Develop an efficient and specific AAV-based labeling system for Muller glia in mice

Yanxia Gao[1,#], Kailun Fang[1,#], Zixiang Yan[2,#], Haiwei Zhang[1,#], Guannan Geng[1], Weiwei Wu[3], Ding Xu[4], Heng Zhang[5], Na Zhong[1], Qifang Wang[1], Minjing Cai[1], Erwei Zuo[2], Hui Yang[1, *]

[1]Institute of Neuroscience, CAS Center for Excellence in Brain Science and Intelligence Technology, Shanghai Research Center for Brain Science and Brain-Inspired Intelligence, Chinese Academy of Sciences, Shanghai, China.
[2]Shenzhen Branch, Guangdong Laboratory for Lingnan Modern Agriculture, Genome Analysis Laboratory of the Ministry of Agriculture, Agricultural Genomics Institute at Shenzhen, Chinese Academy of Agricultural Sciences, Shenzhen, China.
[3]Huigene Therapeutics Inc., Shanghai, China.
[4]Department of Vascular Surgery, Changhai Hospital, Navy Medical University, Shanghai, P.R. China.
[5]Department of Vascular Surgery, The Affiliated Hospital of Qingdao University, Qingdao, China.
[#]These authors contributed equally.
*Correspondence: huiyang@ion.ac.cn (H.Y.)

Abstract

Cell degeneration in the retina leads to several ocular diseases and vision loss. Considerable research efforts focus on reprogramming Muller glia (MG) into functional cells to rescue vision as a promising therapeutic strategy, although whether MG can convert into functional amacrine cells, bipolar cells, retinal ganglia cells (RGCs), rods or cones in mammals remains controversial. The broad applicability of tracking MG differentiation thus presents a need for improved labeling efficiency and specificity. Here, we compared AAV-based labeling strategies with conventional lineage-tracking by crossing transgenic mouse lines. We found that reporter expression was weak and not MG-specific in *mGFAP-Cre* transgenic mice. Different AAV serotypes showed a range of efficiency and specificity in labeling MG, leading us to optimize *a human GFAP-Cre* reporter system packaged in the AAV9 serotype with the *WPRE* (WPRE, woodchuck hepatitis virus post-transcriptional regulatory element) removed. The *hGFAP-Cre- ΔWPRE* reporter could label 20-73.8% MGs, with non-specific RGC labeling rates ranging from 0-0.08% at doses of 1×10^8 to 10^{10} vector genomes (vg) per eye, an approximate 40-fold reduction compared with the *AAV9-hGFAP-Cre-WPRE* labeling system. The *AAV9-hGFAP- Cre-ΔWPRE* system thus represents a highly efficient and specific labeling system for Muller glia, providing a valuable tool for tracking cell fate *in vivo*.

Introduction

Muller glia (MG) represents the main type of glial cell which are responsible for maintaining retinal structure and support for neurons in the retina. In lower vertebrates (e.g., zebrafish, *Danio rerio*), MG can re-enter the cell cycle to proliferate and subsequently

differentiate into one of multiple cell types following injury, such as photoreceptors or retinal
ganglia cells (RGCs) (Bernardos, Barthel, Meyers, & Raymond, 2007; Fimbel, Montgomery,
Burket, & Hyde, 2007; Goldman, 2014; Sherpa et al., 2008). However, the process does not
occur in mammals. As a result, many ocular diseases that are difficult to treat, such as
glaucoma or retinitis pigmentosa, develop from functional degeneration or loss of neurons.
Thus, decades of research efforts have been committed to investigating the regenerative
machinery in adult mammals with the ultimate goal of inducing MG regeneration and
reprogramming. Several major insights have emerged from this work. For example, in mice
Ascl1 overexpression or simultaneous deletion of three nuclear factors I (NFI) genes can both
induce MG proliferation and transformation into amacrines or bipolar cells (Hoang et al., 2020;
Ueki et al., 2015). Similarly, MG to conversion to RGCs was also observed in mice following
deletion of Ptbp1 or simultaneous ectopic expression of Pou4f2 (Brn3b) and Atoh7 (Math5)
(Xiao et al., 2021; Zhou et al., 2020). Moreover, photoreceptors could be generated from MG
under simultaneous overexpression of Otx2, Crx and Nrl after a period of β-catenin ectopic
expression (Yao et al., 2018).

