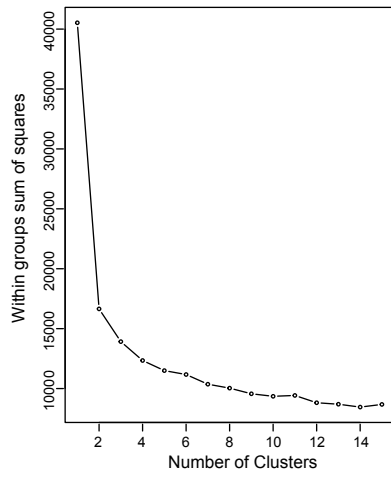


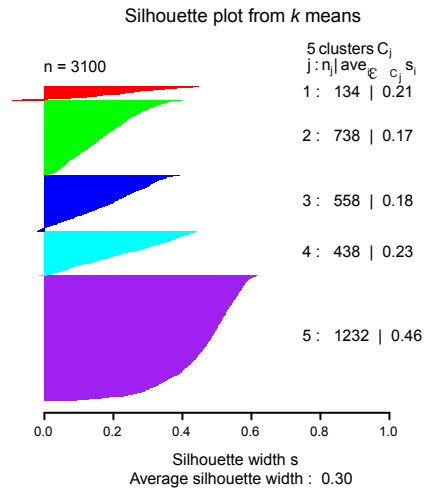


# Supplemental Fig. S2

A



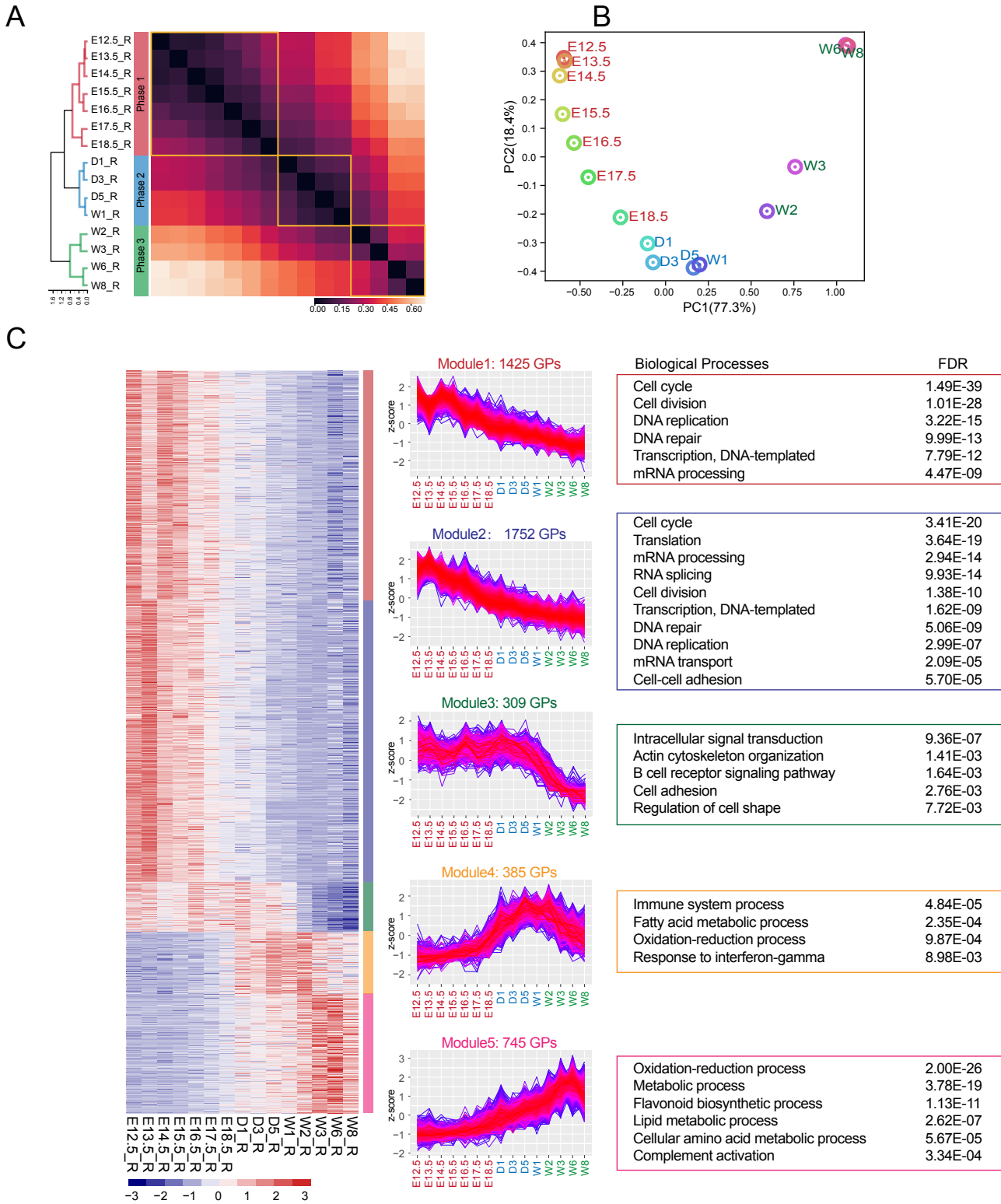
B



