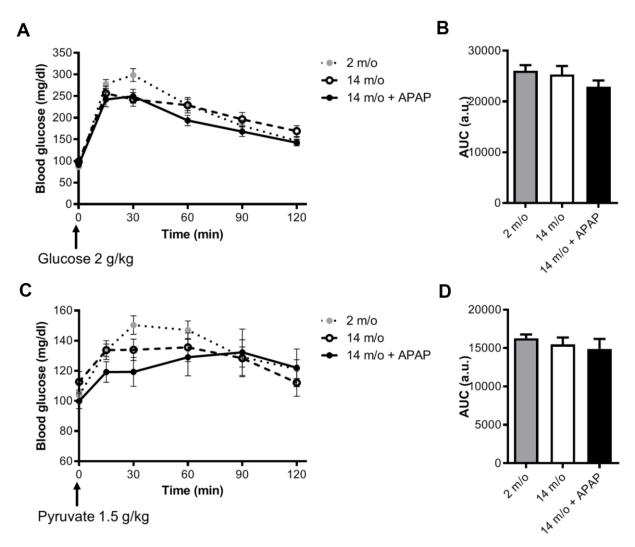
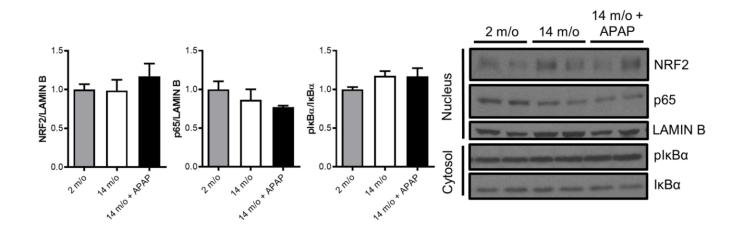
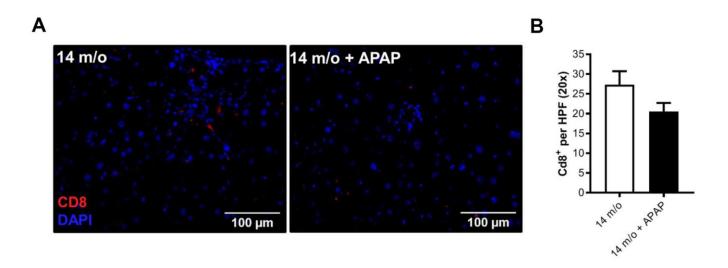
## SUPPLEMENTARY FIGURES



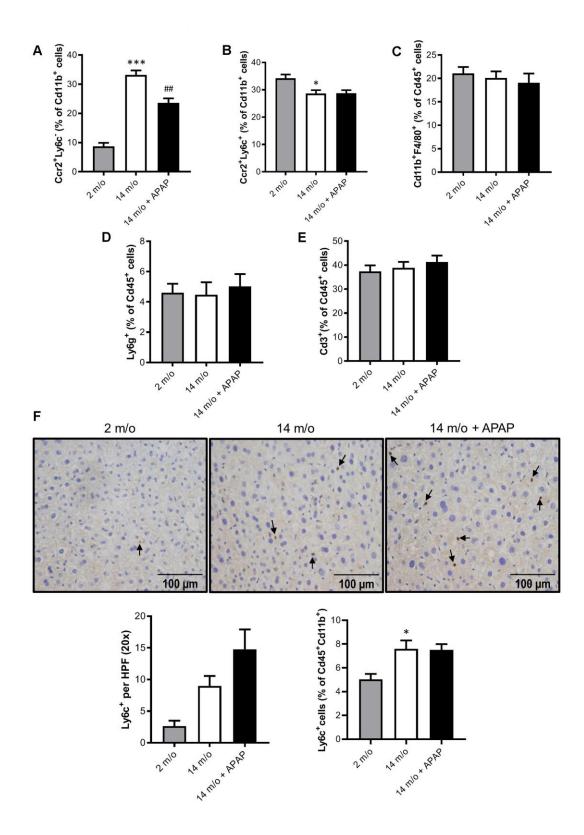
Supplementary Figure 1. Chronic APAP exposure at an infratherapeutic dose did not alter glucose homeostasis in 14 m/o mice. (A) GTT from 2 m/o, 14 m/o and 14 m/o + APAP mice. Values showing blood glucose (mg/dl) correspond to mean  $\pm$  S.E.M. (n = 18-22 mice per group). (B) Graph depicts the area under the curve (AUC) from (A). (C) PTT from 2 m/o, 14 m/o and 14 m/o + APAP mice. Values showing blood glucose (mg/dl) correspond to mean  $\pm$  S.E.M. (n = 17-22 mice per group). (D) Graph depicts the area under the curve (AUC) from (C).



