Transcriptomic comparison of two selective retinal cell ablation paradigms in zebrafish reveals shared and cell-specific regenerative responses

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Abstract

Retinal Müller glia (MG) can act as stem-like cells to generate new neurons in both zebrafish in mice. In zebrafish, retinal regeneration is innate and robust, resulting in the replacement of lost neurons and restoration of visual function. In mice, exogenous stimulation of MG is required to reveal a dormant and, to date, limited regenerative capacity. Zebrafish studies have been key in revealing factors that promote regenerative responses in the mammalian eye. Increased understanding of how the regenerative potential of MG is regulated in zebrafish may therefore aid efforts to promote retinal repair therapeutically. Developmental signaling pathways are known to coordinate regeneration following widespread retinal cell loss. In contrast, less is known about how regeneration is regulated in the context of retinal degenerative disease, i.e., following the loss of specific retinal cell types. To address this knowledge gap, we compared transcriptomic changes between two selective cell ablation paradigms, targeted loss of rod photoreceptors or bipolar cells. Our study spanned twelve time points encompassing the entire degenerative and regenerative process of each targeted cell type. 2,531 differentially expressed genes (DEGs) were identified. Interestingly, the majority of DEGs were paradigm specific, including during MG activation phases, suggesting the nature of the injury/cell loss informs the regenerative process from initiation onward. For example, early modulation of Notch signaling was implicated in the rod but not bipolar cell ablation paradigm. Components of JAK/STAT signaling were activated in both paradigms but were more strongly induced during rod cell regeneration. We functionally validated the role of JAK/STAT signaling during rod cell regeneration using CRISPR/Cas9-based knockdown of *stat3* which inhibited both MG proliferation and rod cell regeneration kinetics. Additionally, although more than a third of all DEGs are implicated as immune-system regulators, individual immune-related factors were

largely paradigm specific. These data support emerging evidence that discrete “fate-biased” regenerative processes follow from selective retinal cell loss.

Author Summary

Blinding diseases are linked to the loss of specific types of neurons in the retina. In humans, this eventually leads to loss of sight. In zebrafish, however, lost retinal neurons are regenerated resulting in restored vision. Our lab has developed zebrafish models that allow us to selectively induce the loss of disease-relevant retinal neurons, thereby allowing us to study how individual retinal cell types are regenerated. Here, to better understand how the regeneration of individual cell types is regulated, we compared gene expression changes occurring during the loss and regeneration of two different retinal cell types, rod photoreceptors and bipolar interneurons. We found that the majority of gene changes were specific to each cell type studied, providing strong evidence that genetic programs underlying stem cell activation in zebrafish vary depending on the cell type damaged. We also found that the immune system was strongly implicated as a regulator of regeneration in both models, but that individual genes immune-related genes tended to be more strongly associated with one of the two models.. We hope that a better understanding of how retinal cell regeneration is regulated in zebrafish will aid efforts to develop regenerative therapeutics designed to restore sight to patients who have lost their vision.

Introduction

Regenerative therapeutics aimed at replacing lost retinal cells have the potential to restore visual function. One category of therapeutics in development aims to stimulate endogenous retinal Müller glia (MG) to act as stem-like cells to replace lost neurons[1,2]. The capacity of MG to drive

retinal repair differs markedly between species. In mammals, MG regenerative potential is intact but remains dormant unless exogenously stimulated. In contrast, zebrafish MG robustly regenerate lost retinal neurons[3]. Zebrafish are therefore an established model for exploring mechanisms controlling MG regenerative potential, including factors that enhance the regenerative potential of mammalian MG[4–8]. Studies of the mechanisms regulating regeneration following widespread retinal cell loss, e.g., damage across multiple cell types/nuclear layers , have focused largely on the role of known developmental pathways and reprogramming factors[3,9–12]. In contrast, mechanisms governing responses to the loss of specific neuronal types are less well defined. Intriguingly, recent studies in zebrafish suggest that the loss of discrete retinal cell types elicits a fate-biased regenerative response; i.e., where progenitors cells give rise predominantly to the lost cell type[13–16]. A deeper understanding of the mechanisms controlling fate-biased regeneration has the potential to facilitate the development of novel cell-type targeted regenerative therapeutic strategies.

Retinal regenerative research in fish has utilized three main injury paradigms: light-induced ablation[17–20], toxin-induced ablation[21,22] and mechanical wounding[23,24]. Early mechanical wounding studies involved surgical excisions of retinal quadrants which induce classic hallmarks of epimorphic regeneration: rapid wound closure and the formation of blastema-like zones of proliferative cells[23]. Other paradigms eliminate all or most cells in a retinal somal layer, e.g., light-induced ablation of rod and cone photoreceptor cells in the outer nuclear layer (ONL)[17–20], excitotoxin-induced ablation of interneurons in the inner nuclear layer (INL) and retinal ganglion cells (RGCs)[21,22]. Collectively, these studies have identified two injury-inducible stem cell niches in the teleost retina; ONL progenitor cells committed to producing rod cells[25,26], and an INL-

localized retinal stem cell[27,28]. Subsequent studies demonstrated that the INL stem cells were Müller glia (MG), which function as injury-induced multipotent stem-like cells. These cells can divide asymmetrically giving rise to a transit-amplifying pool of retinal progenitor cells that then differentiate to regenerate the lost retinal cells[3,9–11]. Intriguingly, mammalian MG can also produce new neurons upon exogenous expression of neurogenic factors, such as *achaete-scute family bHLH transcription factor 1* (*ascl1*)[4,5] or inhibition of factors such as *nuclear factor I a/b/x* (*nfia/b/x*), which function to sustain MG identity[29]. However, the types of neurons produced by mammalian MG are not typically well correlated to types of cells lost; for instance, *ascl1* overexpression is largely limited to the production of bipolar cells[30]. More recently, combinatorial application of exogenous neurogenic factors have overcome this limitation to produce ganglion-like cells capable of responding to light[7]. These studies highlight the need to better understand the regulation of MG regenerative potential, and fate choices of MG-derived neural progenitors, are regulated.

Retinal degenerative diseases typically involve the loss of discrete cell types. Thus, methods for replacing specific cell types are being sought as a strategy to restore vison to patients. To study how discrete cell types are regenerated we adapted a targeted cell ablation method, the nitroreductase (NTR) prodrug converting enzyme system[31–35], to zebrafish[36–41]. Transgenic expression of NTR renders cells susceptible to prodrugs, such as metronidazole (Mtz). Exposing fish to Mtz results in the selective loss of NTR-expressing cells by a DNA-damage induced cell death process[40–43]. Co-expression of a fluorescent reporter in NTR-targeted cells allows the regenerative process to be characterized in detail using *in vivo* time-lapse imaging[38,44] or quantified using high-throughput screening methods[39,45]. This approach affords key advantages

to the investigation of cellular regeneration. For instance, it can be genetically targeted to individual cell types and is prodrug inducible, allowing temporal synchronization of the regenerative process across many samples. While several mutant zebrafish lines exhibit cell-type specific losses, the lack of control over the onset and duration of cell death make it more difficult to profile regenerative responses in these models. Additionally, several retinal degeneration mutants also fail to regenerate[46] suggesting that a threshold of cell death is required to trigger retinal regeneration. Using this approach, recent studies have shown that selective retinal cell loss elicits a fate-biased regenerative response[13–16], although subtler fate-biases have also recently been acknowledged in widespread injury paradigms as well. This suggests limited/selective retinal cell loss and widespread/non-selective retinal injury may trigger regenerative processes that are differentially regulated.

Here, to increase understanding of fate-biased regenerative processes, we used time-resolved gene expression profiling to compare two retinal cell-type specific ablation paradigms in zebrafish. Comparisons between the targeted loss of either 1) bipolar cells[44], or 2) rod photoreceptors[45] involved profiling gene expression changes across 12 timepoints spanning the entire degenerative and regenerative processes. Differential gene expression analysis across a total of 138 microarrays revealed both shared and paradigm-specific profiles. Paradigm-specific expression changes predominated at early and late time points, and shared expression profiles peaked at 24 and 32 hours after induction of cell loss. While paradigm-specific mechanisms were expected to be prevalent during late phases, corresponding to progenitor cell differentiation, predominance at early time points suggests that MG stem cell activation involves signals that may be informative regarding cell type lost, thus facilitating fate-biased responses. Given the

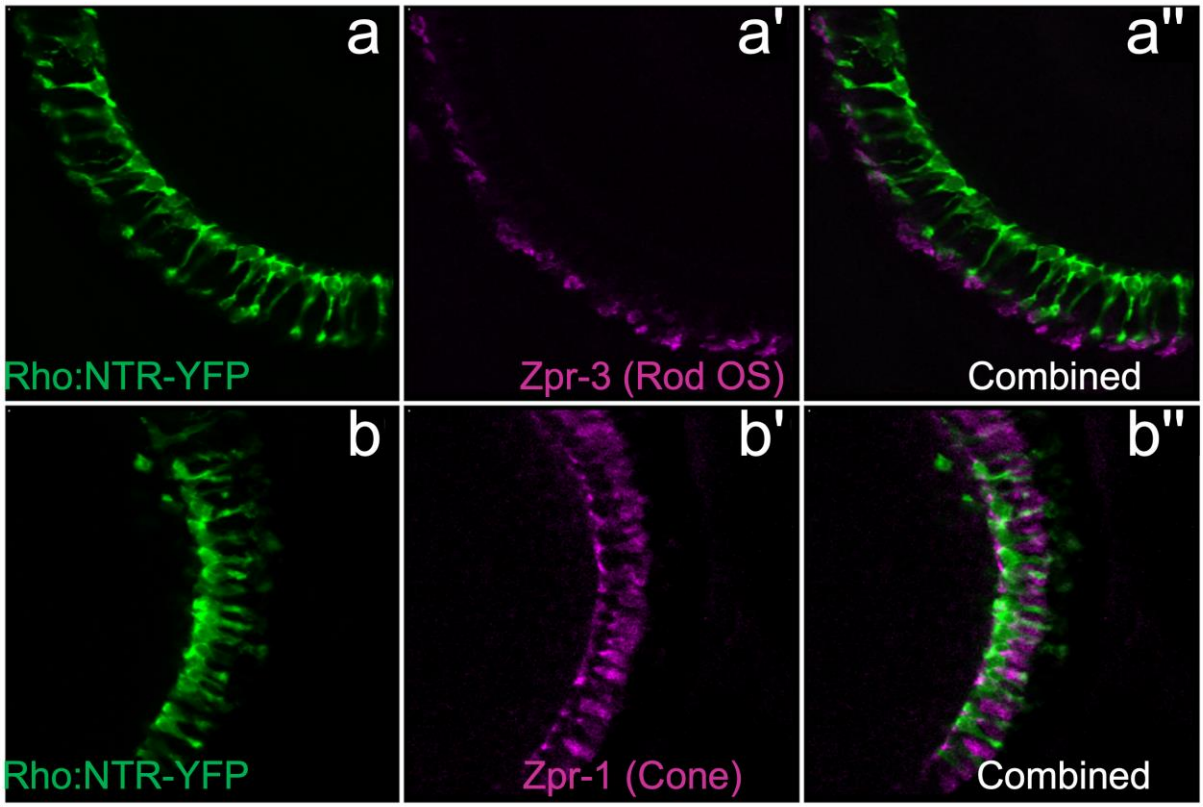
relevance to numerous degenerative diseases, greater understanding of the mechanisms regulating stem cell responses to selective cell loss and subsequent fate-biased regenerative processes is needed as this information could enable the development of cell-type specific regenerative therapeutics.

Results

Specificity of NTR/Mtz-induced Cell Death and Assessments of Regeneration

To expand our understanding of mechanisms regulating the regeneration of discrete retinal cell types, gene expression changes attending two cell-specific ablation paradigms were compared. Specifically, transgenic zebrafish lines expressing NTR-reporter fusions in either a bipolar interneuron subtype (*nyctalopin* or *nyx*-expressing) or rod photoreceptor cells were used, referred to hereafter as “NTR-bipolar”[44] and “NTR-rod”[45], respectively (see Methods for full description). We first confirmed that NTR expression was specific to the targeted cell types within the retina. Prior studies have shown that expression in the NTR-bipolar line is restricted to retinal bipolar cells, with labeling of the pineal gland (epiphysis) in the brain as well[44,47]. For the NTR-rod line, immunohistochemistry confirmed that expression of the NTR-YFP fusion protein was restricted to rod cells, as previously shown for this line[40] and corresponding promoter element[48]. NTR-YFP expressing cells were co-labeled with a rod-specific antibody marking outer segments, zpr-3[49,50] (Supp. Fig. 1a-a"), and interdigitated with cells marked by a cone-specific antibody, zpr-1[51] (Supp. Fig. 1b-b"). Co-labeling levels with zpr-3 suggested that the majority of rod cells express the NTR-YFP transgene. The NTR-bipolar line uses the Gal4/UAS bipartite system to express two different transgenes, a membrane-tagged YFP and an NTR-mCherry fusion protein that enables cell ablation. In this background, NTR-mCherry expression

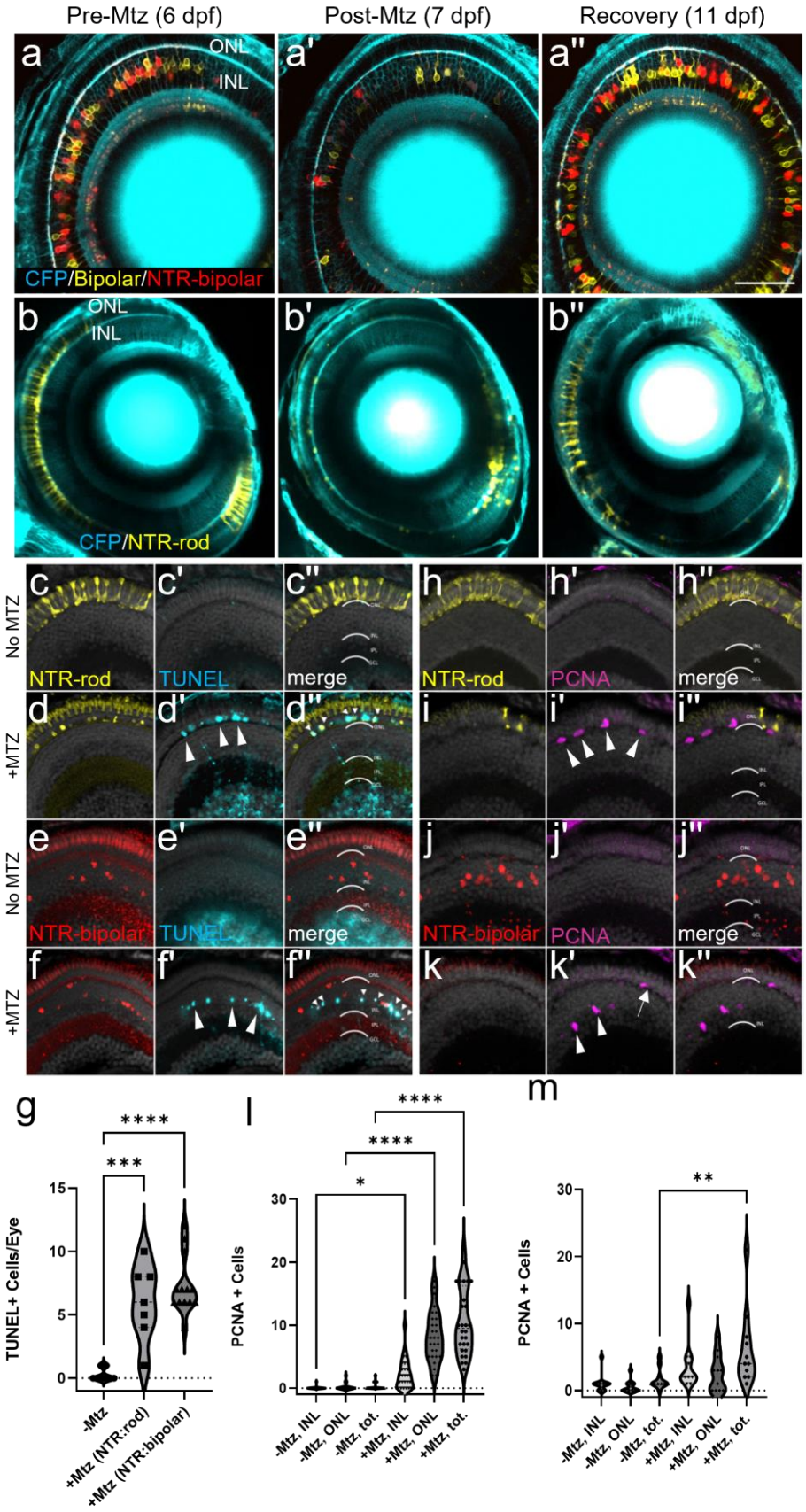
is sporadic, with the number of NTR+ cells varying from low (~25 cells/retina) to high (hundreds of cells/retina)[44]. To account for this variability, mid-level expressing NTR-bipolar larvae (~100 targeted cells) were visually selected for these studies.



Supp. Fig. 1. Confirmation of NTR-rod transgene specificity

(a-a’’) Histological staining in the NTR-rod model showing transgenic Rho:YFP-NTR expression (green) along with antibody staining for rod outer segment marker Zpr-3 (purple). (b-b’’) Histological staining in the NTR-rod model showing transgenic Rho:YFP-NTR expression (green) along with antibody staining for cone marker Zpr-1 (purple).

We next verified that a 24 hr 10 mM Mtz prodrug treatment was sufficient to induce selective loss of NTR-expressing cells and that regeneration occurs upon Mtz washout. Confocal time series imaging was used to follow this process in individual NTR-bipolar and NTR-rod larva. (Fig. 1a-a'' and b-b'', respectively). After a 24 hr 10 mM Mtz treatment (from 6-7 days post-fertilization, dpf) followed by 24 hr washout, NTR+ cells are largely absent or appear fragmented (Fig. 1a', b') in comparison to pre-treatment images (Fig. 1a, b). Four days after Mtz was removed (11 dpf), both NTR+ bipolar and rod cells had regenerated (Fig. 1a'', b''). DMSO controls showed sustained NTR expression in the absence of Mtz (Supp. Fig. 2a-a'', c-c''). Terminal deoxynucleotidyl transferase (TdT)-mediated dUTP nick end labeling (TUNEL)[52] staining confirmed layer-specific cell death in both paradigms (Fig. 1c-f series). Quantification showed a statistically significant increase in DNA damage (TUNEL staining) following Mtz exposures for both transgenic lines (Fig. 1g).


