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Running Title: GSK3 controls displaced retinal ganglion cell genesis in the retina

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ABSTRACT

Glycogen Synthase Kinase 3 (GSK) proteins (GSK3α and GSK3β) are key mediators of signaling pathways, with crucial roles in coordinating fundamental biological processes during neural development. Here we show that the complete loss of GSK3 signaling in mouse retinal progenitors leads to microphthalmia with broad morphological defects. A single wild-type allele of either Gsk3α or Gsk3β is able to rescue this phenotype. In this genetic context, all cell types are present with a functional retina. However, we unexpectedly detect a large number of cells in the inner nuclear layer expressing retinal ganglion cell (RGC)-specific markers (called displaced RGCs, dRGCs) when at least one allele of Gsk3α is expressed. Excess dRGCs lead to increased number of axons projecting into the ipsilateral medial terminal nucleus, an area of the brain belonging to the non-image-forming visual circuit and poorly targeted by RGCs in wild-type retina. Transcriptome analysis and optomotor response assay suggest that at least a subset of dRGCs in Gsk3 mutant mice are direction-selective RGCs. Our study thus uncovers a unique role of GSK3 in controlling the production of ganglion cells in the inner nuclear layer, which correspond to dRGCs, a rare and poorly characterized retinal cell type.
Significance Statement

Glycogen Synthase Kinase 3 (GSK) proteins (Gsk3α or Gsk3β) are key mediators of signaling pathways, especially in the central nervous system but poorly described in the retina. Here we show that the complete loss of GSK3 in mouse retinal progenitors leads to microphthalmia. However, when only one allele of Gsk3α or Gsk3β are present, all cell types are present with a functional retina. More importantly, we unexpectedly uncover a unique role of GSK3 in controlling the genesis of retinal ganglion cells in the inner nuclear layer which could correspond to a rare and poorly characterized retinal cell type. Therefore, our mouse models potentially offer a unique and powerful model system to study the visual function of dRGCs in mammals.
INTRODUCTION

Glycogen Synthase Kinase 3 alpha (GSK3α) and beta (GSK3β) are functionally redundant serine/threonine kinases encoded by two different genes, sharing 95% identity in their kinase domain (Doble et al., 2007). GSK3 exists at the crossroads of multiple signaling pathways and acts as a key molecular switch to mediate their output and guide distinct cellular processes (Cole, 2012; Doble and Woodgett, 2003; Espinosa et al., 2003; Jin et al., 2009; Shimizu et al., 2008; Wang and Li, 2006). Among the signaling pathways regulated by GSK3 kinases, Wnt canonical pathway is the most well described, with GSK3β inhibition triggering an increase in β-catenin protein levels and its nuclear translocation to activate target gene expression (Doble and Woodgett, 2003).

GSK3 is a key regulator of neural stem/precursor cell proliferation in developing as well as adult brain (Eom and Jope, 2009; Hur and Zhou, 2010; Kim et al., 2009; Pachenari et al., 2017). Conditional deletion and gain of function experiments indicate that GSK3 promotes neuronal differentiation (Hur and Zhou, 2010; Kim et al., 2009). GSK3 exerts its effects through phosphorylation of keys proteins involved in neural development, including proneural factors such as Neurogenin 2 and NeuroD (Li et al., 2012; Moore et al., 2002). In addition, GSK3 fine-tunes the balance between cell death and survival, and its altered function is associated with neurodegenerative pathologies including Alzheimer’s disease, bipolar disorders, and Parkinson’s disease (Golpich et al., 2015; Jacobs et al., 2012; Kremer, 2011; Li et al., 2014; Maurer et al., 2014; Medina et al., 2011).

GSK3 kinases are widely expressed in the developing retina (Pérezleón et al., 2013). GSK3-dependent phosphorylation is shown to control the timing of proneural factor activity and thereby regulate retinal cell fate determination. For instance, inhibition of GSK3 signaling in the developing Xenopus retina leads to increase in
early-born cell types at the expense of late-born cells (Marcus et al., 1998; Moore et al., 2002).

To elucidate GSK3 function in mammalian retina development, we generated conditional loss-of-function alleles of Gsk3α and Gsk3β in retinal progenitor cells. We show that complete loss of both GSK3 kinases severely impacts retinal morphology with microphthalmia phenotype, which could be completely rescued with the expression of just one Gsk3α or Gsk3β wild-type allele. We also noted the presence of a large number of displaced retinal ganglion cells (dRGCs) in the inner nuclear layer in the absence of either Gsk3α or Gsk3β. In normal conditions, this is a rare retinal cell subtype, poorly characterized so far. Anterograde labeling of the axonal ganglion cell projections into the brain of Gsk3 mutant mice, allowed us to further support their dRGCs identity. Our study thus identifies GSK3 as a possible determinant of dRGC genesis. We also provide transcriptomic data and visual tests suggesting that at least a subset of these supernumerary dRGCs in Gsk3 mutant retinas are direction-selective RGCs.

**MATERIALS AND METHODS**

**Animals and tissue collection**

All animal experiments have been carried out in accordance with the European Communities Council Directive of 22 September 2010 (2010/63/EEC), European Union guidelines effective and with the Association for Research in Vision and Ophthalmology statement for the use of animals in ophthalmic and visual Research. All animal care and experimentation were also conducted in accordance with guidelines, under the license APAFIS#1018-2016072611404304 by the Institutional animal care committee n°059 in France and by Animal Care and Use Committee at
the National Institutes of Health (ASP#650). Gsk3α and Gsk3β floxed mice were generously provided by Dr. Jim Woodgett (University of Toronto, Canada). Floxed Gsk3 mice were mated with those carrying the retina-specific regulatory element of murine Pax6 driving the expression of the Cre recombinase (α-Cre) in retinal progenitors as early as E10.5 generously provided by Peter Gruss (Roger et al., 2012). Mice are on a mixed background C57Bl6/J and 129/SvJ. Animals from either sex were used for experimental procedures. All mouse genotyping was performed as described (Hamon et al., 2019).

**Hematoxylin & eosin (H&E) staining, and immunostaining**

Methacrylate sections were used for H&E staining as previously described (Hamon et al., 2019). For IHC on frozen sections, enucleated eyeballs were fixed at the required stage in 4% PFA for 60 min on ice and incubated in an increasing concentration of sucrose (10%, 20% and 30%), then embedded in OCT. Embedded eyeballs were serially cut to 12 μm sections using a cryostat. For embryonic stages, pregnant females were euthanized and whole heads of pups were harvested in paraffin. IHC was performed as described (Kretschmer et al., 2015, 2013). Primary and secondary antibodies are listed in Table 1. Sections were counterstained with 1:1000 4′,6-diamidino-2-phenylindole (DAPI) (1 mg/mL, Thermo Scientific).

