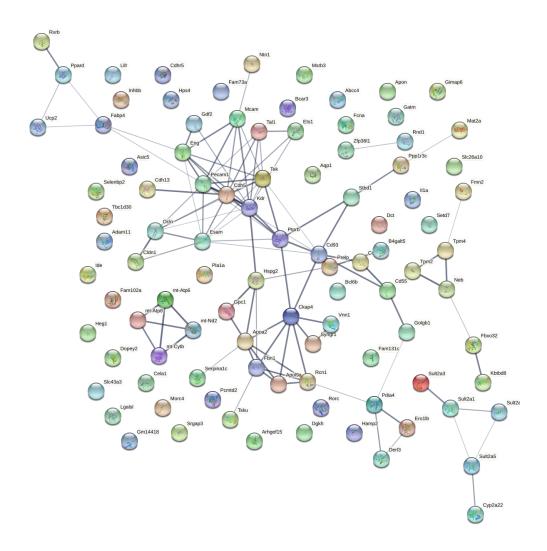
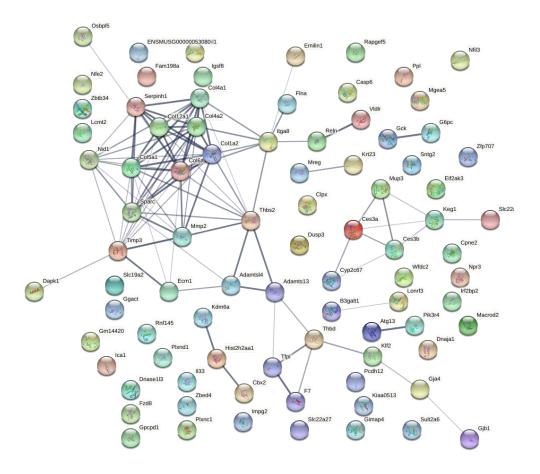
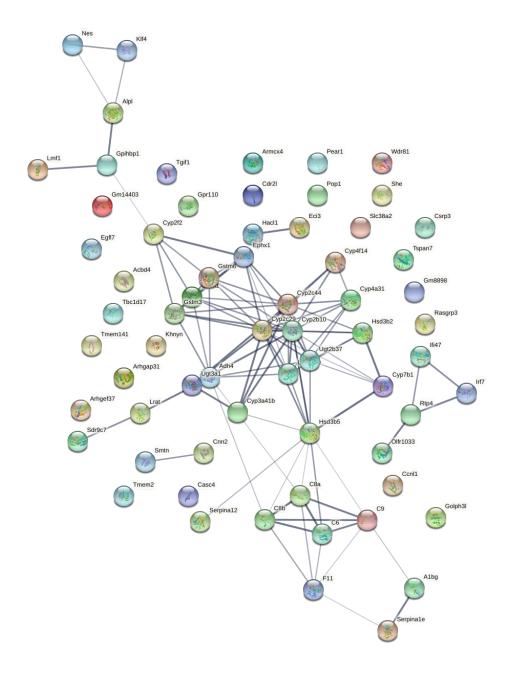
Supplementary Figures: Alterations in the hepatocyte epigenetic landscape in steatosis



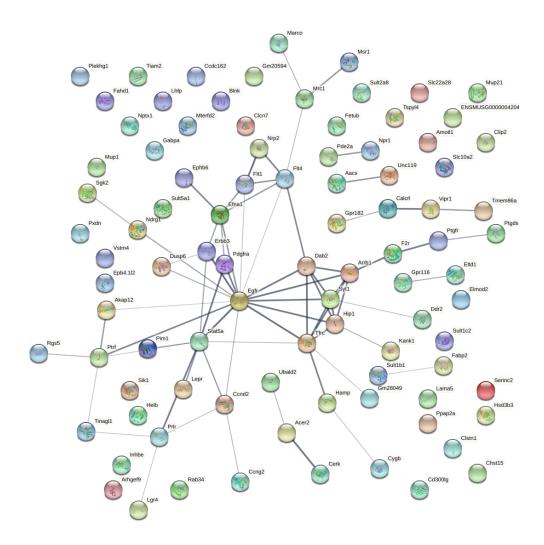
Supplementary Figure 1: The 1st cluster of the PPI network. The constituent genes in this cluster are enriched in Mitochondrial dysfunction.



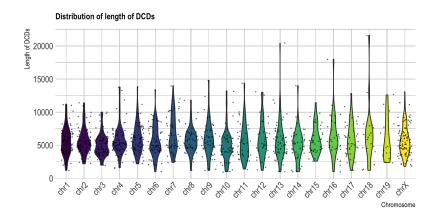
Supplementary Figure 2: The 2nd cluster of the PPI network. The constituent genes are enriched in extra cellular matrix collagen.



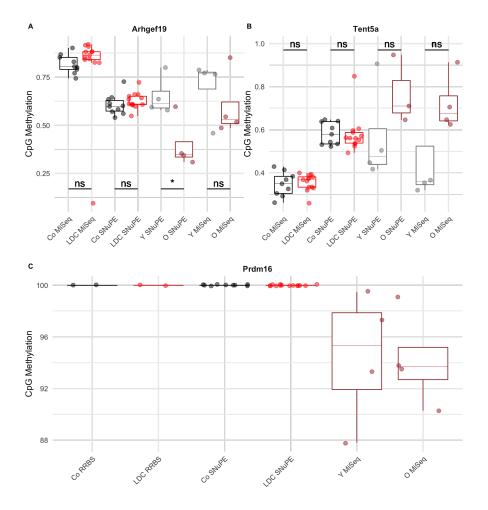
Supplementary Figure 3: The 3rd cluster of the PPI network. The constituent genes are enriched in alcohol metabolism.



Supplementary Figure 4: The 4th cluster of the PPI network. The constituent genes are enriched in steatohepatitis associated pathways.



Supplementary Figure 5: Violin plot showing the distribution of the lengths of the DCD regions over all the chromosomes. The DCD regions were obtained using SCIDDO (p-value ≤ 0.05).



Supplementary Figure 6: Validation of age associated CpG loci 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. ns means non-significant (p > 0.05), * p <= 0.05, ** p <= 0.01, *** p <= 0.001.