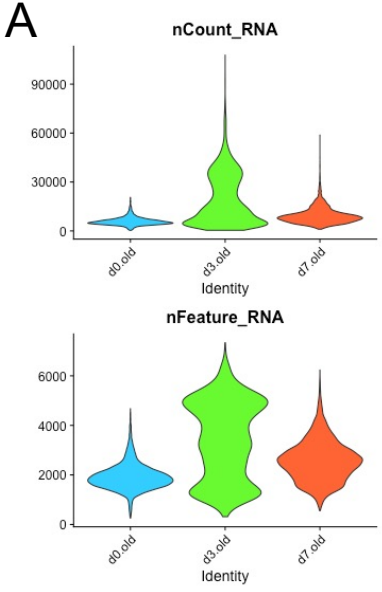
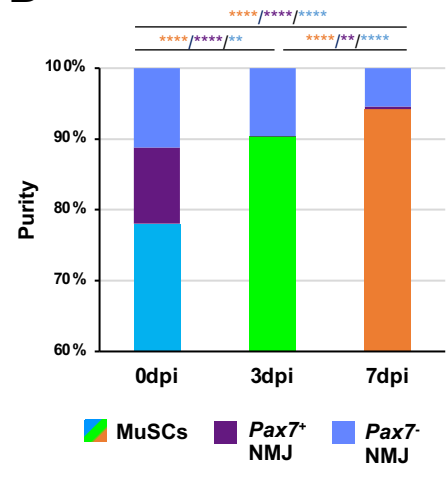


A



B



C

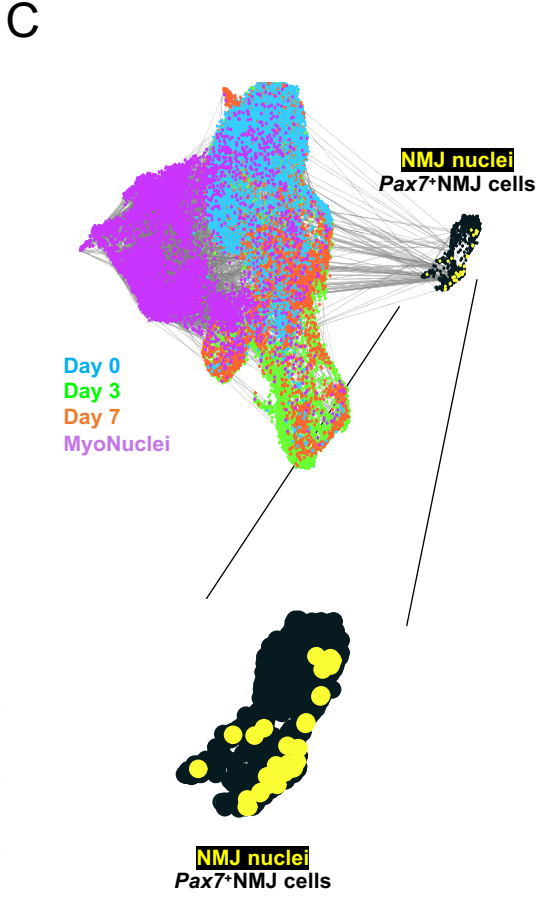


Figure 4 – figure supplement 1. A) Violin plot of the number of unique molecular identifiers (top) and number of genes (bottom) in each dataset. B) Stacked bar graph showing Pax7- NMJ, Pax7+ NMJ, and MuSCs as a percent of FACS-enriched MuSCs. **** denotes $p < 0.0001$ and ** denotes $p < 0.01$ by two-sided z-test for proportions with pairwise comparisons using holm p-value adjustment. Threshold for significance was considered $p < 0.05$. Sample sizes (n) were 5951, 6404, and 6264 for 0dpi, 3dpi, and 7dpi, respectively. Orange asterisk indicates comparison of MuSCs, purple indicates comparison of Pax7+ NMJ cells, and blue indicates comparison of Pax7- NMJ cells. (C) (left) UMAP colored by timepoint showing velocity-inferred cell-cell connections (grey lines), which suggests a decision to acquire a synaptic fate. (right) Expanded view of the NMJ cluster showing Pax7+ NMJ cells (black) and Pax7+ NMJ myonuclei (yellow), which originate from the snRNA-Seq datasets. Blue, orange and green points represent Pax7-NMJ cells recovered in the time course datasets.