Pre-Mtz (6 dpf)
Post-Mtz (7 dpf)
Recovery (11 dpf)
a
a'
a''
ONL
INL
CFP/Bipolar/NTR-bipolar
b
b'
b''
ONL
INL
CFP/NTR-rod
No MTZ
+MTZ
No MTZ
+MTZ
c
c'
c''
h
h'
h''
NTR-rod
TUNEL
merge
NTR-rod
PCNA
merge
d
d'
d''
i
i'
i''
e
e'
e''
j
j'
j''
NTR-bipolar
TUNEL
merge
NTR-bipolar
PCNA
merge
f
f'
f''
k
k'
k''
g
TUNEL+ Cells/Eye
****
***
-Mtz
+Mtz (NTR:rod)
+Mtz (NTR:bipolar)
l
PCNA + Cells
****
****
*
-Mtz, INL
-Mtz, ONL
-Mtz, tot.
+Mtz, INL
+Mtz, ONL
+Mtz, tot.
m
PCNA + Cells
**
-Mtz, INL
-Mtz, ONL
-Mtz, tot.
+Mtz, INL
+Mtz, ONL
+Mtz, tot.

196

Fig. 1. Two NTR models enabling inducible retinal cell-type specific ablation

(a-a'', b-b'') In vivo time-series imaging following the NTR-bipolar (a-a'') or NTR-rod (b-b'') response to metronidazole (Mtz) treatment to induce cell death and regeneration. Images were taken in the same fish at 6 dpf (before Mtz onset, a, b), 7 dpf (after treatment, a', b') and 11 dpf (following recovery, a'', b'').

(c-c'', d-d'', e-e''. f-f'') Representative histological staining for TUNEL (terminal deoxynucleotidyl transferase dUTP nick end labeling) at 7 dpf in uninjured NTR-rod larvae (c-c'') and Mtz treated NTR-rod larvae (d-d'') as well as in uninjured and Mtz-treated NTR-bipolar larvae (e-e'', f-f'', respectively).

(g) Quantification of TUNEL+ cell counts at 7 dpf in untreated fish (-Mtz) or following the ablation of each cell type [+Mtz (NTR:rod) and +Mtz (NTR:bipolar)] .

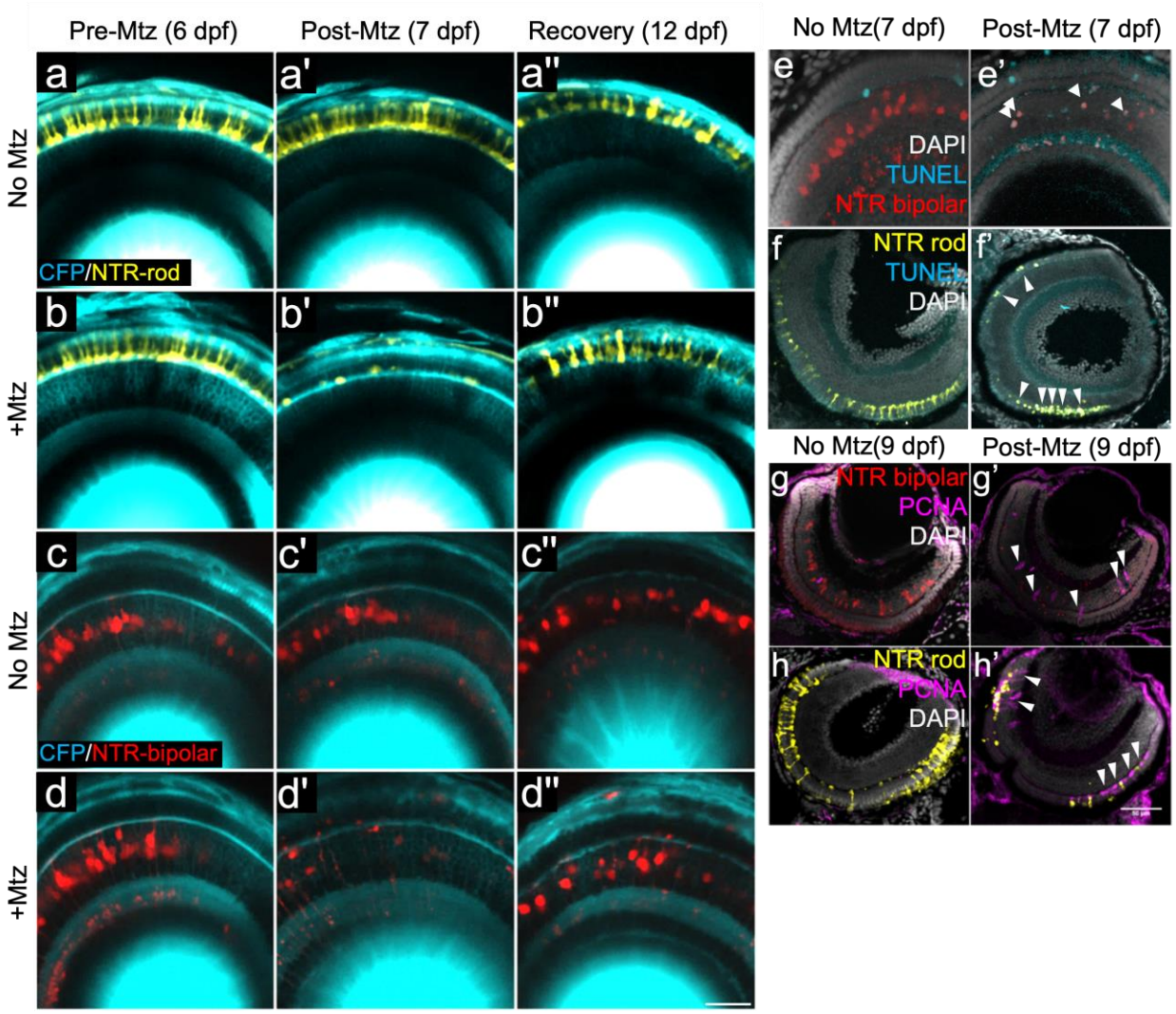
(h-h'', i-i'', j-j''. k-k''). Representative histological staining for PCNA (proliferative cell nuclear antigen) at 9 dpf in uninjured NTR-rod larvae (h-h'') and Mtz treated NTR-rod larvae (i-i'') as well as in uninjured (j-j'') and Mtz-treated NTR-bipolar larvae (k-k'').

(l,m) Quantification of PCNA+ cell counts at 9 dpf in untreated NTR-rod fish or following the ablation of rods (l)and in untreated NTR-bipolar fish or following the ablation of bipolar cells (m). For both paradigms, quantification is split into total number of proliferative cells and those in the INL or ONL.

Asterisks indicate significant statistical difference (* = <0.05, ** = <0.01, *** = <0.001, and **** = <0.0001) across groups, non-significant comparisons are not shown.

Characterization of Retinal Stem Cell Niches Responding to Bipolar and Rod Cell Death

As the NTR-rod line consistently labels the majority of rod photoreceptor cells (Supp. Fig. 1), we anticipated rod cell loss would trigger proliferation in both the INL and ONL stem cell niches (multipotent MG and dedicated rod precursors, respectively), consistent with data from the Hyde lab using a similar transgenic line[53]. Conversely, we expected bipolar cell ablation would result in proliferation predominantly within the INL, i.e., localized to MG cells and daughter progenitor cells. To test which retinal stem cell niche(s) were responsive to cell loss in the two ablation cell paradigms, Mtz-treated and DMSO control retinas were immunolabeled with proliferative cell nuclear antigen (PCNA) 72h post-onset of Mtz at 9 dpf (Fig. 1h-k series, during the peak of proliferation following ablation in our NTR models[38]). The data showed cell-specific trends, with a bias toward ONL, rod-committed precursor proliferation, after rod loss (Fig. 1i', arrowheads) and INL (presumed MG/progenitor cell) proliferation following bipolar cell loss (Fig. 1k', arrowheads). On average more proliferation was seen in NTR-rod lines (~14 PCNA+ cells/retinal slice) versus NTR-bipolar fish (~5 PCNA+ cells/retinal slice, Fig. 1l-m). This difference was due to elevated levels of ONL proliferation following rod ablation as the amount of INL proliferation was similar in both paradigms (Fig. 1l,m). Proliferation within the INL in Mtz-treated NTR-rod lines was typically clustered near the periphery (Supp. Fig. 2h' where the density of cell loss was highest, consistent with increased rod cell death activating MG stem cells[53]. Note, cells dividing in the ONL following bipolar cell ablation (Supp. Fig. 2g', arrowheads) were presumed to be MG-derived progenitors that had migrated to the ONL, consistent with prior studies[3].



Supp. Fig. 2. Additional in vivo imaging and TUNEL/PCNA histological imaging

(a-a'', b-b'') In vivo time-series imaging following NTR-rod larvae that were uninjured (a-a'') or received Mtz (b-b''). Images were taken in the same fish at 6 dpf (before Mtz onset in +Mtz larvae), 7 dpf (after Mtz removal) and 11 dpf (following recovery).

(c-c'', d-d'') In vivo time-series imaging following NTR-bipolar larvae that were uninjured (c-c'') or received Mtz (d-d''). Images were taken in the same fish at 6 dpf (before Mtz onset in +Mtz larvae), 7 dpf (after Mtz removal) and 11 dpf (following recovery).

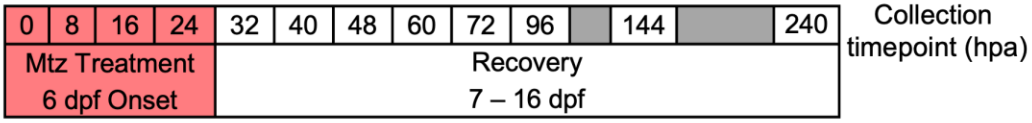
(e-e', f-f') Histological staining in uninjured and +Mtz eyes at 7 dpf for TUNEL in the NTR-bipolar (e-e') and NTR-rod (f-f') paradigms.

(g-g', h-h') Histological staining in uninjured and +Mtz eyes at 9 dpf for PCNA in the NTR-bipolar (g-g') and NTR-rod (h-h') paradigms.

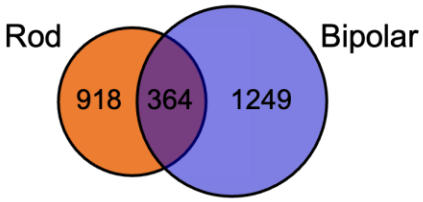
Microarray Analysis of Two Cell-specific Regeneration Paradigms

We next turned to a differential gene expression comparison of our two retinal neuron ablation paradigms. To account for expression changes spanning cell loss and regeneration, eyes were collected from NTR-bipolar and NTR-rod larvae treated ±Mtz across a total of 12 time points, from 0 to 240 hours post ablation (hpa; Fig. 2a). As above, cell death was induced by the addition of 10 mM Mtz from 6 to 7 dpf (0 to 24 hpa), followed by wash out and recovery from days 7-16 dpf (24 to 240 hpa; Fig. 2a). To assess initial MG stem cell responses to retinal cell loss, early time points were emphasized by collecting samples every 8 hr from 0 to 48 hpa. Eight-hour intervals were used to minimize representation of gene expression changes due solely to circadian cycles. For the later time points, samples were collected at 60, 72, 96, 144, and 240 hpa. Across three biological repeats per time point, a total of 96 eyes were collected per time point for each paradigm (48 DMSO controls and 48 +Mtz samples, Supp. Table 1).

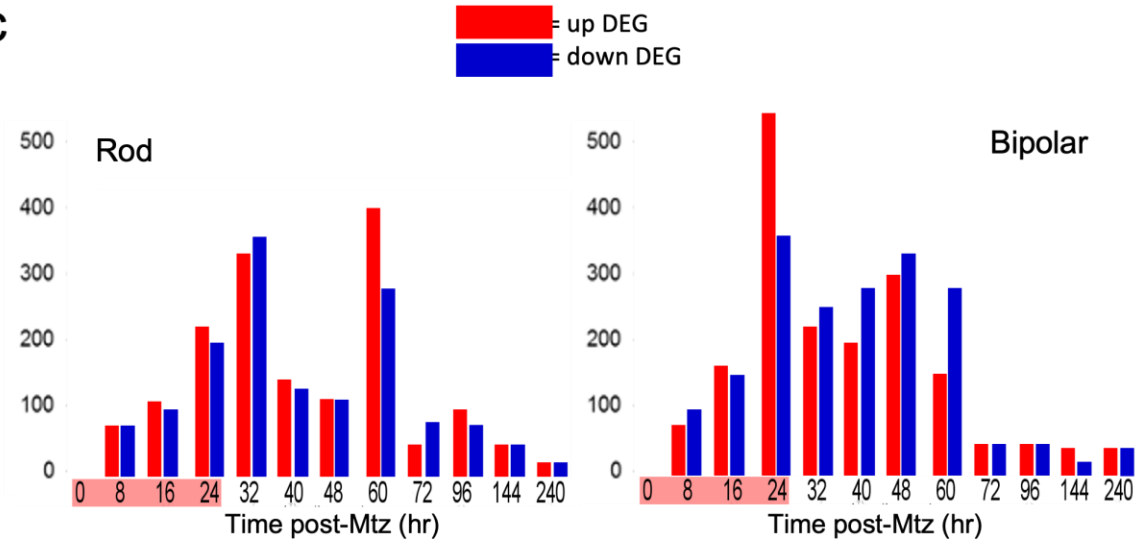
a



b



c



d

Top NTR-rod genes	fold (log2)	p-value	# of DEG timepoints
mala.2	2.49	1.70E-10	9
txn	1.87	6.25E-10	7
sepw2b	2.07	1.87E-09	8
prdx1	1.90	3.02E-09	7
wu:fb18f06	2.07	4.30E-09	8
gstp1	2.78	5.77E-09	7
cyp24a1	1.94	1.53E-08	3
stat2	1.68	1.57E-08	5
si:dkey-87o1.2	1.62	2.52E-08	5
nqo1	1.60	3.21E-08	5
cki	-2.66	6.65E-10	6
wu:fb15e04	-1.85	7.89E-10	7
nfil3-5	-1.44	1.86E-08	2
zgc:136930	-2.04	8.68E-08	6
cyt1l	-1.47	1.53E-07	6
ptprn2	-1.24	2.57E-07	2
cry1b	-1.78	2.68E-07	4
brdt	-1.46	4.57E-07	1
per3	-1.23	4.94E-07	4
myo3a	-1.34	6.71E-07	2

Top NTR-bipolar genes	fold (log2)	p-value	# of DEG timepoints
wu:fj05g07	3.05	3.66E-10	6
zgc:174888	2.14	4.46E-09	6
irf1b	2.23	6.42E-09	4
prdx1	1.89	7.59E-09	6
esm1	2.38	8.26E-09	6
atf3	2.45	2.21E-08	5
hsp70	1.77	3.23E-08	3
stat3	2.08	4.21E-08	5
irf9	1.75	5.81E-08	4
rpe65a	2.36	5.83E-08	1
si:ch211-195b15.7	-1.29	4.27E-07	8
Dr.12789.1.A1_at	-1.38	5.26E-07	8
pdca	-1.90	5.91E-07	6
arl3l2	-1.44	8.60E-07	7
pde6a	-1.76	9.99E-07	8
guca1b	-1.43	3.14E-06	6
s100w	-1.59	3.20E-06	3
gngt2a	-1.74	3.60E-06	3
zgc:162144	-1.66	4.62E-06	4
mb	-1.29	5.00E-06	2

264

Fig. 2. Microarray data collection, DEG identification and top hits

(a) Experimental design for tissue collection of whole eyes for microarray analysis. Treatment with Mtz for 24h was induced at 6 dpf following screening for NTR-rod+ or NTR-bipolar+ fish. Eyes were collected in triplicate at the following 12 timepoints including t0, t8, t16, 24, t32, t40, t48, t60, t72, t92, t144 and t240.

(b) Venn diagram illustrating the total number of differentially expressed genes (DEGs) unique to either cell type or shared between the two at all timepoints.

(c) Chart showing distribution of upregulated and downregulated DEGs in each paradigm.

(d) Top 10 up and downregulated genes across the entire data set based on p-value as well as the number of timepoints that gene was identified as differentially expressed out of 12.

