

Figure S1. Expression of *RBP-J* and Notch pathway-related genes in the retina.

(A,D) *RBP-J* mRNA in the retina at E11.5 (A) and E13.5 (D). (B-F) *Notch1* was expressed in the central part of the retina (B, E), while the *Notch3* expression domain covered the entire retina (C, F) at E11.5 (B, C) and E13.5 (E, F). (G-K) *Dll1* and *Jagged1* showed somewhat complementary patterns of expression, with *Dll1* mostly in the central areas of the retina (G, J) and *Jagged1* enriched in the periphery (H, K) at E11.5 (G, H) and E13.5 (J, K). (I) Sense *RBP-J* probe detects no *in situ* signal. Arrowheads (E, G, H, J, K) point to peripheral region of the retina. Scale bars, 100

μm.

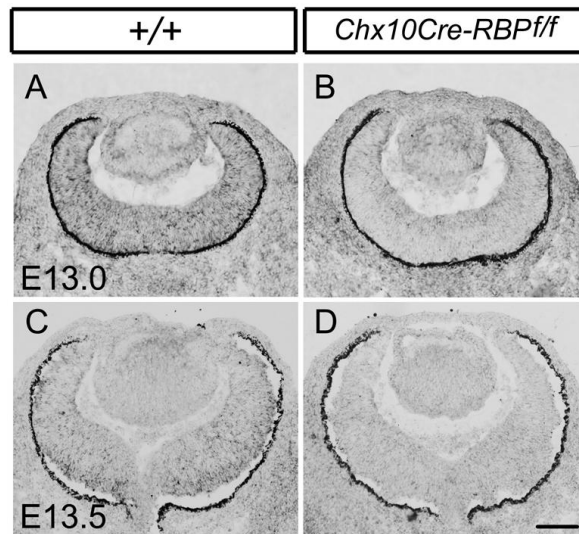


Figure S2. Effective inactivation of *RBP-J* in the retinae of *Chx10Cre-RBP^{ff}* mice. (A-D) *In situ* hybridization shows that *RBP-J* expression is reduced at E13.0, and almost completely lost by E13.5. Scale bar, 100 μm.

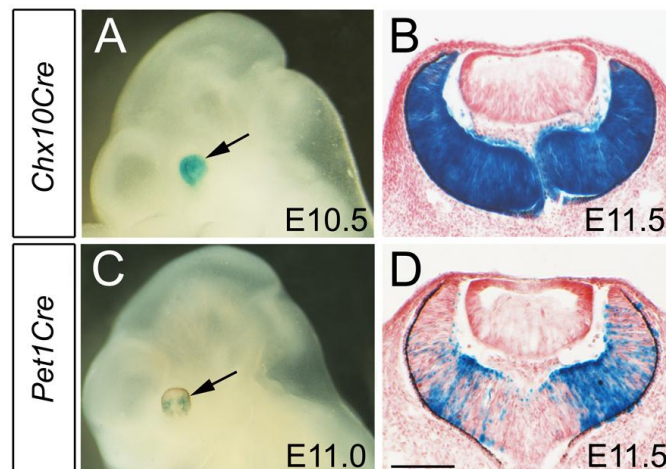


Figure S3. Comparison of Cre activity in the retina between *Chx10Cre* and *Pet1Cre* transgenic mice. (A-D) Cre activity initiates in the retina at approximately E10.5 in *Chx10Cre* mice (arrow in A), and at E11.0 in *Pet1Cre* mice (arrow in C), as shown by X-gal staining. Note that at E11.5, robust X-gal staining is observed throughout the retina of *Chx10Cre* mice (B), whereas X-gal staining in retinae of

E11.5 *Pet1Cre* mice is neither as strong, nor as uniform (D). Scale bar, 100 μ m.

