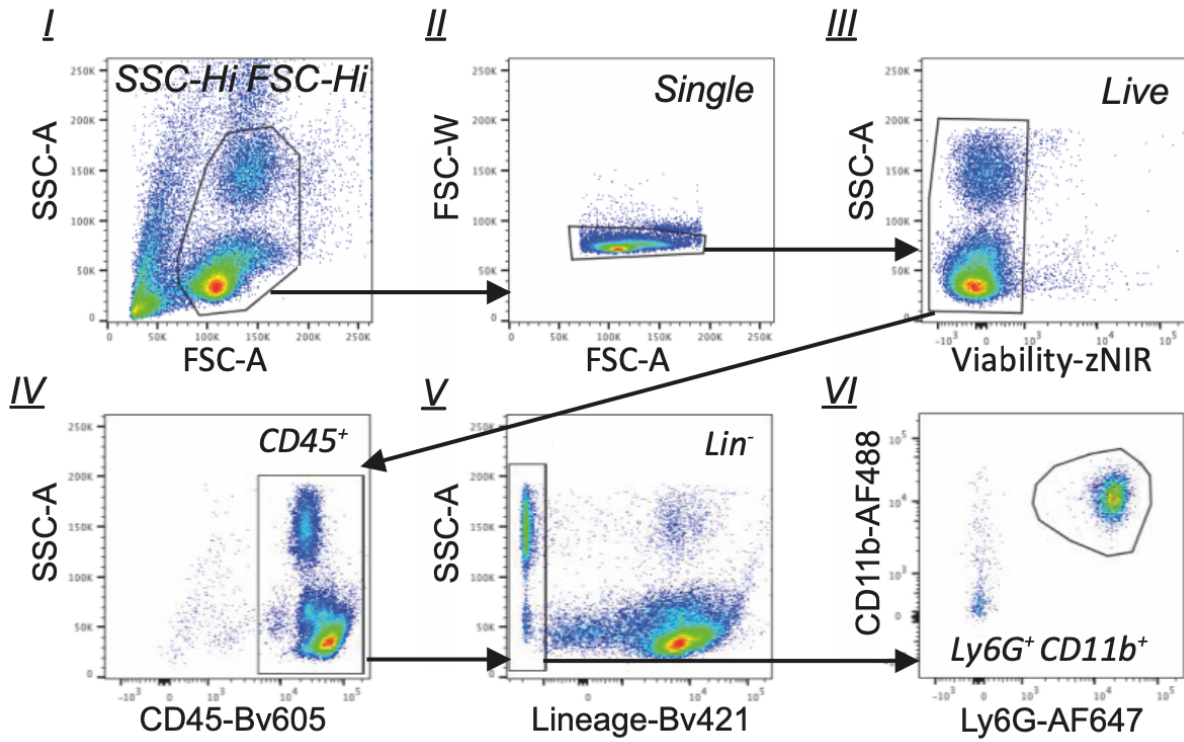


1 **Extended Data:**

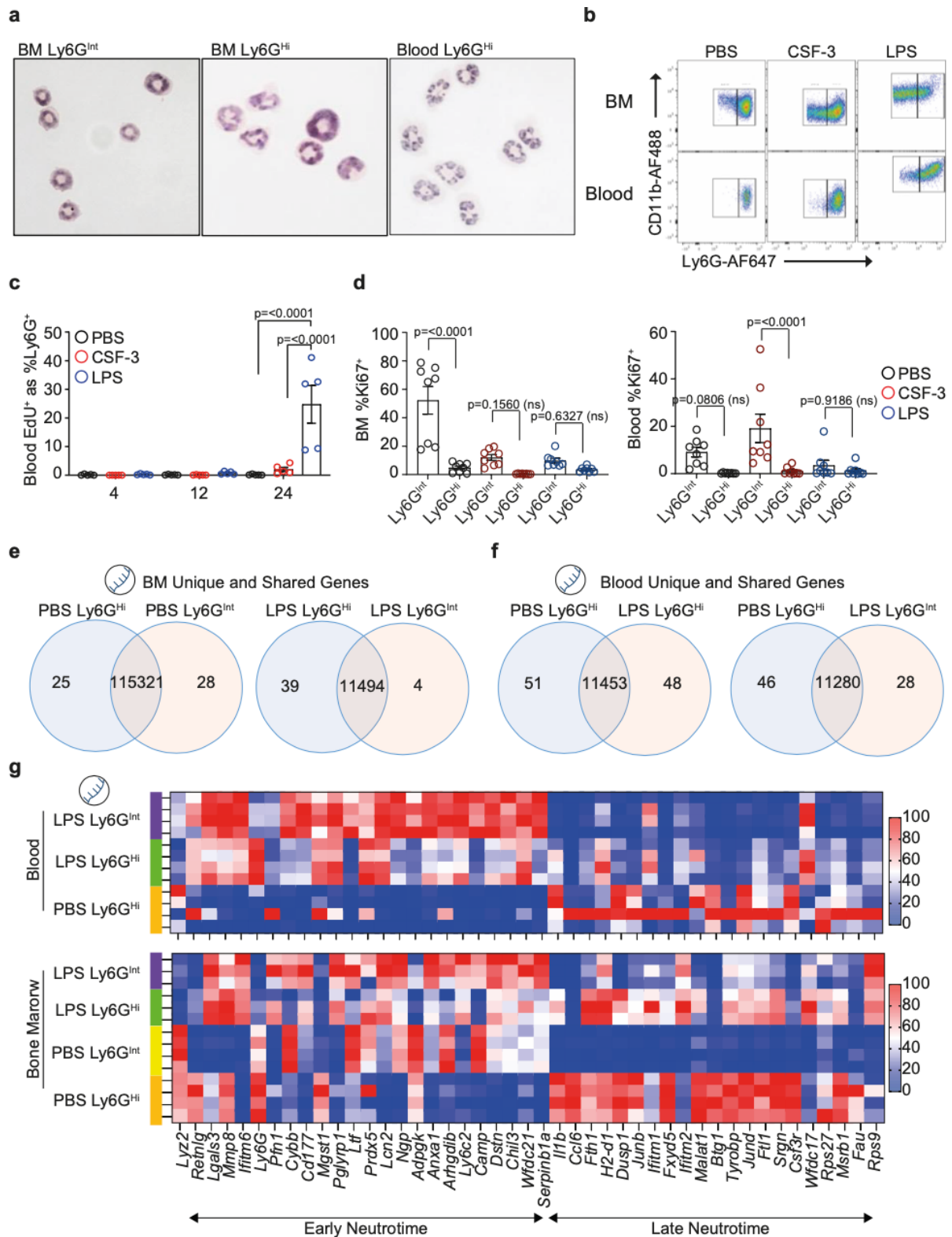
**a**



2

3 **Extended Data Fig. 1. Gating strategy for identification of Ly6G<sup>+</sup>CD11b<sup>+</sup> neutrophils. a,** SSC<sup>Hi</sup>FSC<sup>Hi</sup> (I), single  
4 cells (II), live cells (III), CD45<sup>+</sup> (IV), Lineage<sup>-</sup> (CD3, CD19, Ter119, CD115, Nkp46, Siglec-F and F4/80; (V)) and  
5 Ly6G<sup>+</sup>CD11b<sup>+</sup> (VI).

