

Supplementary Figure Legends

Figure S1. The levels of STAT3 in mitochondria of phagocytes or tissues from inducible mitochondrial STAT3 knock-in mice, as shown in Figure. 1

(A) The amounts of STAT3 were quantified by densitometry, normalized to HSP60, and plotted. (B) The relative amounts of STAT3 in the indicated cell fractionation were quantified, normalized to the indicated loading marker, and plotted. (A and B) The data shown represent a combination of three independent experiments. ** $P < 0.01$. (C) Immunofluorescence of p-STAT3 (Ser727, gray), p-STAT3 (Tyr705, red), HSP60 (green), and DAPI (blue) in MEFs. The data are representative of one of three independent experiments. (D) The relative amounts of STAT3 in the livers, intestines or colons were quantified, normalized to actin, and compared. The data shown represent a combination of three independent experiments and were compared using Multiple t test—one per row. ** $P < 0.01$. (E) The STAT3 expression was assessed in livers and colons harvested from the indicated mice by a Western blot analysis. The relative amounts of STAT3 in these tissues were quantified and normalized to actin, and plotted.

Figure S2. Mitochondrial STAT3 didn't influence the development of HSC, as shown in Figures. 1 and 2

(A) 6-week-old mice were treated with 4-OHT for 7 times. 2 days later, the development of HSC with different genotypes was assessed by flow cytometry. The data shown were representative of one of two independent experiments. (B) The graph shows the percentage of indicated cells in BM gating strategy in (A). The data shown was representative of one of two independent experiments ($n = 7$ mice/group) with similar results. Significance was calculated using an unpaired Student's t-test. (C) The graph shows the number of indicated cells in BM gating strategy in (A). The data shown was representative of one of two independent experiments ($n = 7$ mice/group) with similar results. Significance was calculated using an unpaired Student's t-test. (D) BMDMs were stimulated with or without 100 ng/mL LPS for the indicated time point. p-STAT3 (Ser727),

p-STAT3 (Tyr705), STAT3 and actin were analyzed by a Western blot analysis. The relative levels of the indicated protein were quantified, normalized to actin, and plotted. The plot data shown represent a combination of three independent experiments and were compared using two-way ANOVA followed by multiple comparisons. ** $P < 0.01$, * $P < 0.05$.

Figure S3. The genes involved in mediating inflammation and metabolism were validated by real-time RT-PCR, as shown in Figure. 3

(A and B) RNA was extracted and cDNA was synthesized, and subjected to real-time RT-PCR. Data are shown as the mean \pm SD and are representative of one of two independent experiments performed in triplicate. ** $P < 0.01$, * $P < 0.05$. **(C)** Induced BMDMs were treated with 100 nM 4-OHT for 3 days. Nuclear, cytoplasmic, and mitochondrial fractions were extracted. The amounts of indicated protein were quantified by densitometry, normalized to loading control, and plotted. The data shown represent a combination of three independent experiments. ** $P < 0.01$.

Figure S4. Mitochondrial STAT3 was involved in mediating CPT1a stabilization, as shown in Figure. 6

(A-B) The amounts of indicated protein were quantified by densitometry, normalized to loading control, and plotted. The data shown represent a combination of three independent experiments. ** $P < 0.01$.

Figure S5. USP50 is critical for CPT1a stabilization, as shown in Figure. 7

(A) BMDMs of the indicated genotypes were treated with 4-OHT for 3 days, followed by treatment with 100 ng/mL LPS for an additional 6 h before harvesting. The levels of indicated protein were examined. **(B)** *Rosa26^{LSL-MLS-Stat3}* macrophages were transfected with a negative control siRNA or a siRNA against USP50. The levels of CPT1a, USP50 and actin were assessed. **(C)** The levels of p65 in the indicated cell fractionation were examined. **(A-C)** The amounts of indicated protein were quantified by densitometry, normalized to loading control, and plotted. The data shown represent a combination of three

