

Expanded View Figures

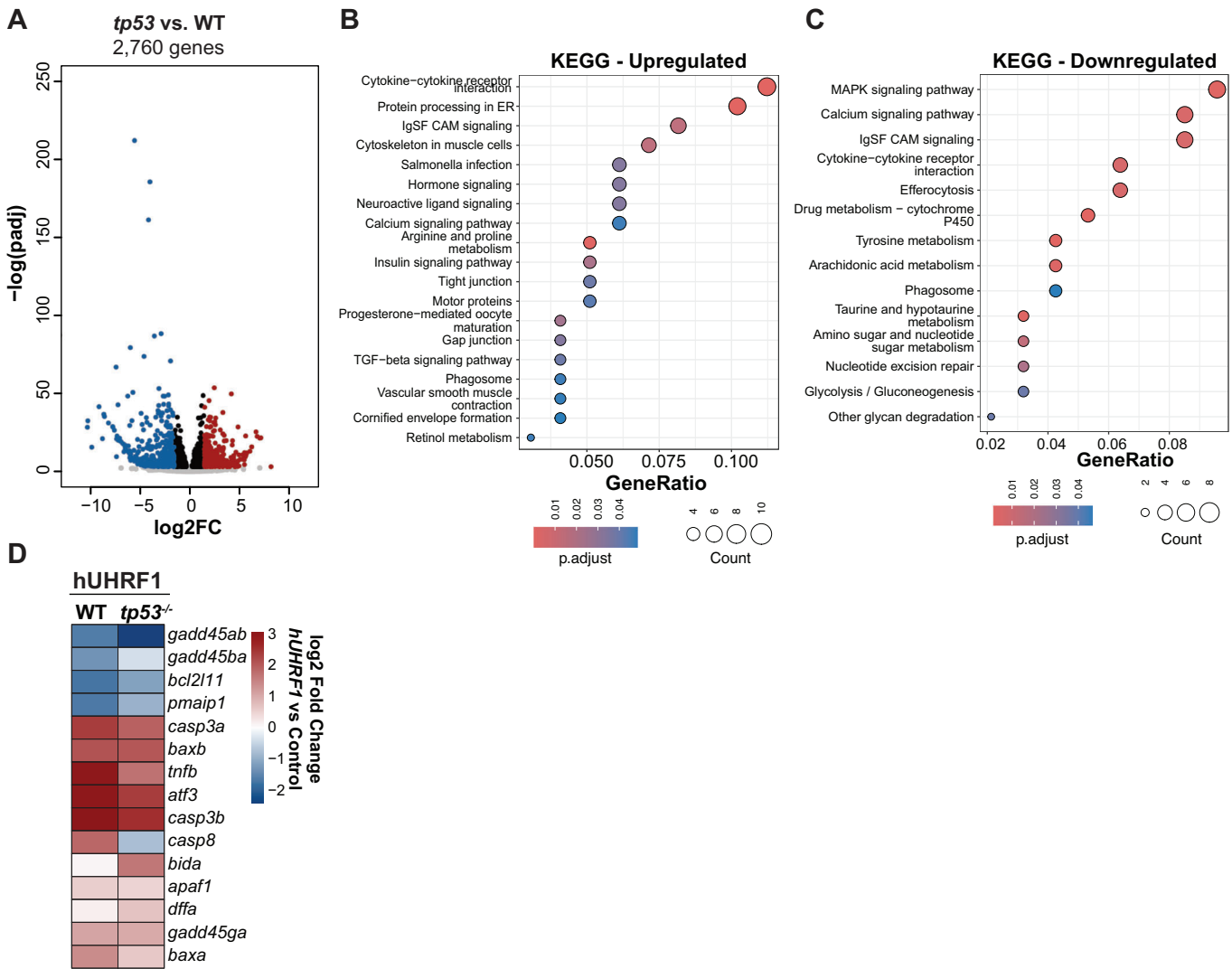


Figure EV1. Bulk RNAseq shows many differentially expressed genes in the liver of *tp53*^{-/-} mutants.

(A) Volcano plot of differentially expressed genes in the liver of *tp53*^{-/-} larvae compared to wild-type at 120 hpf in five biological replicates. Gray dots indicate genes with *P* value adjusted >0.05, black dots indicate genes with *P* value adjusted <0.05, red dots indicate genes with *P* value adjusted <0.05 and log2 fold change >1.5, and blue dots indicate genes with *P* value adjusted <0.05 and log2 fold change <-1.5. *P* values were calculated using the Wald test implemented in DESeq2 and adjusted for multiple testing using the Benjamini-Hochberg method. Genes with an adjusted *P* < 0.05 were considered significantly differentially expressed. (B) KEGG pathway analysis of upregulated genes (*P* value adjusted <0.05 and log2 fold change >0). KEGG pathways enrichment was assessed using a one-sided hypergeometric test with Benjamini-Hochberg correction for multiple testing. Dot size represents the gene ratio, and color represents -log10 of the adjusted *P* value. (C) KEGG pathway analysis of downregulated genes (*P* value adjusted <0.05 and log2 fold change <0). KEGG pathways enrichment was assessed using a one-sided hypergeometric test with Benjamini-Hochberg correction for multiple testing. Dot size represents the gene ratio, and color represents -log10 of the adjusted *P* value. (D) Heatmap of log2 fold change of genes involved in apoptosis in samples overexpressing hUHRF1, comparing *hUHRF1* to WT (WT) and *hUHRF1;tp53*^{-/-} to *tp53*^{-/-} (*tp53*^{-/-}).