6



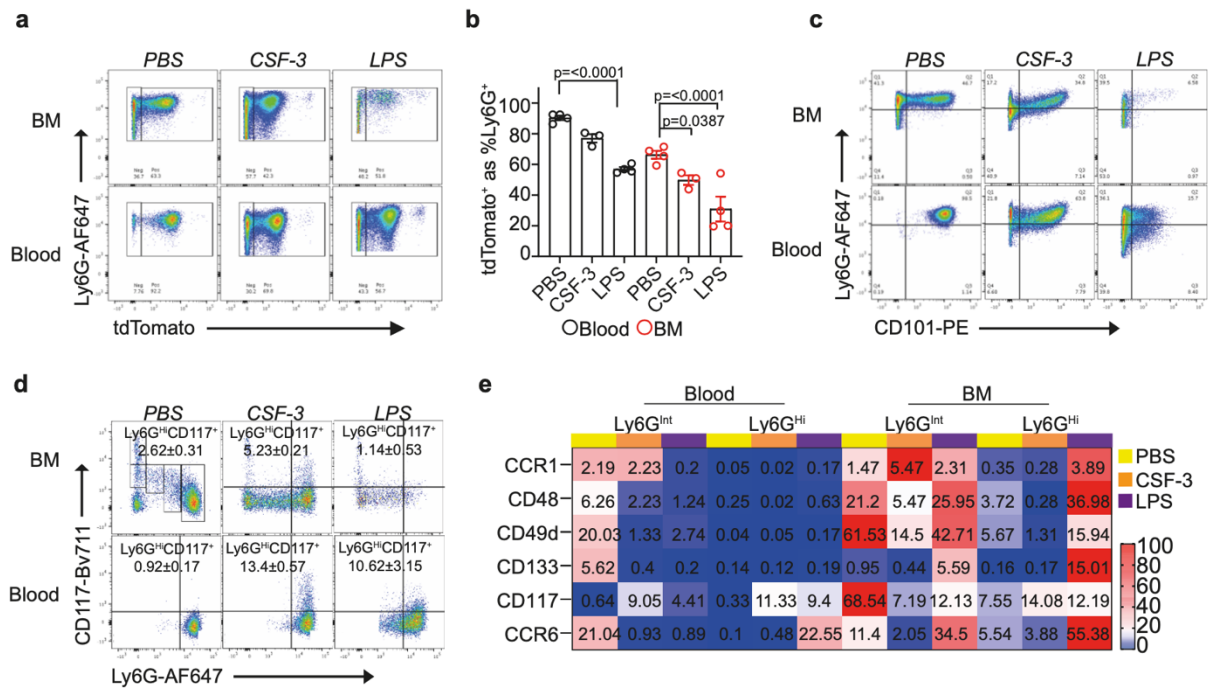
7

8 **Extended Data Fig. 2. Intermediate Ly6G expressing (Ly6G<sup>int</sup>) neutrophils are immature.** **a**, H&E stained  
 9 cytopins of FACS isolated BM Ly6G<sup>int</sup>, BM Ly6G<sup>hi</sup> and peripheral blood Ly6G<sup>+</sup> neutrophils from naive mice. Data  
 10 are representative of n=5 mice. **b**, Flow cytometry plots for Ly6G<sup>+</sup>CD11b<sup>+</sup> neutrophils in PBS-control, CSF-3- and  
 11 LPS-challenged mice. Data representative of: PBS n=11 mice; CSF-3 n=9 mice; LPS n=5 mice. **c**, Quantification of  
 12 EdU<sup>+</sup> as %Ly6G<sup>+</sup> neutrophils in the peripheral blood. PBS n=5 mice; CSF-3 n=5 mice, LPS n=5 mice. Data were  
 13 analysed by 2way ANOVA with Tukey's multiple comparisons test. **d**, Quantification of Ki-67<sup>+</sup> as %Ly6G<sup>int</sup> and  
 14 Ly6G<sup>hi</sup> neutrophils in the BM (left) and peripheral blood (right). Ly6G<sup>int</sup> and Ly6G<sup>hi</sup> neutrophils: PBS n=8 mice;

15 CSF-3 n=8 mice; LPS n=8 mice. Data were analysed by 2way ANOVA with Sidak's multiple comparisons test. **e**,  
16 Venn diagrams for genes with unique and shared expression between Ly6G<sup>Int</sup> and Ly6G<sup>Hi</sup> neutrophils isolated  
17 from the BM of PBS-control (left) and LPS-challenged (right) mice. Data from transcriptomic analysis. **f**, Venn  
18 diagrams for genes with unique and shared expression between; PBS-control Ly6G<sup>Hi</sup> and LPS-challenged Ly6G<sup>Hi</sup>  
19 (left) and LPS-challenged Ly6G<sup>Hi</sup> and Ly6G<sup>Int</sup> neutrophils (right). Data from transcriptomic analysis. **g**, Heatmap  
20 showing row scaled expression for genes associated with early and late stages of neutrophil development  
21 (neutrotime, identified by Grieshaber-Bouyer *et al.*, 2020) for Ly6G<sup>Int</sup> and Ly6G<sup>Hi</sup> neutrophils in the peripheral  
22 blood and BM of PBS-control and LPS-challenged mice. Data from transcriptomic analysis.

23 Bulk Ly6G<sup>Int</sup> and Ly6G<sup>Hi</sup> neutrophil RNA-Seq data in Extended Data Fig. 2e-g. PBS BM: Ly6G<sup>Int</sup> n=4 mice; Ly6G<sup>Hi</sup>  
24 n=4 mice. LPS-BM: Ly6G<sup>Int</sup> n=3 mice; Ly6G<sup>Hi</sup> n=3 mice. PBS peripheral blood: Ly6G<sup>Hi</sup> n=4 mice. LPS peripheral  
25 blood: Ly6G<sup>Int</sup> n=4 mice; Ly6G<sup>Hi</sup> n=4 mice. Dots in Extended Data Fig. 2c, d represent individual mice. Error bars  
26 in Extended Data Fig. 2c, d represent mean±SEM.

