

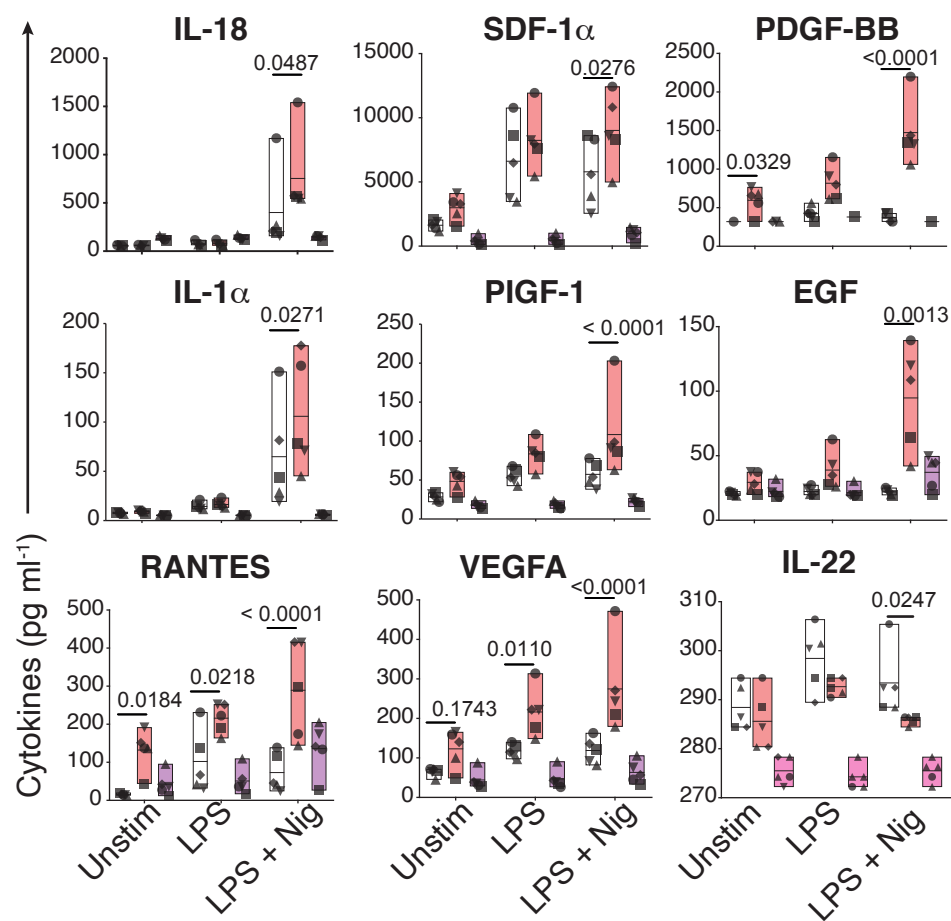
**Supplemental Information**

**Platelets Fuel the Inflammasome Activation  
of Innate Immune Cells**

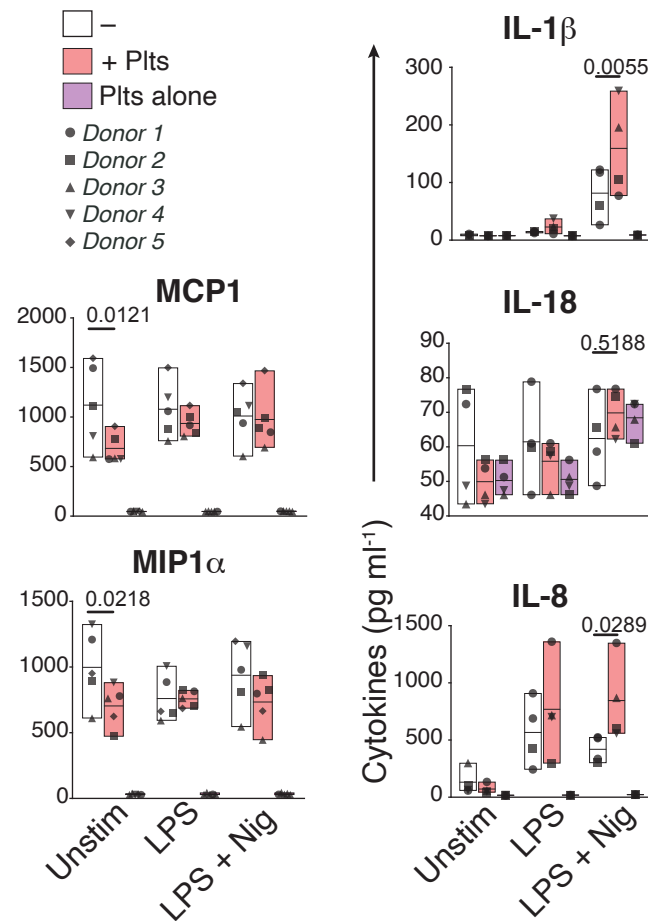
**Verena Rolfes, Lucas Secchim Ribeiro, Ibrahim Hawwari, Lisa Böttcher, Nathalia Rosero, Salie Maasewerd, Marina Lima Silva Santos, Tomasz Próchnicki, Camila Meirelles de Souza Silva, Carlos Wagner de Souza Wanderley, Maximilian Rothe, Susanne V. Schmidt, H. James Stunden, Damien Bertheloot, Magali Noval Rivas, Cor Jesus Fontes, Luzia Helena Carvalho, Fernando Queiroz Cunha, Eicke Latz, Moshe Arditi, and Bernardo Simoes Franklin**

