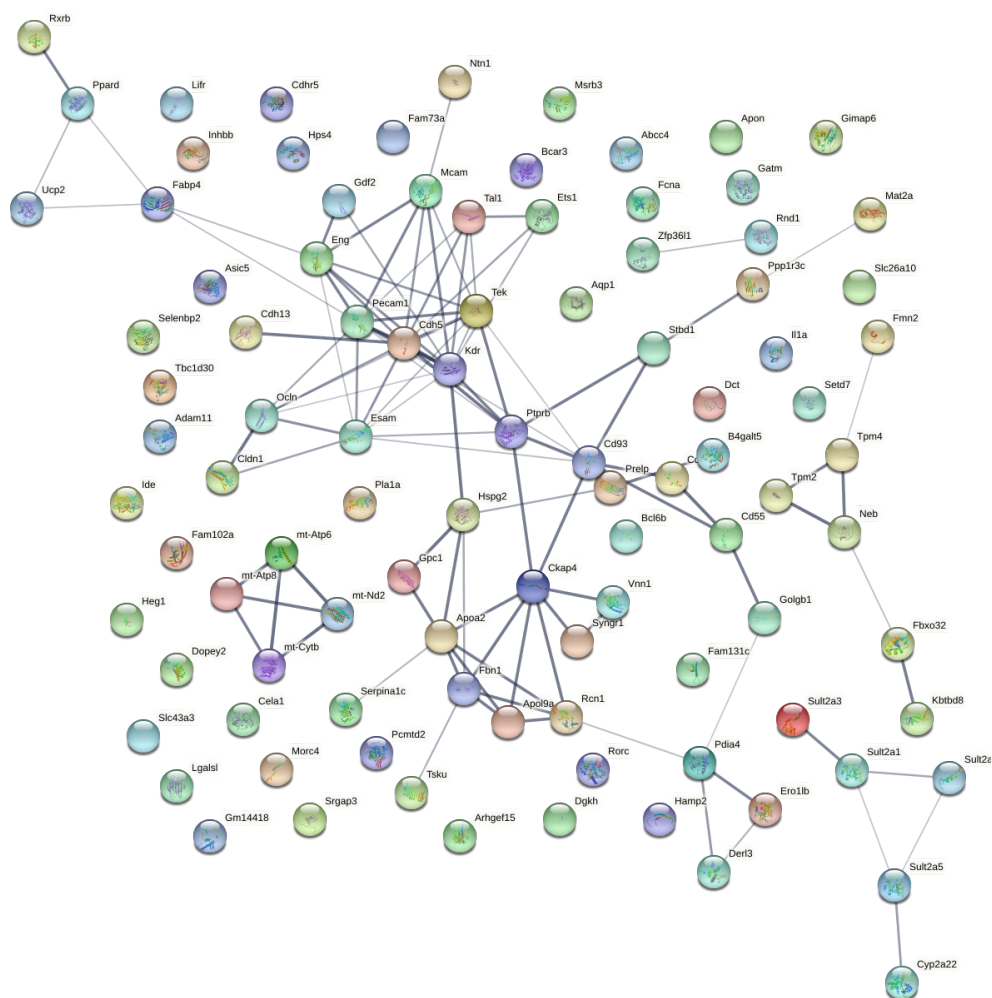
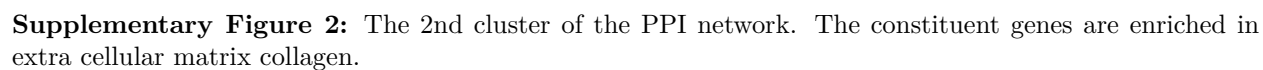


Supplementary Figures: Alterations in the hepatocyte epigenetic landscape in steatosis

