Supporting Information

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SI Materials and Methods

Immunohistochemistry and Histological Analysis. Dissected retinas or retinal explants were fixed in cold 4% paraformaldehyde for 30–60 min at room temperature. The samples were rinsed in PBS and cryoprotected in 30% sucrose overnight at 4 °C. Samples were then embedded in O.C.T. (Sakura, Finetek) and quickly frozen using dry ice. Frozen samples were sectioned at 12 μm using a Leica CM 1850 cryostat. For immunofluorescence studies, cryosections were blocked in 10% Normal Goat Serum/0.5% Triton X-100 in PBS for 1 h and incubated overnight at 4 °C with primary antibodies in the same solution. Primary antibody dilutions were as follows: goat anti-Brn3 (1:300) (sc6026; Santa Cruz), mouse anti-Mash1 (1:200) (BD Pharmingen), mouse anti-RFP (1:500) (Abcam), rabbit anti-RFP (1:500) (Clontech), chicken anti-GFP (1:500) (Abcam), sheep anti-Prtg (1:100) (R&D Systems), rabbit anti-Lin28 (1:50) (sc-67266; Santa Cruz), sheep anti-Oncut2 (1:200) (R&D Systems), goat anti–Otx2-biotin (1:500,) (R&D Systems), and goat anti-Trim71 (Lin41) (1:100) (Santa Cruz). The sections were rinsed in PBS and incubated with appropriate fluorescent conjugated secondary antibodies (Invitrogen) in block solution for 1 h at room temperature. Cell nuclei were counterstained with DAPI. The sections were rinsed with PBS and mounted for microscopy.

MicroRNA Microarray. Whole RNA samples were labeled using the miRCURY LNA microRNA array labeling kit and hybridized onto miRCURY v.11.0 LNA microRNA Arrays (Exiqon) according to the manufacturer's instructions by the Genomics Resource DNA Array Laboratory at the Fred Hutchinson Cancer Research Center (Seattle, WA). This array contains probes for 613 mouse miRNAs, 851 human miRNAs, and 349 rat miRNAs, which represent coverage of miRBase v.13.0 of 96.2%, 89%, and 100%, respectively. It also contains probes for 428 "miRPlus" human miRNAs, proprietary miRNAs not included in the miRBase miRNA database. Because of the proprietary nature of these miRNAs, they have not been included in this analysis. For mean signal intensity, array data were normalized by local background subtraction, and the signal of the four probe spots was averaged. For intersignal comparison, array data were normalized by background subtraction, loess intraslide normalization, and scale interslide normalization using GEPAS (http://gepas.bioinfo.cipf.es; Department of Bioinformatics and Genomics, Principe Felipe Centro De Investigacion, Valencia, Spain). An arbitrary cutoff value for mean fluorescence intensity of 2,000 was used to determine real signal. Additional manual normalization was done for fluorescence values at postnatal day 1 (P1) by determining the mean signal of each condition, and multiplying each miRNA average signal intensity by this factor.

mRNA Microarray. After genotyping, FACS-sorted cells in Qiazol from several animals across two litters were pooled and processed. RNA was hybridized to an Affymetrix Mouse Gene ST 1.0 Array according to the manufacturer's protocols. Array hybridization and postprocess normalization were performed by the Institute for Systems Biology (Seattle, WA). Data analysis was performed in Microsoft Excel and Multiexperiment Viewer 4.6 Version 10.2 (Dana-Farber Cancer Institute).

RT-qPCR. mRNA Real-time PCR was performed as described in ref. 1. For miRNA RT, whole RNA was reverse transcribed in multiplex using custom designed stemloop reverse transcription primers as described previously (2) using SuperScript II RT and associated buffers (Invitrogen). For mRNA RT, RNA was reverse transcribed using oligo(dT) primers (Invitrogen) and SuperScript II RT following the manufacturer's protocols. qPCR was performed using SYBR Green PCR Mastermix (ABI) according to the manufacturer's protocols on an Opticon DNA Engine (Bio-Rad). Each sample was run in triplicate, with $n = 3$ for the number of samples. Statistical analysis on ΔCt values was performed using an unpaired two-tailed t test with Prism 4. Data are presented as mean ± SD. Product specificity was confirmed by agarose gel electrophoresis, and all positive signals were at least five cycles higher than RT controls.

RT primers are as follows: let-7a/f, CGCTACACGCTTGCGTGTTATTTCCTGATGGCGTGTAGCGAACTATACA; miR-9, AAATCGCAGCTGCAGGGTCCGAGGTATTCGGCTGCGATTTTCATACAG; miR-125, CGCTAGACGCTTGCGTGTTATTTCCTGATGGCGTGTAGCGTCACAGGT; miR-183, GGCTAGCAGCGATCAAGGGGCAGCACGTAGGCTGCTAGCCCGGTGTGAG.

PCR primers are as follows (gene, FW primer sequence, RV primer sequence): *beta-Actin*, FW, AGTGTGACGTTGACATCCGTA; RV, GCCAGAGCAGTAATCTCCTTCT; *let-7a*, FW, CGGCCTGAGGTAGTAGGTTG; RV, GCTTGCGTGTTATTTCCTGATGG; *let-7f*, FW, CGCCGCTGAGGTAGTAGATTG, RV, GCTTGCGTGTTATTTCCTGATGG; *miR-9*, FW, GCCGGTCTTTGGTTATCTAGC; RV, TGCAGGGTCCGAGGTATTCG; *miR-125b*, FW, CCGCTCCCTGAGACCCTAA; RV, CGAAGGAACTTGGGATATGACG; *miR-183*, FW GCGCCTATGGCACTGGTAGAA; RV, TGCAGGGTCCGAGGTATTCG.

FACS of Retinal Cells. Embryonic day (E)16 or E17 retinas were dissected in HBSS (Sigma), rinsed in calcium and magnesium free HBSS, and dissociated by trituration after incubation in 0.25% Trypsin-EDTA (Invitrogen). Cells were collected by centrifugation at 180 × g and resuspended in HBSS. Cells were sorted for YFP by flow cytometry using a BD Influx flow cytometer (Becton Dickinson) with 60 mW of 488-nm argon excitation and a bandpass filter of 525/30 nm. Cells were collected by centrifugation and placed in TRIzol (Invitrogen) or Qiazol and processed using the miRNeasy Mini Kit according to the manufacturer's instructions (Qiagen).