**Figure S1**

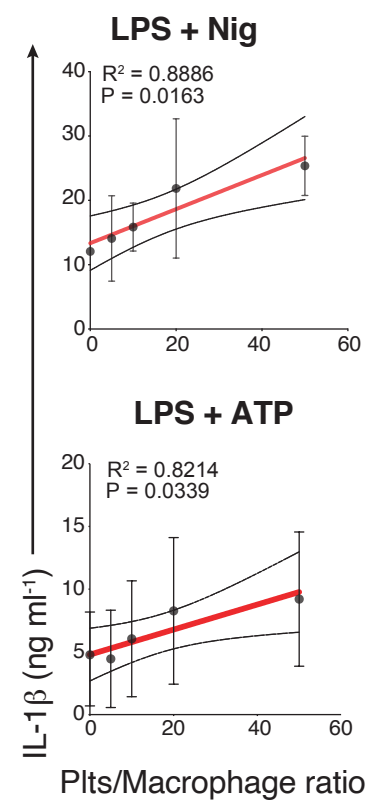
**A**



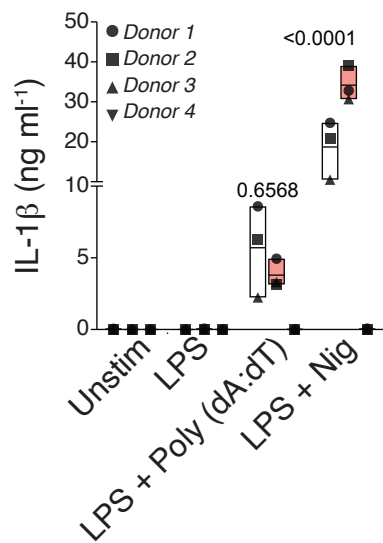
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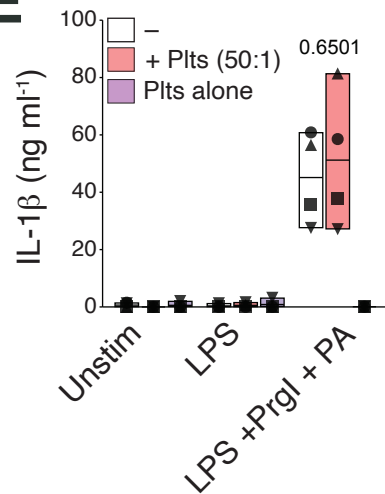
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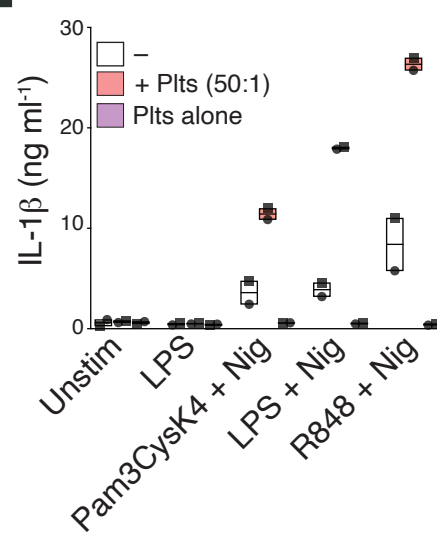
**D**



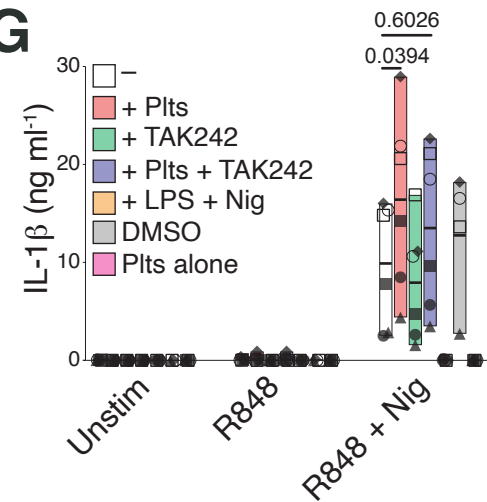
**E**



**F**



**G**





## Figure S1, Related to Figure 1

Multiplex measurement of cytokines in cell-free supernatants of unstimulated (Unstim), or LPS-primed (200 ng ml<sup>-1</sup>, 3 hours), and Nigericin-activated (10 μM, 90 min) human macrophages (**A**), or human neutrophils (**B**). Cells were cultivated alone (—), or in the presence of platelets (+ Plts, 50:1 ratio). The adjusted P values from Tukey's multiple comparison test are indicated.

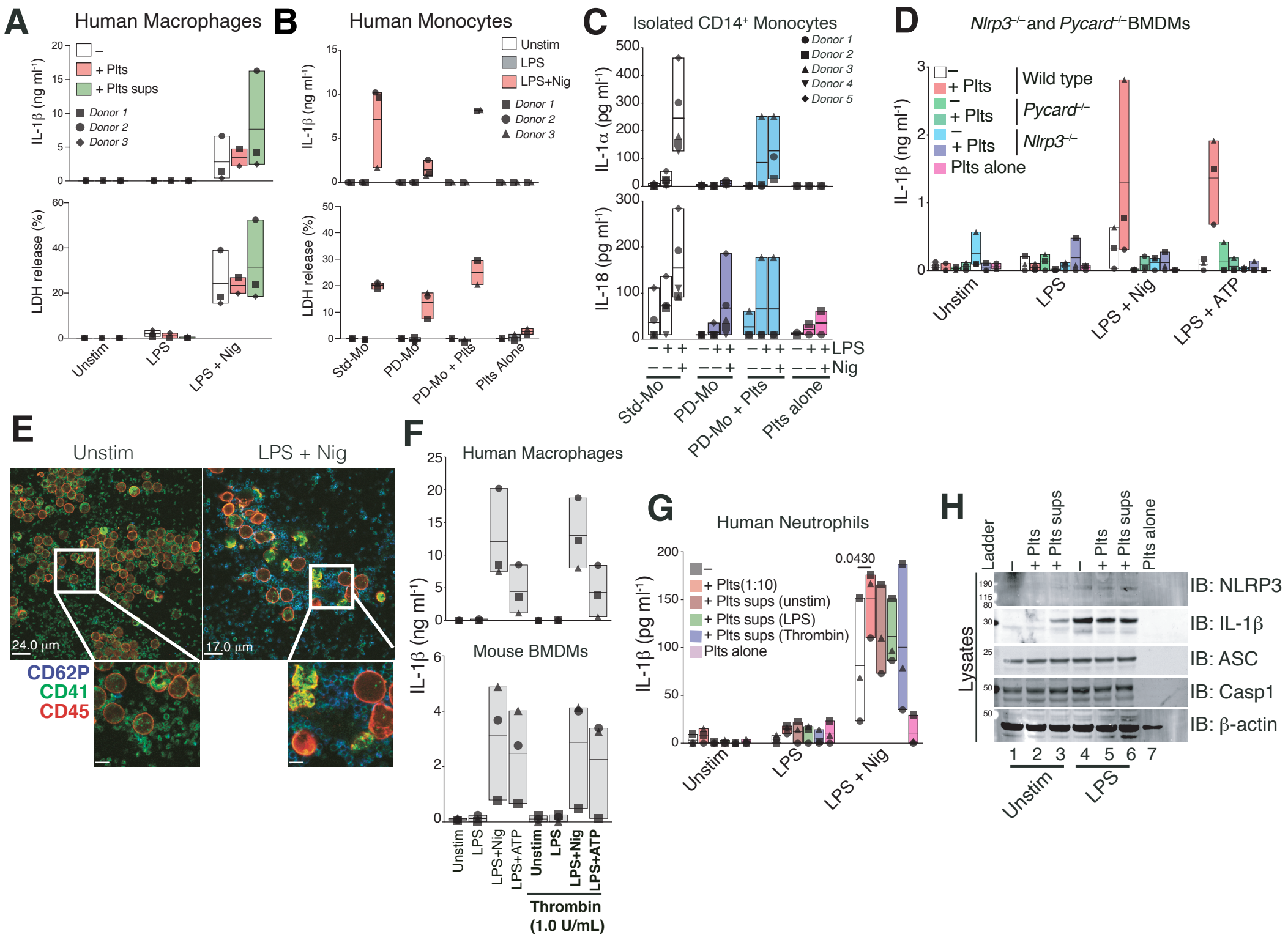
(**C**) Sigmoidal curve fit of IL-1β levels produced by inflammasome-activated (LPS + Nig, or LPS + ATP) human macrophages vs. the platelet-to-macrophage ratios. Pooled from 3 independent experiments represented in **Fig. 1B**.