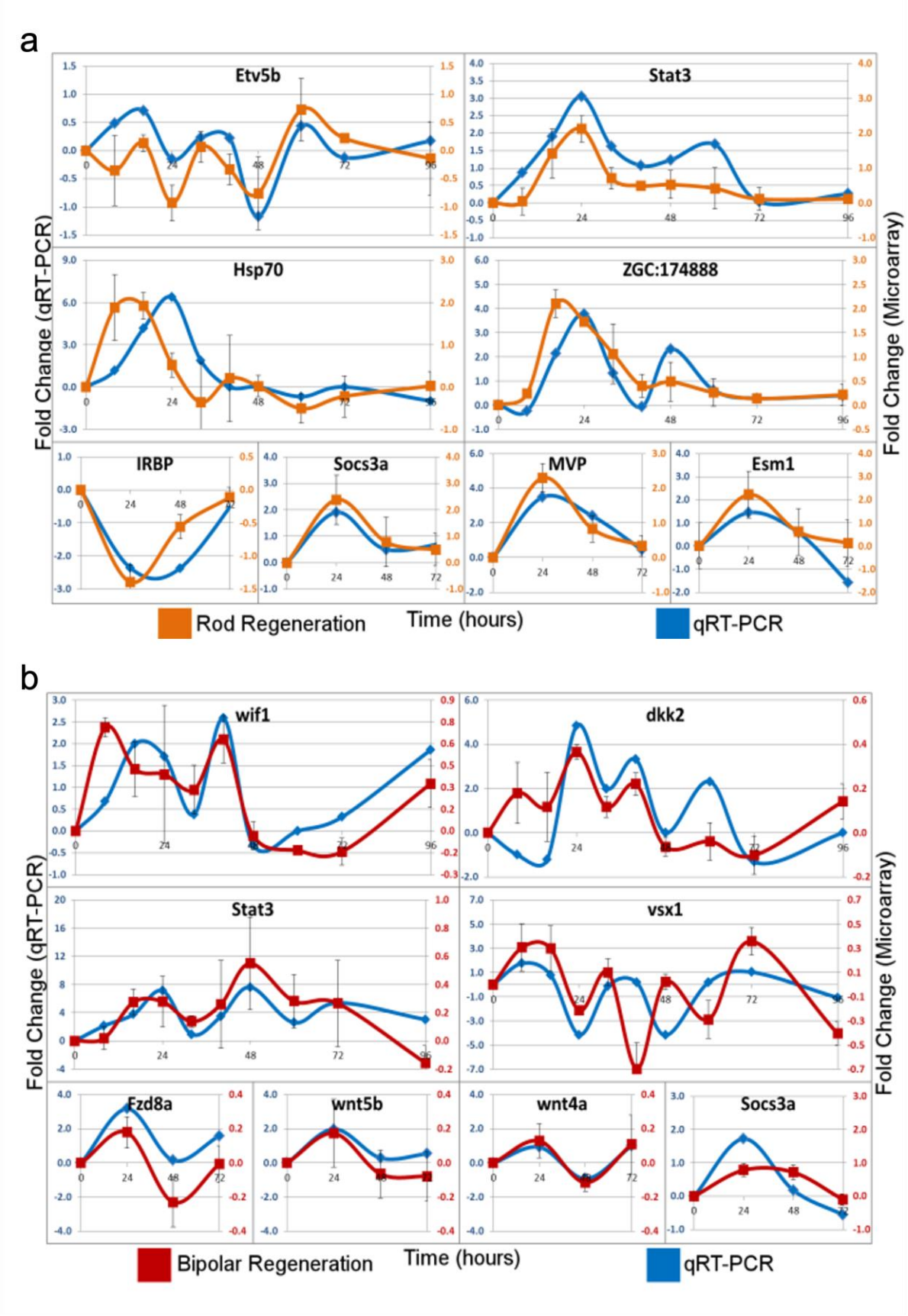
Supp. Table 1. mRNA quality of samples collected for microarray analysis

Run	Cell Type	Concentration (ng)	mRNA Quality (RIN)
1	Rod	128.8 - 2327	6.6-10
2	Rod	109.2 - 992	7.8-9.8
3	Rod	136.0 - 1728	9.8-10
4	Bipolar	141.0 - 1029	5.9-9.4
5	Bipolar	145.4 - 990.8	8.2-9.3
6	Bipolar	204.5 - 685.4	8.4-9.4

Genetic Differences Observed Between Two Cell-specific Regeneration Paradigms

Using a 1.5-fold change and ≤ 0.05 *p*-value cutoff compared to expression values at 0 hpa, a total of 2,531 differentially expressed genes (DEGs) were observed across both paradigms. Across all timepoints 918 and 1,249 DEGs were unique to the rod or bipolar cell ablation paradigm, respectively, and 364 DEGs were shared between the two (Fig. 2b). Plotting the number of

DEGs per each time point showed two peaks at 32 and 60 hpa for the NTR-rod line, and a single peak at 24 hrs post ablation (hpa) for the NTR-bipolar line (Fig. 2c). Next, quantitative reverse transcriptase PCR (qRT-PCR) was used to validate gene expression changes for 8 genes per each paradigm at 0, 24, 48, 72 and 96 hpa (Supp. Fig. 3, primers used are listed in Supp. Table 2). Genes in the Janus kinase-signal transducer and activator of transcription (JAK/STAT) and Wnt pathways were selected for qRT-PCR analysis as both have been implicated in regeneration of the targeted cell types[10,54]. Temporally-resolved expression trends, rather than absolute fold change, were utilized for validation as differences in normalization methods have the potential to impact overall expression levels[55]. These data revealed only minor differences in expression patterns between the microarray and qRT-PCR suggesting the microarray data accurately reflect gene expression changes (Supp. Fig. 3). The top 10 up and down DEGs at all timepoints for each paradigm were then identified by lowest single *p*-value, many passing the DEG threshold at multiple timepoints during out study (Fig. 2d).


a
Etv5b
Stat3
Hsp70
ZGC:174888
IRBP
Socs3a
MVP
Esm1
Fold Change (qRT-PCR)
Fold Change (Microarray)
Rod Regeneration
Time (hours)
qRT-PCR
b
wif1
dkk2
Stat3
vsx1
Fzd8a
wnt5b
wnt4a
Socs3a
Fold Change (qRT-PCR)
Fold Change (Microarray)
Bipolar Regeneration
Time (hours)
qRT-PCR

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Supp. Fig. 3. qRT-PCR validation of mRNA expression changes.

(a, b) A subset of tested genes were selected for validation using quantitative Reverse Transcription – Polymerase Chain Reaction (qRT-PCR). 8 genes were selected for a temporal analysis from 0-72h post Mtz in either the NTR-rod (A) or NTR-bipolar (B) paradigm with beta actin serving as a control.

Supp. Table 2. qPCR primers used

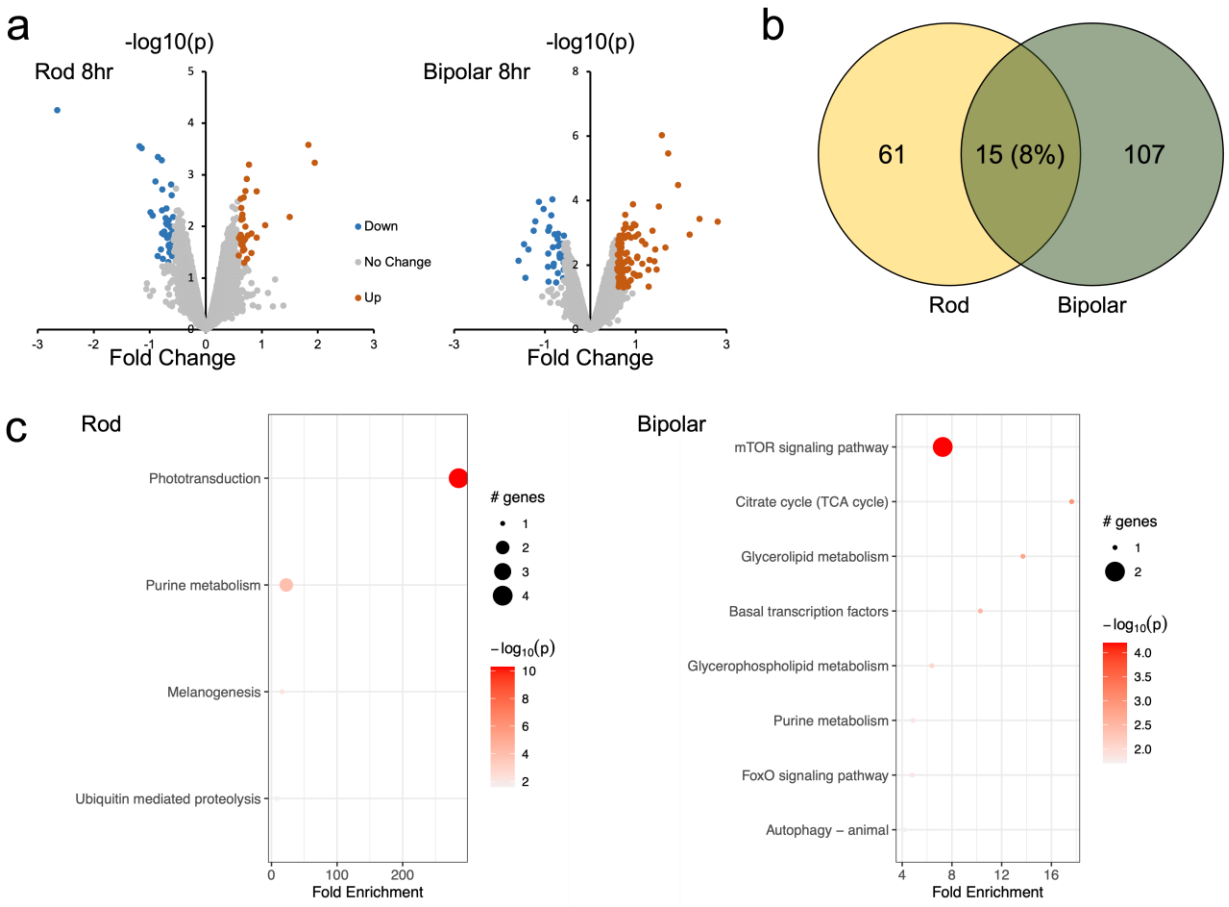
Gene	Ensembl ID	Sequence 5'-3'
stat3	ENSDARG00000022712	F, CTCATGCACAACGAAGCTGCTG
		R, TCCATGTCCGAGGTGAGGGATTCG
etv5b	ENSDARG00000044511	F, ACACCTGTCAATCACCCAGATGC
		R, AAAGCTGCCGATGGAACCTGTG
zgc:174888	ENSDARG00000077176	F, AGAAGCATGTCACCAACAGTGC
		R, TCGCACCCACTTCTTCCTTGAACAG
irbp	ENSDARG00000059163	F, GGAACAAAGTGGTGGACACTGACG
		R, GCATGCCCACCGATGTTATTTCTC
socs3a	ENSDARG00000025428	F, ACTCTGTGGGCACCAATCACTG
		R, CTGGTTTCTGTCGAACGTCTCC
hsp70	ENSDARG00000021924	F,GACCAGGGCAACAGAACAAC
		R, GGTCTCAATACCCAGAGACAGTGG
mvp	ENSDARG00000021242	F, GAGTGCAAAGAGTTACTGGTGAGG
		R, TCATGAGCTCCAGGCAGATACG

*wif-1**	ENSDARG00000005541	F, GCCAGTGCGCTTTAAACCAACC
		R, TCACCTCAAATGCTGCCACACC
*dkk2**	ENSDARG00000076420	F, ATGCCTCTTTTAAGCCGAAGTGC
		R,GCCTTTTTTGCGCTGTTTGG
*fzd8a**	ENSDARG00000045444	F, TACTTCATGTGCCTTCTGGTGG
		R, TGGGCACTAAGACGTTAAGGC
*wnt5b**	ENSDARG00000034894	F, CAGCTGACGGGCCTATCTCAGG
		R, AAAGCTCACCCTCACGGCACG
*wnt4a**	ENSDARG00000071208	F, CAATGCGAGCAACTGGCTATAC
		R, AATGCAGCTTCCCTCGTACCTT
vsx1	ENSDARG00000056292	F, CCAGAGGACAGGATACAGGTATGG
		R, TTCTGGGAGTGGAATGGAGGT
*β-actin***	ENSDARG00000037746	F, CGAGCAGGAGATGGGAACC
		R, CAACGGAAACGCTCATTGC

Transcriptomic Differences Following Regeneration of Uniquely Targeted Neurons

To identify differentially regulated signaling pathways at each time point, and across broader temporally-resolved expression patterns, several analysis methods were used. First, volcano plots and pathfindR[56] analyses were performed to reveal paradigm-specific and shared DEG-associated signaling pathways at each time point (Supp. Figs. 4-14). Volcano plots correlate log-fold changes in gene expression to *p*-values, with upregulated and downregulated DEGs indicated by orange and blue dots, respectively (Supp. Figs. 4a-14a). Venn diagrams show the

total number of DEGs unique to each paradigm and the number of shared DEGs (Supp. Figs. 4b-14b). Kyoto Encyclopedia of Genes and Genomes (KEGG) analysis via the pathfindR package revealed the top enriched pathways associated with either the rod or bipolar paradigm-specific DEGs, as well as shared DEGs (Supp. Figs. 4c-14c).

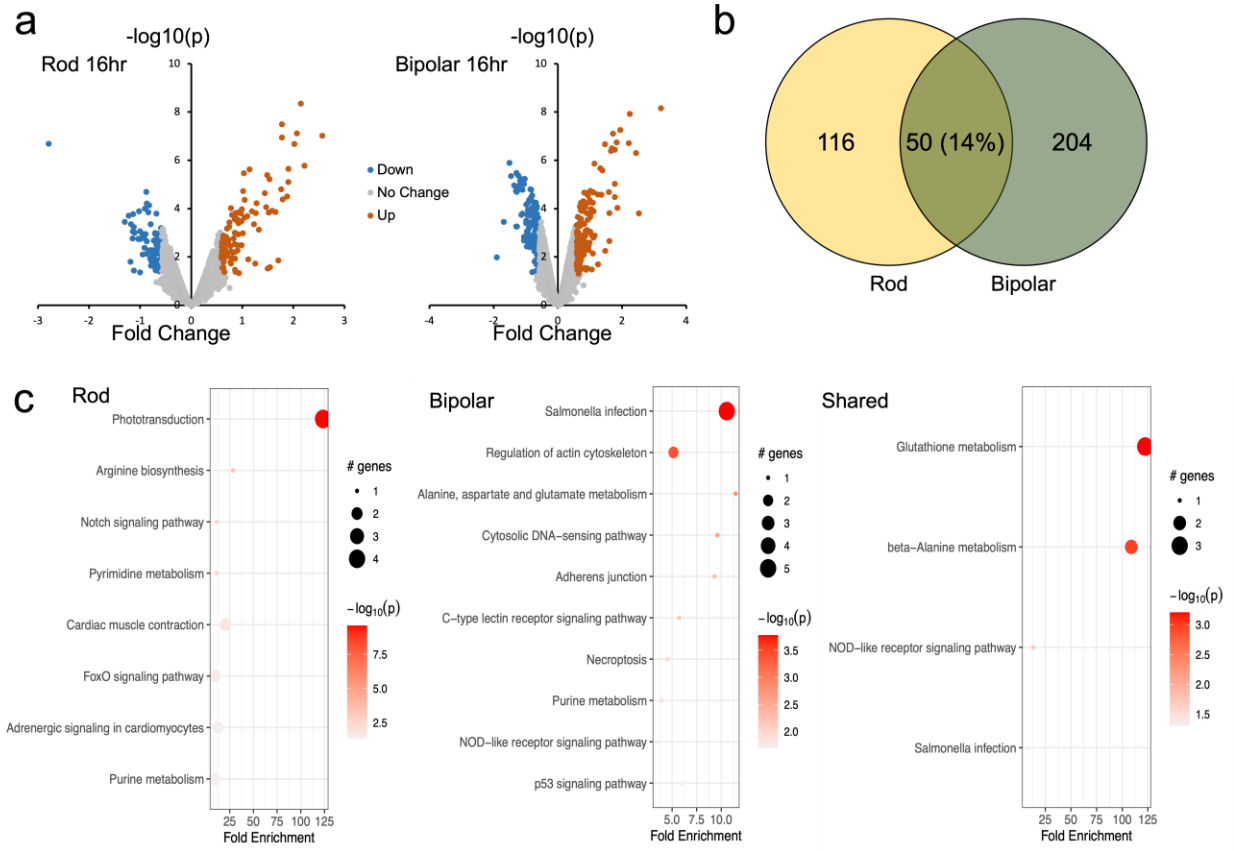


Supp. Fig. 4. Analysis of DEGs and associated pathway terms at timepoint 8 hours following Mtz.

(a) Volcano plot showing the identified up (orange) and down (blue) DEGs in both NTR-rod and NTR-bipolar treatment paradigms.

(b) Venn diagram showing the unique as well as shared (and % of shared) DEGs between the two paradigms.

(c) KEGG pathfindR identified significantly enriched pathways in the NTR-rod and NTR-bipolar paradigms.

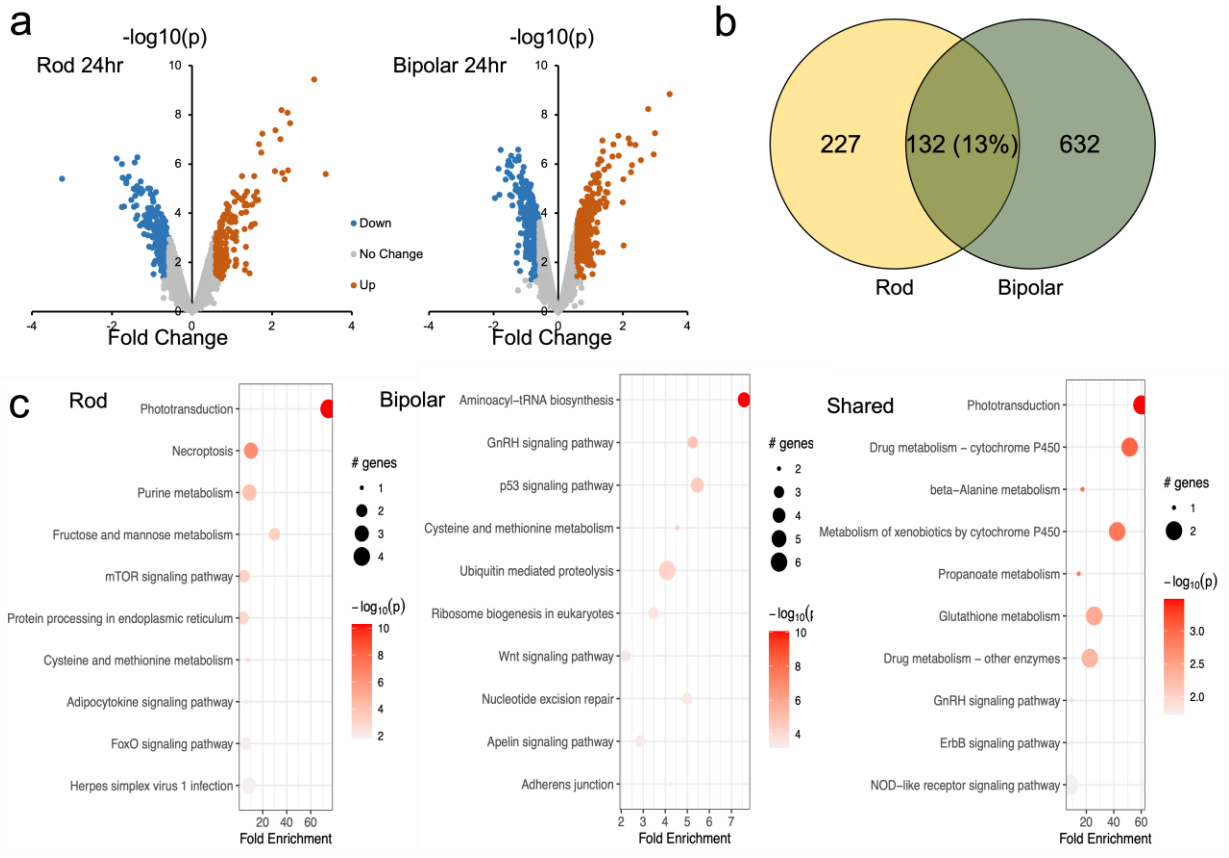


Supp. Fig. 5. Analysis of DEGs and associated pathway terms at timepoint 16 hours following Mtz.

