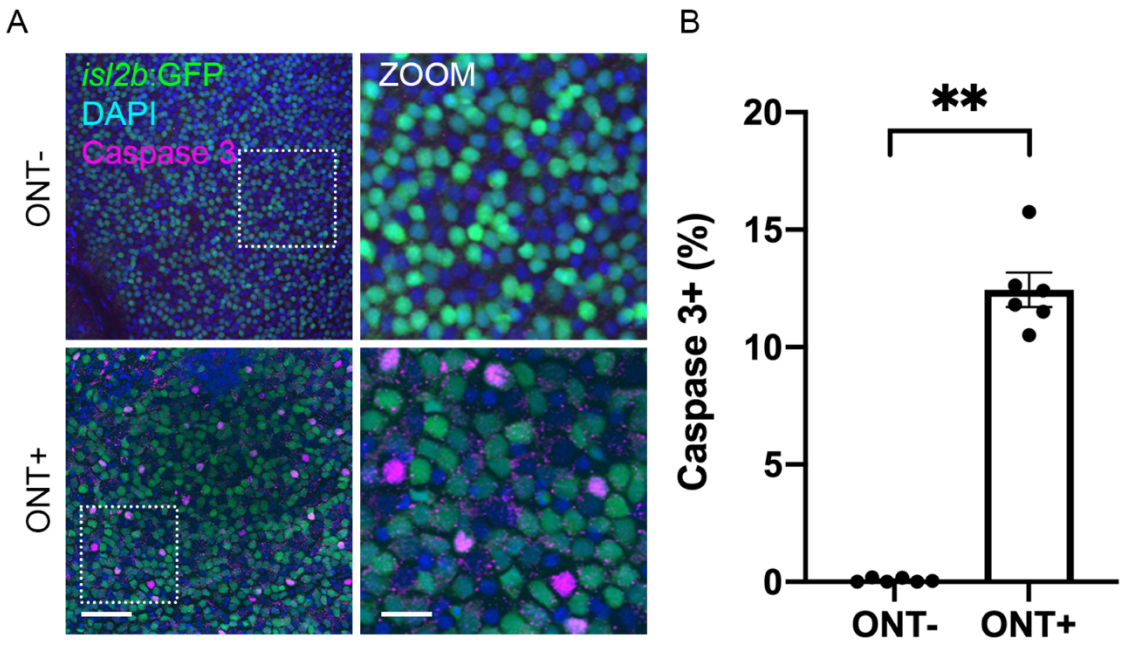


Fig. S1. Cleaved caspase-3 expression in the ganglion cell layer after optic nerve transection.

(A) Cleaved caspase-3 (magenta) expression in *isl2b*:GFP^{+} (green) flat-mount retinae at 7dpi. DAPI (blue) counterstain for nuclei. **(B)** Quantification of the percentage of cleaved caspase-3^{+} RGCs in the ganglion cell layer after ONT(n=6/condition). Shown are mean±SEM; **p<0.01; Mann-Whitney test. Data derived from 3 experiments. Scale bars = 50µm and 150µm on zoomed images.

