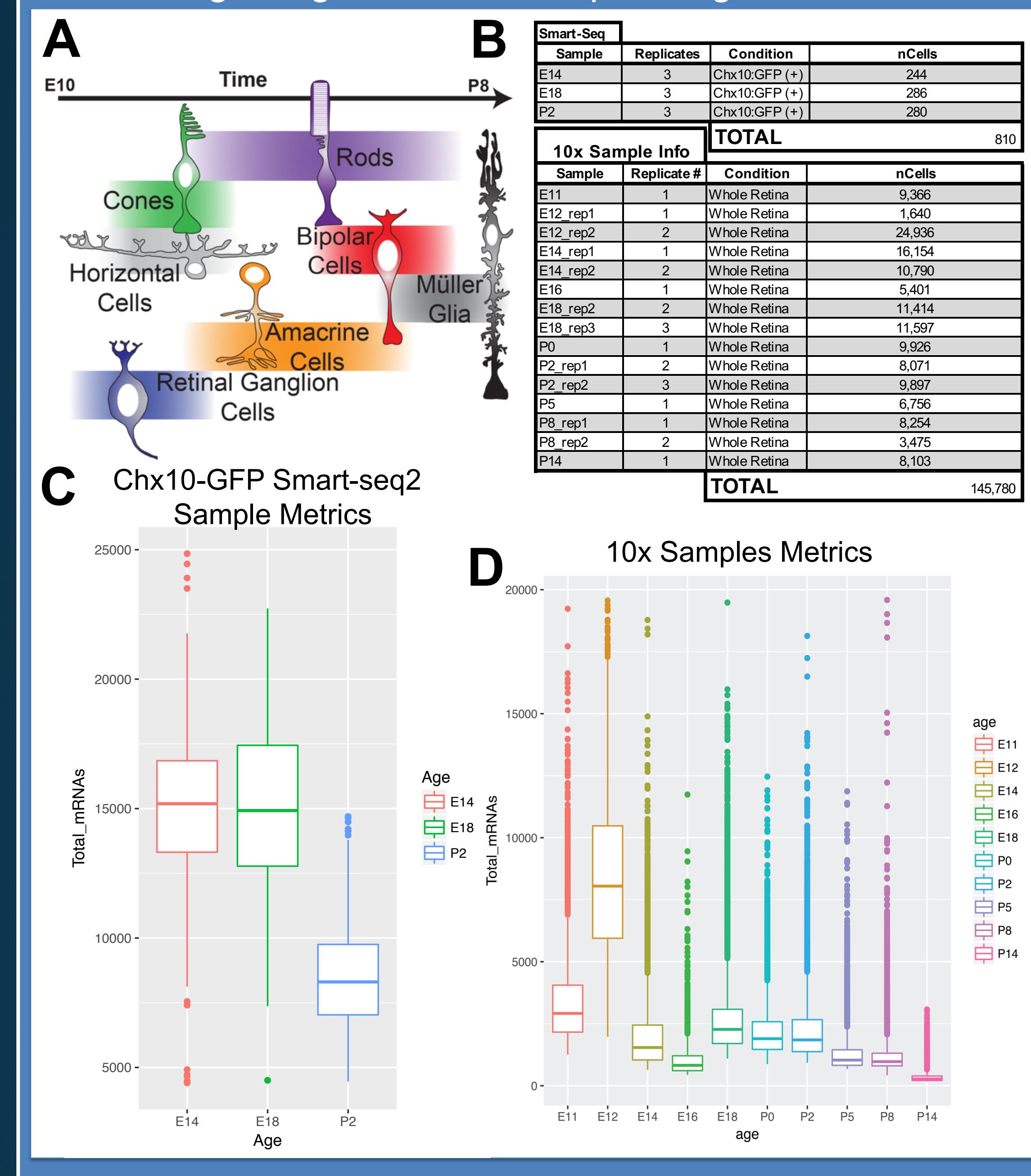


# Mouse retinal development at single-cell resolution

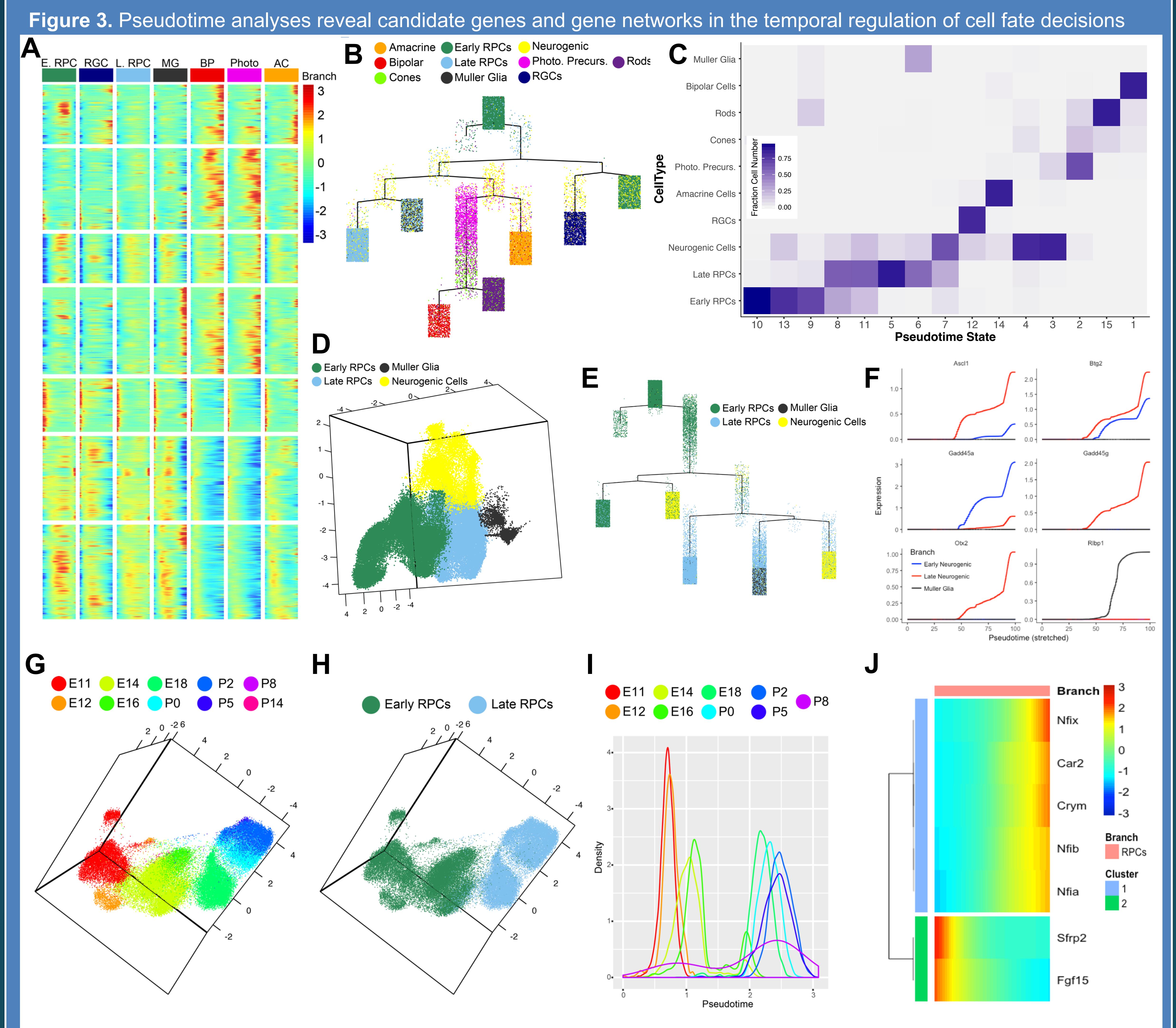
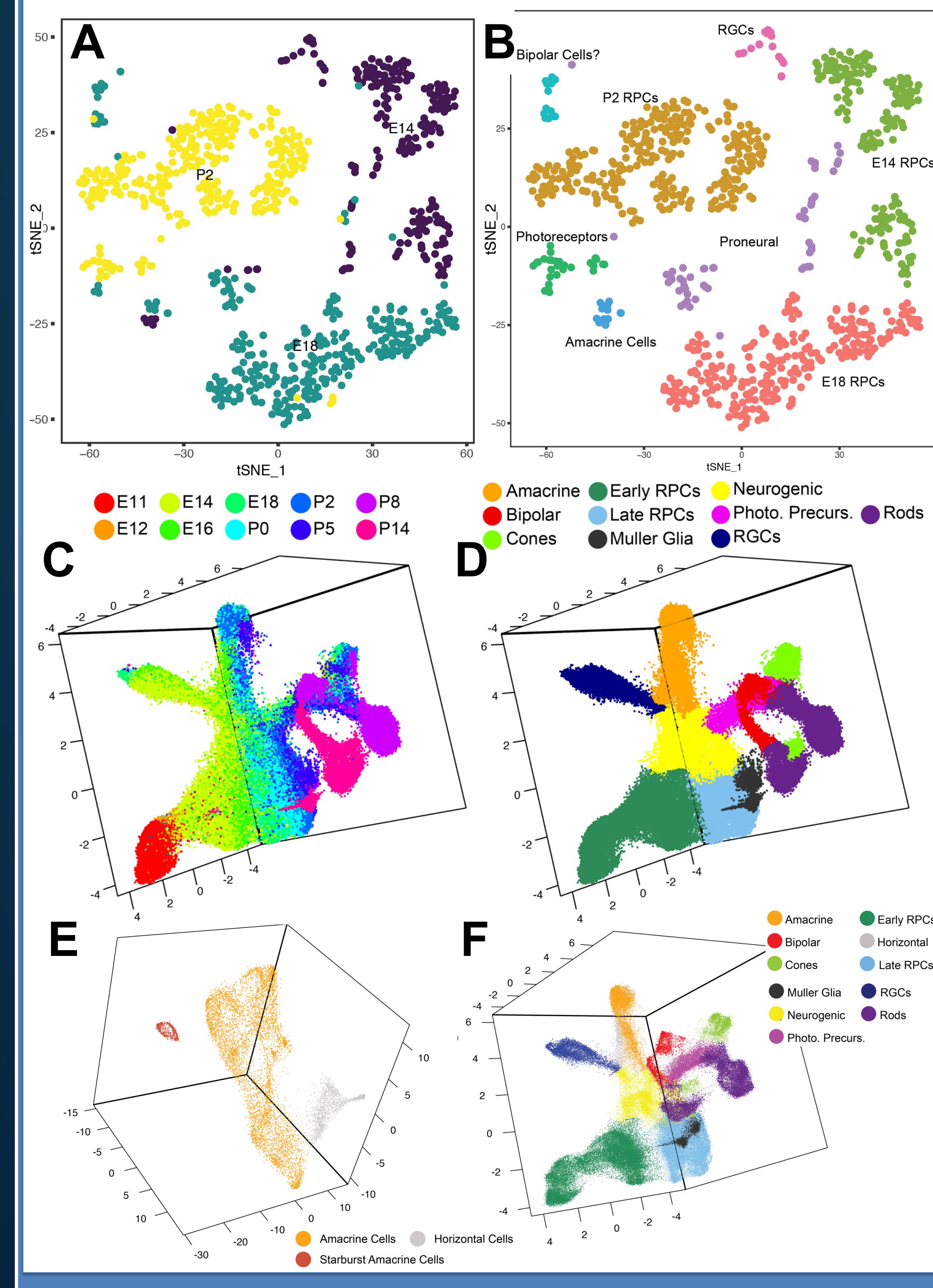
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**Purpose:** Work on retinal development over the past decades has begun to elucidate the transcriptional networks required for cell type specification; however, few efforts have focused on identifying the mechanisms by which an individual retinal progenitor cell (RPC) is selected at a given point in developmental time to differentiate as a specific retinal neuron or Müller glia. Additionally, our knowledge of the transcriptional changes within RPCs that govern the ability of RPCs to gain and/or lose the ability to generate a specific cell type over developmental time (competence model) remains limited. We seek to identify the genes and transcriptional networks that facilitate temporally-regulated cell fate specification.