(a) Volcano plot showing the identified up (orange) and down (blue) DEGs in both NTR-rod and NTR-bipolar treatment paradigms.

(b) Venn diagram showing the unique as well as shared (and % of shared) DEGs between the two paradigms.

(c) KEGG pathfindR identified significantly enriched pathways in the NTR-rod and NTR-bipolar paradigms as well as those shared between the two paradigms.

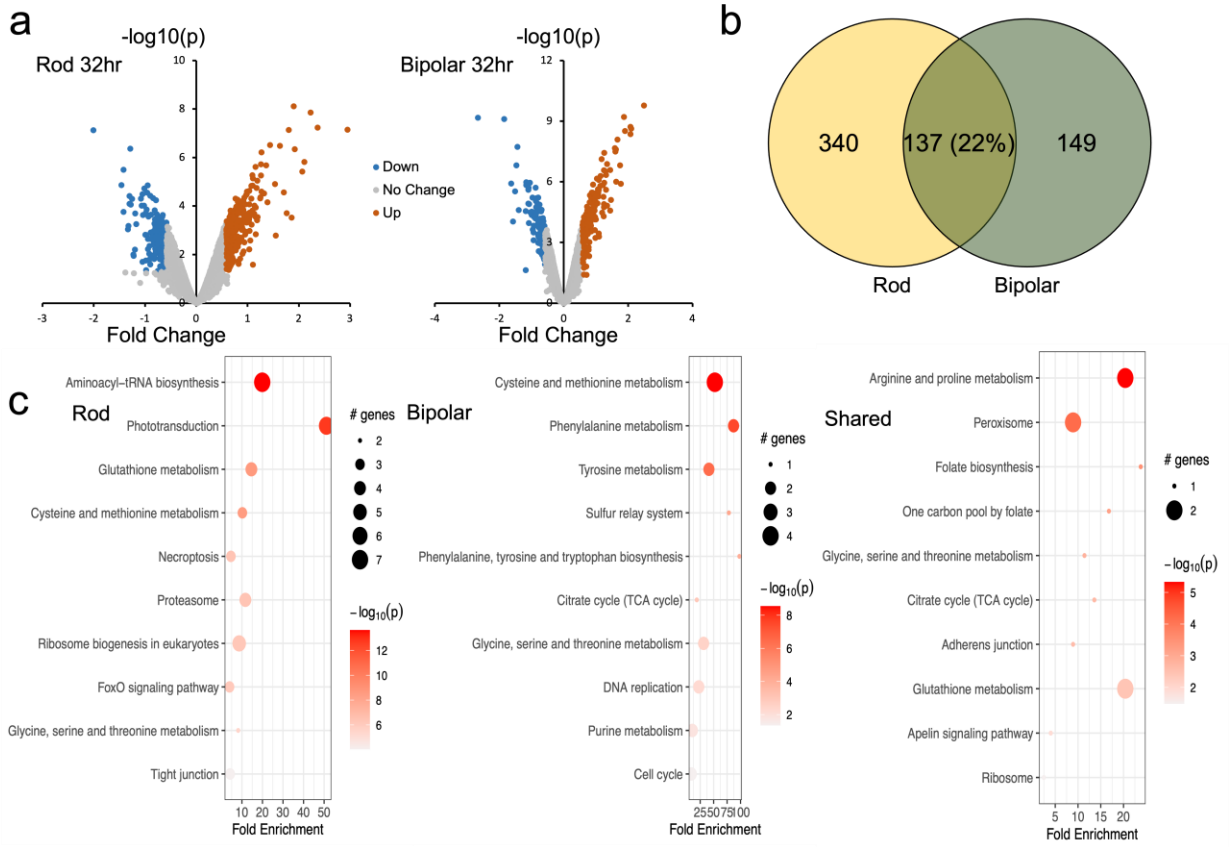


Supp. Fig. 6. Analysis of DEGs and associated pathway terms at timepoint 24 hours following Mtz.

(a) Volcano plot showing the identified up (orange) and down (blue) DEGs in both NTR-rod and NTR-bipolar treatment paradigms.

(b) Venn diagram showing the unique as well as shared (and % of shared) DEGs between the two paradigms.

(c) KEGG pathfindR identified significantly enriched pathways in the NTR-rod and NTR-bipolar paradigms as well as those shared between the two paradigms.

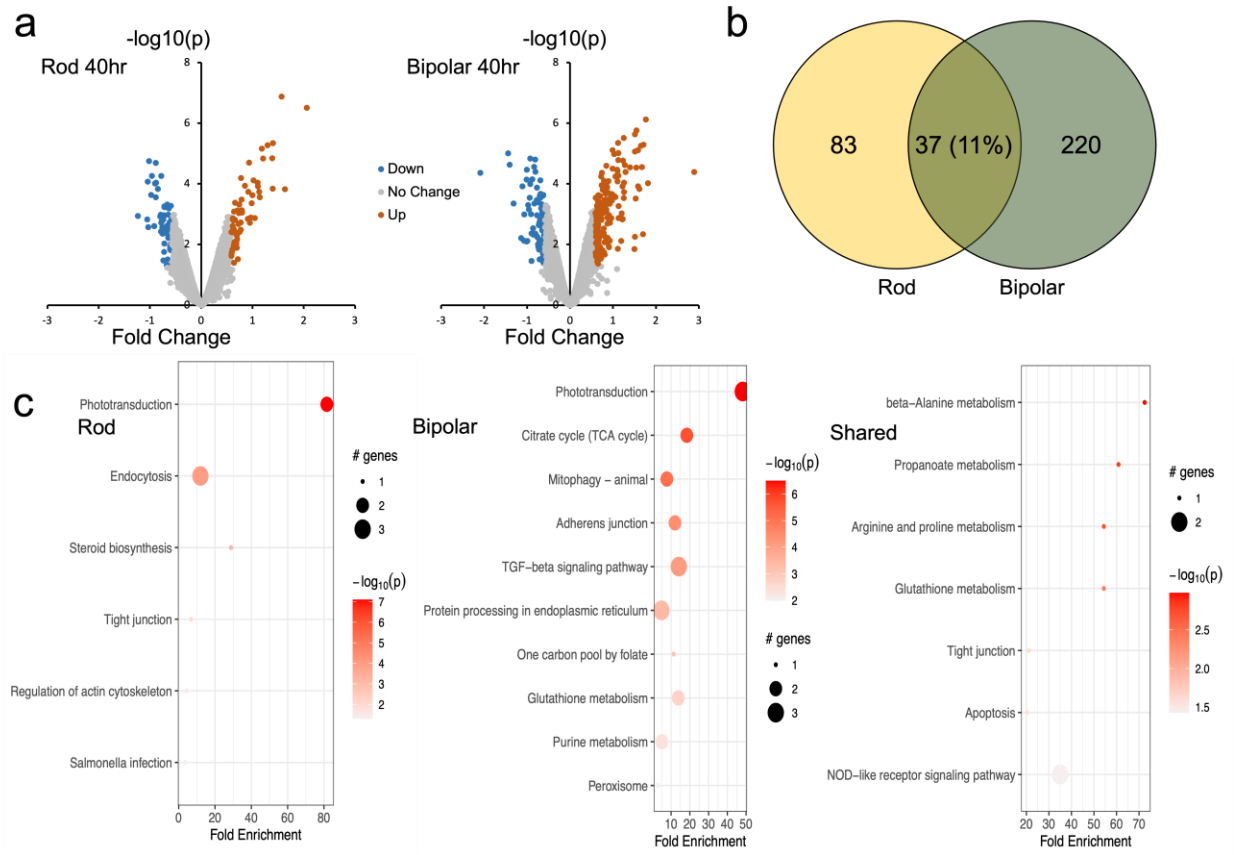


<u>Supp. Fig. 7. Analysis of DEGs and associated pathway terms at timepoint 32 hours following Mtz.</u>

(a) Volcano plot showing the identified up (orange) and down (blue) DEGs in both NTR-rod and NTR-bipolar treatment paradigms.

(b) Venn diagram showing the unique as well as shared (and % of shared) DEGs between the two paradigms.

(c) KEGG pathfindR identified significantly enriched pathways in the NTR-rod and NTR-bipolar paradigms.

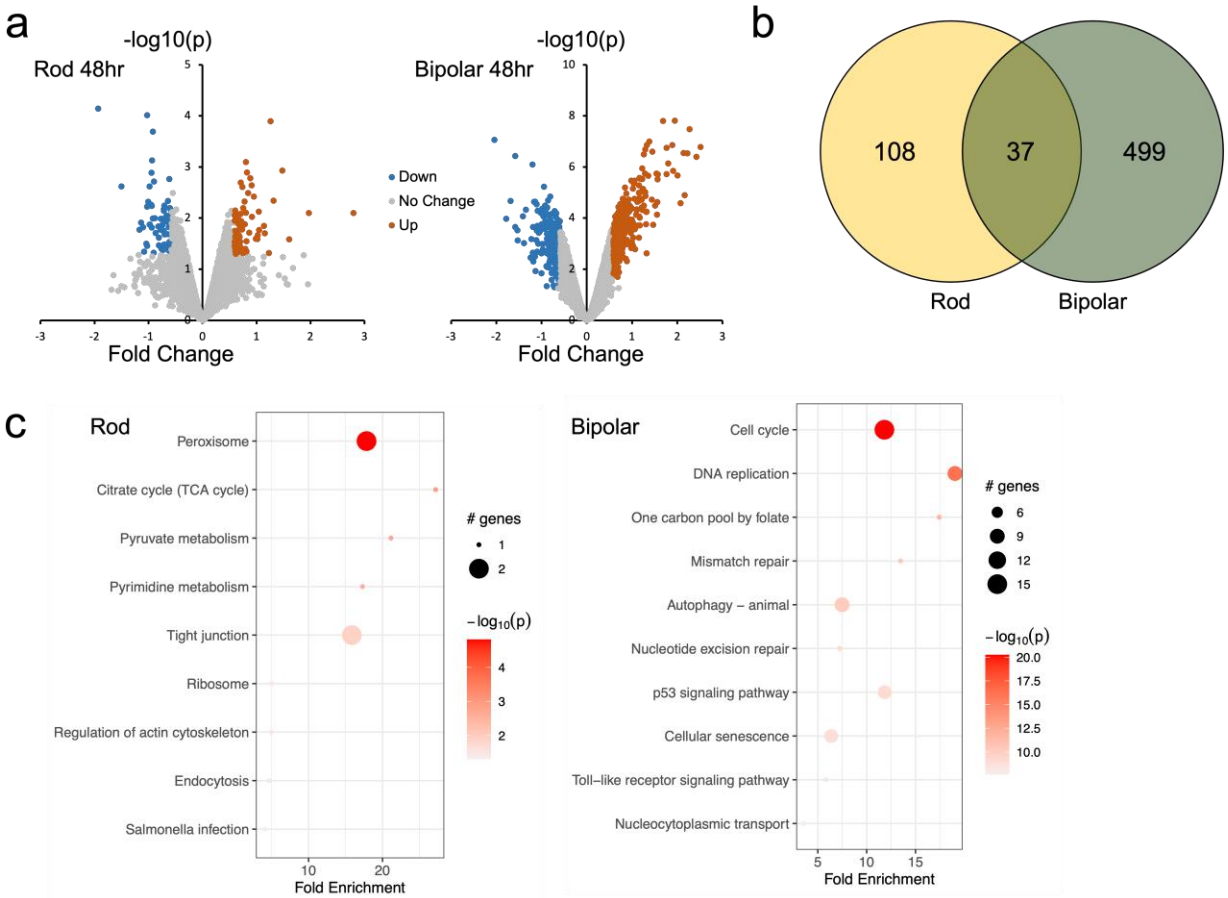


Supp. Fig. 8. Analysis of DEGs and associated pathway terms at timepoint 40 hours following Mtz.

(a) Volcano plot showing the identified up (orange) and down (blue) DEGs in both NTR-rod and NTR-bipolar treatment paradigms.

(b) Venn diagram showing the unique as well as shared (and % of shared) DEGs between the two paradigms.

(c) KEGG pathfindR identified significantly enriched pathways in the NTR-rod and NTR-bipolar paradigms as well as those shared between the two paradigms.

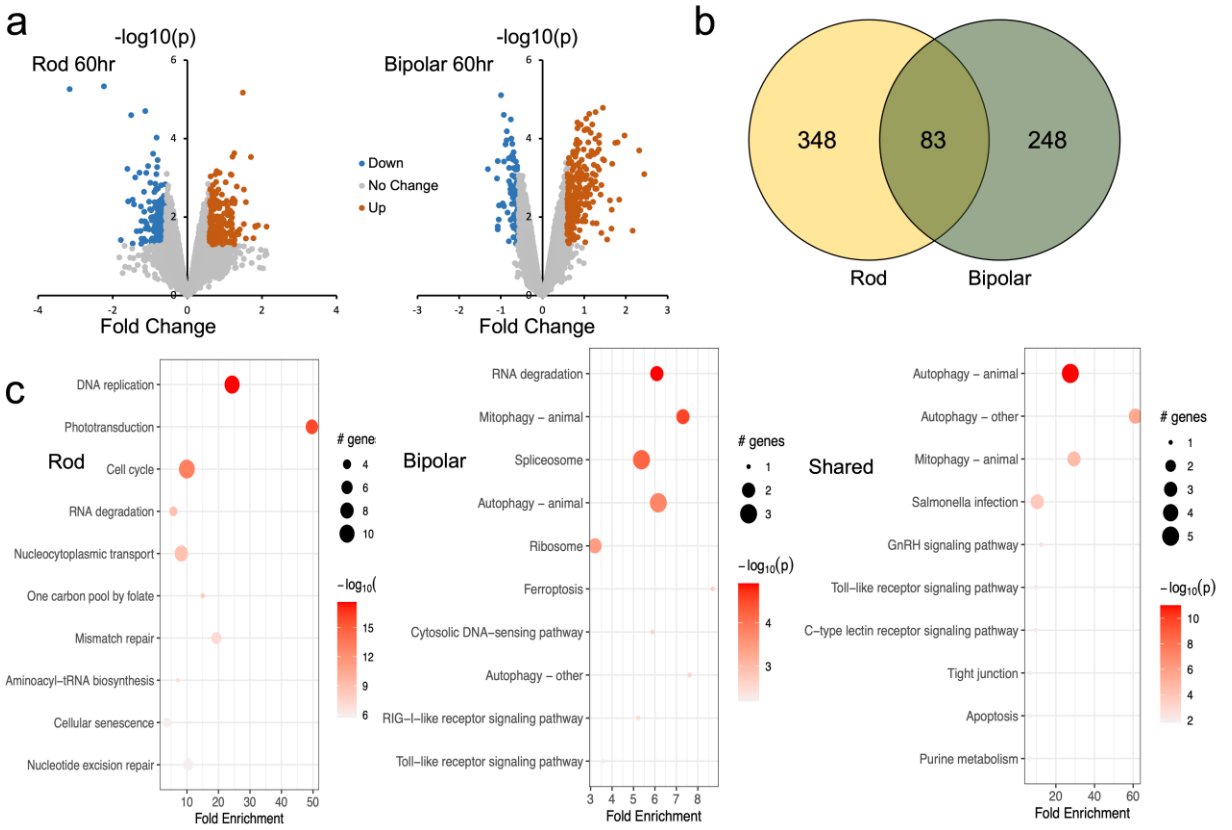


Supp. Fig. 9. Analysis of DEGs and associated pathway terms at timepoint 48 hours following Mtz.

(a) Volcano plot showing the identified up (orange) and down (blue) DEGs in both NTR-rod and NTR-bipolar treatment paradigms.

(b) Venn diagram showing the unique as well as shared (and % of shared) DEGs between the two paradigms.

(c) KEGG pathfindR identified significantly enriched pathways in the NTR-rod and NTR-bipolar paradigms.