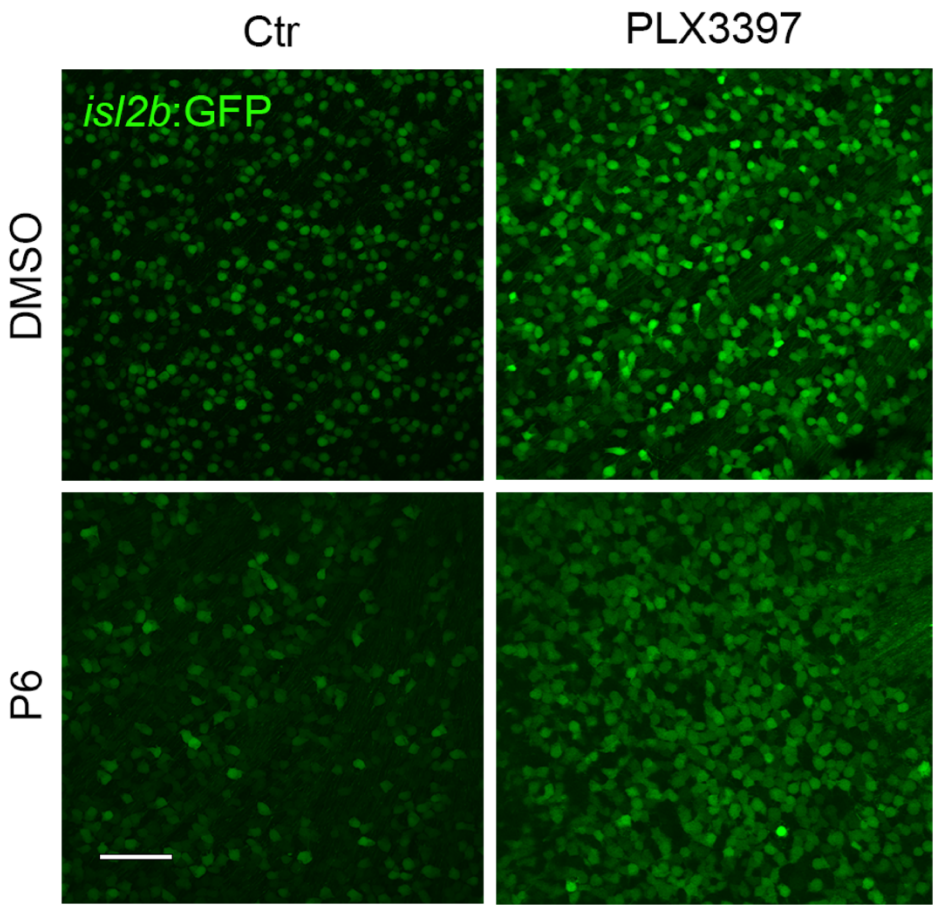


Fig. S2. RGC survival after Jak inhibition and macrophage/microglia depletion.

Flat-mount images of *isl2b*:GFP retinae after intravitreal injection of P6 or DMSO +/- PLX3397 treatment at 7dpi. Data derived from 3 experiments. Scale bars = 50μm.