Western Blotting. Retinas were collected in lysis buffer (50 mM Tris [pH 7.5], 150 mM NaCl, 1.5 mM MgCl, 1 mM EDTA, 10% glycerol, and 1% Triton X-100) containing a protease inhibitor mixture (Roche). Lysates were then centrifuged at maximum speed for 20 min, and the pellet was discarded. Samples were run in a 4–20% Tris·HCl gel (Bio-Rad) at 100 V, after which they were transferred to a nitrocellulose membrane in 120 mM glycine, 125 mM Tris, pH 8.5, and 20% methanol. Filters were then saturated in 3% BSA in TBS and incubated with the antibodies overnight at 4 °C. Primary antibodies were as follows: sheep anti-Prtg (1:1,000) (R&D Systems), rabbit anti-Lin28 (1:2,000) (sc-67266; Santa Cruz), mouse anti-Ascl1 (1:1,000) (BD Pharmingen), and mouse anti–beta-Actin (1:10,000) (Abcam). The membranes were rinsed five times with TBS/0.5% tween and incubated for 1 h with appropriate HRP-conjugated secondary antibodies (Bio-Rad). Signals were exposed to X-ray films using the Immun-Star HRP Chemiluminescence Kit (Bio-Rad).

mRNA Production. To generate mRNA, we used pSLU plasmid as described previously (3). We used the Ambion mMessage

mMachine (AM1345; Ambion) according to the manufacturer's instructions. One microgram of linearized pSLU plasmid was added to a total reaction volume of 20 μL including 10 μL of ribonucleotides (2× NTP and ARCA:anti-reverse cap analog), 2 μL of 10× T7 reaction buffer, and 2 μL of T7 enzyme and RNase-free water and incubated at 37 °C for 2–2.5 h. The RNA was then tailed using E-PAP according to the manufacturer's directions, for 45 min, and then recovered by lithium chloride precipitation and isopropanol precipitation. Thirty to forty micrograms of RNA is a typical yield from a 20-μL reaction.

Electroporation. Retinas were dissected, and retinal explants were placed in an electroporation chamber filled with HBSS; the positive electrode was placed below the explant and the negative electrode above. The RNA was carefully added over the explant. Voltage was then applied: three 50-ms pulses of 40 V using an ECM 830 BTX electroporator. The explants were then returned to the tissue culture medium for up to 48 h.

Tissue Culture. Retinas from E14 or E16 mouse embryos were dissected free of surrounding ocular tissue and lens. Whole retinas were placed into 24-well plates and incubated for 1 or 2 d in DMEM/F12 (1:1, Invitrogen/Gibco) containing 10% heat-inactivated FBS and 10 ng/mL BDNF (R&D Systems).

Mimics and Antagomirs. miRIDIAN microRNA mimics as well as the miRIDIAN microRNA Hairpin Inhibitor antagomirs were purchased from Thermo Scientific.

1. Nelson BR, Hartman BH, Georgi SA, Lan MS, Reh TA (2007) Transient inactivation of Notch signaling synchronizes differentiation of neural progenitor cells. *Dev Biol* 304(2): 479–498.
2. Chen C, et al. (2005) Real-time quantification of microRNAs by stem-loop RT-PCR. *Nucleic Acids Res* 33(20):e179.
3. Hayashi T, Lamba DA, Slowik A, Reh TA, Bermingham-McDonogh O (2010) A method for stabilizing RNA for transfection that allows control of expression duration. *Dev Dyn* 239(7):2034–2040.

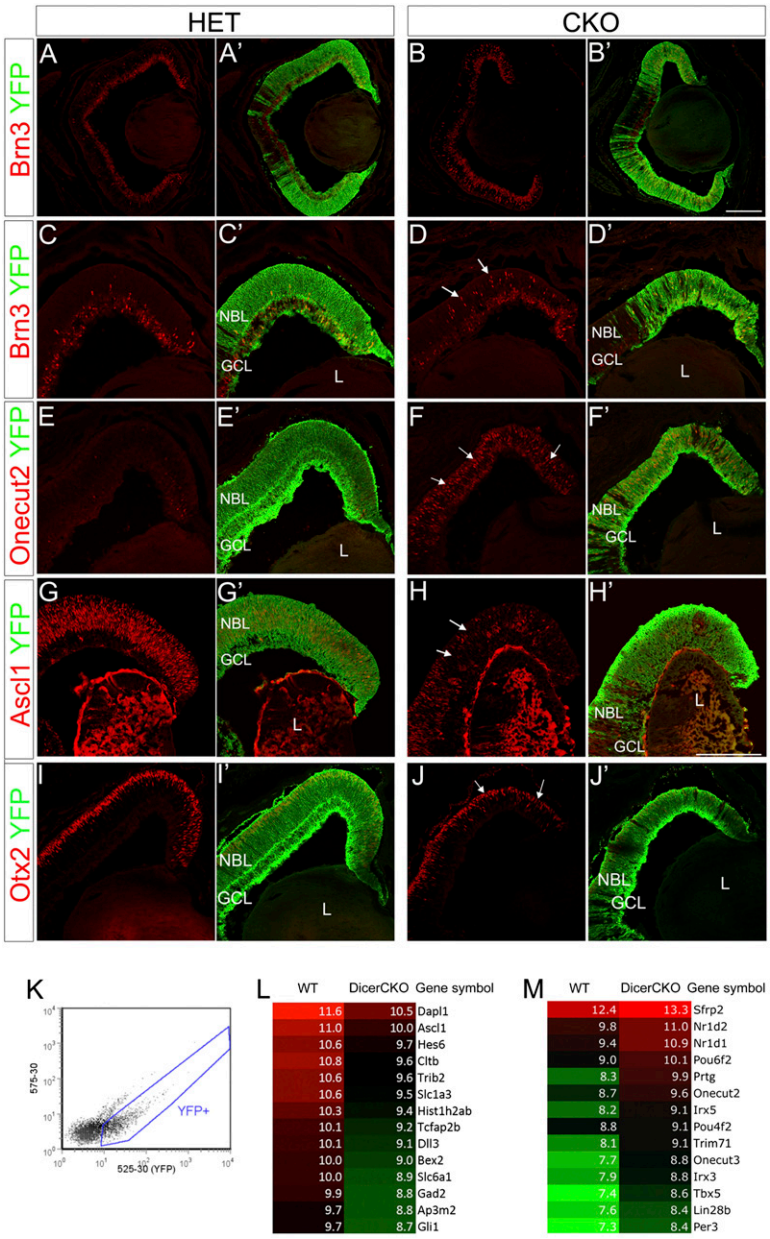

Fig. S1. Changes in Dicer conditional knockout (CKO) retinas. (*A*–*J*′) Dicer-depleted retinal areas generated supernumerary ganglion cells but did not express later progenitor markers. YFP staining (green) indicates areas of cre-mediated recombination and Dicer-CKO. POU class 4 homeobox2 (Brn3) staining (red, *A*–*D*′) in Dicer-HET (*A* and *A*′, *C* and *C*′) and Dicer-CKO E18 retinas (*B* and *B*′, *D* and *D*′) revealed an increase in Brn3+ ganglion cells in the Dicer-deficient areas (arrows, *D*). Similarly, there were more Onecut2+ cells (red) in Dicer-CKO areas (arrow, *F* and *F*′) compared with DicerHET controls (*E* and *E*′). Achaete-scute homolog 1 (Ascl1) immunofluorescence staining (red) in Dicer-HET (G and G′) and Dicer-CKO E18 retinas (H and H′). Note the deficiency of Ascl1 in Dicer-depleted regions (arrows, *H*). Photoreceptor marker orthodenticle homeobox 2 (Otx2) (red) was reduced in Dicer-CKO retinas (arrows, *J* and *J*′) compared with controls (*I* and *I*′). (*K*–*M*) Gene miRNA analyses. (*K*) Retinas from E17 Dicer-HET and Dicer-CKO littermate embryos were dissociated and sorted using FACS. (*L* and *M*) Normalized Affymetrix Mouse Gene ST 1.0 microarray data represented as green-black-red gradients showing the greatest down-regulated genes in Dicer-CKO cells (*H*) and the mostly highly up-regulated genes (*I*). (Scale bars: *A*–*B*′, 200 μm; *C*–*F*′, 100 μm.) NBL, neuroblastic layer; GCL, ganglion cell layer; L, lens.