However, *in vivo* glial lineage-tracing methods represent a long-standing research
objective. For instance, an AAV-mediated glial reporter in the brain has been used by different
research groups to observe the conversion of neuroD1-induced astrocytes into neurons
(Boutin et al., 2010; Brulet et al., 2017; Chen et al., 2020; Wang et al., 2021). However, this
phenomenon was not detectable using a more stringent, inducible, transgenic lineage-tracing
strategy (Wang et al., 2021). One proposed explanation is that AAV-mediated reporters also
non-specifically label neurons, suggesting that no conversion was observed, or alternatively,
that inducible transgene methods cannot label all astrocytes, and thus do not label the
resulting reprogrammed neurons. Similar confounding factors have been reported in MG
lineage-tracing systems, such as the low or extremely variable labeling efficiency in inducible
CreER mouse lines (Jorstad et al., 2017; Rueda et al., 2019; Thanh Hoang et al., 2021; Ueki et
al., 2015), or potential non-specific labeling of other cell types by AAV-based methods, similar
to the problems in astrocyte studies mentioned above (Yao et al., 2016; Yao et al., 2018). It is
therefore crucial to develop an efficient and stringent tool for tracing MG proliferation and
reprogramming in the retina.

Here, we compared the labeling efficiency and specificity of two different reporter systems:
those based on crossing *mGFAP-Cre* transgenic mice and those based on transfection with
AAV-*hGFAP-Cre* constructs in Ai9 mice, which harbor the *Rosa26-CAG-loxp-stop-loxp-*
tdTomato inducible reporter. By optimizing the AAV reporters through WPRE (WPRE
woodchuck hepatitis virus post-transcriptional regulatory element) cassette deletion, selecting
the most suitable serotype, conducting immunofluorescence microscopy to quantify construct
specificity and efficiency *in vivo*, we provide a novel, highly specific and reproducible labeling
system for MG cells in the retina tissue of mice.
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Result
MGs are not accurately labeled in *Ai9;mGFAP-Cre* mice
We first sought to test the specificity of MG labeling by *mGFAP-Cre* transgenic mouse, as
reported in previous work to label astrocytes (Garcia, Doan, Imura, Bush, & Sofroniew, 2004).
To this end, we generated an *Ai9;mGFAP-Cre* mouse line to label MGs (figure 1A) and found

that these tdTomato-labeled cells were distributed throughout the inner nuclear layer (INL)
(Figure 1B, C), whereas MGs were distributed within a relatively tight layer in the middle of the
INL (Figure 1B). Immunofluorescence staining showed the tdTomato reporter poorly labeled
MGs, since only 6.42% ± 0.59% of total tdTomato$^+$ cells (501/7722) were co-labeled with the
MG marker Sox9 (Figure 1D). However, we also found that a small proportion of tdTomato$^+$
cells scattered in the ganglia cell layer (GCL) (Figure 1B), and these cells did not strictly
co-localize with the RGC markers Rbpms or Brn3a (i.e., only overlapped with each marker in
five cells, or <2% of total RGCs, per eye section) (Figure 1E-F). Cumulatively, these results
indicated that the endogenous GFAP-driven reporter did not leak to RGCs, nor accurately
label MGs in this mouse line.

AAV-based reporter labels MGs efficiently but not specifically

AAV-based Cre expression is also commonly used to label MG cells in mice due to its
relatively easier introduction compared to generating transgenic mouse lines (Xiao et al., 2021;
Yao et al., 2016; Yao et al., 2018; Zhou et al., 2020). However, the efficiency of AAV-based
labeling also depends on transfection efficiency, which can be affected by AAV serotype. To
evaluate the labeling efficiency of different AAV serotypes, we packaged the
hGFAP-Cre-WPRE construct into commonly used AAV vectors, including AAV1, AAV2, AAV5,
AAV8, AAV9, and AAV.ShH10 (Buck & Wijnholds, 2020; Yao et al., 2018), and separately
delivered them to the retinas of Ai9 mice by subretinal injection (Figure 2A). The results
showed distinct patterns of transfection for the different serotypes. In particular, AAV1 and
AAV5 showed less diffusion in the retina and their transfection area was smaller than that of
other vectors, while AAV8 and AAV9 exhibited higher transfection efficiency than other vectors,
with >500 labeled cells per section, on average (Figure 2B-D). Unexpectedly, the tdTomato
reporter showed highly variable leakage (i.e., RGC labeling) among serotypes (Figure 2E).
Notably, AAV2 and AAV.ShH10 labeled a greater number of RGCs (>50, or 10% of total
tdTomato$^+$ cells on average per eye section) than other vectors (Figure 2F-G). These results
implied that the selection of specific AAV serotypes could improve transfection efficiency, but
could not prevent non-specific labeling of RGCs (or possibly other cell types). Thus, an
alternative method was necessary to improve labeling specificity.

