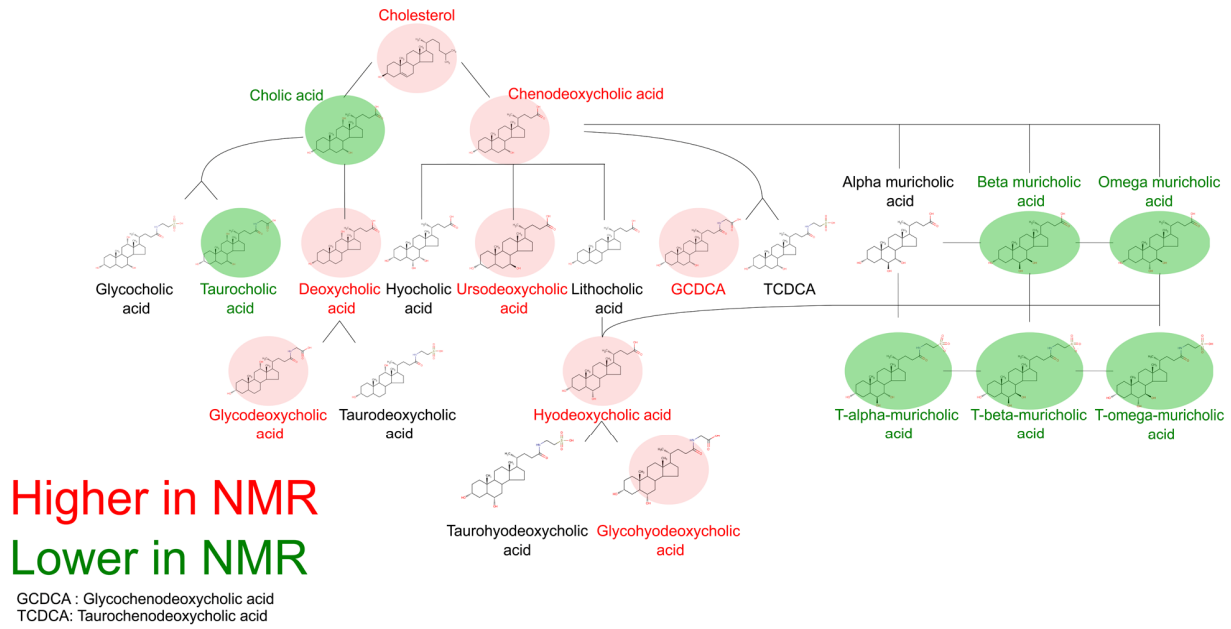
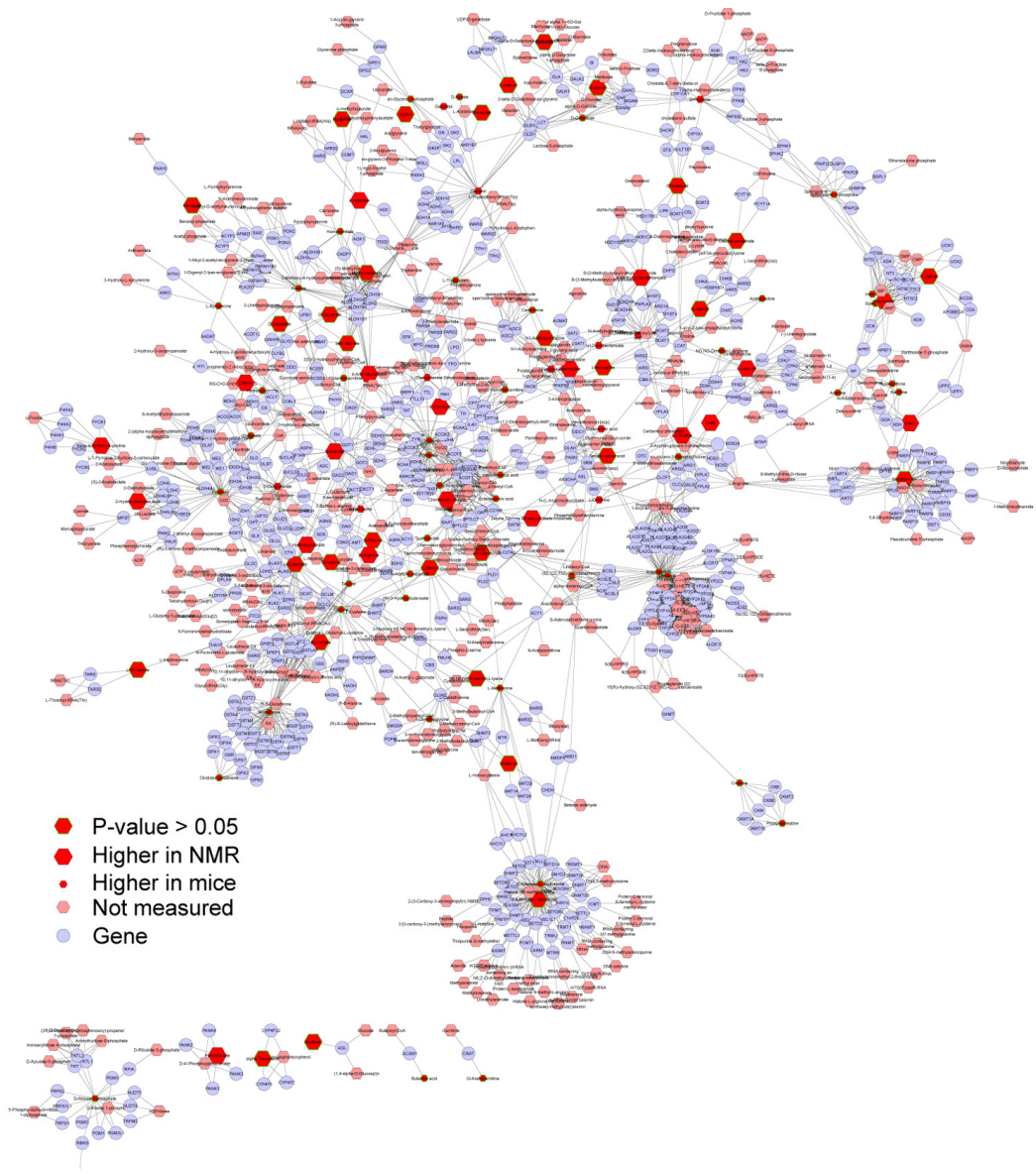


