

Supplementary_Fig_S1:

(A) LC-MS/MS analysis of 293T cells as quality control samples. (B) Data sets (Dataset1-3) with different confident levels by stepwise filtering criteria. Dataset 1 contains all 11,984 GPs with 1% FDR on the peptide level; Dataset 2 contains 7,675 GPs with at least one unique peptide (sequence specific to a gene product) and two strict peptides (mascot ion score > 20); and Dataset 3 contains 6,458 GPs that were detected in at least 2 of the 3 replicates in at least one time point. (C) 2,242 core proteins that were seen in all experiments. (D) GO enrichment analysis of the core proteins. (E) The dynamic range of the mouse liver proteome. (F) Dynamics of housekeeping proteins and hepatic markers. (G) Number of GPs quantified in Dataset 1-3 across 15 time points.



Supplementary_Fig_S2: (A) Optimal number of clusters in k-means clustering determined by within groups sum of squares. (B) Silhouette plot from k-means clustering.



Supplementary_Fig_S3: RNA-Seq analyses of the mouse liver transcriptome

(A) 3 clusters of the mouse liver transcriptome by hierarchical clustering or (B) by principal component analysis. (C) Five gene modules and their functions revealed by k-means clustering.







Supplementary_Fig_S4: RNA-Seq analysis of core liver functions and five hepatic cell types across 15 time points (A) The measurements of 8 liver functions by RNA-Seq across all time points. (B) The mRNA levels of 5 hepatic cell types represented by their selective markers.



Supplementary_Fig_S5:

(A) Counts of TFs by their families based on the TF database - AnimalTFDB 3.0 (Hu et al. 2019). The 3 largest TF families are C2H2zf (n = 272), Homeobox (n = 70), and bHLH (n = 51). (B) Developmental phases by PCA analysis of TFs. (C) Chi-square tests of the distributions of TGs in RNA or protein-based clusters.
(D) Changes of key members in Cytochrome 450s complex measured by protein or RNA expressions.



Supplementary_Fig_S6: (A) Categories of 8,544 RNA-only transcripts. (B) Classes of 1,996 non-protein coding RNA transcripts. (C) mRNA-TF correlation measured by Spearman's correlation coefficient. (D) Protein-TF correlation measured by Spearman's correlation coefficient.



Supplementary_Fig_S7:

(A) The relative protein levels of the 19 prognosis signature proteins (from HCC paper) across all time points during liver development.

(B) The relative levels of subtype-specific (iCluster 1-3) proteins or TFs across all time points during liver development (from TCGA paper).