*, *TNFR1* and *IKK $\beta$*  KO cell lines were generated using the CRISPR/Cas9 technology<sup>30,49</sup>. *Rip1-Rip3* DKO L929 cells were generated by targeting *Rip1* in *Rip3* KO L929 cells. The targeting sequences are: Ppm1b-5'-CTGGGAATGGTCTGCGTTA-3'; Ppm1a-5'-TGTAATCGAAATCCCCAA-3'; Rip1-5'-AACCGCGCTAGTGAGTTGG-3'; TNFR1-5'-GCTTCAACGGC ACGTGACA-3'; IKK $\beta$ -5'-ACCGTGACCGTTGACTAC-3'. Thioglycollate-elicited peritoneal macrophages were obtained from eight-week-old WT or *Rip3* KO mice using a method described previously<sup>50</sup>. Primary WT and *Ppm1b*<sup>+/d</sup> MEF cells were generated from day 14 embryos of the same litter of *Ppm1b*<sup>+/d</sup> heterozygous breeding. The primary MEF cells were immortalized by infection with retrovirus encoding E1A. Mouse BMDMs were differentiated *in vitro* from isolated bone marrow cells. Bone marrow cells collected from mouse femurs and tibias were incubated for seven days in DMEM containing 20% heat-inactivated FBS, penicillin, streptomycin and 30% L929 conditional medium<sup>28</sup>. Three pairs of *Ppm1b*<sup>+/d</sup> and WT mice were used to produce MEF cells and BMDM cells in this work, respectively. HT-29 cells were cultured in McCoy's 5A culture medium (Invitrogen); L929, HEK-293T, NIH3T3-A, NIH3T3-N, HeLa, peritoneal macrophage, J774 and MEF cells were cultured in DMEM. All media were supplemented with 10% FBS (vol/vol), 2 mM L-glutamine, 100 IU penicillin and 100 mg ml<sup>-1</sup> streptomycin at 37 °C in a humidified incubator containing 5% CO<sub>2</sub>.

**Cell death assay.** Cell death was analysed by measuring plasma membrane integrity to incorporate propidium iodide (PI). To measure the spontaneous cell death, PI (5  $\mu$ g ml<sup>-1</sup>) was directly added in the medium and incubated for 10 min. Total cell numbers and PI-positive cells were counted under an inverted fluorescence microscope. Four fields of cells for each sample (more than 1,000 cells) were counted. The data are expressed as the percentage of PI-positive cells per total cells counted.

For TNF-induced cell death, cells were trypsinized and re-plated in 12-well plates to remove dead cells 12 h before TNF treatment. Cells were treated with TNF for the

indicated time and then trypsinized, collected by centrifugation, and resuspended in PBS containing 5  $\mu$ g ml<sup>-1</sup> PI. The level of PI incorporation was quantified by flow cytometer (BD, FACSCalibur). Cell size was evaluated by forward-angle light scattering. PI-negative cells with a normal size were considered as living cells.

Apoptosis of MEF cells was measured by Annexin V staining according to the manufacturer's instructions (Biotium).

**Mass spectrometric analysis.** *Rip3* KO L929 cells expressing Flag-Rip3 or empty vector (control) were treated with or without TNF for 4 h. Protein complex was immunoprecipitated with M2 beads, and eluted with 3X FLAG peptides. Proteins from elution were precipitated by addition of TCA to 20% (vol/vol) and incubated on ice for at least 30 min, followed by centrifugation at 16,000g for 10 min at 4 °C. Protein pellets were washed with ice-cold acetone and dried briefly by vacuum centrifugation and then resuspended in 8 M urea in 50 mM NH<sub>4</sub>HCO<sub>3</sub>. Cysteines were reduced (5 mM dithiothreitol, 30 min) and alkylated (15 mM iodoacetamide, 30 min in dark), and the urea concentration was reduced to 1.33 M by dilution with 50 mM NH<sub>4</sub>HCO<sub>3</sub>. Proteins were digested overnight at 37 °C by the addition of trypsin at a ratio of protein/trypsin (1:100). Formic acid was added to 1% (vol/vol), peptides were loaded onto a STAGETip for desalting, and peptides were eluted directly into inserts with 70% acetonitrile/1% formic acid. The tryptic peptides were analysed on an AB Sciex TripleTOF 5600 mass spectrometer interfaced to an Eksigent NanoLC Ultra 2D Plus HPLC system, essentially as previously described<sup>51</sup>. Peptides were chromatographed using a 60-min gradient from 2–35% (buffer A 0.1% (vol/vol) formic acid 2% (vol/vol) acetonitrile, buffer B 0.1% (vol/vol) formic acid, 98% (vol/vol) acetonitrile) after injection onto a 15-cm emitter (New Objective) packed with New Objective C18 3- $\mu$ m. MS1 spectra were collected in the range 350–1,250 *m/z* for 250 ms, and the 20 most intense precursors with charge state 2–5 were selected for fragmentation; MS2 spectra were collected in the range 100–1,800 *m/z* for 100 ms. For each IP sample, triple injections were performed to achieve depth identification. All wiff files were searched against the mouse Uniprot proteome database (July 2013) appended with common contaminants and reversed-sequence decoys (101,970 sequence including decoys) using ProteinPilot V4.5 beta. 'Iodoacetamide' was selected for Cys alkylation, and 'Trypsin' as protease, and Search Effort was set as 'Rapid ID'. Proteins were filtered with 5% FDR. Phosphatases identified in either TNF-treated or untreated samples were selected as potential Rip3 phosphatases.

**Immunoprecipitation and immunoblotting.** Cells were lysed with lysis buffer (20 mM Tris-HCl, pH 7.5, 150 mM NaCl, 1 mM Na<sub>2</sub>EDTA, 1 mM EGTA, 1% Triton X-100, 2.5 mM sodium pyrophosphate, 1 mM  $\beta$ -glycerophosphate, 1 mM Na<sub>3</sub>VO<sub>4</sub>) on ice for 15 min. Cell lysates were then centrifuged at 20,000g for 30 min. The supernatant was immunoprecipitated with antibody-coupled beads at 4 °C for 3 h or overnight. After the immunoprecipitation, the beads were washed four times in lysis buffer and the immunoprecipitated proteins were subsequently eluted by SDS sample buffer. For endogenous Rip3 immunoprecipitation, anti-Rip3 antibody was coupled to beads by the GlycoLink Immobilization Kit according to the manufacturer's instructions. The luminescent signals of immunoblotting were analysed using an ImageQuant LAS 4000 Scanner (GE Healthcare) or X-ray film.