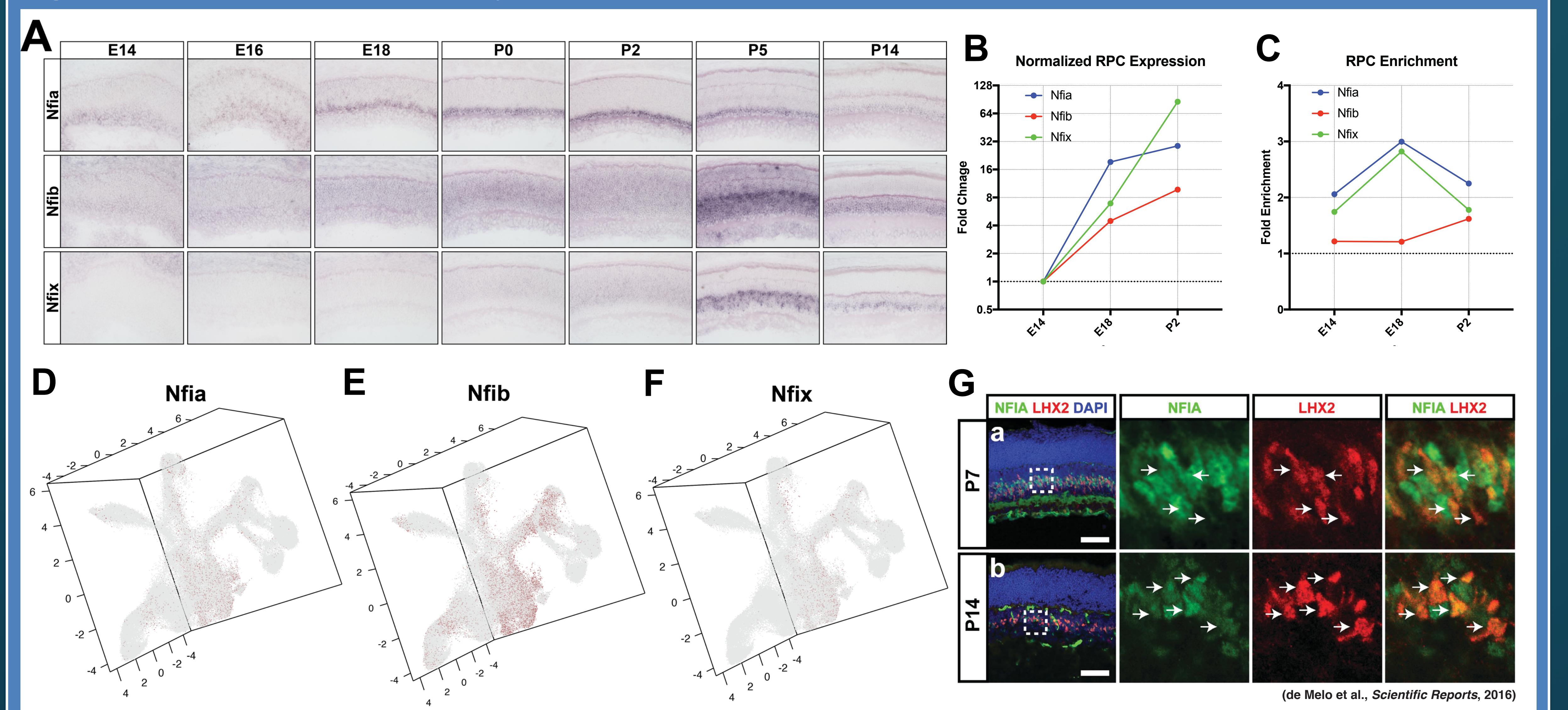
**Figure 1. Analyzing temporal specification of retinal cell fates through single-cell RNA-sequencing.**



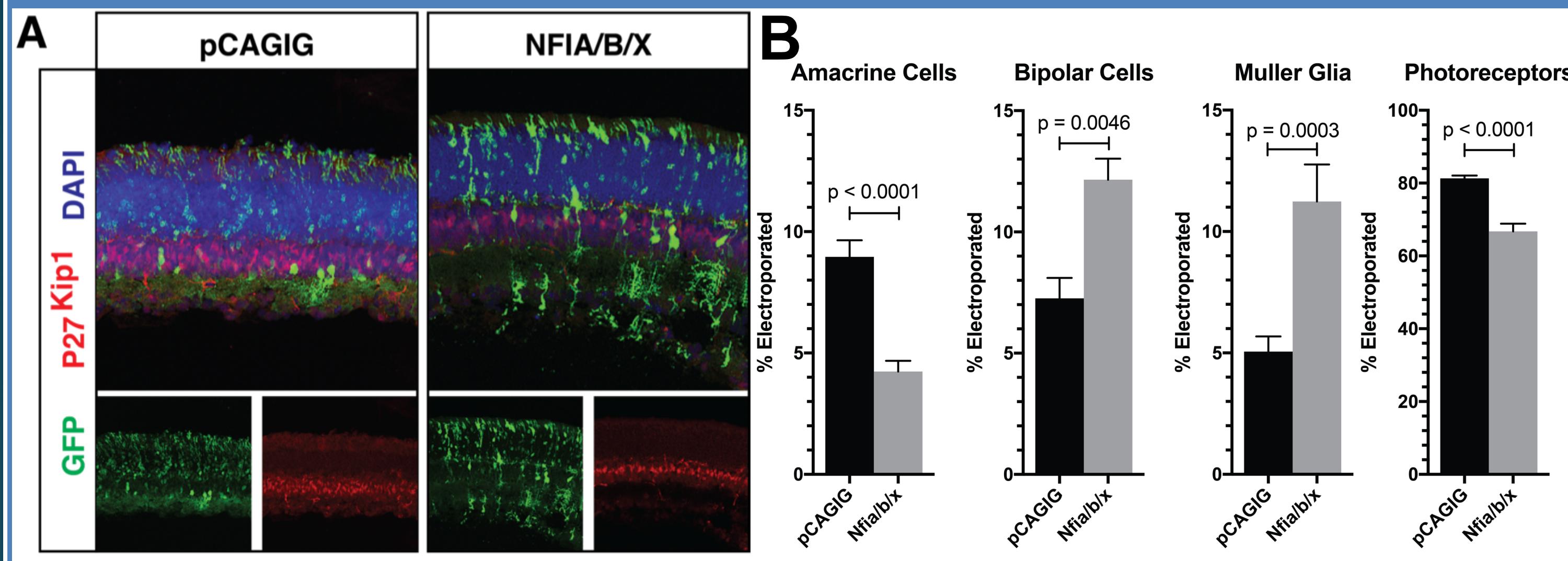
**Figure 2. Dimension reduction and cell-type designation**



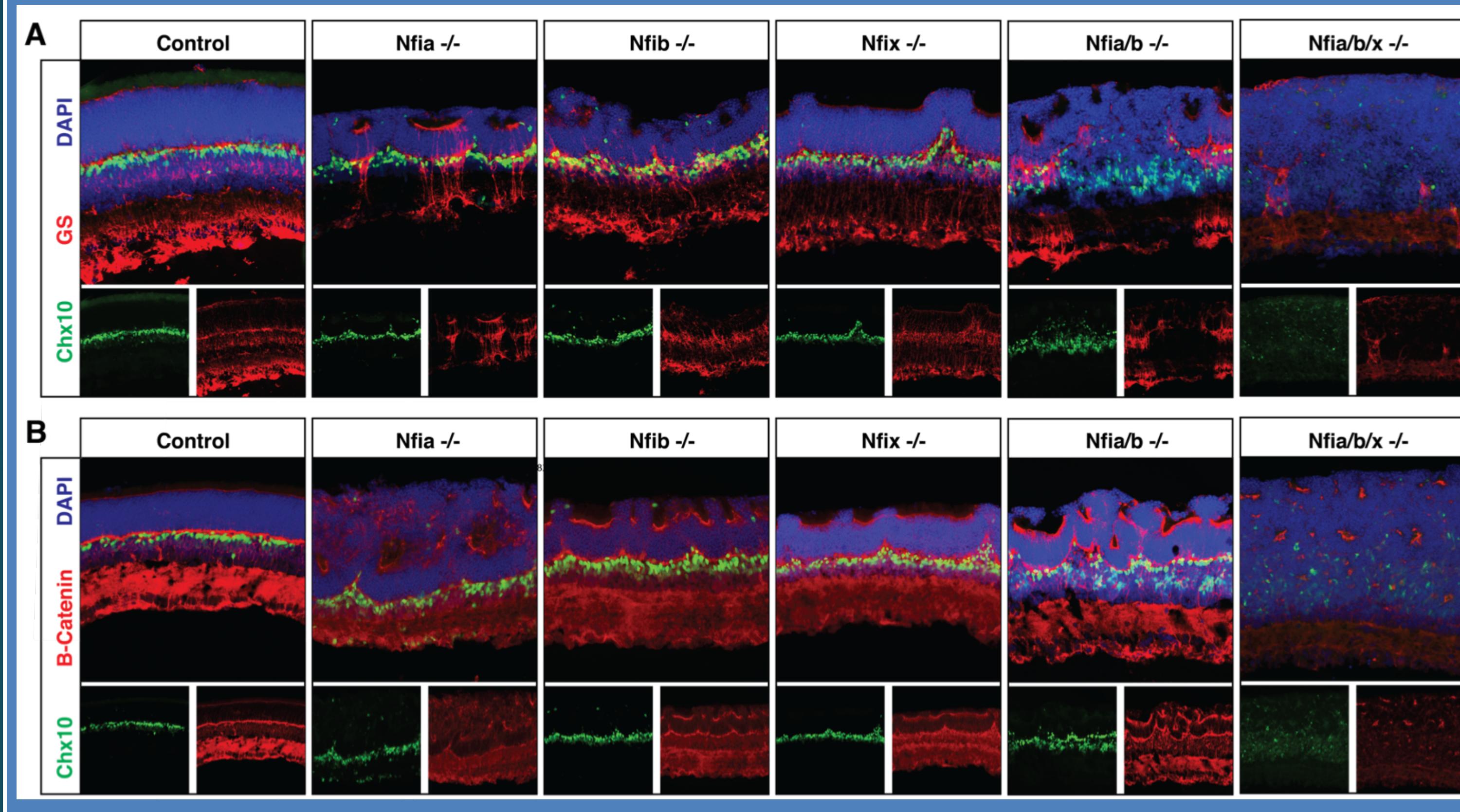
