Fig. S4. Temporal gene expression of non-regenerating digits is distinct from regenerating digits. (**A**) Heat map shows the scaled z-score of the average RPKM of 1400 differentially expressed genes (DEGs) from Non-Regen groups at 12, 14, and 21 DPA, alongside the corresponding z-score of Regen groups. Red and blue cells indicate relative gene upregulation and downregulation, respectively. Green cells indicate cluster type, and black cells indicate genes that are significantly different between time points for Non-Regen and Regen groups (Benjamini corrected $P<0.05$). (**B**) Temporal expression of Non-Regen DEGs (red) and corresponding Regen genes (blue) for each cluster type. Solid lines represent the mean relative log2 fold change in expression level (RPKM) compared to 12 DPA. Lighter shades indicate 95% confidence interval.