**In vitro phosphatase assay.** GST-Ppm1b and GST-R179G were expressed and purified from *Escherichia coli* Flag-mRip3 protein was immunoprecipitated using anti-Flag beads from cell lysates of transfected 293T cells and eluted with  $\times$ 3 Flag peptide. GST-Ppm1b, GST-R179G and GST were incubated with Flag-Rip3 in buffer (20 mM HEPES, 20 mM MgCl<sub>2</sub>, 0.03%  $\beta$ -mercaptoethanol) at 30 °C for 30 min with gentle shaking. The reactions were stopped by the addition of  $\times$ 2 SDS sample buffer followed by boiling for 5 min.

For  $\lambda$ -phosphatase treatment, endogenous Rip3 was immunoprecipitated by Rip3 antibody-coupled beads and washed three times with  $\times$ 1 phosphatase buffer (50 mM HEPES (pH 7.5), 100 mM NaCl, 2 mM dithiothreitol, 0.01% Brij 35, 1 mM MnCl<sub>2</sub>). The immunoprecipitate was then divided into two parts. One was augmented with 200 units of  $\lambda$ -phosphatase (NEB) but the other was mock treated. After incubation at 30 °C for 30 min with gentle shaking, the reactions were stopped by the addition of  $\times$ 2 SDS sample buffer followed by boiling for 5 min.

**Chemical-induced forced Rip3-Rip3 interaction and Mkl1 oligomerization.** To generate the FKBP-Rip3<sup>RHIM</sup> and FRB-Rip3<sup>RHIM</sup> constructs the Rip3<sup>RHIM</sup> (QIG449-451AAA) mutant was fused to the C terminus of the FKBP domain (FK506 binding protein) and FRB domain (domain of mTOR with a point mutation T2098L). Plasmids used as templates containing FKBP and the mutant FRB domain were obtained from the ARGENT Regulated Heterodimerization Kit kindly provided by ARIAD (now iDimerize™ Inducible Heterodimer System by Clontech). The interaction of FKBP and FRB fusion proteins can be induced by a rapamycin analogue AP21976. The FKBP-Rip3<sup>RHIM</sup> and FRB-Rip3<sup>RHIM</sup> were introduced to *Rip1-Rip3* DKO L929 cells by co-infection of lentiviral vectors. To evaluate the



Ppm1b function, these cells were then co-infected with lentiviral vectors encoding Ppm1b-L and Ppm1b-S, or infected with empty vectors. As the infection efficiency was nearly 100% (evidenced by parallel infection or co-infection with lentiviral-GFP), it was unnecessary to select cells that express both proteins. Twenty-four hours after infection, AP21976 (250 nM) was added to induce Rip3–Rip3 interaction. Cell death was analysed 2 h later.

The chemical-induced Mkl1 oligomerization has been described previously<sup>17</sup>. Briefly, Mkl1 was fused to the N terminus of oestrogen-induced homodimerization of the hormone binding domain (HBD) with a G521R mutation (termed Mkl1–HBD). A synthetic antioestrogen 4-hydroxytamoxifen (4-OHT) can induce dimerization of the HBD fusion protein. Mkl1–HBD was introduced to *Mkl1* KO L929 cells by lentiviral vector. Thirty-six hours after infection, 4-OHT (1  $\mu$ M) was added to induce Mkl1 oligomerization. Cell death was analysed 2 h later.

**Generation of *Ppm1b<sup>d/d</sup>* and *Ppm1b<sup>d/d</sup> Rip3<sup>-/-</sup>* mice.** The mouse Ppm1b-disrupted embryonic stem cell clone (AW0406) with a retrovirus vector based on the gene-trap technology employed at Sanger Institute was purchased from the Mutant Mouse Regional Resource Center (MMRRC, University of California Davis). The exact gene-disruption position was determined by 3' RACE and genomic DNA PCR. *Ppm1b<sup>d/d</sup>* embryonic stem cells were injected into C57BL/6 blastocysts, and chimaeric male mice were bred to C57BL/6 wild-type female mice. The resulting *Ppm1b<sup>d/d</sup>* offspring were bred to C57BL/6 mice for more than ten generations. Genotyping was carried out by genomic DNA PCR with the following three primers: P1-5'-TCTCGTTGCATTAGTGTTTACCACTGT-3' (forward sequences in *Ppm1b* genome); P2-5'-GGCTTCTGAATAACCGAATTCAAGG-3' (reverse sequences in *Ppm1b* genome); P3-5'-CTCCCTGGCCTCCAGACAAGTAGA-3' (reverse sequences in retrovirus intron). P1 and P2 are for wild-type allele PCR to produce a 217-bp band, and P1 and P3 are for mutated allele PCR to produce a 310-bp band.

*Rip3<sup>-/-</sup>* mice were generated by the transcription activator-like effector nucleases (TALENs)-mediated gene-disruption method in a C57BL/6 background, as described previously<sup>28</sup>. Genotypes were confirmed by tail-snip PCR. *Rip3<sup>-/-</sup>* and *Ppm1b<sup>d/d</sup>* were subsequently intercrossed.

**SIRS mice model.** Mice were housed in a specific pathogen-free environment. All experiments were conducted in compliance with the regulations of Xiamen University. Six- to eight-week-old female mice (average weight approximately 20 g) were injected intravenously with 15  $\mu$ g TNF (75  $\mu$ g ml<sup>-1</sup>) diluted in endotoxin-free PBS. Mice injected with PBS alone were included as a control. Animals were under permanent observation and survival was checked every 30 min. Littermates of *Rip3<sup>-/-</sup>* and WT, *Ppm1b<sup>d/d</sup>* and WT, *Ppm1b<sup>d/d</sup> Rip3<sup>-/-</sup>* and *Ppm1b<sup>+/+</sup> Rip3<sup>-/-</sup>* mice were used in the experiments. The investigator was blinded to allocation when the mice were injected with TNF and when mice deaths were counted.

In total, 44 pairs of *Rip3<sup>-/-</sup>* and WT mice, 79 pairs of *Ppm1b<sup>d/d</sup>* and WT mice, and 26 pairs of *Ppm1b<sup>d/d</sup> Rip3<sup>-/-</sup>* and *Ppm1b<sup>+/+</sup> Rip3<sup>-/-</sup>* mice were used in these experiments and the subsequent histology analyses.