**EdU labeling and TUNEL assay**

For EdU labelling, females were injected intraperitoneally with 10 mM of 5-ethynyl-20-deoxyuridine (EdU) (Life Technology). EdU incorporation was detected on paraffin sections or frozen sections using the Click-iT EdU Imaging Kit following manufacturer's recommendations (Life Technology). Apoptosis was detected by terminal deoxynucleotidyl transferase-mediated biotinylated UTP nick end labeling (TUNEL) assays using *in situ* cell death detection kit (Promega). All images were acquired using a Zeiss LSM710 confocal microscope and Zen software (Zeiss).
**Immunoblotting**

Frozen retinas were lysed by sonication in lysis buffer (20 mM Na₂HPO₄, 250 mM NaCl, 30 mM NaPPi, 0.1% NP40, 5mM EDTA, 5mM DTT) supplemented with protease inhibitor cocktail (Sigma-Aldrich). Lysates concentration was determined using a Lowry protein assay kit (Bio-Rad) following sonication and centrifugation. Protein supernatants were separated under denaturing condition by SDS-PAGE, transferred onto nitrocellulose membrane and probed with antibodies (listed in Table 1), as described (Belle et al., 2017, 2014). Proteins were visualized using enhanced chemiluminescence kit (Bio-Rad). α-tubulin was used for normalization. Quantification was performed using ImageJ software (http://imagej.nih.gov/ij/; provided in the public domain at NIH).

**Retinal flat mount**

Fixed retinas were permeabilized and blocked in a solution containing 0.5% Triton-X100, 5% donkey normal serum, 1XPBS, 0.1 g/L thimerosal for 1 day at RT under agitation. Primary antibodies were diluted in a solution containing 0.5% Triton-X100, 5% donkey normal serum, 10% Dimethyl Sulfoxide, 1XPBS, 0.1 g/L thimerosal for 3 days at RT under agitation. The retinas were then washed for 1 day in PBST (1XPBS, 0.5% Triton-X100). Secondary antibodies were diluted in the same solution as primary antibodies and left for 2 days. After washing retinas for 1 day, they were mounted on slides and imaged using a scanning confocal microscope (Olympus, FV1000). Primary and secondary antibodies are listed in Table 1.

**Electroretinography**

Electroretinogram (ERG) recordings were performed using a focal ERG module attached to Micron IV (Phoenix Research Laboratory). Briefly, mice were dark-adapted overnight and prepared for the experiment under dim-red light. The mice were anesthetized with ketamine (100 mg/kg) and xylazine (10mg/kg) and received...
Topical proparacaine hydrochloride (0.5%, Alcon) via eye drops. Pupils were dilated with tropicamide (1%, Alcon) and phenylephrine (2.5%, Alcon) and lightly coated with GONAK hypromellose ophthalmic demulcent solution (2.5%, Akorn). Lens of the Micron IV was placed directly on the cornea, and a reference electrode was placed on the mouse head. Scotopic responses were elicited with a series of flashes of increasing light intensities from -1.7 to 2.2 cd.s/m². Photopic responses were elicited under rod-desensitizing background light with a series of flashes of increasing light intensities from -0.5 to 2.8 cd.s/m². Values of a- and b-wave were extracted and plotted for comparisons between groups of interest.

**Optomotor response (OMR)**

Real time video tracking and automated measurements of compensatory head movements in freely moving mice were performed using an OMR recording setup (Dobin et al., 2013) (Phenosys, Berlin, Germany). Each mouse was placed on a platform in the center of four computer-controlled LCD monitors. Visual stimuli were sinusoidally modulated luminance gratings generated by four LCD screens (60 Hz refresh rate; OkrArena, PhenoSys GmbH, Berlin, Germany), presented with a constant rotation. Video tracking considered the animal’s distance to the monitors, thereby keeping the spatial frequency of the retinal image constant and providing data for automated OMR quantifications.

OMRs were recorded using two different Michelson contrasts and different spatial frequencies (presented in random order) in the two mouse groups: 100% contrast or 50% contrast (n=13 for Gsk3αf/+βff and 18 for Gsk3αf/+βff;α-Cre genotype). All stimuli were presented for 60 s randomly in either clockwise or counterclockwise direction. The measurements were completed in three trials for each animal. At 100% and 50% contrast, OMRs were recorded in response to sinusoidal gratings at 12 spatial frequencies between 0.0125 and 0.5 cycles per degree (cpd). The number of head
movements recorded at a speed range from 2 to 14 degrees per second in the same direction as the stimulus (T_Correct) and in the opposite direction (T_Incorrect) were used to calculate the OMR indices (T_Correct / T_Incorrect) at each spatial frequency.

**Retrograde labeling of retinal ganglion cells**

For retrograde labeling, eyes were enucleated with a piece of the optic nerve and fixed in 4% PFA for 30 min. Rhodamine B isothiocyanate–Dextran (Sigma-Aldrich) was applied on the top of the optic nerve and incubated for 60 min. Eyes were flat mounted after the remaining dye was washed out for 48 hours in PBS at 4°C. Z series images were acquired using SP5 confocal microscope (Leica Biosystems), and 3D reconstruction was performed using Volocity (Perkin Elmer).

**Anterograde labeling of retinal ganglion cell projections**

**Anterograde labeling**

For anterograde tracing of retinal projections, a Cholera Toxin beta subunit (CTB) was used. Animal were anesthetized using a cocktail of ketamine (60 mg/kg) and xylazine (10 mg/kg) and a subsequent bilateral injection of 1.2uL CTB at 1mg/ml coupled to either an Alexa-555 or -647 (Lifesciences) were performed intravitreally. Three days following the injection, mice were perfused with 4% PFA.

**Tissue Clearing and 3D imaging**

For 3D imaging of CTB-labeled brains, a methanol clearing protocol was carried out using modification from the iDISCO+ protocol (Dobin et al., 2013). Briefly, brains were dehydrated by immersion in progressive baths of methanol/1X PBS (20%, 40%, 60%, 80%, 100%, 100%) for 2 hours each at RT on a tube rotator (SB3, Stuart) at 14rpm, using a 15 mL centrifuge tube (TPP, Dutcher) protected from light. Following these baths, samples were immersed overnight in 2/3 Dichloromethane (DCM;
Sigma-Aldrich) and then a 30-min bath in 100 % DCM before being transferred in Di-
benzyl Ether (DBE; Sigma-Aldrich) overnight prior imaging.

3D imaging/Image acquisition for all samples was performed as previously described
(Liao et al., 2014). Acquisitions were done using an ultramicroscope I (LaVision
Biotec) with the ImspectorPro software (LaVision Biotec). The step size between
each image was fixed at 2 μm with a numerical aperture of 0.120 and 150ms
acquisition using a PCO Edge SCMOS CCD camera (2,560 x 2,160 pixel size,
LaVision BioTec).

*Image analysis*

Imaris x64 software (Version9.1.2, Bitplane) was used for all image analysis. Stack
images were first converted from .tiff to .ims files using the Imaris file converter
v9.1.2. 3D reconstruction was visualized with the “volume rendering” function. To
isolate ipsi- and contralateral MTN volumes, manual segmentation was carried out
using the “surface” tool and the isoline selection (density, 10%). Each ipsi-
and contra-lateral projection of the MTN was segmented to generate a volume (μm³).
Movie reconstruction with .tiff series were done with ImageJ (1.50e, Java 1.8.0_60,
64-bit) and iMovie (version 10.1.1).