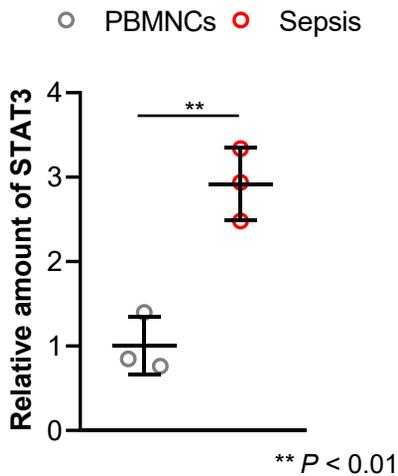
independent experiments. ** $P < 0.01$, n.s., not significant.

Figure S6. Curcumin suppressed the activation of STAT3 and NF- κ B, as shown in Figure. 8

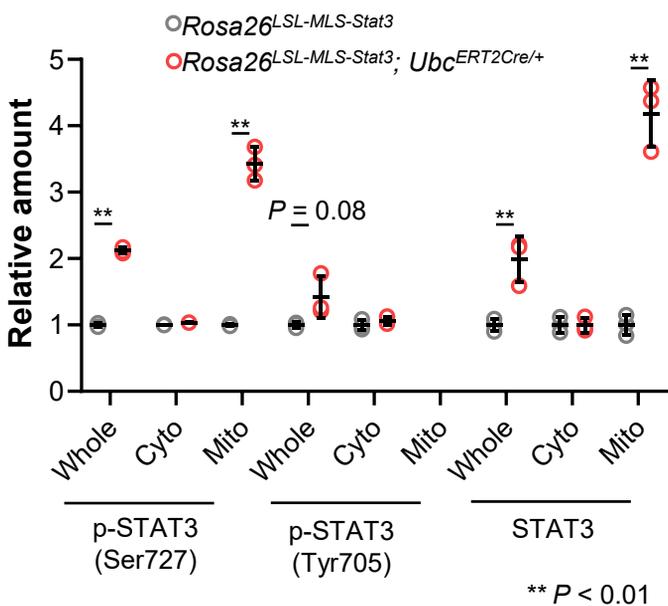
The levels of serum LDH (**A**) and albumin (**B**) were assessed. (A and B) The data shown are representative of one of two independent experiments. Numerical data are shown as the mean \pm SD. ** $P < 0.01$, * $P < 0.05$. (**C-F**) The amounts of indicated protein were quantified by densitometry, normalized to loading control, and plotted. The data shown represent a combination of three independent experiments. ** $P < 0.01$, * $P < 0.05$.