27

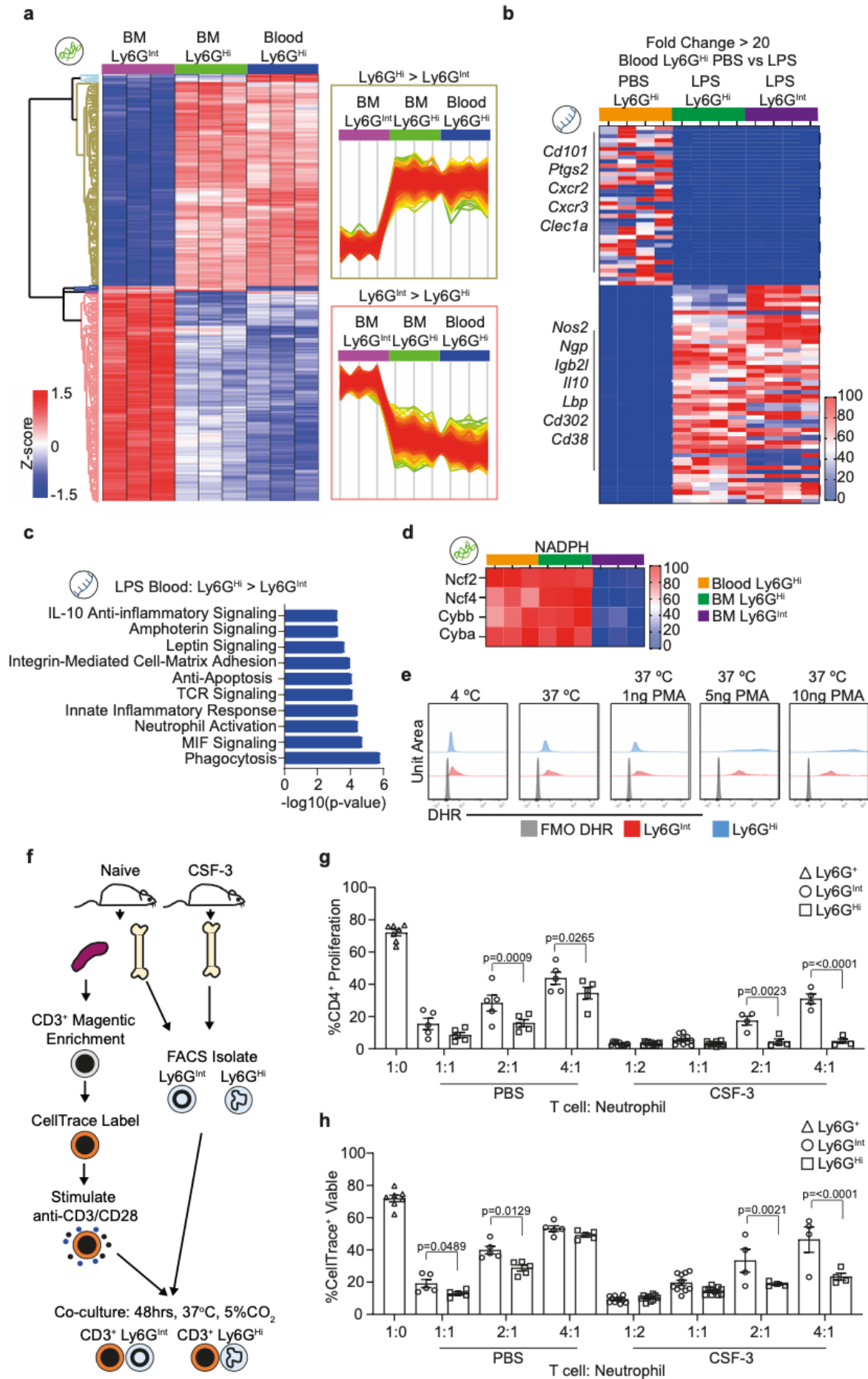


28

29 **Extended Data Fig. 3. Haematopoietic stress reduces the accuracy of alternative methods for identification of**  
 30 **neutrophil maturity.** **a**, Flow cytometry plots for TdTomato expression by Ly6G<sup>+</sup> neutrophils in PBS-control, CSF-  
 31 3- and LPS-challenged mice. BM representative of: PBS n=4 mice; CSF-3 n=3 mice; LPS n=4 mice. Peripheral blood  
 32 representative of: PBS n=4 mice; CSF-3 n=3 mice; LPS n=4 mice. **b**, Quantification of TdTomato<sup>+</sup> as %Ly6G<sup>+</sup>  
 33 neutrophils. Peripheral blood Ly6G<sup>+</sup> neutrophils: PBS n=4 mice; CSF-3 n=3 mice; LPS n=4 mice. BM Ly6G<sup>+</sup>  
 34 neutrophils: PBS n=4 mice; CSF-3 n=3 mice; LPS n=4 mice. Data were analysed by 2way ANOVA with Tukey's  
 35 multiple comparisons test. **c**, Flow cytometry plots for CD101 expression by Ly6G<sup>+</sup> neutrophils in PBS-control,  
 36 CSF-3- and LPS-challenged mice. BM representative of: PBS n=5 mice; CSF-3 n=5 mice; LPS n=5 mice. Peripheral  
 37 blood representative of: PBS n=5 mice; CSF-3 n=5 mice; LPS n=5 mice. **d**, Flow cytometry plots for CD117  
 38 expression by Ly6G<sup>+</sup> neutrophils in PBS-control, CSF-3- and LPS-challenged mice. Data are presented as  
 39 mean±standard deviation. BM representative of: PBS n=3 mice; CSF-3 n=3 mice; LPS n=3 mice. Peripheral blood  
 40 representative of: PBS n=3 mice; CSF-3 n=3 mice; LPS n=3 mice. **e**, Heatmap showing row scaled CCR1<sup>+</sup>, CD48<sup>+</sup>,  
 41 CD49d<sup>+</sup>, CD133<sup>+</sup>, CD117<sup>+</sup> and CCR6<sup>+</sup> as %Ly6G<sup>Int</sup> and Ly6G<sup>Hi</sup> neutrophils isolated from the peripheral blood and  
 42 BM of PBS-control, CSF-3- and LPS-challenged mice. Data from flow cytometry analysis. Peripheral blood Ly6G<sup>Int</sup>  
 43 and Ly6G<sup>Hi</sup> neutrophils: CCR1 PBS n=7 mice, CSF-3 n=4 mice, LPS n=4 mice; CD48 PBS n=7 mice, CSF-3 n=4 mice;  
 44 LPS n=4 mice; CD49d PBS n=5 mice, CSF-3 n=7 mice, LPS n=7 mice; CD133 PBS n=4 mice, CSF-3 n=4 mice, LPS  
 45 n=4 mice; CD117 PBS n=5 mice, CSF-3 n= 7 mice, LPS n=7 mice; CCR6 PBS n=4 mice, CSF-3 n=4 mice, LPS n=4  
 46 mice. BM Ly6G<sup>Int</sup> and Ly6G<sup>Hi</sup> neutrophils: CCR1 PBS n=7 mice, CSF-3 n=4 mice, LPS n=4 mice; CD48 PBS n=7 mice,  
 47 CSF-3 n=4 mice; LPS n=4 mice; CD49d PBS n=4 mice, CSF-3 n=7 mice, LPS n=7 mice; CD133 PBS n=4 mice, CSF-3  
 48 n=4 mice, LPS n=4 mice; CD117 PBS n=5 mice, CSF-3 n= 7 mice, LPS n=7 mice; CCR6 PBS n=4 mice, CSF-3 n=4  
 49 mice, LPS n=4 mice.

