Figure 1-figure supplement 1

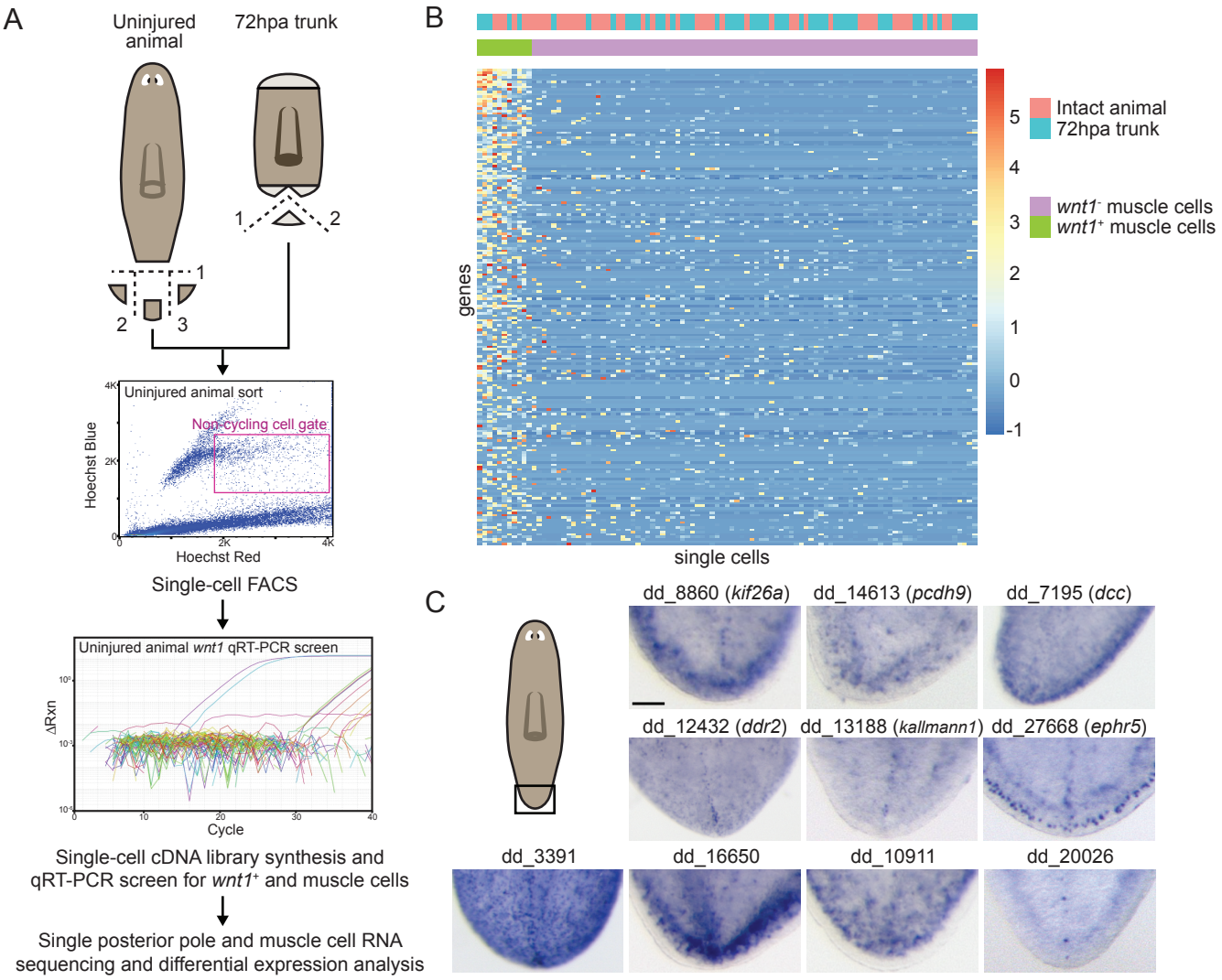

Figure 1-figure supplement 1. Single-cell RNA sequencing of tail tip fragments identifies new genes expressed in the posterior pole region. (**A**) Posterior pole single-cell RNA sequencing approach: Posterior-pole-containing fragments were excised from tail tips of uninjured animals and posterior blastemas of regenerating trunks 72 hours post amputation (hpa) (cartoons; dotted lines are cut planes, and dotted line numbers denote cut sequence). Excised fragments were dissociated and single cells were sorted (gate in magenta) onto 96-well plates via fluorescence-activated cell sorting (FACS). cDNA libraries synthesized from single cells were screened by qRT-PCR for *wnt1* and *collagen* expression (qRT-PCR plot), sequenced, and analyzed for differential gene expression. (**B**) Heatmap of all 101 single cells sequenced (columns: 11 *wnt1*$^{+}$; *collagen*$^{+}$ posterior pole cells and 90 *wnt1*$^{-}$; *collagen*$^{+}$ muscle cells) was generated by clustering by normalized transcript counts of the genes (rows) differentially expressed in posterior pole cells over non-pole muscle cells ($p < 0.05$) (**C**) Tail expression of posterior pole candidates by whole-mount *in situ* hybridization: Gene names represent best human BLAST; numerical names indicate the Smedv4.1 Dresden transcriptome assembly transcript number (See “Gene nomenclature” in Methods). Area imaged is indicated by the box in the cartoon on the left. Images are representative of results seen at least 4 animals. Scale bar represents 50μm.