

Supplementary Materials for  
**Neuroinflammation as a cause of differential Müller cell regenerative responses to retinal injury**

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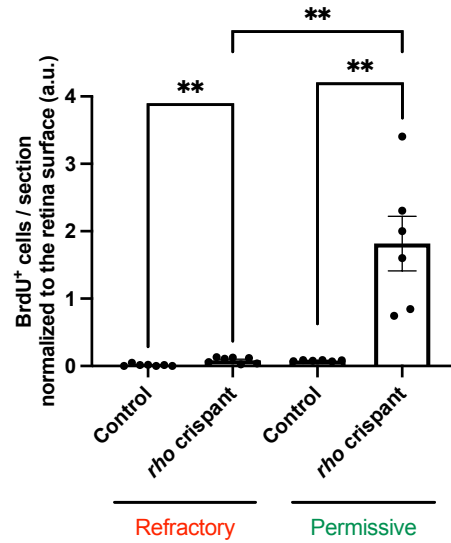
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*Sci. Adv.* **10**, eadp7916 (2024)  
DOI: 10.1126/sciadv.adp7916

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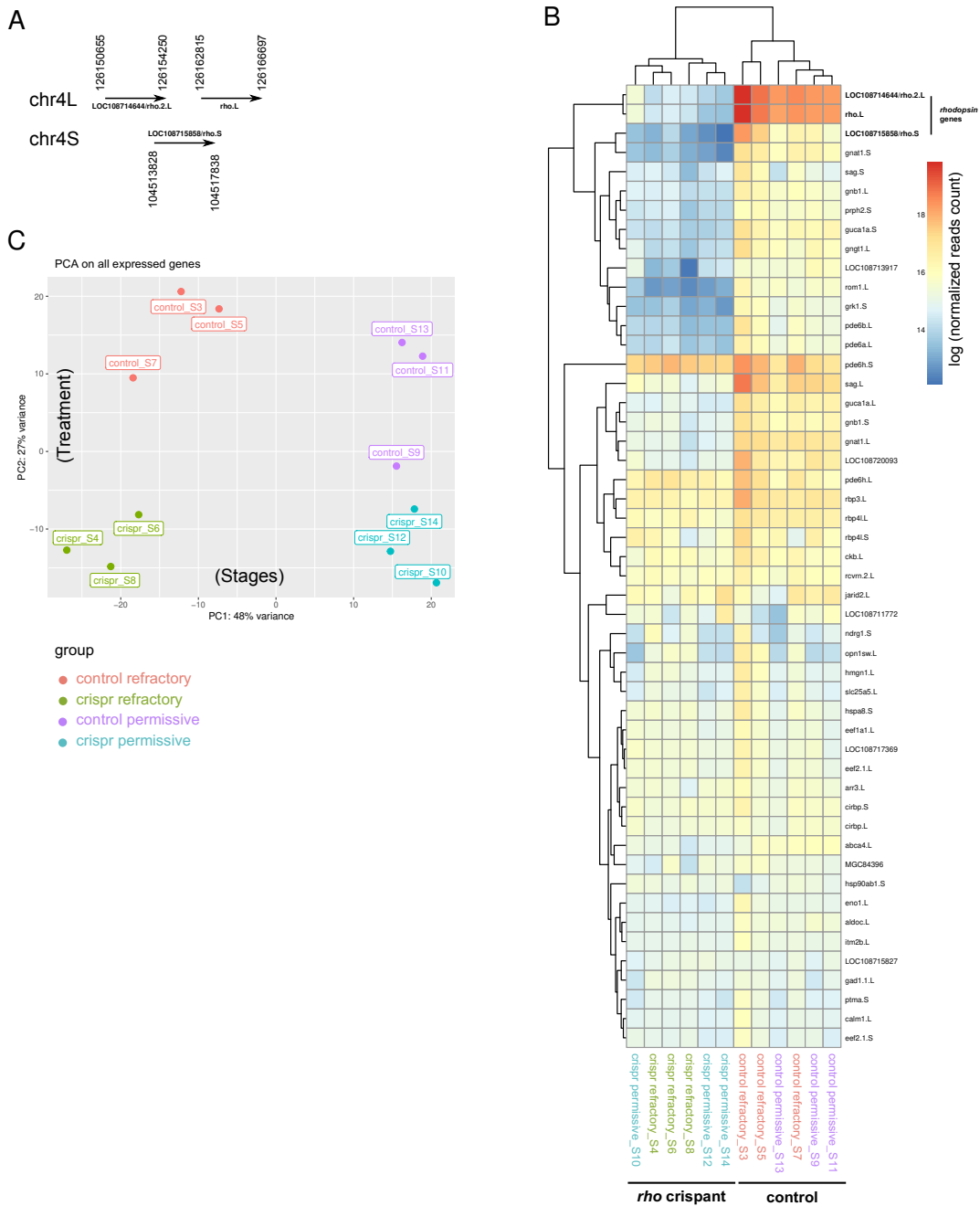
Figs. S1 to S9  
Tables S1 to S5

Figure S1



**Figure S1. The response of Müller cells to injury varies along with aging in *Xenopus* tadpoles.** Quantification of BrdU-positive cells (3-day exposure) in retinal sections of young (refractory) or old (permissive) control and *rho* crispant tadpoles. Data were normalized to the entire surface of the retinal section and are represented as mean  $\pm$  SEM. Each point represents one retina. \*\* $p < 0.01$  (Mann-Whitney test).

Figure S2



**Figure S2. Mapping data.** Following adapter trimming, the RNAseq data were mapped to *Xenopus laevis* genome 9.2 and uniquely mapped reads were assigned to genes using the annotation available on Xenbase. **(A)** Chromosomal locations of the three *rho* loci targeted by CRISPR/Cas9. **(B)** Clustered heatmap of the 50 most expressed genes of the RNAseq dataset. It highlights the clear separation between *rho*-crippant and control tadpoles. **(C)** Principal component analysis (PCA) on expressed genes of the RNAseq dataset. PC1 (48%) is most likely associated with the developmental stage of the tadpoles, while PC2 (27%) is most likely associated with the treatment condition. Components 1 and 2 explain together 75 % of the variance.



