

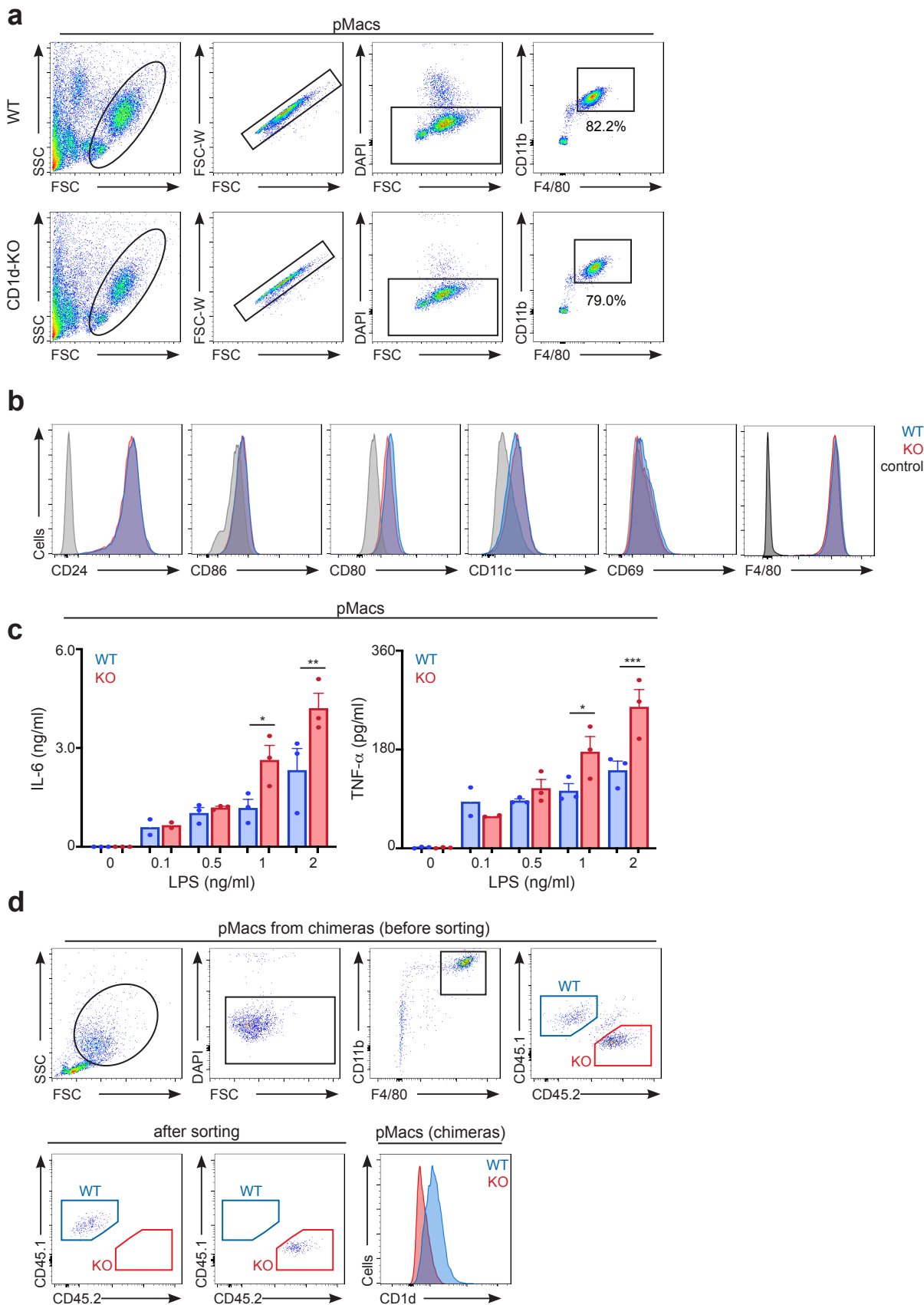
## **SUPPLEMENTARY INFORMATION**

### **CD1d-dependent rewiring of lipid metabolism in macrophages regulates innate immune responses**

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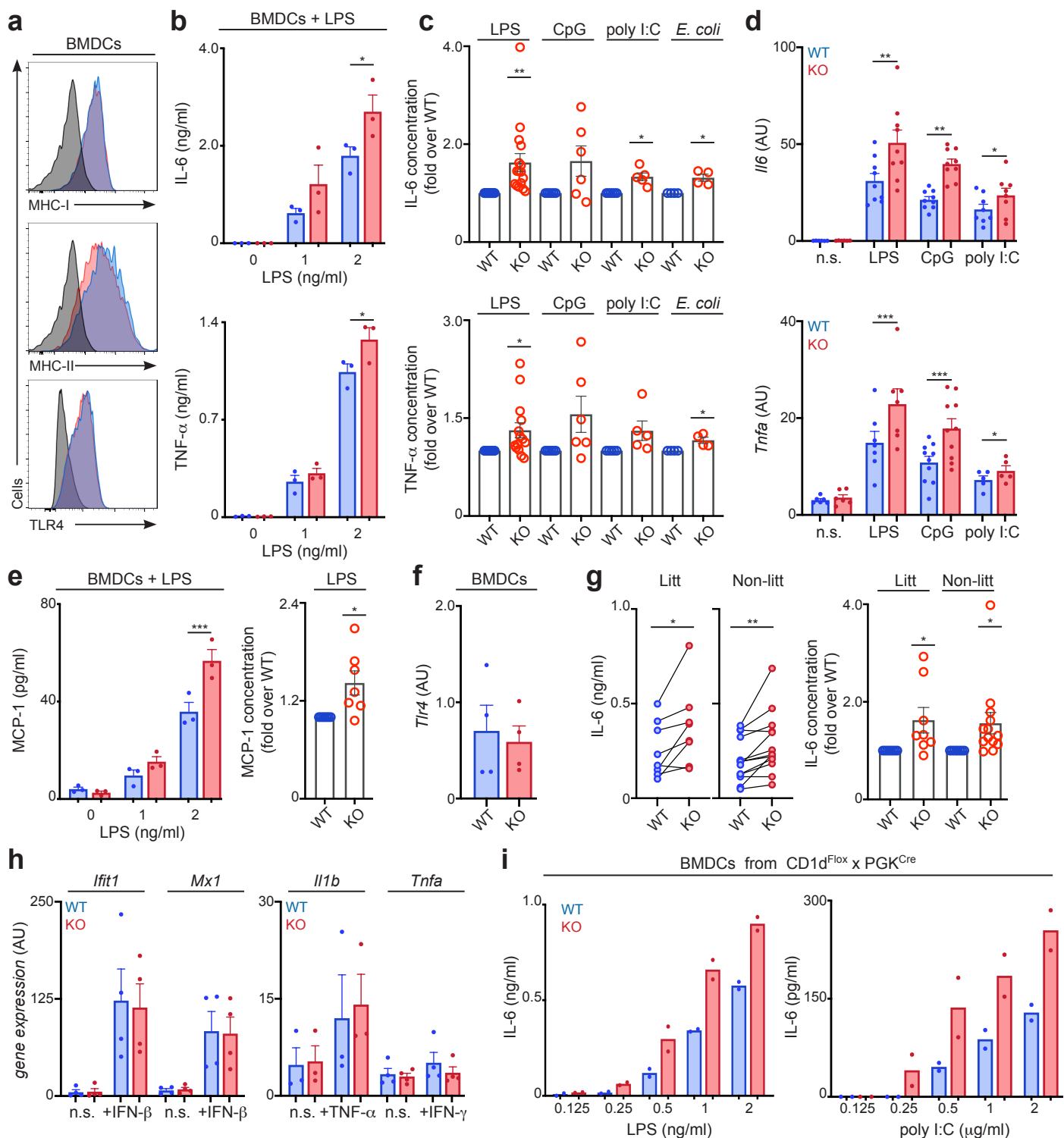
This PDF file includes Supplementary Figures 1 to 6 and Supplementary Table 1

# Supplementary Figure 1



**Supplementary Figure 1. Characterization of WT and CD1d-KO pMacs.** (a) Flow cytometry profile showing populations of WT and CD1d-KO pMacs. (b) Representative flow cytometry for WT (blue) and CD1d-KO (red) pMacs showing expression of the depicted markers. (c) Secretion of IL-6 (left) and TNF- $\alpha$  (right) in WT and CD1d-KO pMacs stimulated with LPS at the indicated concentrations (n=2-3). Bars represent mean  $\pm$  SEM; \*p<0.05; \*\*p<0.01, \*\*\*p<0.001, 2-way ANOVA. (d) Flow cytometry profiles showing gating strategy for purification of WT and CD1d-KO pMacs from BM chimeras. Values for n represent biologically independent samples (as shown by the number of data points in each graph). n= cells isolated from individual mice. Source data are provided as a Source Data file

