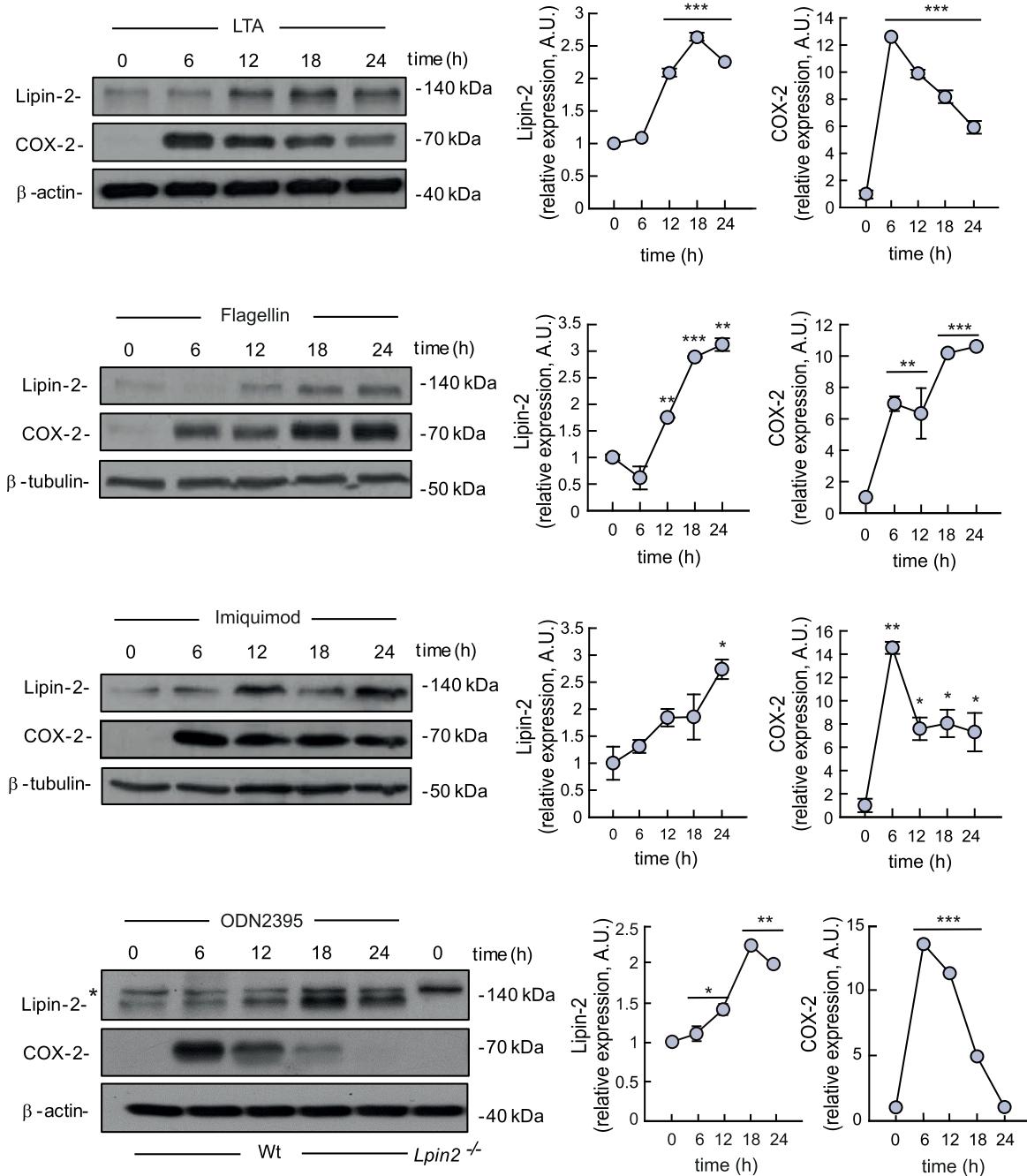


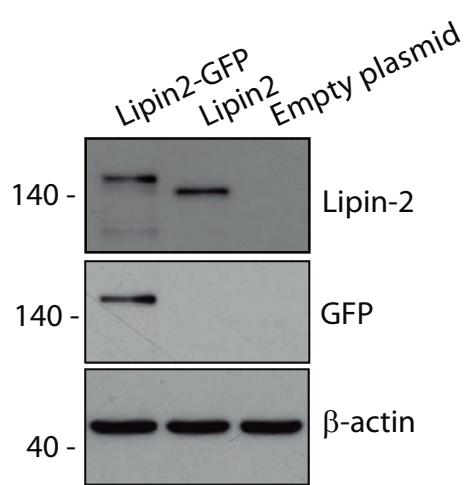
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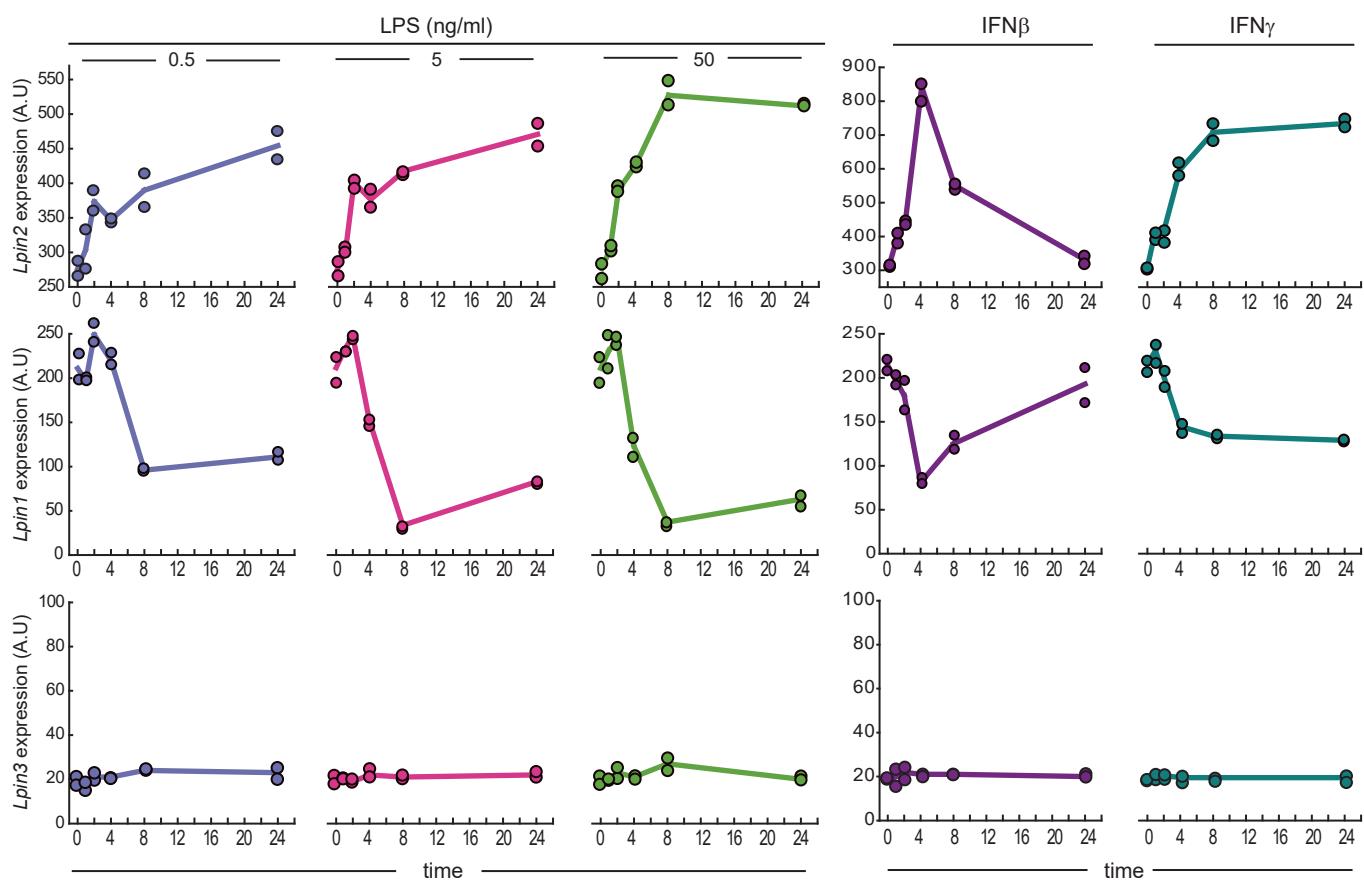
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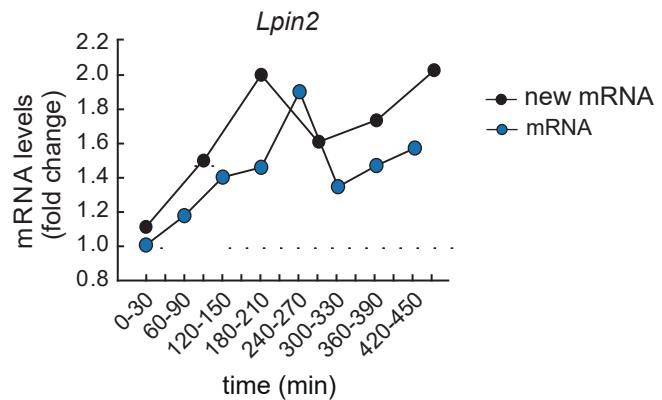
Appendix Figure S1. (continuation of Fig 1). *Effect of TLR agonists on lipin-2 expression.* BMDMs were treated with 1 µg/ml LTA (TLR2), 50 ng/ml Flagellin (TLR5), 5 µg/ml Imiquimod (TLR7) or 1 µM ODN 2395 (TLR9) for the indicated periods of time. Cells lysates were analyzed by immunoblot using specific antibodies against lipin-2, COX-2, and β-actin or tubulin as loading controls. Quantifications of the bands from technical replicates are shown on the right. Shown are representative experiments of three ones. *, P < 0.05, ** P < 0.01, *** P < 0.001, by Student's t test.