Figure S4

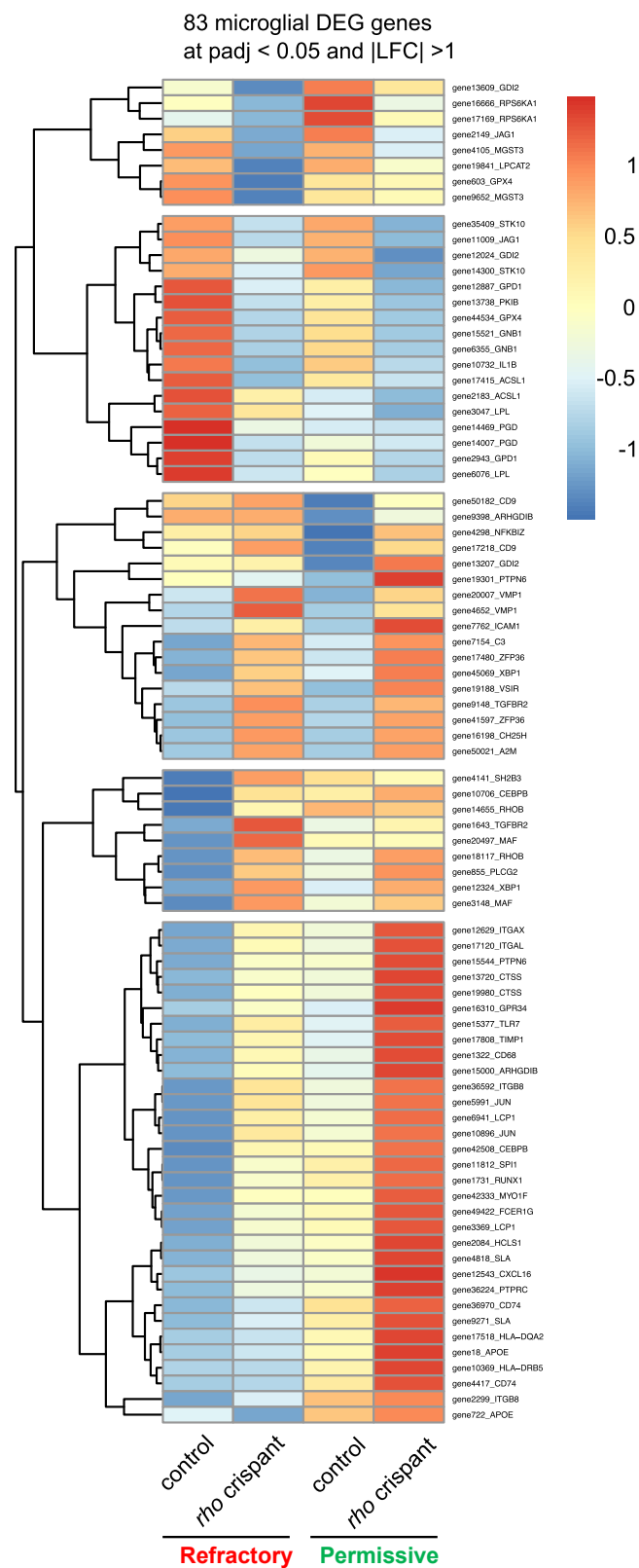
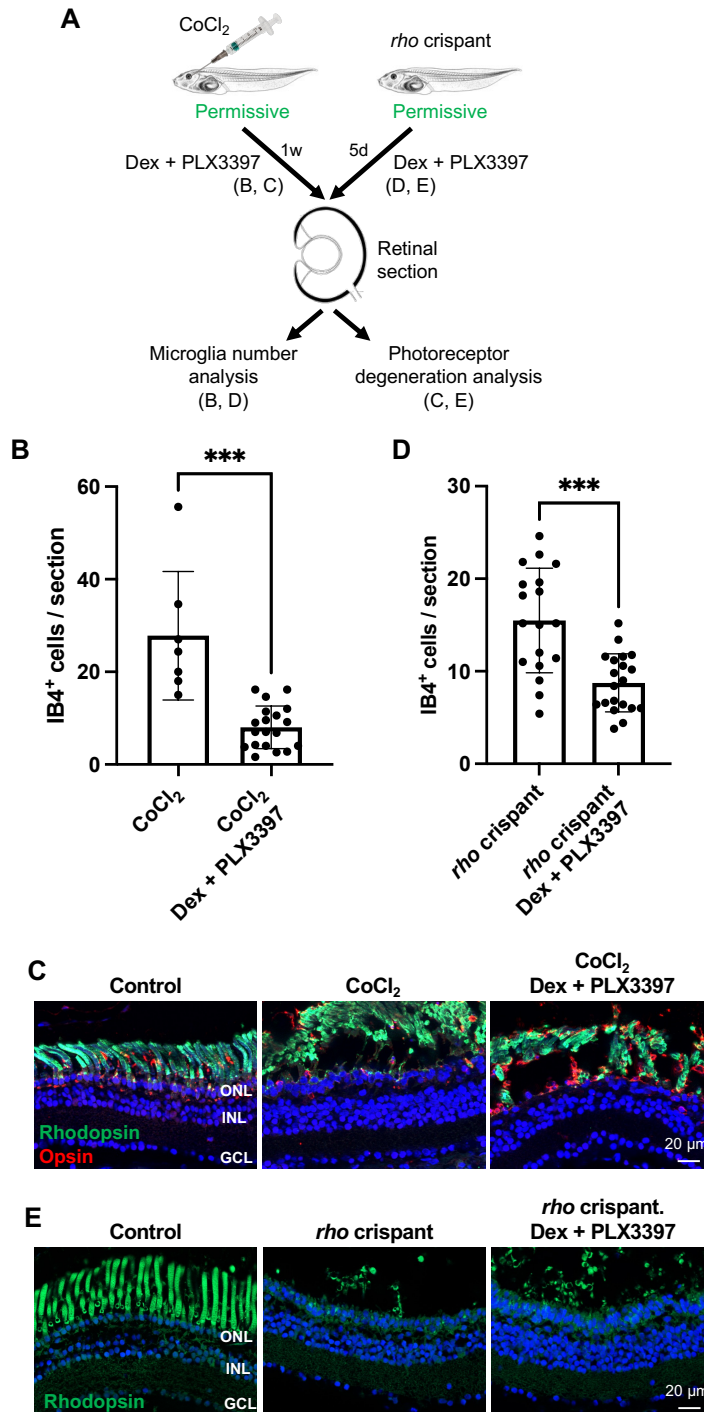
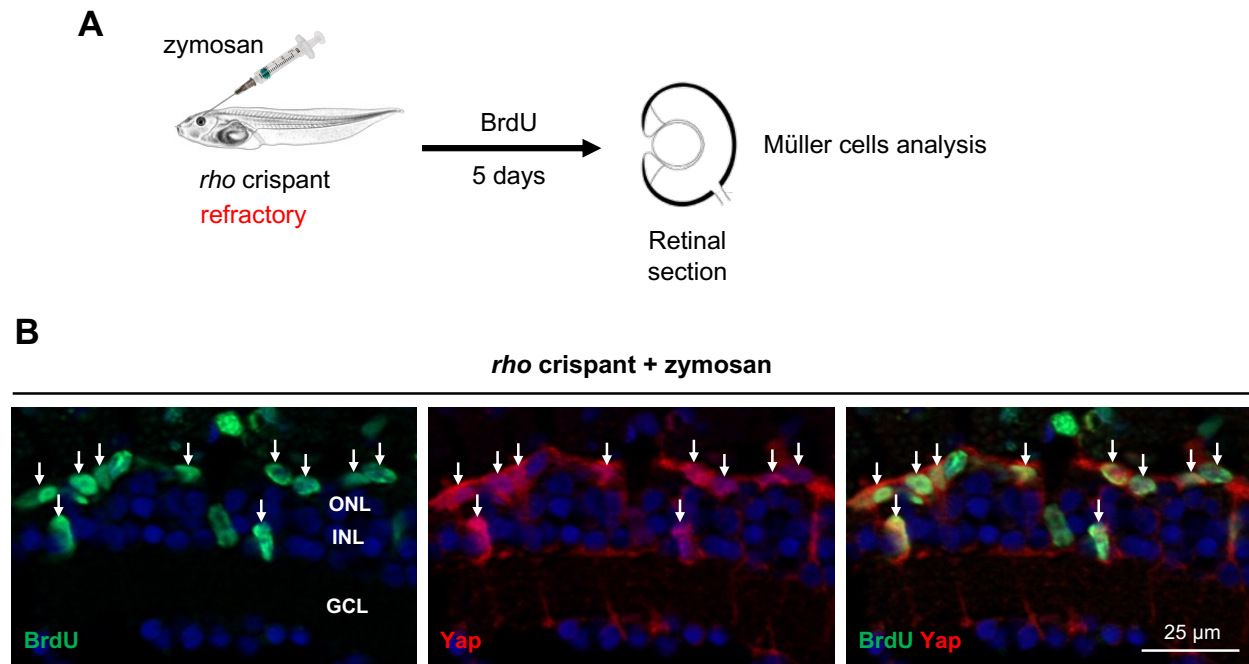