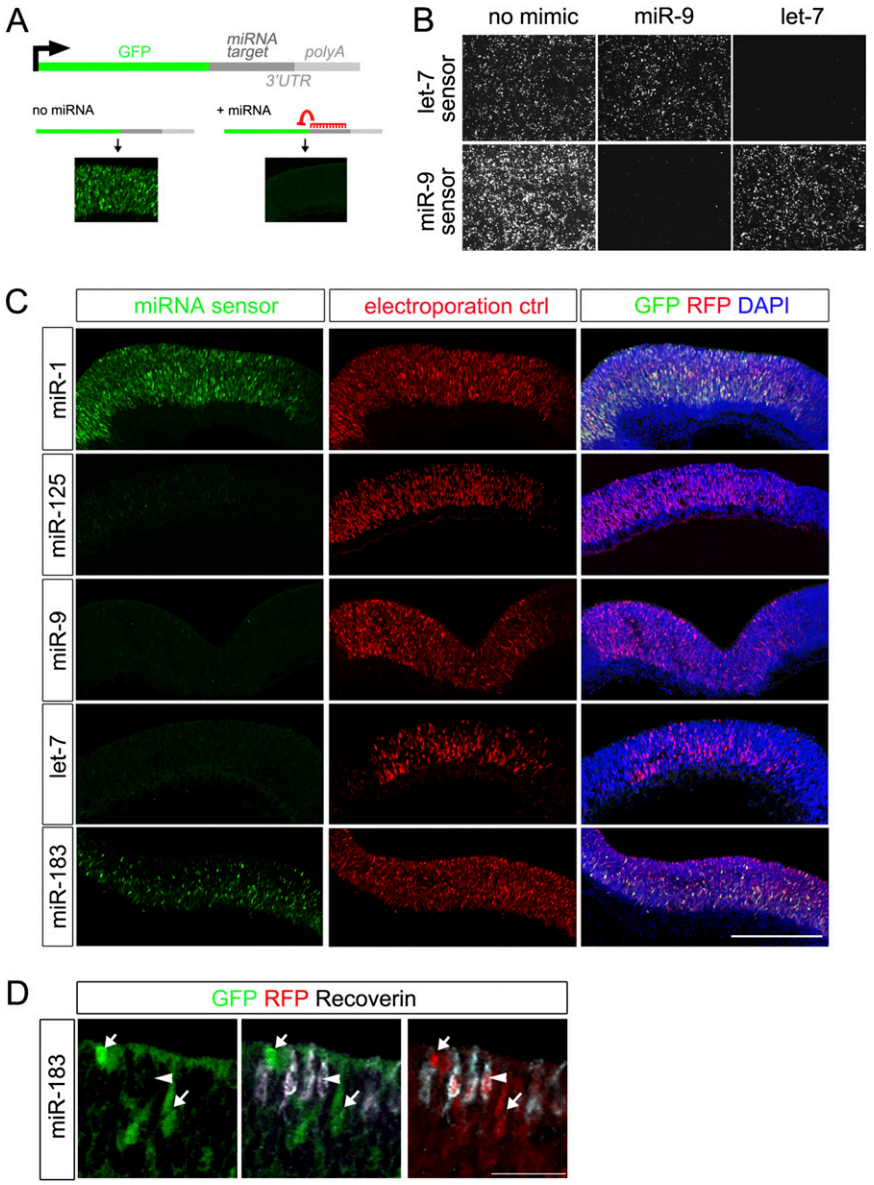

Fig. S2. miRNA expression patterns in P0 retinas. (*A*) Schematic representation of negative nGFP-based miRNA sensor constructs and mechanism. (*B*) miRNA sensors are specific. GFP expression analyses of HEK 293T cells transfected with miRNA sensors for microRNA-9 (miR-9) or let-7a alone or along with miR-9 or let-7 mimics. GFP expression was elevated after 24 h of transfection and reduced after transfection with the corresponding mimic only. (*C*) P0 retinal explants were electroporated with nCherry (electroporation control, red) together with GFP-based sensors for miR-1, miR-125b, miR-9, let-7a, or miR-183 and cultured for 24 h. GFP and nCherry expression were analyzed by immunofluorescence. (Scale bar: 200 μm.) (*D*) GFP-based miRNA sensors allow the detection of miRNA expression at cell resolution. In vivo electroporation of the mouse P0 retinal explants with an miR-183 sensor together with nCherry showed a specific degradation of GFP in Recoverin+ photoreceptors (arrow heads) whereas GFP was expressed in Recoverin cells (arrows). (Scale bar: 50 μm.)

