

Figure S1. Spatial distribution of Iba1 and Chx10 staining of retinal sections from plx and inter groups

Panel C is a representative mouse retina from the plx28 group of rd10 mice that underwent 7-day plx3397 administration (350 ppm) starting at p21. The two treatments starting from the plx28 group resulted in two outcomes (plx groups to the left and inter groups to the right). The first row of panels (i) is the ciliary margin of a retina from each group, the second row of panels (ii) is the mid-peripheral portion of a retina from each group, and the third row of panels (iii) is the optic papilla or areas close to it for each group. Scale bar: 100 μ m.

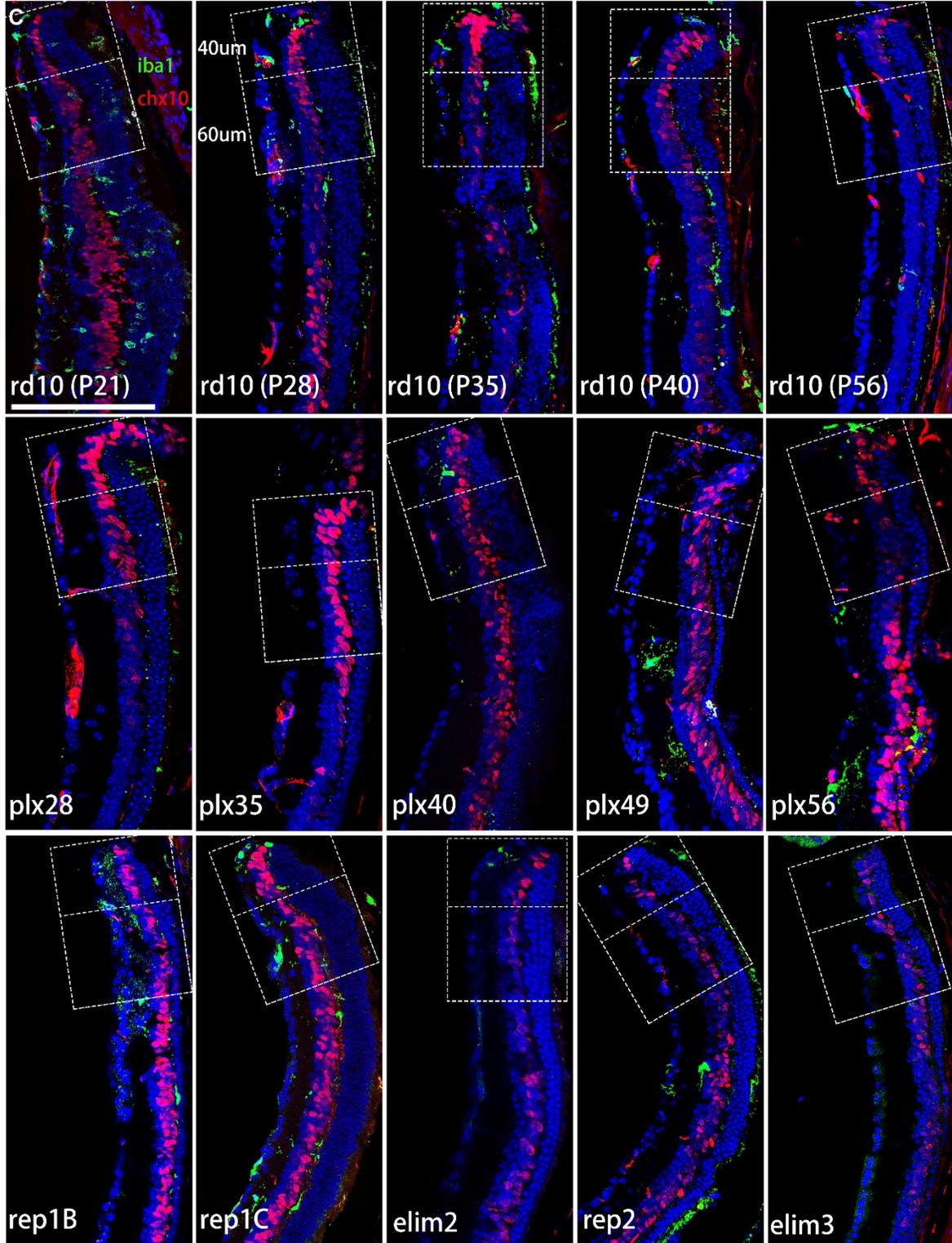
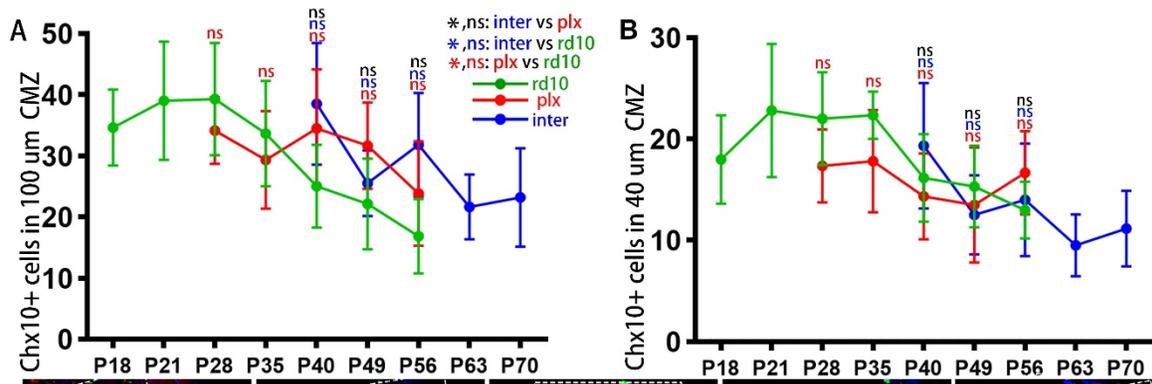


