Regulation of Diseases-Associated Microglia in the Optic Nerve by Lipoxin B_4 and Ocular Hypertension

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Keywords: Glaucoma, microglia reactivity, lipoxins, neurodegeneration, retina, optic nerve

Abstract

Background

The resident astrocyte-retinal ganglion cell (RGC) lipoxin circuit is impaired during retinal stress, which includes ocular hypertension-induced neuropathy. Lipoxin B_4 produced by homeostatic astrocytes directly acts on RGCs to increase survival and function in ocular hypertension-induced neuropathy. RGC death in the retina and axonal degeneration in the optic nerve are driven by the complex interactions between microglia and macroglia. Whether LXB_4 neuroprotective actions include regulation of other cell types in the retina and/or optic nerve is an important knowledge gap.

Methods

Cellular targets and signaling of LXB_4 in the retina were defined by single-cell RNA sequencing. Retinal neurodegeneration was induced by injecting silicone oil into the anterior chamber of the mouse eyes, which induced sustained and stable ocular hypertension. Morphological characterization of microglia populations in the retina and optic nerve was established by MorphOMICs and pseudotime trajectory analyses. The pathways and mechanisms of action of LXB_4 in the optic nerve were investigated using bulk RNA sequencing. Transcriptomics data was validated by qPCR and immunohistochemistry. Differences between experimental groups was assessed by Student's t-test and one-way ANOVA.

Results

Single-cell transcriptomics identified microglia as a primary target for LXB_4 in the healthy retina. LXB_4 downregulated genes that drive microglia environmental sensing and reactivity responses. Analysis of microglial function revealed that ocular hypertension induced distinct, temporally defined, and dynamic phenotypes in the retina and, unexpectedly, in the distal myelinated optic nerve. Microglial expression of CD74, a marker of disease-associated microglia in the brain, was only induced in a unique population of optic nerve microglia, but not in the retina. Genetic deletion of lipoxin formation correlated with the presence of a CD74 optic nerve microglia population in normotensive eyes, while LXB_4 treatment during ocular hypertension shifted optic nerve microglia toward a homeostatic morphology and non-reactive state and downregulated the expression of CD74. Furthermore, we identified a correlation between CD74

and phospho-phosphoinositide 3-kinases (p-PI3K) expression levels in the optic nerve, which was reduced by LXB_4 treatment.

Conclusion

We identified early and dynamic changes in the microglia functional phenotype, reactivity, and induction of a unique CD74 microglia population in the distal optic nerve as key features of ocular hypertension-induced neurodegeneration. Our findings establish microglia regulation as a novel LXB_4 target in the retina and optic nerve. LXB_4 maintenance of a homeostatic optic nerve microglia phenotype and inhibition of a disease-associated phenotype are potential neuroprotective mechanisms for the resident LXB_4 pathway.

Introduction

Ocular hypertension (OHT) is the primary risk factor responsible for initiating the cascade of events leading to the irreversible retinal neurodegeneration that we know as glaucoma. The only existing therapeutic approach for glaucoma involves the use of topical hypotensive drugs to lower intraocular pressure (IOP)[1–4]. However, glaucoma has a multifactorial etiology, and the precise sequence of events and effector cells that trigger and drive the cascades resulting in retinal ganglion cell (RGC) degeneration[5] are largely unknown. Consequently, there is a pressing need to elucidate these mechanisms, identify new therapeutic targets, and develop treatments to prevent and counteract glaucomatous neurodegeneration.

We recently identified a resident neuroprotective lipid mediator pathway in the retina[6]. Metabolomic screening of homeostatic astrocytes identified lipoxins (LXA_4 and LXB_4) as endogenous neuroprotective signals. The canonical role of lipoxins is the regulation of leukocyte and T-cell functions to ensure healthy immune responses[7–10]. However, our recent study established direct protection of RGC and neurons by lipoxins as new bioaction[6]. In response to retinal excitotoxic stress, formation of LXA_4 and LXB_4 in the retina and optic nerve is downregulated, suggesting a homeostatic function. More importantly, inhibition of the lipoxin pathway amplifies RGC death in the retina[6,11] whereas LXB_4

therapeutic treatment rescued RGC function in a chronic OHT model of neurodegeneration[6]. Notably, LXB_4, whose mechanism of action is not yet well defined, consistently demonstrated more potent neuroprotective activity than LXA_4 *in vitro* and *in vivo*[6]. LXB_4's action are not mediated by the LXA_4 receptor, and it has distinct bioactions from LXA_4 with monocytes and macrophages[12]. The mechanisms through which LXB_4 exerts its protective effects and the specific cellular targets of LXB_4 within the retina and optic nerve is not fully understood and was the focus of this study.

A cell type of interest in the cascade of glaucomatous neurodegeneration are microglia, which reside around ganglion cell somata in the retina and their axons in the optic nerve[13–15]. They are in constant communication with astrocytes[16] and continually monitor the retinal and optic nerve environments as part of their essential homeostatic function. Microglial activation and the phenotypic switch from highly ramified, homeostatic microglia to amoeboid-reactive microglia are key features of retinopathy and neurodegeneration[17,18]. Their role in initiating or driving the pathogenesis of glaucoma remains to be clearly defined[19–21]. However, microglia-secreted cytokines regulate astrocyte reactivity in other neurodegenerative disease models including Alzheimer's disease[22–24].

Using single-cell transcriptomics, bulk RNA-seq, and morphological analysis approaches, we investigated the mechanism and cell targets for LXB_4 in healthy and OHT-injured retinas. We report that resident microglia in the retina and distal myelinated optic nerve are a cellular target for LXB_4. After OHT-induced retinal injury, neuroprotective LXB_4 treatment shifted the functional phenotype of microglia towards homeostasis in the distal myelinated optic nerve and downregulated a key marker of disease-associated microglia. Our findings provide new insights into the functional response of microglia to retinal OHT injury, and identify a new cellular target and mechanism for LXB_4's neuroprotective actions.

Methods

Animals

C57BL/6J and *Alox5*$^{-/-}$ (B6.129S2-*Alox5*^{tm1Fun}/J, stock number 004155) male mice were obtained from Jackson Laboratory (Bar Harbor, ME). C57BL/6J mice were used as a congenic control for the *Alox5*$^{-/-}$ (5-LOX KO) mice. All animal procedures were approved by the Institutional Animal Care and Use Committee (IACUC) at the University of California, Berkeley. Mice were housed in a controlled environment, maintained on a 12-hr light-dark cycle, and provided unrestricted food and water access throughout the study.

Silicone oil injections

OHT was induced in C57BL/6J and 5-LOX KO mice using an established silicone oil model[25,26]. Briefly, male mice were anesthetized at 8 wks of age using intraperitoneal injection of ketamine/xylazine (100 mg/kg and 10 mg/kg, respectively). A topical anesthetic (0.5% proparacaine hydrochloride; Sandoz, Princeton, NJ) was applied to the eye. Under microscopic guidance, a sterile 31 G paracentesis needle was used to create an incision in the anterior chamber of the eye, ensuring no damage to the iris or lens. The needle was slowly withdrawn to release approximately 1-2 μL of aqueous humor. Subsequently, 1.2 or 1.8 μL of silicone oil (Alcon, Fort Worth, TX) was injected into the anterior chamber using a 33 G Hamilton syringe (Reno, NV). The syringe was slowly withdrawn after holding it for 10 seconds. To minimize silicone oil leakage, the eyelids were gently closed to cover the corneal incision. After the injection, an antibiotic drop (0.3% Tobramycin Ophthalmic Solution, Bausch and Lomb, Laval, Canada) was applied to the eye. Silicone oil was injected into both eyes, and the uninjected eyes from separate groups of animals were used as controls. Mice were kept on a heating pad until fully recovered from anesthesia. Intraocular pressure (IOP) was measured by Tonometer (TonoLab, Vantaa, Finland) at different time points after dilating the eyes with tropicamide solution (Akorn, Lake Forest, IL) for 10 mins. At designated time points (1, 2, 4, and 6 wks) post-injection, mice were euthanized, and eyes were enucleated in sterile phosphate buffer saline (PBS) at 4 °C. Retina and optic nerve were dissected and stored in 4% paraformaldehyde (4 °C) and TRIzol (-80 °C) for immunostaining and RNA isolation.

Ocular coherence tomography

Anesthetized mice were maintained on a water-based heating pad at 37 °C. Before imaging, lubricant eye drops were instilled on the eyes (Systane Ultra, Alcon), and pupils were dilated using 0.5% tropicamide (Akorn). A lubricant gel (Tears, Alcon) was used to avoid further drying. A Bioptigen Spectral Domain OCT System (Envisu R2300, Durham, NC) was used for image acquisition. OCT imaging and analysis procedures have been described previously[27,28]. In brief, a rectangular scan with dimensions of 1.8 x 1.8 mm was employed to capture an en-face retinal fundus image centered around the optic nerve head. Each image consisted of 100 B-scan images, with 1536 A-scans for each B-scan. Using a script written in ImageJ software (NIH, Bethesda, MD), masked observers analyzed the retinal layer B-scan images. Retinal layer thickness was quantified from both the left and right locations relative to the center of the optic nerve head. The average value obtained from these locations represented the thickness measurement.

Electroretinography (ERG)

The mice were subjected to overnight dark adaptation before the ERG measurements. Anesthesia was induced under red light using intraperitoneal injection of ketamine/xylazine (100 mg/kg and 10 mg/kg, respectively). Corneal anesthesia was achieved using topical proparacaine hydrochloride. To dilate pupils, 0.5% tropicamide (Akorn) and 2.5% phenylephrine (Paragon BioTeck, Portland, OR) were applied. ERG measurements were conducted using the Celeris system (Diagnosys LLC, Lowell, MA), employing a range of stimulus intensities from -5.90 to 2.25 log cdm-2. The subdermal needle electrode at the tail served as the ground electrode. The positive scotopic threshold response (pSTR) was elicited using an intensity of -2.50 log cdm-2 to assess RGC function. The pSTR was recorded as the average of 20 repeats with an inter-stimulus interval of 2 seconds. The amplitude at ~110 ms after stimulus onset was measured and used for analysis.

LXB_4 treatment

For scRNA-seq experiments, mice were treated with 1μg of LXB_4 methyl ester (Cayman Chemicals, Ann Arbor, MI) by intraperitoneal injection (IP) once a day and 1μg of LXB_4 methyl ester by topical application 3 times a day for 3 days. Vehicle (ethanol) for LXB_4 methyl ester was removed under a stream of nitrogen, and LXB_4 methyl ester was resuspended in sterile PBS immediately prior to injection or topical treatment. For RNA-seq experiments, mice were treated with 250 ng of LXB_4 methyl ester by IP and 25ng of LXB_4 methyl ester by topical application every other day for 2 wks. For morphometric analysis, mice were treated with 1μg of LXB_4 methyl ester by IP and 1μg of LXB_4 methyl ester by topical application once daily for 1 wk. For the sham group, mice were treated with LXB_4 equivalent volume of sterile PBS via IP and a topical route.