**Histology.** After animals were euthanized, tissues of different organs were collected immediately, and fixed in 10% neutral buffered formalin for 24 h. The fixed tissues were dehydrated in ethanol, cleared in xylene, and embedded in paraffin blocks. Five-micrometre sections were cut and mounted on adhesion microscope slides (ZSGB-BIO), and then stained with haematoxylin and eosin (H&E) or periodic acid–Schiff (PAS) for analyses.

The degree of caecum damage was assessed by a method described previously<sup>42</sup>. Then the sum of the average scores of four fields per sample was calculated as the

caecum damage score. Representative images were captured and processed using identical settings in the Leica DM2500 at Xiamen University.

The investigators were blinded to allocation when the histology experiments were performed and tissue damage was scored.

**IL-6 level determination.** Following the manufacturer's instructions, the supernatants of the cell culture were collected and the IL-6 level was measured by commercial ELISA kits for mouse IL-6 (R&D). For the *in vivo* SIRS model, the sera were collected before (0 h) and after (2 h, 4 h) TNF injection, and were analysed for their IL-6 levels by ELISA kits.

**Isolation of nucleus and cytosol.** Cells were trypsinized, collected by centrifugation, and washed with pre-cold PBS three times. Then cells were resuspended in Buffer A (10 mM HEPES, pH 7.9; 1.5 mM MgCl<sub>2</sub>; 10 mM KCl; 300 mM sucrose; 0.5% NP-40) for 10 min on ice with gentle tapping. Cell lysate was then centrifuged at 1,000g for 5 min. The suspension (cytosol) was collected and centrifuged further at 1,000g for 10 min to get rid of nucleus contamination; the pellets (nucleus) were resuspended and washed with Buffer A twice.

**Subcellular fractionation.** L929 cells were fractionated and heavy membrane (HM), mitochondria (Mito) and heterotypic membrane (HeteroM) were isolated as described previously<sup>41</sup>. Briefly, approximately  $3 \times 10^8$  cells were washed with cold PBS and collected into 50 ml tubes. Cells were homogenized by glass homogenizer (Kontes) in homogenization buffer (225 mM mannitol, 75 mM sucrose, 0.1 mM EGTA and 30 mM Tris–HCl (pH 7.4)). The lysate was centrifuged at 800g to remove nuclei. The supernatant was centrifuged at 100,000g for 10 min at 4 °C and the subsequent pellet was collected as HM. For further purification, HM was resuspended and loaded on 20% Percoll and centrifuged at 10,000g for 30 min at 4 °C. Mitochondria were recovered from the bottom of the gradient; the heterotypic membranes were collected from the upper gradient. Each fraction was quantified and indicated proteins were analysed by western blot.

**Statistical evaluation.** Statistical analysis was performed with Prism software (GraphPad Software). Data are expressed as means  $\pm$  s.e.m. Two-tailed Student's *t*-test was used to compare differences between treated groups and their paired controls. Mice survival is presented as a Kaplan–Meyer plot and compared by log-rank (Mantel–Cox) Test. To evaluate the caecum damage between the two genotypes, a Wilcoxon signed-rank test was performed. Differences in compared groups were considered statistically significantly different with *P* values lower than 0.05; \*, *P* < 0.05; \*\*, *P* < 0.01; \*\*\*, *P* < 0.001.

No statistical method was used to predetermine sample size. The experiments were not randomized. The investigators were blinded to allocation during the SIRS mouse model experiments and histology experiments (see the SIRS mice model and Histology section above). For other experiments, the investigators were not blinded to allocation during experiments and outcome assessment.

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# ERRATUM

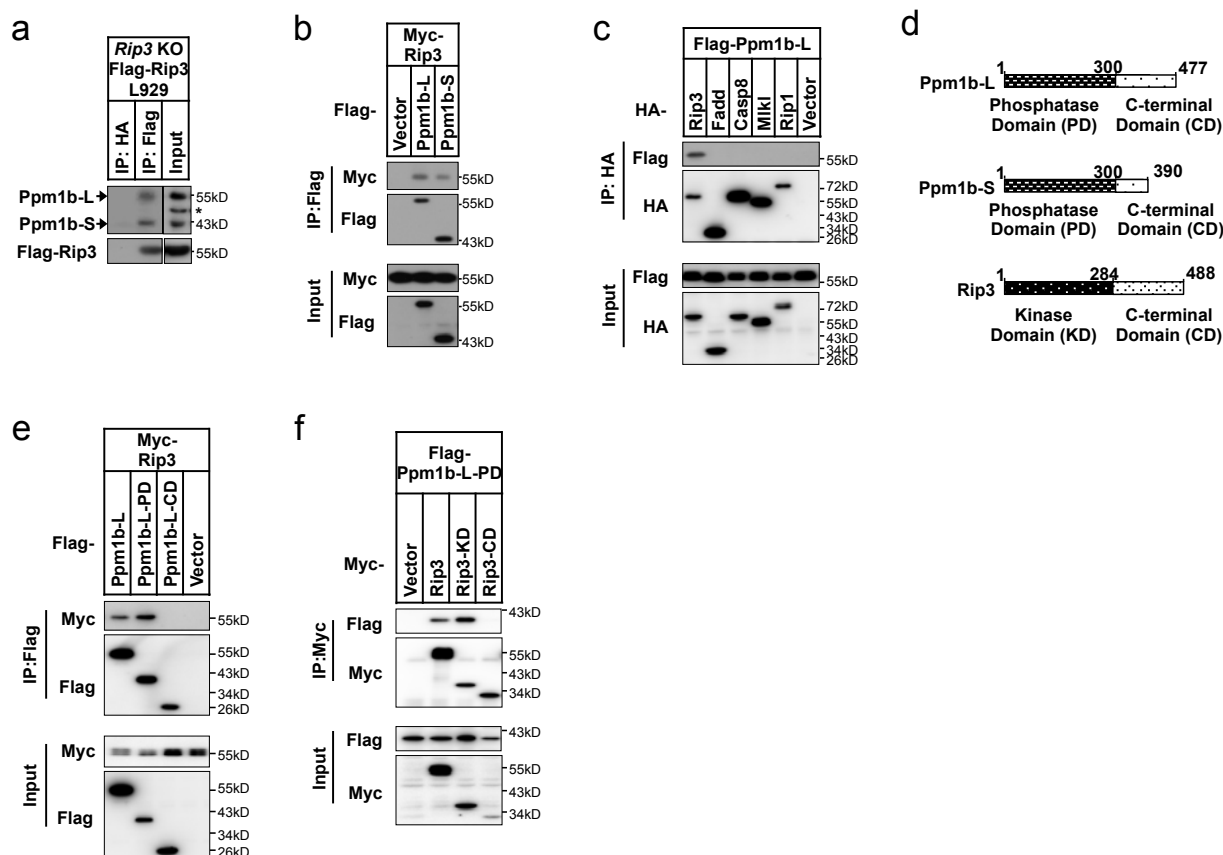
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## Ppm1b negatively regulates necroptosis through dephosphorylating Rip3

