

Figure 2 supp. info. Clustering of proteins differentially expressed in *MAT1A*^{-/-} mice according to their subcellular location. Proteins differentially expressed were identified and clustered by their subcellular location according to gene ontology criteria. The subcellular components accumulating most of the differential proteins were mitochondria, cytoeskeleton, endoplasmic reticulum, and nucleus.

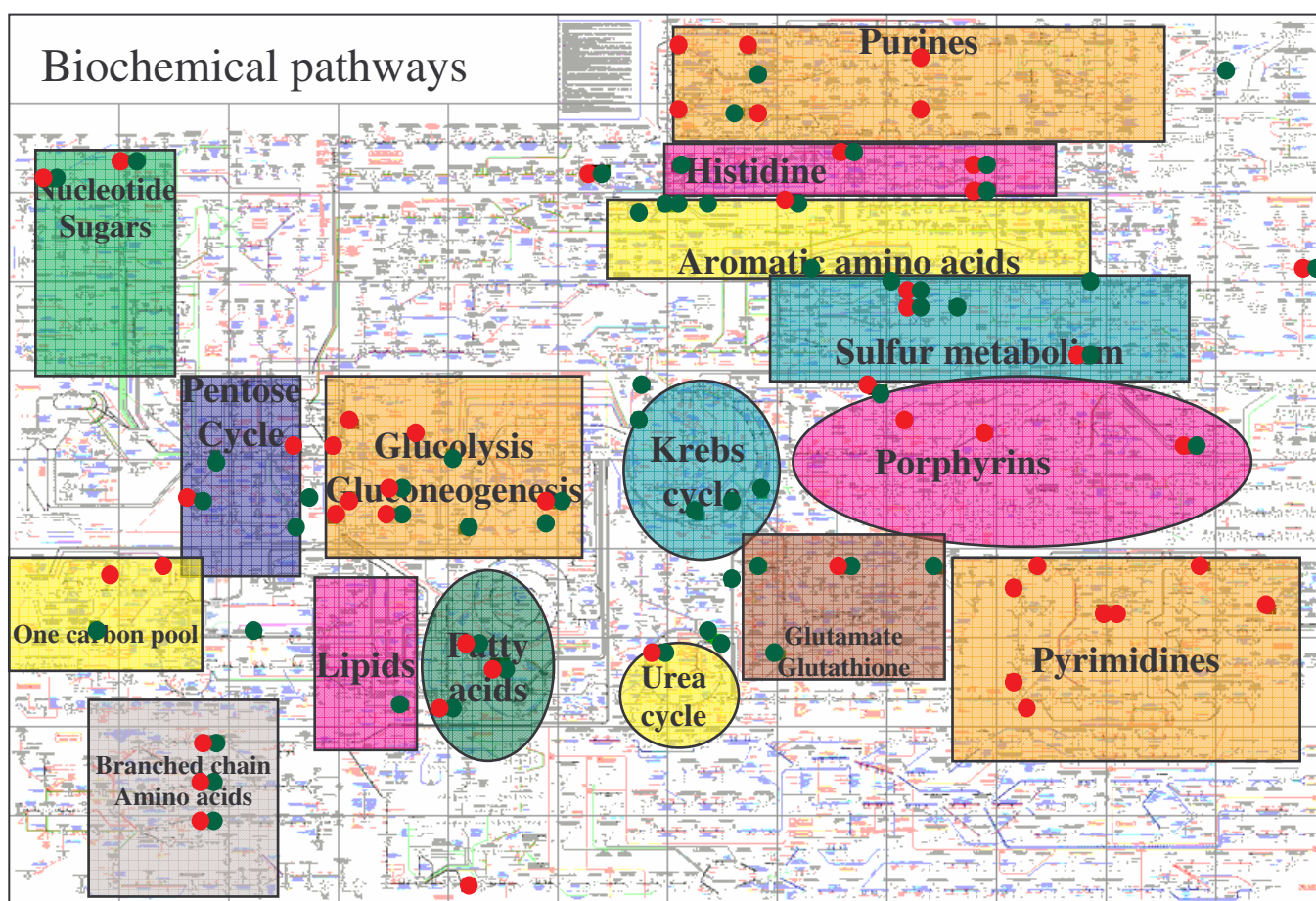


Figure 3 Supp. Info. Metabolic alterations in *MAT1A*^{-/-} liver tumors. Metabolic enzymes which expression is up- or down-regulated in the liver tumors of *MAT1A*^{-/-} mouse were mapped on the Biochemical Pathways chart from Roche () using the GARBAN software developed at CIMA-CEIT. Up-regulated proteins are in red and down-regulated proteins in green.