Figure S4. Heatmap of differentially expressed genes. Clustered heatmap of differentially expressed genes belonging to the microglia molecular signature. Enlargement of the cluster of interest is shown in Fig. 1D.

Figure S5

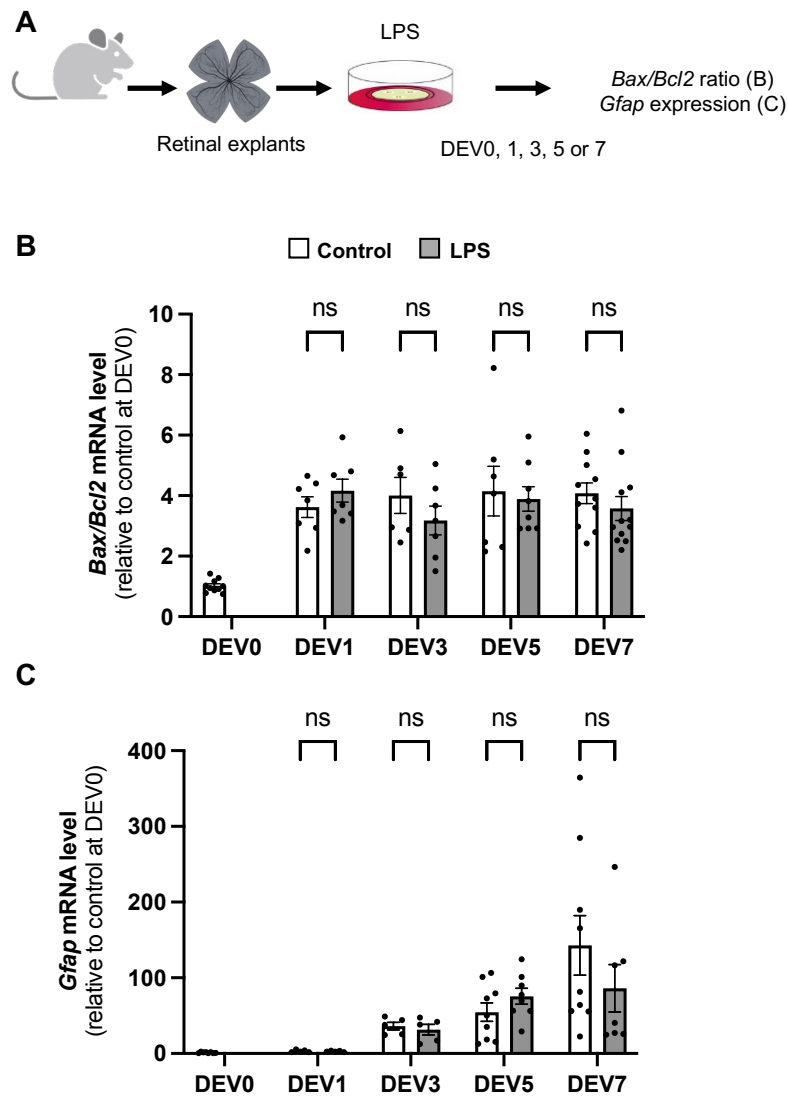


**Figure S5. Dex plus PLX3397 treatment efficiently decreases the number of microglial cells in *CoCl<sub>2</sub>*-injected or *rho* crisprant tadpoles, without impacting retinal degeneration. (A)** Outline of the experimental procedure used in (B-E). Stage 56/62 (permissive stage) *CoCl<sub>2</sub>*-injected (B, C) or *rho* crisprant (D, E) tadpoles were soaked in PLX3397 plus Dex solution for 5 days (5d) or 1 week (1w) as indicated, starting one day before *CoCl<sub>2</sub>* injection. They were then processed for immunolabeling on retinal sections. **(B, D)** Quantification of IB4-positive cells (microglia). **(C, E)** Representative images of retinal sections labeled for Opsins (cones) and/or Rhodopsin (rods). Nuclei are counterstained with Hoechst. Data are represented as mean  $\pm$  SEM, and each point represents one retina. \*\*\* $P < 0.001$  (Mann-Whitney test). GCL, ganglion cell layer; INL, inner nuclear layer; ONL, outer nuclear layer.



**Figure S6. Proliferative cells upon zymosan injection at the refractory stage are Müller cells. (A)** Outline of the experimental procedure used in (B). Stage 48/49 (refractory) *rho* crispant tadpoles were intraocularly injected with zymosan and then exposed to BrdU solution for 5 days before being processed for immunolabeling on retinal sections. **(B)** Representative images of retinal sections co-labeled for BrdU and Yap. Arrows point to double-labeled cells. GCL, ganglion cell layer; INL, inner nuclear layer; ONL, outer nuclear layer.