Wanze Chen, Jianfeng Wu, Lisheng Li, Zhengmao Zhang, Junming Ren, Yaoji Liang, Fenfang Chen, Chao Yang, Zhenru Zhou, Sheng Sean Su, Xinru Zheng, Zhirong Zhang, Chuan-Qi Zhong, Haoqiang Wan, Mu Xiao, Xia Lin, Xin-Hua Feng and Jiahuai Han

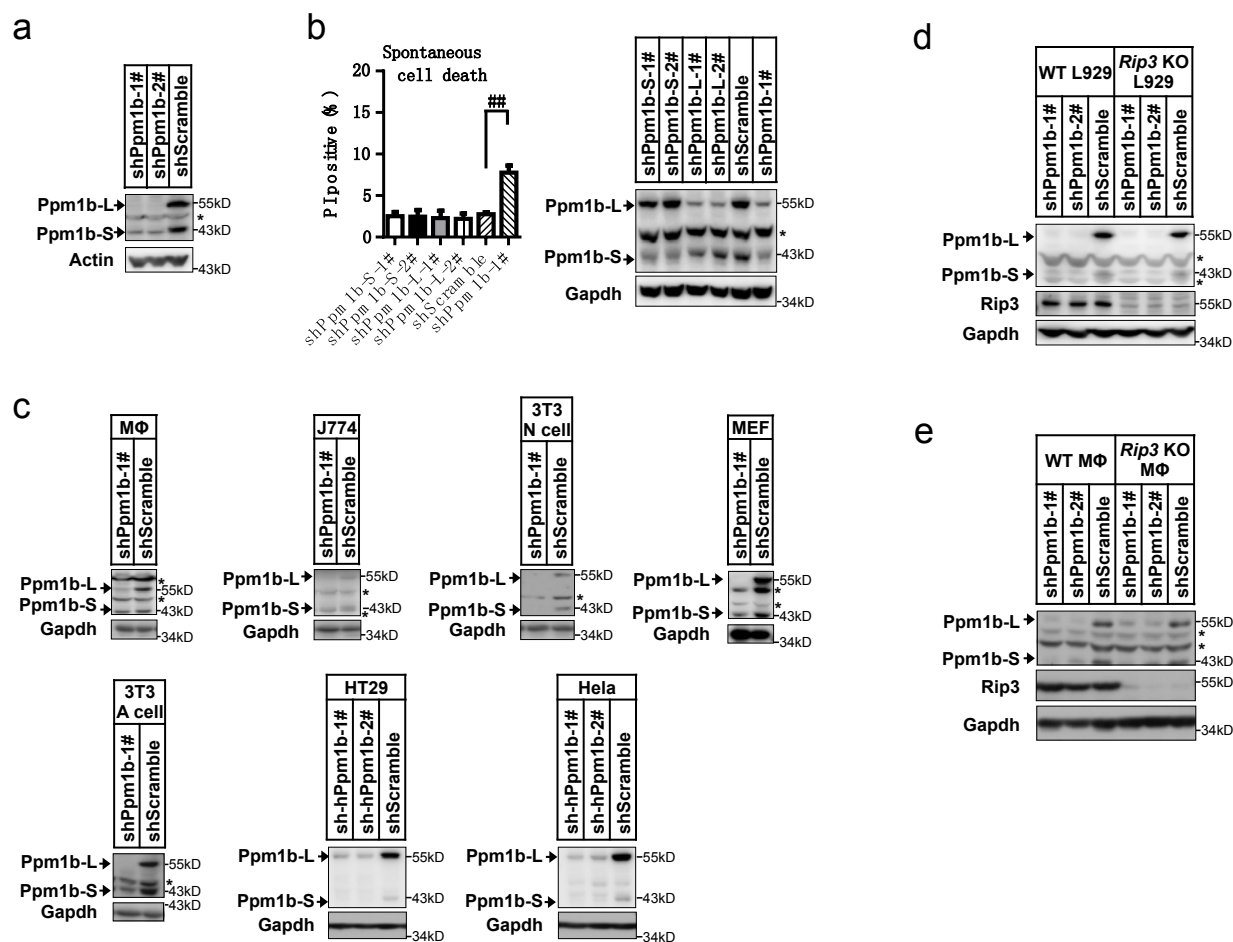
*Nat. Cell Biol.* <http://dx.doi.org/10.1038/ncb3120> (2015); published online 9 March 2015; corrected online 19 March 2015

In the version of this Article originally published online the molecular mass of Ppm1b-S (isoform 2) should have read  $M_r43K$ . This has been corrected in all versions of the Article.



**Supplementary Figure 1** Ppm1b interacts with Rip3. (a) Ppm1b interacts with Rip3 in resting stage in L929 cells. Rip3-KO-Flag-Rip3 L929 cells were lysed and the cell lysates were immunoprecipitated with anti-HA (IP: HA) and anti-Flag (IP: Flag) antibodies. Both the cell lysate (Input) and immunoprecipitates were analyzed by immunoblotting with indicated antibodies. The vertical line represents a splice mark. The samples were obtained and processed in the same experiment, and the gels/blots were processed in parallel. (b) Both Ppm1b-L and Ppm1b-S co-immunoprecipitate with Rip3 in 293T cells. Myc-Rip3 was coexpressed with Flag-tagged Ppm1b-L, Ppm1b-S or empty vector. Then co-immunoprecipitation experiments were performed with anti-Flag antibody. Both the immunoprecipitates and lysates were analyzed by immunoblotting with indicated antibodies. (c) Ppm1b selectively interacts with Rip3 but not the other necrosome components in 293T cells. Flag-Ppm1b-L was

