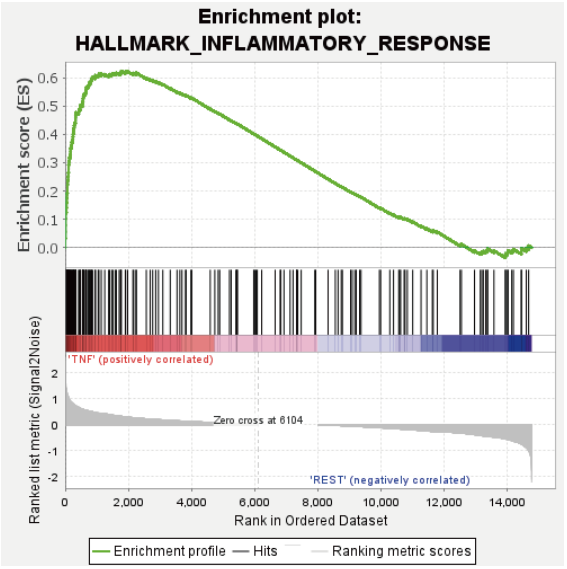
# Figure S2

a

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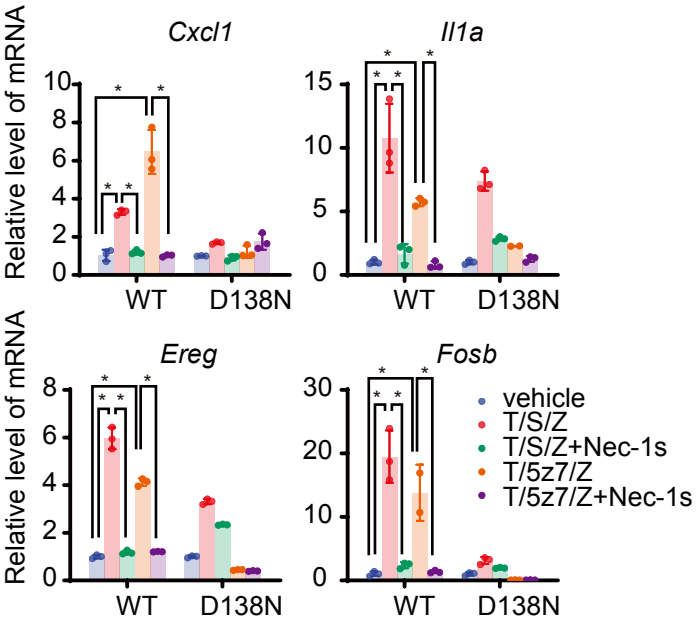


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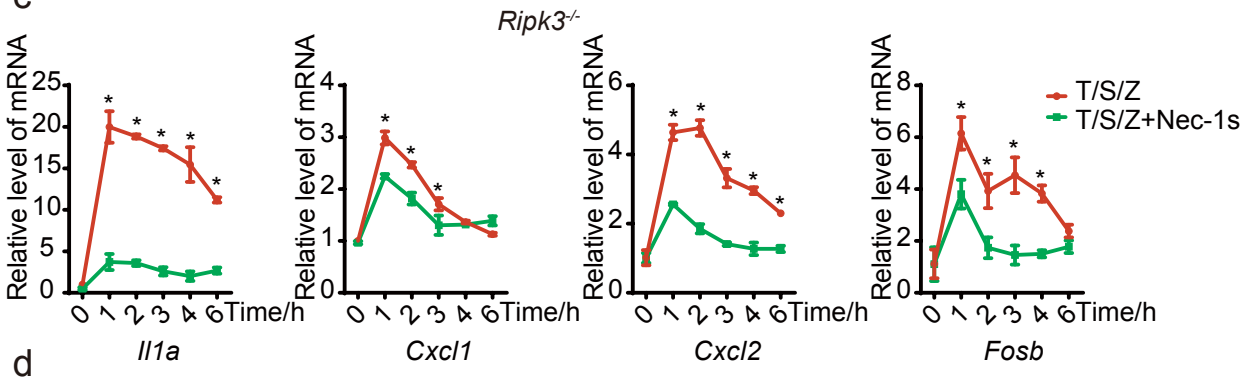
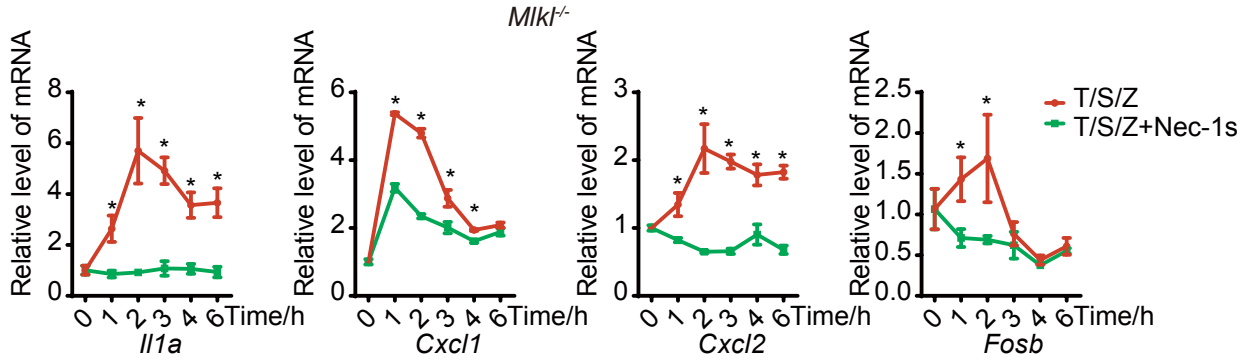