*Whole transcriptome sequencing and data analysis*

Whole transcriptome analysis was performed on three independent biological
replicates from Gsk3αβf/+;α-Cre and Gsk3αβf/+ retina at P60. After harvesting, both
retinas for each animal were immediately frozen. RNA was extracted using
Nucleospin RNA Plus kit (Macherey-Nagel). RNA quality and quantity were evaluated
using a BioAnalyzer 2100 with RNA 6000 Nano Kit (Agilent Technologies). Stranded
RNA-Seq libraries were constructed from 100 ng high-quality total RNA (RIN > 8)
using the TruSeq Stranded mRNA Library Preparation Kit (Illumina). Paired-end
sequencing of 40 bases length was performed on a NextSeq 500 system (Illumina).
Pass-filtered reads were mapped using STAR and aligned to mouse reference genome GRCm38.94 (Chen et al., 2015). Count table of the gene features was obtained using FeatureCounts (Zhou et al., 2019). Normalization, differential expression analysis and FPKM (fragments per kilobase of exon per million fragments mapped) values were computed using EdgeR (Walter et al., 2015). An FPKM filtering cutoff of 1 in at least one of the 6 samples was applied. A False Discovery Rate (FDR) of less than or equal to 0.05 was considered significant and a fold change cutoff of 1.5 was applied to identify differentially expressed genes. Comprehensive gene list analysis, enriched biological pathways, gene annotation, were based on Gene Ontology classification system using Metascape (Sajgo et al., 2017). Data visualization was done using GOplot R package (Livak and Schmittgen, 2001). To evaluate the expression of the DEGs in RGCs, we used published whole transcriptome analysis from purified RGCs available on Gene Expression Omnibus database (GSE87647) (Livak and Schmittgen, 2001).

**Gene expression analysis by Real-Time PCR (RT-qPCR)**

After RNA extraction using Nucleospin RNA Plus kit (Macherey-Nagel), 500 ng of total RNA was reverse transcribed using the iScript cDNA Synthesis Kit according to manufacturer instructions (BioRad). Primers used for RT-qPCR are shown in Table 2. For each RT-qPCR, 2 μL of a ten-fold dilution of synthetized cDNA was used, and the reactions were performed in technical triplicates on a C1000 thermal cycler (CFX96 real-time system, BioRad) using SsoFast EvaGreen Supermix (BioRad) as previously described (Livak and Schmittgen, 2001). RT-qPCR experiments were performed on three independent biological replicates. Differential expression was determined using the ΔΔCt method with the geometric average of Rps26 and Srp72 as endogenous controls (Livak and Schmittgen, 2001).
Statistical analysis

Statistical analysis was performed with GraphPad Prism 8.3.0 (GraphPad Software, La Jolla California USA). Results are reported as mean ± SEM. Nonparametric Mann-Whitney U test was used to analyze cell counting and qPCR data. P value ≤ 0.05 was considered significant. For OMR assay statistical analysis, a Grubbs test was performed at 5% to remove outliers followed by 2-way ANOVA (genotype and spatial frequency) with Bonferroni Post Hoc test. P value ≤ 0.05 was considered significant.

RESULTS

Retinal progenitor-specific deletion of both Gsk3α and Gsk3β results in microphthalmia

We crossed the floxed Gsk3α<sup>fl/fl</sup>β<sup>fl/fl</sup> mice with α-Cre (<i>αPax6-Cre</i>) line to generate Gsk3α<sup>fl/fl</sup>β<sup>fl/fl</sup>;α-Cre mice in which Gsk3 deletion occurs only in retinal progenitors as early as E10.5 (Marquardt et al., 2001). We first validated our model by assessing the efficacy of Gsk3α and Gsk3β deletion at E12.5 (Figure 1A). Immunohistochemistry (IHC) using an antibody recognizing both GSK3 proteins showed ubiquitous expression in control retinas (Figure 1A). Both Gsk3 genes were efficiently deleted in the peripheral retina of Gsk3α<sup>fl/fl</sup>β<sup>fl/fl</sup>;α-Cre mice, but their expression in the central retina remained preserved consistent with the previously described α-Cre expression pattern (Marquardt et al., 2001).

Hematoxylin and Eosin (H&E) staining revealed major morphological defects with profound retinal disorganization, including the loss of radial arrangement as well as folds and aggregates of retinal progenitor cells (RPCs), in Gsk3α<sup>fl/fl</sup>β<sup>fl/fl</sup>;α-Cre retina as early as E12.5 (Figure 1B). In addition, blood was detected inside the retinal
neuroblastic layer. Structure of the retina worsened rapidly during development although the central part remained unperturbed, consistent with continued Gsk3 expression in this region. At and after E14.5, the retina was largely reduced whereas the eye size itself was comparable to littermate controls (Figure 1B). A large quantity of blood accumulated inside the eyeball at P2. Finally, growth of the eyeball was severely reduced leading to microphthalmia in the adult (data not shown).

Multiple allelic combinations revealed functional redundancy of Gsk3α and Gsk3β in retinal development

Severe deleterious effect by the loss of both Gsk3α and Gsk3β in RPCs in early development precludes the analysis of late retinal histogenesis. To circumvent this, we generated animals with different combinations of Gsk3 deletion (loss of only one Gsk3 gene: Gsk3α<sup>f/f</sup>β<sup>+/+</sup>;α-Cre or Gsk3α<sup>+/+</sup>β<sup>f/f</sup>;α-Cre, or ¾ deletion: Gsk3α<sup>f/f</sup>β<sup>+/+</sup>;α-Cre or Gsk3α<sup>+/+</sup>β<sup>f/f</sup>;α-Cre). Immunoblot analysis using anti-GSK3 antibody (recognizing both proteins) in 2-month-old animals with different combinations of Gsk3α and Gsk3β floxed alleles demonstrated the efficacy of Gsk3α and Gsk3β deletion in areas where the Cre recombinase was expressed during early retinal development (all retinal progenitors at the exception of a stripe located in the dorso-central region (Roger et al., 2012)) (Figure 2A). IHC analysis using anti-GSK3β showed ubiquitous expression of Gsk3β in adult control retina and its complete loss in Gsk3α<sup>f/f</sup>β<sup>f/f</sup>;α-Cre retina (Figure 2B). At 2-month, retinal histology revealed the correct laminated architecture with normal photoreceptors and interneurons when even one allele of Gsk3α (Figure 2C, D) or Gsk3β (data not shown) was present. Photopic and scotopic electroretinogram (ERG) recordings, corresponding to cone and rod function respectively, did not show any significant difference between
Gsk3αf/+βf/f;α-Cre and control retina (Figure 2E, 2F). These results were similar in mice carrying any combination of Gsk3 deletion (data not shown). We therefore conclude that a single allele of wild-type Gsk3α or Gsk3β is sufficient to rescue obvious structural and functional defects in the complete absence of GSK3 signaling.