**Figure 4. Nfi transcription factors display enriched expression in late RPCs and Müller Glia.**



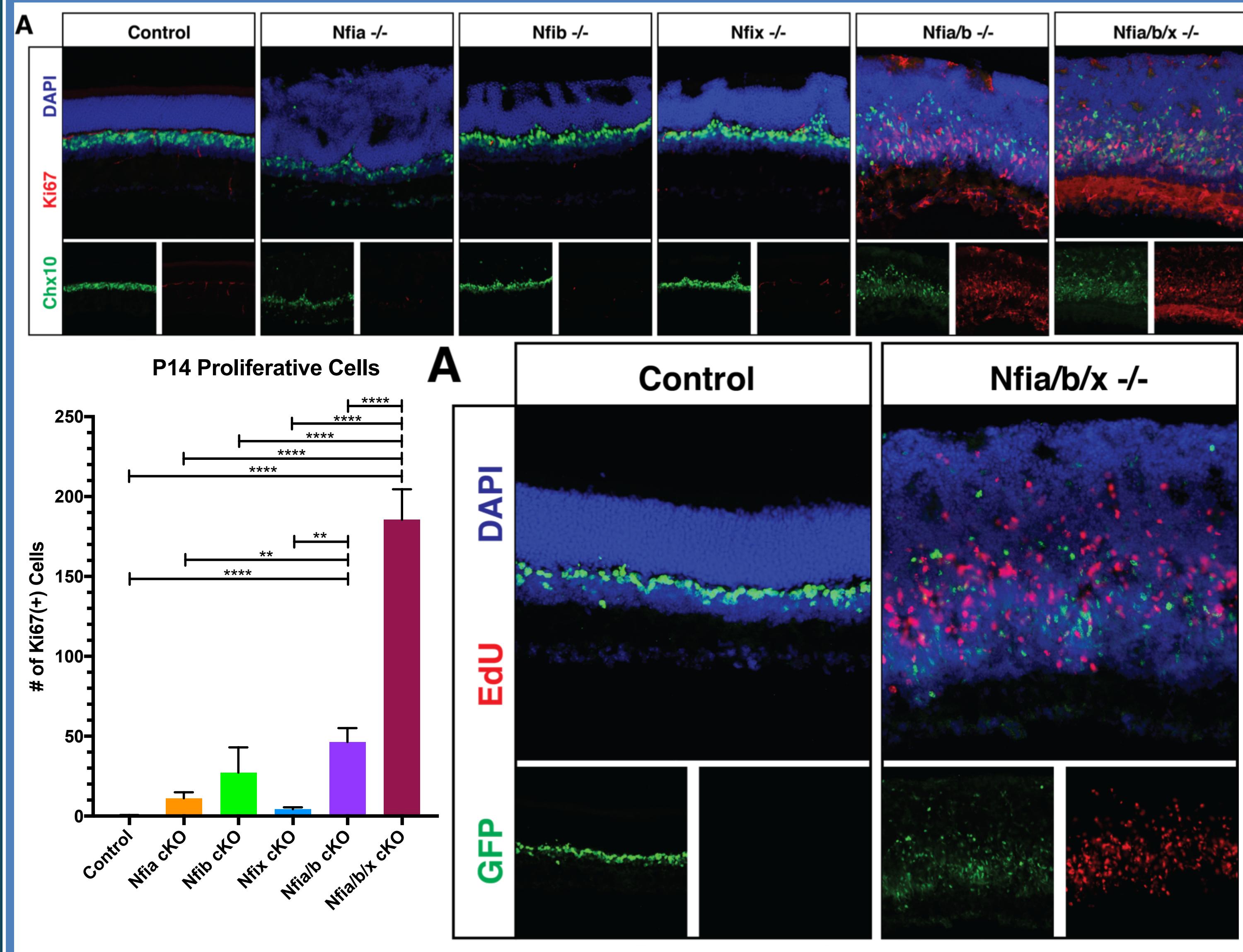
**Figure 5. Nfi transcription factors promote late retinal cell fates.**



**Figure 6. Nfi transcription factors are required for retinal gliogenesis.**



**Figure 7. Nfi transcription factors are required for RPC quiescence.**



**Conclusions:** Using single-cell RNA-sequencing we are able to capture snapshots of cellular transitions of retinal progenitors through cell fate specification and differentiation. Using bioinformatic analyses, we have identified genes and gene networks that correlate with 1) retinal progenitor competence and 2) temporal specification of retinal cell fates. In particular, we show that the Nfi family of transcription factors regulate late retinal cell fates and RPC proliferative quiescence.

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