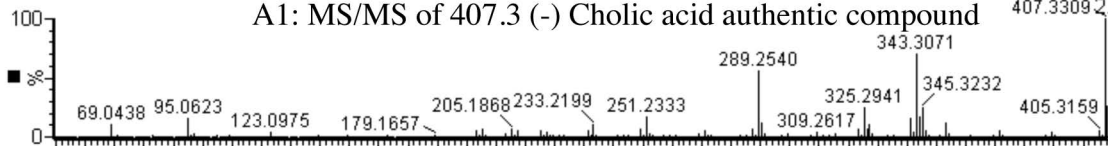


Supplementary Figure 1. Fibrogenesis changes in alcohol-fed *PPAR α ^{-/-}* mice. (A) Immunohistochemical staining of α -smooth muscle actin (α -SMA) of mice fed for six-month. (B) Microarray results of three genes in hepatic fibrogenesis after two- and four- month feeding. Y-axis represents the relative mRNA levels of the specified gene comparing to wt control. * indicates significant difference was observed between two groups (P value < 0.05)

20130423_HH_Std_MSMS_NEG_2 1033 (5.870)

A1: MS/MS of 407.3 (-) Cholic acid authentic compound

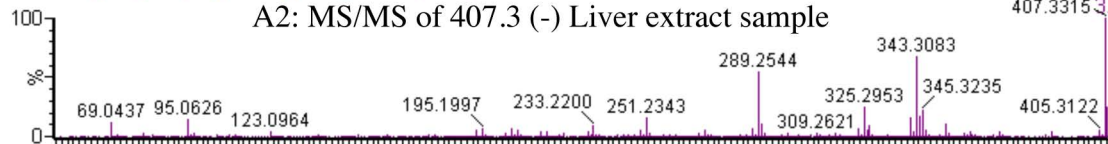
1: TOF MSMS 407.28ES-
407.3309 2.03e4



20130423_HH_Sample_MSMS_NEG_8 1030 (5.850)

A2: MS/MS of 407.3 (-) Liver extract sample

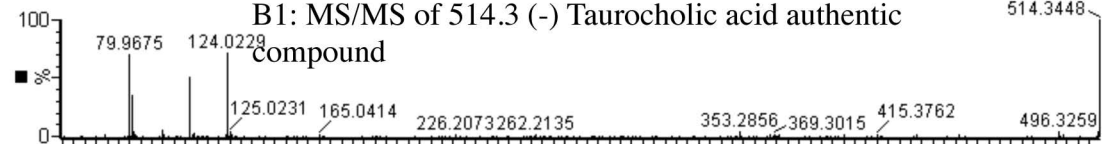
1: TOF MSMS 407.28ES-
407.3315 3.81e3



20130423_HH_Std_MSMS_NEG_1 937 (5.323)