(**D**) HTRF measurements of IL-1β in cell-free supernatants of unstimulated (Unstim), or LPS-primed human macrophages that were stimulated with dsDNA (Poly(dA:dT), and cultured alone, or with platelets.

(**E**) HTRF measurements of IL-1β in cell-free supernatants of unstimulated (Unstim), or LPS-primed, and Prgl (2 μg ml<sup>-1</sup>) + PA (0.5 μg ml<sup>-1</sup>) stimulated human macrophages that were cultured alone, or with platelets.

(**F**) HTRF measurements of IL-1β in cell-free supernatants of hMDMs primed with LPS, Pam3CysK4 (1 μg ml<sup>-1</sup>), or R848 (3.5 μg ml<sup>-1</sup>) for 3 hours, followed by activation with nigericin. (**G**) HTRF measurements of IL-1β in cell-free supernatants of hMDMs cultured as in **A**. Cells were pre-treated with TAK242 (0.5 μg ml<sup>-1</sup>) before priming with R848 (10 μM, 3 hours) and activation with nigericin (10 μM, 90 minutes).

**A, B, D-G** - Floating bars (with mean and minimum to maximum values) from pooled data from several independent experiments. Each symbol represents the average of technical triplicates of cultures from one donor. **E** - Mean ± SD pooled from two independent experiments with platelets and hMDMs from different donors. P values are indicated and were determined by: two-way ANOVA with Tukey's multiple comparison test (**A, B, D, E** and **G**).