50 Dots in Dots in Extended Data Fig. 3b represent individual mice. Error bars in Extended Data Fig. 3b represent  
 51 mean±SEM.

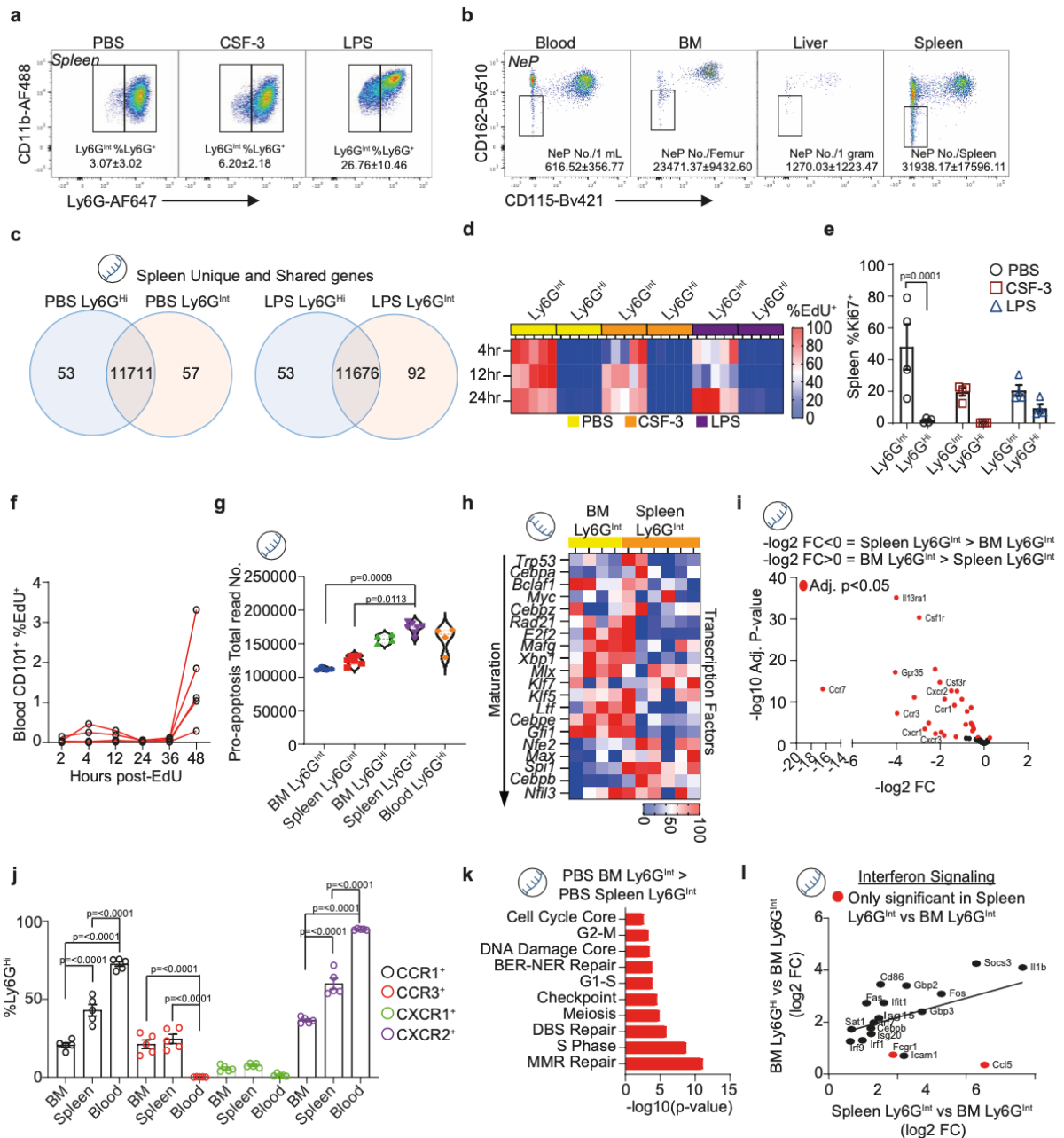
52



54 **Extended Data Fig. 4. Ly6G<sup>Int</sup> display transcriptomic, proteomic and functional differences to Ly6G<sup>Hi</sup>**  
55 **neutrophils. a**, Heatmap showing row scaled protein abundance between Ly6G<sup>Int</sup> and Ly6G<sup>Hi</sup> neutrophils isolated  
56 from the peripheral blood and BM of CSF-3-challenged mice. Data from proteomic analysis. **b**, Heatmap showing  
57 row scaled expression for genes with >20 fold change between peripheral blood Ly6G<sup>Hi</sup> neutrophils isolated from  
58 PBS-control and LPS-challenged mice. Data from transcriptomic analysis. **c**, Top 10 most enriched Process  
59 Networks from DEGs with increased expression in peripheral blood Ly6G<sup>Hi</sup> compared to Ly6G<sup>Int</sup> neutrophils from  
60 LPS-challenged mice. Data from transcriptomic analysis. **d**, Heatmap showing row scaled protein abundance for  
61 NADPH components between Ly6G<sup>Int</sup> and Ly6G<sup>Hi</sup> neutrophils isolated from the peripheral blood and BM of CSF-  
62 3 challenged mice. Data from proteomic analysis. **e**, Histograms showing intracellular-DHR-123 fluorescence for  
63 *ex vivo* PMA stimulated Ly6G<sup>Int</sup> and Ly6G<sup>Hi</sup> neutrophils isolated from the BM of naïve mice. Data representative  
64 of Ly6G<sup>Int</sup> and Ly6G<sup>Hi</sup> neutrophils n=6 mice for each condition. **f**, Schematic for *ex vivo* neutrophil suppression  
65 assays. **g**, Quantification of %CD4<sup>+</sup> T cell proliferation when cultured *ex vivo* with Ly6G<sup>Int</sup> or Ly6G<sup>Hi</sup> neutrophils  
66 isolated from the BM of PBS-control or CSF-3-challenged mice, at different T cell: neutrophil ratios. Data from  
67 flow cytometry analysis. Ly6G<sup>+</sup> neutrophils 1:0 ratio n=7 mice. Ly6G<sup>Int</sup> and Ly6G<sup>Hi</sup> neutrophils: PBS 1:1, 2:1 and  
68 4:1 ratios n=5 mice; CSF-3 1:2 and 1:1 ratios n=11 mice; CSF-3 2:1 and 4:1 ratios n=4 mice. Data were analysed  
69 by 2way ANOVA with Sidak's multiple comparisons test. **h**, Quantification of %Viable CellTrace<sup>+</sup> CD3<sup>+</sup> T cells when  
70 cultured *ex vivo* with Ly6G<sup>Int</sup> or Ly6G<sup>Hi</sup> neutrophils isolated from the BM of PBS-control or CSF-3-challenged mice,  
71 at different T cell: neutrophil ratios. Data from flow cytometry analysis. Ly6G<sup>+</sup> neutrophils 1:0 ratio n=7 mice.  
72 Ly6G<sup>Int</sup> and Ly6G<sup>Hi</sup> neutrophils: PBS 1:1, 2:1 and 4:1 ratios n=5 mice; CSF-3 1:2 and 1:1 ratios n=11 mice; CSF-3  
73 2:1 and 4:1 ratios n=4 mice. Data were analysed by 2way ANOVA with Sidak's multiple comparisons test.