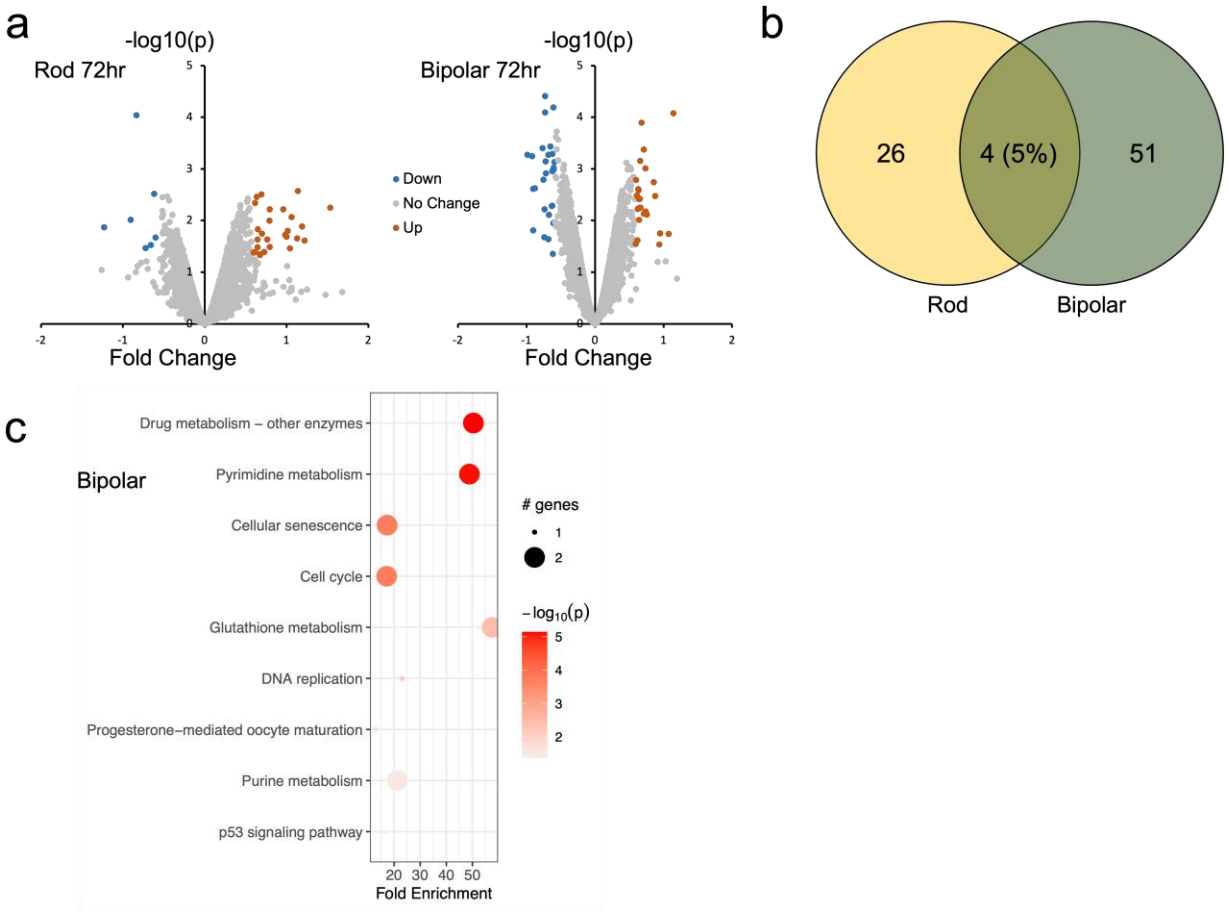


Supp. Fig. 10. Analysis of DEGs and associated pathway terms at timepoint 60 hours following Mtz.

(a) Volcano plot showing the identified up (orange) and down (blue) DEGs in both NTR-rod and NTR-bipolar treatment paradigms.

(b) Venn diagram showing the unique as well as shared (and % of shared) DEGs between the two paradigms.

(c) KEGG pathfindR identified significantly enriched pathways in the NTR-rod and NTR-bipolar paradigms as well as those shared between the two paradigms.

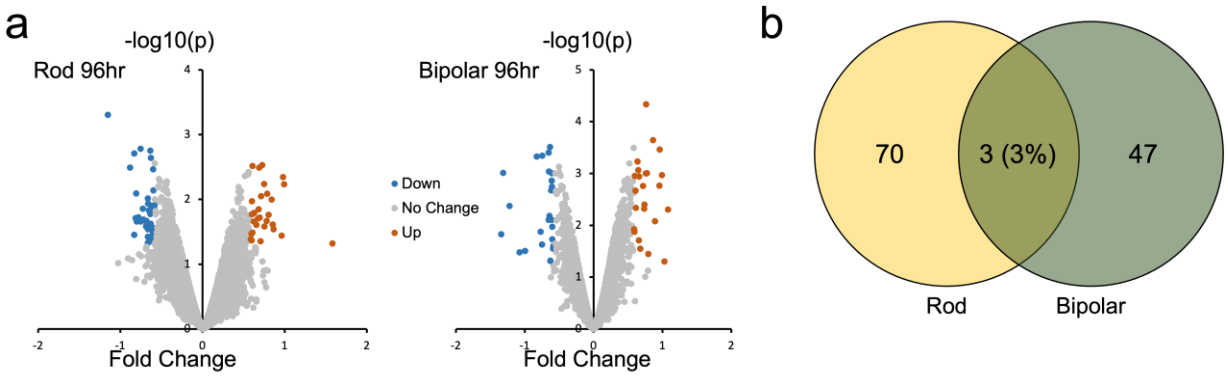


Supp. Fig. 11. Analysis of DEGs and associated pathway terms at timepoint 72 hours following Mtz.

(a) Volcano plot showing the identified up (orange) and down (blue) DEGs in both NTR-rod and NTR-bipolar treatment paradigms.

(b) Venn diagram showing the unique as well as shared (and % of shared) DEGs between the two paradigms.

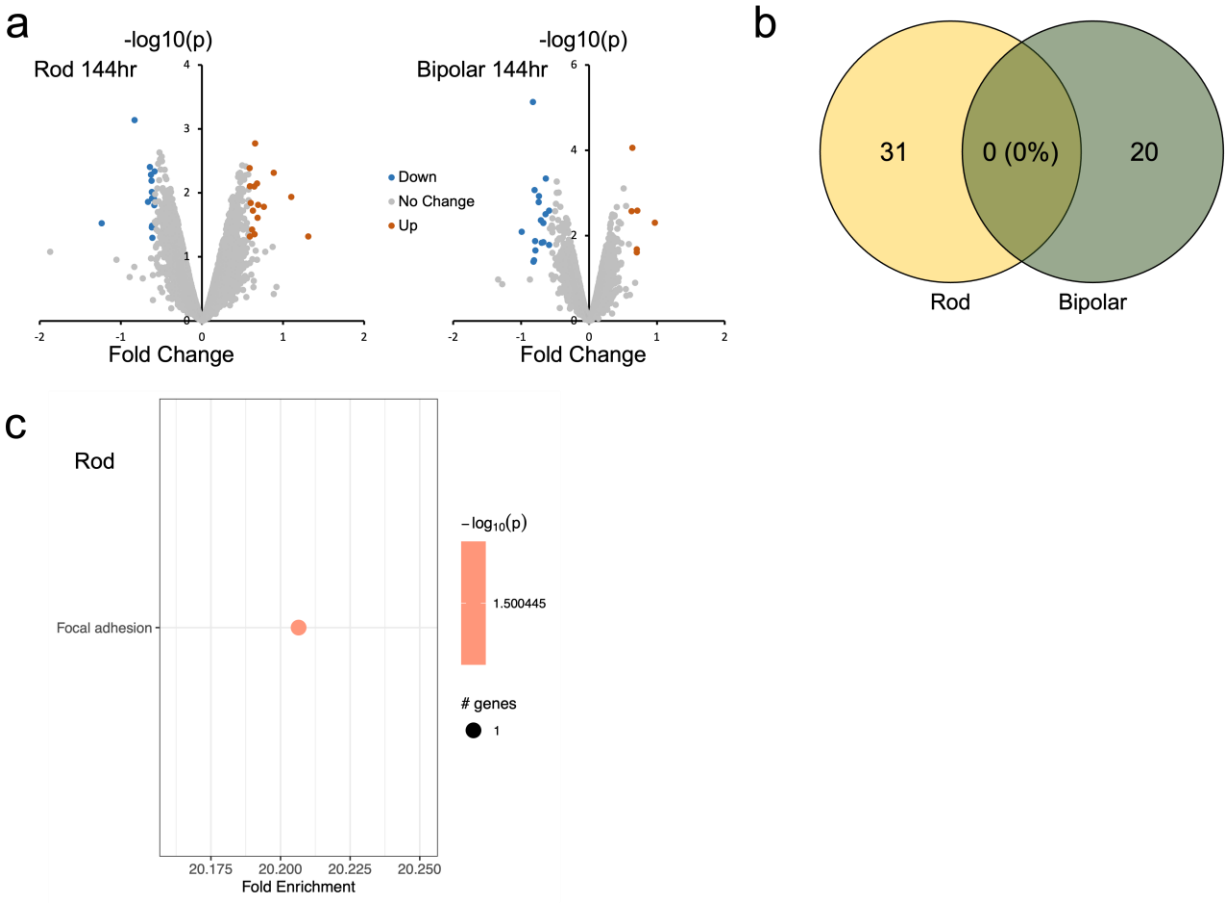
(c) KEGG pathfindR identified significantly enriched pathways in the NTR-bipolar paradigm.



Supp. Fig. 12. Analysis of DEGs and associated pathway terms at timepoint 96 hours following Mtz.

(a) Volcano plot showing the identified up (orange) and down (blue) DEGs in both NTR-rod and NTR-bipolar treatment paradigms.

(b) Venn diagram showing the unique as well as shared (and % of shared) DEGs between the two paradigms.

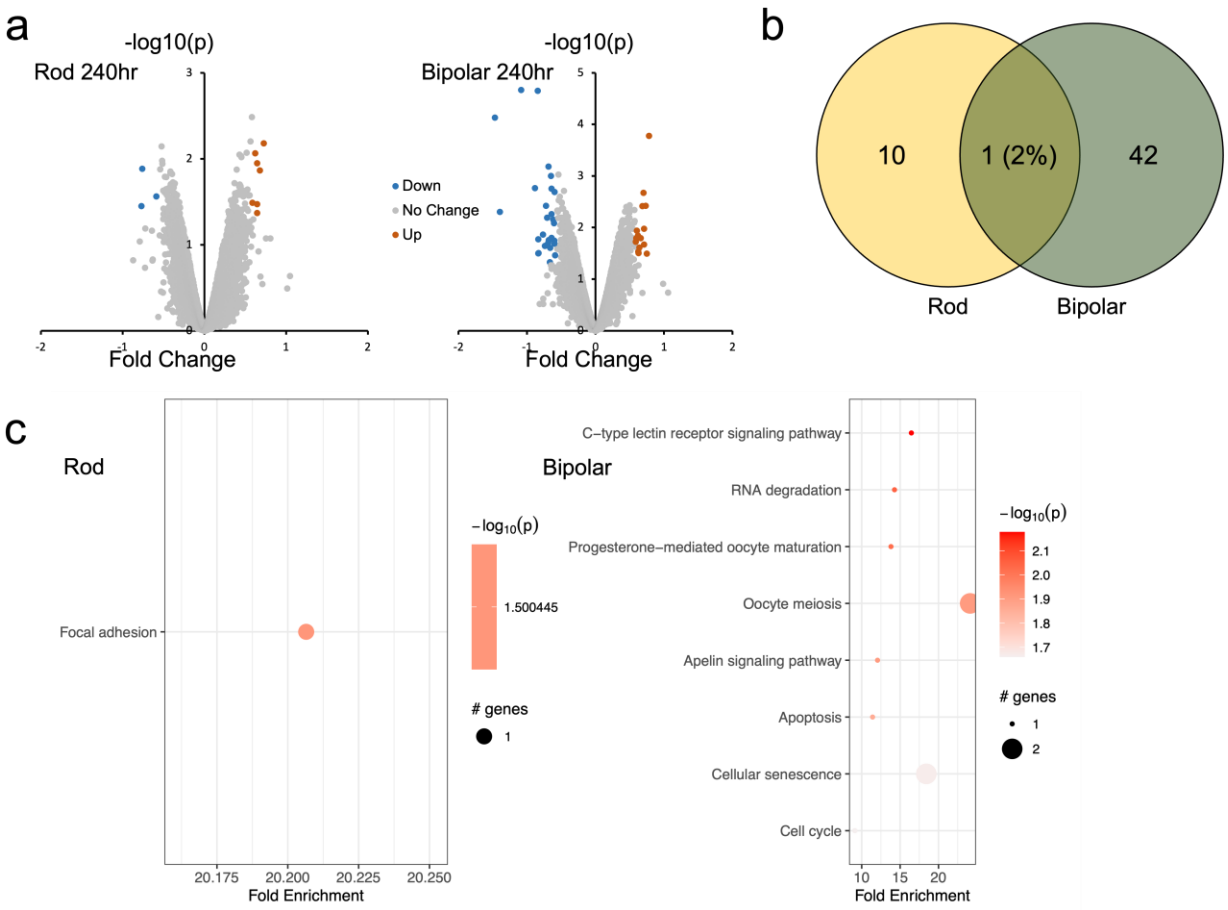


Supp. Fig. 13. Analysis of DEGs and associated pathway terms at timepoint 144 hours following Mtz.

(a) Volcano plot showing the identified up (orange) and down (blue) DEGs in both NTR-rod and NTR-bipolar treatment paradigms.

(b) Venn diagram showing the unique as well as shared (and % of shared) DEGs between the two paradigms.

(c) KEGG pathfindR identified significantly enriched pathways in the NTR-rod paradigm.



Supp. Fig. 14. Analysis of DEGs and associated pathway terms at timepoint 240 hours following Mtz.

(a) Volcano plot showing the identified up (orange) and down (blue) DEGs in both NTR-rod and NTR-bipolar treatment paradigms.

(b) Venn diagram showing the unique as well as shared (and % of shared) DEGs between the two paradigms.

(c) KEGG pathfindR identified significantly enriched pathways in the NTR-rod and NTR-bipolar paradigms.

In order to examine DEGs contributing to different stages of the regeneration process, we identified DEGs whose expression profile fit one of four gaussian-type patterns during the regenerative process: increased (up early) or decreased (down early) from16 to 32 hpa, and increased (up late) or decreased (down late) from 48 to 72 hpa (Fig. 3a). Notably, this captured the majority of DEGs observed. Heatmaps are shown for the top 50 DEGs for each pattern in both the NTR-rod and NTR-bipolar paradigms (Fig. 3b, c). The two reciprocally regulated DEG patterns – up/down early (Fig. 4) and up/down late (Fig. 5) – were evaluated using KEGG, Gene Ontology (GO) and Ingenuity Pathway Analysis (IPA). For early pattern DEGS (Fig. 4a), the top 10 pathfindR KEGG terms were plotted for rod-specific, bipolar-specific and shared gene sets (Fig. 4b-d). Predictably for the rod paradigm, phototransduction was the most enriched term. Additional rod-specific KEGG pathways included RNA degradation, proteosome, and necroptosis (Fig. 4b). For the bipolar paradigm, p53 signaling was the most enriched term, other pathways included autophagy, nucleoside excision repair, and cysteine and methionine metabolism (Fig. 4c). Shared KEGG pathway terms for early pattern DEGs included phototransduction, mTor signaling, and glutathione metabolism (Fig. 4d). Gene Ontology (GO) analysis of the same datasets revealed additional terms, such as circadian rhythm and ncRNA processing for the rod paradigm, cellular apoptotic processes and response to stress for the bipolar paradigm, and response to temperature stimulus and DNA conformation change among shared terms (Fig. 4e-g). Lastly, IPA was used to generate unsupervised networks from the early DEG lists for the NTR-rod and NTR-bipolar paradigms (Fig. 4h, i). For the rod paradigm, signal transducer and activator of transcription 3 (STAT3) was identified as the central mediator of the early DEG network along with multiple cytokine terms (e.g, interleukin-1b and 6, IL-1B, IL-6) and associated terms for the oxidative stress response (Fig. 4h). In the bipolar paradigm, the

central mediator was peroxisome proliferator-activated receptor gamma (PPARG), other noteworthy genes included tumor protein 53 (*tp53*), the cytokine *il10*, *stat5a* and *stat5b* (Fig. 4i). We then produced a summary bar chart of all related immune terms identified from IPA. Early pattern IPA-implicated pathways of the rod paradigm included JAK family kinases, chemokine (C-X-C motif) receptor 4 (CXCR4), IL-6, interferon, and iNOS signaling, as well as multiple other IL-family cytokines (Supp. Fig. 15). For the bipolar paradigm, early pattern IPA terms included similar IL-family cytokines but also added prolactin and leukocyte extravasation signaling, as well as phagosome maturation (Supp. Fig. 16). Combined, KEGG, GO, and IPA analysis revealed that factors implicated in regulating the early stages of regeneration are linked more to the loss of individual retinal cell types than to a common signature across cell types.