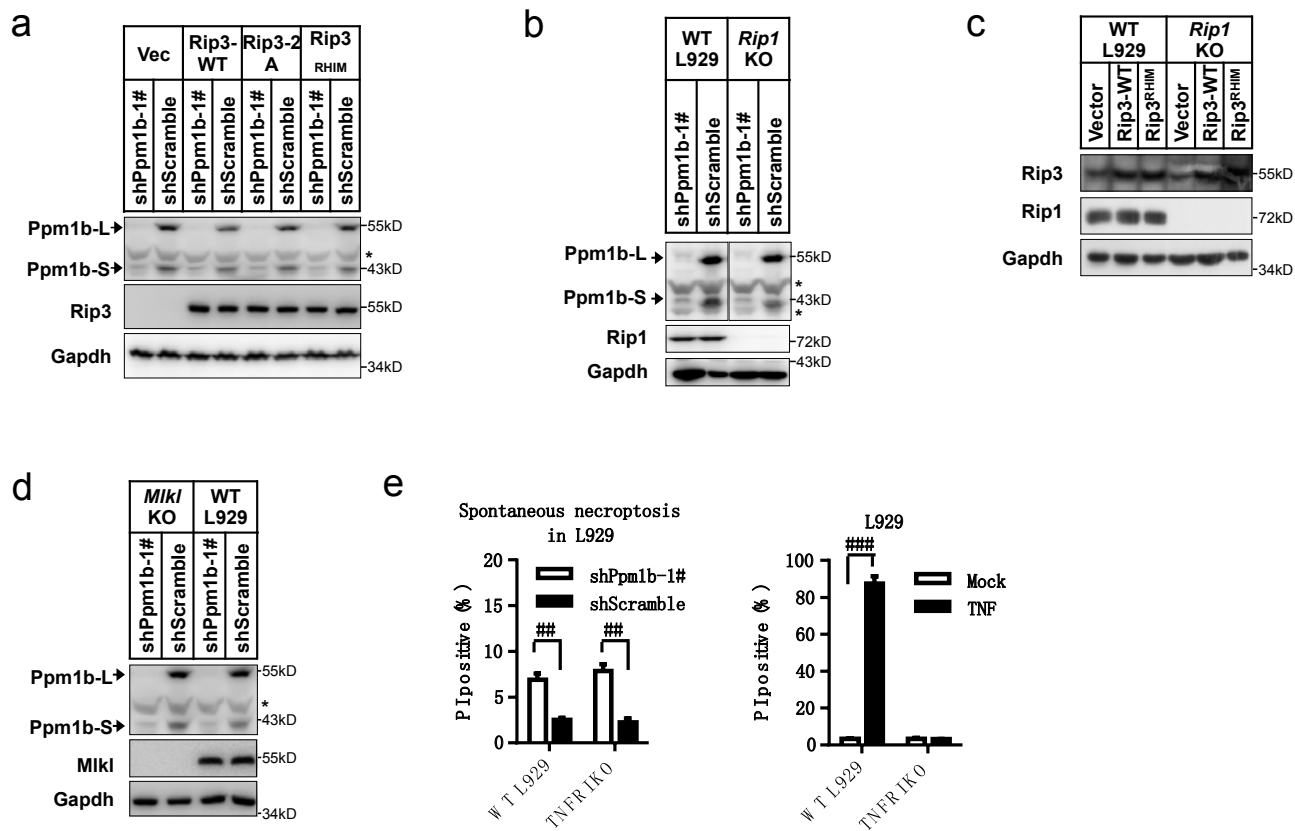
coexpressed with HA-tagged proteins as indicated. Co-immunoprecipitation experiments were performed with anti-HA antibody and analyzed as in (b). (d) Schematic of the domain structures of Ppm1b-L and Ppm1b-S and Rip3. (e) The phosphatase domain of Ppm1b interacts with Rip3. Myc-Rip3 was coexpressed with Flag-tagged full length and truncated Ppm1b in 293T cells. Then co-immunoprecipitation experiments were performed as in (b). Ppm1b-L-PD: Ppm1b-L phosphatase domain; Ppm1b-L-CD: Ppm1b-L C-terminal domain. (f) The kinase domain of Rip3 interacts with Ppm1b. Flag-Ppm1b-L-PD was coexpressed with Myc-tagged full length and truncated Rip3 in 293T cells. Then co-immunoprecipitation experiments were performed with anti-Myc antibody and analyzed as in (b). Rip3-KD: Rip3 kinase domain; Rip3-CD: Rip3 C-terminal domain. Data shown were representative of two or more independent experiments. Uncropped images of blots are shown in Supplementary Figure 7.



**Supplementary Figure 2** Related to Figure 2. (a) The protein amounts in Ppm1b knocked down and control L929 cells were analyzed by immunoblotting with indicated antibodies. Related to Figure 2a. (b) Ppm1b-S, Ppm1b-L and both isoforms were knocked down with isoform-specific shRNAs in L929 cells. Left, 48 hours later, spontaneous cell death was measured. Right, the protein amounts were analyzed by immunoblotting with indicated antibodies. Results shown were mean  $\pm$  s.e.m.;  $n = 3000$  cells pooled from 3 independent experiments. (c) The protein amounts in Ppm1b knocked down and control cells were analyzed by immunoblotting with indicated antibodies. Related to