## Supplementary Figure 2

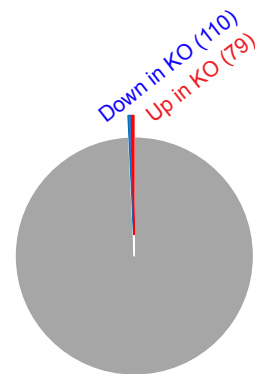


### Supplementary Figure 2. CD1d functions as a negative regulator of TLR responses

(a) Representative flow cytometry of WT (blue) and CD1d-KO (red) BMDCs. (b) Cytokine secretion by WT (blue) and CD1d-KO (red) BMDCs stimulated with LPS as indicated (n=3). \* $p < 0.05$ ; 2-way ANOVA. (c-d) Normalised concentration of secreted cytokines (fold over WT, c) and gene expression (d) in WT and CD1d-KO BMDCs cultured with the depicted stimuli for 6h (n=4-16). \* $p < 0.05$ ; \*\* $p < 0.01$ ; \*\*\* $p < 0.001$  one-sample (c) or paired two-tailed t-test (d). n.s.=non stimulated. (e) Secretion of MCP-1 (left, n=3) and normalised concentration of MCP-1 (fold over WT, right, n=7) for BMDCs after stimulation with LPS. \* $p < 0.05$ ; \*\*\* $p < 0.001$ ; 2-way ANOVA (left), or one-sample t-test (right). (f) qPCR expression data of *Tlr4* in WT and CD1d-KO BMDCs (n=4). (g) Secretion of IL-6 (left) and normalised concentration of IL-6 (fold over WT, right) for BMDCs after stimulation with LPS as above (n=8-13). Cells were either isolated from littermate controls (Litt) or from age and sex matched WT and CD1d-KO mice (Non-Litt). \* $p < 0.05$ ; \*\* $p < 0.01$ ; two-tailed paired (left) or one-sample t-test (right). (h) Expression of the depicted genes in WT and CD1d-KO BMDCs after stimulation with IFN- $\beta$ , TNF- $\alpha$  or IFN- $\gamma$  (n=4). n.s.=non stimulated. (i) WT or CD1d-KO BMDCs were generated from CD1d<sup>Flox</sup> x PGK<sup>Cre</sup> mice and stimulated with TLR ligands. IL-6 secretion was measured by ELISA. Data are representative results pooled from 2 experiments. Bars in all graphs represent mean  $\pm$  SEM. Values for n represent biologically independent samples (as shown by the number of data points in each graph). n= cells isolated from individual mice. Source data are provided as a Source Data file