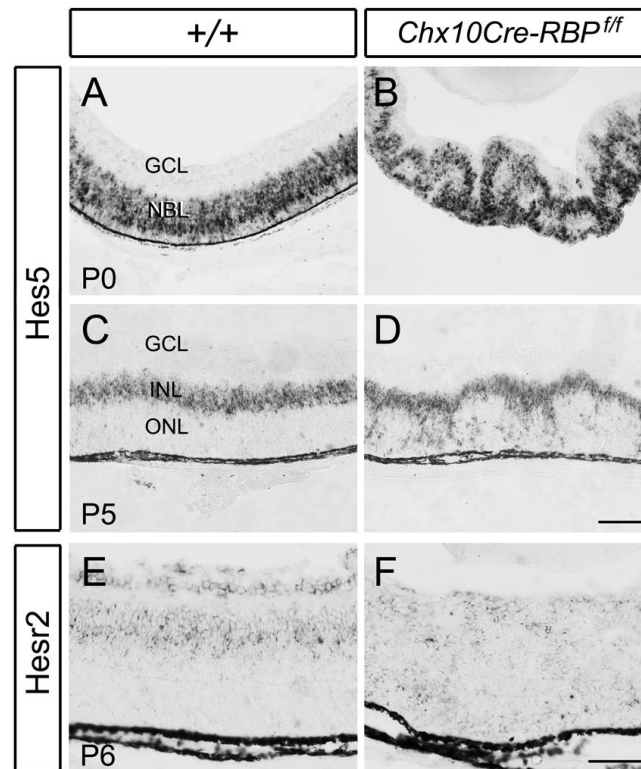


Figure S4. Expression of *Hes5* and *Hesr2* is maintained in *Chx10Cre-RBP^{ff}* retinae. (A-D) The mRNA level of *Hes5* is comparable in *Chx10Cre-RBP^{ff}* retinae to wild-type controls at P0 and P5. (E,F) Expression level of *Hesr2* remains similar in *RBP-J* deficient retinae at P6 relative to age-matched wild-type controls. GCL, ganglion cell layer; NBL, neuroblastic layer; INL, inner nuclear layer; ONL, outer nuclear layer. Scale bars, 100 μ m.