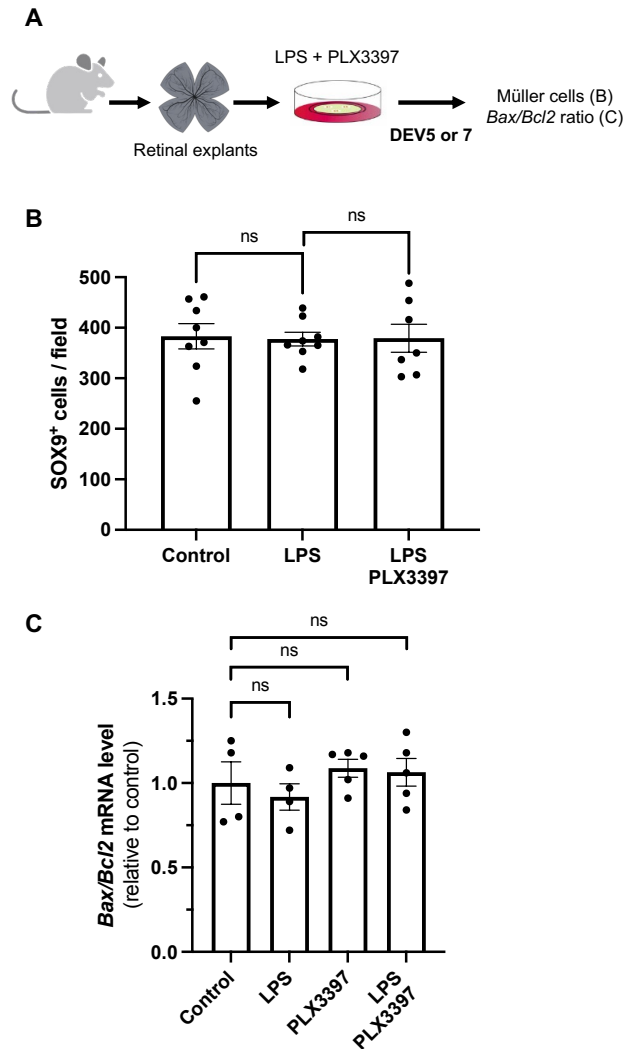
Figure S7



**Figure S7. Absence of toxicity of LPS on retinal cells in mouse explants. (A)** Outline of the experimental procedure used in (B, C). Retinas from wild-type mice were flattened and cultured for up to 7 days in the presence of LPS. They were then processed for qPCR analysis. **(B, C)** qPCR analysis of *Bax/Bcl2* expression ratio (B) or *Gfap* expression (C) in control and LPS-treated retinal explants at different culture time points relative to uncultured control condition (DEVO). Data are represented as mean  $\pm$  SEM, and each point represents one retinal explant. ns: non-significant (Mann-Whitney test).

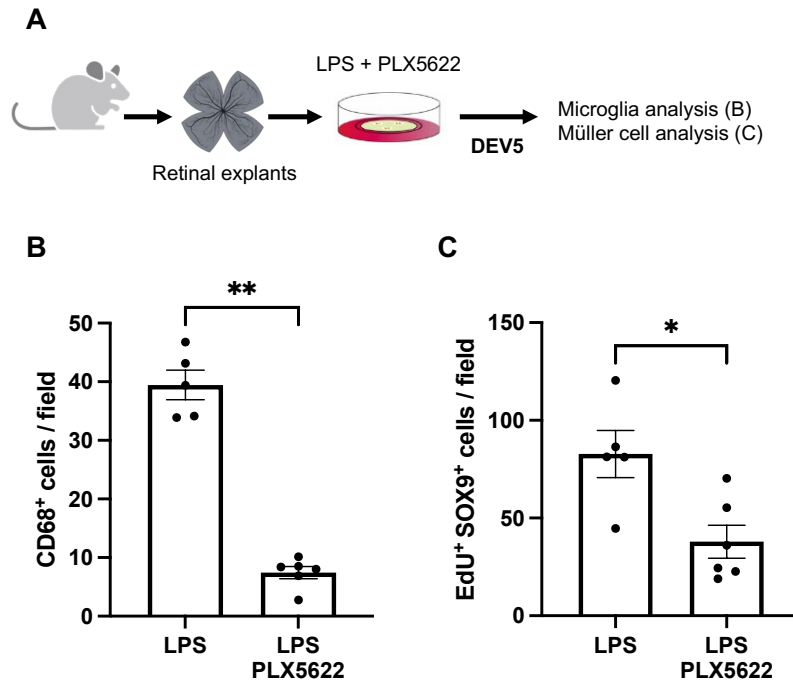


Figure S8



**Figure S8. Impact of LPS plus PLX3397 treatment on the survival of mouse Müller glial cells. (A)** Outline of the experimental procedure used in (B, C). Retinas from wild-type mice were flattened and cultured in the presence of LPS, PLX3397 or LPS plus PLX3397. Retinal explants were processed for immunostaining analysis at DEV7 (B) or processed for qPCR analysis at DEV5 (C). **(B)** Quantification of SOX9-positive cells (Müller cells). **(C)** Retinal qPCR analysis of *Bax/Bcl2* expression ratio. Data are represented as mean ± SEM, and each point represents one retinal explant. ns: non-significant (Mann-Whitney test).

Figure S9



**Figure S9. PLX5622 counteracts the LPS-driven proliferation of Müller glial cells in mouse retinal explants.** (A) Outline of the experimental procedure used in (B, C). Retinas from wild-type mice were flattened and cultured for 5 days in the presence of EdU plus LPS, or plus LPS and PLX5622. Retinal explants were processed for immunostaining analysis at DEV5. (B, C) Quantification of CD68-positive cells (activated microglia, B) or double EdU- and SOX9-positive cells (proliferative Müller cells, C) in LPS or LPS plus PLX5622-treated retinal explants. Data are represented as mean  $\pm$  SEM, and each point represents one retinal explant. \* $P < 0.05$ , \*\* $P < 0.01$  (Mann-Whitney test).

Supplementary Table S1.

## Refractory Stage

ID	Description	setSize	Enrichment Score	Normalized Enrichment Score	pvalue	p.adjust	qvalue
GO:0009583	<u>Detection of light stimulus</u>	45	-0,82	-2,98	1,00E-15	4,96E-13	3,23E-13
GO:0019646	Aerobic electron transport chain	66	-0,75	-2,95	1,00E-15	4,96E-13	3,23E-13
GO:0009584	<u>Detection of visible light</u>	36	-0,85	-2,92	1,00E-15	4,96E-13	3,23E-13
GO:0042773	ATP synthesis coupled electron transport	71	-0,72	-2,89	1,00E-15	4,96E-13	3,23E-13
GO:0042775	Mitochondrial ATP synthesis coupled electron transport	71	-0,72	-2,89	1,00E-15	4,96E-13	3,23E-13
GO:0022904	Respiratory electron transport chain	88	-0,69	-2,83	1,00E-15	4,96E-13	3,23E-13
GO:0002521	<b>Leukocyte differentiation</b>	339	0,47	2,40	1,02E-15	4,96E-13	3,23E-13
GO:0048858	Cell projection morphogenesis	453	0,44	2,28	3,63E-15	1,38E-12	8,98E-13
GO:0032990	Cell part morphogenesis	469	0,43	2,25	3,57E-15	1,38E-12	8,98E-13
GO:0002088	<u>Lens development in camera-type eye</u>	61	0,76	2,97	4,64E-15	1,59E-12	1,03E-12

## Permissive Stage

ID	Description	setSize	Enrichment Score	Normalized Enrichment Score	pvalue	p.adjust	qvalue
GO:0050776	<b>Regulation of immune response</b>	382	0,59	2,14	2,74E-15	9,37E-12	7,46E-12
GO:0002684	<b>Positive regulation of immune system process</b>	465	0,56	2,05	1,11E-13	1,90E-10	1,51E-10
GO:0009583	<u>Detection of light stimulus</u>	45	-0,86	-2,61	1,15E-12	1,31E-09	1,05E-09
GO:0045087	<b>Innate immune response</b>	343	0,59	2,10	2,95E-12	2,17E-09	1,73E-09
GO:0045321	<b>Leukocyte activation</b>	463	0,54	1,99	3,17E-12	2,17E-09	1,73E-09
GO:0098542	<b>Defense response to other organism</b>	442	0,54	1,99	7,51E-12	4,28E-09	3,41E-09
GO:0009584	<u>Detection of visible light</u>	36	-0,87	-2,56	1,53E-11	7,46E-09	5,94E-09
GO:0042110	<b>T cell activation</b>	260	0,61	2,13	2,39E-11	1,02E-08	8,14E-09
GO:0007602	<u>Phototransduction</u>	33	-0,87	-2,53	4,39E-11	1,67E-08	1,33E-08
GO:0002263	<b>Cell activation involved in immune response</b>	138	0,69	2,25	5,61E-11	1,92E-08	1,53E-08

**Table S1. GSEA top 5 most enriched or depleted biological processes at refractory or permissive stages between *rho* crispants and control retinas.** Log<sub>2</sub>FC ranked gene list from differential analysis performed at refractory or permissive stages. Biological processes pertaining to the visual system are underlined and biological processes pertaining to inflammatory response are in bold.