Quantitative PCR

Total RNA was isolated from retinas using TRIzol extraction method (Invitrogen, Waltham, MA). mRNA was converted to cDNA using an iScript cDNA synthesis kit (Bio-Rad, Hercules, CA). Transcripts for *C5ar1, Clec4a2, C3ar1, Ccl5, Tnf-α, Cxcl10,* and *Cd68* were quantified by using GoTaq PCR master mix (Promega, Madison, WI) in OneStep Plus qPCR (Applied Biosystems, Waltham, MA) system by $2^{-\Delta\Delta CT}$ method.

Immunostaining

For whole mounts of the retina and optic nerve, the tissues were dissected and fixed in 4% PFA at 4 °C overnight. The next day, tissues were blocked and permeabilized in blocking buffer (10% normal donkey serum + 2% Triton x-100) for 24 hrs at 4 °C. Further, tissues were incubated with primary antibodies at 1:1000 dilution (anti-Iba1, Cell Signaling (Danvers, MA); anti-CD68, BioLegend (San Diego, CA); anti-RBPMS, Phosphosolutions (Aurora, CO)) for 72 hrs at 4 ^{o}C. Tissues were rinsed three times with washing buffer (PBS+ 0.25% Triton x-100) solution, each for 10 mins, on a rocker at room temperature. Secondary antibodies were diluted in blocking buffer at 1:2000 dilution (Alexa Fluor 594 and Alexa Fluor

488, Invitrogen), and tissues were incubated with a secondary antibody cocktail overnight at 4 ^{o}C. The next day, whole mounts were rinsed three times in a washing buffer and incubated with DAPI (1:5000, Invitrogen) for 10 mins at room temperature. Whole mounts were mounted using gold antifade mounting medium (Invitrogen) on a slide in a coverslip grove. For staining of optic nerve sections, the optic nerves were dissected and fixed in 4% PFA at 4 °C overnight. The next day, optic nerves were washed in PBS and dehydrated in a sucrose gradient (10%, 20%, and 30% sucrose) before embedding them in optimal cutting temperature medium (Thermo Fisher, Waltham, MA). 10µm sections were taken in Leica CM1900 cryostat (Wetzlar, Germany). Sections were washed in PBS, blocked, and permeabilized in blocking buffer (10% normal donkey serum + 0.25% Triton x-100) for 1 hr. Sections were then incubated in primary antibodies (anti-CD74, 1:100, BioLegend; anti-Iba1, 1:100; anti-p-PI3K, 1:100, Invitrogen) dissolved in blocking buffer overnight at 4 ^{o}C. The next day, sections were washed in PBS three times for 10 mins each and were incubated with secondary antibodies (Alexa Fluor 488 and Alexa Fluor 594, 1:200) for 2 hrs at room temperature. Sections were washed with PBS, incubated with DAPI (1:2500) for 10 mins, and mounted using FluorSave™ mounting media (Sigma Aldrich, St. Louis, MO).

Image Analysis

RGCs were counted using a macro written in ImageJ, which sets the auto threshold, performs water-shedding and counts RGCs by Analyze Particles(). After adjusting the threshold, Iba1 and CD74 positive microglia were counted using Analyze Particles(). CD74 and phospho-PI3K were colocalized using Coloc2 and BIOP plugins in ImageJ. Pixel intensities were measured using the Measure() function in ImageJ software. Pearson's correlation coefficient was calculated in RStudio by cor.test().

Confocal microscopy

Images of microglia whole mounts were acquired using a Zeiss LSM710, Axio Imager 2 with Plan-Apochromat 20x objective, 0.8 NA and Plan-Apochromat 63x objective, 1.4 NA. Z-stacks of the retina and optic nerve whole mounts and sections were taken at 1024x1024 resolution. For retina, at least 4

different images of different regions were taken, and for the optic nerve, at least 3 different images were taken from different regions.

Morphometric analysis

Microglia feature analysis

The features of microglia morphology were analyzed by the method published by Heindl et al[29]. using custom scripts in MATLAB (R2022a, MathWorks, Natick, MA), which relies on the Image Processing Toolbox and Statistics and Machine Learning Toolbox for its functionalities. The fully automated analysis of morphological features extracted from confocal image stacks of Iba1 stained microglia involved four primary steps. First, the image quality and preprocessing were controlled to ensure reliable results. Second, microglial cells were segmented from the background, and within each cell, further segmentation was performed to distinguish the nucleus, soma, and branches. Third, a skeleton representation is constructed to capture the spatial structure of the cell bodies and branches. Finally, morphological features were extracted using the properties derived from the cell surface area, volume, and skeleton. The output feature file was imported into RStudio v.4.2.0, and the mean values were calculated for each replicate. Mean values were plotted using GraphPad Prism 9 software (La Jolla, CA).

Reconstruction of microglia morphology

Microglia morphology was reconstructed using Imaris 9.2.v (Oxford Instruments, Abingdon, UK) software. Briefly, raw z-stack confocal image files were imported into Imaris, and the surface module was used to construct the surfaces on the Iba1 channel by setting smoothing=1. The new masked channel was created on the surface. Further, microglial processes were analyzed in three dimensions using a filament-tracing plugin. Starting points (soma) for tracing were identified by setting a maximum diameter of 12 µm, and the seeding points (dendrites) were identified by setting a diameter of 1 µm. Following the tracing process, we manually excluded cells located at the image border that were only partially traced, thereby ensuring that these cells were not included in the analysis. The .ims files were then converted to

.swc files for individual microglia using the ImarisReader toolbox (https://github.com/rcubero/Matlab_Imaris_converter).

MorphOMICs analysis

Microglia morphology was mapped using MorphOMICs (https://github.com/siegert-lab/MorphOMICs). MorphOMICs uses microglia's topological morphology descriptor (TMD) combined with bootstrapping and dimension reduction techniques, Principal Component Analysis (PCA) and Uniform Manifold Approximation and Projection (UMAP), to visualize unsupervised clustering of microglia from different treatment conditions. The bootstrap sample size was 100, and the number of bootstraps collected was 400. The first ten principal components were used as input to UMAP with n_neighbors = 50, min_dist = 1.0, and spread = 3.0.

Monocle trajectory analysis

Each bootstrapped sample is represented by an array of 10,000 pixels from its persistence image, therefore a pixel from a sample can be seen as analogous to a gene from a cell within a single-cell transcriptomic setting. Pixels in proximity covary with one another in a manner similar to how genes may covary.

A pseudo-temporal trajectory-inference algorithm called Monocle[30–32] was used. Monocle uses a partitioned approximate graph abstraction-like algorithm for Louvain clustering, which learns a principal graph using reversed graph embedding to generate lineages and pseudotimes (https://github.com/cole-trapnell-lab/monocle3/).

The bootstrapped samples from MorphOMICs were used as input for Monocle. The principal components were obtained using preprocess_cds with num_dim = 10, after which UMAP dimension reduction was performed using reduce_dimension with umap.metric = ‘manhattan’, umap.min_dist = 1.0, and umap.n_neighbors = 50. Clusters were determined using cluster_cells with cluster_method = ‘leiden’, and the pseudo-temporal trajectory was obtained using learn_graph with use_partition = FALSE and close_loop = FALSE.

Single-cell transcriptomics

Single-cell dissociation

Retinas were dissociated into single-cell suspensions using a papain dissociation kit (Worthington, Columbus, OH). Briefly, dissected retinas were placed in papain solution for 30 mins at 37 ^{o}C with exposure to 5% CO_2 in the incubator. Retinas were gently tapped and incubated for 15 more mins for complete dissociation. The reaction was quenched by adding ovomucoid inhibitor solution, and cells were collected after centrifugation and dissolved in resuspension buffer containing PBS+5%BSA+ DNASE to form a single-cell solution of cells. Cells were passed through a 40µM cell strainer (Sigma) to remove debris and clumps. Before processing the cells for single-cell transcriptomics, rod cells were depleted to enrich the rest of the population. Cells were incubated with Biotin-CD133 antibody for rod-specific labeling and were depleted in the magnetic column after anti-biotin-magnetic bead labeling (Miltenyi Biotech, Bergisch Gladbach, Germany).

Barcoding and Library Preparation

Barcoding and library preparation was achieved using a 10X Chromium Single Cell 3' reagent (v3.1 chemistry, 10x Genomics, Pleasanton, CA), according to the manufacturer's instructions. Briefly, cells were loaded on the chromium chip to create gel beads containing unique oligo barcodes with single cells, creating cell-gel droplets. RNA from each cell was captured within the droplets, and cell-specific barcodes were linked to their respective transcripts. Reverse transcription and amplification of captured RNA were performed to generate cDNA libraries. Quality of cDNA preparation was checked using Bioanalyzer (Applied Bioscience)

Sequencing

The cDNA libraries were subjected to high-throughput sequencing on the Illumina Novaseq S1 100SR platform (San Diego, CA). Sequencing reads containing cell-specific barcodes and transcript information were obtained for each cell. Raw files were demultiplexed using Illumina bcl2fastq2 software for downstream analysis. Library preparation and scRNA-seq were performed at the QB3 Genomics Core Facility, UC Berkeley, Berkeley, CA, RRID: SCR_022170.

Downstream Data Analysis

The sequencing reads were processed using Cellranger software (10x Genomics). Cellranger 'count' pipeline aligned the sequencing reads to the existing mouse genome (mm10, University of California Santa Cruz). Each read was assigned to its respective cell barcode, enabling cell identification and quantification. The output matrix was used for further downstream analysis and clustering of the cell populations in RStudio v.4.2.0 using Seurat V4.0[33]. Briefly, quality control and filtering were performed after determining the percentage of mitochondrial transcripts. The data were normalized using the NormalizeData() function, ensuring that gene expression values were comparable across cells. Variable features were selected using the FindVariableFeatures() function to identify the genes that exhibited significant variation and contributed to heterogeneity within the dataset.

The FindIntegrationAnchors() function was executed on both objects to enable comparisons across different datasets. This process identified cell-to-cell pairings between the two datasets based on the first 30 principal components (PCs). The objects were then integrated using the IntegrateData() function on the anchorset and the first 30 PCs. This integration step combined the gene expression profiles from different datasets while preserving the underlying biological variability.

After integration, counts were scaled using the ScaleData() function to normalize the expression values across cells. Principal components (PCs) were computed using the RunPCA() function, capturing the major sources of variation within the integrated dataset. Furthermore, clustering analysis was performed by executing the FindNeighbors() function on the first 30PCs, identifying the nearest neighbors for each cell based on their gene expression profiles. Subsequently, the FindClusters() function (resolution- 0.8) was used to assign cells to distinct clusters based on their similarity in gene expression. A uniform manifold approximation and projection (UMAP) was constructed using the RunUMAP() function on the first 30 PCs, allowing for the visualization of the cells in a lower-dimensional space while preserving the global structure of the data.

