

Figure S1. ERG analysis was performed on caChREBPRP mice at three time points: 20 dB, 0 dB, and 10 dB. Statistical significance (*t*-test) was assessed across groups: NS- non-significant; $p < 0.05$, $n = 3-6$ per group.

Figure S2. Quantitative spectrum counts for the proteomic analysis of caChREBPRP retinas.

Fig. S3. Ingenuity pathways significantly changed by ChREBP overexpression in rods of caChREBPRP mice. Upstream regulator MLXIPL/ChREBP had the highest positive Z score activating transcriptional program.

Figure S4. Quantitative spectrum counts for the proteomic analysis of the ARPE-19 cells overexpressing ChREBP.

Figure S5. A violin plot was generated using single-cell RNA-seq (scRNA-seq) data from the human retina, retinal pigment epithelium (RPE), and choroid, uploaded to the Spectacle database <https://singlecell-eye.org/app/spectacle>. This dataset was contributed by the Institute for Vision Research at the University of Iowa, based on studies conducted between 2019 and 2020.

Figure S6. A violin plot was generated using single-cell RNA-seq (scRNA-seq) data from the mouse retina uploaded to the Spectacle database <https://singlecell-eye.org/app/spectacle/>. This dataset was generated by the study titled “Molecular characterization of foveal versus peripheral human retina by single-cell RNA sequencing” by AP Voigt, SS Whitmore, MJ Flamme-Wiese, MJ Riker, LA Wiley, BA Tucker, EM Stone, RF Mullins, TE Scheet published in experimental eye Research in 2019.