**Supplementary Table S2.****Primary antibodies and lectin used in *Xenopus***

Antigen	Host species	Distributor	Reference	Dilution
BrdU	Rat	Abcam	ab6326	1/400
BrdU	Mouse	Becton Dickinson	347580	1/100
Isolectin B4 – Alexa Fluor 594 Conjugate		Thermo Fisher Sc.	I21413	1/500
S-Opsin	Rabbit	Millipore	AB5407	1/500
M-Opsin	Rabbit	Millipore	AB5405	1/500
PCNA	Mouse	DAKO	M0879	1/500
Rhodopsin	Mouse	Millipore	MABN15	1/1000
Yap	Rabbit	Abcam	ab52771	1/50

**Primary antibodies used in mice**

Antigen	Host species	Distributor	Reference	Dilution
CD68	Rat	Bio-Rad	MCA1957GA	1/300
SOX9	Rabbit	Abcam	ab185966	1/300

**Secondary antibodies**

Antibody	Host	Company	Reference	Dilution
Anti-mouse IgG, Alexa 488	Goat	ThermoFisher Sc.	A-11001	1/1000
Anti-rabbit IgG, Alexa 555	Goat	ThermoFisher Sc.	A-21428	1/1000
Anti-rat IgG, Alexa 555	Goat	ThermoFisher Sc.	A-21434	1/1000
Anti-rat IgG, Alexa 647	Goat	ThermoFisher Sc.	A-21247	1/500

**Table S2. List of antibodies.**

Supplementary Table S3.

Primers for qPCR (*Xenopus*)

Target	Forward (5'-3')	Reverse (5'-3')
<i>anxA1</i>	TGCACTGCTGAAGAATCGG	TTGCTGTCGTTCCAGAGTTGG
<i>cd68</i>	AGAAATGGAGGCCCTTTGG	CTTGGCGGGTCCATAGTTGA
<i>eef1a1</i>	TGGTGGCATCGACAAGAGAAC	CCACCTTCACGCTCTGCCTTC
<i>il1-beta</i>	CATTCCCATGGAGGGCTACA	TGACTGCCACTGAGCAGCAT
<i>il10</i>	TGCTGGATCTTAAGCACACCCTGA	TGTACAGGCCTTGTTACGCATCT
<i>odc1</i>	GCTTCTGGAGCGGGCAAAGGA	CCAAGCTCAGCCCCCATGTCA
<i>socs3</i>	CCGGTGCCTAGGAAGAAGA	CCTTAAAGCAGCCECCATC
<i>tnf-alpha</i>	GCTCAAGGATAACTCCATCG	AACCAAGTGGCACCTGAATG

Primers for qPCR (mice)

Target	Forward (5'-3')	Reverse (5'-3')
<i>Ascl1</i>	TCTCCTGGGAATGGACTTTG	GGTTGGCTGTCGGTTTGTT
<i>Bax</i>	AGGCCTCCTCTCCTACTTCG	CTCAGCCCATCTTCTTCCAG
<i>Bcl2</i>	GGACTTGAAGTGCCATTGGT	AGCCCCTCTGTGACAGCTTA
<i>Ccl2</i>	GAAGGAATGGGTCCAGACAT	ACGGGTCAACTTCACATTCA
<i>Gfap</i>	CCAGTTACCAGGAGGCACTTG	CGATGTCCAGGGCTAGCTTAA
<i>Il1-beta</i>	GCACTACAGGCTCCGAGATGAAC	TTGTCGTTGCTTGGTTCTCCTTGT
<i>Il-6</i>	GCCTTCTTGGGACTGATGCTGGT	TCCTCTGTGAAGTCTCCTCTCCG
<i>Rps26</i>	CCCAAGGATAAGGCCATCAAG	AAGCACGTAGGCGTCGAAGA
<i>Srp72</i>	GCACTCATGGTAGCGTTCCA	CACCCAGCAGACAGACAAACTG
<i>Tbp</i>	CACAGGAGCCAAGAGTGAAGAAC	ATCACAGCTCCCCACCATGT
<i>Tnf-alpha</i>	AAGTCAACCTCTCTGCC	TCCAAAGTAGACCTGCCCG

Table S3. List of primers.

Supplementary Table S4.

Sample	Condition	Raw reads	Uniquely mapped reads	Mapped length
S13	Permissive control	37519396	32584008	294.26
S11	Permissive control	55667307	48249728	294.84
S9	Permissive control	37134505	32022113	294.80
S14	Permissive <i>rho</i> crispant	55470492	48437975	294.47
S12	Permissive <i>rho</i> crispant	42054660	36682819	293.81
S10	Permissive <i>rho</i> crispant	44074067	38604360	293.86
S3	Refractory control	31671086	27404733	294.53
S5	Refractory control	38540883	33584757	294.89
S7	Refractory control	48274813	41542934	294.17
S4	Refractory <i>rho</i> crispant	49009929	42877033	294.80
S6	Refractory <i>rho</i> crispant	55657807	48465273	294.08
S8	Refractory <i>rho</i> crispant	50338069	44186472	293.79

Table S4. RNAseq samples.

## Supplementary Table S5.

**Figure 1A**

BrdU+ cells / section							
Control	<i>rho</i> crispant	Control	<i>rho</i> crispant	Control	<i>rho</i> crispant	Control	<i>rho</i> crispant
0.00	1.44	0.80	4.22	1.25	4.38	5.29	46.00
0.20	1.40	1.20	3.10	1.50	4.88	6.29	134.60
0.60	0.70	1.60	2.50	1.50	7.28	5.67	75.67
0.25	0.38	0.60	3.80	1.75	8.95	6.00	51.50
0.00	0.40	2.20	6.40	2.50	9.88	6.00	160.00
0.00	1.25	1.60	5.63	2.88	10.99	5.17	114.00
0.25	1.22	0.00	6.44	3.88	23.13		
		0.00	4.33	4.63			
			5.80				
			3.40				

**Figure 2A**

IB4+ cells / section							
Stages							
45/46	47/48	49/50	51/52	53/54	55/56	60	66
0.125	0	0	1.83	1.33	3	11.6	13.8
0	0.166	0.5	1	3.5	2.16	10.7	9
0	0	0.5	1	1.83	3.3	9.5	10.3
0.25	0.166	0.833	1.17	1.66	3.1	7.8	6.1
0.125	0.33	1.16	1.17	1.33	1.83	9.3	
0.25	0.83	1	0.6	1.5	3	6.5	
0.125	0	0.5	0.5	2.16	2.67		