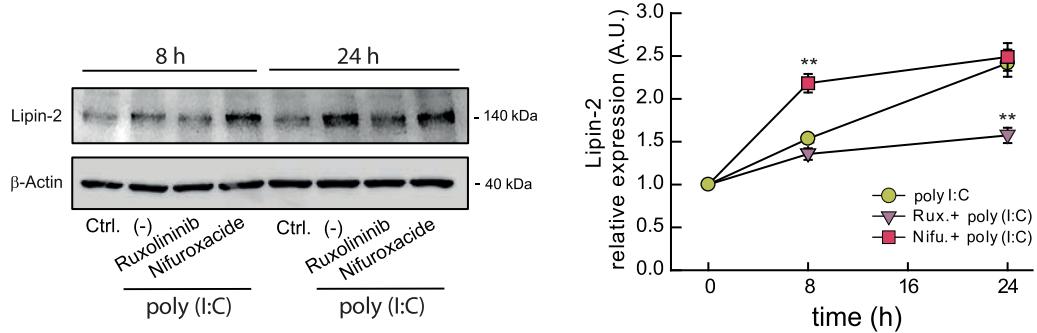
Appendix Figure S2. Overexpression of *lipin-2* in HEK-239 cells. HEK-239 cells were transfected with 2 µg of the plasmid mlipin-2-EGFP (Valdearcos et al., 2012, J. Biol. Chem. 287: 10894-10904) containing the murine sequence of lipin-2 fused with EGFP, a plasmid containing only the lipin-2 sequence or with an empty plasmid. Lysates were analyzed by immuno-blot using antibodies against lipin-2, GFP and β -actin.



Appendix Figure S3. *Lpin* mRNA expression levels in activated BMDMs. BMDMs were treated with the indicated doses of LPS (left panels), or 10 U/ml of IFN β or IFN γ (right panels). Duplicate samples were collected at 0, 1, 2, 4, 8 and 24 h. mRNA levels for the indicated lipins were analyzed using Affymetrix Mouse Gene 1.1ST Array (GSE44292) (Raza et al., 2014, J. Leukoc. Biol. 96:167-183).



Appendix Figure S4. New synthesis of *Lpin2* mRNA induced by IFN- γ . BMDMs were treated or not with 100 U/ml INF- γ at different time points and newly transcribed mRNA and total RNA was analyzed as described elsewhere (Dölken L et al., 2008, RNA, 14:1959-1972). Fold change of newly transcribed and total levels of *Lpin2* mRNA from stimulated cells is represented.