Figure S1

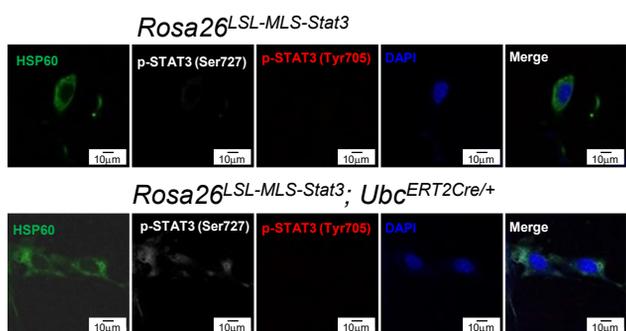
A



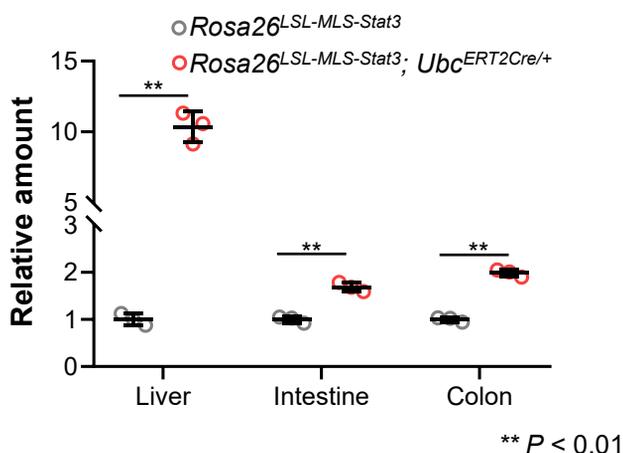
B



C

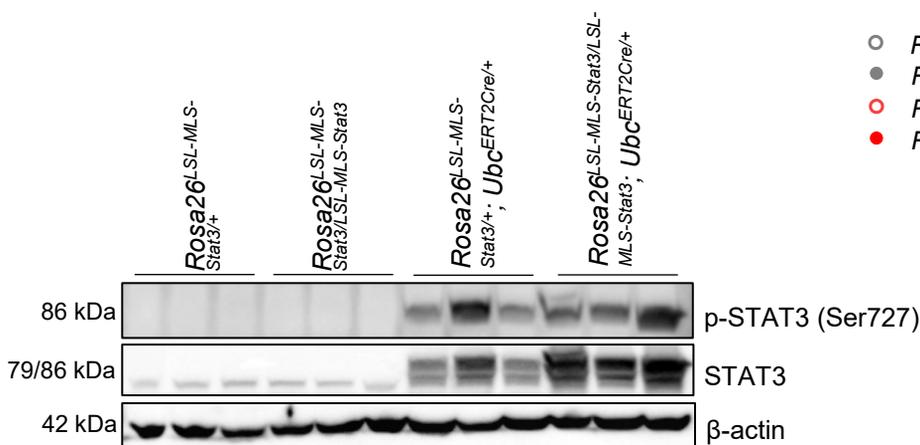


D

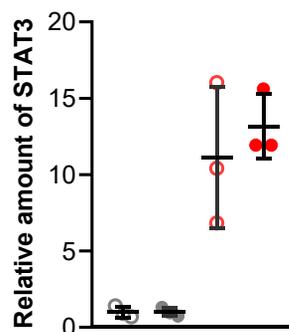


E

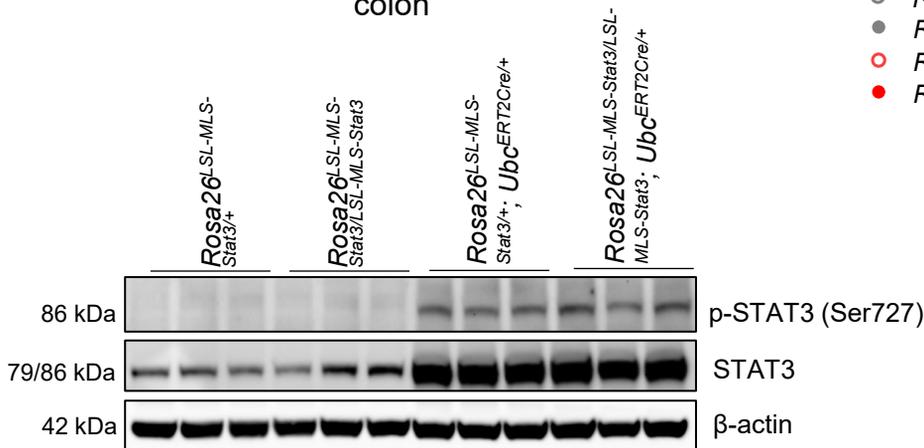
liver



- *Rosa26^{LSL-MLS-Stat3/+}*
- *Rosa26^{LSL-MLS-Stat3/LSL-MLS-Stat3}*
- *Rosa26^{LSL-MLS-Stat3/+}; Ubc^{ERT2Cre/+}*
- *Rosa26^{LSL-MLS-Stat3/LSL-MLS-Stat3}; Ubc^{ERT2Cre/+}*



colon



- *Rosa26^{LSL-MLS-Stat3/+}*
- *Rosa26^{LSL-MLS-Stat3/LSL-MLS-Stat3}*
- *Rosa26^{LSL-MLS-Stat3/+}; Ubc^{ERT2Cre/+}*
- *Rosa26^{LSL-MLS-Stat3/LSL-MLS-Stat3}; Ubc^{ERT2Cre/+}*