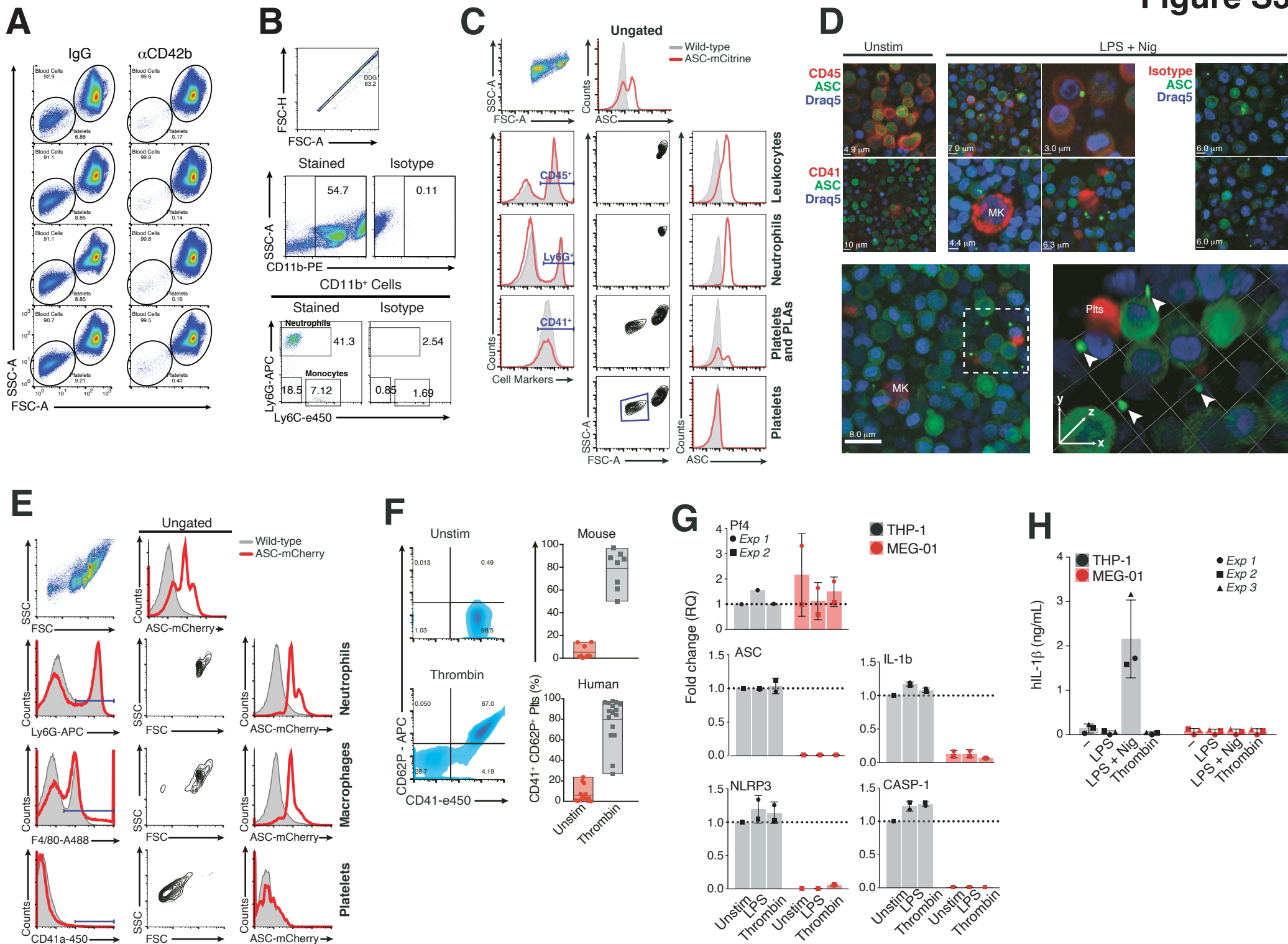


## Figure S2, Related to Figures 1, 2, and 5

(**A**) IL-1 $\beta$  and LDH levels in cell-free supernatants of human macrophages that were cultured alone or in the presence of platelets, or platelet supernatants. Co-cultures were left untreated or primed with LPS and activated with Nigericin. (**B**) IL-1 $\beta$  and LDH levels in cell-free supernatants of standard (MoStd), platelet-depleted (MoPD), or monocytes that were depleted of platelets and later reconstituted with autologous platelets (MoPD + Plts). Cells were stimulated as in A. (**C**) Multiplex Cytokine measurement of IL-1 $\alpha$  and IL-18 in cell-free supernatants of Std-Mo, PD-Mo, or PD-Mo that were added with freshly isolated autologous platelets (PD-Mo + Plts) on a 50:1 platelet-to-monocyte ratio, and platelets cultivated alone. (**D**) IL-1 $\beta$  levels in cell-free supernatants of wild-type, *Nlrp3*<sup>-/-</sup>, or *Pycard*<sup>+/-</sup> BMDMs cultivated alone (—), or in the presence of wild-type platelets (+Plts, 5:1 ratio). (**E**) Confocal imaging of unstimulated (Unstim), or LPS-primed (200 ng ml<sup>-1</sup>, 3 hours), and nigericin-activated human neutrophils incubated with platelets (50:1 platelet-to-neutrophil ratio). Platelet marker (CD41), platelet activation marker (CD62P), leukocyte marker (CD45). Scale bars are indicated. (**F**) HTRF measurements of IL-1 $\beta$  levels in cell-free supernatants of LPS-primed and nigericin-, or ATP-activated hMDMs (top), or mouse BMDMs (bottom), in the presence or absence of thrombin (1 U ml<sup>-1</sup>). (**G**) IL-1 $\beta$  levels in cell-free supernatants of unstimulated (Unstim), or LPS-primed, and nigericin-activated human neutrophils (10  $\mu$ M, 90 min) incubated with platelets (10:1 ratio) or platelet supernatants from unstimulated, LPS (200 ng ml<sup>-1</sup>, 3 hours) or thrombin (1 U ml<sup>-1</sup>) stimulated platelets. (**H**) Immunoblot of NLRP3, IL-1 $\beta$ , ASC, Caspase-1 and  $\beta$ -actin on whole cell lysates of resting, or LPS-primed human macrophages cultivated alone or in the presence of platelets, or platelet-supernatants.

**A - D, F, G** Floating bars (with mean and minimum to maximum values) from pooled data from 3 - 4 independent experiments. Each symbol represents the average of technical triplicates from different donors, or mice. **E, H**- Representative of two independent experiments.

# Figure S3



### Figure S3, Related to Figures 3 and 4

**(A)** Representative flow cytometry scatter plots with gating strategy to assess the efficiency of platelet-depletion. Samples are from peripheral blood of C57BL/6 mice that were injected i.v. with 2  $\mu\text{g/g}$  of body weight of a rat anti-mouse GPIIb/IIIa monoclonal antibody ( $\alpha\text{CD42b}$ ,  $n = 4$ ) or control rat IgG (IgG,  $n = 4$ ).

**(B)** Representative gating strategy for the quantification of neutrophils ( $\text{CD11b}^+$ ,  $\text{Ly6G}^+$ ) and monocytes ( $\text{CD11b}^+$ ,  $\text{Ly6C}^+$ ) in the peritoneal exudate of mice.

**(C)** Flow cytometric analysis of total bone marrow cells from Wild-type (gray histograms), ASC-mCitrine transgenic, or **(E)** ASC-*knock in* reporter mice (red lines). Gating strategy to identify different cell populations based on surface marker staining and scatter characteristics: CD45 (Leukocytes), F4/80 (Macrophages), Ly6G (neutrophils) and CD41 (platelets and platelet-leukocytes aggregates, PLAs).

**(D)** Confocal microscopy of total bone marrow cells from ASC-mCitrine mice, comparing leukocytes ( $\text{CD45}^+$ ), and platelets ( $\text{CD41}^+$ ). Megakaryocytes (MKs), platelets (Plts) and ASC specks (arrows). Scale bars are indicated.

**(F)** Representative flow cytometric assessment of purity (CD41) and activation (CD62P) of resting, or thrombin ( $0.5 \text{ U ml}^{-1}$ ) stimulated platelets purified from wild-type mice ( $n = 8$ ) or human blood donors ( $n = 18$ ).

**(G)** Real time PCR analysis of PF4, IL-1 $\beta$ , NLRP3, ASC and Caspase-1 (CASP-1) expression and **(H)** HTRF measurements of IL-1 $\beta$  in cell-free supernatants on PMA-differentiated THP-1s or the human megakaryocytic cell MEG-01. Cells were left unstimulated, or treated with LPS ( $1 \mu\text{g ml}^{-1}$ ) or Thrombin ( $1 \text{ U ml}^{-1}$ ).