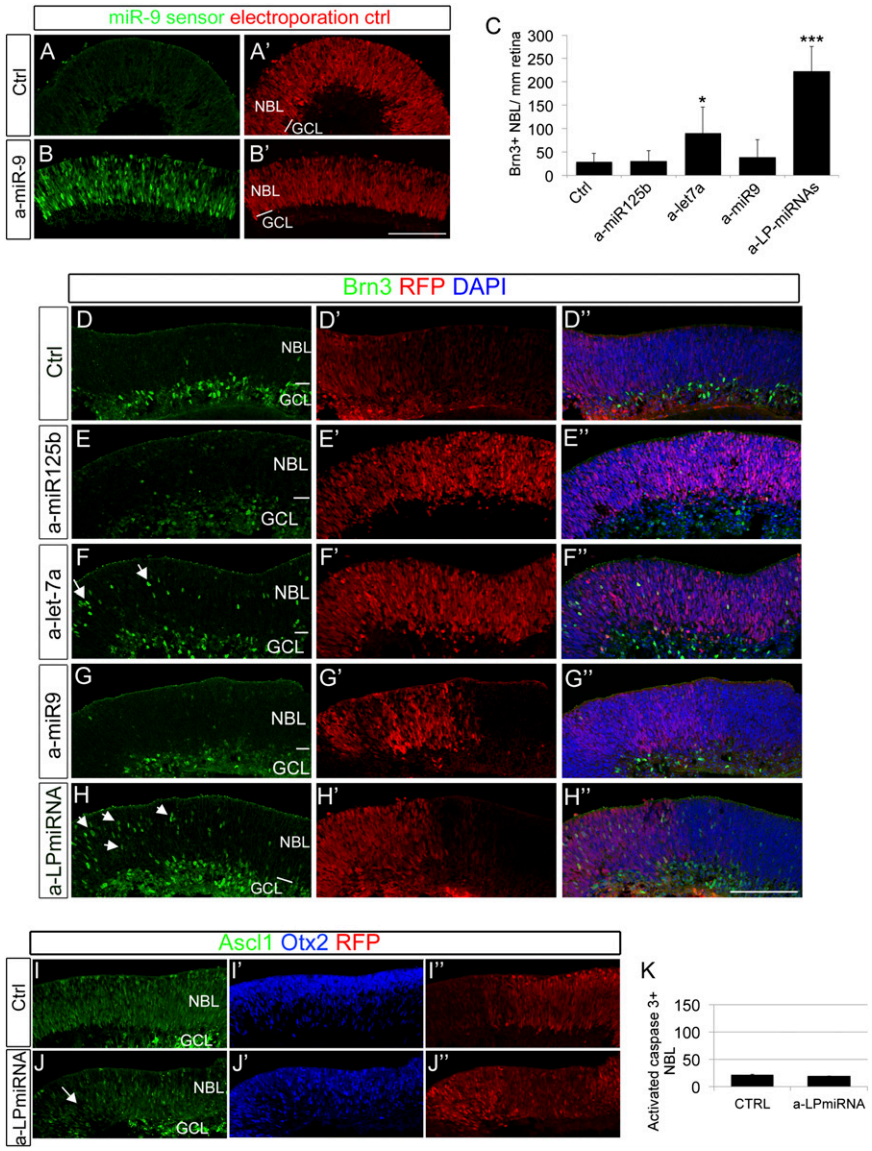

Fig. S3. Late progenitor microRNA (LP-miRNA) loss-of-function. (*A*–*B*′) Antagomirs (small engineered RNA oligonucleotides) are specific silencers of endogenous miRNAs. P0 retinal explants were electroporated with nCherry (electroporation control, red) together with the GFP-based sensors for miR-9 (*A* and *A*′) or with the miR-9 sensor together antagomir against miR-9 (*B* and *B*′). (*C*–*H*′′) Silencing of endogenous LP-miRNAs resulted in an overproduction of ganglion cells. E16 wild-type retinas were electroporated with nCherry together with antagomirs for the different LP-miRNA alone or in combination and labeled with Brn3 (green) and red fluorescent protein (RFP) (red) antibodies. Brn3+ ganglion cells increased in the neuroblastic layer after LP-miRNA inhibition (arrow, *F* and *H*). Ascl1 (green) and Otx2 (blue) were also reduced after LP-miRNA inhibition (I–I′′) compared with control explants (J–J′′). (*K*) There was no significant increase in cell death in the neuroblastic layer after LP-miRNA inhibition in E16 retinas. Error bars indicate mean ± SEM. *P* values: *<0.05; ***<0.001. (Scale bar: 200 μm.)

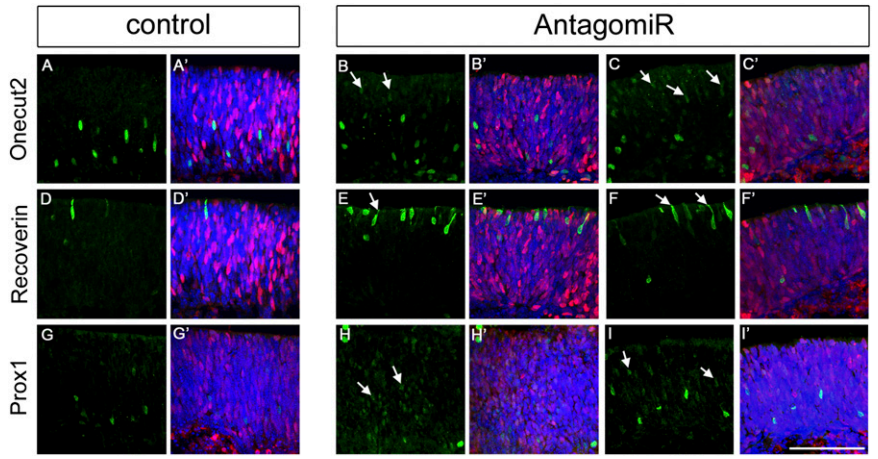

Fig. S4. Silencing of endogenous LP-miRNAs with antagomirs resulted in an overproduction of ganglion cells, horizontal cells, and cone photoreceptors at E16. E16 wild-type retinas were electroporated with nCherry together with antagomirs for LP-miRNA and labeled with Onecut2 (green, *A*–*C*′), Recoverin (green, *D*–*F*′), and Prox1 (green, *G*–*I*′) and RFP (red, *A*–*I*′) antibodies. Onecut2 (*B* and *C*), Recoverin+ photoreceptors (*E* and *F*) and Prox1+ horizontal cells (*H* and *I*) increased in the neuroblastic layer after LP-miRNA inhibition (arrows).

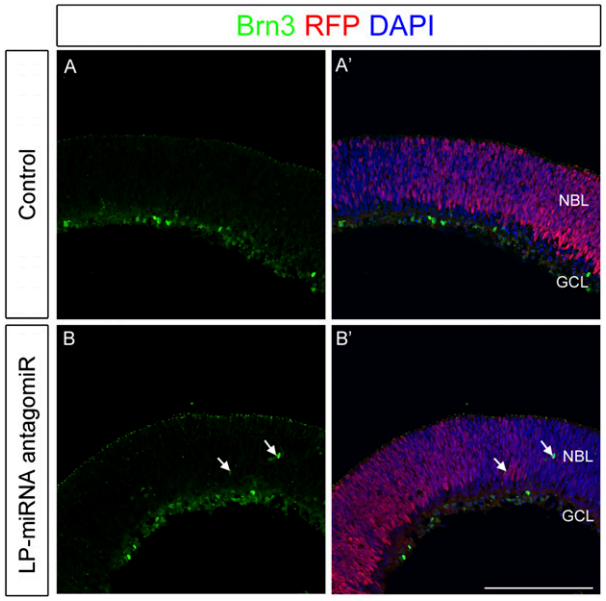

Fig. S5. LP-miRNA antagomirs did not show a robust effect at P1 retinal explants. P1 retinal explants were electroporated with control nCherry mRNA alone (*A* and *A*′) or together with LP-miRNA antagomirs (*B* and *B*′). Only a few Brn3+ cells were observed in the NBL after LP-miRNA inhibition (arrows). NBL, neuroblastic layer; GCL, ganglion cell layer. (Scale bar: 200 μm.)