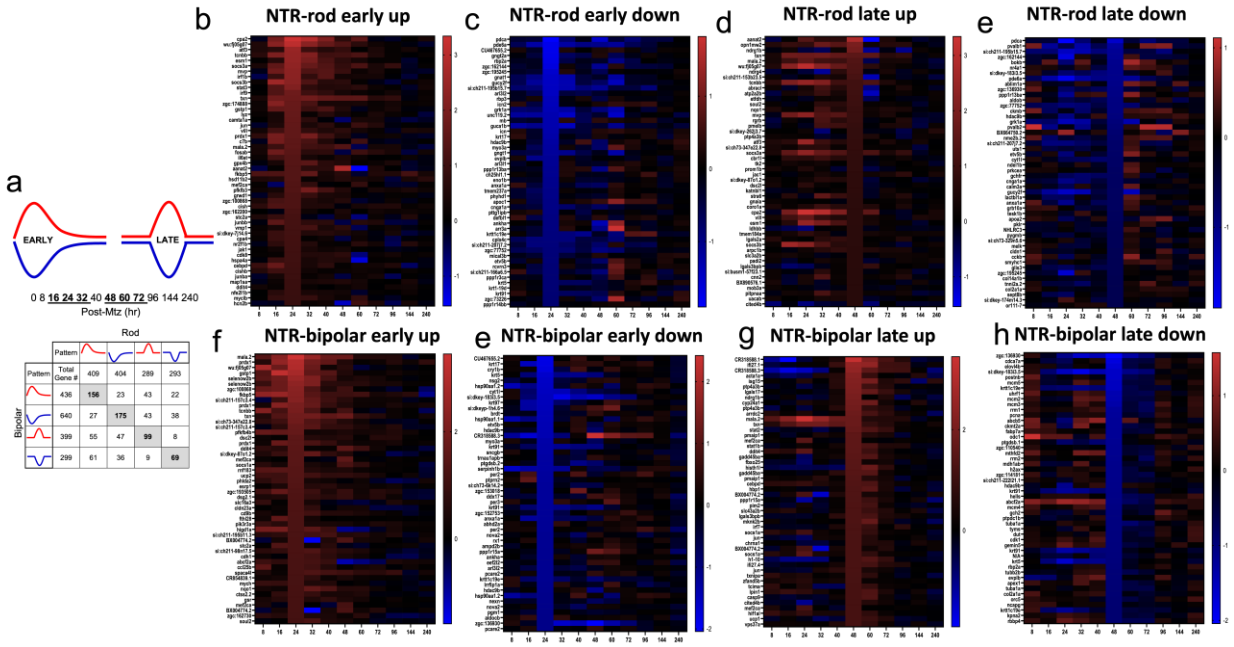
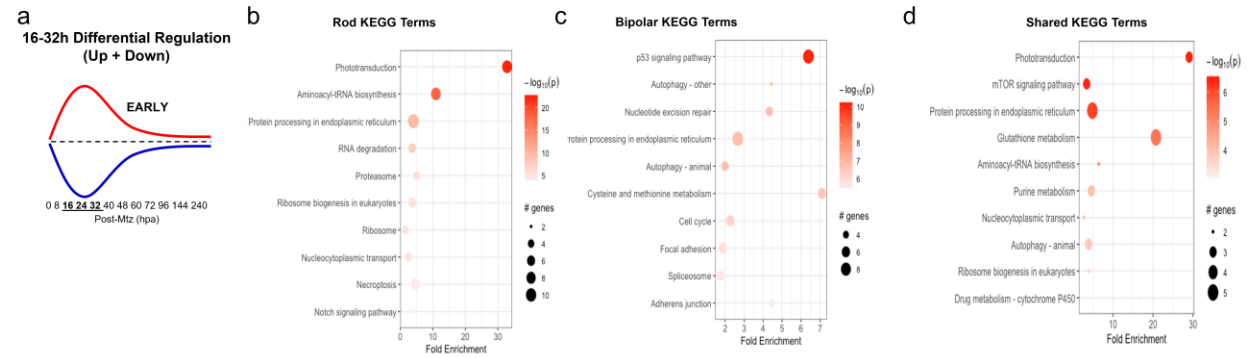


Fig. 3. Identification of early and late DEG patterns and heatmaps for top DEGs in each. (a) DEGs for each paradigm were split into upregulated (red) and downregulated (blue) as well as early (16-32h) and late (48-72h) based on peaks in figure 2. The distribution of DEGs in these 8 patterns is shown in terms of unique and shared DEGs across both cell types.

(b-h) The top 50 genes are plotted in heatmaps as a function of the largest fold changes at the middle timepoint in each pattern (24h and 60h) to demonstrate top genes defining each 8 patterns (NTR-rod and NTR-bipolar for patterns early-up, early-down, late-up and late-down).



e

Rod Early GO Terms	Fold Enrich.	FDR
1. ncRNA metabolic process	4.29	8.46E-06
2. response to light stimulus	6.67	1.50E-05
3. ribosome biogenesis	5.14	1.62E-05
4. anatomical structure development	1.59	1.78E-04
5. circadian rhythm	8.74	1.81E-04
6. oxoacid metabolic process	2.99	3.42E-04
7. visual perception	5.23	3.46E-04
8. rRNA metabolic process	5.29	3.51E-04
9. organonitrogen compound biosynthetic process	2.31	4.47E-04
10. ncRNA processing	3.68	1.55E-03

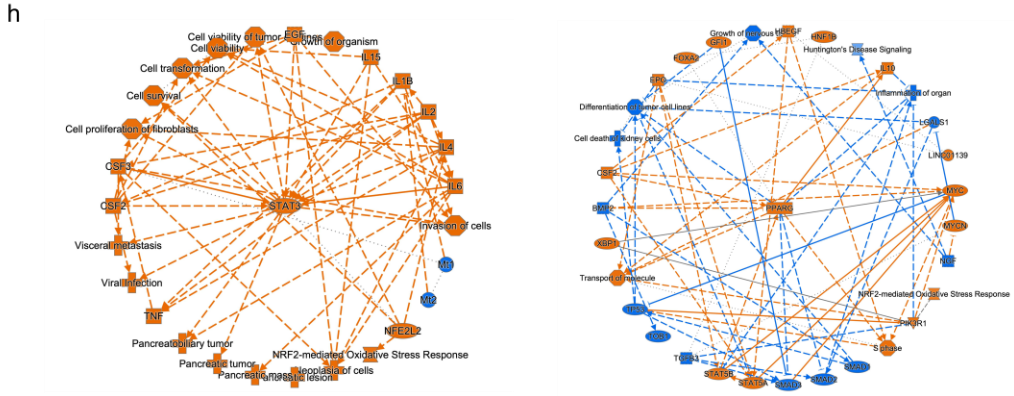
f

Bipolar Early GO Terms	Fold Enrich.	FDR
1. anatomical structure development	1.54	8.69E-06
2. apoptotic process	3.1	2.37E-03
3. protein refolding	19.21	2.90E-03
4. cellular response to stress	2.16	5.59E-03
5. GPCR signaling pathway	0.3	5.89E-03
6. response to light stimulus	4.03	6.00E-03
7. embryo development	1.88	6.23E-03
8. regulation of metabolic process	1.38	8.70E-03
9. eye development	2.22	2.15E-02
10. small molecule metabolic process	1.78	2.17E-02

g

Shared Early GO Terms	Fold Enrich.	FDR
1. response to temperature stimulus	14.75	4.73E-04
2. DNA conformation change	6.15	1.31E-02
3. organic cyclic compound biosynthetic process	2.89	1.66E-02
4. small molecule metabolic process	2.26	1.90E-02
5. protein-chromophore linkage	11.06	1.92E-02
6. anatomical structure development	1.55	2.06E-02
7. circadian rhythm	7.92	2.18E-02
8. response to light stimulus	5.34	2.87E-02
9. cell redox homeostasis	17.86	4.18E-02
10. response to stress	1.99	4.45E-02

h



i

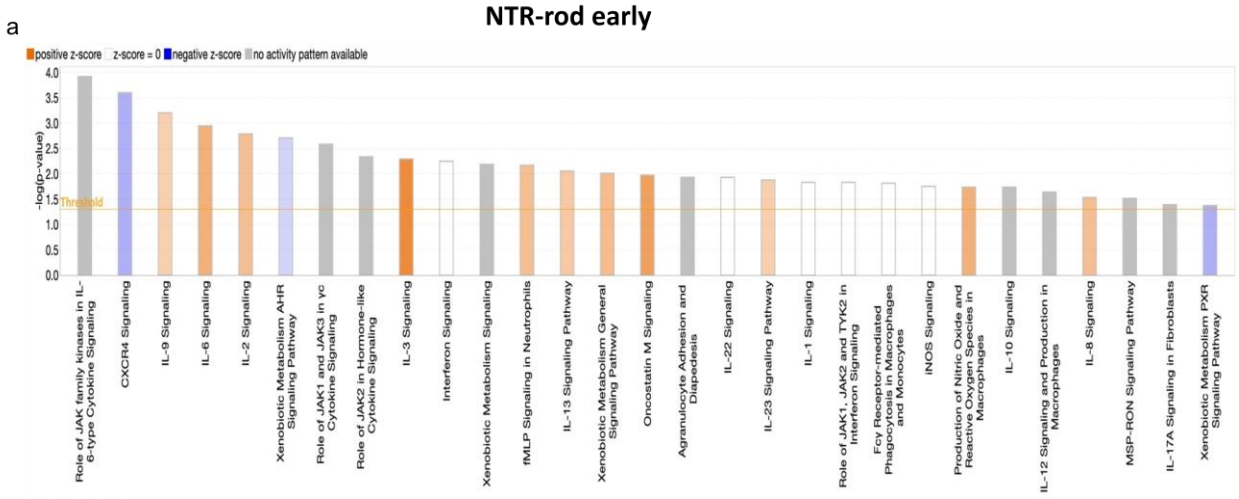
Fig. 4. Pathway analysis of early DEG pattern in both paradigms.

(a) Curve demonstrating expression pattern for early upregulated (red) and downregulated (blue) genes along our timepoints.

(b-d) Top 10 enriched KEGG pathway terms including p-value and # of genes found as DEGs in the NTR-rod (b), NTR-bipolar (c) or from shared DEGs across both paradigms (d).

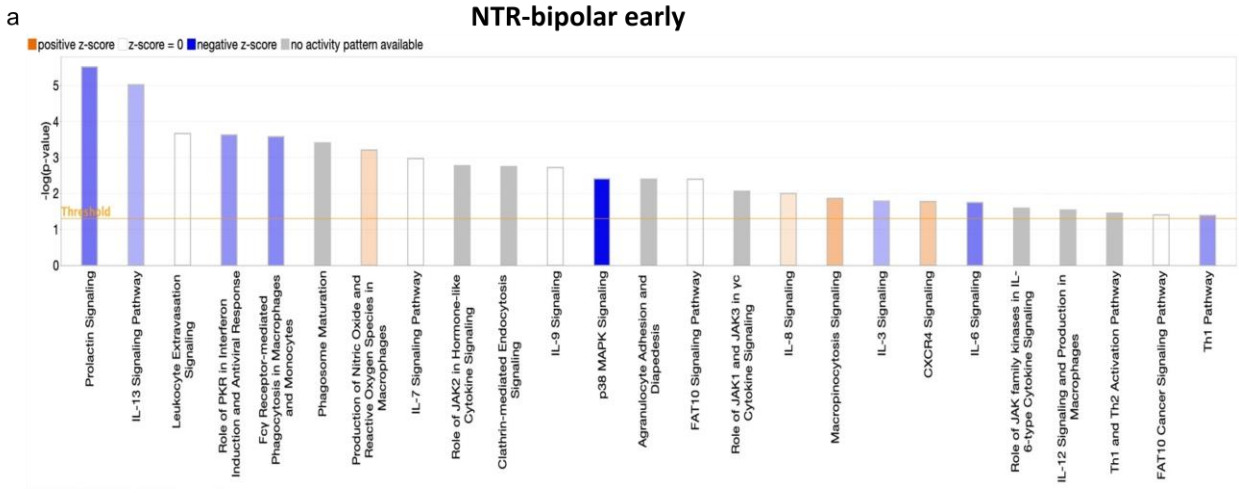
(e-g) Top 10 enriched Gene Ontology pathway terms including fold enrichment and false discovery rate in the NTR-rod (e), NTR-bipolar (f) or from shared DEGs across both paradigms (g).

(h-i) Unsupervised gene networks produced from ingenuity pathway analysis for DEGs in the NTR-rod (h) and NTR-bipolar (i) paradigm. Orange indicates upregulated gene/pathway term while blue indicates downregulated.



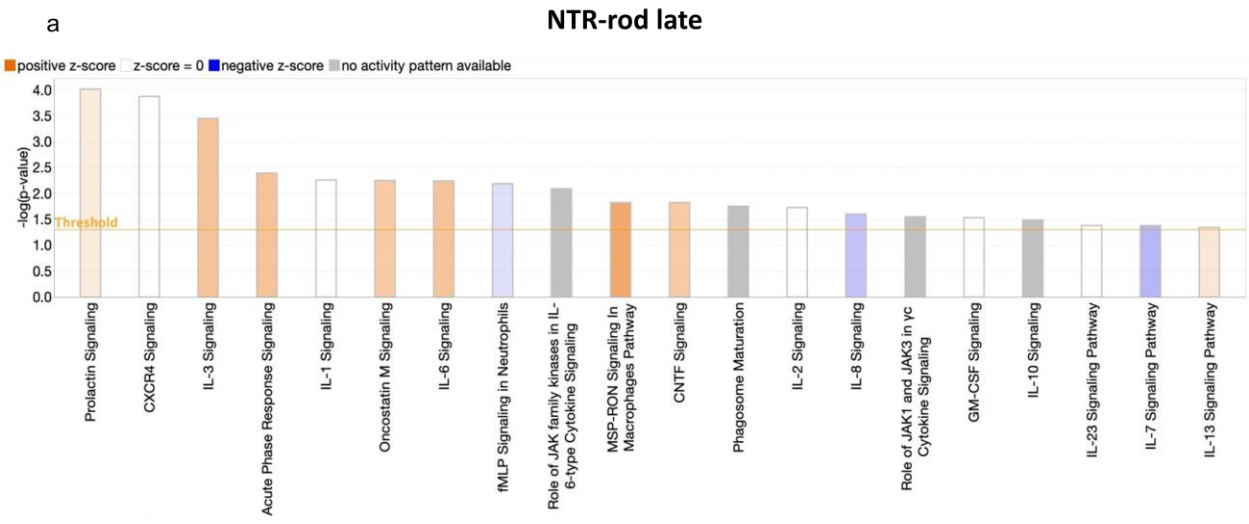
Supp. Fig. 15. Immune related terms identified from IPA for NTR-rod early pattern.

(a-d) IPA was used to test for enriched immune related pathway terms from DEGs for the NTR-rod early pattern.



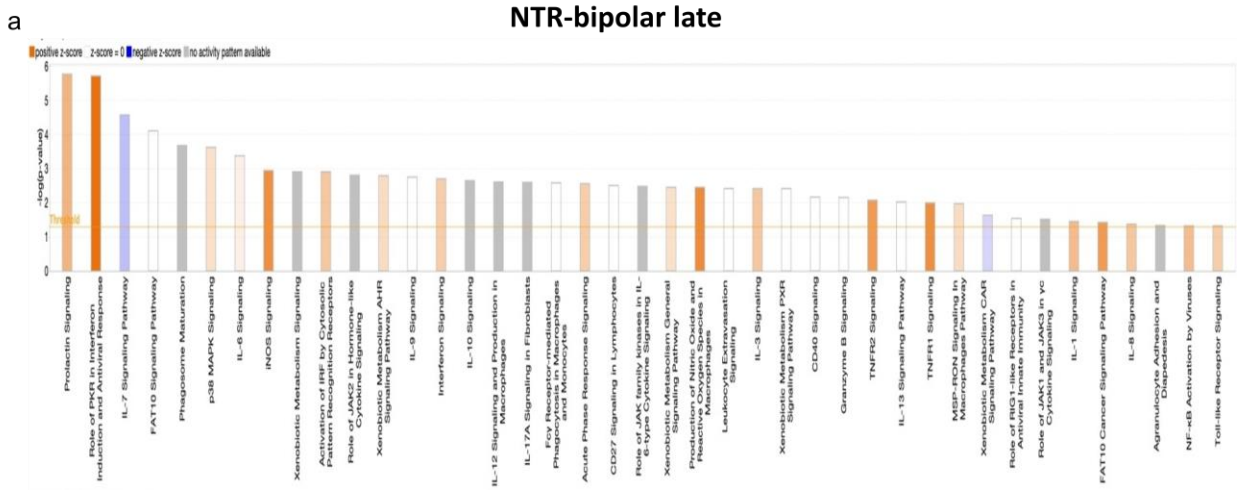
Supp. Fig. 16. Immune related terms identified from IPA for NTR-bipolar early pattern.

(a-d) IPA was used to test for enriched immune related pathway terms from DEGs for the NTR-bipolar early pattern.



Supp. Fig. 17. Immune related terms identified from IPA for NTR-rod late pattern.

(a-d) IPA was used to test for enriched immune related pathway terms from DEGs for the NTR-rod late pattern.

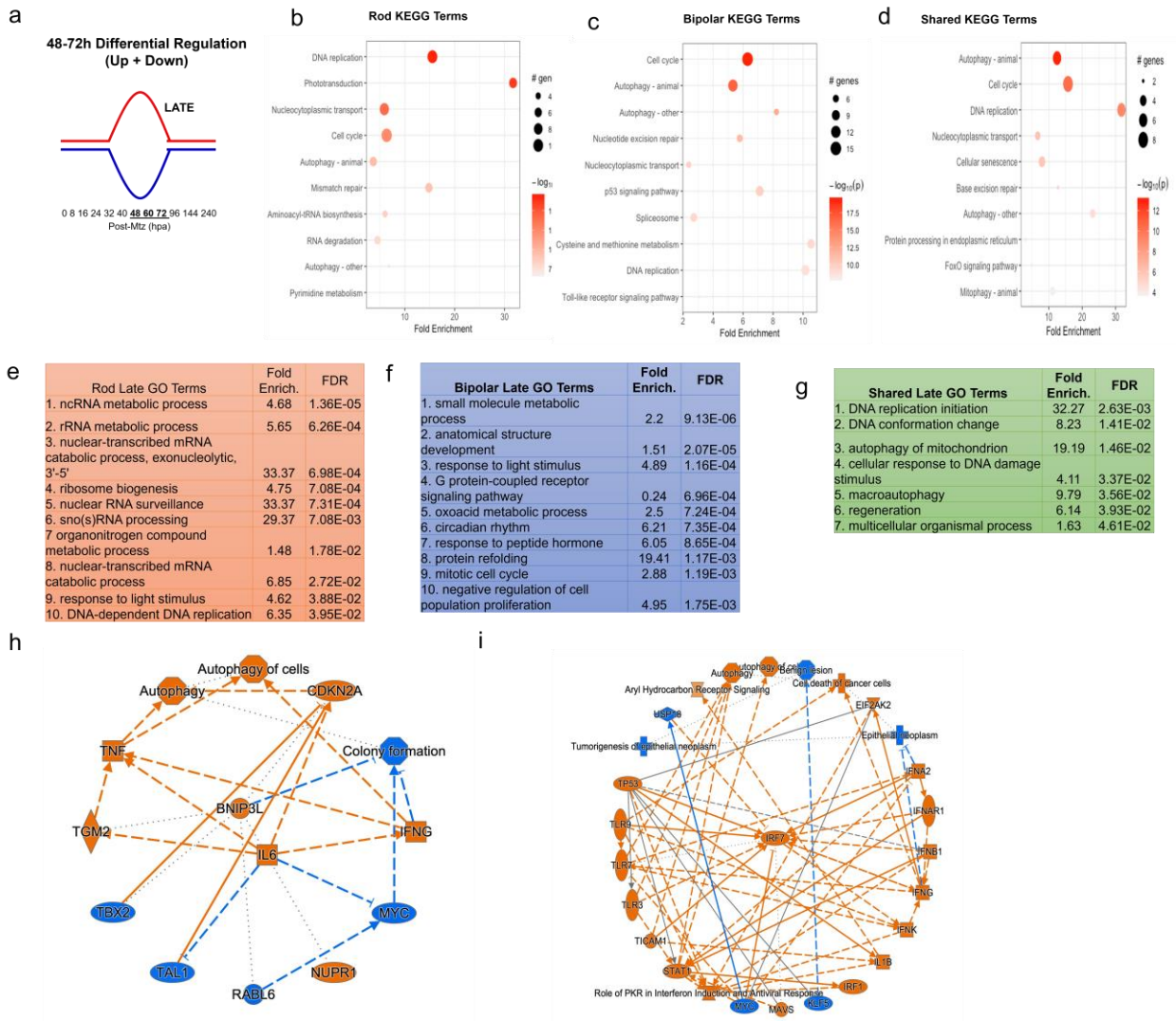


Supp. Fig. 18. Immune related terms identified from IPA for NTR-bipolar late pattern.