# Supplementary Figure 3

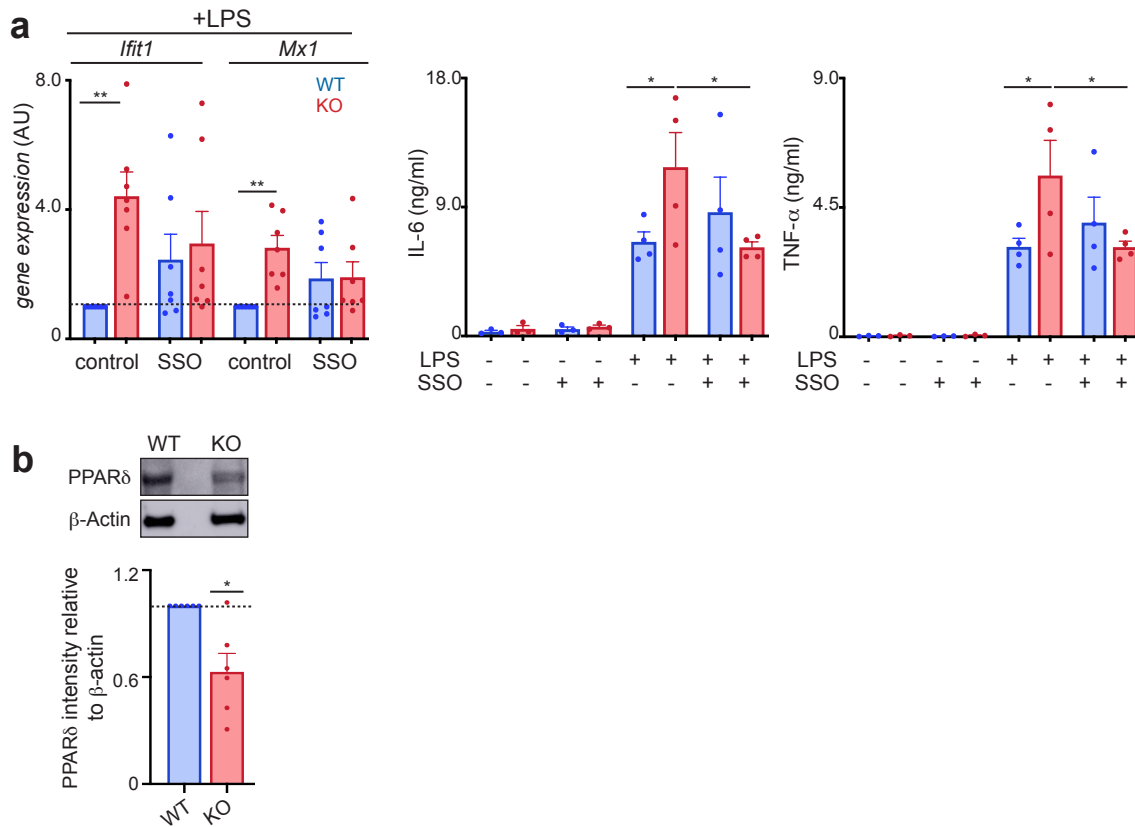
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GO Biological process	
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Cyp51	
Fdft1	
Hsd17b7	
Sc5d	
Idi1	
Hmgcs1	
Fdps	
Abcg1	
Pltp	
Apoc2	
Lpl	
Insig	
Cd244	
Triab3	
Sgms1	
Plk3cb	
Nanp	
Pdgfb	
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secondary alcohol biosynthetic process	
sterol biosynthetic process	
cholesterol metabolic process	
sterol metabolic process	
secondary alcohol metabolic process	
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steroid biosynthetic process	
organic hydroxy compound biosynthetic process	
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alcohol metabolic process	
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organic hydroxy compound metabolic process	

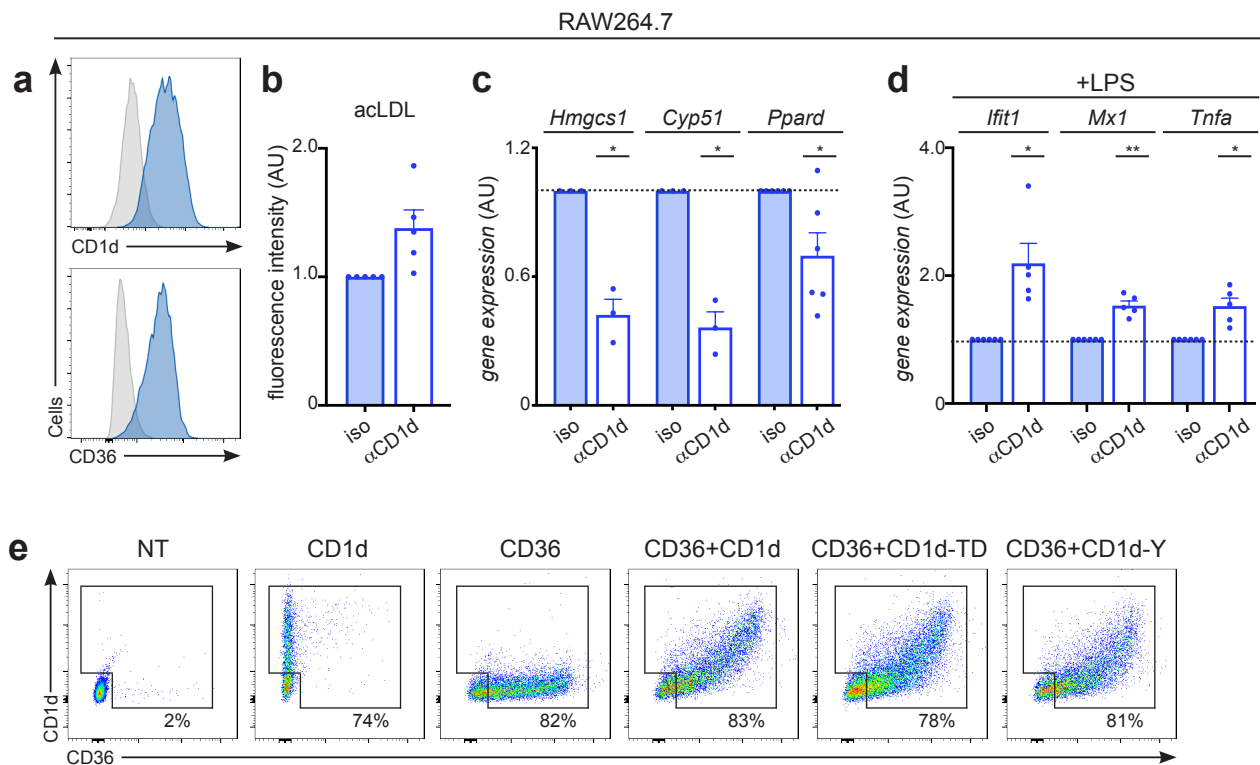
**Supplementary Figure 3. Differentially expressed genes in CD1d-KO vs. WT pMacs.** Left table show genes ID and symbols as well as the fold change for differentially expressed genes between WT and KO pMacs. A fold change cut-off of 1.5 and adjusted p-value cut off of 0.01 were applied. Top right, show numbers of significantly up- or down-regulated genes. Right table shows GO terms and input genes for significantly changed pathways.