To assign cell types to the identified clusters, markers specific to each cluster were identified using the FindAllMarkers() function and compared to known cell-type markers[34–36], facilitating the

annotation of the clusters with specific cell types. Differential gene expression in microglial cells was determined using the FindMarkers() function. Data were visualized using VlnPlot() and DotPlot() functions.

Bulk RNA Sequencing

Total RNA was isolated from optic nerves by TRIzol method (Invitrogen) and RNA quality was measured on Bioanalyzer (Applied Bioscience). mRNA was converted to cDNA using SMARTer v4 Ultra Low Input RNA Kit (Clontech, Mountain View, CA). A Diagenode Bioruptor Pico was used to fragment the cDNA, and libraries were generated using the KAPA Hyper Prep Kit for DNA (Roche, Basel, Switzerland) for sequencing on a NOVAseq S4 flow cell (Illumina). Library preparation and RNA-seq were performed at QB3 Genomics, UC Berkeley, Berkeley, CA, RRID: SCR_022170. The raw sequencing reads were demultiplexed by Illumina bcl2fastq2 software, and read quality was assessed using FastQC v.0.11.9. Adapters were subsequently trimmed from the reads using Trim Galore v.0.6.6. The processed reads were then aligned to the mouse genome (mm39, University of California Santa Cruz) using the STAR alignment tool v.2.7.1a and read counts for each gene were obtained using FeatureCount v.1.5.3. The resulting feature count matrix was imported into RStudio v.4.2.0, and normalization and differential gene expression analyses were conducted using the DeSeq2 package.

Additionally, pathway enrichment analysis was performed using the clusterProfiler package, allowing for the identification of biological pathways enriched with differentially expressed genes. The interaction network of genes was created by String DB, and the Highly interacting network of genes was analyzed by MCODE v. 2.0.2 in Cytoscape v.3.9.1 software. Pathway enrichment of the MCODE-generated networks was performed using ClueGO v. 2.5.9 in Cytoscape v.3.9.1, using a significance cutoff of $p < 0.05$.

Statistical analysis

Student's t-test was used to determine the significance of differences ($p<0.05$) between the two groups. One-way analysis of variance with post-hoc Tukey's multiple comparison tests was used to compare multiple groups. Values are presented as mean ± SEM (standard error of the mean).

Results

LXB_4 regulates microglia functional responses in the healthy and glaucomatous retina

Our previous study established endogenous formation of LXB_4 in the healthy retina and its neuroprotective effect in a rat suture model of OHT by directly acting on RGCs[6]. Data on the mechanism for LXB_4's bioactions and cellular targets are sparse. Hence, we treated healthy mice with LXB_4, *in vivo*, to investigate its homeostatic actions and uncover cellular targets. Cell-specific actions were defined by single-cell transcriptomics (scRNA-seq) analysis (Figure 1). After unsupervised clustering, supervised cell type identification, and differential gene expression analysis, surprisingly, the cell type highly regulated by LXB_4 treatment in the healthy retina was microglia (Figure 1A). A highly selective number of microglia genes (*C5ar1*, *Clea4a2*, *Entpd1*, *Il6ra*, and *CD37*) were downregulated by LXB_4 treatment (Figure 1B). These genes were expressed primarily in microglia (Figure 1C) and are part of the "sensome" encoding proteins expressed on ramified processes of microglia[37]. The function of the sensome is regulation of microglia homeostatic and reactive functions in response to microenvironmental cues[18]. The five genes downregulated by LXB_4 are linked to the transition from a homeostatic phenotype to a reactive microglia phenotype[18]. Pathway enrichment analysis of these genes ($Log2FC< -1$, $p<0.05$) showed enrichment for antigen processing and presentation (Figure 1D), which suggest that LXB_4 can downregulate antigen processing and presentation pathways in microglia that have been linked to neuroinflammation. The role of microglia in the cascade leading to RGC degeneration is of great interest[38] and remains to be defined.

To investigate LXB_4 regulation of microglia function during OHT-induced RGC degeneration, we used the established silicone oil model of chronic moderate OHT[25,39,40] (Supplementary Figure

1A-C) and analyzed microglial sensome and reactivity genes by qPCR. Importantly, sensome gene signatures downregulated by LXB_4 in the healthy retina (Figure 1B) were highly upregulated (~2-fold) under chronic OHT at the 1 wk time point, along with markers of microglial reactivity after 1 or 8 wks (~2 to 10-fold) (Figure 1E). Further, LXB_4 treatment significantly downregulated expression of sensome genes (*C3ar1*, 27.7%, p= 0.0305; *C5ar1*, 39%, p= 0.0271; and *Clec4a2*, 43.5%, p= 0.0140) and the inflammatory marker *Cxcl10* (77.8%, p= 0.0132) in the retina after 4 wks of OHT (Figure 1F). These data identify and confirm microglia as a target for LXB_4 regulation in the healthy normotensive retina and during moderate OHT stress.

Moderate OHT regulates microglia phenotype in both the retina and optic nerve

Since we identified microglia as a new cell target for LXB_4, and the roles of microglia in glaucomatous conditions are complex[19–21], we aimed to better understand the dynamic regulation of microglia function during moderate OHT. While transcriptomics[41] and proteomics[42] studies advanced our understanding of signaling mechanisms in microglia, morphology is a key functional characteristic of microglia behavior and phenotype[43–45], reflecting their spectrum of biological functions[45]. New analytical methods to quantify microglial morphology in detail [29,46] have made it feasible to comprehensively measure the morphological features of microglia and relate them to distinct phenotypes[29,46]. We analyzed the effects of moderate OHT on microglia functional responses in the retina and optic nerve using the methods established by Heindl et al. (2018)[29] and Colombo et al. 2022[46]. The morphologies of retinal and optic nerve microglia stained with Iba1 were analyzed after 2, 4, and 6 wks of OHT. First, we used a feature extraction tool from Heindl et al. [29] to analyze the microglia by their various features (Sphericity, Circularity, Volume of nodes, Total number of nodes, etc.). In the retina, out of 14 features of microglia morphology analyzed, ~14% of features (Reduction in length of branches and Betweenness of nodes) were significantly changed ($p<0.05$) as early as 2 wks when compared to control retinas (Supplementary Figure 2). With sustained OHT, 78% of features were significantly changed ($p<0.05$) at the 4 wks timepoint. At 6 wks, ~93% of features were changed

(p<0.05), representing a time-dependent change in the phenotypes of retinal microglia (Supplementary Figure 2). Next, we analyzed whole mount Iba1-stained microglia in the myelinated optic nerve. None of the optic nerve microglial features significantly changed at the early 2 wks point (Supplementary Figure 3). However, at 4 wks, ~64% of analyzed features exhibited statistically significant changes (p<0.05) when compared to the controls. Furthermore, when comparing the 4 wks data to the 2 wks time point, around 21% of the features showed statistically significant differences (p<0.05), establishing time-course specific increase in microglia morphology changes (Supplementary Figure 3). These results indicate that moderate OHT in both the retina and distal myelinated optic nerve led to specific and dynamic changes in microglia phenotypes.

Next, the morphOMICs method developed by Colombo et al. (2022)[46] was used to capture the complex variability between morphological microglia and to define the distinct microglia subpopulations present in the retina and optic nerve. MorphOMICs involves the conversion of a 3D microglia structure to a 2D persistence barcode[47] and applying bootstrapping and dimension reduction methods to visualize the distinct clusters of microglia with morphological differences[46]. The persistence barcode is generated using Topological Morphology Descriptor (TMD)[47], which maps the start and end of microglia processes as their distance from the soma. After analyzing the retinal microglial whole mount images at different time points of moderate OHT, we observed that retinal microglia clustered differentially at different time points, denoting unique phenotypes at different stages of moderate OHT (Figure 2A-C). These results were concurrent with the feature extraction method, which revealed unique time-course specific morphological characteristics of microglia. To establish the time-dependent changes in microglia morphology, we used pseudo-temporal trajectory-inference algorithm (Monocle3) analysis[30–32], which utilizes reversed graph embedding to generate lineages and pseudotime trajectories. Control microglia represent the starting point of the trajectory. At 4 wks of OHT, microglia in the retina were farthest from the control microglia, denoting the homeostatic-to-reactive phenotype spectrum (Figure 2D). Retinal microglia at the 6 wks time point of OHT aligned between the 2 wks and 4 wks time points on the trajectory (Figure 2D), suggesting a gradual reversal of a microglia inflammatory

functional phenotype in the retina. In addition, we used the microglia reactivity marker CD68[48] to identify reactive microglia at different stages of OHT. Retinal microglia expressed CD68 protein as early as 2 wks and the reactivity marker was expressed throughout the entire time course of 6 wks, with maximum protein expression at 4 wks in the retinal microglia population (Figure 2E, F).

Next, we performed morphOMICs analysis of optic nerve microglia during the time course of OHT. In contrast to retinal microglia, control and 6 wks optic nerve microglia populations clustered together (Figure 3A-C), while microglia populations from the 2 and 4 wks timepoints clustered separately from both the control cluster and the 6 wks cluster (Figure 3C). To further understand these time-dependent phenotypic changes in optic nerve microglia, we performed pseudotime trajectory analysis. Similar to the retina, the microglia populations at 4 wks were farthest on the trajectory compared to the microglia population from healthy optic nerves (Figure 3D), establishing the 4 wks timepoint as the maximal microglia functional response to OHT in both the remote optic nerve and retina. More importantly, similar to the retina, microglia populations at the 6-wks time point partially clustered near the control cluster in the pseudotime trajectory analysis (Figure 3D). Similar to the results from feature extraction, optic nerve microglia showed homeostatic-like morphology at 6 wks of moderate OHT (Figure 3D), denoting similar regulation of microglia functional phenotypes at two distinct sites during the time course of moderate OHT. Consistent with the reactivity markers in retinal microglia, the reactivity marker CD68 was upregulated over the entire time course of OHT at the remote myelinated optic nerve site (Figure 3E, F). Collectively, these data indicate the similar regulation of retinal and optic nerve functional microglia phenotypes under moderate OHT.

Neuroprotective LXB_4 regulates optic nerve microglia during retinal OHT insult.

Both retinal and optic nerve microglia transition from homeostasis to distinct states and dynamic reactivity phenotypes in response to sustained OHT. scRNA-seq data suggest that LXB_4 regulates the microglia homeostatic phenotype in the healthy retina. We used a silicone oil volume that induces severe OHT retinal injury (40% peripheral RGC loss) by 2 wks (Supplementary Figure 1D-H) to investigate the

actions of LXB_4 microglia function in response to significant RGC injury. LXB_4 treatment significantly reduced loss of the nerve fiber layer after 1 wk (~55% improvement from OHT group) based on ocular coherence tomography (OCT) measurements (Figure 4A, B). Microglia morphology in the retina and optic nerve was analyzed by morphOMICs as described above, to define LXB_4 regulation of microglia function. In the retina with severe OHT, microglia were uniquely clustered compared to the microglia population from normotensive retinas (Figure 4C-E). MorphOMICs analysis (Figure 4C-E) and pseudo-time trajectory (Figure 4F) established that LXB_4 treatment during acute and severe OHT did not result in significant morphological changes in the retinal microglia population as they clustered together in the analyses. In addition, CD68 staining, a marker of microglia reactivity did not change in the retina in response to LXB_4 treatment (Figure 4G, H). Taken together, these results indicate that neuroprotection by LXB_4 treatment during acute and severe OHT is not associated with regulating the retinal microglia phenotype.

