Figure S1. Cell type determination workflow. (A) Workflow for determining cell types. **(B-D)** UMAP projections of the whole eye sibCTL and *tet2*$^{-/-}$*;tet3*$^{-/-}$ pooled dataset indicating **(B)** genotype, **(C)** cell category and **(D)** cell type after refinement of neuroblast, bipolar cell, and photoreceptor neuron classes. **(E-G)** UMAP projections used to refine cell type calls on **(E)** bipolar cells **(F)** neuroblasts, and **(G)** photoreceptors. **(H)** Violin plot demonstrating marker specificity for each cell type in the eye.

Figure S2. Removal of non-retinal progenitor cells from retinal progenitor cells. (A-C) UMAP projections of pooled sibCTL and *tet2*$^{-/-}$*;tet3*$^{-/-}$ progenitor cells at all timepoints, colored by **(A)** cluster, **(B)** genotype, and **(C)** timepoint. **(D)** Violin plot representing expression of retinal progenitor and proneural genes. **(E-G)** Violin Plots representing expression of non-retinal progenitor genes including **(E)** lens progenitor genes **(F)** anterior segment progenitor genes and **(G)** pigment genes. **(H)** Retinal progenitor cell (RPCs) and non-retinal progenitor cell designations from pooled progenitor clusters. Clusters 1, 16 and 18 were excluded from further retinal progenitor analyses.

Figure S3. Pooled sibCTL and *tet2*$^{-/-}$*;tet3*$^{-/-}$ retinal datasets visualized across timepoints. (A) UMAP projections of pooled sibCTL and *tet2*$^{-/-}$*;tet3*$^{-/-}$ datasets separated by age. UMAPs are shown segregated by retinal cell type (top row), genotype (middle row), and imbalance score (bottom row). Cluster numbers calculated within each combined dataset are indicated. Pooled 36,48,72, and 120hpf datasets contained 18,18,26, and 25 clusters, respectively.

Figure S4. Raw proportions of each retinal cell type across each age and genotype group in scRNA-Seq datasets. Stacked bar plot representation of proportional cell type contributions to sibCTL and tet2-/-;tet3-/- retinae at 36,48,72, and 120hpf, replicates aggregated.

Figure S5. Characterization of pooled sibCTL and *tet2*$^{-/-}$*;tet3*$^{-/-}$ bipolar cell clusters at 120hpf. (A) Dotplot representing the top six cluster-specific differentially expressed genes across pooled sibCTL and *tet2*$^{-/-}$*;tet3*$^{-/-}$ BC clusters at 120hpf. **(B)** Dotplot representation of BC functional genes across sibCTL and *tet2*$^{-/-}$*;tet3*$^{-/-}$ BC clusters at 120hpf. **(C)** UMAP plots representing AUCell scores for GO-term associated gene sets across the 120hpf BC dataset for the following GO Terms: cell projection (GO:0042995), synapse (GO:0045202), transmembrane transporter (GO:0015318), calcium ion binding (GO:0005509), gated channel activity (GO:0022836). **(D)** Distribution plots of AUCell scores across BC clusters at 120hpf. Y axis = cell density; X axis = AUCell score.

Figure S6. Characterization of pooled sibCTL and *tet2*$^{-/-}$*;tet3*$^{-/-}$ horizontal clusters at 120hpf. (A) Dotplot representing the top six cluster-specific differentially expressed genes across pooled sibCTL and *tet2*$^{-/-}$*;tet3*$^{-/-}$ horizontal cell clusters at 120hpf. **(B)** UMAP and distribution plots representing AUCell scores for GO-term associated gene sets across the 120hpf horizontal cell dataset (UMAP) and across 120hpf horizontal cell clusters (distribution plots) for the following GO Terms: neuron projection (GO:0043005), plasma membrane bounded cell projection (GO:0120025), cell projection (GO:0042995), adenyl ribonucleotide binding (GO:0032559), ATP binding (GO:0005524), cell communication (GO:0007154), protein kinase activity (GO:0004672),

action potential (GO:0001508), neuron to neuron synapse (GO:0098984), axon (GO:0030424), calcium ion binding (GO:0005509), gated channel activity (GO:0022836), and synapse (GO:0045202).

Table S1. Cluster-specific DEGs for all progenitor cells integrated across all genotypes and timepoints.

Table S2. Cluster specific DEGs used for lineage identification

Table S3. Cell type-specific DEGs for retinal cell types from pooled data.

Table S4. Complete differential abundance analysis between sibCTL and *tet2*$^{-/-}$;*tet3*$^{-/-}$ cells across retinal cell types at 36,48,72, and 120hpf.

Table S5. DEGs between sibCTL and t*et2*$^{-/-}$;*tet3*$^{-/-}$ cells of each cell type at 120hpf.

Table S6. GO, KEGG, and REAC terms associated with upregulated sibCTL and *tet2*$^{-/-}$;*tet3*$^{-/-}$ genes for cones at 120 hpf, ShinyGO.

Table S7. Cluster-specific DEGs for pooled sibCTL and *tet2*$^{-/-}$;*tet3*$^{-/-}$ bipolar cells at 120hpf.

Table S8. AUCell scoring statistics for neuronal GO Terms across sibCTL and *tet2*$^{-/-}$;*tet3*$^{-/-}$ BC clusters at 120hpf.

Table S9. Cluster-specific DEGs for pooled sibCTL and *tet2*$^{-/-}$;*tet3*$^{-/-}$ horizontal cells at 120hpf.

Table S10. AUCell scoring statistics for neuronal GO Terms across pooled sibCTL and *tet2*$^{-/-}$;*tet3*$^{-/-}$ horizontal cell clusters at 120hpf.