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.

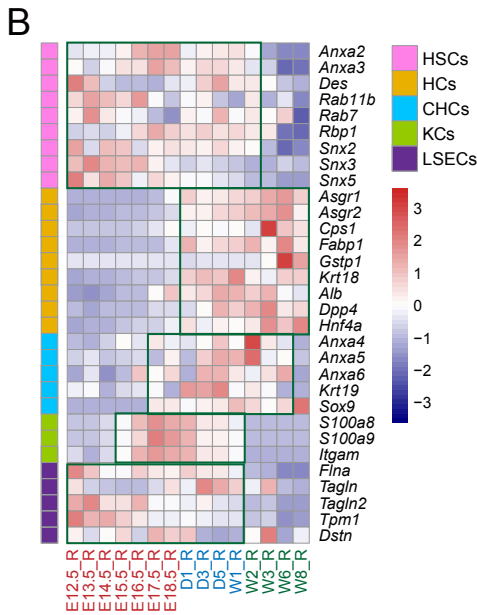
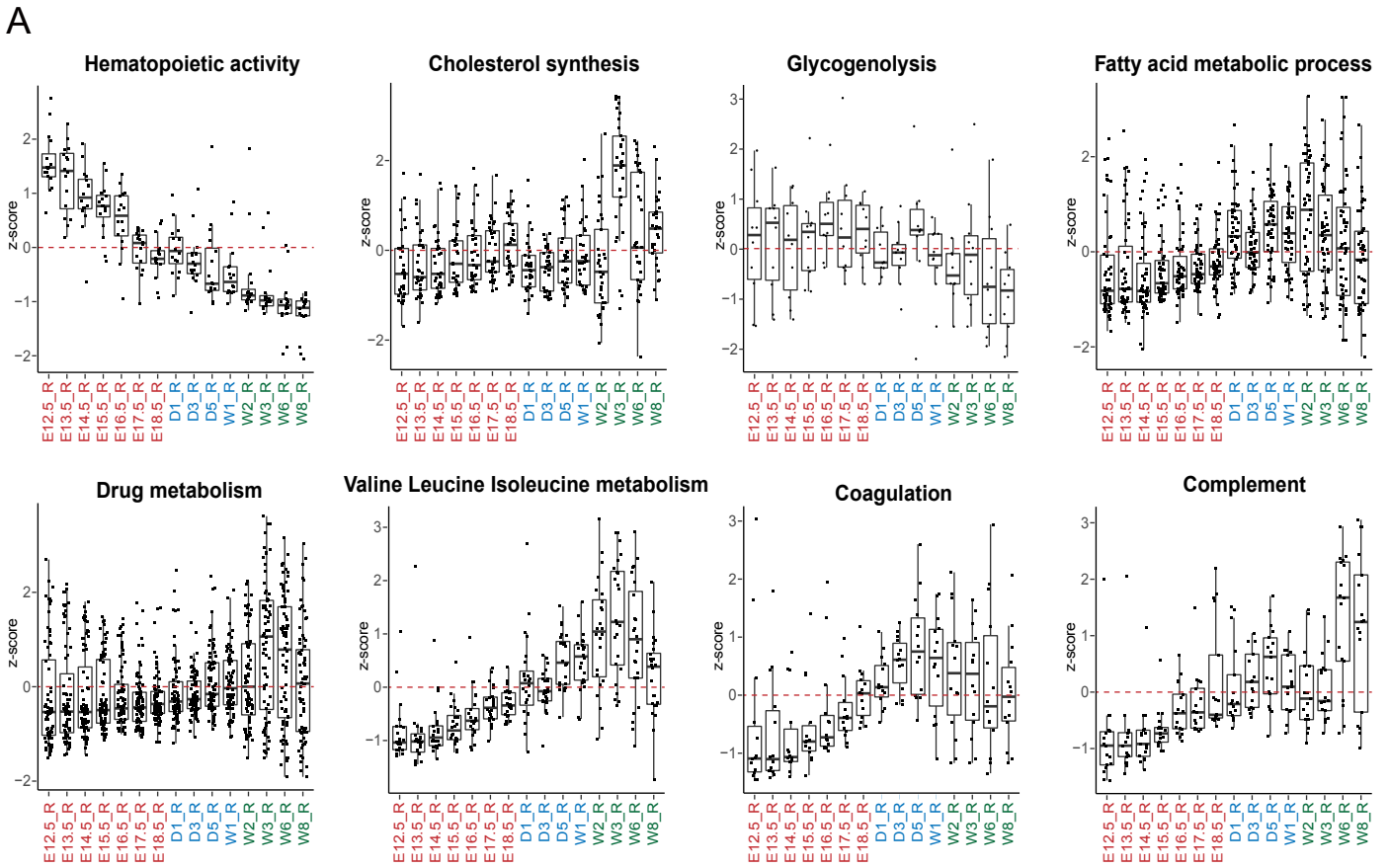
# Supplemental Fig. S3