**Loss of either Gsk3α or Gsk3β in RPCs leads to increased number of displaced retinal ganglion cells**

Even though a single allele of either Gsk3α or Gsk3β permitted normal retinal development (Figure 2), we observed a striking increase in the number of RGCs, as indicated by Brn3a-positive cells, in the inner nuclear layer (INL) of Gsk3αf/+βf/f;α-Cre retina compared to controls (Figure 3A). Brn3a-positive cells in the INL have been described as displaced retinal ganglion cells (dRGCs), a rare cell type in the mammalian retina (Galli-Resta and Ensini, 1996; Young, 1984). All Brn3a-positive cells in the INL of Gsk3αf/+βf/f;α-Cre retina also expressed NF68 that labels cell bodies and axons of RGCs (Figure 3A). To validate that these Brn3a-positive cells in the INL were indeed RGCs with axonal projections included in the optic nerve, we performed retrograde labeling with Rhodamine-Dextran applied onto the optic nerve of Gsk3αf/+βf/f;α-Cre mice. Subsequent 3D reconstructions on flat mount retinas revealed the presence of numerous fluorescent cell bodies located in the INL compared to controls (Figure 3B) demonstrating that axons of dRGCs indeed reached the optic nerve. Thus, Brn3a-positive cells located in the INL of Gsk3αf/+βf/f;α-Cre retinas are indeed RGCs.

Increased dRGCs were observed in retinas carrying any combination of Gsk3 deletions tested (Gsk3αf/+βf/f, Gsk3αf/+βf/f, Gsk3αf/+βf/f or Gsk3αf/+βf/f), with the highest number detected in Gsk3αf/+βf/f;α-Cre mice compared to controls (10-fold increase) (Figure 3C). Notably, Gsk3αf/+βf/f;α-Cre retina did not display excess of dRGCs (data...
not shown). Interestingly, increase in dRGCs number is not associated with a significant reduction in the number of RGCs in the GCL, referred to as orthotopic RGCs (oRGCs) (Figure 3C).

Due to their low number in control retina (around 2% of RGCs), dRGCs have been poorly characterized with very few markers identified, such as Brn3a (Nadal-Nicolás et al., 2014; Nadal-Nicolás et al., 2012). Immunostaining on sections and flat mount retinas with additional RGC marker antibodies revealed that dRGCs in \( Gsk3^{\alpha_{f}/\beta_{f}^{f}; \alpha-Cre} \) retina were also positive for Rbpm (Rodriguez et al., 2014) confirming their increased number in the INL compared to controls (Figure 3D, E). Similar results were observed with Islet1 labeling (Figure 3-1A) (Bejarano-Escobar et al., 2015). Previous work showed that the number of dRGCs varies by retinal domain (Dräger and Olsen, 1980). Counting of Rbpm- or Brn3a-positive dRGCs on \( Gsk3^{\alpha_{f}/\beta_{f}^{f}; \alpha-Cre} \) flat mount retinas did not show any significant differences in their distribution between the dorsal, ventral, nasal and temporal regions (Figure 3-1B). Finally, Brn3a-positive dRGCs did not express markers of other INL neurons such as Choline-Acetyltransferase (CHAT, amacrine cells) or Calbindin (horizontal and amacrin cells) (Figure 3-2). Altogether, our results strongly support the ganglion cell identity of the displaced Brn3a- and RPBMS-positive cells located in the INL of \( Gsk3^{\alpha_{f}/\beta_{f}^{f}; \alpha-Cre} \).

To test whether dRGCs in Gsk3 mutant mice were produced during the same developmental time window as oRGCs, we performed pulse chase experiments by injecting EdU at E12.5, at the peak of RGC birth. Retinal sections from one-month-old animals were then immunolabelled using anti-Brn3a antibody (Figure 4A). In control and \( Gsk3^{\alpha_{f}/\beta_{f}^{f}; \alpha-Cre} \) retina, we identified 40-50% of RGCs that were Brn3a/EdU-positive in all layers examined (GCL and INL), indicating that both dRGCs and oRGCs were born around the same time (Figure 4B).
whether dRGCs are usually overproduced during normal retinal development and eliminated later on. In this context, increased number of dRGCs in Gsk3α<sup>−/−</sup>β<sup>−/−</sup>;α-Cre retinas could result from a defect in dRGC riddance occurring during the first two postnatal weeks, a period of developmental cell death in the retina (Young, 1984). At P0, the number of Brn3a-positive oRGCs was similar between littermate control and Gsk3α<sup>−/−</sup>β<sup>−/−</sup>;α-Cre retina (Figure 4C and D). In contrast, the proportion of Brn3a-positive cells located in the inner part of neuroblastic layer corresponding presumably to dRGCs was much lower in control retinas (6±0.1%) compared to Gsk3α<sup>−/−</sup>β<sup>−/−</sup>;α-Cre retinas (30±1.4%). Thus, dRGCs are not overproduced and eliminated postnatally in control retina. Our results demonstrate that dRGCs are generated during early waves of retinogenesis in Gsk3α<sup>−/−</sup>β<sup>−/−</sup>;α-Cre retina and strongly suggest that GSK3 kinases play a role in restricting their number during normal retinal development.

**dRGCs produced in the absence of either Gsk3α or Gsk3β project to accessory visual system circuitry**

Previous studies in birds and reptiles have reported that dRGCs could be responsible for optokinetic nystagmus, as they mostly project to the accessory optic nuclei (AOS) (Cook and Podugolnikova, 2001), which is critical for non-image forming circuit and image stabilization (Simpson, 1984). To test whether dRGCs in Gsk3 mutants project into specific visual nuclei in the brain, including the AOS, we traced the total pool of RGCs, including dRGCs, with Cholera Toxin beta subunit (CTB). Bilateral injection of CTB, coupled to either an alexa-555 or -647 followed by 3D imaging, allowed us to trace both ipsi- and contra-lateral projecting axons. We first confirmed that CTB injections indeed marked the dRGCs based on flat mounts of retinas after Brn3a and NF68 immunolabelling (Figure 5-1). To visualize the entire
visual projection network, we carried out whole-brain clearing using iDISCO+
followed by light-sheet fluorescent imaging and 3D reconstruction (Figure 5A).
Complete loss of Gsk3β displayed a large increase in ipsilateral projecting RGCs in
one of the three nuclei composing the AOS, the Medial Terminal Nucleus (MTN)
(Simpson, 1984). This terminal nucleus is the main component of the AOS reacting
best to either upward or downward movement and mediates the optokinetic
nystagmus critical for image stabilization (Yonehara et al., 2009). Calculation of the
signal intensity ratio between the ipsilateral and contralateral MTN demonstrated a
significant increase of RGC projections into the ipsilateral MTN in retinas with Gsk3β
deletion (Figure 5B). This result suggests that excess dRGCs might participate to the
non-image forming circuit.

