2-Fold Enrichment Threshold **Liver Tissue** HepG2 Liver (n=1199) Skin (n=1350) Cortex (n=1865) Liver (n=1199) Skin (n=1350) Cortex (n=1865) 9.0 0.6 0.5 **KS Statistic KS Statistic** 0.4 0.4 0.3 Ŋ 0.2 0.1 0.0 3-Fold Enrichment Threshold HepG2 **Liver Tissue** Liver (n=871) Skin (n=809) Cortex (n=1150) Liver (n=871) Skin (n=809) 9.0 0.6 Cortex (n=1150) 0.5 **KS Statistic** Statistic 0.4 0.4 0.3 0.2 0.1 0.0 **4-Fold Enrichment Threshold** HepG2 **Liver Tissue** Liver (n=734) Skin (n=626) Cortex (n=769) Liver (n=734) 90 Skin (n=626) Cortex (n=769) 0.6 0.5 KS Statistic **KS Statistic** 0.4 0.3 0.2 0.1 0.0 5-Fold Enrichment Threshold **Liver Tissue** HepG2 Liver (n=646) Skin (n=507) Cortex (n=481) Liver (n=646) Skin (n=507) Cortex (n=481) 0.6 0.5 **KS Statistic** 0.4 0.3 0.2 0.2 0.1

Supplemental_Fig_S12. Enrichment for proximal binding to liver specific expression analysis, as shown in Figure 3C-D, over a range of fold enrichment threshold cutoffs. From top to bottom, tissue specific transcripts were defined as those with a mean RPKM of 2 in a given tissue of interest and 2, 3, 4, and 5-fold increased mean expression in the tissue of interest relative to the mean expression across all other tissues. Dots represent KS-statistic of enrichment for proximal binding of each DAP to liver (red/purple), skin (blue) and cortex (green) -specific genes in adult liver tissue (left) and HepG2 cell line (right).

ZBTBS ATF FOXA JUN CEBP RES POLR2 HNF4

0.0