74 Bulk Ly6G<sup>Int</sup> and Ly6G<sup>Hi</sup> neutrophil RNA-Seq data in Extended Data Fig. 4b, c. PBS BM: Ly6G<sup>Int</sup> n=4 mice; Ly6G<sup>Hi</sup>  
75 n=4 mice. LPS-BM: Ly6G<sup>Int</sup> n=3 mice; Ly6G<sup>Hi</sup> n=3 mice. PBS peripheral blood: Ly6G<sup>Hi</sup> n=4 mice. LPS peripheral  
76 blood: Ly6G<sup>Int</sup> n=4 mice; Ly6G<sup>Hi</sup> n=4 mice. Bulk Ly6G<sup>Int</sup> and Ly6G<sup>Hi</sup> neutrophil proteomic data in Fig. 2I. CSF-3 BM  
77 Ly6G<sup>Int</sup> n=3, and peripheral blood and BM Ly6G<sup>Hi</sup> n=3 replicates. Each replicate composed of FACS isolated Ly6G<sup>Int</sup>  
78 and Ly6G<sup>Hi</sup> neutrophils pooled from n=4 mice. Dots in Dots in Extended Data Fig. 4g, h represent individual mice.  
79 Error bars in Extended Data Fig. 4g, h represent mean±SEM.

80



81

82 **Extended Data Fig. 5. Splenic Ly6G<sup>int</sup> are immature and distinct from their BM counterparts.** **a**, Flow cytometry  
83 plots for Ly6G<sup>int</sup>CD11b<sup>+</sup> neutrophils in the spleens of PBS-control, CSF-3- and LPS-challenged mice. Data are  
84 presented as mean±standard deviation. Data representative of: PBS n=7; CSF-3 n=7; LPS n=7. **b**, Flow cytometry  
85 plots for the unipotent neutrophil progenitor, termed NeP (characterised by Zhu *et al.*, 2018), in the peripheral  
86 blood, BM, liver and spleen of naïve mice. Data are presented as mean±standard deviation. Data are  
87 representative of: peripheral blood n=5 mice; BM n=5 mice; liver n=5 mice; spleen n=5 mice. **c**, Venn diagrams  
88 for genes with unique and shared expression between Ly6G<sup>hi</sup> and Ly6G<sup>int</sup> neutrophils isolated from the spleen  
89 of PBS-control (left) and LPS-challenged (right) mice. Data from transcriptomic analysis. **d**, Heatmap showing  
90 row-scaled EdU<sup>+</sup> as %Ly6G<sup>int</sup> and Ly6G<sup>hi</sup> neutrophils isolated from the spleen at 4, 12 and 24 hours post-Edu  
91 injection. PBS 4hr, 12hr and 24hr Ly6G<sup>int</sup> and Ly6G<sup>hi</sup> n=5 mice; CSF-3 4hr, 12hr and 24hr Ly6G<sup>int</sup> and Ly6G<sup>hi</sup> n=5  
92 mice; LPS 4hr, 12hr and 24hr Ly6G<sup>int</sup> and Ly6G<sup>hi</sup> n=5 mice. **e**, Quantification of Ki-67<sup>+</sup> as %Ly6G<sup>int</sup> and Ly6G<sup>hi</sup>  
93 neutrophils in the spleen. PBS Ly6G<sup>int</sup> and Ly6G<sup>hi</sup> n=4 mice; CSF-3 Ly6G<sup>int</sup> and Ly6G<sup>hi</sup> n=4 mice; LPS Ly6G<sup>int</sup> and  
94 Ly6G<sup>hi</sup> n=4 mice. Data were analysed by 2way ANOVA with Sidak's multiple comparisons test. **f**, Quantification  
95 of CD101<sup>+</sup> as %Edu<sup>+</sup> neutrophils in the peripheral blood of naïve mice. At all time-points n=5 mice. **g**,  
96 Quantification of total combined read no. for genes associated with pro-apoptosis (GO:0043065). Data from