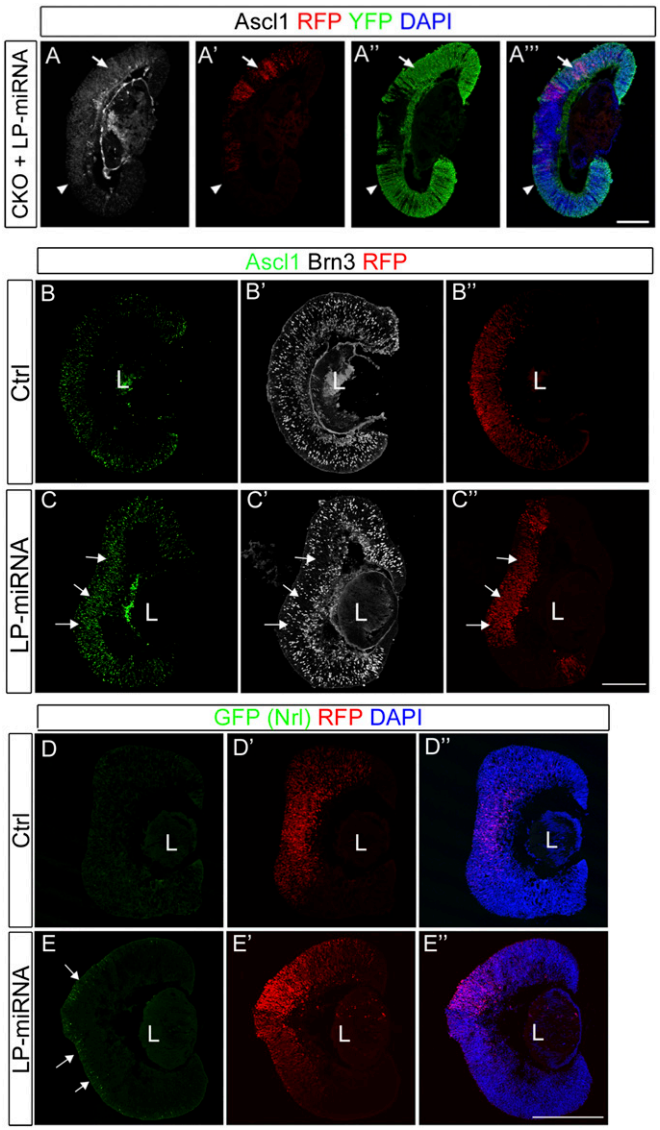

Fig. S6. (*A*–*A*′′′) miR-125, let-7, and miR-9 can rescue the Dicer-CKO phenotype. LP-miRNA electroporation in Dicer-CKO retinas rescued Ascl1 expression. Ascl1 (white) was expressed in the wild-type regions of the retina (YFP–) but absent in Dicer-deficient regions (YFP+) (arrowhead). Coelectroporation of LP-miRNA together with nCherry (red) rescued Ascl1 expression in Dicer-depleted areas (arrow in *A*). (*B*–*E*′′) LP-miRNA transfection accelerates development in normal retina. Brn3 (white, *B*′ and *C*′) and Ascl1 (green, *B* and *C*) in E14 retinas transfected with control mimics (*B*–*B*′′) or LP-miRNA (*C*–*C*′′) together with nCherry (red). (*D*–*E*′′) LP-miRNAs increased the number of neural retina leucine zipper (Nrl)+ photoreceptors in Nrl-GFP E14 retinal explants. NBL, neuroblastic layer; GCL, ganglion cell layer; L, lens.

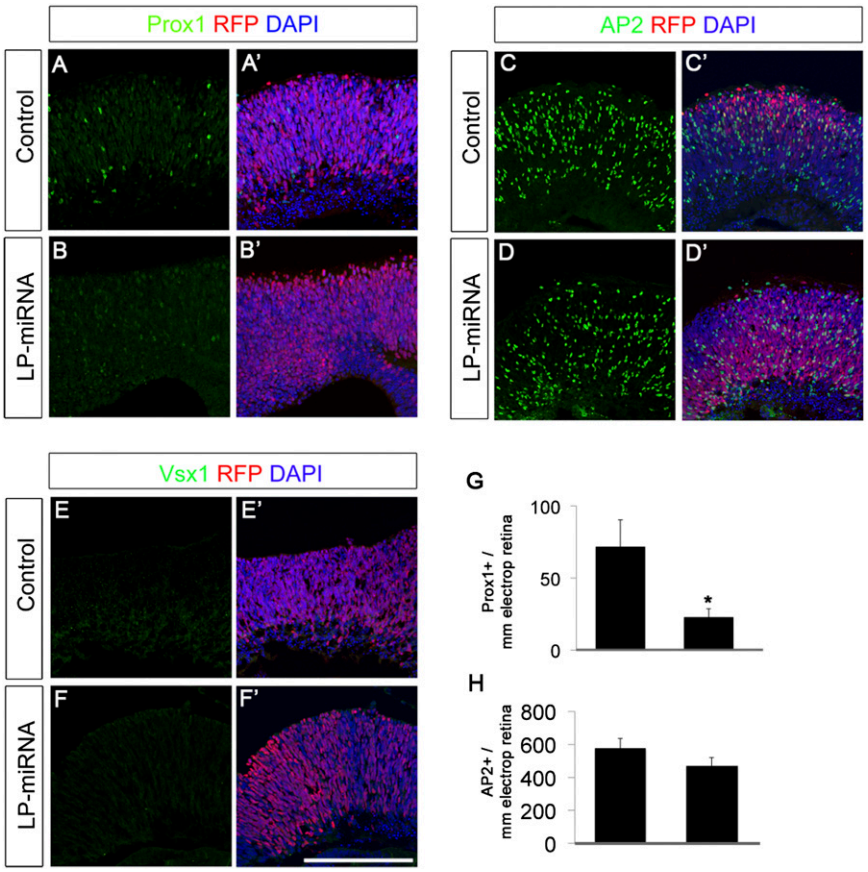

Fig. S7. (*A*–*H*) LP-miRNA electroporation reduced the number of Prox1+ horizontal cells in E14 retinal explants in E14 retinal explants but did not affect amacrine or bipolar cells. Prox1 (green, *A* and *B*), AP2 (green, *C* and *D*), and Vsx1 (green, *E* and *F*) in E14 retinas transfected with control mimics (*A* and *A′*, *C* and *C′*, *E* and *E′*) or LP-miRNA (*B* and *B′*, *D* and *D′*, *F* and *F′*) together with nCherry (red). Error bars indicate mean ± SEM. *P* values: *<0.05. NBL, neuroblastic layer; GCL, ganglion cell layer. (Scale bar: 100 μm.)

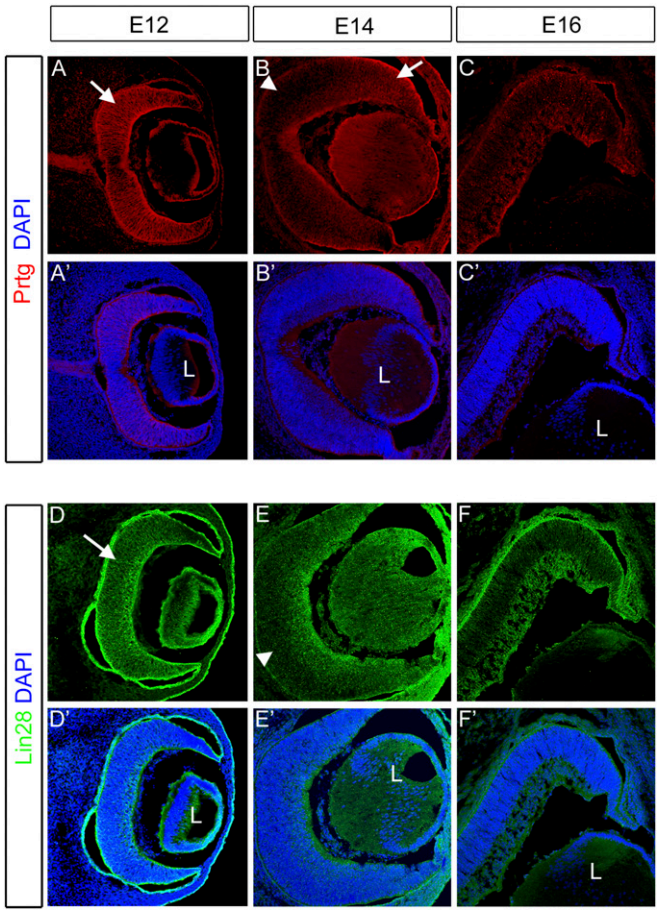

Fig. S8. Protogenin (red, *A*–*C*′) and Lin28b (green *D*–*F*′) stainings in E12, E14, and E16 retinas. Note the high levels of expression of Prtg and Lin28b at E12 (arrow in *A* and *D*). E14 retinas revealed a down-regulation in these proteins in the central retina (arrow heads in *B* and *E*). L, lens.

