

Figure S1

Figure S1. (A) Gel image of a genotyping PCR done on several *Maf1^{hep-/-}* organs and specific Ctrl samples. PCR fragments sizes are 480bp for Maf1LoxP sites inclusion, 376bp for recombinated floxed *Maf1* knock out gene and 450bp for WT mice. As around 20% of liver cells are not hepatocytes, a Maf1LoxP fragment is expected in the liver sample. BAT: brown adipose tissue; WAT: white adipose tissue. **(B)** IGV genome browser view of the region encompassing the *Maf1* gene showing the number of RNAseq reads in Ctrl (black) and *Maf1^{hep-/-}* (green) mice. **(C)** Kaplan-Meier survival curves of male Ctrl and *Maf1^{hep-/-}* mice fed a Chow diet. Ctrl n=26 and *Maf1^{hep-/-}* n=22. **(D)** Fat weight relative to total weight in 24 week-old Ctrl and *Maf1^{hep-/-}* mice fed a HF diet. Ctrl n=17 and *Maf1^{hep-/-}* n=14. **(E)** Representative neutral lipid Oil Red O staining of liver slices from 24 week-old fasted or refed Ctrl and *Maf1^{hep-/-}* mice under a Chow diet. White bars: 100 μ m. **(F)** Hepatic TG content (nmole/mg of tissue sample) in fasted or refed Ctrl and *Maf1^{hep-/-}* mice under a Chow diet. Fasted Ctrl n=8 and *Maf1^{hep-/-}* n=3; Refed Ctrl n=11 and *Maf1^{hep-/-}* n=6. **(G)** Liver FFA content (nmol/mg of tissue sample) in the same samples as in **(E)**. **(H)** FFA content in the liver of fasted or refed Ctrl and *Maf1^{hep-/-}* mice under a HF diet. Fasted Ctrl n=8 and *Maf1^{hep-/-}* n=7; Refed Ctrl n=9 and *Maf1^{hep-/-}* n=7. **(I)** Liver cholesterol content in the same samples as in **(H)**. In **(D)** and **(F)** to **(I)**, the box encompasses upper and lower quartile, the whiskers extend to 1.5 times the interquartile range of the box. Red star, mean; horizontal bar, median.

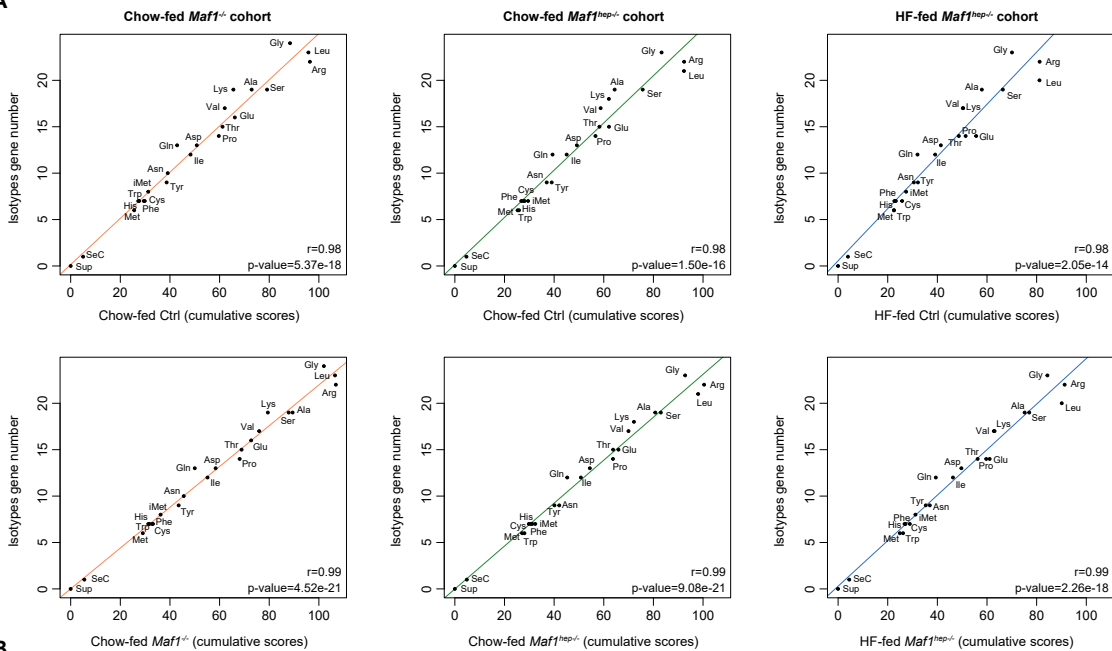
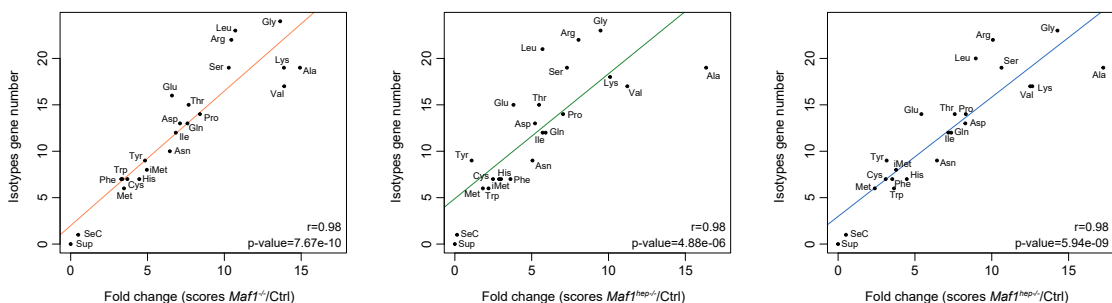
A**B**

