

Figure 1 Supp. info. Functional clustering of proteins differentially expressed in *MAT1A-/-* HCC. Proteins differentially expressed were identified by mass spectrometry and clustered by the biological process which they are involved according to gene ontology criteria: (i) cell communication, (ii) cell growth or maintenance, and (iii) development processes. Each column contains the cluster of differential proteins identified from each single WT vs tumor comparison, which was performed in triplicate. Upregulation and down-regulation in *MAT1A-/-* tumors is indicated by red and green colours respectively. The red name of some proteins indicates that the corresponding GO code could not be assigned automatically by the software and consequently it was programmed manually.

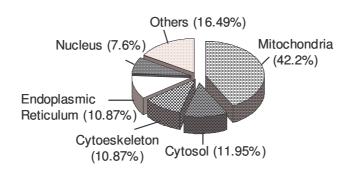


Figure 2 supp. info. Clustering of proteins differentially expressed in *MAT1A-/-* mice according to their subcellular location. Proteins differentially expressed were identified and clustered by their subcellular location according to gene ontology criteria. The subcellular components accumulating most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

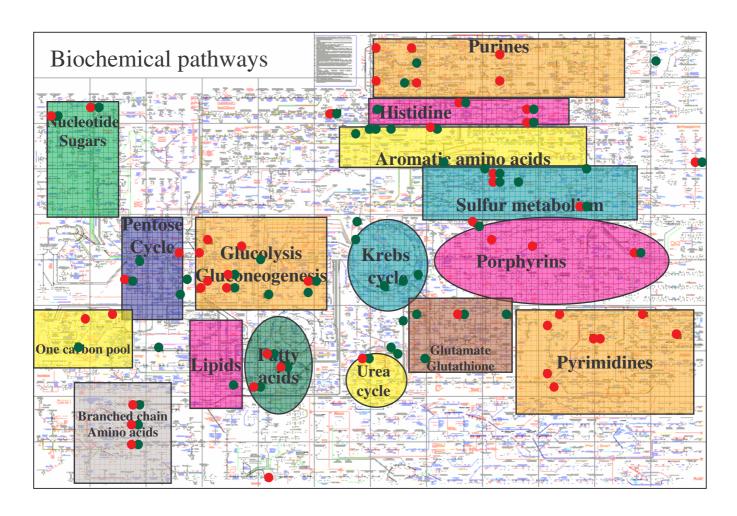


Figure 3 Supp. Info. Metabolic alterations in *MATIA-/-* liver tumors. Metabolic enzymes which expression is up- or down-regulated in the liver tumors of *MATIA-/-* mouse were mapped on the Biochemical Pathways chart from Roche () using the GARBAN software developed at CIMA-CEIT. Upregulated proteins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