(a-d) IPA was used to test for enriched immune related pathway terms from DEGs for the NTR-bipolar late pattern.

The same analysis methods were used to evaluate late pattern DEGs (Fig. 5a). A subset of top KEGG terms stayed consistent with early pattern DEGs including phototransduction and RNA degradation for the rod paradigm, autophagy and p53 for the bipolar paradigm, and also autophagy for shared genes (Fig, 5b-d). The top enriched KEGG terms were DNA replication and cell cycle for the rod and bipolar paradigms, respectively. Newly identified terms included mismatch repair for rods, Toll-like receptor signaling for bipolars, and cellular senescence for the shared set (Fig. 5b-d). Enriched GO terms similarly included some overlap with early pattern terms (Fig. 5e-g), new rod GO terms included ribosome biogenesis, nuclear RNA surveillance, and sno(s) RNA processing (Fig. 5e). New bipolar terms included oxoacid metabolic process, circadian rhythm, and response to peptide hormone (Fig. 5f). Fewer shared DEGs in the late pattern data lead to fewer enriched GO terms, however, the majority were new including cellular response to DNA damage and regeneration (Fig. 5g). IPA analysis of late pattern rod data similarly identified many of the same immune-related pathways implicated in early pattern rod data, including IL-family cytokines. New terms included prolactin, CNTF, and GM-CSF signaling (Supplementary Fig. 17). The late pattern rod network had fewer nodes than the early network and was centered on IL-6 (Fig. 5h). Late pattern bipolar IPA terms also shared many immune-related terms with early pattern data. Additional terms included CD40, granzyme B, and TNFR signaling (Supp. Fig. 18). The late pattern bipolar network was centered on interferon regulatory factor 7 (IRF7, Fig. 5i). Finally, a deep literature search was conducted on the top ~50-60 DEGs in each coordinated pattern for each paradigm. More specifically, given the

importance of the immune system in regulating retinal regeneration in our NTR-rod model previously[38,57], we asked whether genes had previously been linked to immune response or retinal regeneration (Supp. Fig. 19a). In total, we found that ~38 and ~44% of the top DEGs had been linked to immune system function in the rod and bipolar paradigms, respectively. In terms of cell or tissue regeneration, ~27% of the DEGs from both paradigms had been linked to regeneration in prior studies (Supp. Fig. 19b).



Rod Late GO Terms	Fold Enrich.	FDR
1. ncRNA metabolic process	4.68	1.36E-05
2. rRNA metabolic process	5.65	6.26E-04
3. nuclear-transcribed mRNA catabolic process, exonucleolytic, 3'-5'	33.37	6.98E-04
4. ribosome biogenesis	4.75	7.08E-04
5. nuclear RNA surveillance	33.37	7.31E-04
6. sno(s)RNA processing	29.37	7.08E-03
7 organonitrogen compound metabolic process	1.48	1.78E-02
8. nuclear-transcribed mRNA catabolic process	6.85	2.72E-02
9. response to light stimulus	4.62	3.88E-02
10. DNA-dependent DNA replication	6.35	3.95E-02

Bipolar Late GO Terms	Fold Enrich.	FDR
1. small molecule metabolic process	2.2	9.13E-06
2. anatomical structure development	1.51	2.07E-05
3. response to light stimulus	4.89	1.16E-04
4. G protein-coupled receptor signaling pathway	0.24	6.96E-04
5. oxoacid metabolic process	2.5	7.24E-04
6. circadian rhythm	6.21	7.35E-04
7. response to peptide hormone	6.05	8.65E-04
8. protein refolding	19.41	1.17E-03
9. mitotic cell cycle	2.88	1.19E-03
10. negative regulation of cell population proliferation	4.95	1.75E-03

Shared Late GO Terms	Fold Enrich.	FDR
1. DNA replication initiation	32.27	2.63E-03
2. DNA conformation change	8.23	1.41E-02
3. autophagy of mitochondrion	19.19	1.46E-02
4. cellular response to DNA damage stimulus	4.11	3.37E-02
5. macroautophagy	9.79	3.56E-02
6. regeneration	6.14	3.93E-02
7. multicellular organismal process	1.63	4.61E-02

Fig. 5. Pathway analysis of late DEG pattern in both paradigms.

(a) Graphic demonstrating expression pattern for late upregulated (red) and downregulated (blue) genes along our timepoints.

(b-d) Top 10 enriched KEGG pathway terms including p-value and # of genes found as DEGs in the NTR-rod (b), NTR-bipolar (c) or from shared DEGs across both paradigms (d).

(e-g) Top 10 enriched Gene Ontology pathway terms including fold enrichment and false discovery rate in the NTR-rod (e), NTR-bipolar (f) or from shared DEGs across both paradigms (g, only 7 terms enriched in this group).

(h-i) Unsupervised gene networks produced from ingenuity pathway analysis for DEGs in the NTR-rod (h) and NTR-bipolar (i) paradigm. Orange indicates upregulated gene/pathway term while blue indicates downregulated.

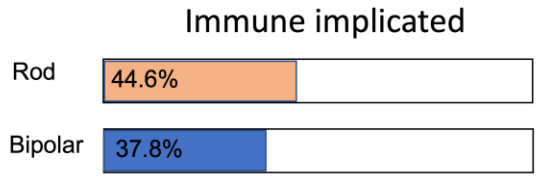
a

NTR-Rod	# genes searched	# Immune role	% Immune role	# Regeneration role	Regeneration role %
Early UP	55	30	54.5	20	36.4
EARLY DOWN	61	18	29.5	10	16.4
LATE UP	62	37	59.7	23	37.1
LATE DOWN	61	11	18.0	6	9.8

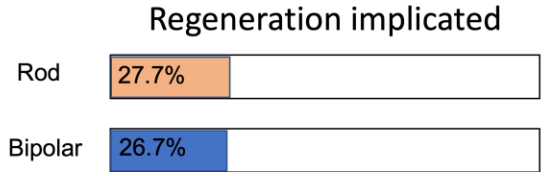
b

NTR-Bipolar	# genes searched	# Immune role	% Immune role	# Regeneration role	Regeneration role %
Early UP	64	24	37.5	15	23.4
EARLY DOWN	58	15	25.9	11	19.0
LATE UP	53	24	45.3	17	32.1
LATE DOWN	53	12	22.6	12	22.6

c



d



Supp. Fig. 19. Literature search for immune or regeneration related terms.

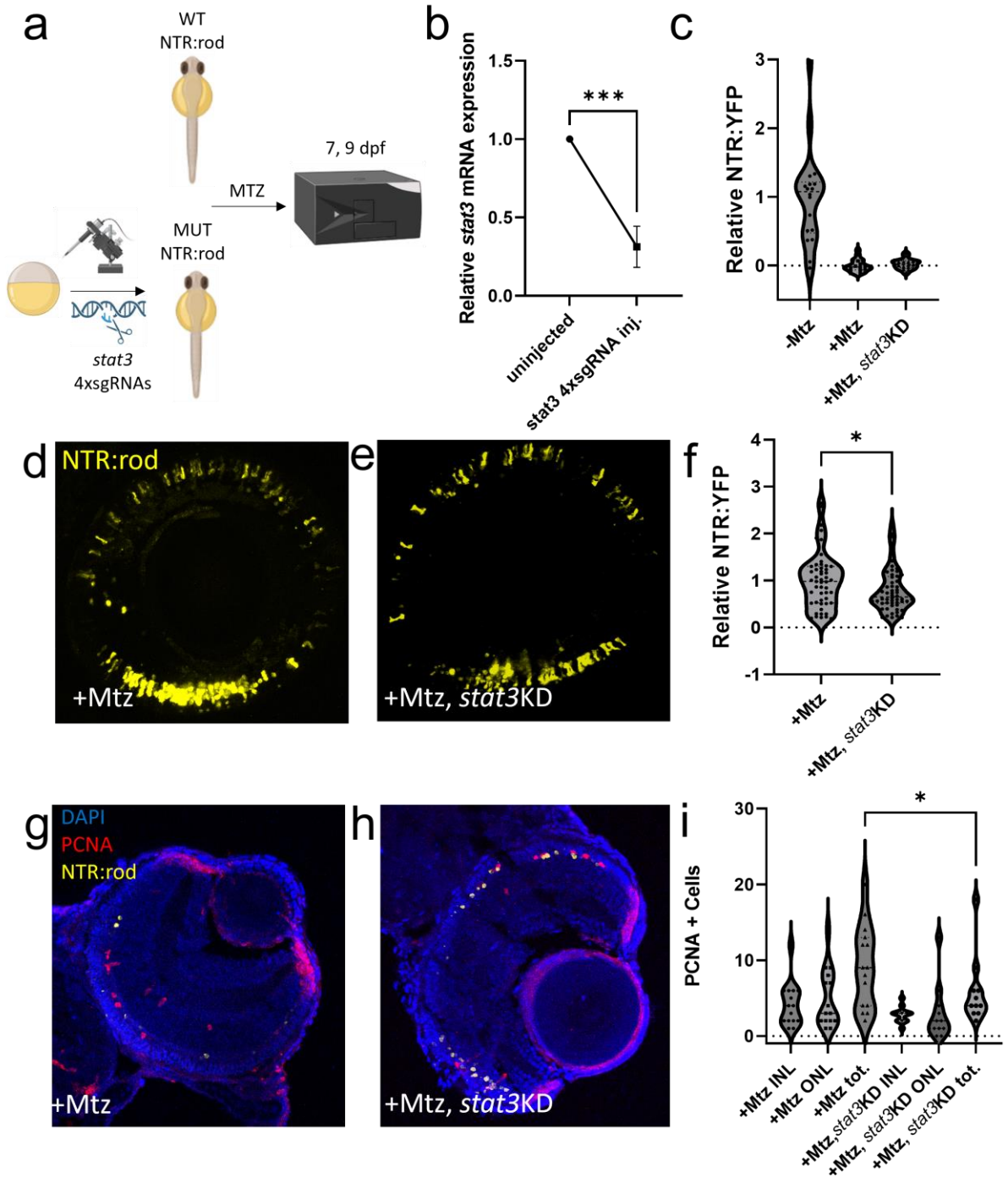
(a-b) The top ~50-60 DEGs for the NTR-rod (a) and NTR-bipolar (b) patterns were searched in the literature for any links to a role in the immune system or in regeneration. The percentage of those with a link to each term are shown.

(c-d) Bar showing the percentage of top DEGs that were implicated in the immune system (c) or regeneration (d).

Validation of role for *stat3* in induced rod photoreceptor regeneration

The expression of *stat3* increased following retinal cell loss in both the NTR:rod and NTR:bipolar paradigms. However, the increase in *stat3* was far more prominent in the NTR:rod fish paradigm regarding both fold change (Supp. Fig. 3a) and the number of timepoints this was observed (8 of 12 for NTR:rod, 4 of 12 for NTR:bipolar). To functionally test the regenerative role of *stat3 in vivo*, we knocked down *stat3* expression in NTR-rod fish using CRISPR/Cas9 redundant targeting, i.e., “crispants” (Fig. 6a). Knockdown was confirmed via qPCR in a subset of injected and non-injected control fish (Fig. 6b). At 5 dpf, rod photoreceptors were ablated (10 mM 24h Mtz). Subsequently, an established Tecan fluorescent plate reader-based assay as well as *in vivo* imaging was used to assess: rod cell death at 7 dpf (Fig. 6c) and rod cell regeneration at 9 dpf (Fig. 6d-f). Knockdown of *stat3* led to significantly impaired rod regeneration compared to wildtype fish, thereby validating the requirement for *stat3* in rod cell regeneration. Lastly, to examine the mechanism by which *stat3* knockdown leads to reduced regeneration, stem-cell proliferation was assessed following ablation in wildtype and mutant fish. Akin to our initial classification of Mtz-induced proliferation (Fig. 1l), death of rods led to proliferation in both the INL and ONL. PCNA immunostaining in *stat3* knockdown fish showed a significant decrease in total proliferation compared to wildtype fish (Fig. 6g-i). This suggests *stat3* loss impairs

557 progenitor cell proliferation at this timepoint, leading to fewer regenerated rods.



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559 Fig. 6. Effect of *stat3* knockdown on rod cell regeneration.

(a) Experimental design depicting CRISPR/Cas9-based targeting of *stat3* via CRISPR/Cas9 in NTR:rod embryos. Control (+Mtz) and knockdown NTR-rod larvae (+Mtz, *stat3*KD) were treated with 10mM Mtz from 5-6 dpf and rod fluorescence was assessed via plate reader assay at 7 dpf (to examine the extend of rod cell loss) and 9 dpf (to examine the extent of rod cell regeneration).

(b) Relative *stat3* mRNA expression (qRT-PCR assay) in non-injected controls compared to *stat3* knockdown fish.

(c) Quantification of NTR-YFP expression in rod cells by plate reader assay at 7 dpf in non-ablated (-Mtz), ablated control (+Mtz) and *stat3*KD ablated larvae (+Mtz, *stat3*KD)

(d-e) Representative *in vivo* confocal images of regenerated rod cells at 9 dpf in control (+Mtz) and *stat3*KD larvae (+Mtz, *stat3*KD)

(f) Quantification of rod cell regeneration by plate reader assay at 9 dpf in control (+Mtz) and *stat3*KD larvae (+Mtz, *stat3*KD).

(g-h) Representative immunohistological staining for PCNA at 7 dpf in control (+Mtz) and *stat3*KD larvae (+Mtz, *stat3*KD) fish.

(i) Quantification of INL, ONL, and total PCNA+ cells at 7 dpf in control (+Mtz) and *stat3*KD larvae (+Mtz, *stat3*KD).

Astericks indicate statistically significant difference (* = <0.05, *** = <0.001) across indicated groups, non-significant comparisons are not shown.

Discussion

Promotion of retinal regeneration would provide a transformative therapeutic approach for patients with blinding degenerative diseases. One strategy to achieve this goal is to induce endogenous human MG to respond to cell loss and regenerate lost retinal neurons, a process that

occurs naturally in zebrafish. Zebrafish studies have identified several genes that regulate retinal regeneration (*ascl1a*[58], *lin-28 homolog A* [8,11], *sry-box transcription factor 2*[59], *stat3*[60]) as well as gene networks coordinating MG states (rest, reactivity, proliferation) following retinal damage [29]. Each of these studies induced widespread retinal damage where the regenerative process largely mirrors retinal development[3,12]. Conversely, retinal degenerative diseases typically involve thez slow progressive loss of specific cell types, such as rod photoreceptors in retinitis pigmentosa[61]. Interestingly, several zebrafish mutants fail to regenerate retinal neurons when loss is slow, progressive, and cell-type specific[46], i.e., akin to disease condtions[46]. This suggests that a threshold of cell death is required to trigger retinal regeneration and that models enabling control over the onset, extent, specificity and duration of cell death can expand our understanding of how regeneration is controlled under disease-mimicking conditions. For instance, Hyde and colleagues have shown that the extent of rod cell loss determines MG responsiveness: limited rod cell loss led to a response solely from “rod-committed” ONL progenitors while widespread rod loss elicited responses in both ONL progenitors and MG cells[53]. Moreover, cell-specific retinal cell ablation models have revealed that regenerative processes can exhibit “fate-bias”, where newly generated cell fates favor the cell type that was lost.[13–16]. Subtler fate biases follow even widespread retinal damage[62], suggesting that the regenerative process is informed by the nature of the injury/cell loss paradigm to guide MG-derived progenitor cell (MGPC) fate decisions. The sequence of temporally-delineated cell fates attending development appear to be recapitulated following widespread retinal injury[12]. However, how biases in MGPC fate decisions are controlled following either widespread or selective retinal cell loss, is unknown. In mice, overexpression of neurogenic factors such as *ascl1*[4,5,7] in MG, and knockdown of inhibitory factors such as the *nfi* genes[29] have been shown to promote limited regenerative

responses. However, the neuronal cell types generated with these methods have been predominantly limited to bipolar-like cells[30], neither well matched to the cell types lost nor particularly relevant to retinal disease. However, inroads into producing more disease-relevant cell types such as retinal ganglion cells have recently been made by adding additional neurogenic factors such as *pou4f2* and *isl1*[7,63,64]. Increased understanding mechanisms driving fate-biased regeneration may help to promote the full regenerative potential of the mammalian retina. Here, we investigated transcriptomic responses to the selective loss of two retinal cell types, rod photoreceptors and bipolar interneurons, to begin to reveal mechanisms that inform the regenerative process about the cell types lost.

We first characterized NTR-rod and NTR-bipolar transgenic lines following prodrug-induced cell loss, confirming the specificity of cell loss and quantifying proliferative response in the INL and ONL (Fig. 1). The latter assay was particularly important as prior studies had shown that the extent of rod cell loss impacts how two distinct stem/progenitor cell populations respond; low rod loss leading to rod-committed progenitor proliferation in the ONL only, while extensive rod loss triggered both MG and ONL progenitor proliferation[53]. Our data showed proliferative responses in both the INL and ONL (Fig. 1l)suggesting both paradigms trigger MG proliferation. Thus, differences in gene expression observed between these paradigms cannot be explained solely by differential stem cell responses, e.g., activation of only rod-committed progenitors in the ONL for the NTR-rod paradigm.