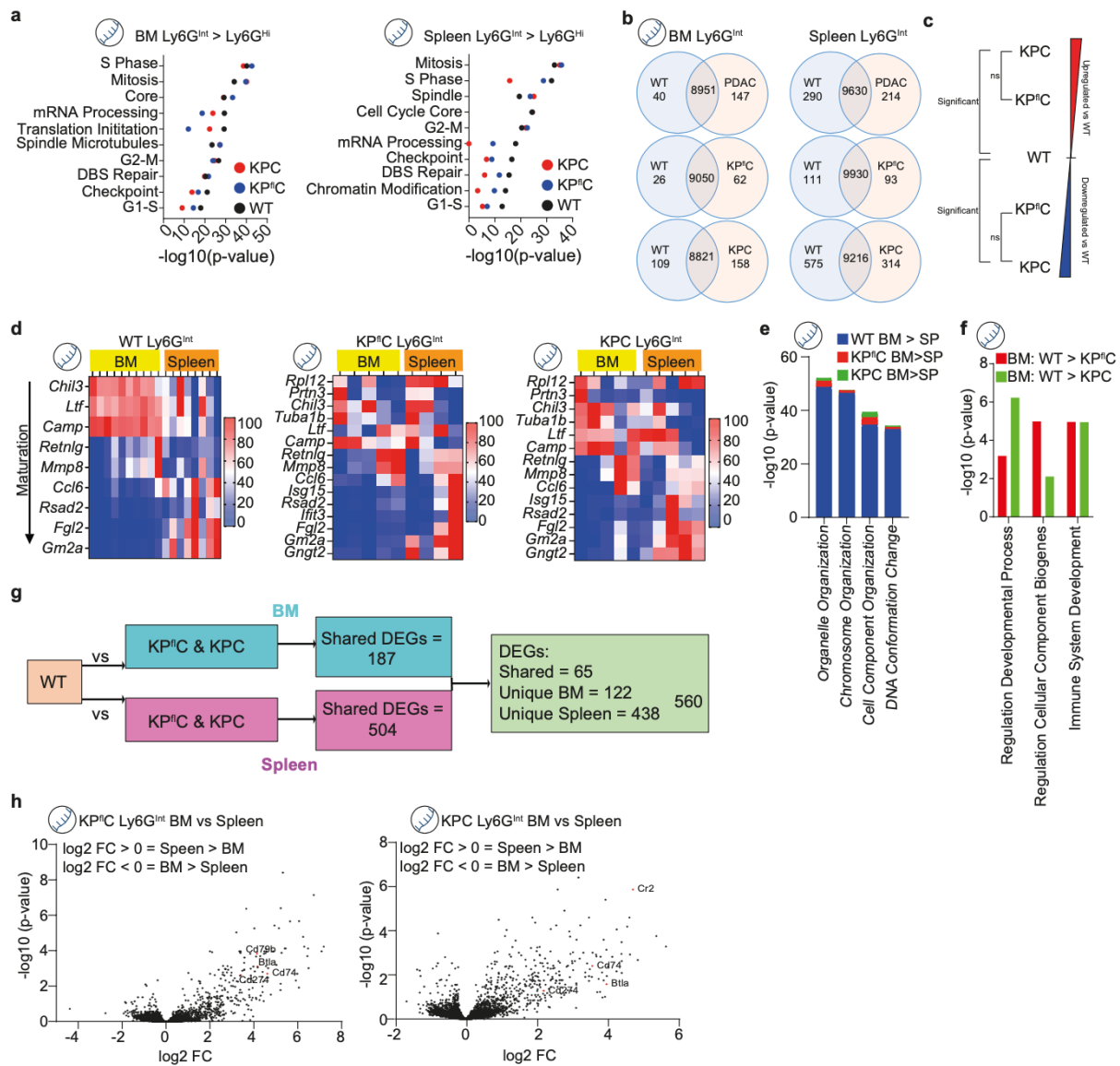


97 transcriptomic analysis. **h**, Heatmap showing column scaled expression for transcription factors associated with  
98 neutrophil maturation. Data from transcriptomic analysis. **i**, Volcano plot for genes associated with leukocyte  
99 chemotaxis (GO:0030595) comparing BM Ly6G<sup>Int</sup> and spleen Ly6G<sup>Int</sup> neutrophils isolated from naïve mice. Data  
100 from transcriptomic analysis. Fold change = FC. **j**, Quantification of CCR1<sup>+</sup>, CCR3<sup>+</sup>, CXCR1<sup>+</sup> and CXCR2<sup>+</sup> as %Ly6G<sup>Hi</sup>  
101 neutrophils in the BM, spleen and peripheral blood of naïve mice. CCR1<sup>+</sup> BM, spleen, peripheral blood n=5 mice;  
102 CCR3<sup>+</sup> BM, spleen, peripheral blood n=5 mice; CXCR1<sup>+</sup> BM, spleen, peripheral blood n=5 mice; CXCR2<sup>+</sup> BM,  
103 spleen, peripheral blood n=5 mice. Data were analysed by 2way ANOVA with Tukey's multiple comparisons test.  
104 **k**, Top 10 most enriched Process Networks from DEGs with increased expression in BM Ly6G<sup>Int</sup> compared to  
105 spleen Ly6G<sup>Int</sup> neutrophils from PBS-control mice. Data from transcriptomic analysis. **l**, Correlation for DEGs  
106 increased in PBS-control spleen Ly6G<sup>Int</sup> compared to BM Ly6G<sup>Int</sup> with DEGs increased in PBS-control BM Ly6G<sup>Hi</sup>  
107 compared to BM Ly6G<sup>Int</sup>, associated with the process network Inflammation Interferon Signaling. Data from  
108 transcriptomic analysis. Fold change = FC.

109 Bulk Ly6G<sup>Int</sup> and Ly6G<sup>Hi</sup> neutrophil RNA-Seq data in Extended Data Fig. 5c, g-i, k, l. PBS BM: Ly6G<sup>Int</sup> n=4 mice;  
110 Ly6G<sup>Hi</sup> n=4 mice. LPS-BM: Ly6G<sup>Int</sup> n=3 mice; Ly6G<sup>Hi</sup> n=3 mice. PBS peripheral blood: Ly6G<sup>Hi</sup> n=4 mice. LPS  
111 peripheral blood: Ly6G<sup>Int</sup> n=4 mice; Ly6G<sup>Hi</sup> n=4 mice. Dots in Extended Data Fig. 5e-g, j represent individual mice.  
112 Error bars in Extended Data Fig. 5e, j represent mean±SEM.

113





114

115 **Extended Data Fig. 6. Ly6G<sup>Int</sup> neutrophils maintain their immature status and tissue specific phenotypes in**  
 116 **tumour bearing mice. a,** DEGs associated with cell cycle regulation with increased expression in BM Ly6G<sup>Int</sup>  
 117 compared to Ly6G<sup>Hi</sup> (left) and spleen Ly6G<sup>Int</sup> compared to Ly6G<sup>Hi</sup> (right) in WT, KP<sup>f</sup>C and KPC mice, shown as -  
 118 Log<sub>10</sub>(p-value). Data from transcriptomic analysis. **b,** Venn diagrams for DEGs shared by KP<sup>f</sup>C and KPC (PDAC),  
 119 unique to KP<sup>f</sup>C and unique to KPC compared to WT for BM Ly6G<sup>Int</sup> (left) and spleen Ly6G<sup>Int</sup> neutrophils (right).  
 120 Data from transcriptomic analysis. **c,** Schematic showing proposed gene expression for Ly6G<sup>Int</sup> neutrophils from  
 121 KP<sup>f</sup>C and KPC mice compared to WT. **d,** Heatmap showing row scaled expression for genes associated with  
 122 neutrophil maturation (identified by Xie *et al.*, 2020) for BM Ly6G<sup>Int</sup> and spleen Ly6G<sup>Int</sup> neutrophils from WT  
 123 (left), KP<sup>f</sup>C (middle) and KPC mice (right). Data from transcriptomic analysis. **e,** Enrichment analysis for GO  
 124 Processes associated with neutrophil development increased in BM Ly6G<sup>Int</sup> compared to spleen Ly6G<sup>Int</sup>  
 125 neutrophils from WT, KP<sup>f</sup>C and KPC mice. Data from transcriptomic analysis. **f,** Enrichment analysis for GO  
 126 Processes associated with neutrophil development increased in WT BM Ly6G<sup>Int</sup> compared to KP<sup>f</sup>C and KPC BM  
 127 Ly6G<sup>Int</sup> neutrophils. Data from transcriptomic analysis. **g,** Schematic for identification and comparison of  
 128 transcriptome changes identified in PDAC bearing compared to WT mice in BM and spleen Ly6G<sup>Int</sup> neutrophils.  
 129 **h,** Volcano plot for 560 DEGs identified between BM and spleen Ly6G<sup>Int</sup> shared by KP<sup>f</sup>C (left) and KPC (right) mice  
 130 compared to WT. Here, 122 DEGs are increased in BM > spleen Ly6G<sup>Int</sup> and 438 DEGs are increased in spleen >  
 131 BM Ly6G<sup>Int</sup>. Data from transcriptomic analysis. Fold change = FC.