**Whole transcriptome analysis suggests that dRGCs in GSK3 mutant retinas are
direction-selective ganglion cells.**

We next performed transcriptome analysis using RNA-sequencing in order to
identify molecular changes in adult Gsk3αf+/βf/+;α-Cre retina and to better characterize
dRGCs. Retinas from Gsk3αf+/βf/+ mice were used as controls. Gene level analysis
revealed 111 differentially expressed genes (DEGs) using filtering criteria of Fold
Change (FC) = 1.5 with a False Discovery rate (FDR) cutoff of ≤ 0.05 and a minimum
mean expression value of one FPKM (fragments per kilobase of exon per million
reads mapped) in at least one of the two experimental groups (Figure 6A and Figure
6-1). Pathway analysis of DEGs revealed several statistically significant
overrepresented pathways (Figure 6-2). Biological processes and molecular functions
pathways included 48 DEGs; of these, 33 genes were expressed in RGCs based on
published whole transcriptomic data from purified RGCs (for a total 69 RGC-
expressed genes among the 111 DEGs) (labeled with stars in Figure 8B) (Sajgo et
Dominance of RGC-expressed genes in our dataset is consistent with the high number of dRGCs observed in $Gsk3\beta^{+/+};\alpha$-Cre retina. Among interesting candidates dysregulated in the biological processes and molecular function pathways (Figure 6B and 6-2), we identified $Chrna2$, $Chrma5$, $Chrma7$, $Chrnb4$ encoding for postsynaptic subunits of the nicotinic cholinergic receptor. With the exception of $Chrma2$, all other genes are upregulated in $Gsk3\beta^{+/+};\alpha$-Cre retina. Most retinal ganglion cells express nicotinic receptors (Kay et al., 2011; Rousso et al., 2016). Among other potentially relevant genes, the $Grik3$ gene product belongs to the kainate family of glutamate receptors functioning as ligand-activated ion channels. In direction-selective ganglion cells (DSGCs), glutamate is proposed to be the main source of excitation (Sweeney et al., 2019, 2014). Finally, $Cartpt$, encoding for the preprotein CART (Cocaine- And Amphetamine-Regulated Transcript Protein) that was upregulated in $Gsk3\beta^{+/+};\alpha$-Cre retina was validated by RT-qPCR (Figure 6C). $Cartpt$ is specifically expressed in direction-selective RGCs (DS-RGCs) (Rousso et al., 2016; Sato et al., 2017), suggesting that dRGCs (or at least a subset) in $Gsk3\beta^{+/+};\alpha$-Cre retina might be DS-RGCs. In support with this hypothesis, we found some dRGCs in $Gsk3\beta^{+/+};\alpha$-Cre and littermate control retina positive for the transcription factor Tbr2, described as essential for RGC specification participating in non-image-forming visual circuits (Figure 6D) (Simpson, 1984; Yonehara et al., 2009). A small subset of dRGCs also expressed Foxp2, a transcription factor involved in DS-RGC differentiation in mice (Figure 6D) (Kim et al., 2009). These two factors were expressed in a mutually exclusive way in Rbpm-positive dRGCs, suggesting that dRGCs in $Gsk3\beta^{+/+};\alpha$-Cre might encompass several subtypes.

**Optomotor response is impaired in GSK3 mutant**

Given that DS-RGCs are reported to drive the optomotor response (OMR) by projecting mainly into the contralateral AOS (Kim et al., 2009), we tested the OMR of
Gsk3$\alpha^{f/+}$β$^{f/f}$;α-Cre mice. The OMR indices (T_correct / T_incorrect) were calculated from three trials at contrast 1 and 0.5 (Figure 6E). At 100% contrast, the OMR indices were significantly reduced in Gsk3$\alpha^{f/+}$β$^{f/f}$;α-Cre mice compared to controls at 0.05, 0.15 and 0.25 cycles per degree (cpd). The maximum OMR index was observed at 0.15 cpd in controls whereas it reached its maximum at 0.1 in Gsk3$\alpha^{f/+}$β$^{f/f}$;α-Cre mice.

At 50% contrast, the OMR indices were also significantly reduced in Gsk3$\alpha^{f/+}$β$^{f/f}$;α-Cre mice compared to controls but to a larger extend between 0.05 and 0.3 cpd. The maximum OMR index was observed at 0.15 cpd in both controls and Gsk3$\alpha^{f/+}$β$^{f/f}$;α-Cre mice. Altogether, these results demonstrate an impaired OMR in Gsk3$\alpha^{f/+}$β$^{f/f}$;α-Cre mice. These data, together with our transcriptomic and axonal projections analyses, suggest that at least a subset of dRGCs expressing only one allele of Gsk3$\alpha$ are DS-RGCs.

**DISCUSSION**

In this study, we report that complete loss of GSK3 in retinal progenitors leads to microphthalmia in adult mice with severe morphological defects. Such a severe phenotype was not observed anymore when only one Gsk3$\alpha$ or Gsk3β allele was expressed, confirming the functional redundancy of these two genes. Our results implicate that the kinase GSK3 as the first reported determinant of dRGCs determinant during retinal histogenesis. We show that mouse retinas with only one allele of Gsk3 exhibit an excessive number of dRGCs. The concomitant large increase of axonal projections to the ipsilateral MTN, our RNA-Seq data and optomotor response tests, have led us to propose that these dRGCs are involved in the detection of image motion direction.
In pigmented wild-type mouse retina, dRGCs in the INL are a very rare and poorly-described type of cells, which represent only 2% of RGCs (Li et al., 2012; Moore et al., 2002). It is therefore striking that dRGC number increases up to 20% of RGCs when a single copy of Gsk3α is present in retinal progenitors. To our knowledge, such a high number of dRGCs has never been reported in a transgenic/mutant animal. A previous study hypothesized that dRGCs are misplaced in the INL due to an ontogenic aberration rather than representing an independent class of RGCs (Fite et al., 1981; Krause et al., 2014). Indeed, differential cell adhesion plays a key role in sorting and migration of retinal cells in their appropriate layers, especially for RGCs. One can therefore hypothesize that enhanced dRGCs in mice with a single copy of Gsk3 is the consequence of increased aberration events. This hypothesis could be supported by our RNA-Seq data showing the upregulation of genes coding for collagen subunits (Col18a1, Col4a3, Col9a1, Col9a2) and extracellular matrix proteins in Gsk3$^{+/\beta^{-}\alpha^{-}\text{Cre}}$ retina, which could favor migration defects. Noticeably, if it were the case, the increase in dRGCs should be accompanied by a decrease in oRGCs. However, we found that the number of oRGC in the GCL is unaltered, strongly suggesting that RGCs in the INL of mice with a single copy of Gsk3 represent a specific subtype of RGCs. In support with this, topographic and quantitative analysis of RGCs in albinos and pigmented rats indicate that dRGCs are not misplaced by ontogenic mistakes but indeed represent a specific subpopulation of RGCs (Nadal-NicolÃ¡s et al., 2014). GSK3β is involved in neural cell fate decision by controlling the timing of the activity of bHLH transcription factors, such as NeuroD or Neurog2 (Karten et al., 1977). If dRGCs are not produced following ontogenic aberrations but are instead determined by a proper genetic program, it would be interesting to identify transcription factors involved and seek for any regulation by GSK3 kinases. Along this line, further studies would allow to better
understand if the excess of dRGCs is only due to an expanded pool of normally occurring dRGCs or if their presence is also a consequence of an aberrant migration during retinal development when GSK3s are not fully active. New sequencing technology such as single cell RNA-Seq would definitively be an asset to shed more light on specific markers for dRGCs and to identify key players of dRGC specification/differentiation. As a distinct cell type, scRNA-seq analysis following high depth sequencing should highlight a distinct cell cluster in tSNE plots in retina with only one $Gsk3\alpha$ allele expressed corresponding to dRGCs. The interest and power of such approach has already been demonstrated for RGC characterization (Rheaume et al., 2018). Whole transcriptome analysis at early time points when RGCs are produced might also complete such analysis.