Next, we analyzed the potential effect of LXB_4 treatment on microglia phenotype in the distal myelinated optic nerve. MorphOMICs identified unique clusters of microglia populations in all three groups, namely normotensive, OHT, and OHT with LXB_4 treatment. Optic nerve microglia from normotensive retina were a single and unique cluster (Figure 5C), while optic nerve microglia populations from severe OHT were spatially distinct and separated into two clusters (Figure 5C). These findings establish that severe OHT induces distinct and rapid morphological changes in microglia populations in the distal optic nerve. Interestingly, unlike in the retina, morphOMIC analysis revealed that LXB_4 treatment induced a unique single microglia population in the optic nerve, which was a distinct cluster from the sham-treated mice with severe OHT (Figure 5C). Trajectory analysis confirmed that the spatially unique subpopulation of optic nerve microglia in mice with severe OHT were the farthest morphological distance (Figure 5D) from the microglia population in normotensive control eyes. The unique microglia population that was induced by LXB_4 treatment was closest to the normotensive microglia population in pseudotime trajectory analysis (Figure 5D), i.e., morphological towards the homeostatic phenotype. Next, we analyzed microglial reactivity in the optic nerve using CD68 as a reactivity marker.

Immunohistochemistry (IHC) analysis demonstrated that severe OHT induced a high expression (297% increase, p=0.0007) of CD68 in microglia in the distal myelinated optic nerve (Figure 5E, F) compared to optic nerves from normotensive eyes. More importantly, LXB_4 treatment significantly reduced (88%, p=0.0343) CD68 expression after 1 wk of severe OHT (Figure 5E, F). These data are consistent with the morphOMIC analysis, which demonstrates that LXB_4 treatment promotes restoration of a microglia homeostatic functional phenotype.

LXB_4 intrinsic regulation of microglia homeostatic phenotype in the optic nerve was confirmed using Alox5 knockout (KO) mice, an established lipoxin-deficient mouse strain[49–51], in which the required enzyme (5-LOX) for lipoxin formation has been deleted. MorphOMICs analysis established that the microglia population in optic nerves from normotensive 5-LOX KO mice was distinct from that in healthy congenic wild-type mice (Supplementary Figure 4A). This suggests an altered homeostatic microglia phenotype in the absence of optic nerve homeostatic 5-LOX activity, i.e., lipoxin signaling. Consistent with the results from healthy optic nerves, morphOMICs and pseudotime trajectory analysis of optic nerve microglia after 1 wk of severe OHT showed that reactive microglia population in 5-LOX KO mice were distinct from wild-type congenic mice and farthest removed from the homeostatic microglia phenotype of congenic normotensive wild-type mice (Supplementary Figure 4B). These results suggest that the deletion of the lipoxin pathway in the optic nerve is associated with a dysregulated microglia phenotype and response to retinal OHT stress.

LXB_4 targets a marker of disease-associated microglia in the optic nerve

To investigate the mechanisms underlying LXB_4 regulation of optic nerve microglia functional phenotypes during severe OHT, we conducted bulk RNA transcriptomics (RNA-seq) analysis of optic nerves from mice treated with or without LXB_4. The myelinated optic nerve is comprised of a heterogeneous population of astrocytes, microglia, and oligodendrocytes. Hence, transcriptomic signatures from all these cell types[52] was expected. A linear regression model (DESeq2) was used to

perform differential gene expression analysis comparing OHT versus normotensive controls and OHT versus OHT with LXB_4 treatment (Figure 6A).

Microglia sensome markers were significantly upregulated ($p<0.05$) in the OHT group (Figure 6B). Consistent with the homeostatic action of LXB_4 in healthy retinas (Figure 1), LXB_4 treatment during OHT significantly downregulated ($p<0.05$) a subset of sensome markers in the optic nerve (Figure 6C). Given the role of LXB_4 in regulating microglia phenotype, we focused on analyzing downregulated genes. STRING[53] protein-protein association clustering of genes downregulated by LXB_4 treatment (Log2FC<-1, p.adjust<0.05) was followed by MCODE[54] analysis to identify highly interactive gene subclusters (Figure 6D). Pathway enrichment analysis of genes in these interactive subclusters revealed an association with *Cd74*, which regulates cytokine production in mononuclear phagocytes (Figure 6E). CD74 is a key marker for a unique subset of disease-associated microglia [55,56] that have been identified in central nervous system pathology[57]. *CD74* is detected at the RNA level in the retina and its RNA expression is increased in the optic nerve crush model[58]. To validate our findings, expression of CD74 was assessed by IHC in optic nerve sections from mice with OHT and mice with OHT that were treated with LXB_4. CD74 expression was increased by 303.68% ($p=0.0017$) in Iba1-positive microglia cells in response to OHT (Figure 6F, G). LXB_4 treatment markedly reduced the number of CD74-expressing cells by 52.56% ($p=0.0054$) (Figure 6F, G). Furthermore, the intensity of CD74 protein expression in the optic nerve was downregulated by 37.96% ($p=0.033$) following LXB_4 treatment (Figure 6H). To assess the impact of endogenous LXB_4 on CD74 in the optic nerve, protein expression was assessed by IHC in 5-LOX KO mice with and without severe OHT. Strikingly, optic nerves from normotensive 5-LOX KO mice showed a 468.9% ($p= 0.0272$) increase in the number Iba1 cells positive for CD74 compared to wild-type congenic control optic nerves (Supplementary Figure 5). OHT in 5-LOX KO mice did not further increase the number of Iba1 cells positive for CD74 in the optic nerves. However, the number of CD74 positive Iba1 cells in optic nerves was 503.3% ($p= 0.0149$) higher in 5-LOX KO mice when directly compared to wild-type congenic controls with OHT (Supplementary Figure 5). Surprisingly, CD74 expressing microglial were only detected by IHC in the optic nerve in both wild-type and 5-LOX

KO mice but not in the retina during severe OHT (Supplementary Figure 6). These results provide evidence that OHT selectively induces a disease-associated microglia phenotype in the distal myelinated optic nerve and that LXB_4 regulates these disease-associated microglia phenotype.

LXB_4 regulates $CD74^+$ disease-associated microglia and the phosphoinositide 3-kinase (PI3K) signaling pathway

Results revealed that LXB_4 could regulate the functional phenotype of optic nerve microglia and downregulate the expression of CD74, a marker of disease-associated microglia in the brain. Subsequently, we investigated the intracellular signaling mechanisms underlying the regulation of disease-associated microglia in the optic nerve. KEGG pathway enrichment[59] analysis of genes downregulated (Log2FC <-1, p.adjust< 0.05) in the optic nerve by LXB_4 treatment identified the PI3K-Akt signaling pathway as a significant candidate (Figure 7A). These results were of interest because PI3K signaling has been implicated in neuroinflammation and reactive glial phenotypes[60–62]. Considering that PI3K signaling is ubiquitously present in most cells[63], we performed co-staining of optic nerve sections with antibodies targeting CD74 and activated PI3K (phospho-PI3K, p-PI3K) to examine their expression specifically in the disease-associated microglia phenotype (Figure 7B). p-PI3K was colocalized with CD74 expressing cells (Supplementary Figure 7A, B). Because of the membrane-binding nature of CD74 and the intracellular localization of p-PI3K, background noise, and expression of p-PI3K in other cells, it was challenging to perform co-localization and expression analysis comparisons between control and severe OHT plus or minus LXB_4 treatment.

Therefore, to establish the regulatory role of PI3K signaling in disease-associated microglia, correlation analysis was used to examine the expression of these markers in the optic nerve. Correlation analysis is a well-established approach for determining regulatory relationships[64]. Significant positive correlation was identified between p-PI3K and CD74 expression in both the OHT (r= 0.74, p=0.004) (Figure 7C) and OHT with LXB_4 treatment groups (r=0.91, p=0) (Figure 7D). Correlation analysis of CD74 and p-PI3K with DAPI signals (nuclear staining in all cells) was used as the negative correlation

control. As expected, DAPI staining did not correlate with p-PI3K (r= 0.34, p=0.258) (Supplementary Figure 7C) or CD74 (r= 0.51, p=0.077) (Supplementary Figure 7D).

Given the consistent correlation between CD74 and p-PI3K co-expression in the optic nerves of mice with OHT, it is of interest that LXB_4 treatment significantly downregulated p-PI3K relative to CD74 (30.4%, p=0.0072) (Figure 7E). Taken together, the correlation analysis suggests that activated PI3K during OHT is a key feature of the optic nerve disease-associated (CD74) microglia phenotype. The mechanism for LXB_4 downregulation of a CD74 microglia phenotype during OHT could potentially be mediated by inhibition of PI3K signaling.

Discussion

The current study identifies microglia as a target for regulation by LXB_4 in the retina and myelinated, retrolaminar optic nerve. Microglia are specialized and tissue resident mononuclear phagocytes that are essential for maintaining retinal and brain homeostasis but are also a key cell type for driving pathogenesis in neurodegenerative diseases such as Alzheimer's and glaucoma[22–24,65]. Our previous study[6] established endogenous LXB_4 formation in the retina and optic nerve head. More importantly, it demonstrated direct regulation of RGCs as a cellular target in the retina for LXB_4's neuroprotective action in both retinal excitotoxicity and OHT injury. The unexpected finding that regulation of the microglia pathway for environmental sensing and transition to a reactive phenotype are primary targets for LXB_4 in the healthy retina is of great interest. Changes in the microglia sensome are key events in neurodegenerative diseases and drive the transition of the microglia phenotype from a neuroprotective to a neurotoxic state[37]. Neurotoxic microglia activate astrocytic reactivity in the brain[23] and sustained activation of microglia is related to the degeneration of RGCs in glaucoma models[66,67]. Hence, the regulation of microglial sensome by LXB_4 is likely a mechanism for its homeostatic and neuroprotective role in the retina and optic nerve.