B1: MS/MS of 514.3 (-) Taurocholic acid authentic compound

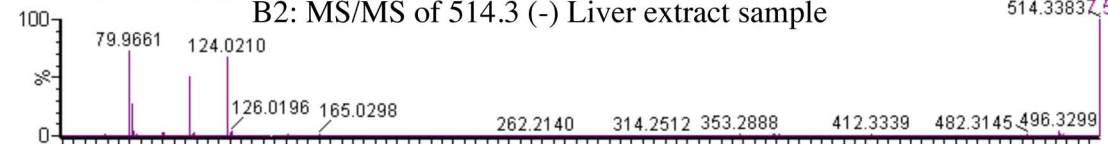
1: TOF MSMS 514.26ES-
514.3448 209



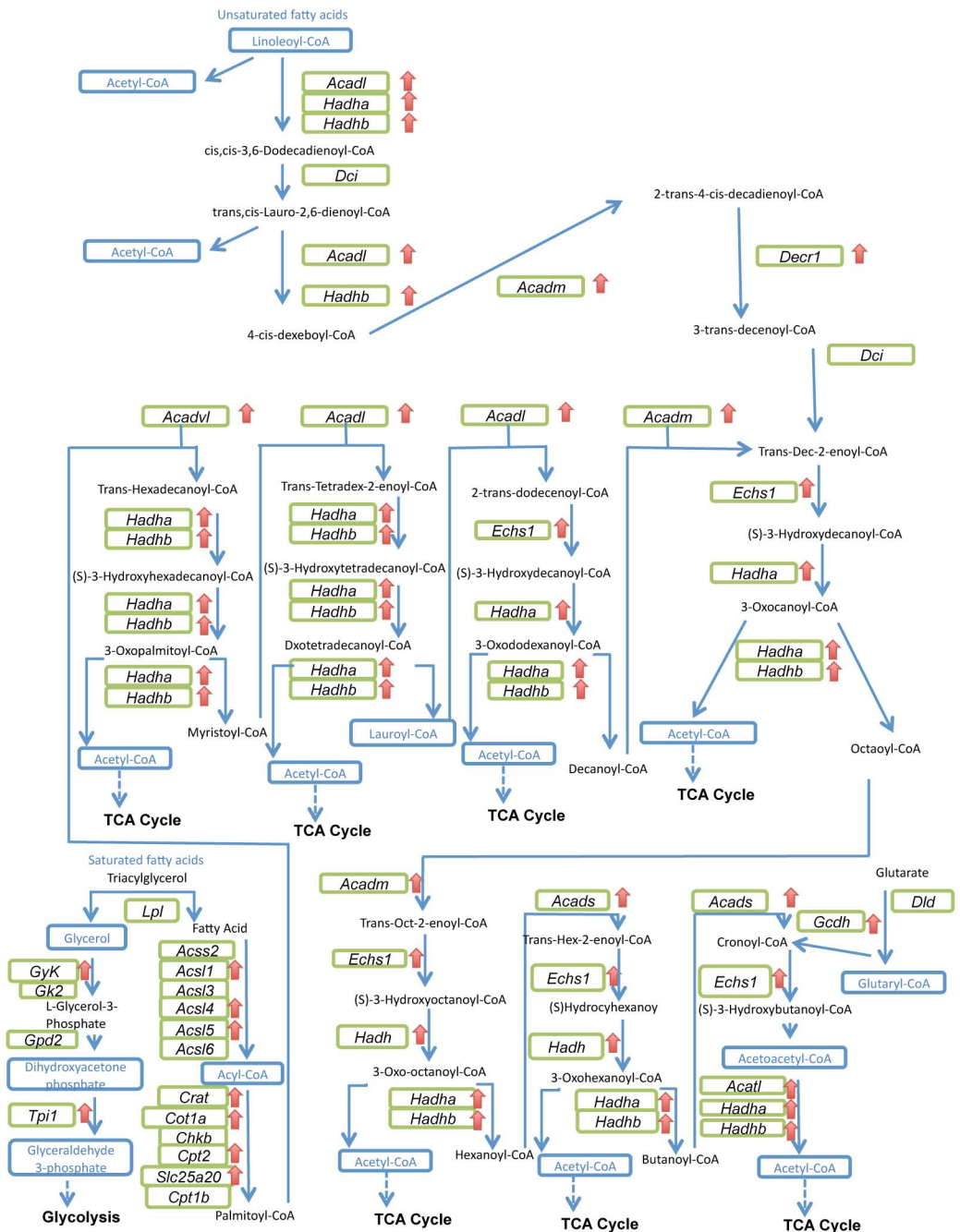
20130423_HH_Sample_MSMS_NEG_5 937 (5.324)