**A - E** - Representative of two or more independent experiments.

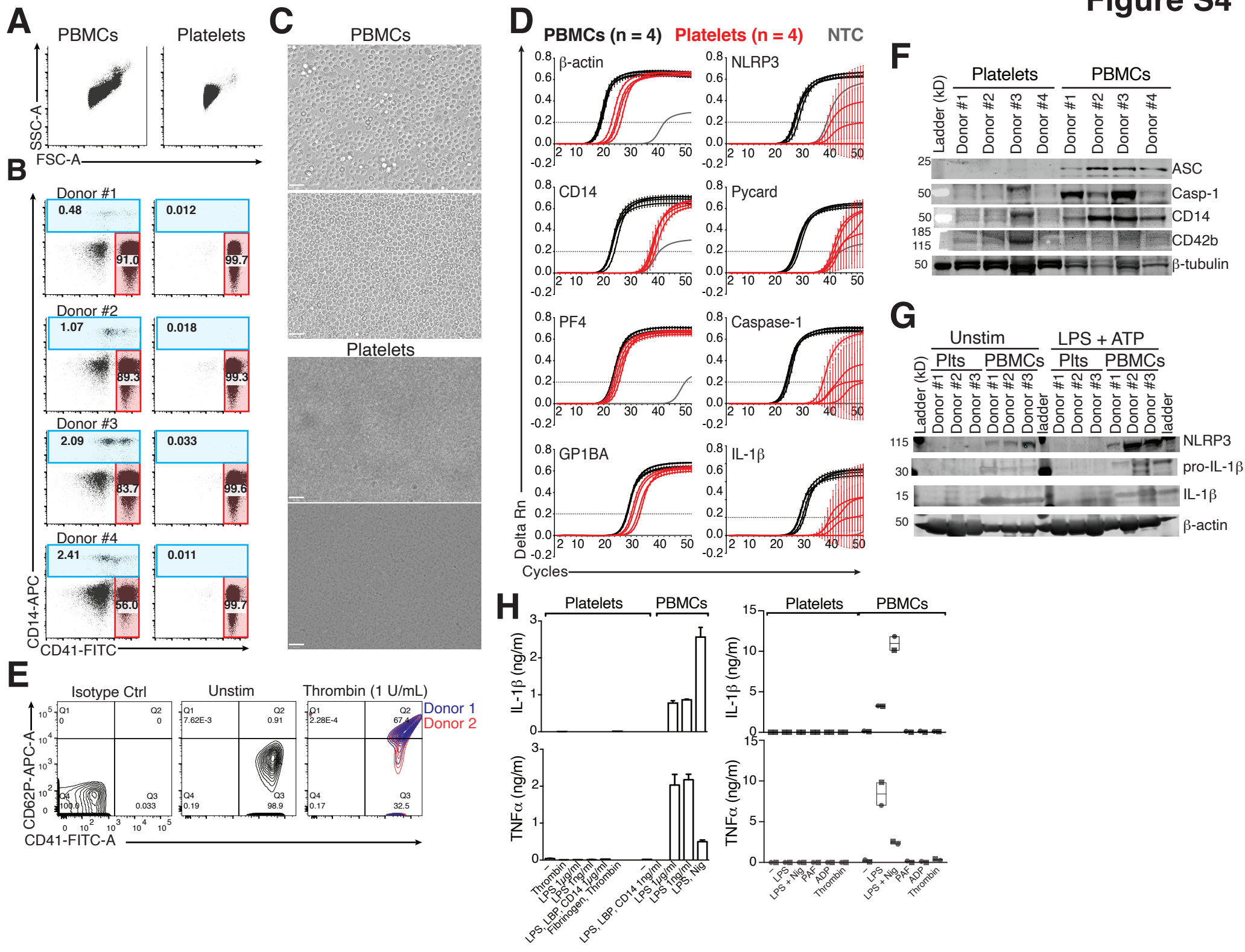
**F** - Floating bars (with mean and minimum to maximum values) from pooled data from several independent experiments, each symbol represents the measurements from platelets of individual mice, or donors.

**G** Mean + SD of pooled data from 2 independent experiments performed in triplicates.

**H** Mean + SD of pooled data from 3 independent experiments performed in triplicates.



# Figure S4



### **Figure S4, Related to Figure 4**

(**A-B**) Representative flow cytometric analysis of PBMCs, or platelets ( $> 10^9$ ) purified from 25 ml of peripheral blood of healthy donors ( $n = 4$ ) showing the purity of platelet preparations with CD14 (monocyte) or CD41 (platelets) surface markers. (**C**) Light microscopy of PBMCs, or isolated platelets. Scale bars: 100  $\mu\text{m}$ . (**D**) Amplification plots of the expression of NLRP3, PYCARD, Caspase-1, and IL-1B, in comparison to Monocyte marker (CD14) and platelet markers (PF4 and GP1BA) from a qPCR performed on total RNA isolated from PBMCs or platelets ( $n = 4$ ). NTC = non-template control. Dotted lines = Cycle Threshold (CT, 0.2). (**E**) Flow cytometric assessment of purity (CD41) and activation (CD62P) of resting, or thrombin ( $1 \text{ U ml}^{-1}$ ) stimulated platelets purified from healthy donors ( $n = 2$ ). (**F**) Immunoblotting of ASC, Caspase-1, CD14, CD42 and  $\beta$ -tubulin in resting platelets, or PBMCs from healthy donors ( $n = 4$ ). (**G**) Immunoblotting of NLRP3, or  $\beta$ -actin in resting, or activated platelets, or PBMCs from healthy donors ( $n = 3$ ). (**H**) IL-1 $\beta$  levels in cell-free supernatants of human isolated Platelets or PBMCs that were stimulated as indicated for 3h (left), or 18h (right) ( $n = 2$ ).

**A - D, F** - Representative of two independent experiments performed with 4 healthy blood donors.

**E** - Representative of several experiments. Two donors are shown.

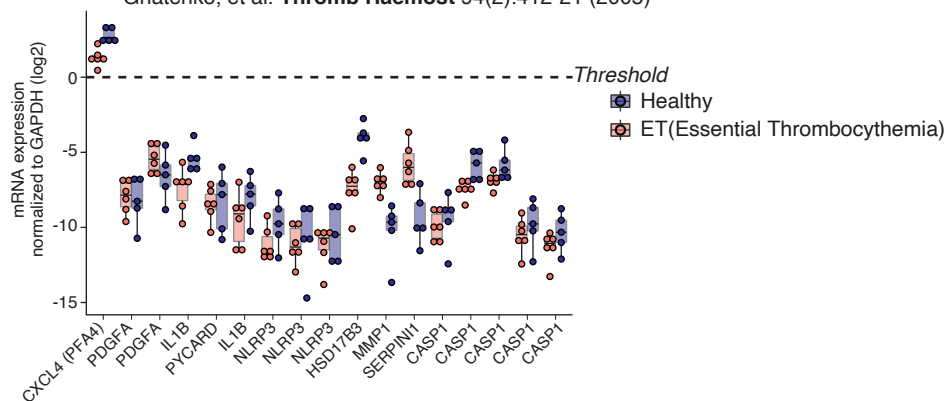
**G** - Data from one experiment with 3 different donors.