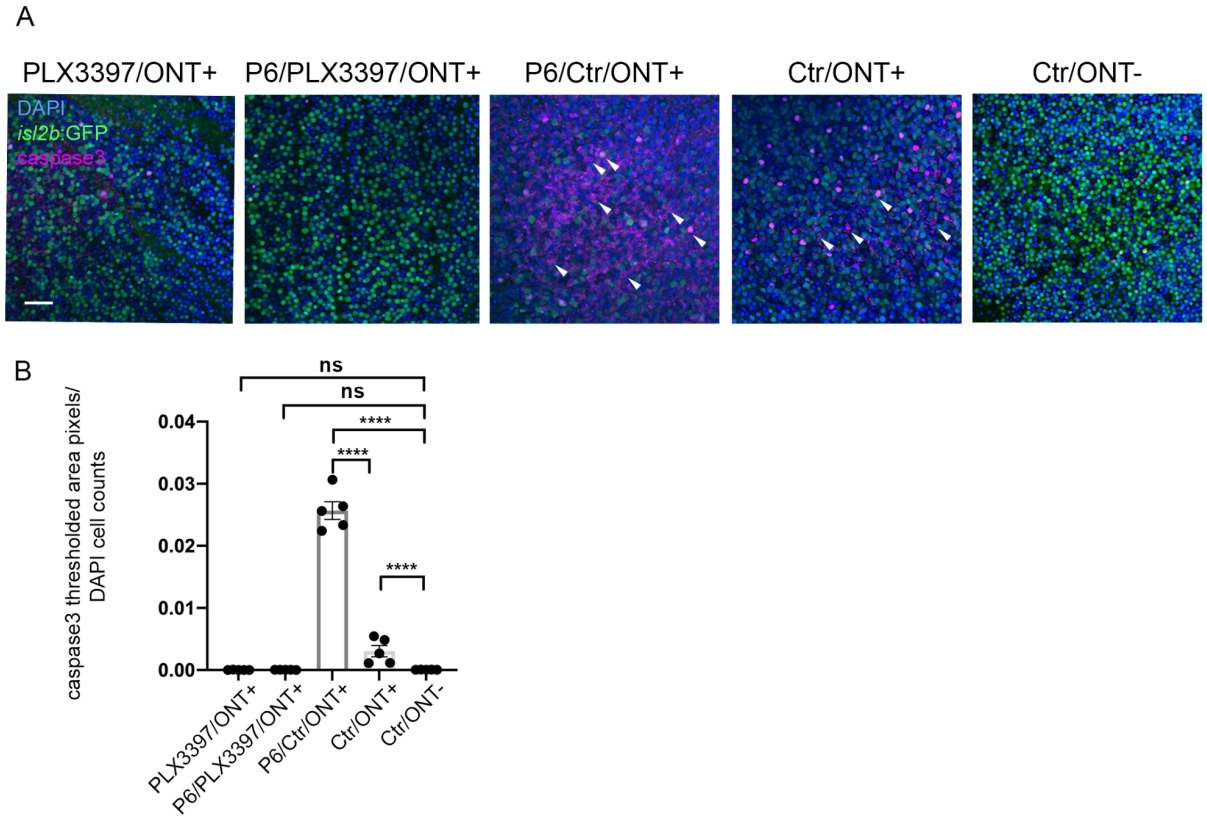


Fig. S3. Cleaved caspase-3 staining after JAK inhibition and macrophage/ microglia depletion.

(A) Cleaved caspase-3 (magenta) expression in *isl2b*:GFP^{+} (green) flat-mount retinae at 7dpi. DAPI (blue) counterstain for nuclei. Scale bar=50 µm. **(B)** Quantification of the ratio of the thresholded area pixels of cleaved caspase-3^{+} staining to counts of DAPI cells in the ganglion cell layer (n=5/condition). Shown are mean±SD; ****p<0.0001; Kruskal Wallis ANOVA with Dunn's multiple comparisons. Data derived from 2 experiments.

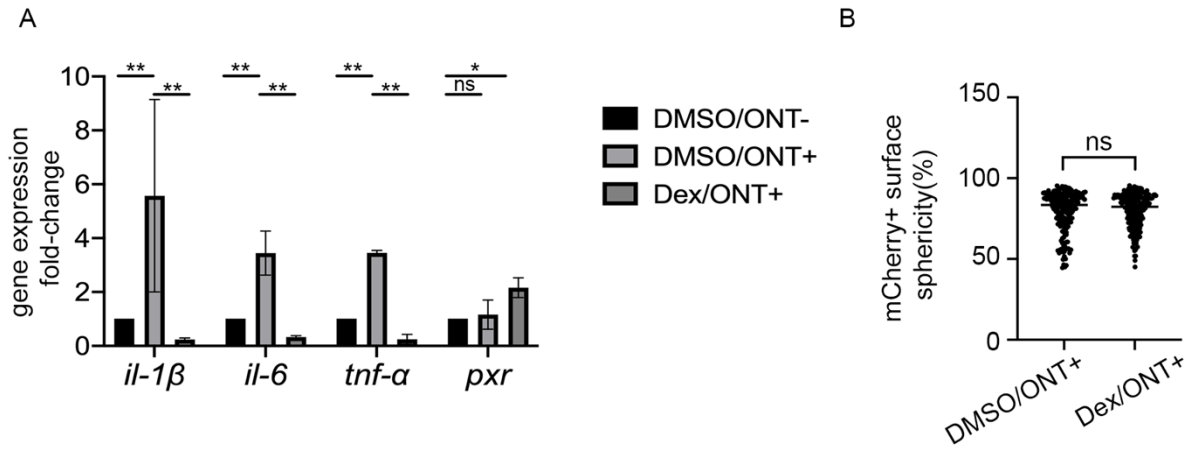


Fig. S4. Quantification of sphericity of macrophages/microglia and qRT-PCR after dexamethasone application.

