Molecular signatures of retinal ganglion cells revealed through single cell profiling

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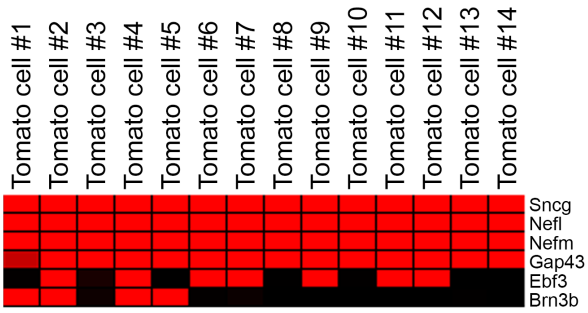
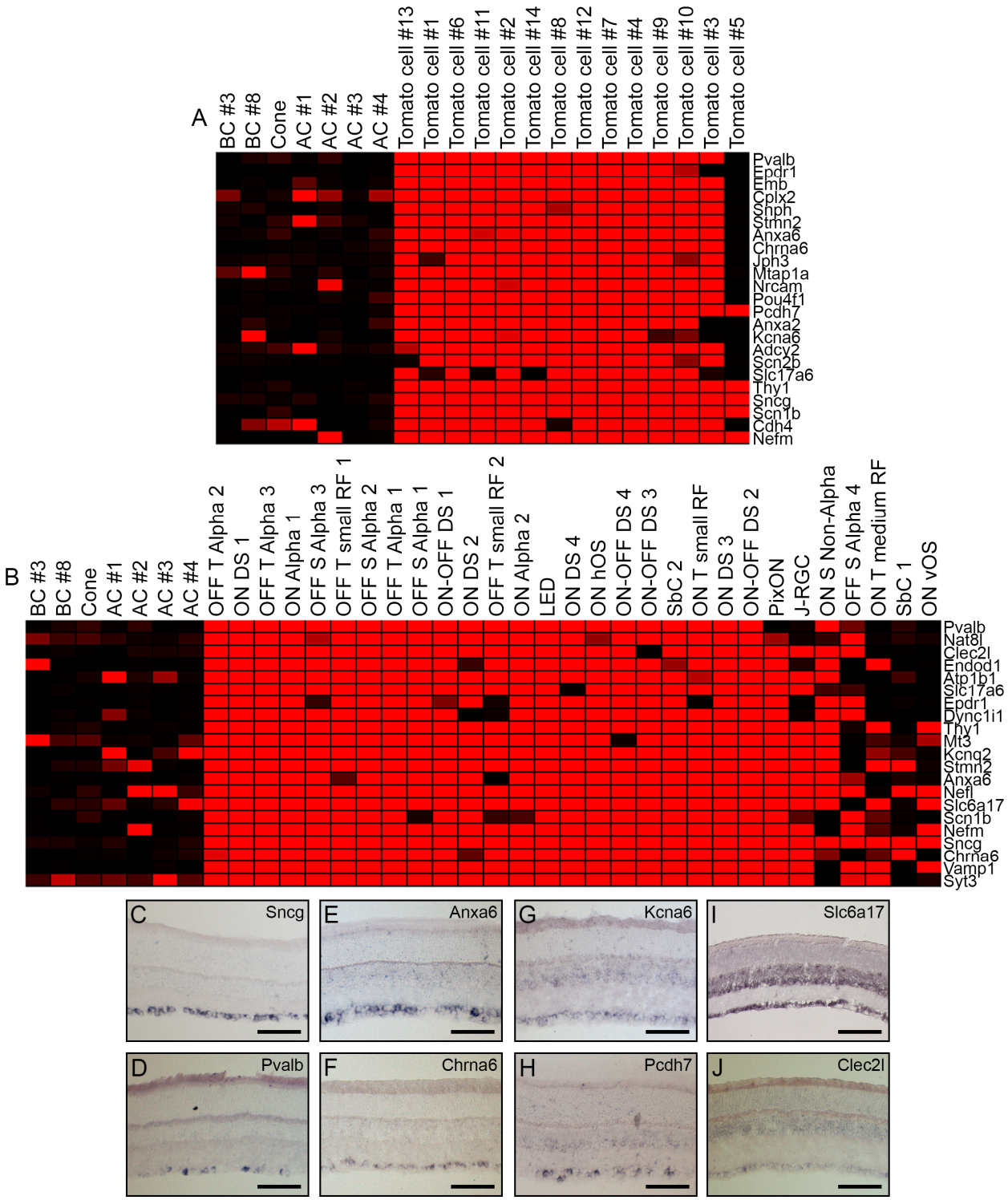
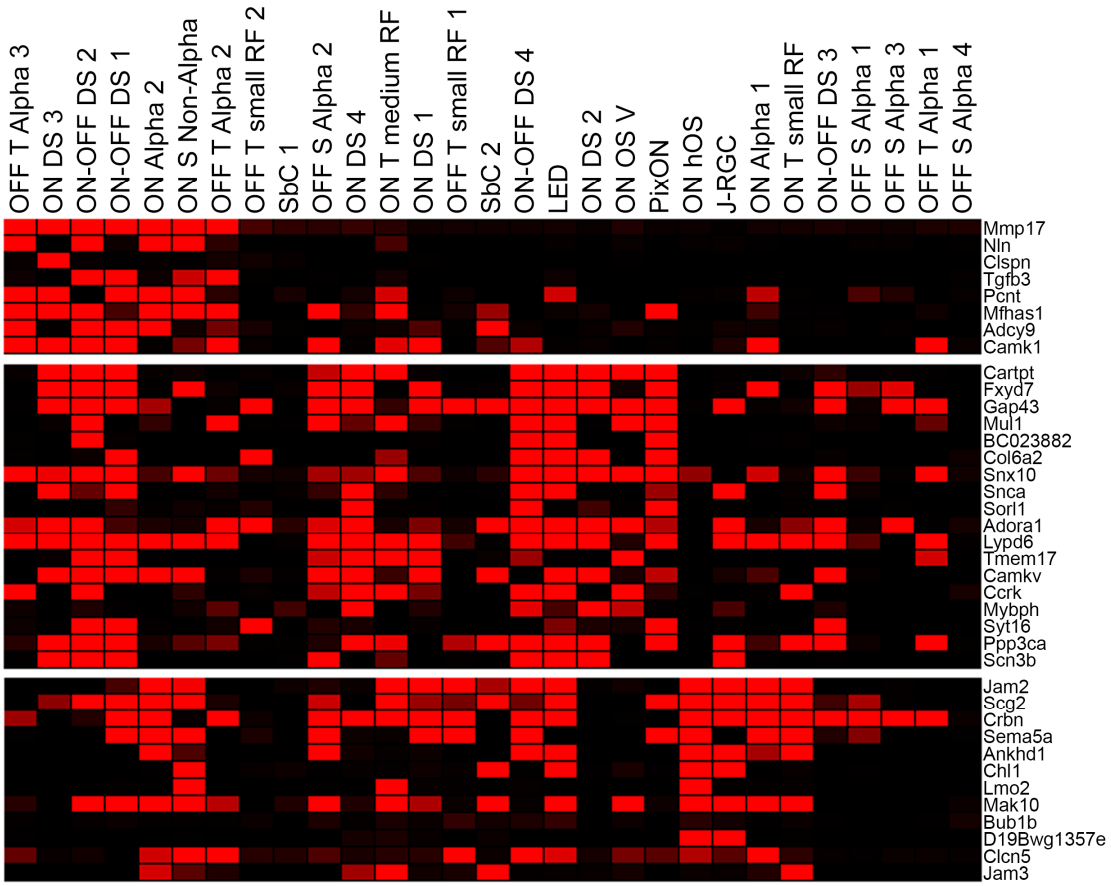