**H** – Mean + SD of technical triplicates. Representative of 2 independent experiments.

A

### E-GEOD-2006 - Transcription profiling of human platelets from patients with essential thrombocythemia

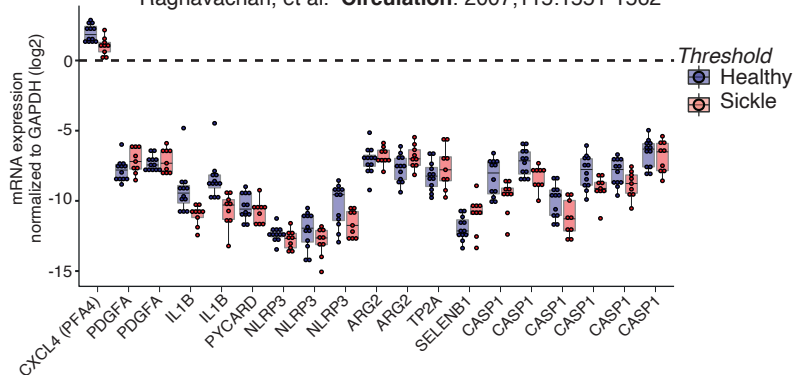
Gnatenko, et al. *Thromb Haemost* 94(2):412-21 (2005)



B

### E-GEOD-11524 - Transcription profiling of human platelets from sickle cell patients reveals changes in arginine metabolic pathways

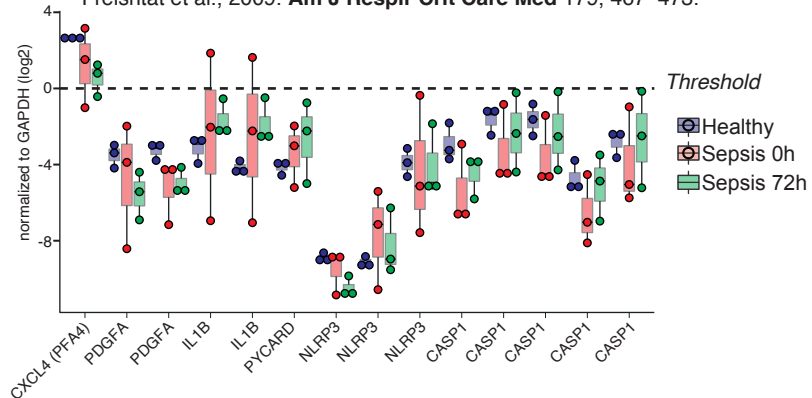
Raghavachari, et al. *Circulation*. 2007;115:1551-1562



C

### E-GEOD-10361 - Transcription profiling of human platelets as cytotoxic mediators in sepsis-induced acute lung injury (ALI)

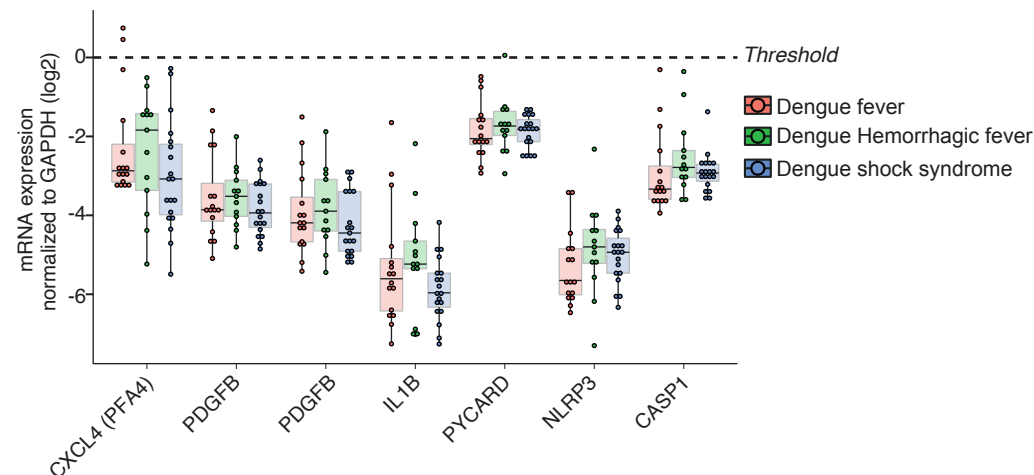
Freisztat et al., 2009. *Am J Respir Crit Care Med* 179, 467-473.



D

### GEOD17924 - Genome-wide expression profiling deciphers host responses altered during dengue shock syndrome and reveals the role of innate immunity in severe dengue

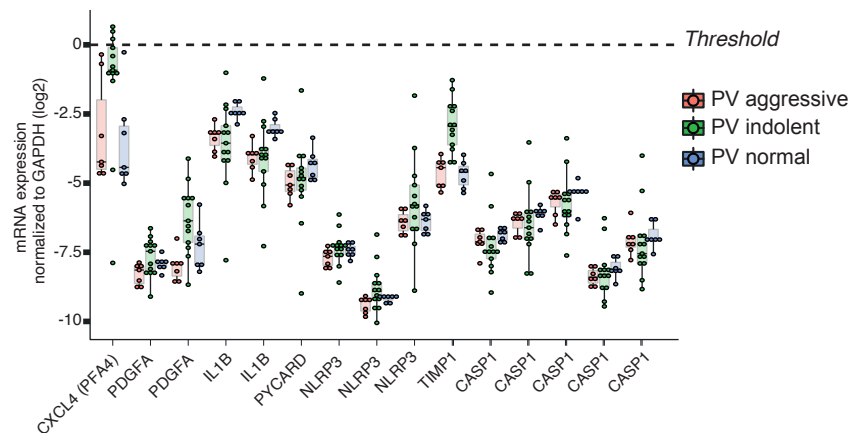
Devignot S. et al. *PLoS one* 20100720 7