**Figure 3G**

-ΔCT					
<i>anx1</i>		<i>il1-beta</i>		<i>il10</i>	
Control	CoCl <sub>2</sub>	Control	CoCl <sub>2</sub>	Control	CoCl <sub>2</sub>
-4.40	-3.03	-15.42	-13.13	-12.20	-10.94
-6.01	-4.42	-13.56	-11.61	-11.98	-11.43
-9.04	-4.46	-11.12	-11.33	-11.62	-10.93
-8.56	-4.89	-11.93	-10.41	-11.14	-10.45
-8.75	-5.22	-13.90	-12.60	-11.79	-10.67
-4.33	-4.20	-12.32	-11.34	-13.37	-12.02
-9.82	-4.82	-12.73	-11.36	-12.04	-10.72
-8.99	-3.67			-11.24	-10.89
<i>sox3</i>		<i>cd68</i>		<i>tnf-alpha</i>	
Control	CoCl <sub>2</sub>	Control	CoCl <sub>2</sub>	Control	CoCl <sub>2</sub>
-7.29	-3.93	-7.04	-3.79	-11.99	-8.69
-7.40	-5.53	-9.10	-5.96	-11.95	-10.83
-7.69	-5.62	-9.88	-5.88	-11.05	-9.32
-8.48	-5.79	-9.74	-6.29	-12.08	-11.86
-9.13	-7.30	-8.95	-6.36	-11.21	-10.39
-8.21	-6.38	-8.58	-5.75	-13.94	-11.72
-9.43	-5.79	-10.50	-7.05	-12.99	-11.49
-9.34	-6.25	-8.63	-5.43		

**Figure 3I**

%PCNA+ cells / Yap+ cells	
Control	CoCl <sub>2</sub>
0	96.88
0	89.55
0	93.44
0	97.89
0	94.19
0	96.55
0	96.15
0	100.00
0	77.50
0	83.78

**Figure 2C**

IB4+ cells / section			
Control	<i>rho</i> crispant	Control	<i>rho</i> crispant
0.56	0.00	4.18	16.20
0.00	0.00	5.55	16.40
0.00	0.10	5.50	13.08
0.00	0.00	7.50	16.91
0.00	0.90	0.58	14.83
0.25	0.00	0.27	14.58
0.00	1.00	2.27	13.92
0.00	0.54	2.83	16.50
0.45	0.38	1.67	
0.10	0.73	4.17	
0.27	0.14	8.18	
0.09	2.67	9.27	
0.00	0.91		
0.00	1.10		
	0.25		
	0.73		
	0.10		

**Figure 3D**

IB4+ cells / section			
Control	CoCl <sub>2</sub>	Control	<i>rho</i> crispant
63.95	305.56	26.67	143.33
35.53	540.06	8.33	88.33
35.53	312.67	16.67	113.33
49.74	312.67	21.67	131.67
42.64	376.62	5.00	103.33
42.64	461.89	0.00	
35.53	390.83	5.00	
71.06	390.83		
92.38	341.09		
63.95	312.67		
85.27	397.94		
71.06	397.94		
49.74	476.11		
85.27	717.71		
49.74			
85.27			
42.64			
78.17			
49.74			
14.21			
28.42			
99.48			
63.95			
56.85			
63.95			
35.53			
56.85			
56.85			

**Figure 3M**

PCNA+ IB4+ cells / section		
Control	CoCl <sub>2</sub>	CoCl <sub>2</sub> Dex + PLX3397
3.40	285.20	134.60
4.20	266.80	119.80
10.40	330.20	22.60
0.00	300.20	20.00
1.00	287.40	97.00
1.00	244.80	132.00
0.80	91.00	190.00
6.20	150.20	120.00
0.20	341.60	38.40
1.33	331.20	125.60
	198.40	74.00
	179.00	105.40

Figure 3O	
PCNA+ IB4+ cells / section	
<i>rho</i> crispant	<i>rho</i> crispant Dex + PLX3397
90.60	134.00
86.20	113.60
127.80	151.60
166.20	135.00
138.40	100.20
174.40	99.40
264.80	98.60
263.40	148.20
194.00	79.80
234.20	102.40
189.00	116.60
128.20	104.80
237.00	132.60
100.60	137.20
215.20	123.00
231.40	220.00
220.80	88.00
184.60	60.40
	83.40
	101.40

Figure 4B		
IB4+ cells / section		
Control	CoCl <sub>2</sub>	CoCl <sub>2</sub> Dex + PLX3397
0.40	18.00	6.40
3.60	14.00	4.67
1.40	11.40	7.20
1.00	9.80	9.80
0.20	31.60	3.60
1.40	8.00	7.20
1.80	9.20	5.20
0.00	9.20	8.40
3.80		0.20
0.80		1.60
0.00		2.00
0.00		1.80
0.80		3.40

Figure 4C		
IB4+ IB4- cells / section		
Control	CoCl <sub>2</sub>	CoCl <sub>2</sub> Dex + PLX3397
0.40	120.50	15.40
1.00	42.60	1.33
0.00	62.00	4.00
1.50	49.20	2.80
0.60	145.40	5.60
1.40	51.80	35.40
2.60	74.20	4.80
0.00	107.60	3.60
2.80		9.20
1.80		3.60
1.00		4.40
1.60		2.60
2.00		4.00

Figure 4F	
IB4+ cells / section	
Control	Zymosan
3.14	18.86
3.86	19.86
3.14	19.88
2.43	9.71
3.83	28.86

Figure 4G	
IB4+ IB4- cells / section	
Control	Zymosan
7.43	11.29
4.57	10.71
3.29	16.25
5.00	6.71
4.00	11.00

Figure 4I	
IB4+ cells / section	
Control	Bacteria
6.33	37.60
7.00	41.33
1.67	22.00
3.25	27.00
6.33	19.00
2.75	22.67
4.71	29.25
2.00	20.33
	13.50
	38.43
	25.00
	31.80
	16.29
	14.20
	29.00
	27.00
	17.00
	25.50
	25.25
	17.00
	30.67
	23.67

Figure 4J	
IB4+ IB4- cells / section	
Control	Bacteria
7.67	8.70
2.00	3.00
1.83	11.75
3.00	6.00
13.67	16.00
2.75	6.33
4.00	3.00
3.50	6.67
	6.00
	12.14
	10.50
	9.60
	6.86
	5.00
	15.00
	16.50
	4.33
	7.50
	6.38
	4.33
	6.67
	2.33

Figure 5B																							
EdU+ Sox9+ cells / field																							
	Control												LPS										
DEV0	0.00	0.00	0.00	0.00																			
DEV1	0.00	0.00	0.00	0.00	0.00																		
DEV3	7.33	2.14	3.75	0.25	0.75																		
DEV5	28.63	15.38	33.00	18.13	8.63	3.00	9.00	12.75	10.25														
DEV7	21.88	30.14	18.33	9.75	14.20	13.60	20.91	14.80	19.40	13.75	23.00	9.50	108.40	163.38	180.89	115.00	43.50	53.42	51.20	24.22	58.00	82.75	113.00



**Figure 5D**

CD68+ cells / field	
LPS	LPS PLX3397
56.92	9.08
51.08	12.19
62.75	11.44
44.50	10.06
39.00	13.58
69.17	14.38
68.69	12.63
30.75	