Figure S2. Chx10 + cell counts in the retinal CMZ

(A, B) Retinal sections were immune-stained, panoramic photographed, and tiled up for the rd10, plx, and inter groups. Chx10 + cells were counted in the ciliary marginal zone (100 μ m or 40 μ m ends of each retinal section) of each retina (rd10 green, plx red, inter, blue). (N = 3 mice, n = 2 images per mouse).

(C) Representative retinal sections from each of the three groups, with areas in the white box outlining the ciliary marginal zone.

Data are presented as the mean \pm SD. *P < 0.05; **P < 0.01; ns, No significance (one-way ANOVA). Red, blue, and black asterisks or ns represent differences in the significance of the data of the plx group vs the rd10 group, the inter group vs the rd10 group, and the inter group vs the plx group. Scale bar, 200 μ m (B).

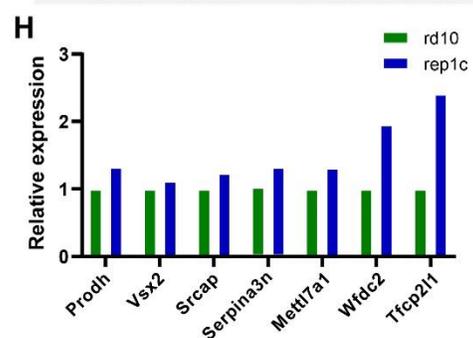
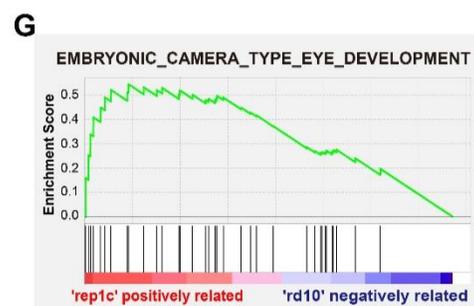
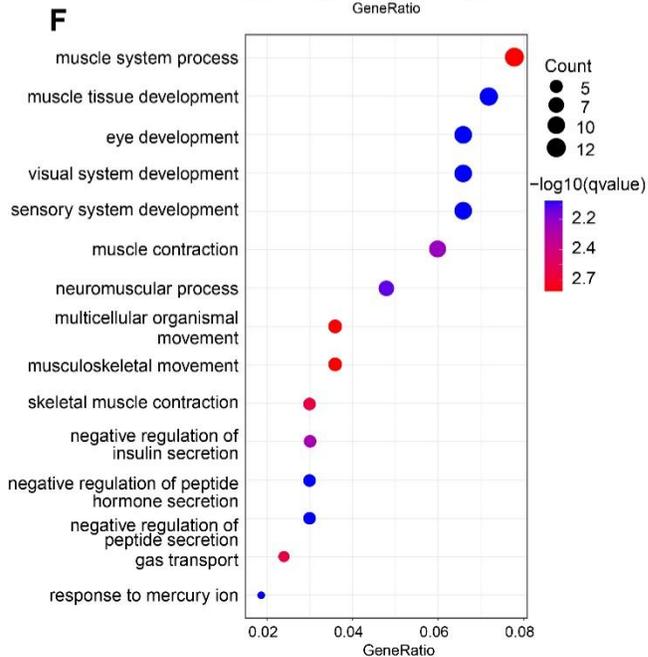
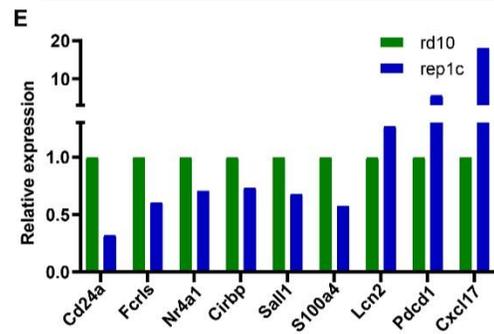
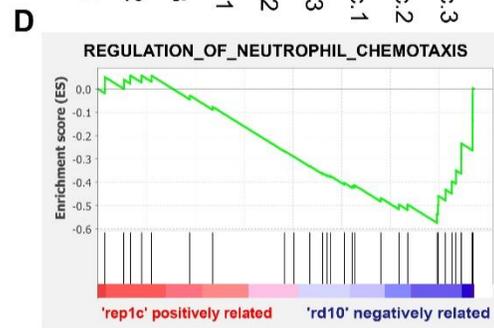
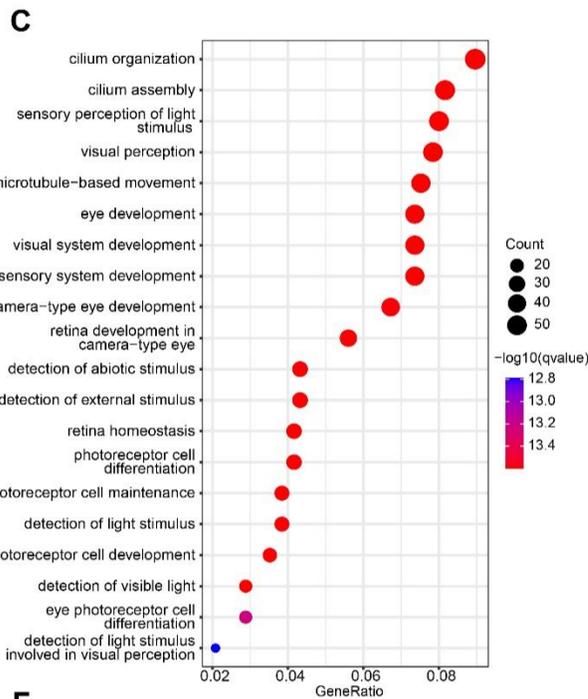
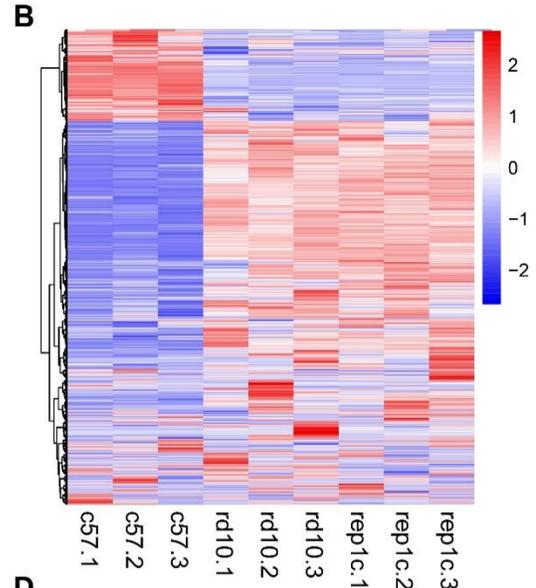