E

### E-GEOD-47018 - Gene Expression Profiling in Polycythemia Vera (PV)

Spivak JL et al. *Europe PMC* 25162887

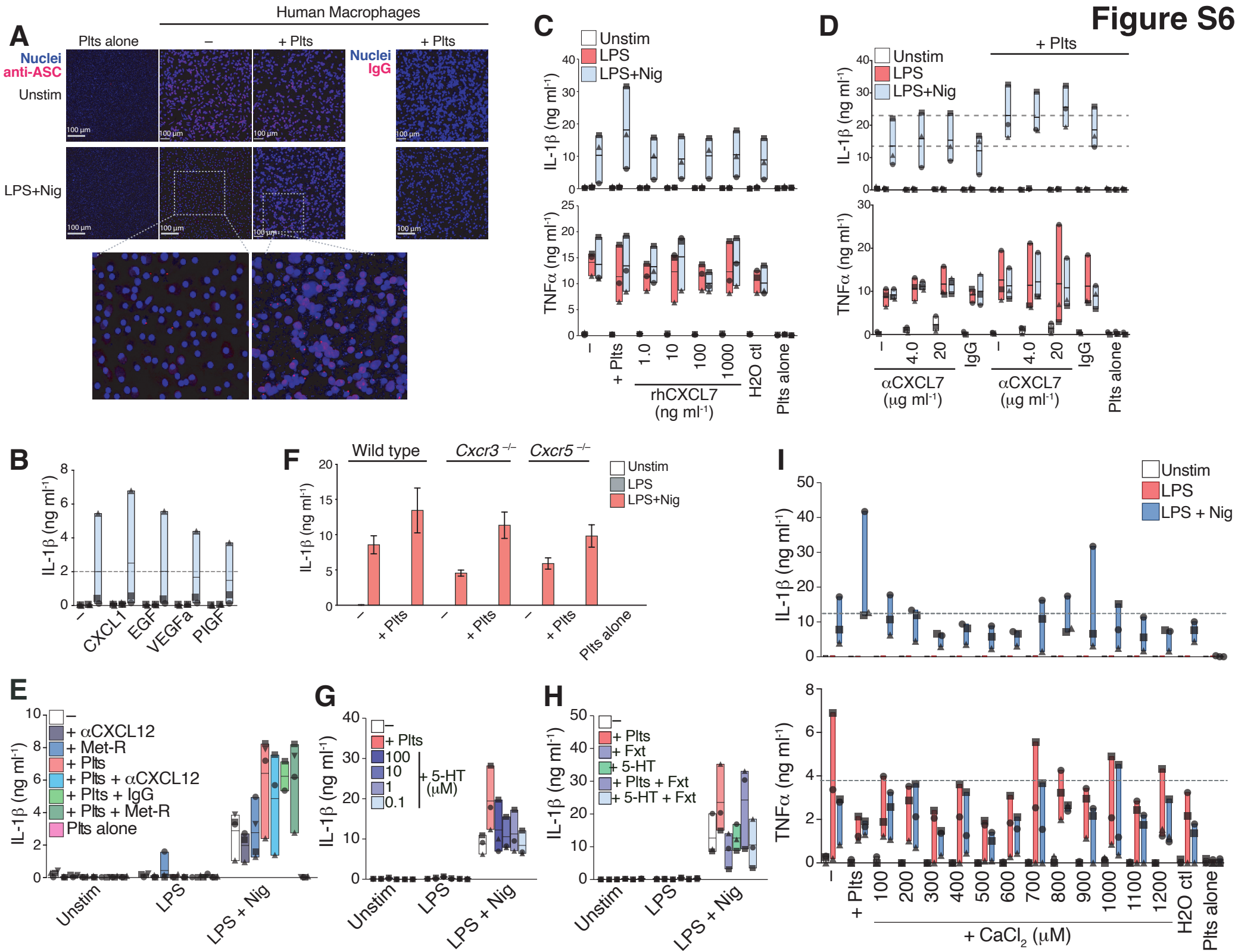




**Figure S5, Related to Figure 4, and STAR METHODS: Meta-analysis of microarray data**

**A – E** Microarray Meta-analysis of transcriptomics of isolated human platelets. Gene expression data from five independent studies that addressed the transcriptomics of platelets isolated from the peripheral blood of healthy donors, or patients with a variety of diseases. Bar charts represent the  $\text{Log}_2$  transformed data for platelet marker (CXCL4, and PDGFA) as well as inflammasome-associated genes (PYCARD, NLRP3, TIMP1, CASP1, ARG2, TP2A, SELENB1). Expression values were normalized against the expression of the constitutive gene GAPDH. Each symbol represents one individual donor, or patient.

**Figure S6**



## Figure S6, Related to Figure 5 and 6

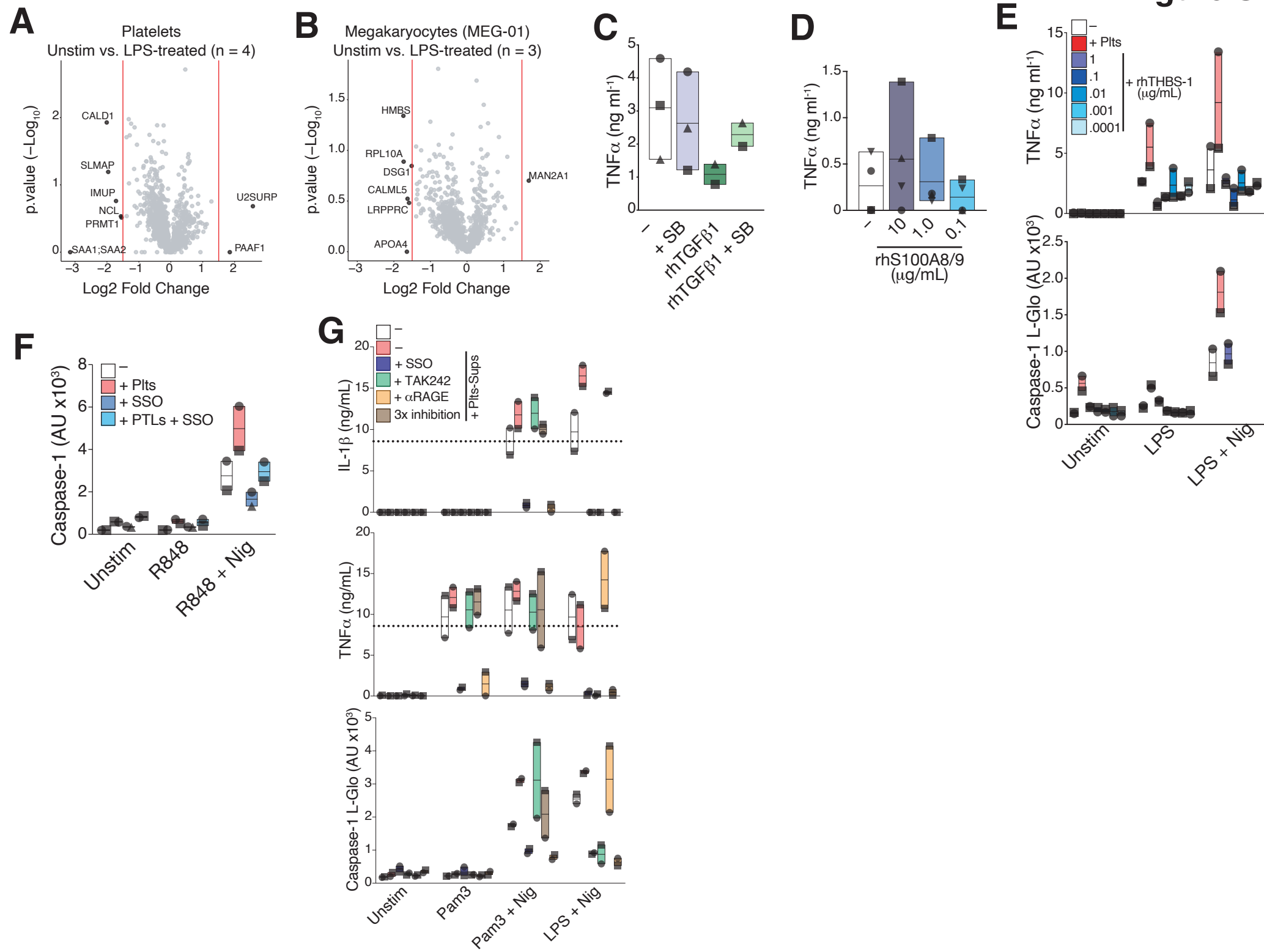
(A) Confocal microscopy of ASC specks in LPS primed (200 ng ml<sup>-1</sup>, 3 hours) and nigericin activated (10 μM, 45 min) human macrophages. Cells were either cultured alone (–) or in the presence of platelets (+Plts, 50:1 ratio). (B - E) IL-1β and TNFα levels in cell-free supernatants of unstimulated (–), LPS stimulated, and nigericin-activated (10 μM, 90 min) human macrophages, either cultivated alone (–), or in the presence of platelets (+Plts, 50:1 platelet-to-macrophage ratio) as indicated. (B) Addition of the following recombinant human proteins to human macrophages: CXCL1 (100 pg ml<sup>-1</sup>), EGF (200 pg ml<sup>-1</sup>), VEGFa (200 pg ml<sup>-1</sup>), PlGF (80 pg ml<sup>-1</sup>) or (C) the indicated concentrations of CXCL7. (D) Blocking antibodies against CXCL7 (4 or 20 μg ml<sup>-1</sup>) or (E) against CXCL12 (10 μg ml<sup>-1</sup>) added to macrophages before the start of the assay. To block CCR5, human macrophages were pre-incubated with met-RANTES (10 ng ml<sup>-1</sup>, 90 minutes) before the start of the assay. Matching IgG isotype controls were added at the same concentrations as the respective blocking antibodies. (F) IL-1β levels in cell-free supernatants of unstimulated (–), LPS stimulated, and nigericin-activated wild-type, *Cxcr3*<sup>-/-</sup>, or *Ccr5*<sup>-/-</sup> BMDMs cultivated alone (–), or in the presence of wild-type platelets (+Plts, 5:1 ratio). (G - H) IL-1b levels in cell-free supernatants of hMDMs stimulated as in B, and added with recombinant human serotonin (5-HT) at the indicated concentrations (G), or pre-incubated with fluoxetine (10 μM) for 30 min before the addition of platelets. (I) IL-1β and TNFα levels in cell-free supernatants of unstimulated (–), LPS stimulated, and nigericin-activated hMDMs cultivated alone (–), or in the presence of platelets (+Plts, 50:1 ratio), added with the indicated concentrations of calcium chloride (CaCl<sub>2</sub>) in Ca<sup>2+</sup>-free medium before the start of the assay.