Supplementary\_Fig\_S3: RNA-Seq analyses of the mouse liver transcriptome

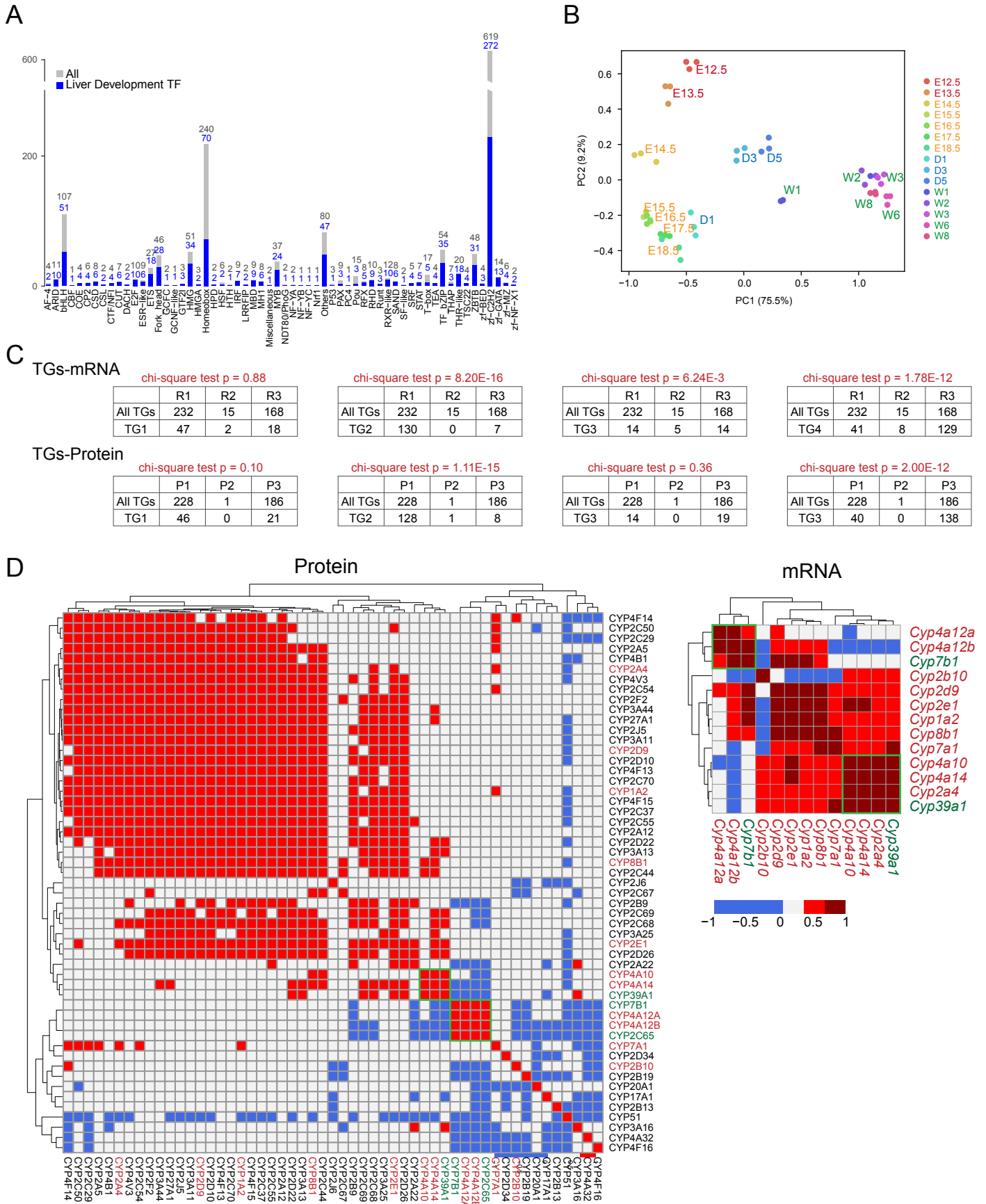
(A) 3 clusters of the mouse liver transcriptome by hierarchical clustering or (B) by principal component analysis. (C) Five gene modules and their functions revealed by k-means clustering.

# Supplemental Fig. S4



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.

# Supplemental Fig. S5

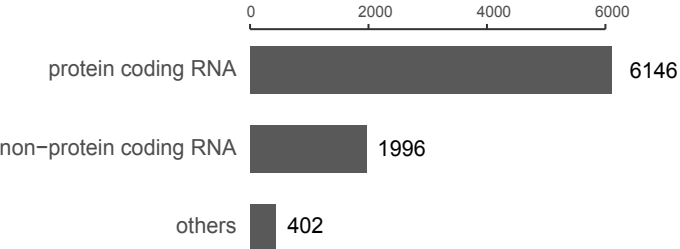


Supplementary\_Fig\_S5:

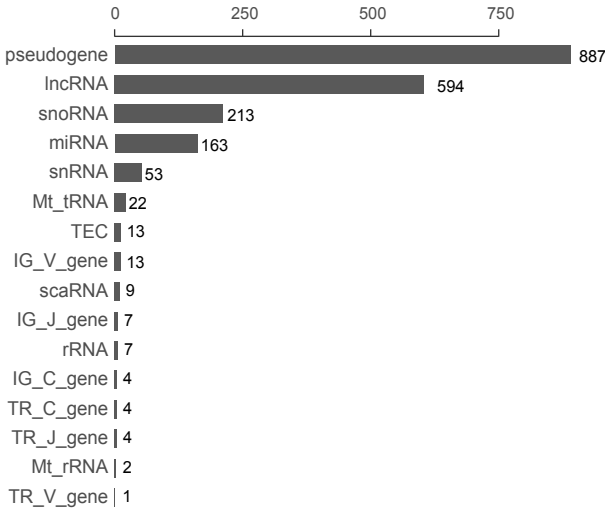
(A) Counts of TFs by their families based on the TF database - AnimalTFDB 3.0 (Hu et al. 2019). The 3 largest TF families are C2H2zf ( $n = 272$ ), Homeobox ( $n = 70$ ), and bHLH ( $n = 51$ ). (B) Developmental phases by PCA analysis of TFs. (C) Chi-square tests of the distributions of TGs in RNA or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