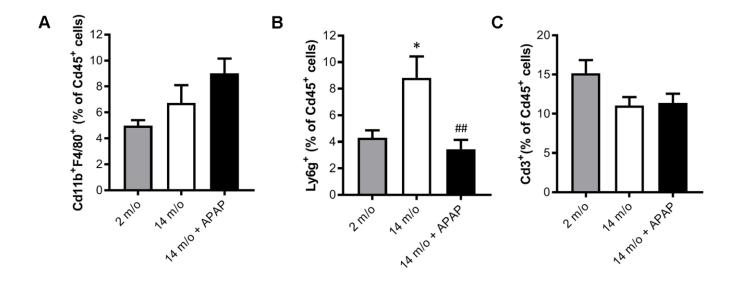
**Supplementary Figure 2. Impact of chronic APAP treatment in NRF2 and NF-\kappaB signaling pathways.** Representative immunoblots showing nuclear NRF2 and p65-NF- $\kappa$ B level using LAMIN B as a loading control, and cytosolic p-I $\kappa$ B $\alpha$  vs. total I $\kappa$ B $\alpha$ . Graphs depict densitometric quantifications of the indicated protein levels. Values are mean ± S.E.M. (n = 6-8 mice per group) (see original western blot in Supplementary Figure 8). Statistical analysis was performed by one-way ANOVA or Brown-Forsythe and Welch ANOVA test followed by their respective post-hoc test.



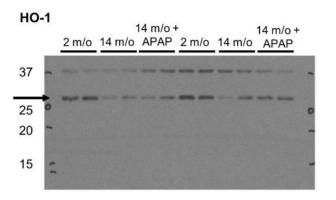
Supplementary Figure 3. Quantification of Cd8 positive cells in liver sections from 14 m/o and 14 m/o + APAP mice by immunofluorescence. (A) Representative images of anti-Cd8 staining performed on various livers cryosections from 14 m/o and 14 m/o + APAP mice. (B) Quantification of Cd8<sup>+</sup> cells per HPF (High Power Field). Data are represented as the mean  $\pm$  S.E.M. (n = 4-6 mice per group). Statistical analysis was performed by Mann-Whitney U test.



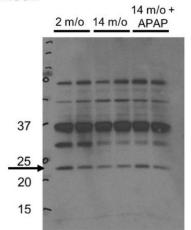
**Supplementary Figure 4. Aging and chronic APAP treatment did not affect non-lymphoid populations in NPCs.** Analysis of different inflammatory populations in liver NPCs from 2 m/o, 14 m/o and 14 m/o + APAP mice by flow cytometry. (**A**) Percentage of Ccr2<sup>+</sup>Ly6c<sup>-</sup> cells from Cd11b<sup>+</sup> cells. (**B**) Percentage of Ccr2<sup>+</sup>Ly6c<sup>+</sup> cells from Cd11b<sup>+</sup> cells. (**C**) Percentage of Cd11b<sup>+</sup>F4/80<sup>+</sup> cells from Cd45<sup>+</sup> cells. (**D**) Percentage of Ly6g<sup>+</sup> from Cd45<sup>+</sup> cells. (**E**) Percentage of Cd3<sup>+</sup> cells from Cd45<sup>+</sup> cells. (**F**) Ly6c<sup>+</sup> per HPF (High Power Field) immunostaining (left) and analysis of total Ly6c<sup>+</sup> cells from Cd45<sup>+</sup>Cd11b<sup>+</sup> cells by flow cytometry (right). Data are represented as the mean ± S.E.M. (n = 5-16 mice per group). Statistical analysis was performed by Kruskal-Wallis, one-way ANOVA or Brown-Forsythe and Welch ANOVA test followed by their respective post-hoc test. \* *P* < 0.05 and \*\*\* *P* < 0.001 *vs*. 2 m/o; ## *P* < 0.01 *vs*. 14 m/o.