Knowledge of the mechanisms of action and cellular targets of LXB_4 is limited, despite several publications establishing endogenous formation of LXB_4 and its ability to counter-regulate the activity of

pro-inflammatory signals in leukocytes during acute inflammation[9,68]. An early study[69] identified a unique ability of LXB_4 to drive migration and adhesion of monocytes, the mononuclear phagocytes in blood, without activating an inflammatory monocyte phenotype. Our *in vivo* findings indicate that LXB_4 regulation of pathways essential to controlling transition to a reactive inflammatory phenotype as a potential mechanism for maintaining the homeostatic functions of the resident mononuclear phagocyte in central nervous system, namely microglia. Interestingly, the structurally and functionally distinct LXA_4, which acts at a different receptor than LXB_4, has been found to inhibit the inflammatory microglial function in spinal cord injury[70] and in severe congenital retinal degeneration[71] mouse models. However, it is important to point out that even though both LXA_4 and LXB_4 are generated in the healthy retina and optic nerve, they act on different receptors and LXB_4 is the most potent lipoxin in terms of *in vivo* and *in vitro* neuroprotective activity[6,11]. We previously reported that glaucomatous injury downregulates enzymes required for LXB_4 formation in the retina[6], which underscores the homeostatic role of lipoxin in the retina. This finding is consistent with a subsequent report in the RD1 mouse strain, which develops severe photoreceptor death and retinal degeneration that correlates with marked downregulation of the lipoxin pathway[71].

An important finding of the study is that both severe and moderate OHT trigger dynamic and temporally defined morphological changes in the distal optic nerve microglia population that paralleled the temporal morphological response of the retinal microglia population. Microglia populations in both the retina and optic nerve transitioned to morphologically distinct populations during the time course of sustained long-term OHT. Interestingly, after polarizing towards a functional phenotype that progressively is more divergent from the homeostatic population in normotensive condition, microglia transition back towards a homeostatic morphology by week 6, despite unchanged and sustained OHT, suggesting an adaptive response. The behavioral response of optic nerve microglia provided compelling evidence that the myelinated optic nerve rapidly responds to OHT in the retina. Research to understand the pathogenesis of glaucomatous RGC degeneration has primarily focused on the retina and optic nerve head. However, emerging evidence points toward RGC axons as a primary site of glaucoma pathogenesis,

including impaired axonal transport and mitochondrial dysfunction as important early events that precede the loss of RGC in the retina[72,73]. At this time, it is unclear how microglia in the distal myelinated optic nerve sense and rapidly respond to OHT. It is tempting to speculate that abnormal axonal transport and energy metabolism are sensed by the abundant resident optic nerve microglia population.

A key finding is that OHT leads to expression of a unique CD74 positive microglia population in the optic nerve. This population was unique to the optic nerve, and CD74 positive microglia were not present in the retina during moderate or severe OHT. CD74 positive microglia have been defined as a disease-associated microglia population (DAM) in the brain. DAM were initially identified in a mouse model of Alzheimer's disease (AD) using single-cell transcriptomics and proteomics analysis[56,74–80]. Subsequently, their association with the disease was confirmed through their presence in affected brain regions and human genome-wide association studies[55]. The regulation of DAM, particularly under neuropathic conditions is of great interest and a potential therapeutic target. DAM activation requires two stage TREM2 mediated signaling which results in upregulation of phagocytic, lysosomal and lipid metabolism pathways[55]. Understanding the role of DAM in neuropathic conditions is challenging because TREM2 plays distinct functional roles at different stages of AD pathology[81].

Hence, it is of great interest that neuroprotective LXB_4 treatment inhibited the induction of an optic nerve CD74 microglia population in response to OHT, in addition to inhibiting microglia reactivity (CD68 expression). LXB_4 treatment correlated with a distinct functional microglia phenotype compared to untreated mice with OHT. More importantly, LXB_4 treatment promoted a microglial phenotype that was morphologically closer to the healthy homeostatic phenotype compared to untreated mice. The relevance of the endogenous lipoxin pathway in regulating microglia homeostatic function is underscored by the loss of function in 5-LOX KO mice. This lipoxin-deficient mouse line exhibited presence of CD74 positive microglia in the optic nerve without OHT, which was equivalent to congenic wild-type mice with OHT. In addition, morphOMIC analysis established that the homeostatic optic nerve microglia population was distinct in 5-LOX KO mice compared to their healthy congenic wild-type controls and exhibited an amplified reactive response to OHT. 5-LOX is also a key enzyme for generating pro-inflammatory

leukotrienes; hence, the phenotype of an amplified optic nerve DAM and reactive microglia response is unexpected. However, we have not detected significant leukotriene generation in mouse or rat healthy or injured retinas or optic nerves[6,50,82]. More importantly, 5-LOX inhibition or deletion amplifies retinal inflammation[82], autoimmune[50] and neurodegeneration pathogenesis[6] indicating that 5-LOX has protective functions in the retina.

Pathway analysis and IHC established that OHT correlated with an increase in PI3K activity in optic nerve microglia, including the unique CD74 positive microglia population. More importantly, downregulation of the CD74 microglia population by LXB_4 treatment correlated with reduced PI3 kinase activity and expression in the optic nerve. These findings suggest that inhibition of the PI3K pathway is a potential target for LXB_4 signaling. The PI3K pathway is expressed in many cell types with broad cell-specific functions[83]. Microglia activation of the PI3K-Akt pathway increases the formation and secretion of pro-inflammatory cytokines such as IL-6, IL-1β, IL-12, and TNF-α, which drive neurodegeneration[60–62], activate NF-kB, and induce pro-inflammatory mediators in *in vitro* microglia models of LPS-induced inflammation[60,84]. Inhibition of PI3K/Akt signaling has been shown to protect RGCs after optic nerve injury in rat models[85]. PI3K signaling also provides pro-proliferative and pro-survival functions towards sustained microglia activation via TREM2 regulation[55,86], and hence becomes an important mediator in regulating DAM. The canonical anti-inflammatory action of LXB_4 is the inhibition of cytokine production by leukocytes[9,87], which is consistent with our finding that LXB_4 treatment inhibits PI3K activation in a reactive microglial phenotype.

In conclusion, our study reveals that OHT triggers early and dynamic functional microglial responses and the presence of a unique disease-associated microglia phenotype in the distal myelinated optic nerve. Treatment with neuroprotective LXB_4 regulates microglia homeostatic function, promotes restoration of a homeostatic microglia phenotype, and inhibits polarization of a disease-associated microglial population in the optic nerve. These findings indicate that the regulation of microglia functions as a potential mechanism for LXB_4-mediated neuroprotection and dynamic optic nerve microglia responses which is an unexpected early event in retinal pathogenesis following OHT.

Declarations

Ethics approval and consent to participate

All animals were handled in accordance with the ARVO Statement for the Use of Animals in Ophthalmic and Vision Research, and all procedures were approved by the Institutional Animal Care and Use Committee (IACUC) at the University of California, Berkeley.

Consent for publication

Not applicable

Availability of data and materials

The dataset generated in this study was deposited to the GEO (GSE251716, scRNA-seq; GSE250615, bulk RNA-seq), and is publicly available at the publication date of this article.

Competing interests

No conflicting relationships exist for any of the authors.

Funding

This work was partly supported by NIH grants R01EY030218 (KG, JGF), P30EY003176, and 1S10RR026866-01, Shaffer Grant from the Glaucoma Research Foundation (KG), and BrightFocus Foundation G2023001F (SM).

Authors' contributions

S.M., J.G.F, and K.G. conceived the study; S.M., M.L., S.K., T.S., and M.K. performed the experiments; S.M. and M.L. performed data analysis; S.M., E.W., J.G.F., and K.G. wrote the manuscript.

Acknowledgments

We acknowledge the QB3 Genomics core RRID: SCR_022170, UC Berkeley, for sequencing support, and The CNR Biological Imaging Facility, CRL Molecular Imaging Center, RRID: SCR_017852, UC Berkeley, for imaging and image analysis support.

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Figures

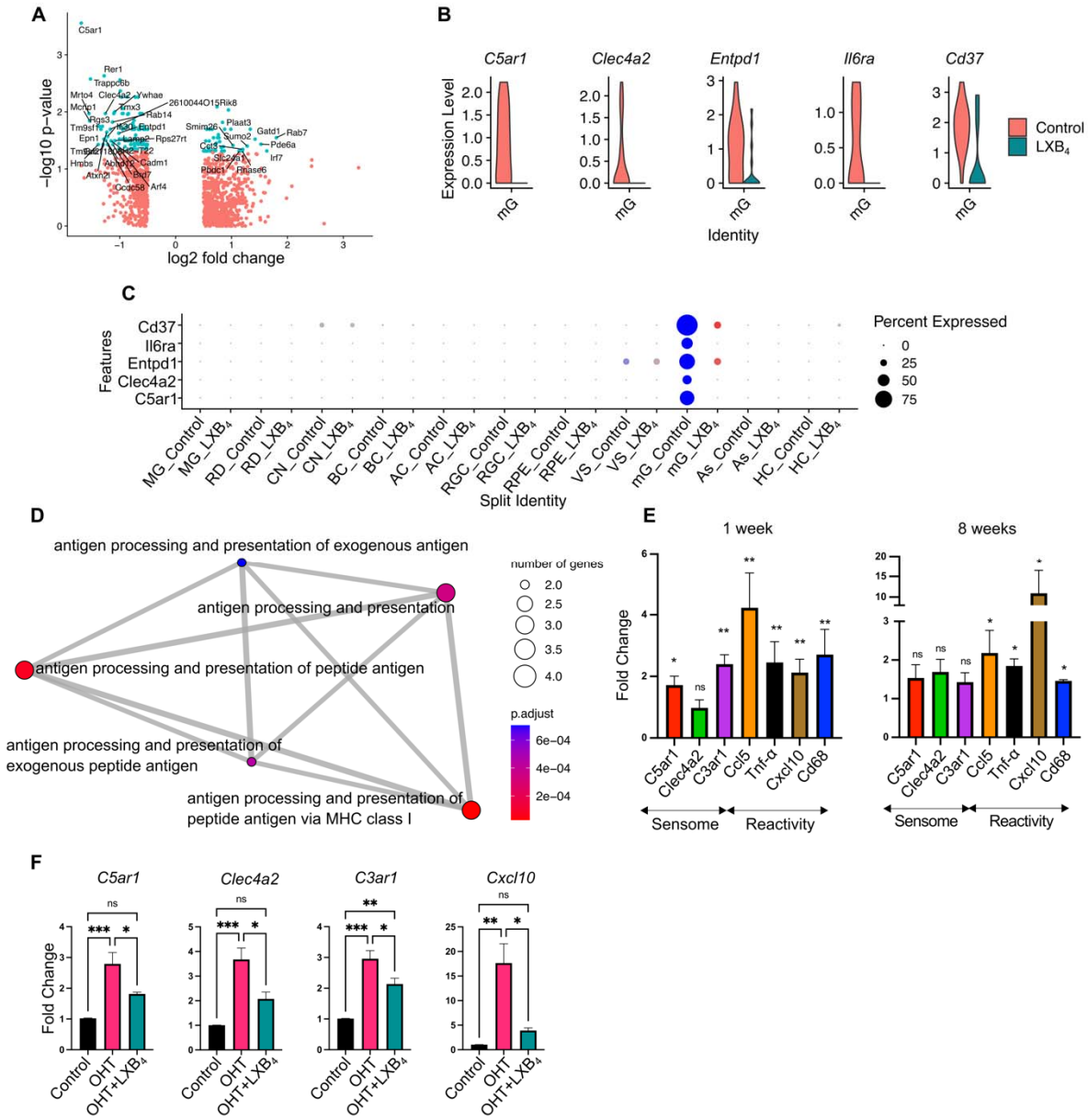

Figure 1: LXB_4 targets retinal microglia in healthy and moderate ocular hypertension conditions. **(A)** Volcano plot of differentially regulated genes in microglia. Genes with $|Log_2$ Fold Change (FC)$|> 0.5$ change in expression are plotted. Significant ($p< 0.05$) changes in grey and not significant in red. Genes with $|Log_2FC|>1$ significant changes are labeled. (**B)** Violin plot of selective sensome genes downregulated in microglia (mG) by LXB_4 treatment in healthy retinas. (**C)** Dot-plot of sensome genes expressed in retinal cells of healthy controls and after LXB_4-treatment. HC: horizontal cells, As:

astrocytes, VS: vascular cells, RPE: retinal pigment epithelium, RGC: retinal ganglion cells, AC: amacrine cells, BC: bipolar cells, CN: cones, RD: rods, MG: muller glia. (**D)** Gene ontology pathway enrichment map for genes downregulated ($Log_2FC < -1$, $p < 0.05$) by LXB_4 in the healthy retina. (**E)** Quantitative PCR analysis of sensome and microglia reactivity gene expression after 1 and 8 wks of moderate OHT. Significance was determined by unpaired t-test (*p< 0.05; **p<0.01; ns, not significant, n=4); each replicate was pooled from two retinas. (**F)** Quantitative PCR analysis of microglia sensome and inflammatory gene expression with or without LXB_4 treatment for 3 wks during OHT compared to normotensive retinas. Data were analyzed by One-way ANOVA with Tukey's multiple comparison test (*p< 0.05; **p<0.01; ***p<0.001; ns-, not significant, n=4). Each replicate is 2 retinas pooled. Data is presented as mean ± SEM.

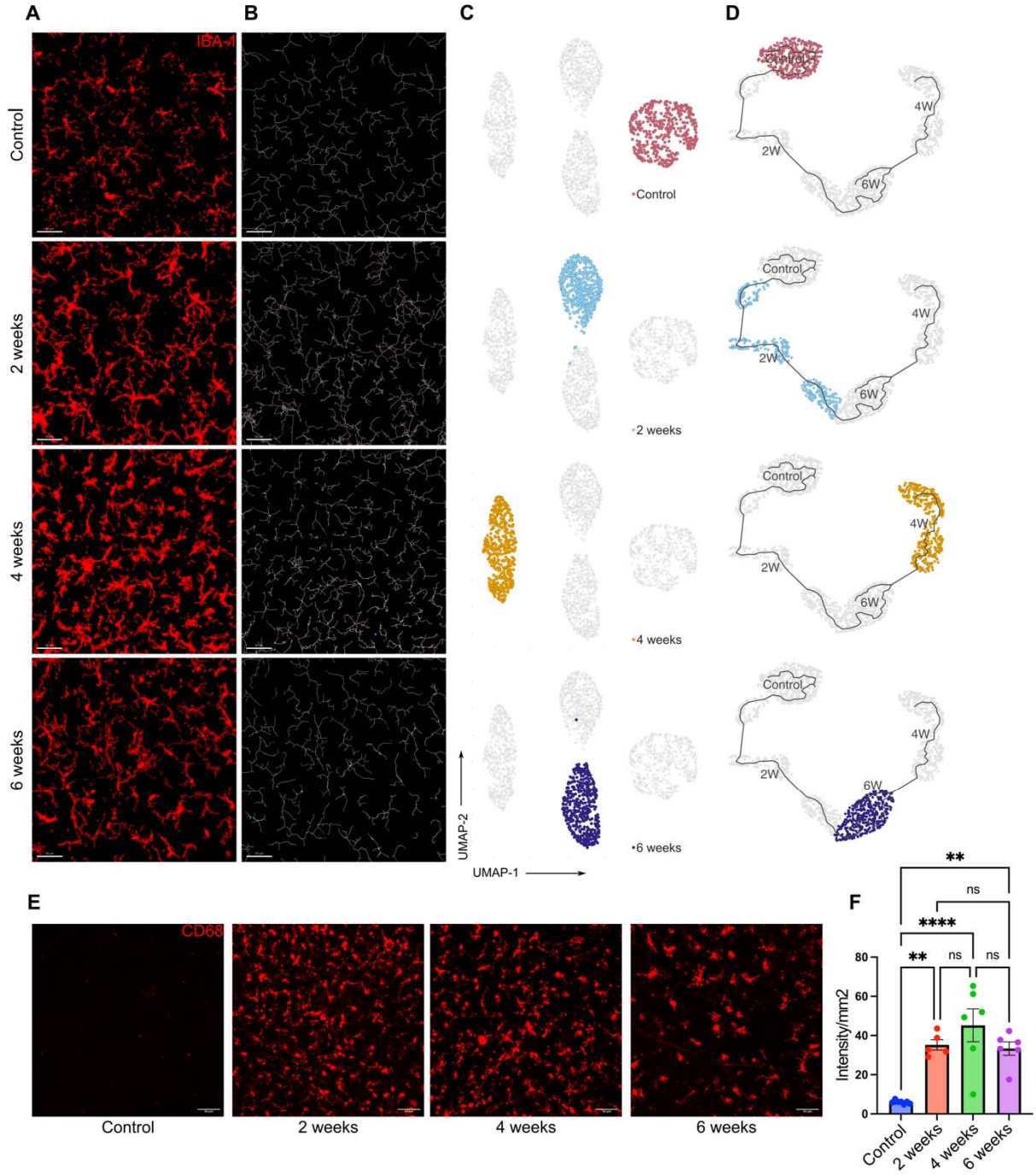

Figure 2: Dynamic changes in retinal microglia morphology during moderate OHT. (A) Representative confocal micrograph of Iba1 (red) stained retinal microglia at different time points of moderate OHT (scale bar- 50µm). **(B)** Representative filament images of microglia morphology over the time course of OHT, generated from the respective Iba1-stained images using IMARIS (scale bar-50µm).

(**C)** UMAP plot displaying the clustering of microglia populations at different time points of OHT. Each dot depicts 100 microglia bootstrapped for their topological morphology descriptor, and 400 dots per group. (**D)** UMAP plot of pseudotime trajectory of microglia population morphology during time course of moderate ocular hypertension; each time point is represented by a different color. (**E)** Representative confocal micrographs of CD68-stained retinal microglia at different time points of OHT (scale bar-50μm). (**F)** Quantification of CD68 expression in retinal whole mounts in normotensive controls (n=6) and 2 wks (n=5), 4 wks (n=6), and 6 wks (n=6) of moderate OHT. Data were analyzed by One-way ANOVA with Tukey's multiple comparison test (**$p<0.01$; ****$p<0.0001$; ns, not significant). Each dot depicts the mean CD68 expression from a single retina. Data presented as mean ± SEM.

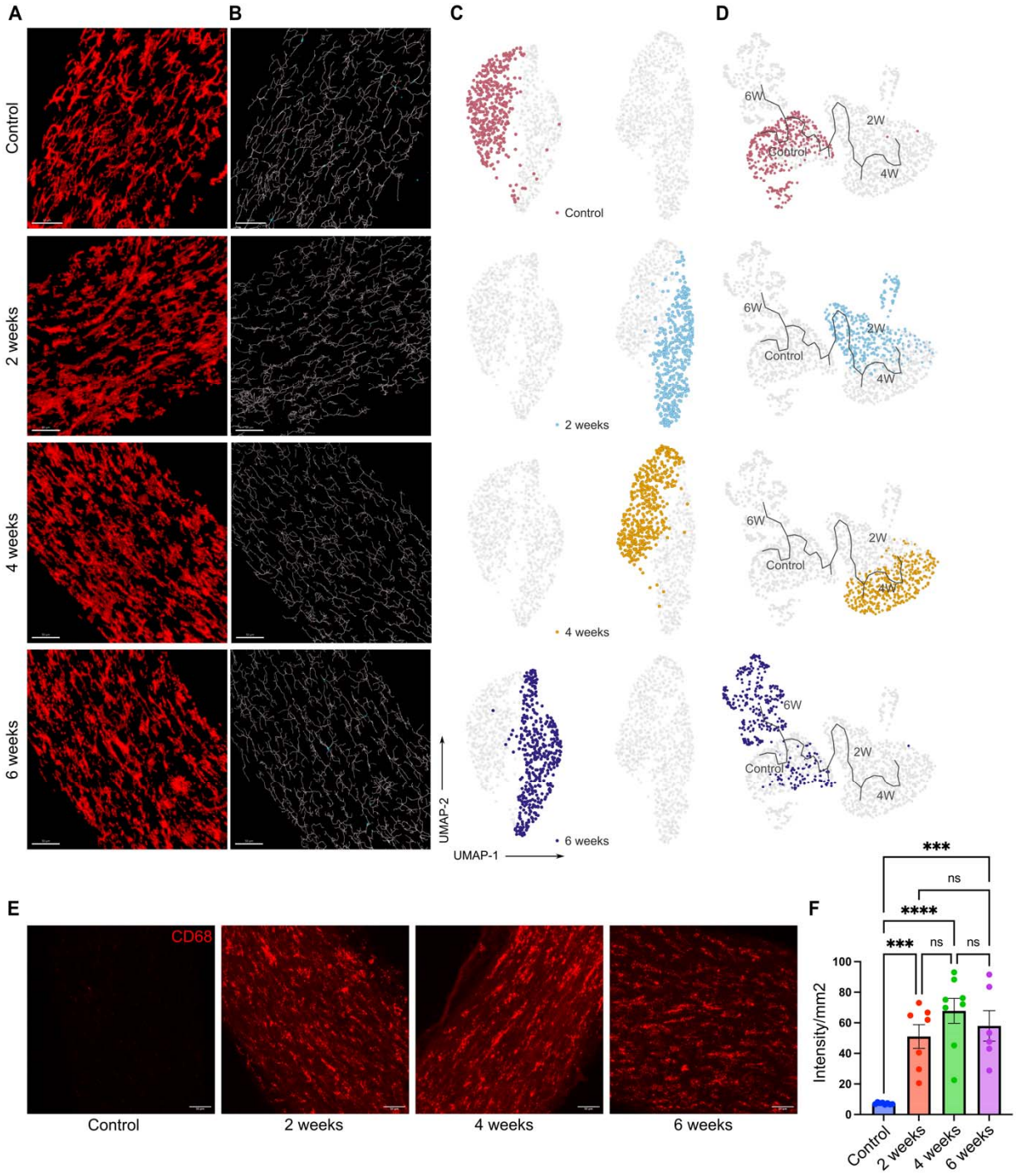

Figure 3: Dynamic changes in optic nerve microglia phenotypes during moderate OHT. (A) Representative confocal micrograph of Iba1 (red) stained optic nerve microglia at different time points of OHT (scale bar- 50µm). (**B)** Representative filament images of microglia morphology during the time course of OHT, generated from the respective Iba1-stained images using IMARIS (scale bar-50µm). (**C)**

UMAP plot displaying clustering of optic nerve microglia during time course of OHT. Each dot depicts 100 microglia bootstrapped for their topological morphology descriptor, and 400 dots are shown per group. (**D)** UMAP plot of pseudotime trajectory of microglia morphology for the time course of moderate ocular hypertension for each time point(**E)** Representative confocal micrographs of CD68-stained optic nerve microglia at different timepoints of OHT (scale bar- 50µm). (**F)** Immunohistochemical quantification of CD68 expression in optic nerve whole-mounts for normotensive controls (n=6), 2 wks (n=7), 4 wks (n=8), and 6 wks (n=6) of OHT. Data were analyzed by One-way ANOVA with Tukey's multiple comparison test (***$p<0.001$; ****$p<0.0001$; ns, not significant). Each dot depicts the mean CD68 expression from a single retina. Data presented as mean ± SEM.