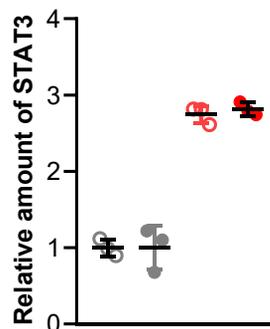


Figure S2

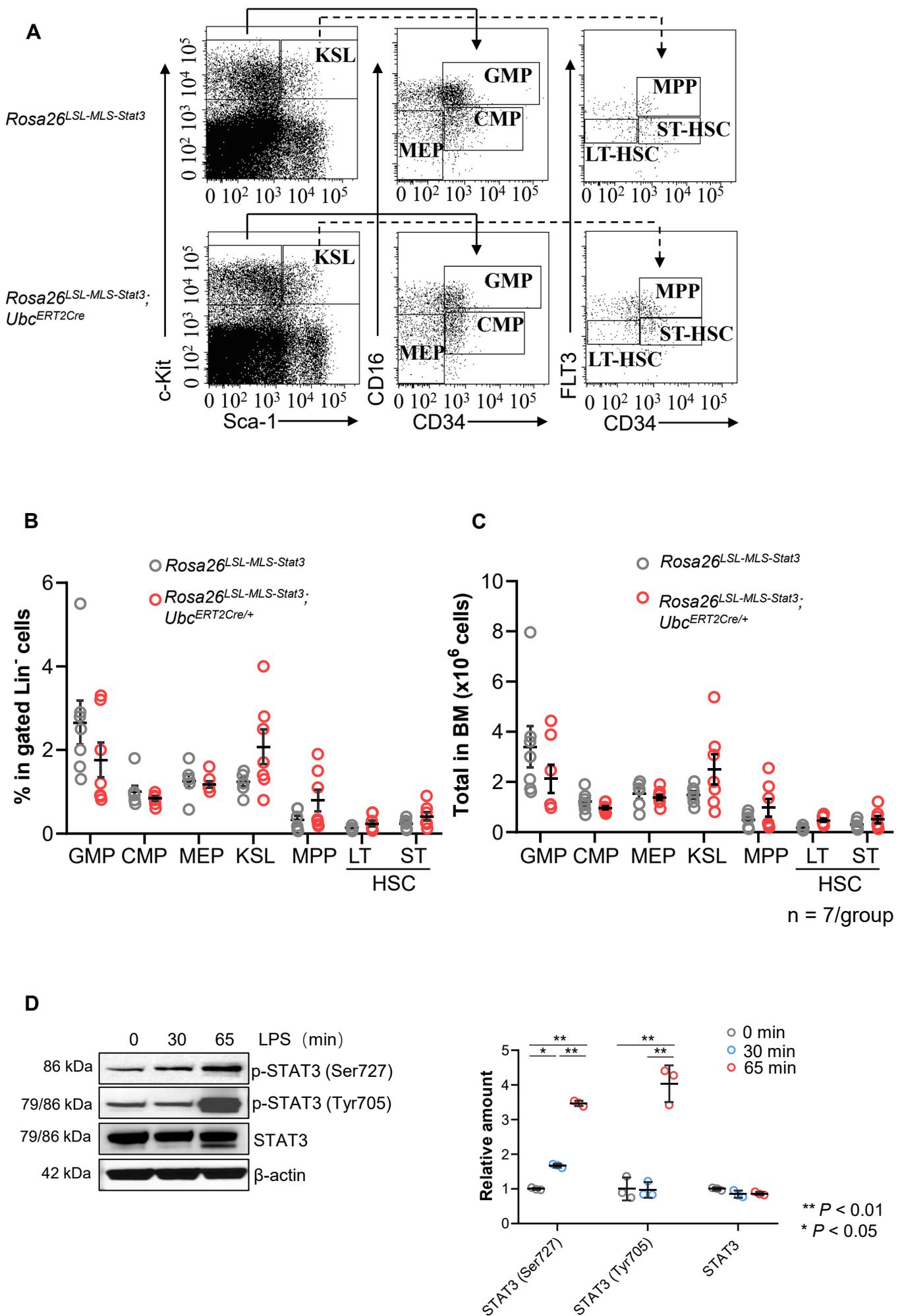