## Supplementary Figure 4



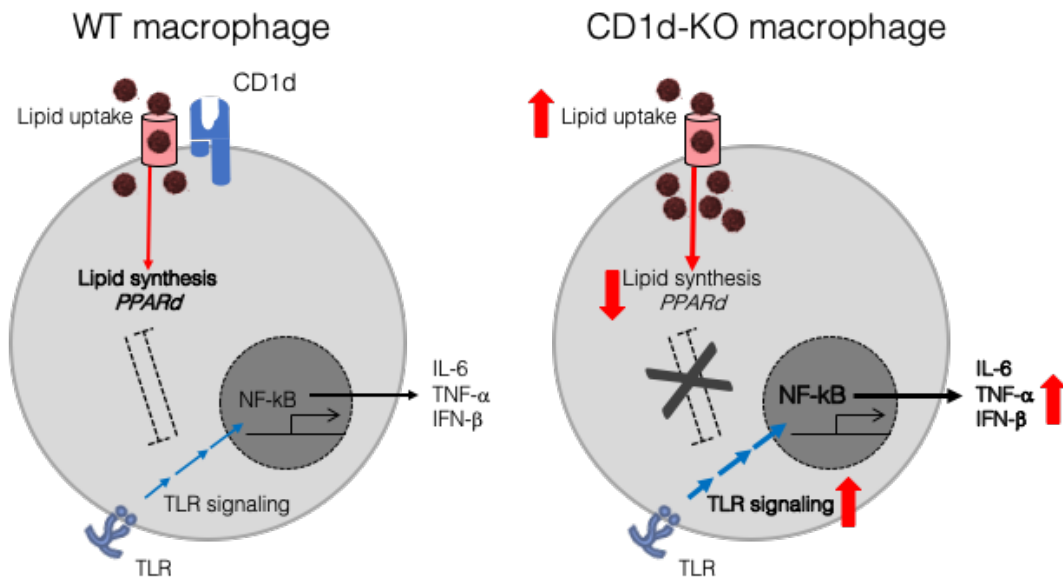
**Supplementary Figure 4. CD1d links metabolism and immunity in macrophages. (a)** BMDCs were cultured in the presence (or absence, control) of SSO overnight prior to stimulation with LPS. Expression of the depicted genes (left,  $n=7$ ) or cytokine secretion (right,  $n=3-4$ ) are shown. Bars represent mean  $\pm$  SEM; \* $p<0.05$ ; \*\* $p<0.01$  2-way ANOVA. **(b)** Western-blot showing total PPAR $\delta$  and  $\beta$ -actin in WT and CD1d-KO BMDCs. Levels of PPAR $\delta$  were quantified and related to  $\beta$ -actin ( $n=6$ ). Bars represent mean  $\pm$  SEM; \* $p<0.05$  one-sample t-test. Values for  $n$  represent biologically independent samples (as shown by the number of data points in each graph).  $n$ = cells isolated from individual mice. Source data are provided as a Source Data file