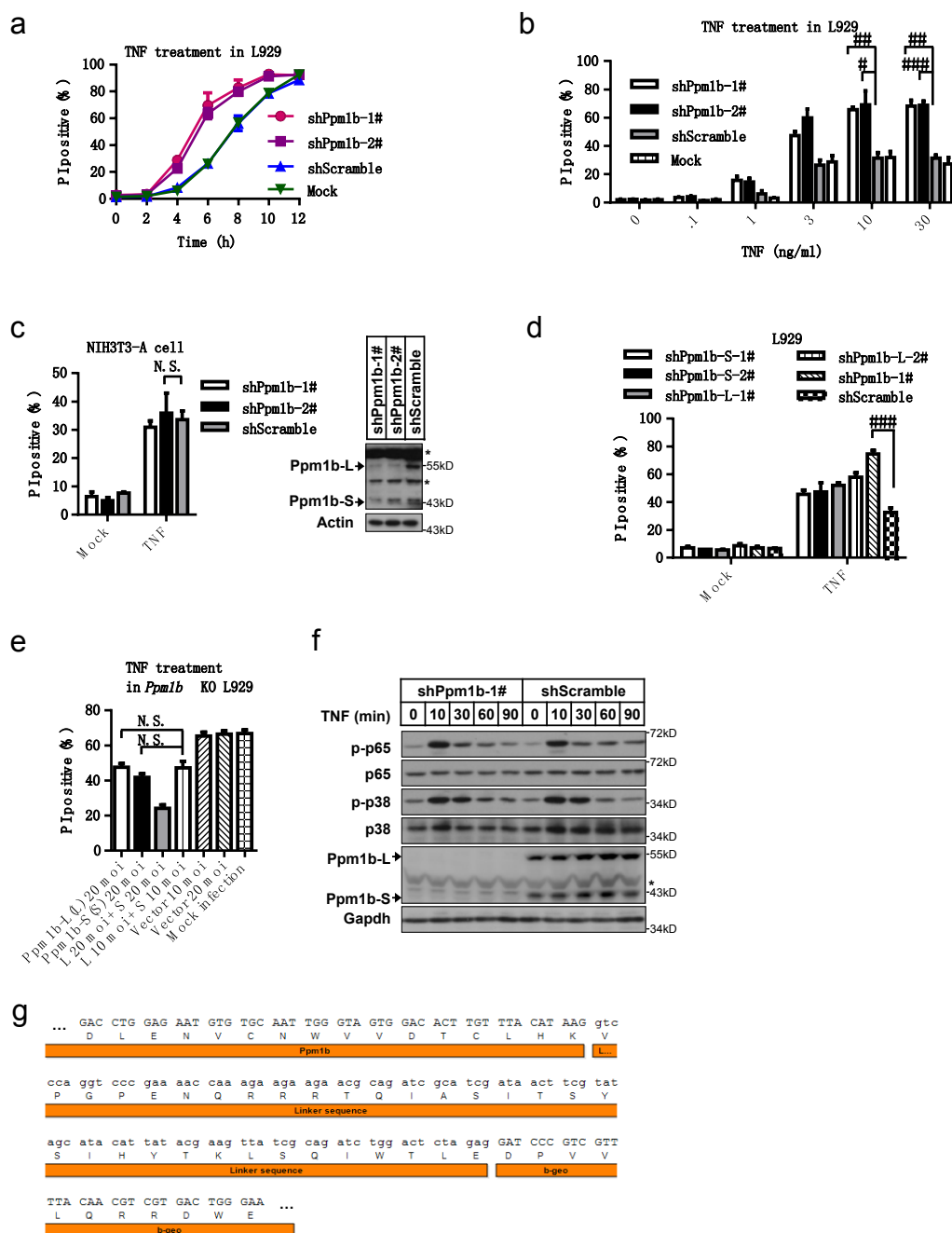
Figure 2c. (d) The protein amounts in WT and *Rip3* KO L929 cells knocked down with shPpm1b or control shRNAs were analyzed by immunoblotting with indicated antibodies. Related to Figure 2f. (e) The protein amounts in WT and *Rip3* KO mouse peritoneal macrophage cells knocked down with shPpm1b or control shRNAs were analyzed by immunoblotting with indicated antibodies. Related to Figure 2g. For Figure a,c,d,e, data shown were representative of two or more independent experiments. The asterisk (\*) denotes a nonspecific band. Statistics source data for this figure can be found in Supplementary Table 2. Uncropped images of blots are shown in Supplementary Figure 7.





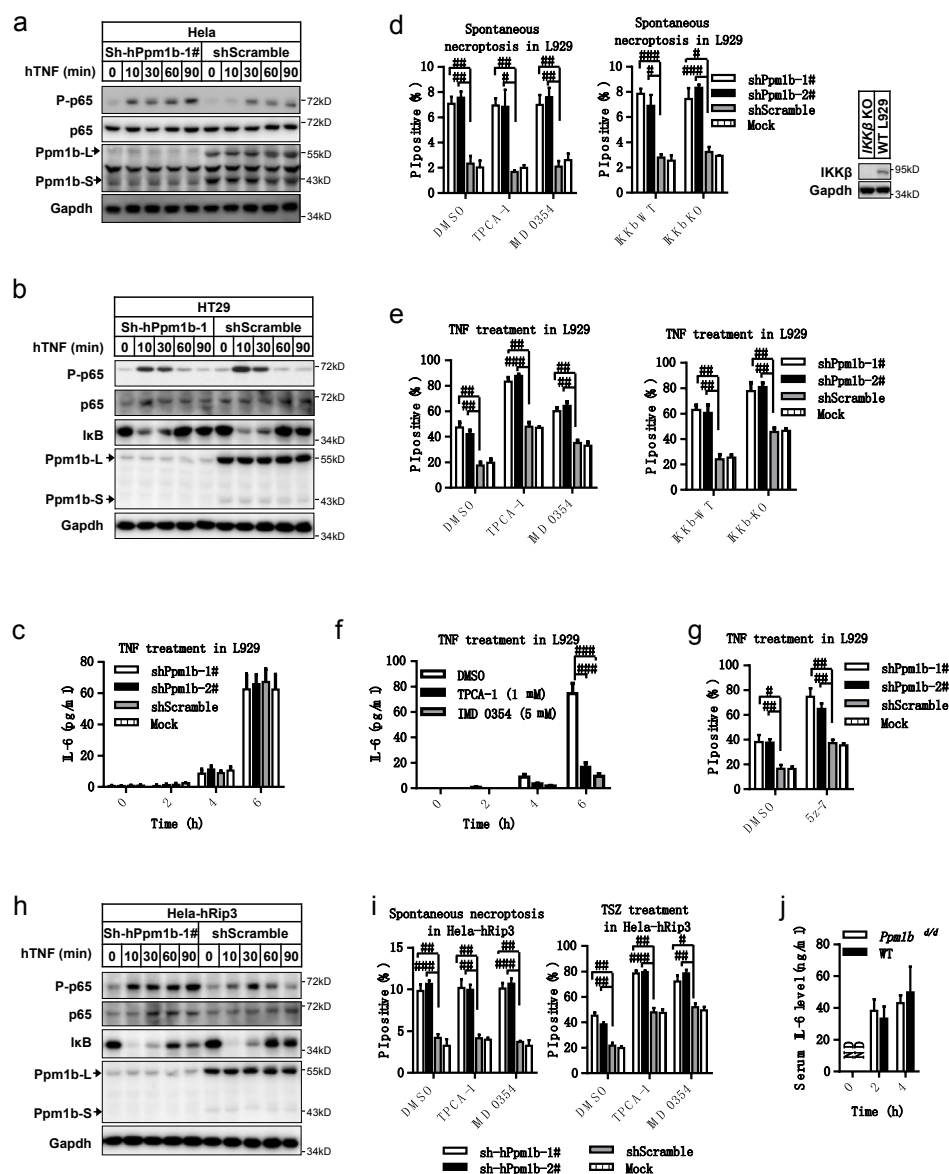
**Supplementary Figure 3** Related to Figure 3. (a) Ppm1b was knocked down in *Rip3* KO L929 cells reconstituted with Rip3-WT, Rip3 phosphorylation deficient mutant (Rip3-2A) mutant and Rip3 RHIM domain mutant (Rip3<sup>RHIM</sup>). The cells were lysed and subjected to immunoblotting with indicated antibodies. Related to Figure 3b. (b) Ppm1b was knocked down in WT and *Rip1* KO L929 cells. The cells were lysed and subjected to immunoblotting with indicated antibodies. The vertical line represents a splice mark. The spliced images were from the same blot. Related to Figure 3c. (c) WT Rip3 and Rip3<sup>RHIM</sup> were introduced into *Rip1* KO and WT L929 cells by lentiviral vectors. The cells were lysed and subjected to immunoblotting with indicated antibodies. Related to Figure 3d. (d) Ppm1b was knocked