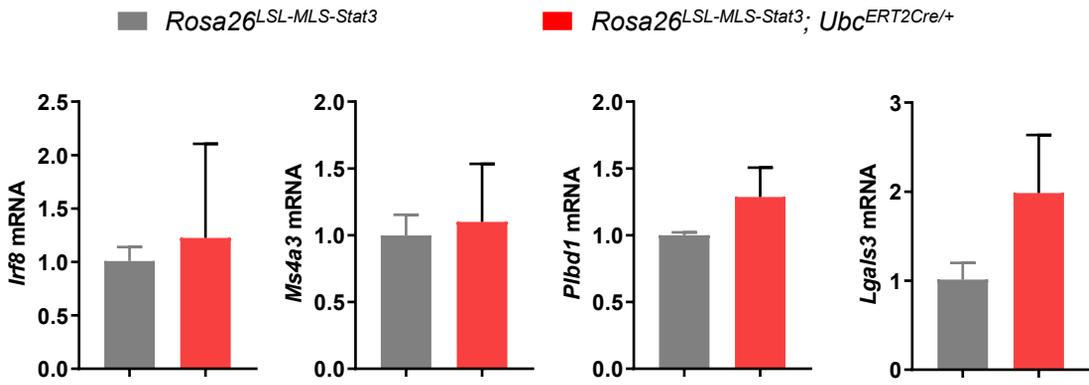
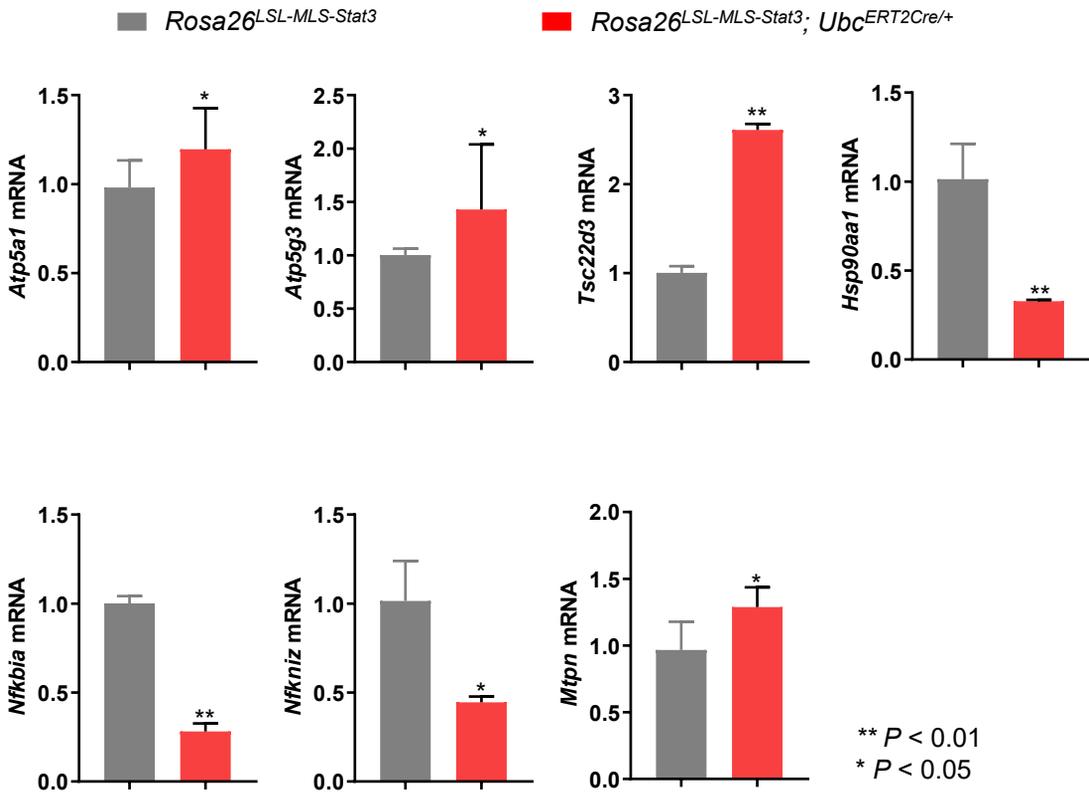