Figure S2. (A) Spearman rank correlations of Pol III occupancy cumulated scores for each tRNA isotope between Ctrl and *Maf1* deficient mice as indicated. The regression line is colored. (B) Spearman rank correlations between score fold change (for each cohort, Ctrl versus *Maf1* deficient mice) for each isotope (X axis) and number of corresponding isotype gene (Y axis), for Ctrl and *Maf1* deficient mice of each of the three cohorts, as indicated. The correlation line is colored.

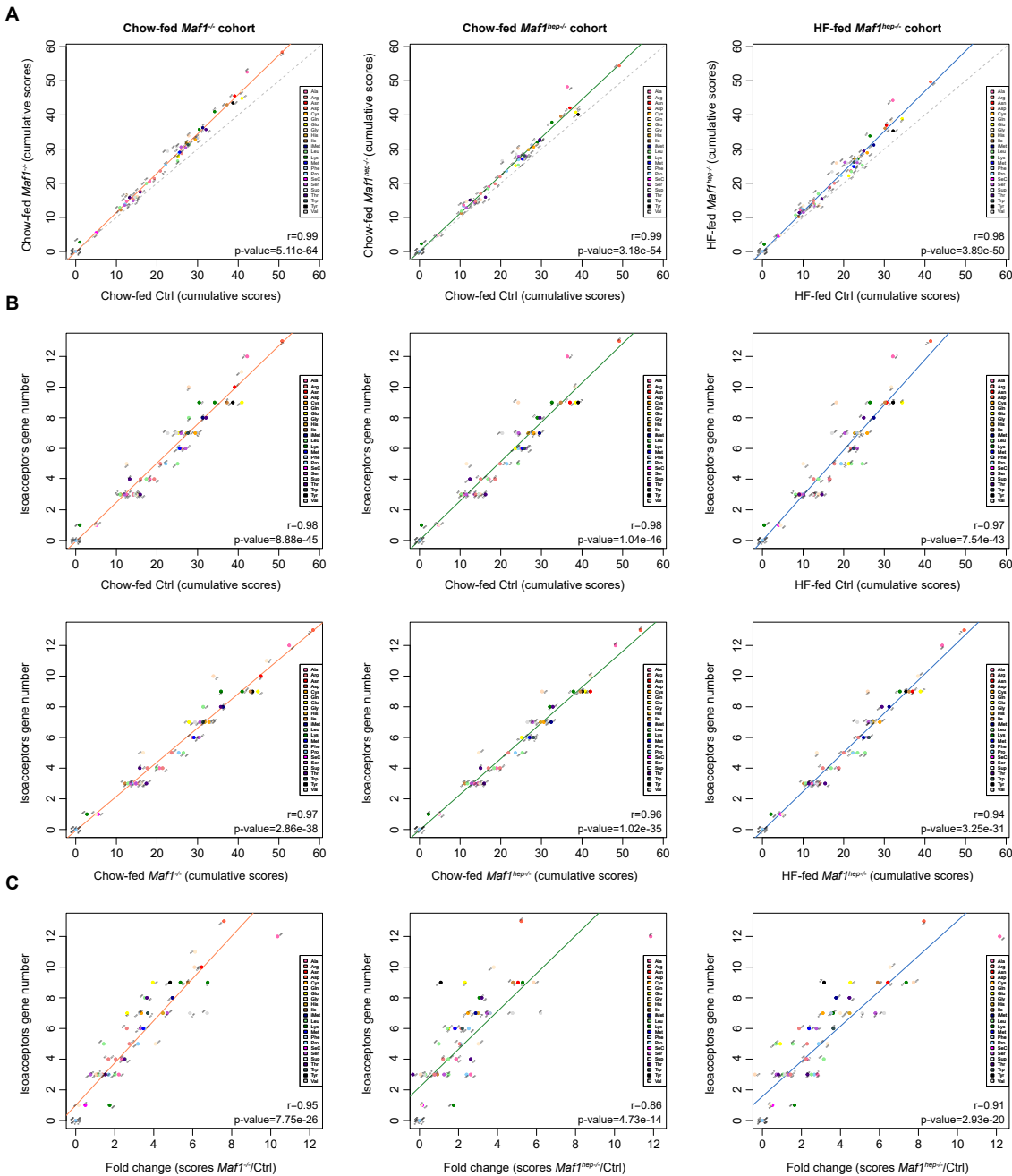


Figure S3

Figure S3. (A) Spearman rank correlations of Pol III occupancy cumulated scores for each tRNA isoacceptor between Ctrl and *Maf1* deficient mice as indicated. The regression line is colored, the $x=y$ line is dotted. (B) Spearman rank correlations between cumulated scores for each isoacceptor (X axis) and number of corresponding isoacceptor genes (Y axis). The correlation line is colored. (C) Spearman rank correlations between score fold change (for each cohort, Ctrl versus *Maf1* deficient mice) for each isoacceptor (X axis) and number of corresponding isoacceptor genes (Y axis), for Ctrl and *Maf1* deficient sample of each of the three cohorts, as indicated. The correlation line is colored.