Deletion of the *WPRE* element in the AAV9 construct eliminates non-specific neuron
labeling

Since *WPRE* is often used to enhance gene expression in AAV vectors (Challis et al.,
2019; Choi et al., 2014; Deverman et al., 2016), we hypothesized that increasing Cre
expression could lead to tdTomato activation in cells with low GFAP promoter activity,
potentially resulting in non-specific labeling of RGCs by AAV-based reporters targeting MG. To
test this hypothesis, we deleted *WPRE* from the reporter construct (Figure 3A) and packaged it
in the AAV9 serotype for delivery by subretinal injection to the eyes of Ai9 mice. We then
evaluated the efficiency and MG specificity of tdTomato$^+$ labeling. We found that transfection
area and cell number varied in a dose dependent manner, with more extensive reporter signal
in the high dose injection groups (1x10^9 and 1x10^{10} vector genomes /eye) and smaller
transfection area and fewer labeled cells in the 1x10^8 group (Figure 3B-C). However,
transfection area and cell number were comparable between the *WPRE* and Δ*WPRE* groups
at 1x10^9 dose (Figure 3C). Among total tdTomato$^+$ cells, an average of 700 (73.8% ± 8.5%),
423 (51.6% ± 9.4%), and 153 (20% ± 4.16%) cells were co-labeled with the Sox9 marker in the

1×10^{10}, 1×10^9, and 1×10^8 groups, respectively, accounting for 99%, 98%, and 96% of the total
labeled cells separately (Figure3 E-F). These results indicated that deletion of *WPRE* could
keep the efficiency and improve the selectivity of in vivo MG labeling.

Moreover, tdTomato⁺Rbpms⁺ cells were largely undetectable in each of the different AAV
dosage groups, even in high density tdTomato⁺ cells (Figure 3G), and with strong statistical
significance, since less than one RGC (15 tdTomato⁺Rbpms⁺ cells in 22269 total labeled cells)
on average was labeled per eye section (Figure 3H-I). Under the same dose (1×10^9 vg/eye),
the Δ*WPRE* group showed a 40-fold reduction in the ratio of tdTomato⁺Rbpms⁺ cells to total
tdTomato⁺ cells (from 3.93% ± 0.61% to 0.08% ± 0.05%), and an 80-fold (from 6.72% ± 1.15%
to 0.08% ± 0.04%) among total Rbpms⁺ cells (Figure 3H), compared with the *WPRE* group. It
warrants mention that the proportion of labeled RGCs remained consistently low across a wide
dosage range, 0.08% to 0% from 1×10^{10} to 1×10^8 vg per eye in the Δ*WPRE* group. These
results indicated that the ΔWPRE AAV reporter system could labeled MGs with high specificity,
with only negligible staining of RGCs, even in experiments requiring high dose transfection.

We observed that a very small proportion of tdTomato⁺ cells were not labeled by Sox9
marker for MG (e.g., 9/431 in the 1×10^9 group in one section, Figure 3G), leading us to
question whether these cells were other neuron types, such as bipolar cells, amacrine cells or
horizontal cells. To explore this possibility, we conducted immunofluorescent staining for
PKC-α (the bipolar cell marker), Calbindin (marked horizontal cells, amacrine cells and RGCs,
but could distinguish horizontal cells in mice) and Calretinin (mainly marked mouse amacrine
cells)(Kovacs-Oller et al., 2019; Liets, Eliasieh, van der List, & Chalupat, 2006) in eye sections
with tdTomato⁺ cells labeled by the Δ*WPRE*-AAV9 system and detected no co-labeling among
these cells (Figure S1A-D). Moreover, as shown in Figure 3D, in the outer nuclear layer (ONL)
composed of photoreceptors, tdTomato⁺ cells were not observed. Collectively, these results
indicated that this *AAV9-hGFAP-Cre-ΔWPRE* reporter system did not label other retina neuron
types either, which could be used to label MG with high specificity and at a wide dosage range
in Ai9 mouse retina.