To comprehensively characterize transcriptomic changes during rod and bipolar cell regeneration, samples were collected across 12 time points encompassing cell loss and

regeneration (Fig. 2a). Prior microarray studies have successfully identified genes associated with MG activation[65] and networks activated following various retinal injury paradigms[60,66–70].. More recently, single-cell RNAseq (scRNA-seq) and ATAC-seq (Assay for Transposase-Accessible Chromatin) were used to compare light and NMDA induced retinal cell ablation paradigms during early phases of the regenerative process[29]. Here, by expanding the number of time points analyzed we sought to identify genes/pathways associated with: 1) inflammation and immune cell activation, 2) stem cell activation, 3) MG/MGPC proliferation, and 4) MGPC differentiation. We emphasized early time points (every 8 hr from 0-48 h) to identify genes linked to the initiation of fate-biased regenerative processes. A total of 364 shared, 918 rod-specific, and 1249 bipolar-specific DEGs were identified (Fig. 2b). Overall, shared DEGs/pathways were limited more to early time points, while paradigm-specific DEGs/pathways were identified throughout the study. The number of DEGs diminished for both cell-types starting at 72 hpa. That paradigm-specific DEGs predominated supports the concept that injury/cell loss specifics inform the regenerative process[13–16 3,11,12].

KEGG pathway analysis per each timepoint identified previously implicated pathways (e.g., mTor, Notch, and Wnt signaling)[8,54,67,71,72], and terms linked to the regulation of stem cell function but not previously associated with retinal regeneration (e.g., glutathione metabolism[73], FoxO signaling[74], and cellular senescence[75]). To enhance pathway analyses, we grouped DEGs into four coordinately regulated sets for each paradigm: up or down early (16-32 hr) and up or down late (48-72 hr, Figs. 3a,b). This accounted for the majority of DEGs and reinforced that paradigm-specific DEGs outnumbered shared DEGs (Fig. 3c). Representative genes in the NTR:rod early up group included known factors (e.g., *activating transcription factor 3- atf3*,

stat3)[60,76] and genes not previously associated with retinal regeneration (e.g., *glutathione S-transferase pi 1- gstp1*). Among the known set, factors associated with immune system reactivity were prevalent, including a number of genes previously shown to be upregulated in MG at 16h post light ablation in adult zebrafish[60] (e.g., *janus kinase 1- jak1*, *stat3*, *suppression of cytokine signaling 3b- socs3b*, *cytokine inducible SH2-containing protein- cish*, *irf9* and *complement component 7b- c7b*). GO analysis additionally identified shared late pattern enrichment for the broad term "regeneration" based on the differential regulation of the genes *annexin A1a- anxa1a, ubiquitin-like with PHD and ring finger domains 1- uhrf1, socs3a, capthespin Ba- ctsba, legumain- lgmn, major vault protein- mvp, v-fos FBJ murine osteosarcoma viral oncogene homolog Ab- fosab,* and *GLIS family zinc finger 3- glis3* (Fig. 5). Next, IPA was used to reveal differential regulation of pathways at early and late stages of regeneration in each model. For both cell types, and at both early and late timepoints, multiple shared and unique immune-related pathways were identified, e.g., cytokines, JAK/STAT, Toll-like receptor and prolactin signaling (Supp. Fig. 15). We then produced unsupervised DEG networks using the coordinated expression pattern data, i.e., rod-early, rod-late, bipolar-early and bipolar-late. Known pro-regenerative and pro-inflammatory factors STAT3 and IL-6[60,77] were identified as central mediators in the rod paradigm (Fig. 4h, 5h), while PPARG and IRF7 were implicated as central mediators for the bipolar paradigm (Fig. 4i, 5i). PPARG has recently been tied to zebrafish retinal progenitor cell function in adults through interactions with metabolic pathways.[78] Interestingly, IRF7 has been implicated as a key regulator of microglia reactivity, its upregulation promoting a phenotypic switch from an inflammatory to anti-inflammatory state, aka stimulating resolution of microglia activation[79,80]. Our prior work suggested that accelerating the resolution process by exposure to the immunosuppressant dexamethasone 24 hrs after

induction of rod cell ablation led to enhanced rod cell regeneration in zebrafish[57]. Together, these studies implicate induction of IRF7 expression as potential strategy for promoting neuronal regeneration.

Both IL-6 and interferons activate JAK/STAT signaling[77,81], a known mediator of the response to retinal damage[60] regulating cell migration[82], proliferation[60], apoptosis[83], immune system[84] and oxidative stress[85] responses. DEGs in the JAK/STAT family were primarily upregulated in the rod (e.g, *stat3, jak1, cish, socs1a/3a/3b*) and bipolar paradigms (e.g, *cish, socs1a/3a/3b, stat1a/1b/2/5a/5b*). However, the specific JAK/STAT family members involved differed between our two paradigms (e.g., *stat3* for rod and *stat1a/b, stat2 and stat5a/b* for bipolar). Similarly, different cell death pathways were also implicated, NTR-rod being linked to necroptosis (Fig. 4b) while NTR-bipolar was linked to apoptosis (Fig. 4c, f), These findings align with a recent drug screen in the same NTR-rod model where inhibitors and genetic disruption of parthanatos and necroptosis pathways protected rods from cell death while inhibition of apoptosis did not[40]. Interestingly, recent work in multiple mouse tumor models links necroptotic signaling to the activation of IL-6 and STAT3[86–88] while apoptotic signaling was linked to STAT5 activation[89], matching gene expression and cell death patterns in our models. JAK/STAT signaling receives feedback inhibition from Suppression of Cytokine Signaling (SOCS) genes[90]. Notably, ablation of both cell types was followed by upregulation of *socs3a, socs3b, socs1a* and *cish*. *Socs3a* has been implicated as a mediator of hair and liver cell regeneration in zebrafish through activation of resident stem cells and progenitor differentiation[91,92], and is strongly upregulated in an adult zebrafish photoreceptor lesion model[68]. In a functional test of STAT3 signaling in the rod cell ablation paradigm, we showed

that CRISPR/Cas9 mediated disruption of *stat3* led to statistically significant reductions in proliferation and rod photoreceptor regeneration kinetics (Fig. 6), consistent with a reduction in photoreceptor regeneration following light-damage in *stat3* morpholino injected eyes[60]. Interestingly, the Reh lab has recently shown that combining overexpression of *ascl1* with inhibition of STAT signaling stimulates enhanced MG-derived regeneration in the mouse retina[30]. Here, *socs1a, socs3a/b* and *cish* likely serve to similarly limit over-activation of JAK/STAT signaling during retinal regeneration following activation of distinct STATs. These results highlight how cell-specific regulation of family members within a given signaling pathway may delineate fate-biased from shared (i.e., developmental) regenerative mechanisms. By extension, further insights into the regulation of fate-biased regenerative mechanisms will likely aid in the development of cell-type targeted therapeutic strategies to restore vision.

Materials and Methods

Aquaculture

Zebrafish were maintained under standard environmental conditions (~28°C, 14hr:10hr light:dark cycle) under an approved ACUC animal use protocol. Larvae were fed paramecia starting at 5 days post-fertilization (dpf), then paramecia and *Artemia salina* from 9-16 dpf. Late stage larvae (e.g., 8 dpf) slated for imaging were kept in 12 well plates in 5 ml of system water until 12 dpf after which they were sacrificed.

Transgenic Lines

A bipartite Gal4/UAS [93] transgenic zebrafish line derived with a 1,482 bp promoter element from the *nyctalopin* (*nyx*) gene [94,95], *Tg(nyx:Gal4-VP16)q16a*, and a Gal4-driven reporter, *(UAS:GAP-YFP)q16b*, expresses membrane-tagged yellow fluorescent protein (YFP) in a subpopulation of

bipolar cells [47]. Crosses to a UAS-reporter/effector line facilitating prodrug-induced cell ablation, *Tg(UAS-E1b:NfsB-mCherry)c264* [96], resulted in triple transgenic fish expressing an NTR-mCherry fusion protein in subsets of *nyx*-promoter targeted bipolar cells (*q16a;q16b;c264*; hereafter, NTR-bipolar lines). A transgenic line derived with a 3.7 kb promoter element from the *rhodopsin (rho)* gene (kind gift of Dr. Shoji Kawamura) [48] expresses a YFP-NTR fusion protein in rod photoreceptor cells, *Tg(rho:YFP-Eco.NfsB)gmc500* [45] (hereafter, NTR-rod lines). Retinal morphology was monitored during imaging studies by crossing both NTR lines with *Tg(pax6-DF4:gap43-CFP)q01* which expresses membrane tagged CFP throughout the retina (see Fig. 1A-B) [97]. Transgenic fish were propagated in the *roy orbison* (aka, $mpv17^{a9/a9}$, hereafter $roy^{a9/a9}$)[98,99] pigmentation mutant background to facilitate intravital imaging [100]. However, for differential gene expression studies, to minimize expression variance due to differences in transgene copy number, outcrosses to an AB wildtype strain (WT) were performed to generate heterozygotes.

Mtz Treatment

For histological experiments, *in vivo* imaging experiments and all microarray tissue collections, transgenic NTR-bipolar and NTR-rod larvae were screened and separated into two equal sized groups at 6 dpf: 1) non-treated controls (Cntl); and 2) those treated with 10mM Mtz for 24 hr to induce cell death, from 6-7 dpf (or DMSO-treated controls where applicable). After Mtz treatment, fish were rinsed into system water and fed paramecia until sacrificed.

mRNA Isolation and Preparation

Whole eye mRNA was prepared across twelve time points: t0 (just prior to Mtz exposure); t8, t16, and t24 hr (during Mtz treatment); and t32, t40, t48, t60, t72, t96, t144, and t240 hr (after Mtz removal during recovery (Fig. 2A). Sample collection started at 8:00 a.m. on the day larvae

reached 6 dpf. At each time point, 16 eyes from 8 larvae were isolated per condition. To isolate eyes, larvae were euthanized in 0.4% tricaine for 5 mins followed by cervical transection. Whole eye pairs were manually isolated under an Olympus SZX16 epifluorescence stereoscope and immediately placed into a chilled/sterile 1.5 ml tube with 50 µl of TriZOL (Life Technologies); samples were then stored at -80°C until extraction. This protocol was followed for three biological repeats per condition/time point for NTR-rod and NTR-bipolar lines. Samples were batch extracted and processed following the final time. All samples were processed in the Medical College of Georgia (MCG, former Mumm lab location) Integrated Genomics Core for mRNA isolation, cDNA library construction, and microarray hybridization.

Microarrays

GeneChip Zebrafish Genome Microarrays (Affymetrix) were processed by the MCG Genomic Core. Each run involved sibling zebrafish and consisted of 23 RNA samples across each regenerative paradigm—1 pretreatment, and 11 time points from the control and Mtz treatment groups. RNA sample quality was assessed by concentration and the RNA Integrity Number (RIN), an algorithm that assigns integrity values to RNA measurements [101]. Only samples attaining a minimal concentration of ≥100ng/µL (5µL total) and a RNA integrity number (RIN) value of ≥8 were used for microarray hybridizations [101]. Runs where a minimum of 21 of 23 samples were deemed of good quality were utilized in the microarray studies. Three runs were processed per regenerative paradigm resulting in six microarray sets (Supplementary Table 1) and a total 138 microarrays overall.

Tissue preparation and immunohistochemistry

For immunohistochemistry, larval zebrafish were euthanized, fixed in 4% paraformaldehyde (PFA) for 8 hr, washed three times in 1x PBS (phosphate buffered saline; EMD Millipore) for 30

min and stored at 4°C. Samples were mounted in cryogel embedding medium within the next 2-4 days, frozen in liquid nitrogen then stored at -80^{0}C until sectioned in the lateral plane at 25 μm thickness with a cryostat. Sliced sections were collected on standard microscope slides and stored at 4°C.

For immunolabeling, slides were air dried at room temperature for ~1 hr, rinsed in 1xPBS and then re-fixed with 4% PFA for 15 min. PBST rinses (1xPBS +0.1% Tween20, Fisher Scientific) were conducted to remove trace PFA followed by 5 min antigen retrieval with SDS (1% Sodium Dodecyl Sulfate; Fisher Scientific) in PBS. The blocking phase was performed with 3% goat serum in PBDT (1xPBS, 1% BSA, 1% DMSO, 0.1% TritonX-100) for 30 min and incubated with primary antibody/1% goat serum/PBDT overnight at 4°C. The next morning, slides were rinsed in PBST, stained with secondary antibody/PBDT ~1 hr in a light protected humidity chamber and cover-slipped (22x50 mm, Fisher Scientific). PBST rinses removed unbound secondary antibody. Samples were protected with Vectashield + DAPI (Vector Laboratories) and cover-slipped (24x50 mm, Fisher Scientific).

Primary antibodies included: mouse anti-PCNA monoclonal antibody (1:1000, clone PC10; Sigma Aldrich), rabbit anti-Caspase-3 monoclonal antibody (1:500, clone C92-605; BD Biosciences), Click-iT Tunel Alexa Fluor 647 (1:500; Life Technologies), mouse anti-zpr-1 monoclonal antibody (1:750; ZIRC), mouse anti-zpr-3 monoclonal antibody (1:750; ZIRC), mouse anti-ZS-4 monoclonal antibody (1:750; ZIRC). Secondary antibodies included: anti-mouse Alexa Fluor 430 (1:500; Life Technologies), anti-mouse Alexa Fluor 635 (1:500; Life Technologies), anti-rabbit Alexa Fluor 430 (1:500; Life Technologies).

Cell Counting and Analysis

Images were collected with an Olympus FV1000 Confocal Microscope (405, 440, 488, 515, 559, and 635nm laser lines). Stacked confocal images were obtained using a 40x oil immersion objective with a 2.5 µm step size, 130 µm aperture, and 10 µm total depth. Five sections were collected per retina centered around the optic nerve. Images (Olympus .OIB format) were analyzed using ImageJ. Manual cell counts were averaged across sections per retina and averaged within each group. Student's t-test and One-way ANOVA were used for statistical comparisons between groups.

Sample Quality and Differential Expression Analysis

Data were collected from 138 Genechip Zebrafish Genome arrays (Affymetrix) across four conditions: NTR-rod cntrl, NTR-rod Mtz, NTR-bipolar cntrl, and NTR-bipolar Mtz. The Bioconductor suite in the R statistical software [102], LIMMA [103], Carmaweb [104], and Microsoft Access were used for data processing, differential expression testing and storage. Prior to statistical analysis, Robust Multi-array Average (RMA) pre-processing routine [105] and Quality control assessments [106] were used for background correction, normalization and quality control. A set of differentially expressed genes was derived using LIMMA with a false discovery rate adjusted p-value of 0.05. Differentially expressed genes were defined as those expressing a 1.5-fold up or downregulation at any time point in regeneration. Pathway analysis was performed using Ingenuity Pathway Analysis (IPA), Gene Ontology (GO) and KEGG pathway analysis (via the pathfindR R studio package). An adjusted p value below 0.05 was used throughout as a cutoff for significance.

qPCR Processing

Extracted mRNA samples were reverse transcribed (Qiagen Omniscript RT kit, Qiagen) and stored at -20°C. Samples were run in triplicate using the BioRad iQ SYBR Green Supermix

(BioRad) in iCycler IQ 96 well PCR plates (Bio-Rad) on a BioRad iCycler equipped with an iCycler iQ Detection System. The protocol consisted of three phases: 1) 92˚C for 10:00 min, 2) 50x 92˚C for 00:15 min, 60˚C for 01:00 min, 3) 81x 55˚c→95˚c for 00:10 min. β-actin served as the house keeping gene and $2^{-\Delta\Delta CT}$ method was used for normalization to ensure equal amounts of cDNA for comparisons. qPCR primers were designed using the online tool QuantPrime.

CRISPR/Cas9 mediated *stat3* targeting

CRISPR/Cas9 mediated redundant targeting injections were performed at the one-cell stage of gmc500 embryos utilizing the published strategy and gRNA table by Wu et al [107]. Published sgRNAs for *stat3* were ordered as DNA oligos, assembled with the general CRISPR tracr oligo, and then transcribed using pooled in vitro transcription (HiScribe T7 High Yield RNA Synthesis kit, New England BioLabs) and cleaned up with the NEB Monarch RNA Cleanup kit. A mixture of all four sgRNAs (1 ng in total) and Cas9 protein (2.5 µM, IDT) was injected into *rho:YFP-NTR* embryos at the one-cell stage for targeting each gene.

Quantitative real-time Polymerase Chain Reaction (qRT-PCR)

To validate *stat3* expression knockdown mediated by CRISPR/Cas9 targeting, 3 groups of 10 larvae of both uninjected and gRNA injected transgenic larvae at 2 dpf were processed through a previously published protocol to measure gene expression with qRT-PCR [40]. Briefly, RNA was purified using NEB Monarch RNA Cleanup kit and reverse transcribed to cDNA using qScript cDNA synthesis kit (QuantaBio). Quantitative PCR was conducted using designed primers with the primerdb database and PowerUp™ SYBR™ Green Master Mix (ABI) in QuantaStudio (ABI). Delta delta CT analysis was performed to calculate relative fold change in gene expression levels between knockdown larvae and controls. Each experiment was performed in triplicate.

ARQiv scans to measure rod photoreceptor loss and regeneration

Wildtype non-injected and *stat3* sgRNA injected *Tg(rho:YFP Eco. NfsB)gmc500* larvae were treated with Mtz at 5 dpf and subsequently rod cell loss or regeneration was measured at 7 dpf and 9 dpf, respectively, using the ARQiv system, as previously described [38].

Competing Interests

JSM holds patents for the NTR inducible cell ablation system (US #7,514,595) and uses thereof (US #8,071,838 and US#8431768).

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