d



# Figure S2

e

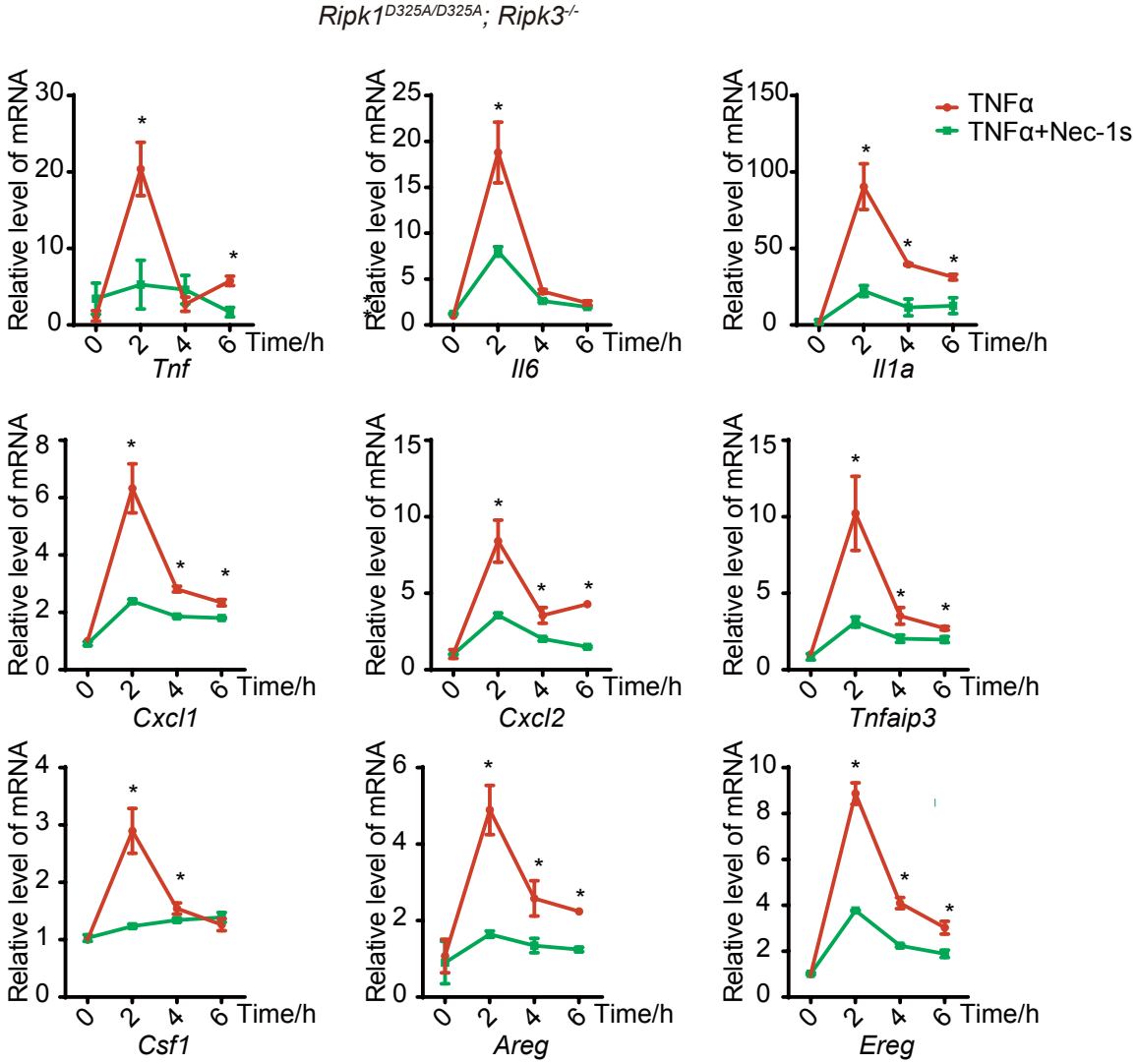



**Fig. S2 RIPK1 regulates gene transcription in a cell death independent manner. a** Inflammatory response pathway analysis was shown by GSEA enrichment plot of RNA-seq data with the genes significantly enriched in *Ripk1*$^{D325A/D325A}$*;Ripk3*$^{-/-}$ MEFs treated with TNFα compared with vehicle or TNFα plus Nec-1s. **b** qPCR verification of the expression of indicated genes from the RNA-Seq results in Wildtype or *Ripk1*$^{D138N/D138N}$ MEFs with indicated treatment. 5 ng/ml mTNFα, 50 μM SM164, 100 nM (5Z)-7-oxozeaeno, 20 μM zVAD-fmk, 10 μM Nec-1s were used. mTNFα was added 0.5h after pretreatment with other compounds and treated for 3h (n = 3, mean ± SD). *p < 0.01. **c, d** qPCR analyses of the expression of indicated genes in *Ripk3*$^{-/-}$ (c), *Mlkl*$^{-/-}$ (d), MEFs treated with vehicle, or 50 μM SM164, 20 μM zVAD-fmk, +/- 10 μM Nec-1s for 0.5h followed by 5 ng/ml mTNFα for the indicated time course (n = 3, mean ± SD). *p < 0.05. **e** qPCR analyses of the expression of indicated genes in *Ripk1*$^{D325A/D325A}$*;Ripk3*$^{-/-}$ MEFs treated with vehicle, or +/- 10 μM Nec-1s for 0.5h followed by 20 ng/ml mTNFα for the indicated time course (n = 3, mean ± SD), *p < 0.05.