SUPPLEMENTARY FIGURES

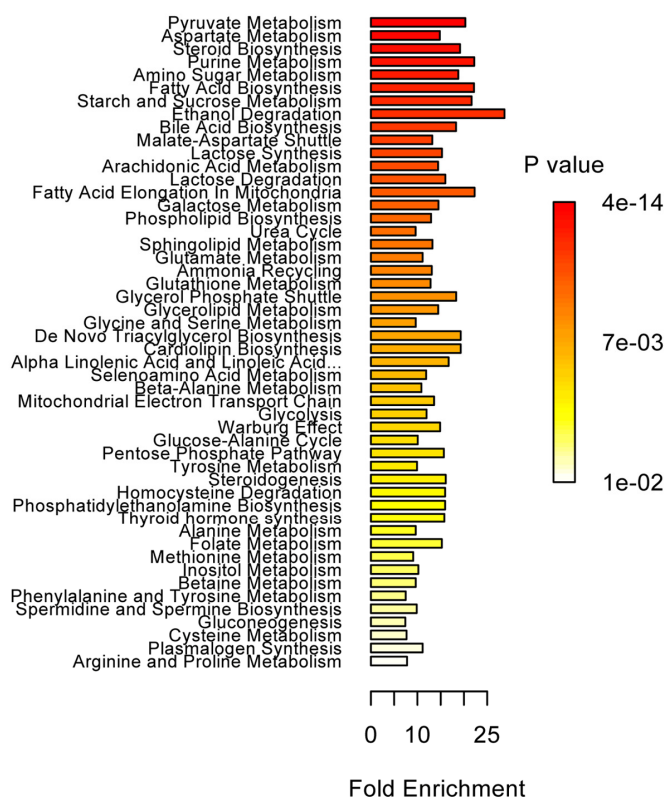


Supplementary Figure 1. Schematic overview of interspecies differences in bile acid metabolism. Note that molecular species that are more abundant in naked mole-rats are marked with pink backgrounds, while molecules that are more abundant in mice are marked in green.



Supplementary Figure 2. Pathway analysis was processed with Metscape app v3.1.3 from Cytoscape software v3.7.1 (ref <http://cytoscape.org>). Fold-changes were calculated by dividing means of groups. P-values were obtained by means of the two-sided Wilcoxon test.

Enrichment Overview (top 50)



Supplementary Figure 3. Quantitative enrichment analysis was processed with MetaboAnalyst 4.0 (<https://www.metaboanalyst.ca/>). Data were log-transformed and mean-centered. SMPDB pathway-associated metabolite sets was used, with a threshold of 3 compounds minimum per pathway.