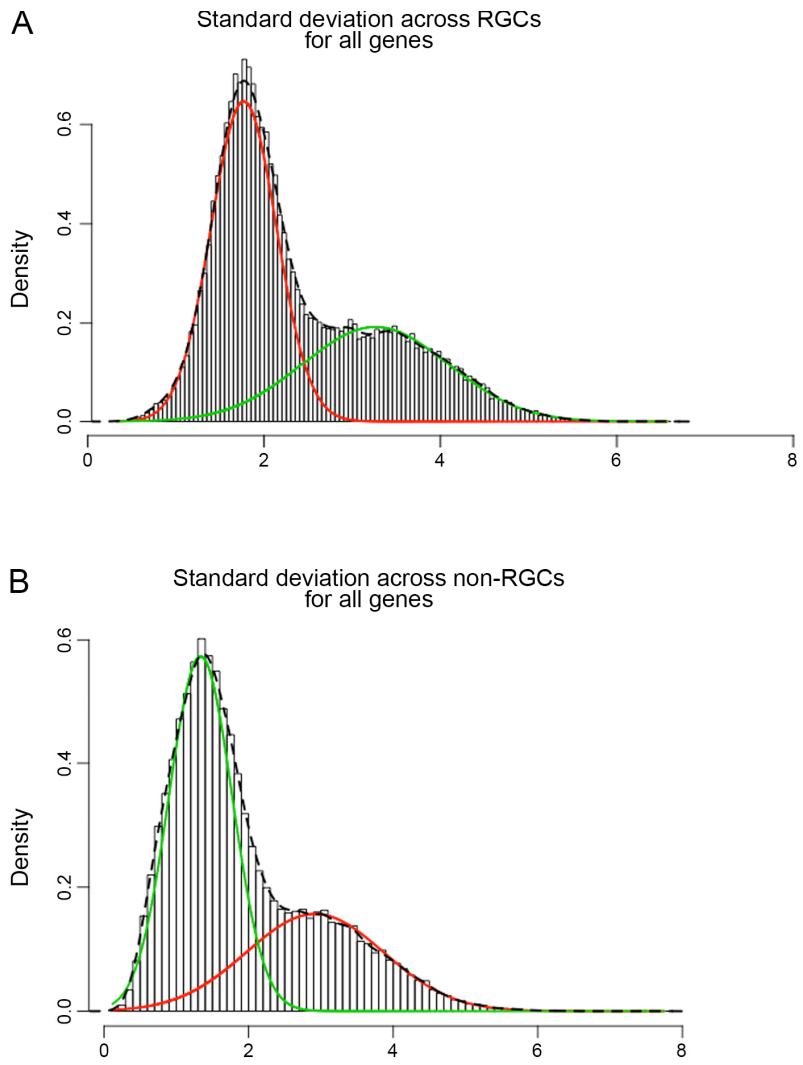
Supplementary Figure 1. RGC marker genes expressed in tdTomato+ cells.
The expression of RGC genes was examined in our tdTomato+ cells and visualized by heatmap. Genes examined included *Sncg, Nefl, Nefm, Gap43, Ebf3,* and *Brn3b.*



Supplementary Figure 2. Parvalbumin gene correlates detected in RGCs.
Genes highly correlated with *Pvalb* in the tdTomato+ cell population were determined through Pearson correlation and visualized by heatmap (A). Among the physiologically classified RGCs, *Pvalb* correlated genes were also defined by Pearson correlation and demonstrated through heatmap (B). *Pvalb* correlated genes from both datasets were then examined by ISH: *Sncg* (C), *Pvalb* (D), *Anxa6* (E), *Chrna6* (F), *Kcna6* (G), *Pcdh7* (H), *Slc6a17* (I), and *Clec2l* (J). Scale bars represent 100 µm.



Supplementary Figure 3. Genes correlated with RGC subtype markers.
The genes which were most highly correlated (Pearson correlation) with previously identified RGC subtype markers, *Mmp17, Cartpt,* and *Jam2*, were identified within the characterized RGCs.



Supplementary Figure 4. Standard deviation of microarray data across RGCs and non-RGCs.
The standard deviation of gene expression among the physiologically characterized RGCs (A) and non-RGCs (B) was examined.