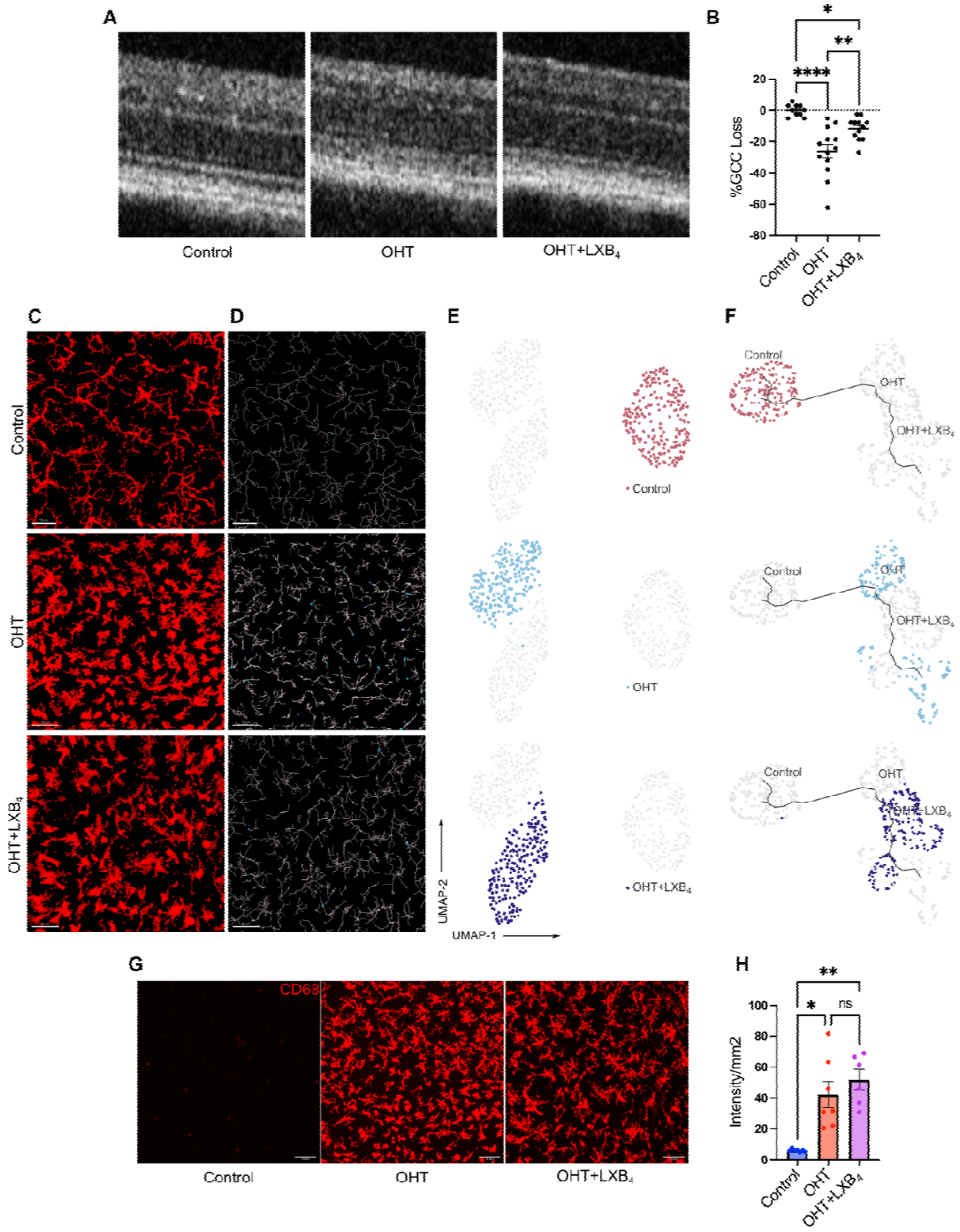

Figure 4: Neuroprotective LXB_4 treatment did not affect retinal microglia phenotype during severe OHT. (A) Representative OCT images of retinal layers for a normotensive control, OHT, and

OHT+LXB_4. (**B)** Scatter plot quantification of ganglion cell complex (GCC) layer thickness for normotensive controls (n=10), OHT (n=13), and OHT+LXB_4 (n=12). Data were analyzed by One-way ANOVA with Tukey's multiple comparison test (*p<0.05; **p<0.01; ****p<0.0001). Each dot depicts the percentage of GCC loss. (**C)** Representative confocal micrograph of Iba1 (red) stained retinal microglia in normotensive control, OHT, and OHT+LXB_4 (scale bar- 50µm). (**D)** Representative filament images of microglia morphology generated from the respective Iba1-stained images using IMARIS (scale bar- 50µm). (**E)** UMAP plot displaying clustering of optic nerve microglia in normotensive, OHT, and OHT+LXB_4 groups. Each dot depicts 100 microglia bootstrapped for their topological morphology descriptor, and 200 dots per group. (**F)** UMAP plot of pseudotime trajectory of microglia morphology; all groups are displayed at once. (**G)** Representative confocal micrographs of CD68-stained retinal microglia for normotensive controls, OHT, and OHT+LXB_4 (scale bar-50µm). (**H)** Quantification of CD68 expression in retinal whole mounts for normotensive control (n=6), OHT (n=6), and OHT+LXB_4 (n=6). Data were analyzed by One-way ANOVA with Tukey's multiple comparison test (*p<0.05; **p<0.01; ns, not significant). Each dot depicts the mean CD68 expression from a single retina. Data presented as mean ± SEM.

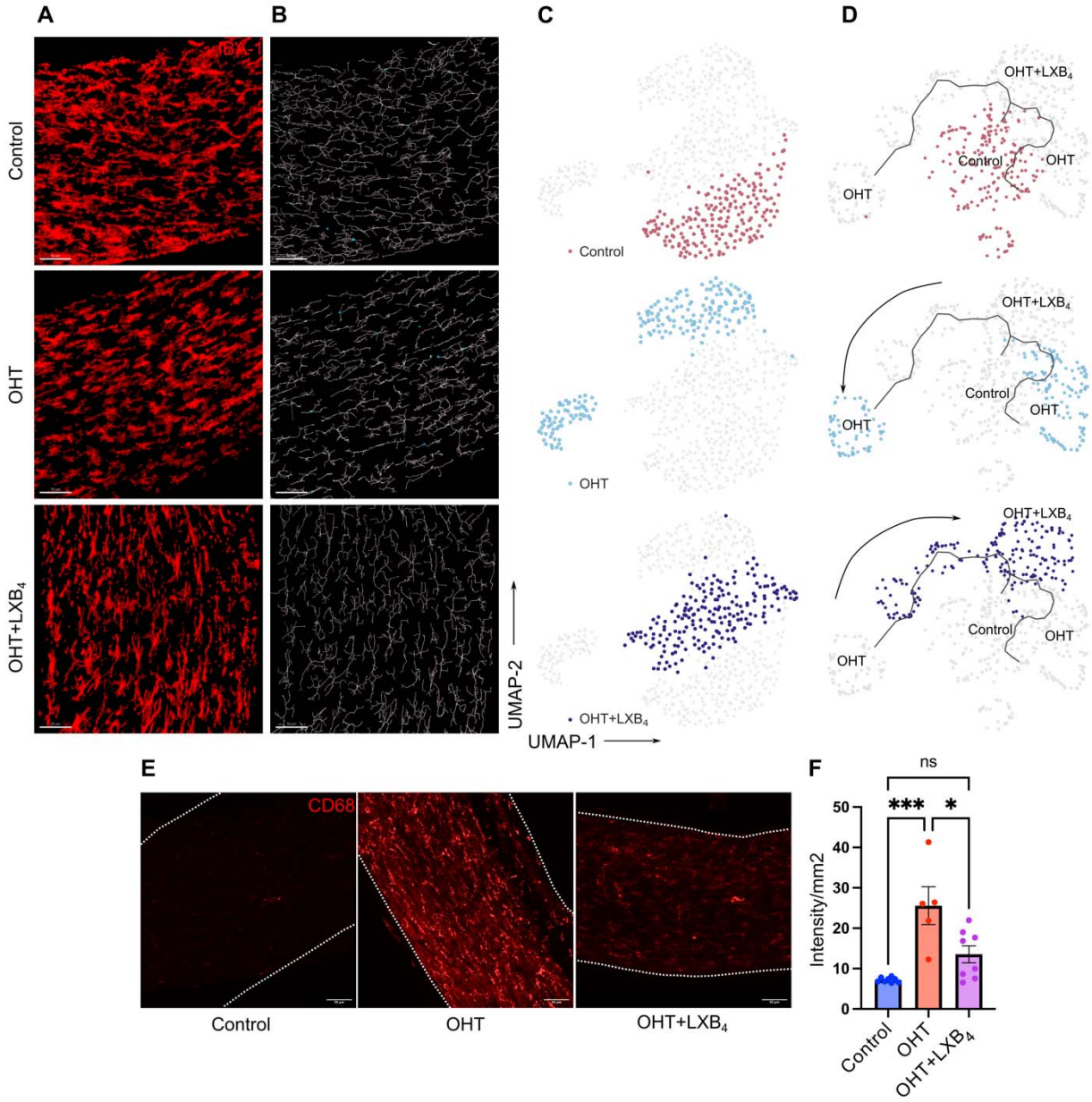

Figure 5: Neuroprotective LXB_4 treatment promotes restoration of a homeostatic optic nerve microglia phenotype. (A) Representative confocal micrograph of Iba1 (red) stained optic nerve microglia in normotensive control, OHT, and OHT+LXB_4 groups (scale bar- 50µm). (**B)** Representative filament images of microglia morphology generated from the respective Iba1-stained images using IMARIS (scale bar-50µm). (**C)** UMAP plot displaying clustering of optic nerve microglia in normotensive control, OHT, and OHT+LXB_4 groups. Each dot depicts 100 microglia bootstrapped for

their topological morphology descriptor, and 200 dots are shown per group. (**D)** UMAP plot of pseudotime trajectory of microglia morphology for all groups. (**E)** Representative confocal micrographs of CD68-stained optic nerve microglia for normotensive control, OHT, and OHT+LXB_4 (scale bar-50μm). (**F)** Quantification of CD68 expression in optic nerve whole-mounts for normotensive control (n=6), OHT (n=5), and OHT+LXB_4 (n=8). Data were analyzed by One-way ANOVA with Tukey's multiple comparison test (*$p<0.05$; ***$p<0.001$; ns, not significant). Each dot depicts the mean CD68 expression from a single retina. Data presented as mean ± SEM.

