Transcriptomic analysis across nasal, temporal, and macular regions of human neural retina and RPE/choroid by RNA-Seq

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Abstract

Proper spatial differentiation of retinal cell types is necessary for normal human vision. Many retinal diseases, such as Best disease and male germ cell associated kinase (\textit{MAK})-associated retinitis pigmentosa, preferentially affect distinct topographic regions of the retina. While much is known about the distribution of cell-types in the retina, the distribution of molecular components across the posterior pole of the eye has not been well-studied. To investigate regional difference in molecular composition of ocular tissues, we assessed differential gene expression across the temporal, macular, and nasal retina and retinal pigment epithelium (RPE)/choroid of human eyes using RNA-Seq. RNA from temporal, macular, and nasal retina and RPE/choroid from four human donor eyes was extracted, poly-A selected, fragmented, and sequenced as 100 bp read pairs. Digital read files were mapped to the human genome and analyzed for differential expression using the Tuxedo software suite. Retina and RPE/choroid samples were clearly distinguishable at the transcriptome level. Numerous transcription factors were differentially expressed between regions of the retina and RPE/choroid. Photoreceptor-specific genes were enriched in the peripheral samples, while ganglion cell and amacrine cell genes were enriched in the macula. Within the RPE/choroid, RPE-specific genes were upregulated at the periphery while endothelium associated genes were upregulated in the macula. Consistent with previous studies, \textit{BEST1} expression was lower in macular than extramacular regions. The \textit{MAK} gene was expressed at lower levels in macular than extramacular regions, but did not exhibit a significant difference.
between nasal and temporal retina. The regional molecular distinction is greatest between macula and periphery and decreases between different peripheral regions within a tissue. Datasets such as these can be used to prioritize candidate genes for possible involvement in retinal diseases with regional phenotypes.

**Keywords**

RNA-Seq; retina; choroid; RPE; gene expression; retinitis pigmentosa; macular degeneration; transcriptome

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1. Introduction

Human visual activities balance the need for high visual acuity, such as reading, driving, and recognizing faces, with comprehensive peripheral vision. High visual acuity is enabled by the macula, a region at the center of the posterior retina with the highest density of cone photoreceptors and ganglion cells. Vision in dim light is made possible by the rod photoreceptor cells which are most concentrated just anterior to the macula.

Many ocular pathologies affect distinct regions of the retina. Macular degenerations, such as age-related macular degeneration, Best disease, Stargardt disease, and North Carolina macular dystrophy, result in loss of photoreceptors and RPE cells in the macula. Other diseases, such as retinitis pigmentosa (RP), cause selective loss of photoreceptors at the periphery of the retina, often sparing central vision until advanced stages of disease. Some diseases manifest further distinction in regional phenotypes. For instance, male germ cell kinase (MAK)-related RP, the most common cause of inherited blindness among the Ashkenazi Jewish population, manifests an unusual inferonasal predilection for the photoreceptor cell death (Stone et al., 2011; Tucker et al., 2011).

Classic studies on the distribution of cell types through the neural retina (Curcio and Allen, 1990; Curcio et al., 1990; Jonas et al., 1992), combined with extensive disease phenotyping and detailed analyses of single molecule expression have provided substantial insight into the structural and functional organization of the neural retina, retinal pigment epithelium (RPE), and choroid in different regions of the eye. Previous large-scale studies aimed at differentiating macula from periphery have utilized reverse transcriptase-polymerase chain reaction (RT-PCR) (Kociok and Joussen, 2007), array-based technologies (Ishibashi et al., 2004; Diehn et al., 2005; Bowes Rickman et al., 2006; Radeke et al., 2007; van Soest et al., 2007) and more recently, RNA sequencing (RNA-Seq) (Li et al., 2014). Unlike the former two technologies, RNA-Seq provides not only estimates of gene expression level and isoform abundance, but also captures sequence-level information, potentially uncovering novel exons and other transcriptional events.

Here we present the first RNA-Seq dataset to investigate the temporal, macular, and nasal regions of the retina and RPE/choroid along with an additional sample with superior and inferior regions represented. Distinct expression profiles clearly differentiated retina from RPE/choroid. Differences between periphery and macula were more pronounced in the
retina than in the RPE/choroid and in both tissues reflected dominant cell-type distributions. In the neural retina, nasal and temporal regions were indistinguishable by our criteria.