Figure S3

A



B



C

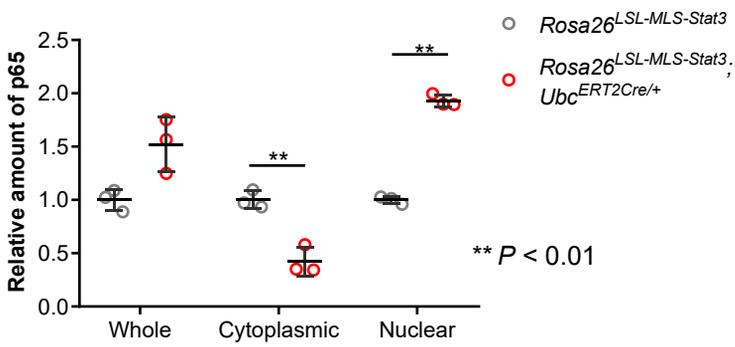


Figure S4

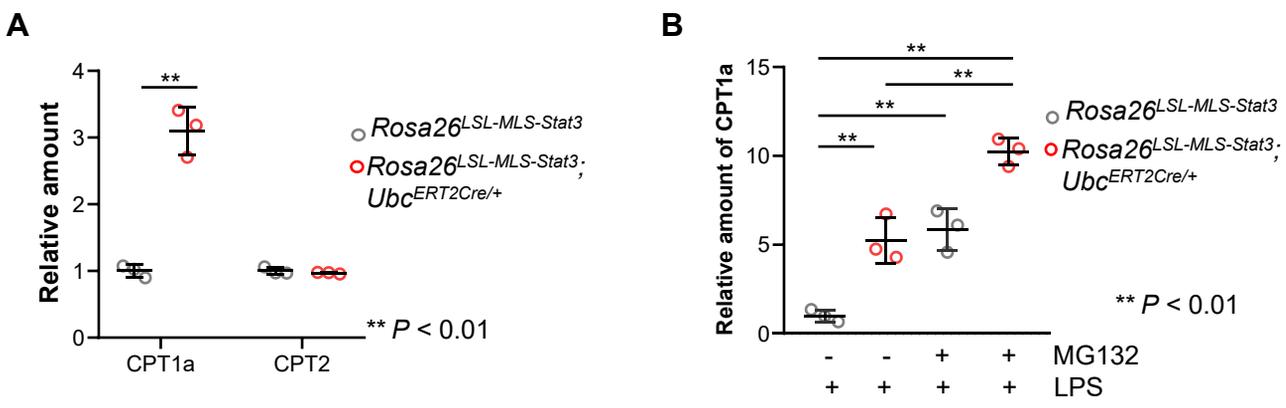
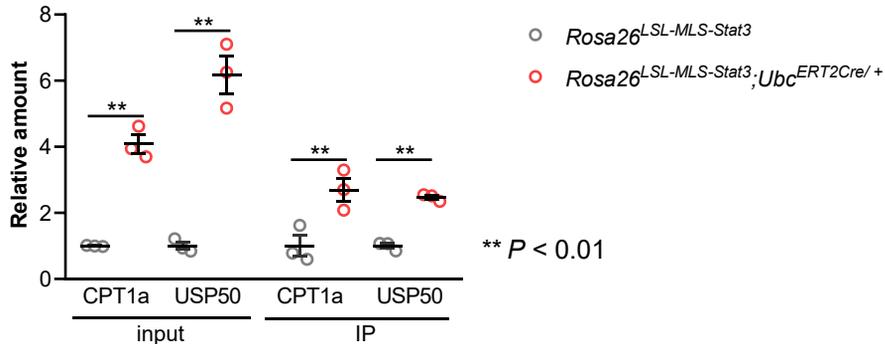
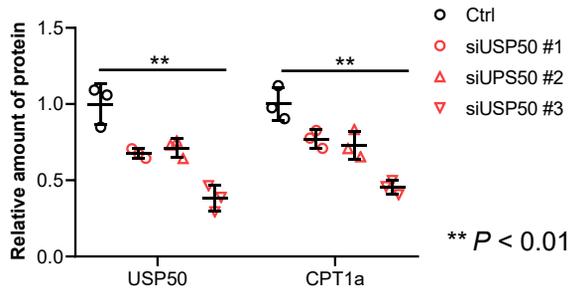