Appendix Figure S5. *Lipin-2 expression in cells treated with poly(I:C).* BMDMs were left untreated (Ctrl.) or stimulated with 25 mg/ml poly(I:C) in the presence or absence of 5 mM Ruxolitinib or 10 mM Nifuroxacide for the indicated periods of time. Protein was analyzed by Immunoblot using specific antibodies against lipin-2 or β-actin (loading control). Quantifications of the bands are shown on the right. Shown is a representative experiment of three ones (three biological samples). **, P < 0.01, by Student's t test.

Peak 1: 71527697-71528898

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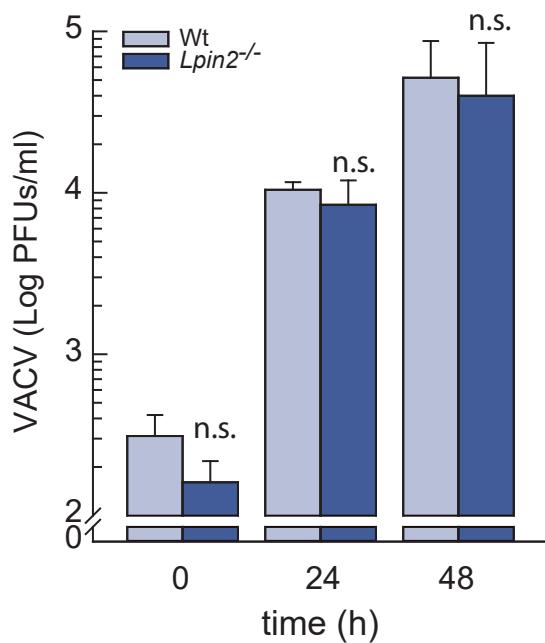
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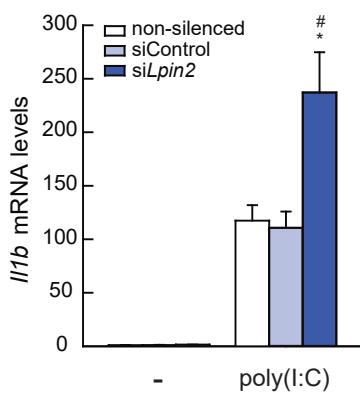
Peak 3: 71541311-71541719

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TTTTCTATGTATAAGAAGTTGTAGGGGGCGTAAGGGGG

Appendix Figure S6. ISRE and GAS sequences present in Stat1 peaks in the Lpin2 gene. DNA sequence motifs recognized by Stat1 in peaks 1, 2 and 3 called by MACS during Chip-Seq analysis were determined by the presence of ISRE (GAAANNGAAA, green) or GAS (TTCNNNGAA or TTCNNNNNGAA, grey) consensus motifs within a 100-bp region centered on the peak summit. Notice that in peak 2 a GAS consensus motif was also found at 128-bp from the center of the peak.



Appendix Figure S7. Infection of BMDMs with VACV is not affected by lipin-2 expression levels. BMDMs from Wt or *Lpin2*^{-/-} animals were infected with VACV (MOI = 0.01, Western Reserve strain). Cells were harvested at the indicated time points and virus yields were determined by plaque assay in BSC40 cells. Results represent the mean \pm SD of three independent experiments. *P* values were calculated by two-tailed t test assuming non-equal variance. No statistical differences(n.s.) were found between Wt and lipin-2 –deficient macrophages.



Appendix Figure S8. Effect of lipin-2 on *Il1b* expression in RAW264.7 macrophages. RAW264.7 macrophages were left untreated (non-silenced), or silenced with control siRNAs (siControl) or against *Lpin2* (si*Lpin2*). After 48 h, cells were left untreated (-) or activated with 25 µg/ml poly(I:C). *Il1b* mRNA levels were analyzed by qPCR, using *Gapdh* as reference. Data from triplicate biological samples are represented as mean ± SE. *, P < 0.05, #, P < 0.05, by Student's t test. *, si*Lpin2* vs siControl. #, si*Lpin2* vs non-silenced cells.