B2: MS/MS of 514.3 (-) Liver extract sample

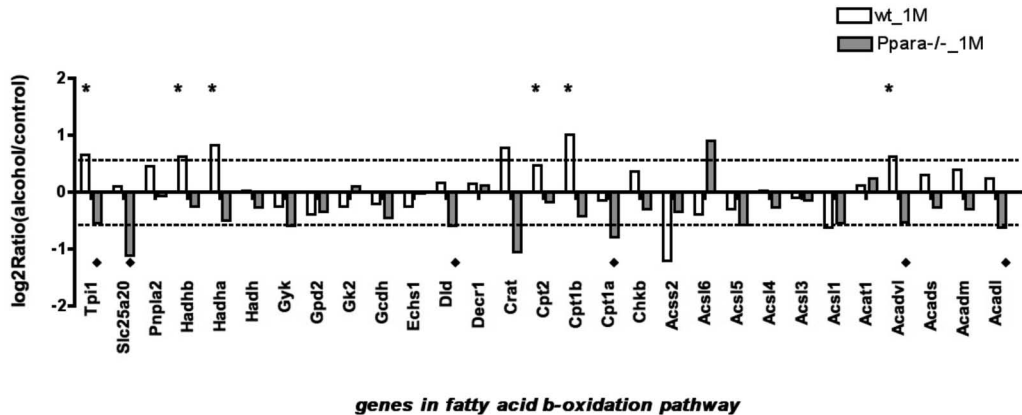
1: TOF MSMS 514.26ES-
514.3383 7.59e4



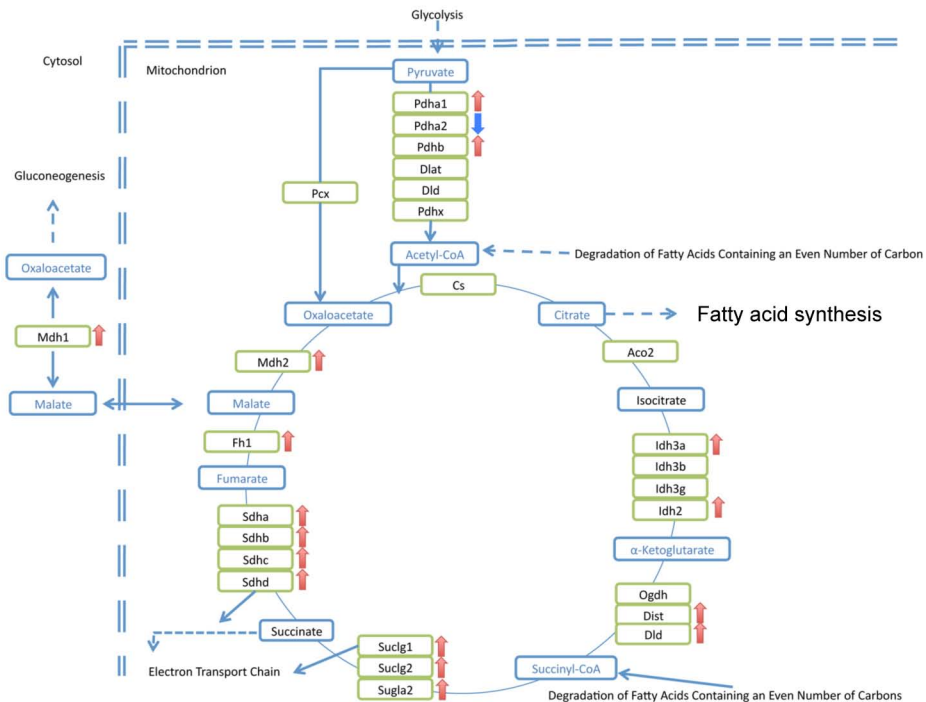
Supplementary Figure 2. Verification of metabolite IDs. A1 and B1 are MS/MS spectra of authentic compounds of cholic acid and taurocholic acid respectively. A2 and B2 are MS/MS spectra of the ions (m/z values 407.3 and 514.3 respectively) obtained in liver extract samples.



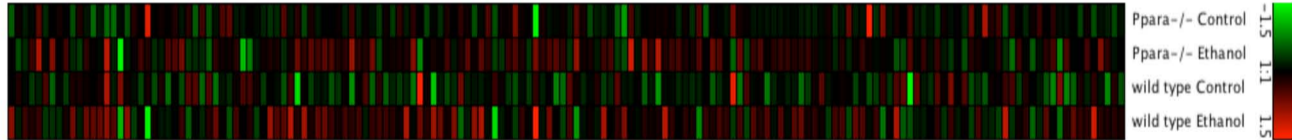
Supplementary Figure 3. A diagram of the fatty acid β -oxidation pathway, the genes with a red up arrow are those showing either an induction with fold change of more than 1.5 or statistical significant difference (P value < 0.05) or those meeting both criteria.



Supplementary Figure 4. Alteration of expression of genes involved in fatty acid β -oxidation at one month of alcohol feeding. Y-axis represents Log2Ratio(alcohol-fed/control). The marks of “*” and “◆” indicate statistically significant difference observed in wild type and Ppara α -nullmice respectively.



Supplementary Figure 5. A diagram of the TCA cycle, the genes with a red up arrow are those showing either an induction with fold change of more than 1.5 or statistical significant difference (P value < 0.05) or those meeting both criteria.



Supplementary Figure 6. Heatmap of transcriptomics data of genes involved in purine metabolism. The raw data was pre-processed with Partek Genomics Suite as described in Material and methods. Processed intensity data was visualized by Genesis (<http://genome.tugraz.at/>).