Figure S5

A



B



C

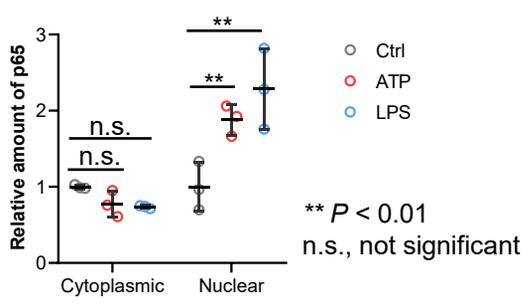
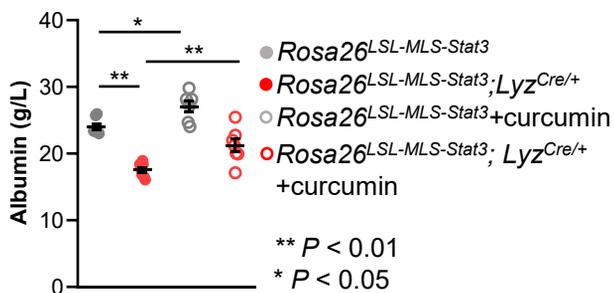
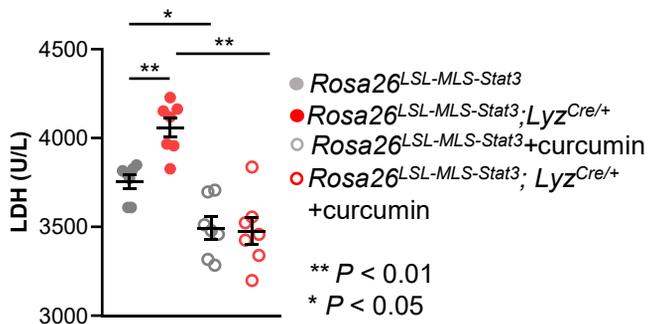