132 Bulk Ly6G<sup>Int</sup> and Ly6G<sup>Hi</sup> neutrophil RNA-Seq data in Fig. 5b-f. BM: WT Ly6G<sup>Int</sup> n=10 mice; WT Ly6G<sup>Hi</sup> n=10 mice;  
 133 KP<sup>f</sup>C Ly6G<sup>Int</sup> n=5 mice; KP<sup>f</sup>C Ly6G<sup>Hi</sup> n=5 mice; KPC Ly6G<sup>Int</sup> n=5 mice; KPC Ly6G<sup>Hi</sup> n=5 mice. Spleen: WT Ly6G<sup>Int</sup> n=8

134 mice; WT Ly6G<sup>Hi</sup> n=10 mice; KP<sup>f</sup>C Ly6G<sup>Int</sup> n=4 mice; KP<sup>f</sup>C Ly6G<sup>Hi</sup> n=5 mice; KPC Ly6G<sup>Int</sup> n=5 mice; KPC Ly6G<sup>Hi</sup> n=5  
 135 mice.

136 **Tables:**

<i>Peripheral blood vs peripheral blood</i>			DEGs	Total DEGs
PBS BL Ly6G <sup>Hi</sup>	>	LPS BL Ly6G <sup>Hi</sup>	2634	4374
LPS BL Ly6G <sup>Hi</sup>	>	PBS BL Ly6G <sup>Hi</sup>	1740	
LPS BL Ly6G <sup>Hi</sup>	>	LPS BL Ly6G <sup>Int</sup>	567	1147
LPS BL Ly6G <sup>Int</sup>	>	LPS BL Ly6G <sup>Hi</sup>	580	
<i>BM vs BM</i>			DEGs	Total DEGs
PBS BM Ly6G <sup>Hi</sup>	>	PBS BM Ly6G <sup>Int</sup>	2004	5915
PBS BM Ly6G <sup>Int</sup>	>	PBS BM Ly6G <sup>Hi</sup>	3911	
LPS BM Ly6G <sup>Hi</sup>	>	LPS BM Ly6G <sup>Int</sup>	353	533
LPS BM Ly6G <sup>Int</sup>	>	LPS BM Ly6G <sup>Hi</sup>	180	
PBS BM Ly6G <sup>Hi</sup>	>	LPS BM Ly6G <sup>Hi</sup>	1421	3672
LPS BM Ly6G <sup>Hi</sup>	>	PBS BM Ly6G <sup>Hi</sup>	2251	
PBS BM Ly6G <sup>Int</sup>	>	LPS BM Ly6G <sup>Int</sup>	1699	2786
LPS BM Ly6G <sup>Int</sup>	>	PBS BM Ly6G <sup>Int</sup>	1087	
<i>Spleen vs spleen</i>			DEGs	Total DEGs
PBS SP Ly6G <sup>Hi</sup>	>	PBS SP Ly6G <sup>Int</sup>	2654	6896
PBS SP Ly6G <sup>Int</sup>	>	PBS SP Ly6G <sup>Hi</sup>	4242	
LPS SP Ly6G <sup>Hi</sup>	>	LPS SP Ly6G <sup>Int</sup>	1509	2717
LPS SP Ly6G <sup>Int</sup>	>	LPS SP Ly6G <sup>Hi</sup>	1208	
PBS SP Ly6G <sup>Hi</sup>	>	LPS SP Ly6G <sup>Hi</sup>	2069	5448
LPS SP Ly6G <sup>Hi</sup>	>	PBS SP Ly6G <sup>Hi</sup>	3379	
PBS SP Ly6G <sup>Int</sup>	>	LPS SP Ly6G <sup>Int</sup>	2673	4000
LPS SP Ly6G <sup>Int</sup>	>	PBS SP Ly6G <sup>Int</sup>	1327	

137

138 **Table 1.** DEGs identified by p-value<0.05 and fold change≥1.5 from comparisons of Ly6G<sup>Hi</sup> and Ly6G<sup>Int</sup> neutrophil  
 139 populations isolated from the peripheral blood (BL), bone marrow (BM) and spleen (SP) of PBS-control and LPS-  
 140 challenged mice. Data from transcriptomic analysis.

<i>Ly6G<sup>Int</sup> Comparisons: Blood, BM, Spleen</i>			DEGs	Total DEGs
PBS BM Ly6G <sup>Int</sup>	>	PBS SP Ly6G <sup>Int</sup>	93	968
PBS SP Ly6G <sup>Int</sup>	>	PBS BM Ly6G <sup>Int</sup>	875	
LPS BM Ly6G <sup>Int</sup>	>	LPS SP Ly6G <sup>Int</sup>	112	684
LPS SP Ly6G <sup>Int</sup>	>	LPS BM Ly6G <sup>Int</sup>	572	
LPS SP Ly6G <sup>Int</sup>	>	LPS PB Ly6G <sup>Int</sup>	18	50
LPS PB Ly6G <sup>Int</sup>	>	LPS SP Ly6G <sup>Int</sup>	32	

141

142 **Table 2.** DEGs identified by p-values<0.05 and fold change≥1.5 from comparisons of Ly6G<sup>Int</sup> neutrophil  
 143 populations from the peripheral blood (PB), bone marrow (BM) and spleen (SP) of PBS-control and LPS-  
 144 challenged mice. Data from transcriptomic analysis.