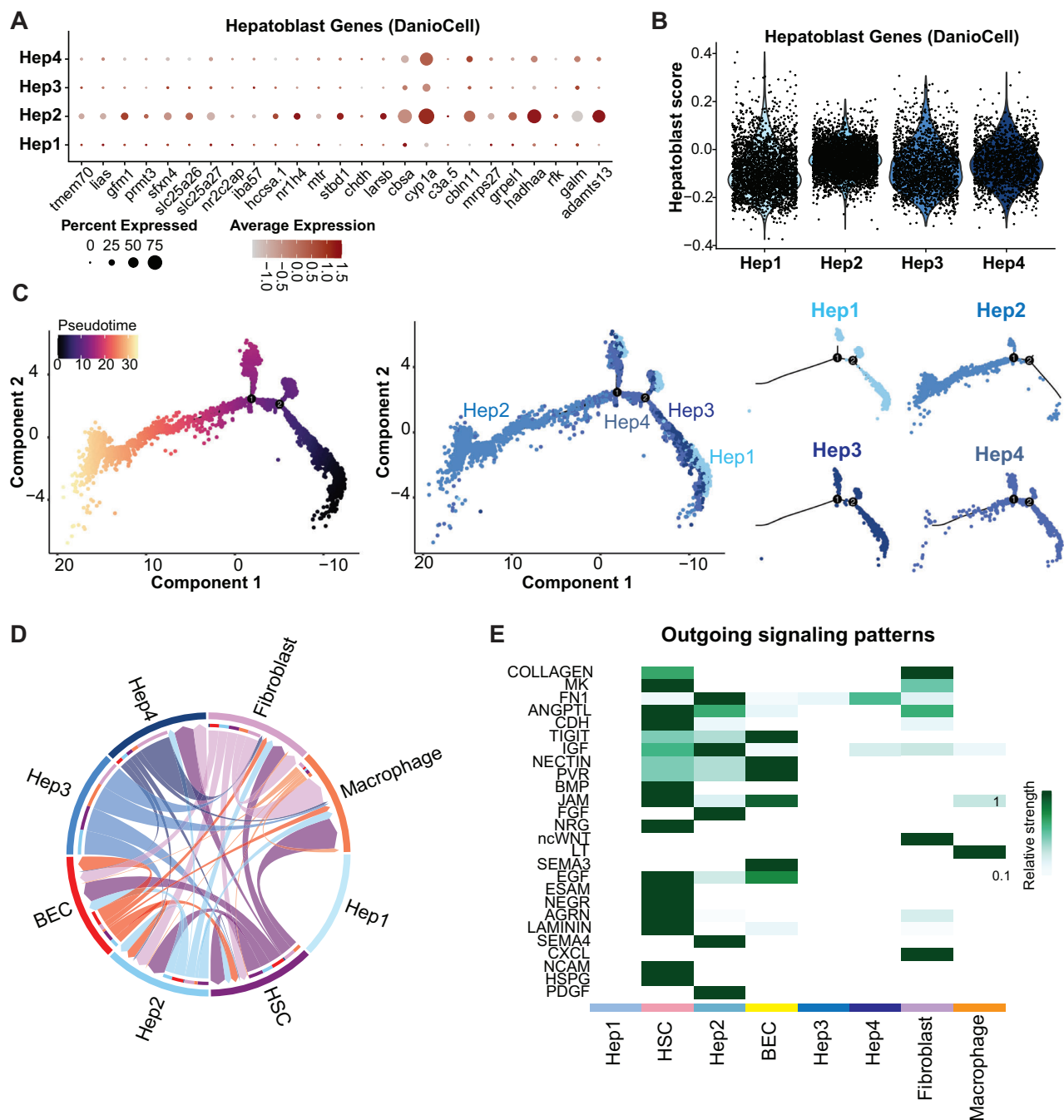


Figure EV2. Hepatocytes in control larvae cluster based on expression profile reflecting maturation.

(A) Expression of hepatoblast genes obtained from DanioCell in hepatocytes from control larvae at 120 hpf. (B) Hepatoblast Score of genes present in A in Hep1-4 in controls graphed in individual cells identified from scRNAseq. (C) Pseudotime projection of hepatocytes in controls. (D) Chord diagram showing cell-cell communication in control, with the width of each chord representing the proportion of cells with that signal and the arrows representing the direction of the signal. (E) The top outgoing signaling molecules in control are inferred based on the relative strength of the signaling.