**Figure 5E**

EdU+ Sox9+ cells / field		
Control	LPS	LPS PLX3397
24.00	79.25	36.50
28.75	149.00	16.50
28.25	59.50	2.75
32.25	61.75	25.50
37.75	108.25	55.75
62.00	77.50	47.00
60.50	182.75	47.75
33.25	65.00	36.50

**Figure 6A**

Cc/2 RNA level																										
Control												LPS														
DEV1	158.64	185.04	268.29	542.75	588.25	140.88	84.56	103.69					838.51	1203.89	2224.19	334.67	2114.17	268.52	176.77	161.79						
DEV3	168.39	162.01	67.45	59.85	247.73	32.16	25.91						506.16	174.68	995.67	508.97	737.61	110.42	81.31							
DEV5	89.96	23.25	42.24	64.47	156.50	24.24	27.86	50.79					821.58	229.13	3380.42	357.97	122.80	198.26	122.72	108.42						
DEV7	37.62	13.54	32.61	100.06	12.00	72.87	29.88	25.82	62.98	8.90	10.22	16.13	491.54	511.80	417.70	2683.91	378.85	617.54	3806.31	600.40	784.05	135.76	134.40	125.67		

Il1-beta RNA level																										
Control												LPS														
DEV1	2.66	3.22	4.28	3.77	11.96	2.18	1.20	2.53					22.77	32.83	41.39	7.31	33.72	4.53	4.19	4.17						
DEV3	1.73	1.68	0.52	3.33	1.30	0.60	0.71						13.14	3.75	23.91	18.42	10.03	2.96	1.55	2.18						
DEV5	0.88	0.79	1.54	0.89	6.03	1.78	9.59	2.51	8.58	0.73	1.49	3.12	17.50	7.41	23.63	11.62	31.68	18.84	18.54	18.26	2.45	2.39	1.97	1.30		
DEV7	2.80	0.76	1.99	0.89	0.87	1.96	0.82	4.13	1.72	0.81	1.16	0.69	34.74	34.13	39.96	17.16	20.40	13.80	57.39	15.24	15.97	4.20	2.74	4.62		

Il6 RNA level																										
Control												LPS														
DEV1	2.57	3.64	13.98	3.86	8.09	10.66	3.39	5.11					19.21	38.17	45.57	13.90	24.08	34.13	17.81	19.11						
DEV3	4.59	2.40	3.69	3.33	2.23	0.98	0.71						12.69	2.52	20.79	12.43	6.60	14.68	5.33	7.79						
DEV5	6.47	0.79	2.44	1.02	6.03	0.73	1.82	3.12					26.65	11.65	4.89	3.56	41.74	88.59	9.64	42.32	5.79	6.08	3.00	6.71		
DEV7	2.00	0.76	1.99	0.81	0.85	1.95	0.76	4.13	1.73	0.82	1.16	1.07	6.92	8.22	6.38	64.49	6.64	5.68	32.94	15.24	8.62	4.99	4.36	3.50		

Tnf-alpha RNA level																										
Control												LPS														
DEV1	3.26	4.38	2.80	9.68	4.80	0.65	0.50	1.29					2.93	11.76	19.84	7.74	4.55	0.72	0.66	0.98						
DEV3	3.38	1.68	1.22	2.62	2.89	1.00	0.71						19.70	5.53	18.36	32.23	9.38	3.13	1.64	1.72						
DEV5	3.27	2.63	7.35	1.82	4.75	8.06	8.96	5.79	6.68	0.73	1.49	3.15	31.18	8.24	25.23	47.04	24.58	40.52	19.09	14.15	2.66	2.16	3.82	2.40		
DEV7	45.94	2.91	6.47	5.13	2.59	9.53	4.28	4.13	6.24	0.81	1.16	1.91	55.47	16.48	16.78	20.43	32.14	13.62	12.02	15.24	16.14	5.62	4.54	4.34		

**Figure 6C**

EdU+ Sox9+ cells / field				
Control	LPS	TNF-alpha	IL6	TNF-alpha + IL-6
8.00	59.67	255.71	7.25	116.50
6.33	101.20	257.63	9.00	132.50
3.43	134.57	157.13	4.33	156.25
27.00	64.25	117.67	4.33	152.29
36.13	93.25	77.29	9.71	117.13
6.63	56.00	138.63	34.88	
8.63		113.13	31.38	
		73.50	17.17	
			15.50	

**Figure 6E**

Tnf-alpha mRNA level		
Control	LPS	LPS PLX3397
2.46	2.82	1.06
0.40	5.61	5.58
1.32	8.22	2.54
0.78	4.42	1.07
0.75	2.90	1.23
1.34	1.85	1.18
0.81	1.68	1.80
1.23	1.53	1.58

**Figure 7B**

EdU+ Sox9+ cells / field			
Control AAV	Control AAV LPS	AAV-YAP5SA	AAV-YAP5SA LPS
57.63	73.00	116.00	377.88
33.13	83.75	264.00	344.63
37.38	106.71	173.50	463.27
48.25	105.75	235.00	330.25
63.50	112.63	308.00	260.00
	101.25	264.75	

<b>Figure 7D</b>			
<b>EdU+ Sox9+ cells / field</b>			
<b>Control</b>	<b>LPS</b>	<b>EGF</b>	<b>EGF LPS</b>
0.38	124.38	331.63	623.25
22.75	132.88	20.50	877.13
7.13	183.38	559.00	672.29
5.00	237.38	351.63	308.83
13.71	308.38	67.71	450.38
8.14	59.25	167.33	310.28
2.00	489.75	90.43	239.88
6.60	116.83	49.00	135.33
9.25	24.67	290.20	312.43
53.38	91.75	639.25	432.88
12.00	172.25	231.00	115.00
10.88	46.50	69.88	408.63
54.63	130.63	27.50	295.00
39.00	23.25	158.63	67.38
	46.88	22.75	217.63
	77.00	410.88	253.00
	156.88		364.25
	85.50		

<b>Figure 7F</b>			
<b>EdU+ Sox9+ cells / field</b>			
<b>Control AAV</b>	<b>Control AAV PLX3397</b>	<b>AAV-YAP5SA</b>	<b>AAV-YAP5SA PLX3397</b>
12.50	1.57	962.14	153.43
30.75	0.88	729.00	226.50
9.56	1.14	924.17	261.67
12.75	2.00	824.13	118.67
11.43	1.88	880.00	135.63
	1.75		131.25
	2.14		137.25
	0.67		206.00
	3.00		273.50
			282.29

<b>Figure 7H</b>			
<b>EdU+ Sox9+ cells / field</b>			
<b>Control</b>	<b>PLX3397</b>	<b>EGF</b>	<b>EGF PLX3397</b>
4.88	0.71	186.80	10.25
3.40	0.13	51.75	8.17
2.20	0.50	49.33	15.67
26.43	0.83	55.33	9.83
43.17	3.86	75.50	71.50
14.80	2.57	181.29	62.75
57.00	4.00	178.75	10.60
		173.60	