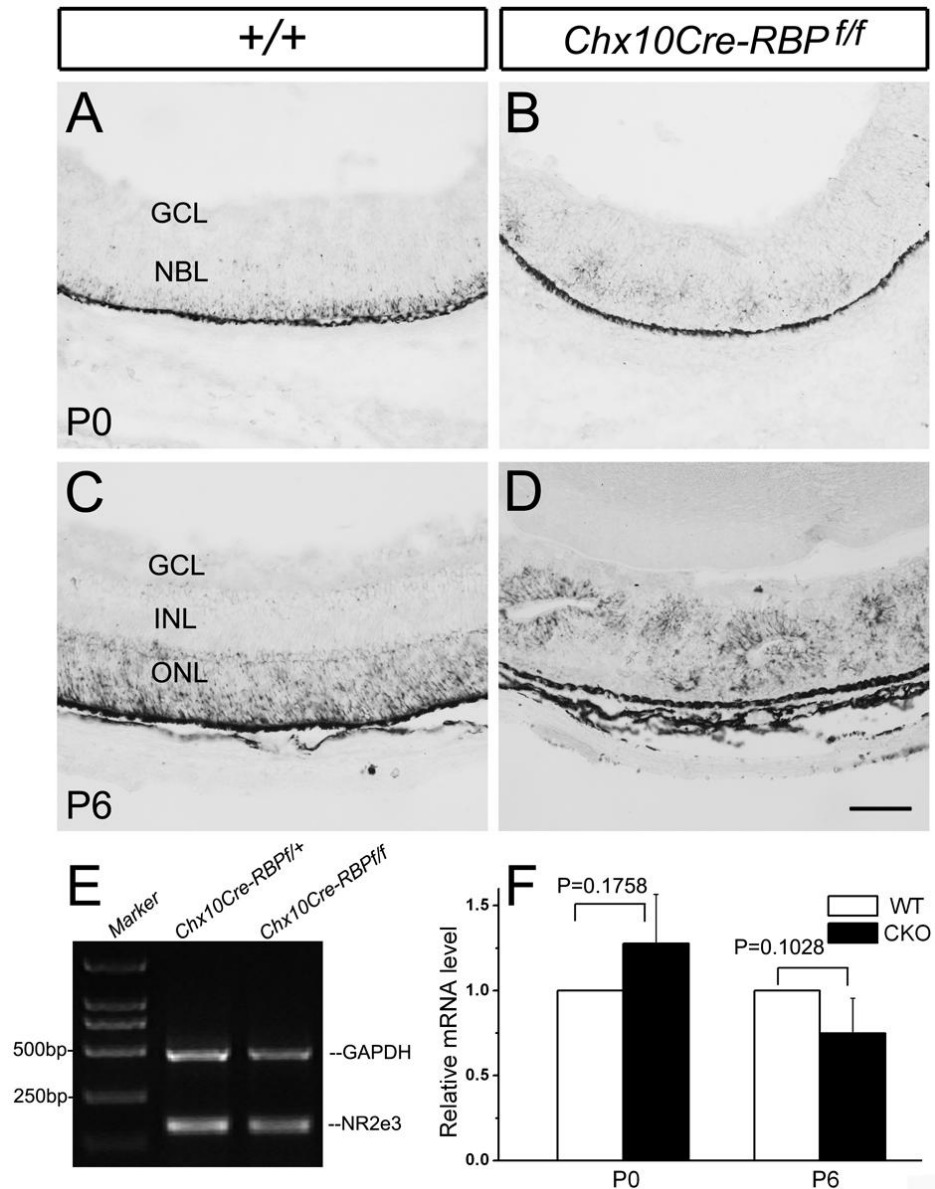


Figure S5. Expression of *NR2e3* appears to be unchanged in *Chx10Cre-RBP^{f/f}*

retinæ. (A-D) Expression level of *NR2e3* remains similar in *RBP-J* deficient retinæ at P0 (B) and P6 (D) compared to age-matched wild-type controls (A, C). (E,F) RT-PCR results show the specifically amplified *NR2e3* DNA fragment at 150 bp, and this pair of primer was used in real-time PCR. qPCR results indicate similar expression levels of *NR2e3* in wild-type and *RBP-J* deficient retinæ. GCL, ganglion cell layer; NBL, neuroblastic layer; INL, inner nuclear layer; ONL, outer nuclear layer.

Scale bar, 100 μ m.

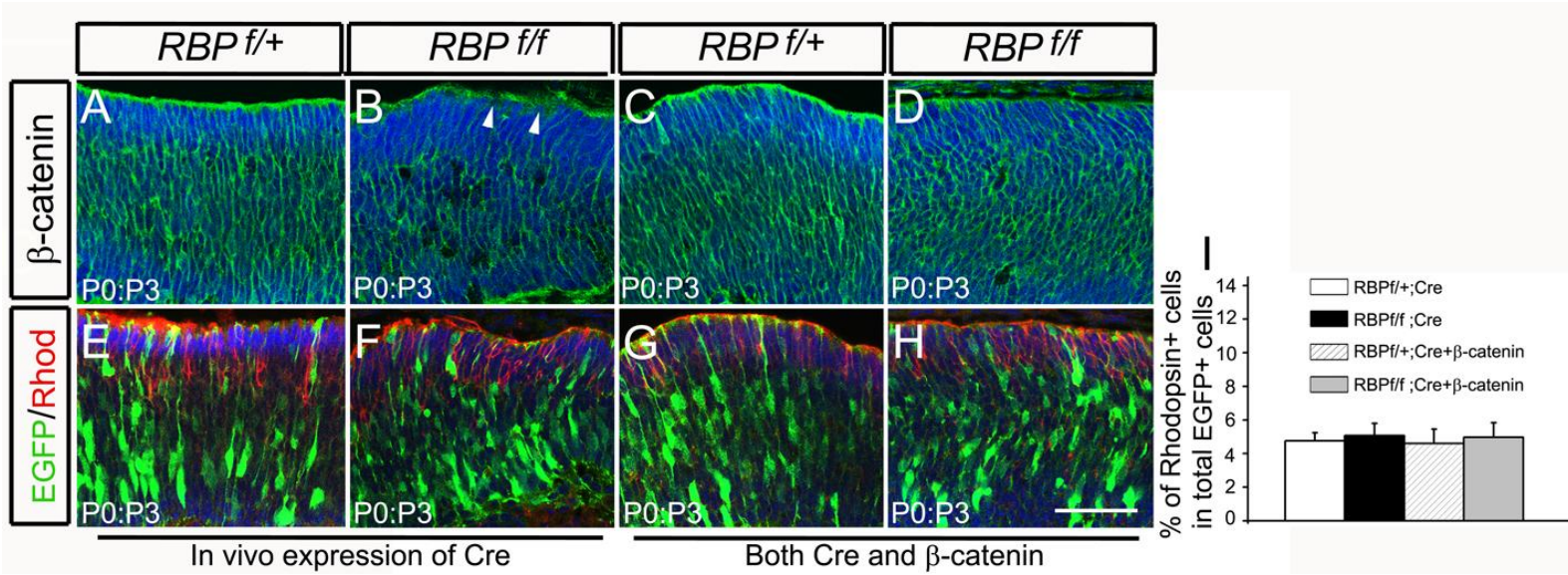


Figure S6. Cell type analysis of P0 electroporated retina at P3. (A-D) Apical β-catenin expression is disturbed in Cre-electroporated *RBP^{f/f}* retinæ (arrowhead in B) at P3 compared with that in *RBP^{f/+}* retinæ (A). Co-electroporation of β-catenin with Cre in *RBP^{f/f}* retinæ rescues the apical disturbance although the accumulation of β-catenin protein is still weak at this stage (D). (E-H) Double labeling on adjacent sections shows that a few EGFP⁺ cells differentiate into rhodopsin⁺ photoreceptors in both electroporated *RBP^{f/+}* and *RBP^{f/f}* retinæ at P3. Hoechst counterstaining is shown in blue. (I) Statistic result shows no significant difference between the percentages of rhodopsin⁺ photoreceptors in the total of EGFP⁺ cells in electroporated *RBP^{f/f}* and *RBP^{f/+}* retinæ. Scale bar, 100 μm.