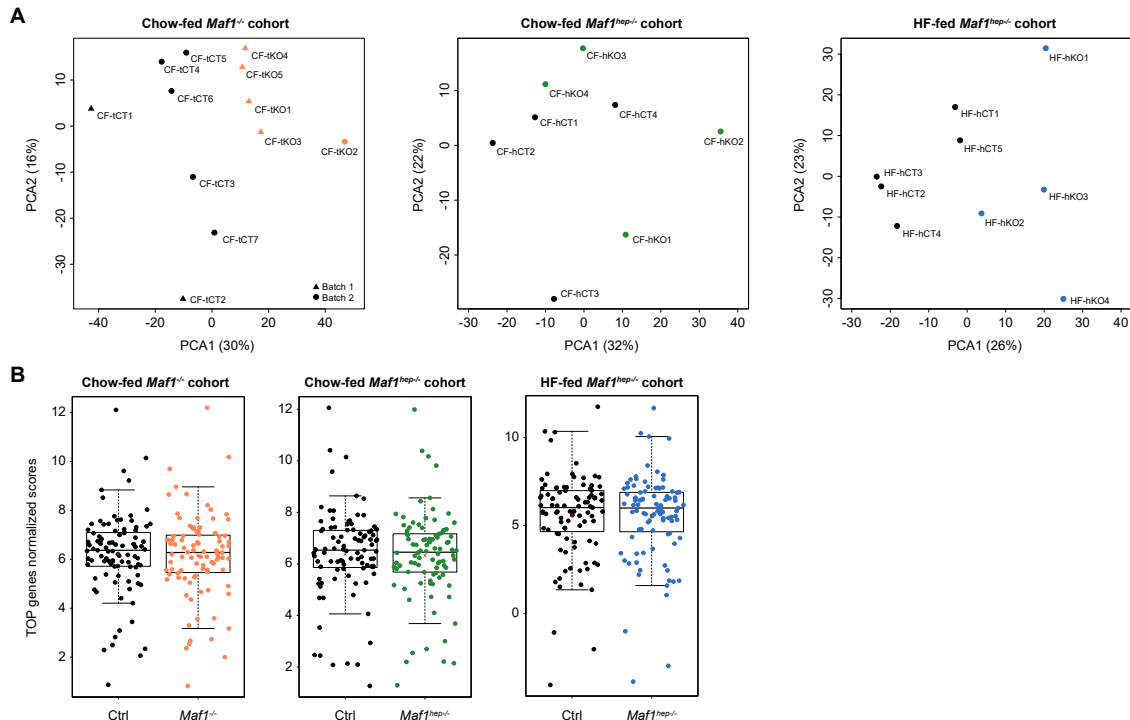


Figure S4. (A) Principal component analysis (PCA) of the samples used for RNAseq. Black symbols: Ctrl samples. Colored symbols: knockout samples from Chow-fed *Maf1*^{-/-} (orange), Chow-fed *Maf1*^{hep-/-} (green), and HF-fed *Maf1*^{hep-/-} (blue) mice. For the Chow-fed *Maf1*^{-/-} cohort, dots and triangles indicate 2 different batches of data acquired at different times. (B) Box plots indicating the scores of TOP mRNAs for indicated mice. The box encompasses upper and lower quartile, the whiskers extend to 1.5 times the interquartile range of the box. Red star, mean; horizontal bar, median.

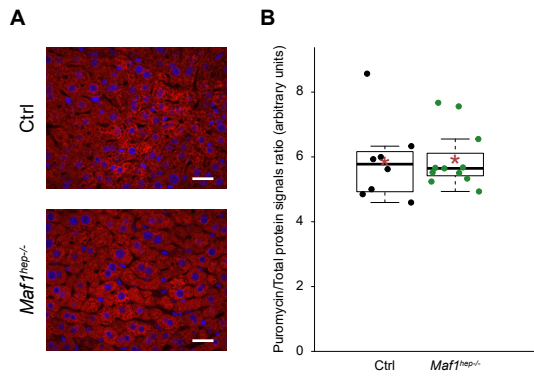


Figure S5. (A) Representative puromycin and DAPI staining of liver slices from 13-14 week-old Chow-fed *Maf1^{hep-/-}* mice. White bars represent 20 μm . (B) WESTTM quantification of puromycin protein incorporation in the livers of mice from the same Chow-fed *Maf1^{hep-/-}* cohort. Ctrl n=8 and *Maf1^{hep-/-}* n=11. The boxes encompass upper and lower quartile, the whiskers extend to 1.5 times the interquartile range of the box. Red star, mean; horizontal bar, median.