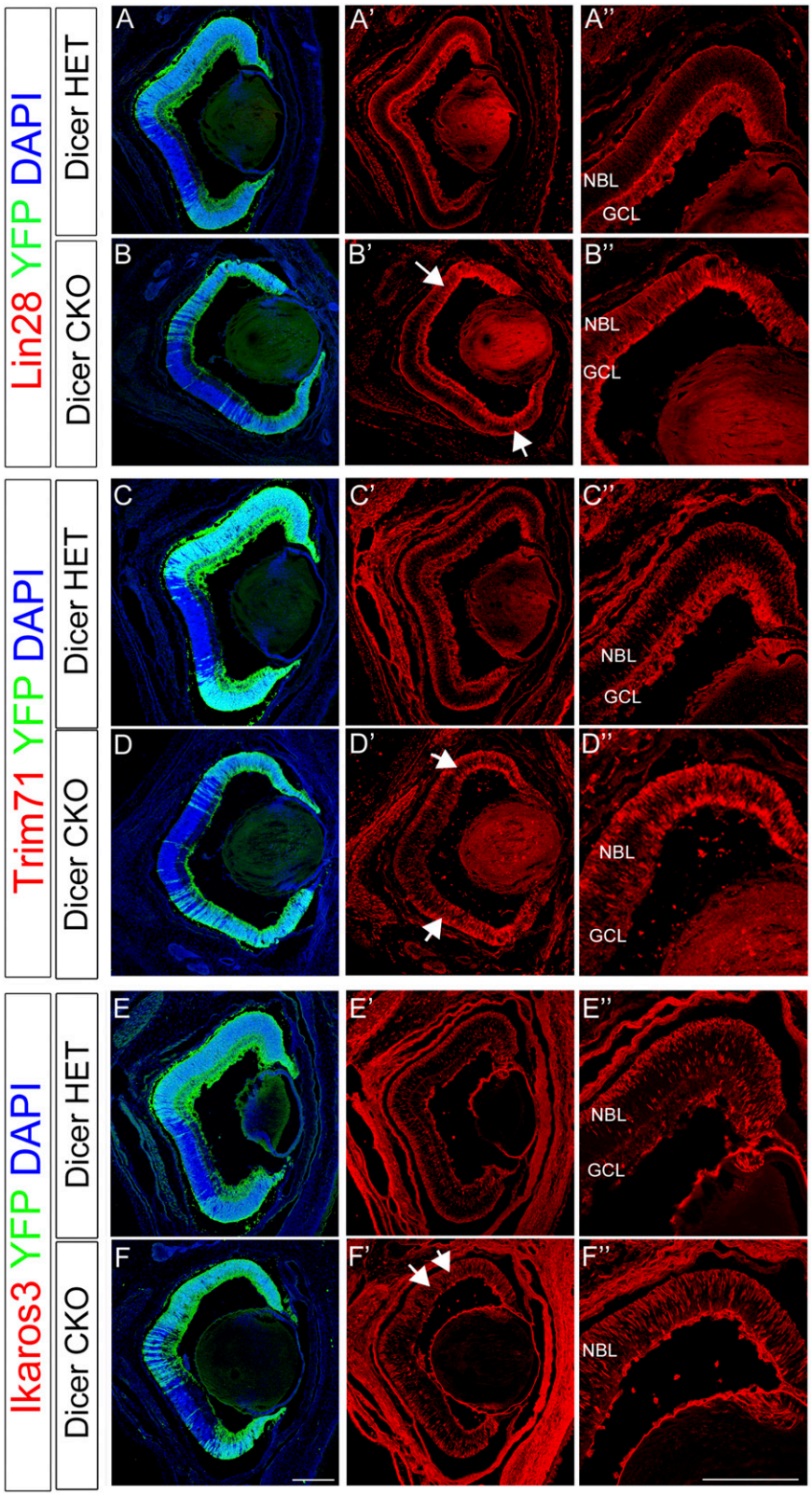

Fig. S9. Lin28, Trim71, and Ikaros3 were up-regulated after Dicer-CKO. (*A*–*B*′′) YFP staining (green) indicates areas of cre-mediated recombination and Dicer-CKO. Lin28 staining (red, *A*′ and *B*′) in Dicer-HET (*A*–*A*′′) and Dicer-CKO E18 retinas (*B*–*B*′′) revealed an increase in Lin28 protein in Dicer-deficient areas (arrows, *B*′). Trim71 immunofluorescence staining (red) in Dicer-HET (*C*–*C*′′) and Dicer-CKO E18 retinas (*D*–*D*′′). Note the up-regulation of Trim71 in Dicer-depleted regions (arrows, *D*′). Ikaros3 (red) was up-regulated in Dicer-CKO retinas (arrows, *F*′) compared with controls (*E*′). (Scale bar: 200 μm.) NBL, neuroblastic layer; GCL, ganglion cell layer; L, lens.