Figure S6

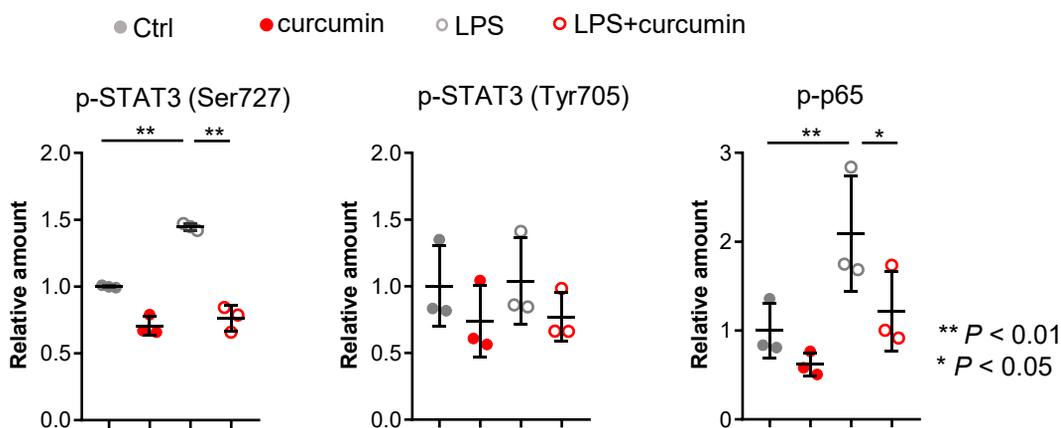
A



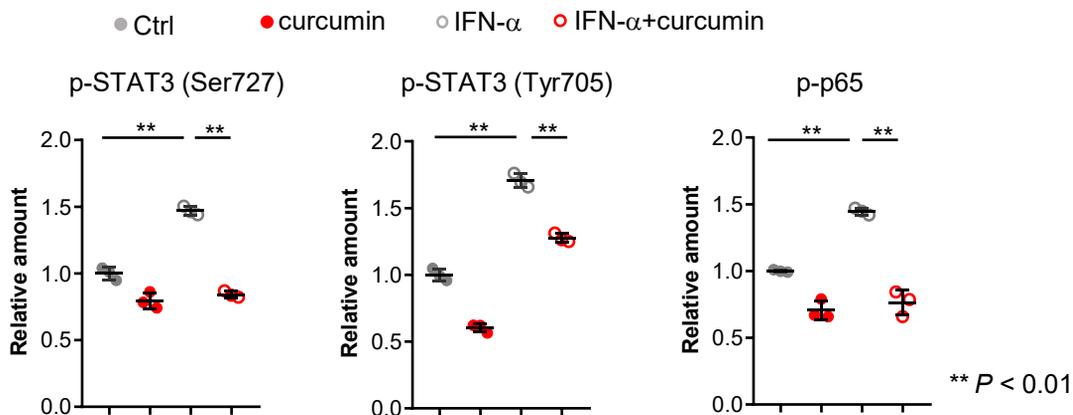
B



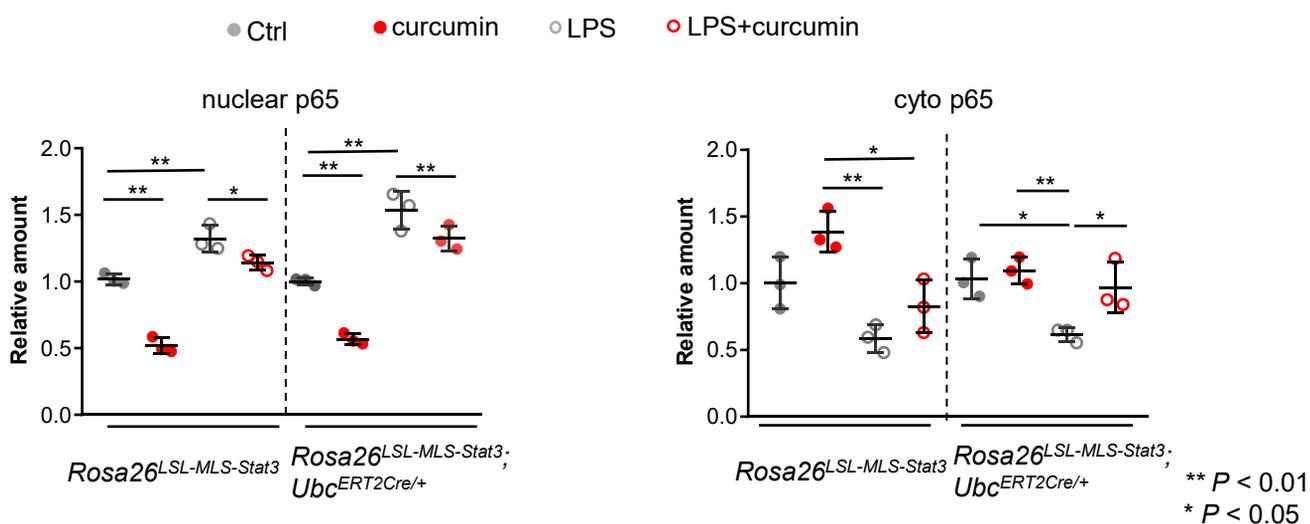
C



D



E



F