In reptiles, amphibians and birds, only dRGCs project into the MTN, whereas in mammals only oRGCs have been reported as projecting into the MTN (Mouritsen et al., 2004). Our results obtained from anterograde labeling clearly demonstrated a large increase in ipsilateral MTN projections in absence of $Gsk3\beta$, whereas it was absent or very dim in control animals. Although this strongly suggests that excess dRGCs in mutant mice are causing this phenotype, we cannot exclude the possibility that mutant oRGCs also participate to these ipsilateral MTN projections. However, contralateral projections did not seem to be affected. Noticeably however, it would be challenging to observe an increase in dRGC projections into the other areas already strongly labeled using our anterograde labeling method, especially into the dLGN or SC. We can speculate that the low number of ipsilateral MTN projections in the control condition reflects the low number of dRGCs present in the WT retina and could therefore explain why such result had not been described so far. Altogether, our results strongly suggest that dRGCs may primarily project into the ipsilateral MTN. In mice, it has been shown by retrograde labeling from the superior colliculus...
(SC), which receive large amount of RGC projections, that dRGCs/oRGCs project to one or both SCs (Nießner et al., 2016). Although challenging, similar experiments, i.e. fluorescent dye injection into the ipsilateral MTN, may allow us to discriminate whether the increased signal in absence of Gsk3βoriginates only from dRGCs and whether these cells also project into this area in WT retina. In regards to our results, it is still unclear whether GSK3 function is to limit the number of dRGCs and actively regulates their correct projection to the contralateral MTN or if GSK3 function is limited to tightly controlling of dRGC number, which project thereafter to the ipsilateral MTN on a GSK3-independent manner.

Given the very low percentage of dRGCs in the control retina, their function is poorly studied in mammals. In contrast, dRGC function, projections and topography have been extensively investigated in bird and reptile retina (Nießner et al., 2016). In birds, cryptochrome-expressing dRGCs are used as a magnetic compass for orientation (Pang and Wu, 2011). In European Robin birds, *Erithacus rubecula*, a low number of dRGCs have been identified but specifically express Cryptochrome 1b only during nocturnal migration period (Pang and Wu, 2011). In rodents, retrograde labeling from the optic nerve led to the identification of 16 classes of dRGCs based on their ramification levels of their dendrites as well as the dendritic field size (Giolli et al., 2006; Yonehara et al., 2009). Based on dRGC dendrite projections into the IPL, it has been proposed that most dRGCs in WT retina are functionally more involved in retinal OFF light pathways (Simpson, 1984; Yonehara et al., 2009). Similar methods applied to *Gsk3αβf/α-Cre* retina should shed more light on dRGC function and establish whether all the different classes are present.

As part of the AOS, the MTN receives afferent signal from the eye and sends efferent signal to motor neurons controlling the position of the eye. As such, optokinetic reflex relies on direction specific retinal projections to the AOS. Neurons
of the dorsal terminal nucleus (DTN) codes for horizontal stimulus whereas neurons of the MTN codes for vertical stimulus (Nadal-Nicolás et al., 2014). Therefore, the direction of image motion relies on DS-RGCs in the retina. The alteration the OMR in $Gsk3^\alpha^{f/+}\beta^{f/f}\alpha-Cre$ mice, support the hypothesis that some of the supernumerary dRGCs are indeed related to motion detection. Although the number of dRGCs was drastically increased, the OMR was not increased but at the contrary reduced. Such result might be caused by the higher number of projections to the ipsilateral side instead of the contralateral one, leading to an alteration of the neuronal circuit regulating the OMR (Nadal-Nicolás et al., 2014). We also identified in $Gsk3^\alpha^{f/+}\beta^{f/f}\alpha-Cre$ and control retinas a small subset of dRGCs, which are positive for the transcription factors Tbr2 and Foxp2, the markers for non-image-forming RGCs and DS-RGCs respectively (Marquardt et al., 2001). Together with the transcriptomic data (upregulation of genes such as Cartpt expressed in DS-RGCs), these results provide strong evidence suggesting that the large number of dRGCs in $Gsk3^\alpha^{f/+}\beta^{f/f}\alpha-Cre$ retina might indeed be DS-RGCs projecting into the MTN. It has been recently proposed that dRGCs might be also involved in predator detection by integrating overhead visual information (Roger et al., 2010). Using suitable and complementary visual tests, our genetic model could be highly valuable to complete the functional identification of the dRGCs in visual process.

Overall, our results demonstrate a critical role of GSK3 in stringently regulating the number of a rare type of dRGCs, which has been poorly described as yet. Gsk3 mutant mice, with a large number of dRGCs in their retina, offer a unique and powerful model system to further study the embryonic origin, synaptic connections and visual function of dRGCs in mammals.
ACKNOWLEDGEMENT

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AUTHOR’S CONTRIBUTION

E.K., R.J.V., C.H., designed and performed the experiments and analyzed the data, S.L. L.T. and P.S. performed the experiments and analyzed the data, A.C. designed the experiments, analyzed the data and revised the manuscript, M.P., A.S., J.E.R. designed the study, analyzed the data, wrote the manuscript with the help of E.K. R.J.V and C.H. J.E.R supervised the study.

REFERENCES


FIGURE AND EXTENDED DATA LEGENDS

Figure 1. Developmental defects and microphthalmia in Gsk3-deficient retina with aberrant nuclear translocation of β-catenin, a key effector of the Wnt canonical pathway. (A) Immunohistochemistry (IHC) of E12.5 retina from Gsk3α<sup>fl/fl</sup>β<sup>fl/fl</sup> mice expressing or not α-Cre using a pan-GSK3 antibody (green) shows efficient deletion at the periphery where the Cre expression has been previously reported (delimited by dashed-line) Scale bar: 100 μm. (B) Hematoxylin and eosin (H&E) staining on methacrylate sections at E12.5, E14.5 and P2 reveals large retinal morphogenesis defects in Gsk3α<sup>fl/fl</sup>β<sup>fl/fl</sup>;α-Cre with blood invasion into the eyeball (showed by white arrow). L, Lens; NR, neural retina. Scale bar: 100 μm at E12.5 and E14.5. 500 μm at P2. For the magnification of P14.5, scale bar: 50 μm.

Figure 2. One allele of either Gsk3α or Gsk3β is sufficient for the development of a functional retina. (A) Immunoblot analysis of protein extracts from 2-month-old animals with different combination of Gsk3α and Gsk3β floxed alleles (Gsk3α<sup>fl/fl</sup>β<sup>+/+</sup>, Gsk3α<sup>+/+</sup>β<sup>fl/fl</sup>, Gsk3α<sup>+/+</sup>β<sup>fl/fl</sup> or Gsk3α<sup>fl/fl</sup>β<sup>+/+</sup>) with or without Cre recombinase using anti-panGSK3 antibody (recognizing both isoforms) reveals decreased expression of GSK3α or GSK3β (arrowheads). α-Tubulin is used as loading control. (B) IHC on 2-month-old retinal sections from control and Gsk3α<sup>fl/fl</sup>β<sup>fl/fl</sup>;α-Cre retinas with or without Cre recombinase using anti-GSK3β antibody (red) showing ubiquitous Gsk3β expression in all retinal layers, whereas its expression is lost in the Cre-expressing retina. (C) Expression of only one Gsk3 allele (Gsk3α) is sufficient for proper photoreceptor development. IHC using anti-Rhodopsin (Rho, red) and anti-Cone arrestin (Arr3, red) antibodies to label rod and cone photoreceptors, respectively. (D) Expression of only one Gsk3 allele (Gsk3α) is sufficient for proper interneuron...
development. IHC using anti-Calretinin (Calr, green) and anti-Calbindin (Calb, red) antibodies to label horizontal and amacrine cells, respectively. (B-D) onl, outer nuclear layer; inl, inner nuclear layer; gcl, ganglion cell layer. Scale bar: 20μm. (E, F) Electoretinogram (ERG) recording in 2-month-old Gsk3αf/βf/α-Cre animals and littermate controls. Photopic (cones) (E) and scotopic (rods) (F) response in Gsk3αf/βf/α-Cre animals are similar to controls. Mean ± SEM intensity response curves of a- and b-wave responses averaged from 8 biological replicates of each genotype.