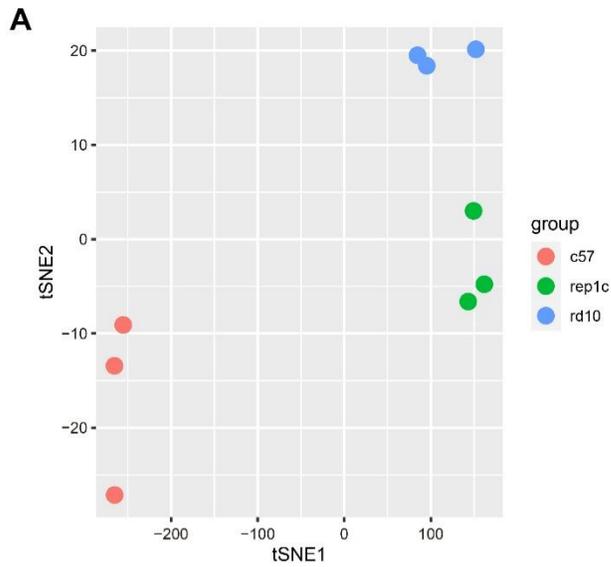


Figure S3. Transcriptomic sequencing in the c57, rd10 and rep1c groups

- (A) t-SNE plot showing the overall presentation of data in all three groups.
- (B) Expression of heatmap based on all genes in the c57, rd10, and rep1c groups
- (C) The 20 most significantly enriched items in the GO analysis of low expression genes in the rd10 group compared to the c57 group.
- (D) GSEA between the rep1c and rd10 groups showed enrichment of the regulation of neutrophil chemotaxis item.
- (E) FPKM relative expression of DEGs associated with inflammation (i.e., cd42a, Fcrls, and S100a4) and anti-inflammation (Lcn2, Pdccl1, Cxcl17) in the rd10 and rep1c groups.
- (F) The 15 most significantly enriched biological process items in the GO analysis of differentially expressed genes (DEGs) between the rd10 and rep1c groups.
- (G) GSEA between the rep1c and rd10 groups showed the enrichment of an embryonic camera-type eye development item.
- (H) FPKM relative expression of DEGs associated with neuroregeneration and stem cell maintenance in the rd10 and rep1c groups.