Discussion

In this study, we developed a relatively straightforward and accessible mouse MG labeling
system in which AAV9-based *hGFAP-Cre-ΔWPRE* was applied in Ai9 transgenic mice. This
system can label MG efficiently and specifically without obvious mislabeling of other functional
neurons, including RGC, photoreceptors, amacrines, bipolar and horizontal cells.

Selecting an appropriate system for tracking MG in vivo is essential for investigations of
MG reprogramming. While the introduction of reporters by crossing with a transgenic Cre
mouse line provides more consistent and stable labeling than AAV-based systems, the labeling
efficiency may be low. In this study, we found that introduction of the *mGFAP-Cre* transgenic
construct by conventional crossing failed to label the majority of MGs, unlike that reported for
astrocytes in brain tissues (Garcia et al., 2004). Mouse lines with inducible Cre, such as
CreER, are considered more stringent than constitutive Cre lines, but the labeling efficiency is
dependent on tamoxifen dose (Hu et al., 2020), and was shown to exhibit particularly low
effectiveness in tracking MG in other studies (Jorstad et al., 2017; Ueki et al., 2015).
Additionally, tamoxifen administration reportedly impairs neurogenesis (C. M. Lee et al., 2020)
and can adversely affect the activity and specificity of promoters driving Cre (Denk et al., 2015;

Donocoff, Teteloshvili, Chung, Shoulson, & Creusot, 2020).

Considering the heterogeneity of MGs including many subtypes (Menon et al., 2019;
Roesch et al., 2008), conclusions regarding the ability of MG to differentiate into other
neuronal types require validation by labeling and detection of all MG subtypes. However, the
labeling efficiency of MG by AAV-based reporters primarily depends on its transfection
efficiency which can be affected by AAV tropisms, enhancer elements in the Cre vector (such
as *WPRE*), and injection methods. The AAV1, 2, 5, 8, 9 and ShH10 serotypes with an eGFP
reporter driven by CMV or CAG promoters have been shown to transfect MG using intravitreal
or subretinal injection (Klimczak, Koerber, Dalkara, Flannery, & Schaffer, 2009; Lebherz,
Maguire, Tang, Bennett, & Wilson, 2008; Surace et al., 2003). We compared the transfection
patterns of these serotypes using an *hGFAP-Cre* vector and found that AAV1, AAV2, or AAV5
were ineffective for MG transfection. Other recent work showed variable specificity by different
serotypes for labeling astrocytes in the brain (Wang et al., 2021), which were in line with our
results in the retina.

In addition, high specificity for tracking MG is indispensable for exclusion of false-positive
results in investigation of MG conversion to neurons. Until now, the efficiency and specificity of
AAV-based labeling of astrocytes remains controversial for study of neurogenesis and
reprogramming, especially in the brain (Thanh Hoang et al., 2021; Wang et al., 2021). We
found that all serotypes exhibited varying degrees of leakage to RGCs in the retina. We further
improved the vector by removing the *WPRE* element and found that labeling efficiency was not
obviously affected, but the proportion of non-specifically labeled cells decreased by at least
40-fold that of systems which include *WPRE,* substantially lower than that of other reported
tracking systems for astrocytes in the brain (Srinivasan et al., 2016; Wang et al., 2021).
Moreover, the system lacking *WPRE* exhibits a consistently low non-specific labeling ratio
across a wide dose range, from 1×10^{8} to 1×10^{10} vg per eye, suggesting its potential reliability
for tracking MG.

However, the specificity of this AAV-mediated reporter system depends on MG-specific Cre
expression driven by the GFAP promoter. If the manipulated gene of interest affects GFAP
promoter activity, its overexpression or knockdown in other cell types, such as neurons, may
activate the GFAP promoter and initiate Cre expression in those neurons, in turn affecting its
specificity for MG. For example, NEUROD1 may function as a *cis*-regulator of the *hGFAP*
promoter (Wang et al., 2021). Under this condition, other tracking strategies, such as labeling
neurons with retrograde virus (Wang et al., 2021), may need to be combined with this method
to further validate the results. In all, our AAV9 *hGFAP-Cre-ΔWPRE* system could offer
conveniences for fundamental research in vertebrate eye development, as well as the
potential for development of MG-targeted therapeutics.