**A** - Representative of three independent experiments

**B – E, G - I** Floating bars (with mean and minimum to maximum values) from pooled data from independent experiments. Each symbol represents the average of technical triplicates from different donors. Representative of three - four independent experiments.

**F** - Mean + SD of technical triplicates from one experiment.

**Figure S7**



### Figure S7, Related to Figure 7

(**A** - **B**) Volcano plots showing the Log2-fold change and -Log10 of the p values of secretome of (**A**) human platelets (n = 4) and (**B**) megakaryocytes (n = 3). Proteins with  $-2 \leq \text{Log2 fold} \leq 2$  are labeled. (**C**)  $\text{TNF}\alpha$  levels in cell-free supernatants of hMDMs that were left untreated or pre-treated with the TGFb-inhibitor SB-431542 (10  $\mu\text{M}$ , for 1 hours), followed by stimulation with recombinant human TGF-b1. (**D**)  $\text{TNF}\alpha$  levels in cell-free supernatants of hMDMs that were left untreated or stimulated with recombinant human S100A8/9 at the indicated concentrations. (**E**)  $\text{TNF}\alpha$  levels and caspase-1 activity in cell-free supernatants of unstimulated, or LPS-primed hMDMs that were co-incubated with platelets, or the indicated concentrations of rhTHBS1. (**F**) Caspase-1 activity measured in cell-free supernatants of unstimulated, or R848-primed hMDMs pre-treated or not with the CD36 inhibitor SSO. (**G**)  $\text{IL-1}\beta$ ,  $\text{TNF}\alpha$  levels and caspase-1 activity in cell-free supernatants of unstimulated, or LPS- or Pam3CysK4-primed hMDMs that were activated with nigericin in the presence of SSO (50  $\mu\text{M}$ ), TAK242 (0.5  $\mu\text{g ml}^{-1}$ ), anti-Rage (10  $\mu\text{g ml}^{-1}$ ), or all those inhibiting strategies combined (3X inhibition).

**C - G** - Floating bars (with mean and minimum to maximum values) from pooled data

from a minimum of 2 independent experiments. Each symbol represents the average of technical replicates from different donors.

**Table S1: Primers used for qPCR analysis. Related to Figure 5, and Figures S3 - S4.**

Gene symbol	Encoding protein	Forward primer sequence (5' - 3')	Reverse primer sequence (5' - 3')
<i>ACTB</i>	$\beta$ -actin	CCACCATGTACCCTGGCATT	CGGAGTACTTGCGCTCAGG
<i>NLRP3</i>	NLPR3	TCGGAGACAAGGGGATCAAA	AGCAGCAGTGTGACGTGAGG
<i>CD14</i>	CD14	GAGCTCAGAGGTTCGGAAGA	CTTCATCGTCCAGCTCACAA
<i>PYCARD</i>	ASC	GAGCTCACCGCTAACGTGCT	ACTGAGGAGGGGCCTGGAT
<i>PF4</i>	CXCL4	CTGAAGAAGATGGGGACCTG	GTGGCTATCAGTTGGGCAGT
<i>CASP1</i>	Caspase-1	ACAACCCAGCTATGCCCACA	GTGCGGCTTGACTTGTCCAT
<i>GP1BA</i>	CD41	CTGCTCTTTGCCTCTGTGGT	CTCCAGGTGTGTGGTTTGTG
<i>IL1B</i>	IL-1 $\beta$	TGGGCAGACTCAAATTCCAGCT	CTGTACCTGTCCTGCGTGTTGA