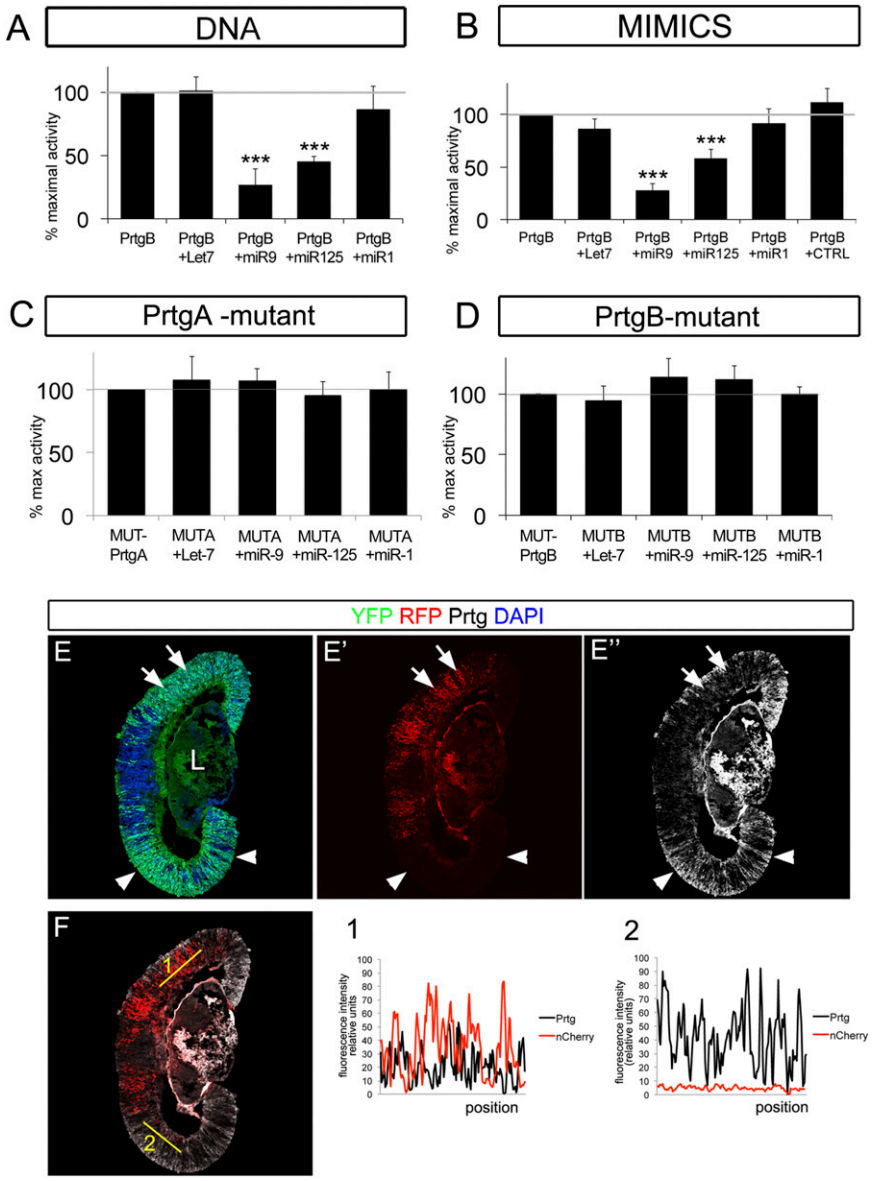

Fig. S10. Prtg is a target of LP-miRNAs. (*A*–*D*) The luciferase reporter constructs were cotransfected, together with control vectors, with miRNA expression constructs (*A*, *C*, and *D*) or with miRNA mimics (*B*) in HEK293T cells. Firefly luciferase activity was measured and normalized with Renilla luciferase activity in the same well. Data are expressed as percentage of induction relative to control. Values are mean ± SD of four independent experiments. (*E* and *F*) Endogenous Prtg protein (white) in Dicer-CKO retinas transfected with LP-miRNA together with nCherry (red). YPF staining (green) indicates areas of cre-mediated recombination. Graphs *1* and *2* are line scan measurements for nCherry (red) and Prtg (black) represented as fluorescence intensity (arbitrary units). Note the reduction in Prtg intensity in LP-miRNA electroporated areas (arrows).

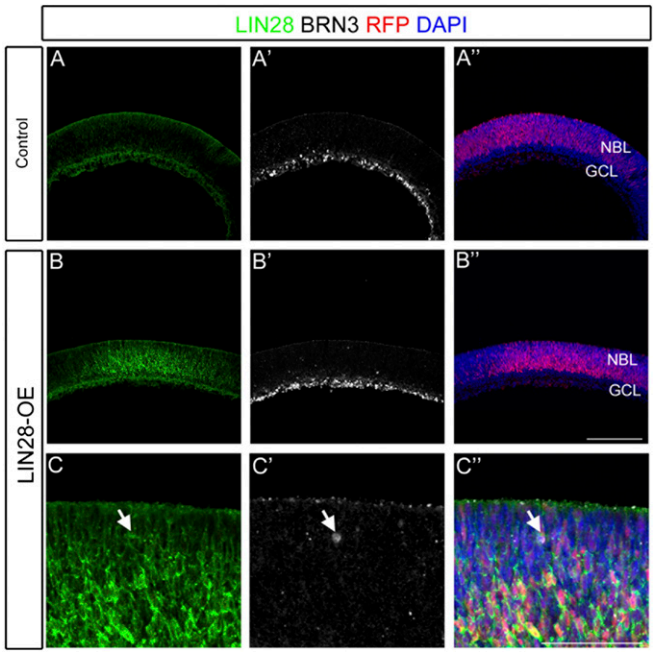

Fig. S11. Lin28b overexpression (OE) in P1 retinal explants. nCherry mRNA (red) alone or together with Lin28b mRNA (green) was electroporated in retinal explants (*A*–*C*′′). Only a small number of Brn3+ ganglion cells (white) were detected in the neuroblastic layer after Lin28 overexpression (arrows in *C*–*C*′). NBL, neuroblastic layer; GCL, ganglion cell layer. (Scale bars: *A*–*B*′′, 200 μm; *C*–*C*′′, 50 μm.)

Table S1. Genes with greatest upregulation in Dicer CKO retinas

WT signal	Dicer CKO signal	Fold change	Gene symbol
8.19	10.87	6.43	Mt2
7.14	8.86	3.30	Polr3g
8.25	9.90	3.14	prtg
9.40	10.93	2.88	Nr1d1
9.01	10.49	2.78	Tom1l1
8.59	10.01	2.67	Gm73
7.08	8.45	2.59	Lpp
7.66	9.02	2.57	Vtn
7.23	8.58	2.54	Th
8.57	9.91	2.53	Slc38a4
7.02	8.32	2.46	Ano5
9.17	10.45	2.43	Ret
8.15	9.41	2.40	Ubash3b
10.17	11.43	2.39	Crabp1
10.40	11.65	2.38	Anxa5
7.38	8.63	2.38	Tbx5
7.74	8.99	2.38	Bche
9.17	10.40	2.35	Ankrd52
8.59	9.80	2.32	Crhbp
9.77	10.97	2.30	Nr1d2
7.76	8.91	2.22	Lgr5
9.45	10.59	2.20	Hipk3
7.85	8.98	2.19	Col1a2
9.10	10.21	2.17	Slc25a24
8.98	10.09	2.16	Pou6f2
8.77	9.87	2.14	Rragd
7.06	8.14	2.12	Oasl2
7.75	8.83	2.11	Onecut3
7.74	8.81	2.09	Slc9a9
8.59	9.65	2.09	Zbtb20
8.32	9.38	2.07	Ak3l1
8.30	9.35	2.07	Gsbs
8.43	9.46	2.04	Man2a1
7.24	8.27	2.04	Map3k5
7.64	8.65	2.03	Gja1
7.35	8.36	2.02	Per3
8.03	9.04	2.02	Stk32a
8.58	9.59	2.01	Col4a1
10.13	11.14	2.01	Pam
8.25	9.26	2.01	Igdcc3
7.51	8.52	2.00	Clec18a
9.20	10.20	1.99	Zbtb16
8.07	9.06	1.99	Trim71
8.06	9.05	1.99	Mylip
7.57	8.56	1.99	Mtap7d2
9.17	10.15	1.98	Zfp568
7.82	8.80	1.98	Dusp9
9.65	10.63	1.98	Reck
8.86	9.84	1.96	Slc6a15
7.91	8.88	1.96	Pdzd2
7.92	8.88	1.94	Dbp
9.18	10.13	1.94	Bcl2l11
7.07	8.02	1.93	Alpk1
10.03	10.98	1.93	Tnrc6a
10.24	11.19	1.93	Uhmk1
8.64	9.59	1.92	Ezr
8.67	9.61	1.92	Onecut2
7.16	8.10	1.92	Slc16a12
8.52	9.45	1.90	Car14
8.89	9.81	1.90	Akap6
9.06	9.98	1.89	Atp7a
7.84	8.75	1.88	Fbn1
9.59	10.50	1.88	Magt1

Table S1. Cont.