## Supplementary Figure 5



**Supplementary Figure 5. CD1d regulates CD36-dependent lipid uptake.** (a-d) RAW264.7 cells were treated with  $\alpha$ CD1d antibody or isotype control (iso) as indicated. (a) Flow cytometry panel showing expression of CD1d and CD36; (b) Uptake of Dil-acLDL (n=5); (c) Relative expression of the depicted genes (n=3-6); (d) Expression of the depicted genes after LPS stimulation (n=5). Bars represent mean  $\pm$  SEM; \*p<0.05, \*\*p<0.01 one-sample t-test. (e) HEK293T cells were transiently transfected with the indicated constructs to express CD1d, mutant CD1d (CD1d-TD or CD1d-Y) and/or CD36. Surface expression of CD1d and CD36 was measured by flow cytometry. Values for n represent biologically independent samples (as shown by the number of data points in each graph). Source data are provided as a Source Data file

## Supplementary Figure 6



**Supplementary Figure 6. Schematic model of the CD1d-dependent regulation of metabolism and immunity in macrophages.** CD1d-deficient macrophages display an increased lipid uptake and transcriptional downregulation of metabolic enzymes involved in lipid synthesis pathways as well as the transcription factor PPAR $\delta$ . These metabolic alterations underpin increased responses of CD1d-KO cells to TLR stimulation, resulting in increased TLR signalling and cytokine production. Red arrows represent pathways up- or down-regulated in CD1d-KO cells vs. WT controls.

**Supplementary Table 1. Primers used for qPCR**

<b>Target</b>	<b>Forward Sequence</b>	<b>Reverse Sequence</b>
<i>Cd36</i>	ATGGGCTGTGATCGGAACTG	TTTGCCACGTCATCTGGGTTT
<i>Cyp51a1</i>	CTGCCCGCTGGAGCGAAAAG	CACAGGTGTTGTCAGCCGACC
<i>Gapdh</i>	AACGACCCCTTCATTGAC	TCCACGACATACTCAGCA
<i>Hmgcs1</i>	GGAAGCCTTTGGGGACGTTA	ACACTCCAACCCTCTTCCCT
<i>Ifit1</i>	CTGAGATGTCACTTCACATGGAA	GTGCATCCCAATGGGTTCT
<i>Il6</i>	CAGAGGATACCACTCCCAACA	TCCAGTTTGGTAGCATCCATC
<i>Lpl</i>	GGGAGTTTGGCTCCAGAGTTT	TGTGTCTTCAGGGGTCCTTAG
<i>Msra</i>	TGGAGGAGAGAATCGAAAGCA	CTGGACTGACGAAATCAAGGAA
<i>Mx1</i>	GACCATAGGGGTCTTGACCAA	AGACTTGCTCTTTCTGAAAAGCC
<i>Nrlh3</i>	CTGATTCTGCAACGGAGTTGT	GACGAAGCTCTGTTCGGCTC
<i>Nrlh2</i>	CCACCATCGAGATCATGTTG	TCTCGTGGTTGTAGCGTCTGG
<i>Plin1</i>	GGGACCTGTGAGTGCTTCC	GTATTGAAGAGCCGGGATCTTTT
<i>Pltp</i>	CGCAAAGGGCCACTTTTACTA	GCCCCATCATATAAGAACCAG
<i>Ppara</i>	ACTCCACCTGCAGAGCAACCA	TAFATCTCCTGCAGTAGCGGG
<i>Ppard</i>	CCCTGGCAAAGCATTGTAT	AATCCTTGGCCCTCTGAGAT
<i>Pparg</i>	TTGAGCCCAAGTTCGAGTTTGCTG	ATTCTAGAGCCCGCAGAATGGTGT
<i>Srebf1</i>	ACAGTGACTTCCCTGGCCTAT	GCATGGACGGGTACATCTTCAA
<i>Srebf2</i>	GCAGCAACGGGACCATTCT	CCCCATGACTAAGTCCTTCAACT
<i>Tlr4</i>	TGGCTGGTTTACACATCCATCGGT	TGGCACCATTGAAGCTGAGGTCTA