

Supplementary Figure 1 – Related to Figures 2 and 4: Extended phenotypic and functional analyses of neonatal myeloid cells.

[A] Gating strategy for phenotyping of myeloid cells in mouse bone marrow.

[B] MFI of CD11b on bone marrow monocytes from mice at different ages [3 days old (3d), n = 4; 6 days old (6d), n = 5; 9 days old (9d), n = 5; JUV, n = 5; AD, n = 10].

[C] CD11b marker expression of monocytes from mass cytometry experiment comparing newborns aged 0-5 days (n = 75) and 31-81 days after birth (n = 31), mean expression from binned days used for coloring.

[D] MFI of CD11b on bone marrow neutrophils from neonatal mice house in either germ-free or conventional, specific pathogen free facility (n = 9 for both groups).

[E] Opsonophagocytic uptake of mouse sera opsonized GFP-fluorescent Spn by monocytes from bone marrow suspensions of neonatal or adult mice at multiplicity of infection (MOI) of 25 (n = 8 for both groups).

[F] MFI of GFP signal on GFP+ monocytes in [D].

[G] Deposition of complement C3 on Spn (left, serotype 4; right, serotype 23F) in 5-10% sera from NNT versus AD mice (n = 2 with 2 technical replicates marked by the same symbol).

[H] Recoverable live bacteria in spleen of $Cd11b^{-/-}$ recipients receiving either $Cd11b^{+/+}$ neonatal neutrophils (solid circle, n = 9), $Cd11b^{+/-}$ neonatal neutrophils (solid orange circles, n = 8) or $Cd11b^{-/-}$ neonatal neutrophils (solid green circle, n = 8) relative to that of recipients receiving $Cd11b^{+/+}$ adult neutrophils (open circle; n = 9, n = 9, n = 7, respectively) at 20 hours post infection with Spn via IP.

[I] Monocyte counts in peripheral blood from NNT (6d old, n = 7; 9d old, n = 10), JUV (n = 6) and AD (n = 11) mice.

[J] Frequency of Ly6C^{hi} monocytes (left) and Ly6C^{lo} monocytes (right) from spleen of NNT (n = 5) versus AD (n = 5) mice. Data with error bars are presented as mean \pm SEM. N.S., not significant.



Supplementary Figure 2 - Related to Figure 3: Assessment of surface markers associated with CD62L¹⁰ 'aged' neutrophils versus CD62L^{hi} 'non-aged' neutrophils in adult peripheral blood.

[A] Gating strategy for phenotyping of neutrophils in mouse blood.

[B-G] MFI analysis of known markers between $CD62L^{lo}$ 'aged' (red dots) and $CD62L^{hi}$ 'non-aged' (blue dots) neutrophils in adult blood (n = 7).







Ε







Supplementary Figure 3 – Related to Figure 4: **Bias of neonatal neutrophils toward an 'aged' phenotype is unlikely driven by lifespan shortening, intrinsic signaling pathways or CD11b expression itself.**

[A] RT-PCR analysis of myeloperoxidase (MPO) mRNA transcript in NNT (n = 11) versus AD (n = 8) neutrophils.

[B] Lymphocyte counts in peripheral blood from uninfected NNT mice (n = 5), NNT mice infected with Spn at 24 hpi (n = 4) and uninfected AD mice (n = 6).

[C] RT-PCR analysis of Cxcl2 mRNA transcript in NNT (n = 9) versus AD (n = 7) neutrophils.

[D] MFI of CXCR4 on peripheral blood neutrophils from NNT (n = 10) versus AD mice (n = 7). **[E]** Frequency of CD62L¹⁰ 'aged' neutrophils from peripheral blood of $Cd11b^{+/+}$ AD mice (n = 5) versus $Cd11b^{-/-}$ AD mice (n = 4). Data with error bars are presented as mean ± SEM. N.S., not significant.











Supplementary Figure 4 – Related to Figure 4: Transcriptional analysis of efferocytosisassociated markers in bone marrow and lung tissues.

Bone marrow and lung expression of [A] *Cd169*, [B] *Lxra*, [C] *Mertk*, [D] *Abca1* and [E] *Gas6* in NNT (bone marrow, n = 4; lung, n = 8-9) versus AD (bone marrow, n = 3; lung, n = 5). Expression was calculated as fold change in NNT relative to AD. Data with error bars are presented as mean \pm SEM.



Supplementary Figure 5 – Related to Figure 5: Extended phenotypic analyses of CD169-DTR and *Cd169^{-/-}* adult mice.

[A] Representative images of spleens from CD169-DTR and WT mice following DT administration as described in STAR Methods.

[B-C] MFI expression of CD11b on bone marrow Ly6C^{hi} [B] and Ly6C^{lo} [C] monocytes in WT (n = 11) versus CD169-DTR mice (n = 8).

[D-G] Absolute counts (neutrophils in [D], monocytes in [E]) or percentage population of all leukocytes (neutrophils in [F] monocytes in [G]) in blood from WT versus $Cd169^{-/-}$ adults (n = 6 for both groups).

[H] Survival of WT (open circle grey line, n = 9) versus *Cd169^{-/-}* adults (open circle teal line, n = 8) following IP challenge with Spn. Data with error bars are presented as mean ± SEM. N.S., not significant.



Β



Lyz2 Cre/+ Mertk fl/fl

Supplementary Figure 6 – Related to Figure 5: Assessment of MerTK expression on macrophages in the $Lyz2^{Cre/+}$ Mertk^{fl/fl} conditional knockout mice.

[**A**] Representative flow plots assessing frequency of MerTK-expressing cells as proportion of macrophages (gated on Live, Singlets, CD11b⁺ F4/80⁺) from bone marrow of $Mertk^{fl/fl}$ versus $Lyz2^{Cre/+}$ $Mertk^{fl/fl}$ mice; FMO, fluorescence-minus-one control.

[**B**] Quantification of data described in [A] of $Mertk^{fl/fl}$ adult mice (n = 6) and $Lyz2^{Crel+}Mertk^{fl/fl}$ adult mice (n = 9). Data with error bars are presented as mean ± SEM.

Gene	Primer Sequence (5' – 3')
Gapdh	Forward: AGG TCG GTG TGA ACG GAT TTG
	Reverse: TGT AGA CCA TGT AGT TGA GGT CA
Itgam	Forward: ATG GAC GCT GAT GGC AAT ACC
(<i>Cd11b</i>)	Reverse: TCC CCA TTC ACG TCT CCC A
Cd169	Forward: CTT GGG TCA GCC AAC AGT TC
	Reverse: GGT GAT GGT GAA ACC TGG AC
Lxra	Forward: CAA CAG TGT AAC AGG CGC T
	Reverse: TGC AAT GGG CCA AGG C
Mertk	Forward: GAG GAC TGC TTG GAT GAA CTG TA
	Reverse: AGG TGG GTC GAT CCA AGG
Abcal	Forward: GGT TTG GAG ATG GTT ATA CAA TAG TT
	Reverse: CCC GGA AAC GCA AGT CC
Gas6	Forward: GGA TTT GCT ACC TAC AGG CTC A
	Reverse: TTA ACT TCC CAG GTG GTT TCC
Мро	Forward: GGA AGG AGA CCT AGA GGT TGG
	Reverse: TAG CAC AGG AAG GCC AAT G
Cxcl2	Forward: CCA CCA ACC ACC AGG CTA C
	Reverse: GCT TCA GGG TCA AGG GCA AA

Table S1 – Related to Figures 2 and 4: List of mouse primer sequences used in this study