Materials and methods

Animals

All mice were housed under a 12 hour light/dark cycle with water and food provided *ad*
libitum at the Animal Center of the Institute of Neuroscience, Chinese Academy of Sciences,
Shanghai, China. All animal procedures were approved by the Animal Care and Use
Committee. All reporters were based on tdTomato expression in Ai9 transgenic mice
(*CAG-Loxp-stop-Loxp-tdTomato*, JAX #007909) purchased from the Jackson Laboratory.

GFAP-Cre (B6.Cg-Tg(Gfap-cre)73.12Mvs/J, JAX#012886) mice were gifted by Dr. Jiawei
Zhou in the Institute of Neuroscience, Chinese Academy of Sciences.

AAVs and vectors

221 AAV vectors, *hGFAP-Cre-ΔWPRE,* and *hGFAP-Cre-WPRE* were constructed by
222 PCR-based subcloning. The 681-bp human GFAP promoter was used in this study, which was
223 derived from the 2.2-kb gfa2 promoter (Y. Lee, Messing, Su, & Brenner, 2008). Different
224 serotypes of AAVs were packaged and titered by Gene Editing Core Facility in the Institute of
225 Neuroscience.

Subretinal and intravitreal injection

AAVs were delivered to eyes via subretinal injection, as previously described (Chiu,
Chang, & So, 2007; Qi et al., 2015). For subretinal injection, adult mice were anaesthetized
with a mixture of ketamine and xylazine, and pupils were dilated with tropicamide
phenylephrine eye drops before injection. A small scleral incision was made using a 30G
needle under a microscope (Olympus, Tokyo, Japan). Then a 32G needle on a Hamilton
syringe was inserted into the subretinal space though the scleral incision. 1 µl of AAV was
slowly (i.e., up to 20s) injected into the subretinal space. After AAV injection, the Hamilton
syringe was removed and a drop of ofloxacin eye ointment was applied to cover the eye.

Immunofluorescent staining and Imaging

Mouse eyes were collected after perfusing animals with 4% paraformaldehyde (PFA) in
PBS, and post-fixed for half an hour in PFA at room temperature after removing the cornea.
Then, retinas were dissected and dehydrated overnight using 30% (*w/v*) sucrose in PBS and
embedded in O.C.T (Sakura). Sections were performed by a cryostat (HM525, Thermo).

Before staining, sections were dried for 30 minutes at 65℃ and then were washed in PBS
3 times for 5 minutes per wash. Antigen recovery was performed using heated sodium citrate.
Blocking was performed in 150 µl blocking buffer (0.1 M PBS: 10% goat serum, and 0.1%
Tween-20). Primary antibodies were incubated at 4℃ overnight. Details of primary antibodies
used in this study were as follows: rabbit anti-Rbpms (1:200, Proteintech, 15187-1-AP), mouse
anti-Brn3a (1:100, Millipore, MAB1585), mouse anti-Sox9 (1:200, Sigma, Amab90795), rabbit
anti-Rfp (1:200, Rockland, 600-401-379), Mouse-anti-PKC α (1:200, Santa Cruz
Biotechnology, sc-8393), Rabbit-anti-Calbindin (1:200, Proteintech, 14479-1-AP) and
mouse-anti-Calretinin (1:200, Proteintech, 66496-L-IG). Sections were washed 3x for 10
minutes per wash on the second day. Secondary antibodies were also incubated at 4℃
overnight. These secondary antibodies included: Alexa Fluor 647-AffiniPure goat anti-mouse
IgG (H+L) (1:500, Jackson ImmunoResearch, 115-605-003), Alexa Fluor 647-AffiniPure goat
anti-rabbit IgG (H+L) (1:500, Jackson ImmunoResearch, 111-605-003), Fluorescein (FITC)
AffiniPure goat anti-mouse IgG (H+L) (1:500, Jackson ImmunoResearch, 115-095-003),
Cy™3 AffiniPure goat anti-rabbit IgG (H+L) (1:500, Jackson ImmunoResearch, 111-165-003).
Sections were washed 3x for 10 minutes per wash on the third day. After nucleic DNA staining
by 4′,6-diamidino-2-phenylindole (DAPI), sections were mounted with fluorescent anti-fade
mounting medium (Southern Biotech, 0100-01). All sections were imaged by confocal
microscopy (Olympus, FV3000). Images were processed using ImageJ.

