



**Fig. S5. Temporal dynamics of transcription factors (TFs) during digit regeneration. (A)** Heat map shows the average log<sub>2</sub> fold change in gene expression (RPKM) of TFs in the gene regulatory network at 12, 14, and 21 DPA for Regen and Non-Regen groups, normalized to R12 values (n=4 mice, 4 digits/group/time point). Black cells indicate genes that are significantly different between time points for Regen and Non-Regen groups (Benjamini corrected  $P < 0.05$ ). **(B)** Venn diagrams show number of TFs present in Regen, Non-Regen, or both groups for each cluster.