down in WT and *Mik1* KO L929 cells. The cells were lysed and subjected to immunoblotting with indicated antibodies. Related to Figure 3h. (e) *TNFR1* KO and WT L929 cells were infected with lentivirus encoding shPpm1b or control. Left, spontaneous cell death was analyzed 48 hours later.  $n = 3000$  cells pooled from 3 independent experiments. Right, *TNFR1* KO and WT L929 cells were treated with or without TNF for 12 hours. Cell death was analyzed.  $n = 3$  independent experiments. Results shown were mean  $\pm$  s.e.m.; ## $P < 0.01$ ; ### $P < 0.001$ . For Figure a-d, data shown were representative of two or more independent experiments. The asterisk (\*) denotes a nonspecific band. Statistics source data for this figure can be found in Supplementary Table 2. Uncropped images of blots are shown in Supplementary Figure 7.



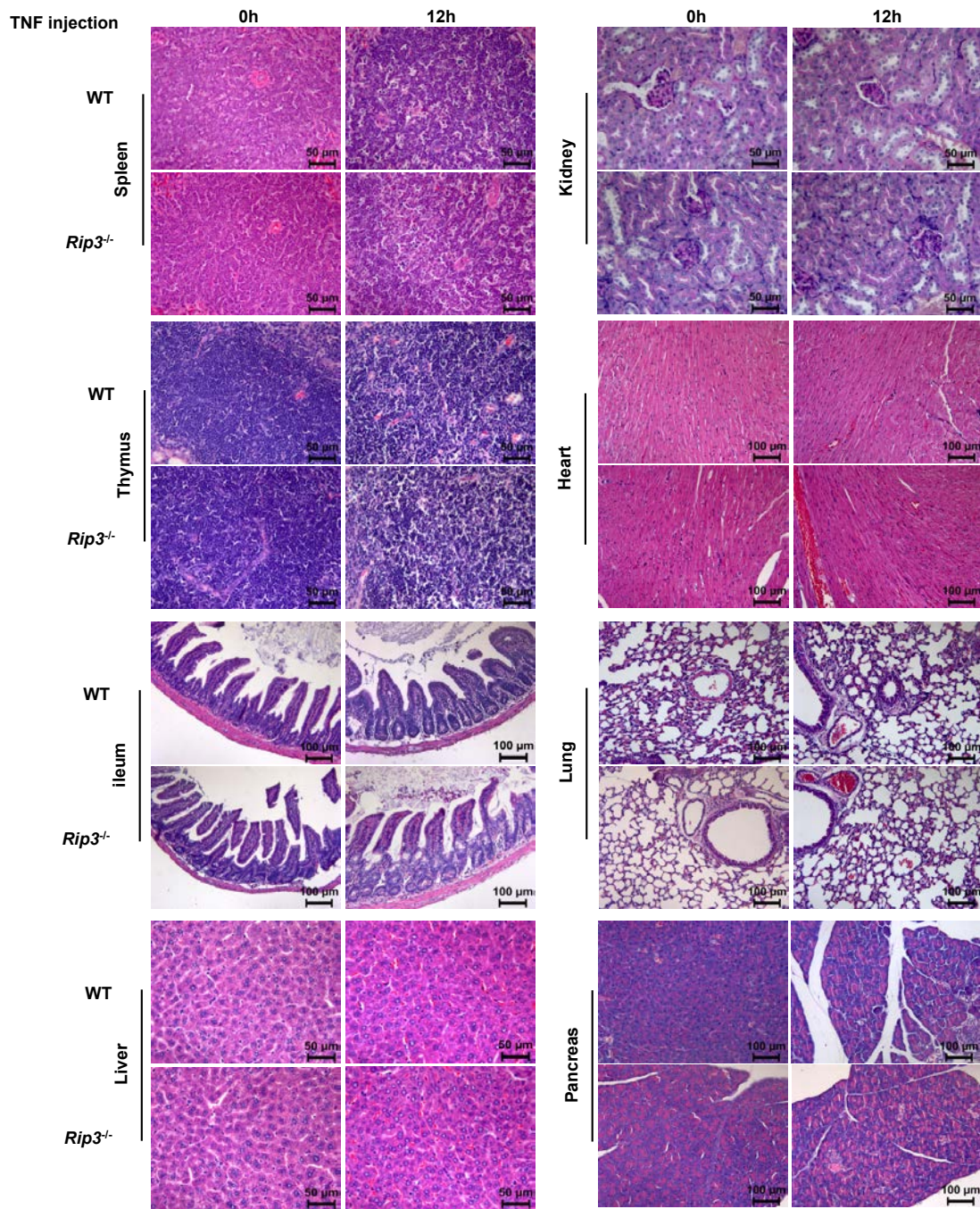
**Supplementary Figure 4** Ppm1b targets TNF-induced necroptosis but not apoptosis. **(a-b)** L929 cells were infected with lentivirus encoding shPpm1b or control, or not infected (Mock). 48 hours later, (a) the cells were treated with TNF (10 ng/ml) for indicated time periods and cell death was analyzed by flow cytometer; (b) the cells were treated with different doses of TNF as indicated for 6 hours and cell death was analyzed.  $n = 3$  independent experiments. **(c)** Ppm1b does not affect TNF-induced apoptosis in NIH3T3-A cells. Ppm1b was knocked down in NIH3T3-A cells. Left, 48 hours later, the cells were treated with or without TNF (100 ng/ml) for 24 hours and cell death was analyzed.  $n = 3$  independent experiments. Right, the cell lysates were analyzed by immunoblotting with indicated antibodies. **(d)** Both Ppm1b-L and S isoforms restrict TNF-induced necroptosis in L929. Ppm1b-S, Ppm1b-L or both isoforms were knocked down with isoform specific shRNAs in L929 cells. 48 hours later, the cells were treated with or without TNF (10 ng/ml) for 6 hours and cell death was measured.  $n =$

