

Supplemental Figure 1: Flow cytometry gating strategy for the detection of APANs and the effect of LPS on APAN formation. (A) Human peripheral blood neutrophils  $(1\times10^6/\text{mL})$ 

obtained from healthy volunteers were stimulated with various doses of eCIRP for 4 h. The cells were then stained with anti-CD66b, CXCR4, CD62L, CD86, CD40, HLA-DR, and isotype Ab, followed by the detection of APANs by flow cytometry. Representative images of the gating strategy are shown. (B) HLA-DR expression in eCIRP-treated human blood neutrophils was assessed in various neutrophil populations (APANs, naAPNs, and nAPANs) by flow cytometry as presented in the histogram. BMDNs  $(1\times10^6)$  were treated with eCIRP at different (C) doses and (D) time-points and then the cells were stained with anti-Ly6G, CD40, CD86, CXCR4, and CD62L and subjected to flow cytometry. (E) MHC-II expression was assessed in various cell population by flow cytometry as presented in the histogram. (F) Morphology of APANs. APANs were sorted from splenic cells of CLP mice, placed on a slide glass, and stained with Wright-Giemsa solution (Sigma-Aldrich). Samples were observed with microscope at 1000× magnification. n=3 APAN cells are shown as representative images. (G) Effect of LPS on APAN formation. Mouse BMDNs ( $1\times10^6$ /mL) were treated with LPS at various doses for 12 h. The frequency of APANs was then assessed by flow cytometry. Experiments were performed at least 3 times, and all data were analyzed. Data are expressed as mean  $\pm$  SEM and compared by oneway ANOVA and SNK test. n=6/group. \*p<0.05 vs. PBS. BMDNs, bone marrow-derived neutrophils; APAN, antigen-presenting aged neutrophil.

#### Supplemental Figure 2 В nCount\_RNA percent.mito nCount\_RNA nFeature\_RNA percent.mito 4000 0.75 3000 PRS eCIRP PBS С D Ε F 20 GN UrAc APAN (%) Thio Arth -APAN · PBS eCIRP Log2 odds ratio, eCIRP vs PBS G Н 114 II21 0.050 0.050 no reads mapped to this gene no reads mapped to this gene Expression Level **Expression Level** 0.025 0.025 0.000 0.000

Supplemental Figure 2: Quality control data of single-cell RNA sequencing. (A) Plots showing the number of genes detected in each cell (nFeature\_RNA), the number of molecules