Figure 3. Gradual loss of Gsk3α and/or Gsk3β leads to an increased number of Brn3a-positive retinal ganglion cells displaced in the inner nuclear layer (INL) of adult retina. (A) Brn3a (red) and NF68 (green) IHC on 2-month-old Gsk3αf/βf/α-Cre mouse retina reveals the presence of supernumerary displaced retinal ganglion cells (dRGCs, arrows) in the INL of Gsk3αf/βf/α-Cre compared to littermate controls. Top panel represents control retinas, middle panel a peripheral retinal area, and bottom panel a more central area. Scale bar: 20 μm. (B) dRGCs send their axons into the optic nerve. Visualization of dRGCs after 3D reconstruction of 2-month-old flat mounted retina of control and Gsk3αf/βf/α-Cre animals following retrograde labeling with Rhodamin-Dextran applied onto the optic nerve. inl: inner nuclear layer, gcl: ganglion cell layer. (C) Gradual loss of Gsk3α and Gsk3β alleles (Gsk3αf/βf/+, Gsk3αf/βf/+, Gsk3αf/βf/ or Gsk3αf/βf/+) leads to a gradual increase of Brn3a-positive RGCs located to the INL, with the highest number observed in Gsk3αf/βf/α-Cre animals. Left Histograms represent counting of the total number of Brn3a-positive cells per section located in the GCL (left panel) or in the INL (middle panel). Right histogram represents the percentage of the dRGCs among the total number of Brn3a-positive cells per section for each combination. Mean ± SEM values
are presented from 4 biological replicates. A nonparametric Mann-Whitney U test was applied, * indicates $P \leq 0.05$. (D) Brn3a (red) and Rbpms (green) IHC on 2-month-old mouse retina reveal the co-expression of these two RGC markers (dRGCs, arrows) in the INL of both $Gsk3\alpha^{+/}\beta^{ff}; \alpha$-Cre dRGCs and in littermate controls. Scale bar: 20 $\mu$m. (E) Flat mounted retina from $Gsk3\alpha^{+/}\beta^{ff}; \alpha$-Cre and littermate controls labelled with anti-Rbpms antibody demonstrated the large number of Rbpms-positive dRGCs in the INL of $Gsk3\alpha^{+/}\beta^{ff}; \alpha$-Cre mice. See Extended Data Figure 3-1 for Islet1 and Rbpms co-localization used to complete dRGC characterization and the repartition of the dRGCs in the retina. See Extended Data Figure 3-2 showing that Brn3a-positive dRGCs are not positive for amacrine or horizontal cell markers.

Figure 4. dRGCs are produced in the same differentiation wave as oRGC located in the GCL. (A) EdU- (green) and Brn3a-positive cells (red) were found both in the GCL and in the INL of 30-days old $Gsk3\alpha^{+/}\beta^{ff}; \alpha$-Cre animals after a single injection of EdU at E12.5. (B) Percentage of EdU- and Brn3a-positive cells located either in the GCL or in the INL among total number of Brn3a-positive cells. Mean ± SEM values are presented from 3-4 biological replicates. A nonparametric Mann-Whitney U test was applied, ns: not significant (C) Brn3a (red) and NF68 (green) immunostaining on P0 mouse retina revealed that a large number of dRGCs were already present in $Gsk3\alpha^{+/}\beta^{ff}; \alpha$-Cre but they were fewer in littermate controls (white arrows). (D) Left stacked histogram represents counting of the total number of Brn3a-positive cells per section located in the GCL (white bars) and in the INL (black bars) of $Gsk3\alpha^{+/}\beta^{ff}; \alpha$-Cre retina. Right histogram represents the percentage of the dRGCs among the total number of Brn3a-positive cells per section. Mean ± SEM values are presented from 6 biological replicates. A nonparametric Mann-Whitney U test was
applied, ** indicates $P \leq 0.01$. inl, inner nuclear layer; gcl, ganglion cell layer. Scale bar: 20μm.

Figure 5. Lack of Gsk3β results in RGC projections into the ipsilateral Medial Terminal Nucleus. (A) All panels are light sheet fluorescence microscopy of solvent-cleared adult brain from control, $Gsk3^{\alpha-\beta^{+/+}}$; α-Cre, $Gsk3^{\alpha^{+/-}\beta^{+/-}}$; α-Cre and $Gsk3^{\alpha^{+/-}\beta^{+/-}}$; α-Cre animals after intravitreal injection of CTB coupled to either an Alexa-555 or -647. Ipsilateral projections of RGCs into the MTN was observed in the absence of Gsk3β expression. SC, superior colliculus; NOT, nucleus of optic tract; dLGN, dorsal lateral geniculate nucleus; vLGN, ventral lateral geniculate nucleus; IGL, intergeniculate leaflet; OPT, Olivary Pretectal Nucleus; dMTN, dorsal medial terminal nucleus; MTN, medial terminal nucleus; vMTN, ventral medial terminal nucleus; OT, Optic tract; SCN, suprachiasmatic nucleus; ON, optic nerve. Scale bar: 1mm; * indicates the ipsilateral MTN. (B) Quantification of the signal intensity ratio between ipsilateral and contralateral MTN in controls and Gsk3 mutants (including $Gsk3^{\alpha^{+/-}\beta^{+/-}}$; α-Cre, $Gsk3^{\alpha^{+/-}\beta^{+/-}}$; α-Cre, and $Gsk3^{\alpha^{+/-}\beta^{+/-}}$; α-Cre). A nonparametric Mann-Whitney U test was applied, ns: non-significant, ** $P \leq 0.01$. See Extended Data Figure 5-1 for co-staining of the CTB-positive cells with Brn3a and NF68.

