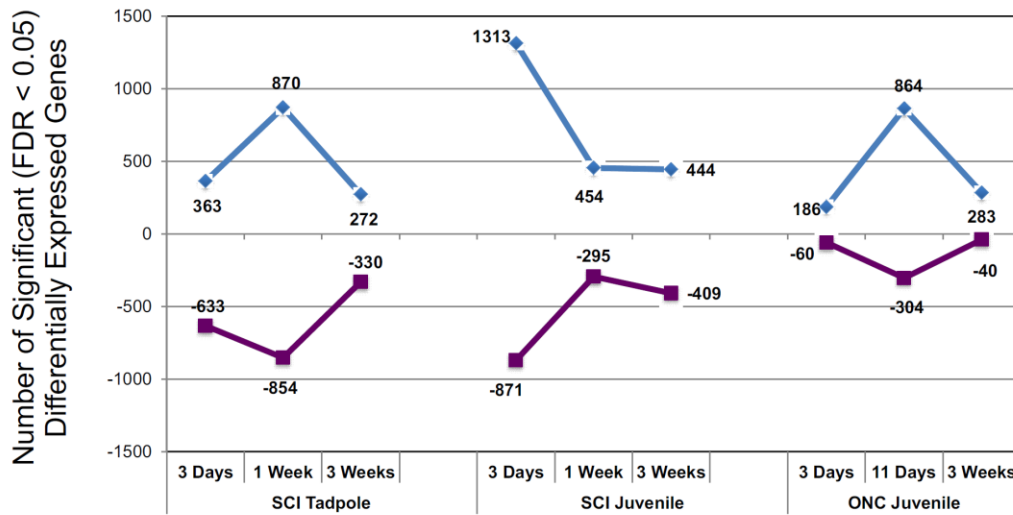


Additional_File3_DESeq2_Metadata.pdf. Temporal patterns of gene expression and shared injury-response genes between regenerative vs. non-regenerative tissues, as determined by DESeq2. **A)** Regenerative tissues [*i.e.*, SCI tadpole hindbrain (SCI Tadpole) and ONC juvenile frog eye (ONC Juvenile)] shared similar temporal patterns of numbers of significant (FDR < 0.05) differentially expressed genes, which differed markedly from that of the non-regenerative tissue [SCI juvenile frog hindbrain (SCI Juvenile)]. Whereas the expression response of the two regenerative tissues peaked during the mid recovery phase (1 week/11 days), that of the non-regenerative tissue peaked at the early, post trauma phase (3 days). Up- and down-regulated genes are shown in green and red, respectively; S & L gene homeologs were tallied separately. **B)** Plot illustrating the percentage of annotated genes that were significantly (FDR < 0.05) differentially expressed with injury (100% = 24,382 genes).

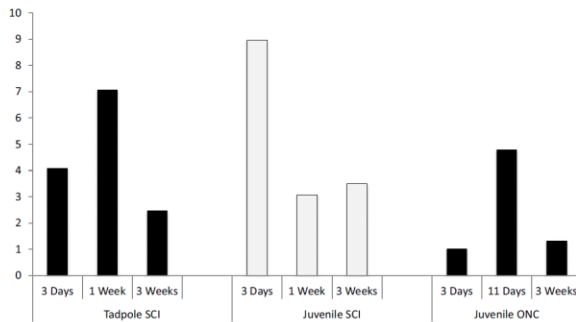
Additional_File2_Differential_Expression_Analysis_by_DESeq2.xlsm contains the DESeq2 output files from which A and B were derived. **C – E)** UpSet plots illustrating the number of genes overlapping between the samples indicated by the circles below each bar at 3 days (**C**), 7/11 days (**D**), and 3 weeks (**E**) after injury. Numbers of shared up- and down-regulated genes are indicated above and below each bar, respectively. The maximum number of overlapping genes between the two successfully regenerative tissues (DESR: Differentially Expressed in Successful Regeneration) occurred during the peak phase of regenerative CNS axon outgrowth.

DESeq2 Metadata

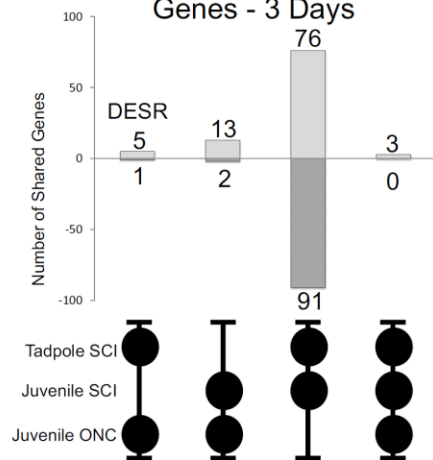
A. Temporal Changes in Injury-Induced Differential Gene Expression



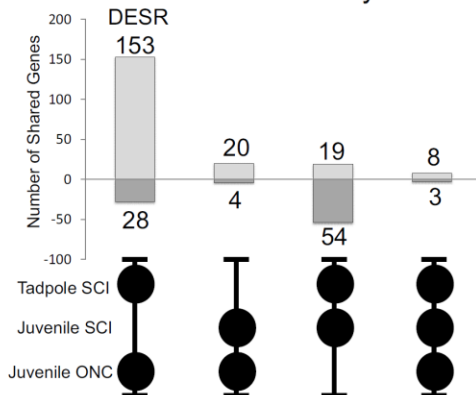
B. % of Annotated Genes that were Differentially Expressed



C. Shared Differentially Expressed Genes - 3 Days



D. Shared Differentially Expressed Genes - 7/11 Days



E. Shared Differentially Expressed Genes - 3 Weeks