(A) qRT-PCR for *il1-β, il6*, *tnf-α* and a downstream transcriptional target of dexamethasone *pxr* (Pascussi et al. 2000) expression in retinae treated with 10μM dexamethasone or 0.05%DMSO at 7dpi,expression fold change of above genes in DMSO/ONT- retinae were normalized to 1 as the control. *gapdh* were used as the housekeeping gene. Shown are mean±SD; **p<0.01; *p<0.05. Kruskal Wallis ANOVA with Dunn's multiple comparisons. Data derived from 3 experiments. **(B)** Quantification of the sphericity of mCherry+ surfaces after dexamethasone application at 7dpi. Violin plot showing no significant differences in sphericity of mCherry+ macrophages/microglia in Dex/ONT+ retinae compared to DMSO/ONT+ controls (n=180 in Dex/ONT+ and n=198 in DMSO/ONT+); p=0.4235, unpaired t-test with Welch's correction.

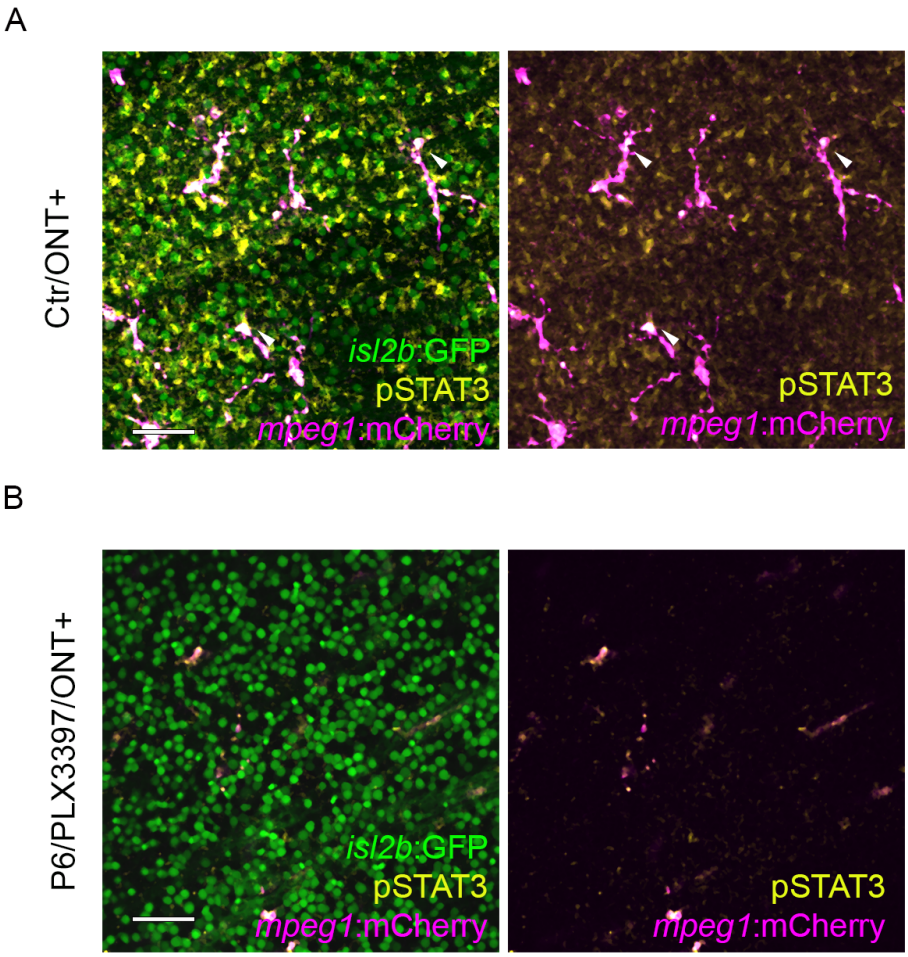


Fig. S5. JAK/STAT pathway activity in macrophages/microglia and after P6/ PLX3397 treatment.

(A) Flat-mount images showing pSTAT3 staining (yellow) on *isl2b*:GFP;*mpeg1*:mCherry (*isl2b*:GFP – green; *mpeg1*:mCherry - magenta) retinae at 7dpi. Image to right has *isl2b*:GFP channel removed. **(B)** Flat-mount images showing pSTAT3 staining on *isl2b*:GFP;*mpeg1*:mCherry (*isl2b*:GFP – green; *mpeg1*:mCherry - magenta) retinae after P6/PLX3397 treatment or housed in system water and injected with 0.05% DMSO (Ctr) at 7dpi. Image to right has *isl2b*:GFP channel removed. Scale bar=50μm.