Figure 6. Whole transcriptome meta-analysis suggests that dRGC in $Gsk3^{\alpha^{+/-}\beta^{+/-}}$; α-Cre retina are direction-selective ganglion cells. (A) Volcano plot representation of differentially expressed genes between $Gsk3^{\alpha^{+/-}\beta^{+/+}}$; α-Cre and control retina plotted on the x-axis (log2 scale). FDR adjusted significance is plotted on the y-axis. Orange and blue dots: significantly up-regulated and down-regulated genes in $Gsk3^{\alpha^{+/-}\beta^{+/-}}$; α-Cre retina, respectively. Vertical dashed lines represent FC=1.5. Horizontal dashed line represents FDR=0.05. (B) Chord plot representation
of DEGs related to GO annotations belonging to either molecular functions (MF) or biological process (BP). Overlaps in GO annotation amongst genes within each category are visualized. * correspond to genes expressed in previously published purified RGCs (blue, slightly expressed genes in RGCs between 1 and 5 FPKM; red, highly expressed genes in RGCs more than 5 FPKM). (C) RT-qPCR validation of selected DEGs identified by RNA-seq analysis. Differential expression analysis by RT-qPCR of Cartpt, Th, Eph2, Cplx1, Chn5, Chn2, Chn7, Chn4 in Gsk3αf/+; a-Cre retina at 2-months of age, relative to littermate control retina levels. All values are expressed as the Mean ± SEM from three biological replicates. A nonparametric Mann-Whitney U test was applied, * indicates \( P \leq 0.05 \). (D) IHC on 2-month-old mouse retina reveals the presence of a subset of dRGCs (Rbms-positive dRGCs, red) in Gsk3αf/+; a-Cre expressing either the transcription factor Tbr2 (grey) or Foxp2 (green). Arrows indicate Tbr2 and Rbms-positive dRGCs; arrowheads represent Foxp2 and Rbms-positive dRGCs. onl, outer nuclear layer; inl, inner nuclear layer; gcl, ganglion cell layer. Scale bar: 50 μm. (E) The mean OMR indices (±SEM) are plotted as a function of spatial frequency for each genotype (n=13 for Gsk3αf/+ and 18 for Gsk3αf/+; α-Cre genotype). The baseline (1; dashed line) represents unspecific head movements and no response to the stimulus. OMR at 100% and 50% contrast in Gsk3αf/+; a-Cre mice (dashed line) and controls (black line). A Grubbs test was performed at 5% to remove outliers followed by 2-way ANOVA, * indicates \( P \leq 0.05 \), ** indicates \( P \leq 0.01 \), *** indicates \( P \leq 0.001 \). See Extended Data Figure 6-1 for the hierarchical clustering of the DEGs. See Extended Data Figure 6-2 for pathway analysis results.
Figure 3-1. dRGCs express the nuclear factor Islet-1. (A) IHC on 2-month-old mouse retina reveals that most dRGCs (Rbpms-positive dRGCs, white arrows, red) in the INL of Gsk3αβf/f; α-Cre and littermate controls were positive for Islet-1 (green), a marker expressed in the nuclei of ganglion cells, and of cholinergic amacrine cells, ON-bipolar cells, and subpopulations of horizontal cells. onl, outer nuclear layer; inn, inner nuclear layer; gcl, ganglion cell layer. Scale bar: 50 μm. (B) Counting on flat mount of Rbpms- or Brn3a- positive cells located in the INL at the dorsal, ventral, nasal and temporal part of control and Gsk3αβf/f; α-Cre retina. Histogram represents the number of Brn3a- or Rbpms-positive cells per field. Mean ± SEM values are presented from 4 biological replicates.

Figure 3-2. Brn3a-positive cells located in the INL of Gsk3αβf/f; α-Cre retina are dRGCs. Brn3a-positive RGCs located in the INL of Gsk3αβf/f; α-Cre retina do not express markers of other INL neurons such as Choline-Acetyltransferase (Chat) or Calbindin (Calb). onl, outer nuclear layer; inn, inner nuclear layer; gcl, ganglion cell layer. Arrowheads indicates Brn3a-positive dRGCs. Scale bar: 20μm.

Figure 5-1. Intravitreal injection of CTB labels dRGCs. After intravitreal injection of CTB coupled to an Alexa-555 (red) in Gsk3αβf/f; α-Cre eye led to the labelling of Brn3a- (green) and NF68-positive (grey) cells located in the INL. Scale bars: 20μm.

Figure 6-1. Hierarchical clustering of the identified differentially expressed genes. Hierarchical clustering representing the 111 DEGs (abs(FC)>1.5; FDR≤0.05; FPKM>1) between 2-month-old Gsk3αβf/f; α-Cre retina and littermate control were clustered by their Z-score. Each column for each genotype corresponds to one
sample. For both groups, triplicates were analyzed. Left panel corresponds to the
downregulated genes; Right panel corresponds to the upregulated genes.

Figure 6-2. Identification of enriched pathways from DEGs identified in 2-
month-old Gsk3α<sup>f/+</sup>β<sup>f/f</sup>; α-Cre retina. (A) Gene ontology (GO) annotations of DEGs in Gsk3α<sup>f/+</sup>β<sup>f/f</sup>; α-Cre retina compared to littermate controls. Top over-represented pathways for Biological process (BP), Molecular Function (MF), KEGG (Kyoto Encyclopedia of Genes and Genomes) and TRRUST (Transcriptional Regulatory Relationships Unrevealed by Sentence-based Text mining) were identified by enrichment analysis using Metascape. (B) Circular visualization for BP and MF of GO enrichment analysis. Down-regulated genes (blue dots) and up-regulated genes (red dots) within each GO pathway are plotted based on logFC. Z-score bars indicate if an entire GO category is more likely to be increased or decreased based on the genes within it.
Table 1. List of primary and secondary antibodies used for immunohistochemistry (IF) and western blot (WB)

**Primary antibodies**

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<td></td>
<td></td>
</tr>
</tbody>
</table>
Table 2. List of primers used for RT-qPCR

<table>
<thead>
<tr>
<th>Gene name</th>
<th>Primer F</th>
<th>Primer R</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>Carpt</em></td>
<td>5’-TAAAGTTTTCCTCCCCTCCGAGGCA-3’</td>
<td>5’-CAACACCACATTCGAGGCTTCT-3’</td>
</tr>
<tr>
<td><em>Th</em></td>
<td>5’-ACTATGCTCTTCGATCCTCCGGGA-3’</td>
<td>5’-CGGATGTTGAGGACTTGAGGTA-3’</td>
</tr>
<tr>
<td><em>Epha2</em></td>
<td>5’-GACCCTCCAGATTCCTTTTGC-3’</td>
<td>5’-GCGTACTTCCTAGTTGTCATA-3’</td>
</tr>
<tr>
<td><em>Cplx1</em></td>
<td>5’-GGGTAGAGGAAGAGGACCCG-3’</td>
<td>5’-CTTGGCGTACTTTGCTTTG-3’</td>
</tr>
<tr>
<td><em>Chrna5</em></td>
<td>5’-CCTGACTCCAGACACTGTCGGG-3’</td>
<td>5’-CCAGTACTCCAAAGATGCCCT-3’</td>
</tr>
<tr>
<td><em>Chrna2</em></td>
<td>5’-CTTGGAGCCACATGAGGGA-3’</td>
<td>5’-CTTGGAGCCACATGAGGGA-3’</td>
</tr>
<tr>
<td><em>Chrna7</em></td>
<td>5’-CTTGGAGCCACATGAGGGA-3’</td>
<td>5’-CTTGGAGCCACATGAGGGA-3’</td>
</tr>
<tr>
<td><em>Chrnb4</em></td>
<td>5’-AAACTGATCCTGACCTTCCGAG-3’</td>
<td>5’-GTAGAGAGGTCCAGGAGATGCC-3’</td>
</tr>
</tbody>
</table>