145

<i>Ly6G<sup>hi</sup> PBS Comparisons: Blood, BM, SP, LV</i>			DEGs	Total DEGs
PB Ly6G <sup>Hi</sup>	>	BM Ly6G <sup>Hi</sup>	2274	3608
BM Ly6G <sup>Hi</sup>	>	PB Ly6G <sup>Hi</sup>	1334	
PB Ly6G <sup>Hi</sup>	>	SP Ly6G <sup>Hi</sup>	1628	1790
SP Ly6G <sup>Hi</sup>	>	PB Ly6G <sup>Hi</sup>	162	
PB Ly6G <sup>Hi</sup>	>	LV Ly6G <sup>+</sup>	1466	2106
LV Ly6G <sup>+</sup>	>	PB Ly6G <sup>Hi</sup>	640	
BM Ly6G <sup>Hi</sup>	>	SP Ly6G <sup>Hi</sup>	1882	3090
SP Ly6G <sup>Hi</sup>	>	BM Ly6G <sup>Hi</sup>	1208	
BM Ly6G <sup>Hi</sup>	>	LV Ly6G <sup>+</sup>	2652	5555
LV Ly6G <sup>+</sup>	>	BM Ly6G <sup>Hi</sup>	2903	
SP Ly6G <sup>Hi</sup>	>	LV Ly6G <sup>+</sup>	1451	3733
LV Ly6G <sup>+</sup>	>	SP Ly6G <sup>Hi</sup>	2282	

146

147 **Table 3.** DEGs identified by p-value<0.05 and fold change≥1.5 from comparisons of Ly6G<sup>hi</sup> and Ly6G<sup>+</sup> neutrophils  
 148 isolated from the peripheral blood (PB), bone marrow (BM), spleen (SP) and liver (LV) of PBS-control mice. Data  
 149 from transcriptomic analysis.

<i>Ly6G<sup>hi</sup> LPS Comparisons: Blood, BM, SP, LV</i>			DEGs	Total DEGs
PB Ly6G <sup>Hi</sup>	>	BM Ly6G <sup>Hi</sup>	591	1604
BM Ly6G <sup>Hi</sup>	>	PB Ly6G <sup>Hi</sup>	1013	
PB Ly6G <sup>Hi</sup>	>	SP Ly6G <sup>Hi</sup>	5	11
SP Ly6G <sup>Hi</sup>	>	PB Ly6G <sup>Hi</sup>	6	
PB Ly6G <sup>Hi</sup>	>	LV Ly6G <sup>+</sup>	108	323
LV Ly6G <sup>+</sup>	>	PB Ly6G <sup>Hi</sup>	215	
BM Ly6G <sup>Hi</sup>	>	SP Ly6G <sup>Hi</sup>	1153	1831
SP Ly6G <sup>Hi</sup>	>	BM Ly6G <sup>Hi</sup>	678	
BM Ly6G <sup>Hi</sup>	>	LV Ly6G <sup>+</sup>	2121	3236
LV Ly6G <sup>+</sup>	>	BM Ly6G <sup>Hi</sup>	1115	
SP Ly6G <sup>Hi</sup>	>	LV Ly6G <sup>+</sup>	71	211
LV Ly6G <sup>+</sup>	>	SP Ly6G <sup>Hi</sup>	139	

150

151 **Table 4.** DEGs identified by p-value<0.05 and fold change≥1.5 from comparisons of Ly6G<sup>hi</sup> and Ly6G<sup>+</sup> neutrophils  
 152 isolated from the peripheral blood, BM, spleen and liver of LPS-challenged mice. Data from transcriptomic  
 153 analysis.

<i>PDAC Ly6G<sup>int</sup>: BM vs BM between genotypes</i>						
Geno	Pop	vs	Geno	Pop	DEGs	Total DEGs
WT	BMInt	>	KPflC	BMInt	66	275
WT	BMInt	<	KPflC	BMInt	209	
WT	BMInt	>	KPC	BMInt	149	454
WT	BMInt	<	KPC	BMInt	305	
KPflC	BMInt	>	KPC	BMInt	1	1
KPflC	BMInt	<	KPC	BMInt	0	

154

155 **Table 5.** DEGs identified by p-value<0.05 from comparisons of Ly6G<sup>int</sup> neutrophils from the BM of WT, KPflC and  
 156 KPC mice. Data from transcriptomic analysis. Genotype = Geno; population = Pop.

<i>PDAC Ly6G<sup>int</sup>: Spleen vs Spleen between genotypes</i>						
Geno	Pop	vs	Geno	Pop	DEGs	Total DEGs
WT	SPInt	>	KP <sup>f</sup> C	SPInt	401	707
WT	SPInt	<	KP <sup>f</sup> C	SPInt	306	
WT	SPInt	>	KPC	SPInt	865	1419
WT	SPInt	<	KPC	SPInt	554	
KP <sup>f</sup> C	SPInt	>	KPC	SPInt	0	0
KP <sup>f</sup> C	SPInt	<	KPC	SPInt	0	

157

158 **Table 6.** DEGs identified by p-values≤0.05 from comparisons of Ly6G<sup>int</sup> neutrophils from the spleen of WT, KP<sup>f</sup>C  
 159 and KPC mice. Data from transcriptomic analysis. Genotype = Geno; population = Pop.

<i>PDAC Ly6G<sup>int</sup>: Unique and Shared DEGs compared to WT</i>						
Tissue	Geno	Comparison			DEGs	Total DEGs
BM	WT	BMInt	>	KP <sup>f</sup> C & KPC	40	187
		BMInt	<	KP <sup>f</sup> C & KPC	147	
	WT	BMInt	>	KP <sup>f</sup> C Only	26	88
		BMInt	<	KP <sup>f</sup> C Only	62	
	WT	BMInt	>	KPC Only	109	267
		BMInt	<	KPC Only	158	
Spleen	WT	SpleenInt	>	KP <sup>f</sup> C & KPC	290	504
		SpleenInt	<	KP <sup>f</sup> C & KPC	214	
	WT	SpleenInt	>	KP <sup>f</sup> C Only	111	204
		SpleenInt	<	KP <sup>f</sup> C Only	93	
	WT	SpleenInt	>	KPC Only	575	916
		SpleenInt	<	KPC Only	341	

160

161 **Table 7.** DEGs identified by p-values≤0.05 from the BM and spleen that are shared by KP<sup>f</sup>C and KPC compared to  
 162 WT, only identified in WT vs KP<sup>f</sup>C and only identified in WT vs KPC mice. Data from transcriptomic analysis.  
 163 Genotype = Geno.

<i>PDAC Ly6G<sup>int</sup>: BM vs Spleen within each genotype</i>					
Geno	Comparison			DEGs	Total DEGs
WT	BMInt	>	SPInt	461	1135
	BMInt	<	SPInt	674	
KP <sup>f</sup> C	BMInt	>	SPInt	6	155
	BMInt	<	SPInt	149	
KPC	BMInt	>	SPInt	12	228
	BMInt	<	SPInt	216	

164

165 **Table 8.** DEGs identified by p-values≤0.05 from comparisons of Ly6G<sup>int</sup> neutrophils from the BM and spleen in  
 166 WT, KP<sup>f</sup>C and KPC mice. Data from transcriptomic analysis. Genotype = Geno.

167

168

169

170

171