-0.025

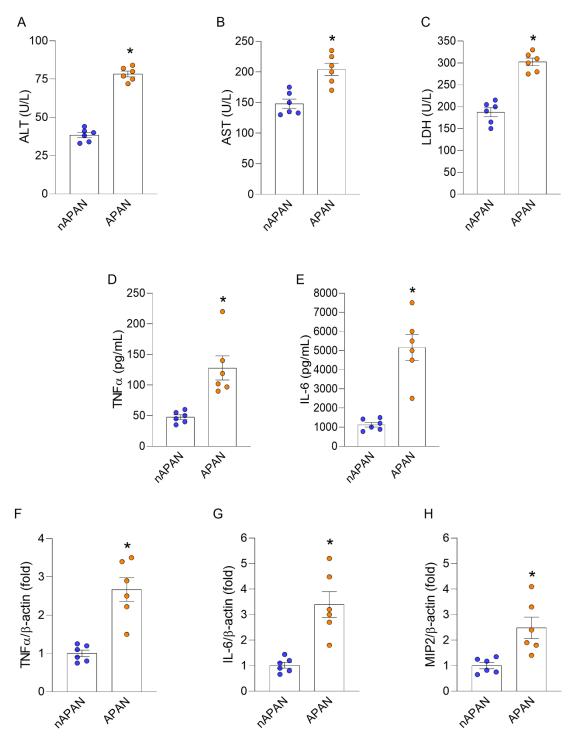
-0.050

-0.025

-0.050

detected in each cell (nCount\_RNA), and percent mitochondrial genes (percent.mito) prior to and (**B**) after filtering. (**C**) Plots showing the percentage and counts of each cell type in the PBS group and (**D**) in the eCIRP-stimulated group. (**E**) Increase in the percentage of APANs after stimulation with eCIRP. (**F**) eCIRP-induced changes in the percentage of cells matching ImmGen mouse neutrophil transcriptomes. (**G**) Graphs showing differential expression of *Il4* and (**H**) *Il21* across different neutrophil transcriptomes. No reads were detected to these genes. BMDN, bone marrow-derived neutrophils; APANs, antigen-presenting aged neutrophils; eCIRP, extracellular cold-inducible RNA-binding protein; Immunological Genome Project, ImmGen; unstimulated circulating neutrophils, GN; arthritic mouse neutrophils, Arth; thioglycolate-simulated peritoneal neutrophils, Thio; uric acid-simulated peritoneal neutrophils, UrAc. APAN, antigen-presenting aged neutrophil; eCIRP, extracellular cold-inducible RNA-binding protein.

#### Supplemental Figure 3



**Supplemental Figure 3:** BMDNs were isolated from WT mice and stimulated with eCIRP for 6 h and after that the cells were stained with anti-Ly6G, CXCR4, CD62L, CD40, and CD86 Ab and then APANs and nAPANs were sorted by FACS. A total of  $1\times10^6$  each of APANs, and

nAPANs were adoptively transferred into neutropenic mice (PMN<sup>DTR</sup> mice) via retro-orbital injection at the time of CLP. At 20 h later, blood and lungs were collected to assess several parameters. Serum (**A**) ALT, (**B**) AST, and (**C**) LDH were determined using specific colorimetric enzymatic assays. Serum (**D**) TNF $\alpha$ , and (**E**) IL-6 levels were measured by ELISA. Lung mRNA levels of (**F**) TNF $\alpha$ , (**G**) IL-6, and (**H**) MIP2 were measured by real-time PCR. Data are expressed as means  $\pm$  SE (n=6 mice/group) and compared by one-way ANOVA and SNK method (\*p<0.05 vs. CLP+nAPAN-injected mice). APAN, antigen-presenting aged neutrophil; nAPAN, non-antigen-presenting aged neutrophil; CLP, cecal ligation puncture; ALT, alanine aminotransferase; AST, aspartate amino transferase; LDH, lactate dehydrogenase; IL, interleukin; TNF, tumor necrosis factor; MIP2, macrophage chemoattractant protein 2.

### Supplemental Table 1: Clinical parameters of patients with sepsis

Patient	Age	Sex	SOFA*	APACHE-II*	Hours#	Initiating Clinical Events
1	65	F	7	26	21	Iatrogenic injury of transverse colon with associated feculent peritonitis
2	71	F	5	14	20	Perforated ischemic bowel secondary to parastomal hernia with associated feculent peritonitis, incidentally COVID-19 <sup>+</sup>
3	66	M	6	12	22	Perforated appendicitis
4	69	F	8	19	19	Deep surgical site infection after incarcerated hernia repair

<sup>\*</sup>SOFA and APACHE-II scores upon presentation; \*Time from identification of sepsis to blood sample collection, hours

# Supplemental Table 2: WBC and neutrophil counts in WT and PMN $^{DTR}$ mice (MRP8-Cre $^+\times$ ROSA-iDTR $^{KI})$

Mice strains	WBCs (x10 <sup>3</sup> cells/μL)	Neutrophils (x10 <sup>3</sup> cells/μL)
WT	$7.58 \pm 3.79$	$2.93 \pm 1.46$
PMN mice (MRP8-Cre <sup>+</sup> × ROSA-iDTR <sup>KI</sup> )	$4.12 \pm 2.06$ *	$0.76 \pm 0.38$ *

N=3/5 mice/group; Student's T-Test; \*p<0.05 vs WT mice

## Supplemental Table 3: Mouse primer sequences

Gene	Forward (5'-3')	Reverse (5'-3')
TNFα	AGACCCTCACACTCAGATCATCTTC	TTGCTACGACGTGGGCTACA
IL-6	CCGGAGAGGAGACTTCACAG	CAGAATTGCCATTGCACAAC
KC	GCTGGGATTCACCTCAAGAA	ACAGGTGCCATCAGAGCAGT
MIP2	CCCTGGTTCAGAAAATCATCCA	GCTCCTCCTTTCCAGGTCAGT
β-actin	CGTGAAAAGATGACCCAGATCA	TGGTACGACCAGAGGCATACAG