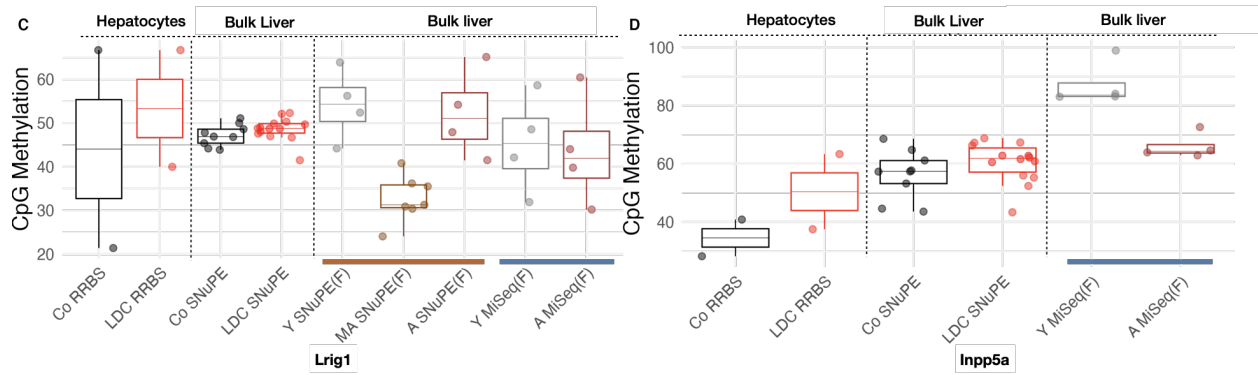


**Supplementary Figure 1:** The 1st cluster of the PPI network. The constituent genes in this cluster are enriched in Mitochondrial dysfunction.

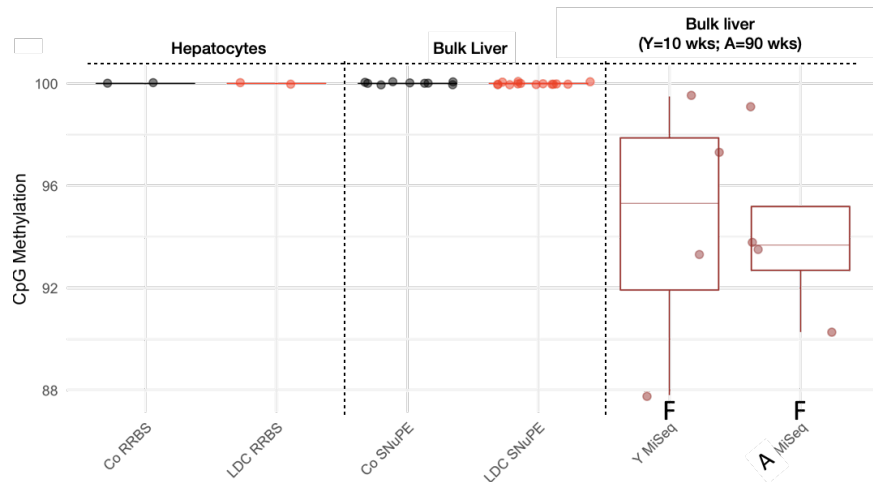








**Supplementary Figure 5:** The CpG methylation status of the Stubbs Loci (as shown in Table 1) in LDC (over Co) mice from liver hepatocytes (using RRBS) and in bulk liver (using SNUPE). The CpG methylation is compared to bulk liver from aging mice using SNUPE and MiSeq (I, J). The CpG methylation of the new aging loci was also measured in LDC (over Co) mice and compared to aging bulk liver using SNUPE and MiSeq. (K, L). t test (parametric, unpaired) was used to compare and evaluate the significance between groups Co vs LDC and young (Y), mid-aged (MA) vs aged (A) for each of the technologies, in both (M) male and (F) female. The gene associated with the measured CpG is mentioned at the bottom of each plot. The source of the sample and the age are mentioned on top. All differences that are significant ( $* p < 0.05$ ) are marked in the plot. In each case, comparisons were made between two groups (LDC vs. Co, Y vs. A or Y vs. MA for each technology). For better comparison, methylation values obtained from SNUPE analyses were plotted as methylation index multiplied by 100. RRBS data was excluded when read coverage for the respective CpG was below 3 (concerns Smarca2). SNUPE analysis with low coverage is excluded from the figure as well.



**Supplementary Figure 6:** Validation of age associated CpG loci: Prdm16 with SNUPE and MiSeq and comparison of CpGs in aging (from miseq and RRBS). The differences of the groups are non significant in these loci. t test (parametric, unpaired) was used to compare and evaluate the significance between groups.  $* p \leq 0.05$ .