



Fig. S3. Transcriptomic dynamics for Regen and Non-Regen groups. (A) Heat map shows the scaled z-score of the RPKM of 1513 differentially expressed genes (DEGs) from individual Regen samples and (B) 1400 DEGs from individual Non-Regen samples at 12, 14, and 21 DPA (n=4 mice, 4 digits/group/time point). Red and blue cells indicate relative gene upregulation and downregulation, respectively, and green cells indicate cluster type. (C) Gene type distribution (% of total mRNA) of each cluster for the Regen and (D) Non-Regen groups. TEC: to be experimentally confirmed.