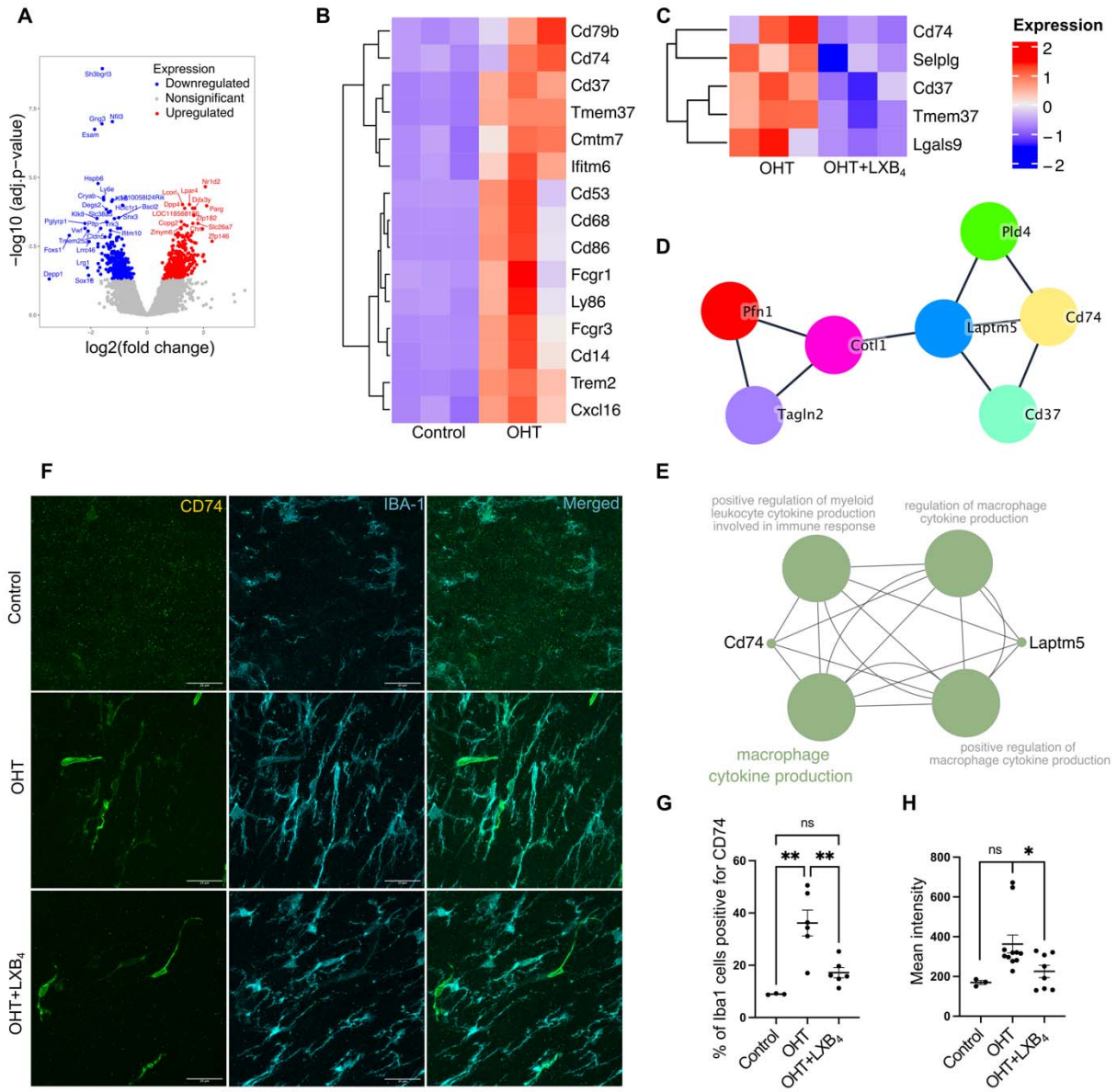

Figure 6: LXB_4 regulates OHT induction of a $CD74^+$ disease-associated microglia phenotype in the optic nerve. (A) Volcano plot for differential gene expression in the optic nerve between OHT and OHT+LXB_4 (Genes: upregulated-red; downregulated-blue; no significant change-grey). (**B)** Heatmap for expression of significantly changed (p.adjust<0.05) genes in normotensive versus OHT. (**C)** Heatmap for expression of significantly changed (p.adjust<0.05) genes in OHT versus OHT+LXB_4. (**D)** Network of highly interacting genes in the optic nerve that were downregulated by LXB_4 treatment during OHT, derived from MCODE analysis of STRING network. (**E)** Pathway enrichment network of genes shown in

(D). **(F)** Representative confocal micrographs of optic nerve sections stained for Iba1 (cyan) and CD74 (red) in normotensive control, OHT, and OHT+LXB_4 groups (scale bar-25 μm). (**G)** Quantification of Iba1 cells positive for CD74 expression ($CD74^+$) in normotensive control (n=3), OHT (n=6), and OHT+LXB_4 (n=6). Data were analyzed by One-way ANOVA with Tukey's multiple comparisons test (**$p<0.01$; ns, not significant). Each dot depicts the mean measurement from a single optic nerve. (**H)** Quantification of CD74 expression intensity in normotensive control (n=3), OHT (n=11), and OHT+LXB_4 (n=8). Data were analyzed by unpaired t-tests between normotensive control versus OHT and OHT versus OHT+LXB_4 (*$p<0.05$; ns, not significant). Each dot depicts the mean measurement from a single optic nerve. Data presented as mean ± SEM.

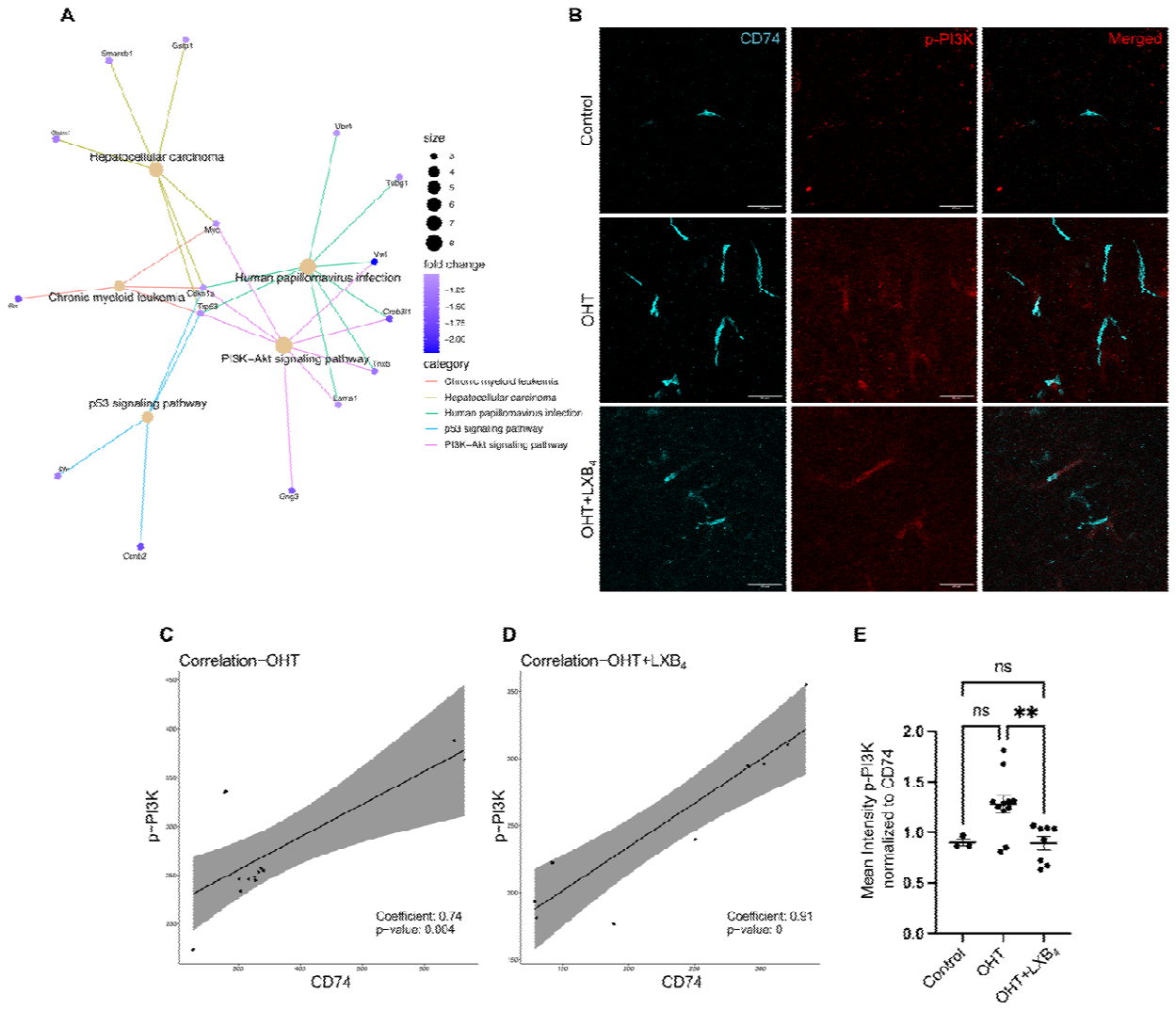

Figure 7: LXB_4 regulates PI3K signaling in optic nerve $CD74^+$ disease-associated microglia. (A) KEGG pathway enrichment map of genes downregulated by LXB_4 treatment during severe OHT. The Pathway circle size depicts number of genes involved in enrichment; genes linked to pathways are shown with their fold change scale. (**B)** Representative confocal micrographs of optic nerve sections stained for CD74 (cyan) and p-PI3K (red) in normotensive control, OHT, and OHT+LXB_4 groups (scale bar- 25 µm). (**C, D)** Correlation plot for CD74 and p-PI3K protein expression in OHT (**C)** and OHT+LXB_4 (**D).** Each dot represents the intensity of CD74 and p-PI3K correlated from a single cell. (**E)** Quantification of normalized p-PI3K to CD74 expression. Data were analyzed One-way ANOVA with Tukey's multiple

comparison test (**$p<0.01$; ns, not significant). Each dot represents normalized expression intensity from a single cell. Data presented as mean ± SEM.