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Author contributions

Y.G., K.F., Z.Y. and H.Y. conceived the project. Y.G., K.F., Z.Y. and H.Z. designed and conducted experiments. W. W. and G.G. assisted with virus package. D.X. and H.Z. performed cryostat section for retinas. N.Z., Q.W. and M.C assisted with animal experiments. H.Y. designed experiments and supervised the whole project. Y.G., K.F., Z.Y. and H.Y. wrote the paper.

Declaration of interests

The authors declare no competing interests.

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Figure 1 Muller glia are not well-labeled in the *Ai9;mGFAP-Cre* mouse line

(A) Schematic illustration of constructs used to establish the *Ai9;mGFAP-Cre* mouse line.

(B) tdTomato reporter co-localization with cell markers in *Ai9;mGFAP-Cre* mice. Rbpms and Brn3a are RGC markers; Sox9 specifically labels Muller glia (MG) in the retina. The tdTomato reporter is weakly co-expressed with these cell markers, which indicates poor labeling of MG by tdTomato and no detection of leakage to RGCs. Scale Bar, 50 µm. RGC, retinal ganglia cell; ONL, outer nuclear layer; INL, inner nuclear layer; GCL, ganglia cell layer.

(C) The tdTomato cell number in each eye section. n = 12 retinas per group.

(D-F) Venn diagram of average number of tdTomato-labeled cells and/or other cell markers in each section. n = 12 retinas per group. All values are presented as means ± S.E.M..

Figure 2 AAV-based systems co-label a small proportion of RGCs along with MG

(A) Schematic illustration of experimental design. Cre expression is driven by the human GFAP promoter and enhanced by the WPRE element. WPRE, woodchuck hepatitis virus post-transcriptional regulatory element.

(B) Representative images of transfection with different AAV serotypes through subretinal injection. Scale bar, 200 μm.

(C) The average number of tdTomato-labeled cells in each eye section infected by different AAVs.

(D) Quantification of transfection area in each section.

(E) Representative images of co-localization of tdTomato signal with Rbpms in the retina for each AAV serotype. Scale Bar, 50 μm.

(F) The number of tdTomato-labeled RGCs.

(G) The ratio of tdTomato-labeled RGCs to total labeled cells. n = 4~5 retinas per group for panels C, D, F and G. All values are presented as means ± S.E.M.

Figure 3 Reduced non-specific labeling in the ΔWPRE system

(A) Schematic diagram of the *hGFAP-Cre-ΔWPRE* vector and the tdTomato reporter construct in the Ai9 mouse line.

(B) Representative images of tdTomato co-localization with the Muller glia marker Sox9 in mouse retinas following subretinal injection with different doses of AAVs (from left to right:1×10^{10}, 1×10^{9}, 1×10^{8} vector genomes per eye, vg/eye). Scale bar, 200 μm.

(C) The average number of tdTomato⁺ cells in each eye section infected by different doses of

AAVs.

(D) Representative images of tdTomato co-labeling with the Sox9 MG marker in different

densities of labeled MG in retina sections. Scale Bar, 50 μm.

(E) The ratio of tdTomato-labeled MG among total labeled cells (left) and MG (right).

(F) Venn diagram of the average number tdTomato-labeled cells and MG in each section.

(G) Representative images of MG cells in retina sections co-labeled with tdTomato and RGC

marker Rbpms in different transfection densities. Scale Bar, 50 μm.

(H) The ratio of tdTomato-labeled RGCs among total reporter cells (left) and RGCs (right).

(I) The Venn diagram of average tdTomato-labeled cells and RGCs in each section.

n = 3~7 retinas per group for panel C, E, H. All values are presented as means ± S.E.M..

Figure S1 Reduced leakage in the ΔWPRE system related to Figure 3

(A) Co-localization of tdTomato and bipolar cell marker PKC-α, horizontal cell marker Calbindin and amacrine cell marker Calretinin. Arrows show horizontal cells. INL, inner nuclear layer. Scale Bar, 50 μm.

(B-D) Venn diagram of average tdTomato reporter and cell markers in each section (up); the number of PKC-α⁺ (C), Calbindin⁺ (C) and Calretinin ⁺ (D) cells in each eye section infected at 10^9 vg/eye (down). PKC-α marked bipolar cells, Calbindin marked horizontal cells, amacrine cells and RGCs in mice but could distinguish horizontal cells, pointed out by arrows) and Calretinin mainly marked mouse amacrine cells. Brackets show the number of both tdTomato and cell marker positive cells among total cell marker positive cells.

n=4~5 retinas for panel B-D. All values are presented as means ± S.E.M..