Table S1. Sequences of q-PCR primers

Click here to download Table S1

Table S2. 56 up-regulated genes at 24hpi (filtering parameters used: the maximum of the average group RPKM value >1.5, fold change >2, false discovery rate (FDR) p-value <0.05. Genes with TPM=0 in one or more replicates were excluded.

Click here to download Table S2

Table S3. 252 down-regulated genes at 24hpi (filtering parameters used: the maximum of the average group RPKM value >1.5, fold change >2, false discovery rate (FDR) p-value <0.05. Genes with TPM=0 in one or more replicates were excluded.

Click here to download Table S3

Table S4. 5 up-regulated genes and 3 down-regulated genes at 12hpi (filtering parameters used: the maximum of the average group RPKM value >1.5, absolute fold change >2, false discovery rate (FDR) p-value <0.05. Genes with TPM=0 in one or more replicates were excluded.)

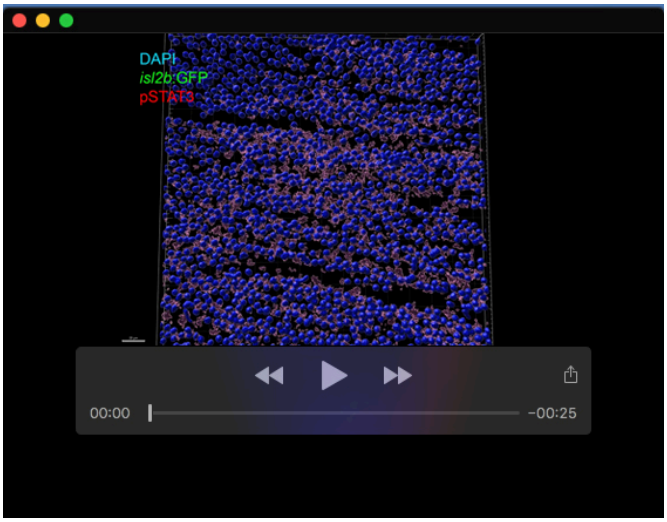
Click here to download Table S4

Table S5. 49 up-regulated genes at 12hpi (filtering parameters used: the maximum of the average group RPKM value >1.5, fold change >2, p-value <0.05. Genes with TPM=0 in one or more replicates were excluded.

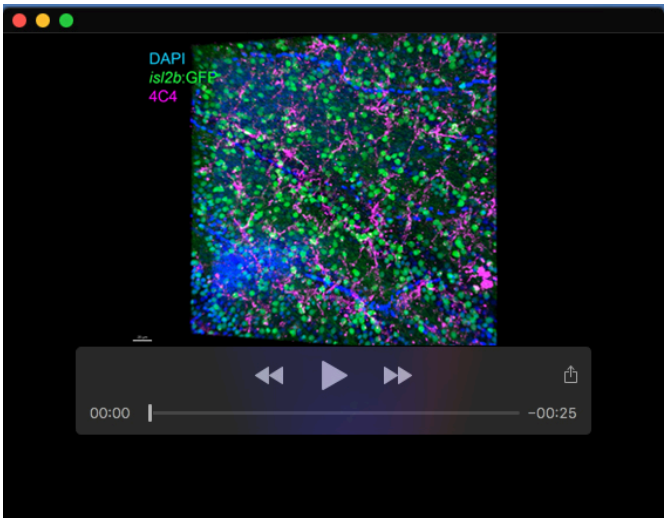
Click here to download Table S5

Table S6. 31 down-regulated genes at 12hpi (filtering parameters used: the maximum of the average group RPKM value >1.5, fold change < -2, p-value <0.05. Genes with TPM=0 in one or more replicates were excluded.

Click here to download Table S6



Movie 1. Surfaces of pStat3 staining generated in Imaris. Scale bar = 20μm.



Movie 2. 3D image of 4C4 staining generated in Imaris. Scale bar = 20μm.