WT signal	Dicer CKO signal	Fold change	Gene symbol
7.85	8.75	1.87	Gm626
12.43	13.33	1.87	Sfrp2
9.03	9.92	1.85	Mt1
8.24	9.13	1.85	Irx5
9.57	10.45	1.84	Mbc2
8.83	9.70	1.84	Cmtm6
8.54	9.42	1.83	Ak3l1
9.34	10.21	1.82	Atl3
7.91	8.77	1.82	Irx3
7.80	8.65	1.81	Clmn
9.04	9.89	1.81	Itgav
9.10	9.95	1.81	Tes
9.25	10.10	1.80	Ptprk
8.58	9.42	1.80	Stra6
9.56	10.40	1.79	Styx
7.44	8.28	1.79	Lancl3
8.91	9.75	1.79	Usp44
9.44	10.27	1.78	Txnip
9.17	9.99	1.76	Foxp1
9.82	10.64	1.76	Fbn2
10.04	10.86	1.76	Elavl4
7.64	8.44	1.74	Lin28b
7.96	8.75	1.73	Unc5a
8.71	9.50	1.73	Sgcb
8.79	9.58	1.73	Cyp1b1
7.69	8.48	1.72	Gm626
10.19	10.97	1.72	Emb
9.76	10.55	1.72	Cacna2d1
8.75	9.53	1.72	Spg20
11.12	11.89	1.71	Aldh1a1
7.49	8.26	1.70	Pmfbp1
8.37	9.13	1.70	Cald1
9.15	9.92	1.70	Onecut1
7.63	8.40	1.70	A2m
7.56	8.32	1.70	Fst
7.60	8.36	1.70	Gm626
8.09	8.85	1.69	Obfc2a

Table S2. Genes with greatest downregulation in Dicer CKO retinas

WT signal	Dicer CKO signal	Fold change	Gene symbol
9.25	7.09	0.22	Fabp7
8.99	6.94	0.24	Cbln2
9.51	7.54	0.25	Eomes
6.48	4.76	0.30	Tac1
9.87	8.19	0.31	Rgs4
7.11	5.43	0.31	Slitrk6
8.66	7.00	0.32	Igf1
6.69	5.23	0.36	B930036N10Rik
9.60	8.15	0.37	Rrh
6.99	5.55	0.37	Glra2
9.28	7.95	0.40	Etv5
9.60	8.30	0.41	Isl2
8.66	7.36	0.41	Tcfap2a
8.72	7.44	0.41	Cacng3
9.70	8.42	0.41	Dusp4
8.16	6.90	0.42	Chrnb3
8.51	7.28	0.43	Dlg2
10.80	9.60	0.43	Cltb
9.33	8.13	0.43	Hhip
8.92	7.73	0.44	Csdc2
8.22	7.03	0.44	Slc10a4
8.60	7.42	0.44	Gria2
9.44	8.26	0.44	Vcan
9.24	8.08	0.45	Car2
9.69	8.53	0.45	Rnd2
9.95	8.80	0.45	Gad2
10.01	8.87	0.45	Slc6a1
9.61	8.46	0.45	Ier5
8.14	7.00	0.45	Grik3
9.78	8.64	0.45	Etv5
10.62	9.52	0.47	Slc1a3
8.78	7.69	0.47	Mdga2
6.70	5.61	0.47	Mgat4c
11.56	10.48	0.47	Dapl1
9.22	8.14	0.47	Socs2
9.10	8.02	0.47	Rabl4
5.82	4.74	0.48	Ppef1
5.94	4.88	0.48	Pcdhb9
6.90	5.85	0.48	Gabrb2
7.37	6.32	0.48	Gjd2
8.52	7.47	0.48	Fgf12
8.77	7.72	0.48	D10Ertd322e
7.72	6.68	0.49	Zmat4
9.72	8.68	0.49	Rgs2
8.86	7.82	0.49	B230399E16Rik
7.95	6.92	0.49	EG620782
9.04	8.01	0.49	Krt73
7.63	6.60	0.49	1810027O10Rik
6.97	5.94	0.49	Hfm1
10.62	9.59	0.49	Trib2
9.18	8.17	0.50	Gsta4
8.93	7.93	0.50	1810035L17Rik
7.49	6.49	0.50	Fstl5
9.99	9.00	0.50	Bex2
7.78	6.79	0.50	Pcdhb17
8.78	7.79	0.51	Crym
8.56	7.57	0.51	Fam19a1
9.55	8.57	0.51	Pou4f1
9.00	8.03	0.51	2610021K21Rik
10.96	9.99	0.51	Ascl1
9.72	8.75	0.51	Gli1
5.74	4.78	0.51	—
8.76	7.80	0.51	AI593442

Table S2. Cont.

WT signal	Dicer CKO signal	Fold change	Gene symbol
9.00	8.04	0.51	Bai2
8.18	7.22	0.52	EG640050
4.95	4.00	0.52	Vmn2r43
6.14	5.19	0.52	—
8.41	7.46	0.52	Spa17
9.33	8.39	0.52	Ndufa1
7.69	6.75	0.52	Stk32b
8.48	7.54	0.52	D030028M11Rik
8.98	8.05	0.52	Kbtbd11
9.62	8.69	0.52	Lmo2
7.65	6.72	0.52	Lrfn5
10.05	9.12	0.53	Dll3
8.98	8.05	0.53	Ass1
3.60	2.68	0.53	ENSMUSG00000057130
10.35	9.42	0.53	Hist1h2ab
8.05	7.13	0.53	Ramp3
8.74	7.82	0.53	Slc7a3
9.59	8.67	0.53	Cisd1
9.71	8.80	0.53	Ap3m2
8.41	7.50	0.53	Rpl22l1
5.07	4.16	0.53	2310042E22Rik
8.95	8.05	0.53	Cd9
8.96	8.06	0.53	Ass1
8.37	7.47	0.54	Mdga2
9.24	8.34	0.54	Gprin1
9.15	8.25	0.54	2010107G23Rik
7.80	6.91	0.54	Nanos1
10.65	9.75	0.54	Hes6
9.14	8.25	0.54	Tomm5
8.32	7.42	0.54	1700048O20Rik
10.09	9.20	0.54	Tcfap2b
6.86	5.97	0.54	Gabra2
6.54	5.66	0.55	LOC629446 // LOC629446
6.98	6.11	0.55	H2-Ab1
8.88	8.01	0.55	3110006E14Rik
9.57	8.70	0.55	0610010E21Rik
7.97	7.10	0.55	AA388235