<b>Figure 8A</b>	
<b>Asc1 mRNA level</b>	
<b>Control</b>	<b>LPS</b>
0.74	0.99
0.90	1.22
0.80	1.10
2.42	1.42
0.64	0.90
0.95	0.41
1.62	0.63
0.78	0.41
0.97	0.39
1.38	0.74
0.75	0.52
1.00	0.40
0.53	1.94
1.40	0.39
1.35	0.47
2.72	0.78
0.53	1.85
0.84	0.65
0.84	0.80
1.20	0.56
0.84	0.98
0.93	0.59
1.08	2.18
1.38	1.17
0.67	0.82
0.83	0.87
1.37	0.73
1.65	1.00
0.69	0.63
0.74	0.79
1.17	1.17
1.10	1.16
0.95	0.65
1.01	0.96
0.83	0.77
1.11	0.91
1.07	0.65
	0.12

<b>Figure 8D</b>			
<b>Ascl1 mRNA level</b>			
		<b>LPS</b>	
<b>Control</b>	<b>PLX3397</b>	<b>LPS</b>	<b>PLX3397</b>
1.18	2.13	5.24	6.10
0.85	1.19	6.04	7.39
0.58	1.42	2.85	9.22
0.42	1.48	1.25	5.06
1.90	2.30	1.29	5.43
0.69	1.15	1.90	4.25
2.09	1.92	3.75	5.12
1.51		1.48	2.80
1.27		2.97	5.44
0.69		1.94	9.29
0.94		1.22	2.37
1.63		1.67	4.28
0.76		1.62	2.93
0.98		1.29	5.13
		0.98	5.01
			2.90

<b>Figure 9A</b>		
<b>Tnf-alpha mRNA level</b>		
	<b>LPS</b>	
<b>Control</b>	<b>LPS</b>	<b>PLX3397</b>
1.07	5.23	2.39
0.68	2.97	1.56
0.88	6.12	5.20
1.02	4.32	2.38
1.16	6.04	0.79
1.33	2.40	0.96
1.33	2.26	0.81
0.67	6.88	1.38
1.46	0.65	0.95
1.63	1.23	0.70
0.62	2.73	0.25
0.75		0.65
0.98		0.76
0.63		1.39
1.95		2.45
1.12		0.42

<b>Figure 9B</b>		
<b>Ascl1 mRNA level</b>		
<b>Control</b>	<b>LPS</b>	<b>TNF-alpha</b>
0.78	0.72	0.59
1.39	0.46	0.44
1.05	0.60	0.52
1.07	0.74	0.50
0.82	0.78	0.45
1.10	1.29	0.57
1.12	0.40	0.37
1.05	1.03	0.53
0.78	0.27	0.21
0.99	0.59	0.31
	0.45	0.52
		0.50

<b>Figure 9C</b>	
<b>Ascl1 mRNA level</b>	
<b>TNF-alpha</b>	<b>TNF-alpha PLX3397</b>
1.79	2.52
1.16	4.53
1.23	2.80
0.73	2.50
1.06	3.26
	6.65

<b>Figure 9D</b>		
<b>Ascl1 mRNA level</b>		
<b>Control</b>	<b>LPS PLX3397</b>	<b>LPS TNF-alpha</b>
0.93	5.59	0.22
1.46	1.95	0.23
0.71	4.18	0.14
	4.30	0.50
	2.67	0.21
		0.41
		0.45
		0.54

<b>Figure S1</b>			
<b>BrdU+ cells / section normalized to the retina surface (a.u.)</b>			
<b>Control</b>	<b>rho crispant</b>	<b>Control</b>	<b>rho crispant</b>
0.00	0.13	0.07	0.74
0.02	0.12	0.09	2.30
0.05	0.06	0.07	1.60
0.02	0.03	0.09	0.84
0.00	0.04	0.09	3.40
0.00	0.11	0.08	2.00
0.02	0.12		

<b>Figure S5B</b>	
IB4+ cells / section	
CoCl <sub>2</sub>	CoCl <sub>2</sub> Dex + PLX3397
24.40	9.60
55.60	14.60
27.00	4.20
34.60	4.00
15.00	9.00
20.00	10.60
18.00	11.40
	9.20
	4.00
	6.80
	1.60
	16.20
	7.00
	16.20
	12.00
	2.60
	2.80
	3.80
	7.00

<b>Figure S5D</b>	
IB4+ cells / section	
rho crispant	rho crispant Dex + PLX3397
19.60	6.60
19.40	4.40
24.60	5.80
5.40	8.40
11.00	3.80
21.60	11.60
15.00	10.60
7.40	11.20
21.80	6.80
18.20	6.40
11.40	6.00
22.60	6.40
9.00	9.80
15.20	13.40
12.00	9.00
15.20	15.20
10.60	11.75
18.60	10.20
	11.60
	6.00

<b>Figure S7B</b>																							
Bax/Bcl2 mRNA level																							
	Control										LPS												
DEV0	0.78	1.28	0.75	1.03	0.92	1.42	0.87	1.17	0.95	1.01													
DEV1	4.41	4.65	2.94	4.22	3.85	3.08	2.18					4.80	3.42	4.68	5.93	3.69	3.48	3.17					
DEV3	2.95	4.70	4.91	6.14	2.45	2.87						5.05	3.67	3.17	4.24	1.96	1.51	2.66					
DEV5	4.07	4.64	8.22	5.20	2.46	2.15	2.31					5.10	5.96	4.23	3.82	2.91	2.92	3.28	2.92				
DEV7	4.35	5.01	6.04	2.80	3.73	5.44	2.42	4.54	3.61	3.91	2.98	4.27	4.12	2.96	6.82	3.20	2.52	2.21	3.16	5.44	2.74	2.50	2.97

<b>Figure S7C</b>																							
Gfap mRNA level																							
	Control										LPS												
DEV0	1.41	0.77	1.83	0.51	0.49	0.47	1.67	2.63															
DEV1	4.14	1.98	1.85	5.34	2.65							1.93	3.92	2.46	2.58	3.44							
DEV3	37.99	48.97	24.37	25.55	44.27							12.60	17.26	41.88	38.03	47.43							
DEV5	15.34	12.70	35.27	18.54	79.47	72.95	101.04	50.19	106.42														
DEV7	64.08	22.55	55.45	165.57	189.83	364.64	284.90	81.62	56.09	25.83	27.19	24.76	40.55	121.73	116.49	246.50							

<b>Figure S8B</b>		
Sox9+ cells / field		
Control	LPS	LPS PLX3397
363	365	307
324	374	303
255	366	416
457	318	488
434	353	337
461	382	454
371	439	350
400	423	

<b>Figure S8C</b>			
Bax/Bcl2 mRNA level			
Control	LPS	PLX3397	LPS PLX3397
0.77	1.09	1.16	1.18
1.25	0.72	1.02	1.30
0.80	0.97	1.17	1.06
1.18	0.89	0.91	0.84
		1.18	0.94

<b>Figure S9B</b>	
CD68+ cells / field	
LPS	LPS PLX5622
34.13	8.00
33.88	10.13
39.38	8.50
43.14	2.75
46.75	8.38
	6.88

<b>Figure S9C</b>	
EdU+Sox9+ cells / field	
LPS	LPS PLX5622
81.25	55.25
86.38	36.00
81.13	70.25
44.63	18.88
120.38	24.38
	22.63

**Table S5. Descriptive Statistics.**