3 independent experiments. **(e)** *Ppm1b* KO L929 cells were infected with different doses of lentivirus encoding Ppm1b-L and Ppm1b-S as indicated, or not infected (Mock infection). Then the cells were treated with TNF (10 ng/ml) for 6 hours and cell death was analyzed.  $n = 3$  independent experiments. **(f)** Ppm1b does not affect the TNF-induced p65 and p38 phosphorylation. Ppm1b was knocked down with shRNA in L929 cells. 48 hours later, the cells were treated with TNF (10 ng/ml) for indicated time. The cell lysates were analyzed by immunoblotting with indicated antibodies. **(g)** The Ppm1b- $\beta$ -geo fusion mRNA sequences in *Ppm1b*<sup>del</sup> mice were determined by 3' RACE. For Figure a-e, results shown were mean  $\pm$  s.e.m.; \* $P < 0.05$ ; \*\* $P < 0.01$ ; \*\*\* $P < 0.001$ ; N.S.: no significant difference. For Figure f, data shown were representative of two independent experiments. The asterisk (\*) denotes a nonspecific band. Statistics source data for this figure can be found in Supplementary Table 2. Uncropped images of blots are shown in Supplementary Figure 7.



**Supplementary Figure 5** The regulation of necroptosis by Ppm1b is independent of NF- $\kappa$ B pathway. (a) HeLa cells were infected with lentivirus encoding sh-hPpm1b or control. 48 hours later, the cells were treated with hTNF (30 ng/ml) for indicated time and subjected to immunoblotting with indicated antibodies. (b) HT29 cells were analyzed as in (a). (c) L929 cells were infected with lentivirus encoding shPpm1b or control, or not infected (Mock). 48 hours later, the cells were treated with TNF for indicated time and the IL-6 level of the cell culture supernatant was analyzed by ELISA. n = 3 independent experiments. (d) Left, L929 cells were infected with lentivirus encoding shPpm1b or control, or not infected (Mock). 5 hours after infection, the cells were treated with DMSO, TPCA-1 (1  $\mu$ M) or IMD 0354 (5  $\mu$ M). 48 hours later, spontaneous cell death was analyzed. Middle, IKK $\beta$  KO and WT L929 cells were infected with lentivirus encoding shPpm1b or control, or not infected. 48 hours later, spontaneous cell death was analyzed. Right, the IKK $\beta$  protein amount in IKK $\beta$  KO and WT L929 cells was determined by immunoblotting. n = 3000 cells pooled from 3 independent experiments. (e) Left, the cells were treated as in (d, left), except that the cells were treated with TNF for 5 hours and the TNF-induced cell death rather than spontaneous cell death was analyzed 48 hours after infection. Right, the cells were treated as in (d, middle), except that the cells were treated with TNF for 5 hours and TNF-induced cell death rather than spontaneous cell death was analyzed 48

hours after infection. n = 3 independent experiments. (f) L929 cells were pretreated with DMSO, TPCA-1 or IMD 0354 for 2 hours followed by treatment with TNF for indicated time. The IL-6 level of the cell culture supernatant was analyzed by ELISA. n = 3 independent experiments. (g) L929 cells were infected with lentivirus encoding shPpm1b or control, or not infected. 48 hours later, the cells were pretreated with DMSO or 5z-7 (1  $\mu$ M) for 2 hours followed by treatment with TNF for 5 hours. Then the cell death was analyzed. n = 3 independent experiments. (h) HeLa cells stably expressing human Rip3 (HeLa-hRip3) were analyzed as in (a). (i) HeLa-hRip3 cells were infected with lentivirus encoding sh-hPpm1b or control, or not infected. Spontaneous cell death and hTNF (30 ng/ml) + Smac mimetic (100 nM) + zVAD (20  $\mu$ M) (TSZ)-induced cell death were analyzed as in (d, left) and (e, left). n = 3 independent experiments. (j) Littermates of *Ppm1b*<sup>+/+</sup> and WT mice were injected with TNF (15  $\mu$ g) via the tail vein. Then the serum IL-6 level was analyzed by ELISA at different time points as indicated. n = 4 mice for each group in single experiment where two independent experiments were performed to assess reproducibility. ND: not detectable. For Figure c-g,i,j, results shown were mean  $\pm$  s.e.m.; #P < 0.05; ##P < 0.01; ###P < 0.001. For Figure a,b,h, data shown were representative of two or more independent experiments. Statistics source data for this figure can be found in Supplementary Table 2. Uncropped images of blots are shown in Supplementary Figure 7.



**Supplementary Figure 6** TNF induces tissue damage in different organs of WT and *Rip3*<sup>-/-</sup> mice. Littermates of WT and *Rip3*<sup>-/-</sup> mice were injected with TNF (15  $\mu$ g) via the tail vein for indicated time. The sections of kidney were analyzed by PAS staining while those of the

other organs were analyzed by H&E staining. The representative images were shown (n=5 mice of each genotype at 12 hour time point; n=3 mice of each genotype at 0 hour time point.). Scale bar: 50 or 100  $\mu$ m as indicated.





Supplementary Figure 7 Uncropped images of blots in Figure 1-7 and Supplementary Figure 1-6.

**Supplementary Table Legends**

**Supplementary Table 1** The mass spectrometric data of Rip3 immunocomplex. Rip3 KO L929 cells were reconstituted with Flag-Rip3 to generate Rip3-KO-Flag-Rip3 L929 cells. Upon TNF treatment for 5 hours, these cells were lysed and subjected to immunoprecipitation with anti-Flag antibody. Then the immunocomplex was analyzed by mass spectrometry and results were listed below. See “Methods” for detail. Protein score: A measure of the protein confidence for a detected protein, calculated from the peptide confidence for peptides. The higher the value is, the more confidently the protein exists in the sample. %Cov (coverage): The percentage of matching amino acids from identified peptides having confidence greater than 0, divided by the total number of amino acids in the sequence. %Cov(95)(coverage): The percentage of matching amino acids from identified peptides having confidence greater than 95%, divided by the total number of amino acids in the sequence. Peptides(95%): The number of the unique, high confident (>95%) peptides in the detected protein.

**Supplementary Table 2** The statistics source data for Figures and Supplementary Figures.