# Supplemental Fig. S6

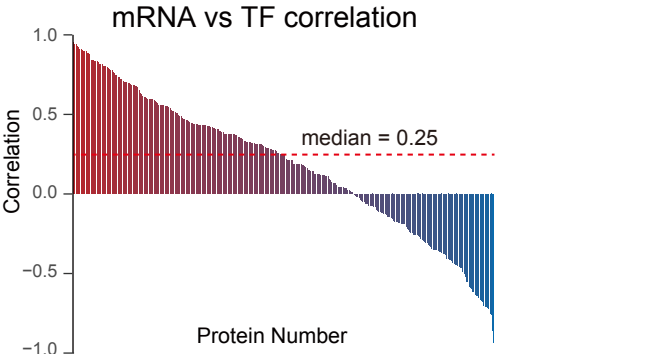
A



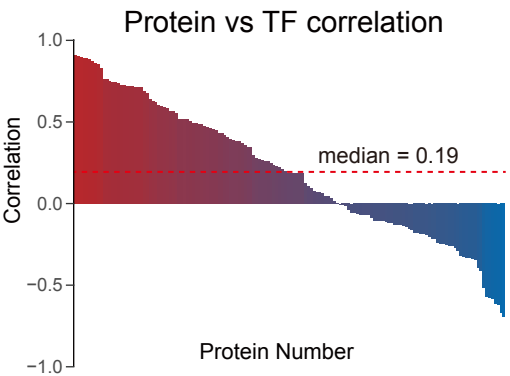
B



C



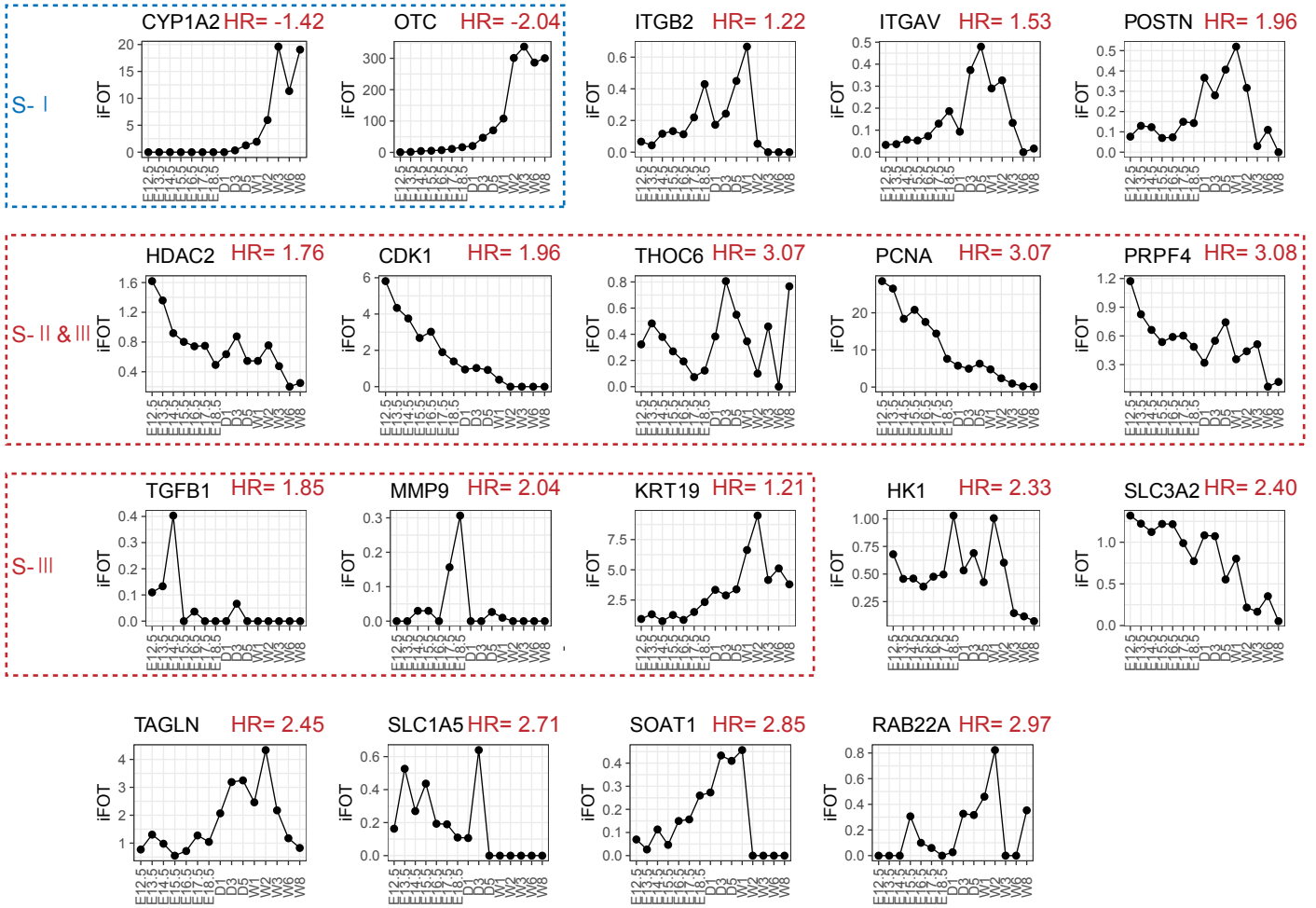
D



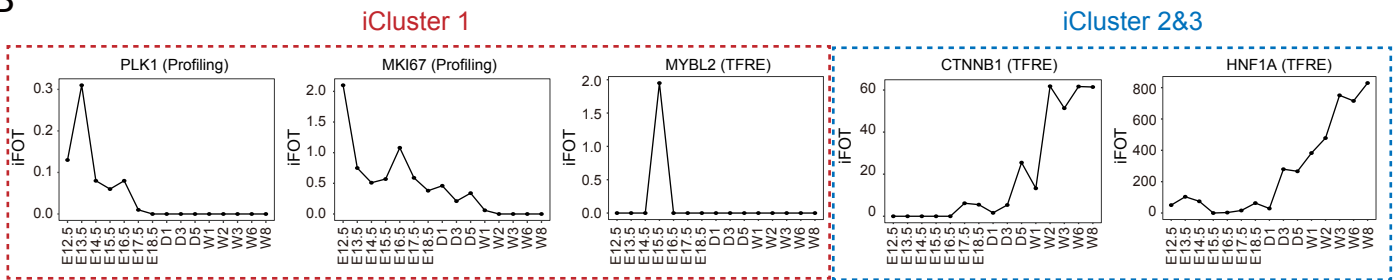
Supplementary\_Fig\_S6:  
(A) Categories of 8,544 RNA-only transcripts. (B) Classes of 1,996 non-protein coding RNA transcripts.  
(C) mRNA-TF correlation measured by Spearman's correlation coefficient. (D) Protein-TF correlation measured by Spearman's correlation coefficient.

# Supplemental Fig. S7

A



B



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).