Supplementary Figure 5. Analysis of non-lymphoid inflammatory population in PBMCs from 2 m/o, 14 m/o and 14 m/o + APAP mice by flow cytometry. (A) Percentage of Cd11b<sup>+</sup>F4/80<sup>+</sup> cells from Cd45<sup>+</sup> cells. (B) Percentage of Ly6g<sup>+</sup> from Cd45<sup>+</sup> cells. (C) Percentage of Cd3<sup>+</sup> cells from Cd45<sup>+</sup> cells. Data are represented as the mean  $\pm$  S.E.M. (n = 9-14 mice per group). Statistical analysis was performed by Kruskal-Wallis or Brown-Forsythe and Welch ANOVA test followed by their respective post-hoc test. \* *P* < 0.05 vs. 2 m/o; ## *P* < 0.01 vs. 14 m/o.



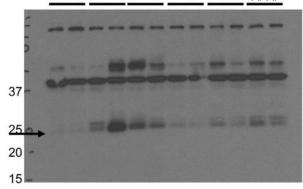
MnSOD



<u>2 m/o 14 m/o +</u> <u>2 m/o 14 m/o APAP</u> <u>37</u> 25 20 15

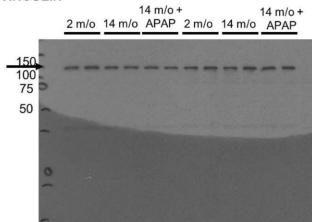
NQO1

14 m/o + 14 m/o + 2 m/o 14 m/o APAP 2 m/o 14 m/o APAP

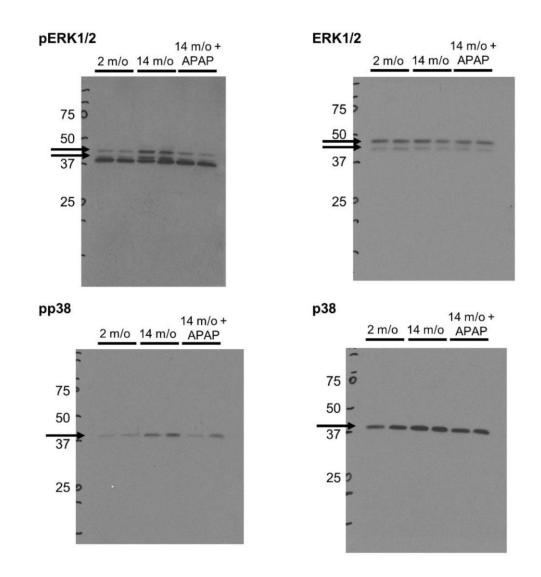


VINCULIN

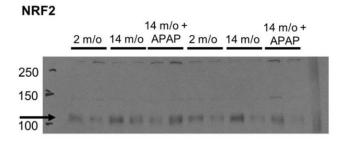
GAPDH

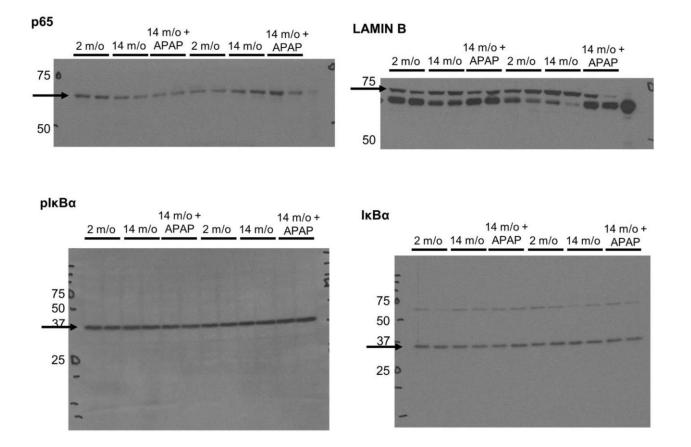


Supplementary Figure 6. Data from Figure 3A.



Supplementary Figure 7. Data from Figure 3E.





Supplementary Figure 8. Data from Supplementary Figure 2.