2. Materials and methods

2.1 Tissue acquisition

Human eyes were obtained through the Iowa Lions Eye Bank after informed consent by family members and in accordance with the tenets of the Declaration of Helsinki. Donor information is presented in Table 1. In four donors, an 8 mm trephine punch was used to remove the macula and a 6 mm punch was used to remove temporal and nasal punches. In one additional sample, a 4 mm punch was used to dissect macular, nasal, temporal, superior and inferior punches (Braun et al., 2013). Neural retina and RPE/choroid were separated, flash frozen in liquid nitrogen, and stored at −80°C. All samples used in this study were preserved in liquid nitrogen within 6 hours of death.

2.2 RNA sequencing

RNA was extracted from frozen tissue punches using a Qiagen RNeasy Mini Prep Kit (Qiagen, Valencia, CA) and kept frozen prior to sequencing. The four temporal-macula-nasal sets were prepared for paired-end sequencing using an Illumina TruSeq Stranded mRNA Sample Prep Kit and sequenced on the Illumina platform in the Genomics Division of the Iowa Institute of Human Genetics. Additional paired-end sequencing of one temporal-macula-nasal-superior-inferior sample was performed on the Illumina platform at HudsonAlpha Institute for Biotechnology (Huntsville, AL).

2.3 Bioinformatic analysis

Sequenced reads were mapped to human genome build hg19 using TopHat2 (ver. 2.0.11; (Kim et al., 2013)), transcript structure and abundance were estimated using Cufflinks (ver. 2.1.1; (Trapnell et al., 2010)), and differential expression analysis was performed using Cuffdiff (ver. 2.1.1; (Trapnell et al., 2012a)). Quality control analysis was performed using RNA-SeQC (ver. 1.1.7; (DeLuca et al., 2012)). The cummeRbund package (ver. 2.4.1; (Trapnell et al., 2012b)) for R (ver. 3.0.2) was used for data visualization. Differential expression analysis was performed for the four donor samples with similar processing (macula, temporal, and nasal retina and RPE/choroid). Spearman’s rank correlation coefficient as implemented in R was used for all correlations. Genes were deemed differentially expressed if the absolute value of the log2 (fold change) was > 1, the q-value < 0.001, and the FPKM (Fragments Per Kilobase of transcript per Million mapped reads) values of either group compared were all > 1.

3. Results

We performed 100 bp paired-end RNA-Seq on retina and RPE/choroid from the temporal, macular, and nasal regions of four clinically normal human donor eyes (Table 1). Hierarchical clustering of samples showed clear separation of neural retina from RPE/choroid samples and evidence of donor effect, i.e., samples derived from the same donor tend to cluster together more often than not (Figure 1) (Rouhani et al., 2014).
3.1 Comparison with previously published data

We compared our dataset to a recently published table of FPKM (Fragments Per Kilobase of transcript per Million mapped reads) values derived from macular and peripheral retina and RPE/choroid/sclera for 91 genes implicated by genome-wide association studies (GWAS) in various eye diseases (Li et al., 2014). To compare the previous results to ours, we averaged our nasal and temporal FPKM values together for one “peripheral” value (Figure 2). Where Cufflinks matched two separate loci to a single gene symbol, we took the higher of the two values. While the values for retina roughly follow the diagonal, FPKM values were consistently higher for genes in our RPE/choroid samples compared to the RPE/choroid/sclera samples of Li, et al., likely reflecting the cellular paucity of the sclera. The obvious exception is COL10A1, which shows higher expression in peripheral RPE/choroid/sclera than in peripheral RPE/choroid alone. In addition, TIMP3, reported by Li et al. as a predominantly retinal transcript, showed robust expression in all RPE/choroid samples in the current report (Figure 2).

3.2 Regional gene expression by tissue

To evaluate gene expression across regions of the retina and RPE/choroid, we used Cuffdiff to perform pairwise tests between groups of punches (Supplemental Table 1). When comparing nasal retina vs. macular retina, 30 genes showed increased expression in nasal retina and 128 genes showed decreased expression (Table 2). When comparing temporal retina vs. macular retina, 37 genes showed increased expression in temporal retina and 323 genes showed decreased expression (Table 3). Notably, of the 40 top differences in expression between nasal retina and macular retina (Table 2), 21 of the same genes were in the list of top 40 differences between temporal retina and macular retina (Table 3). Interestingly, no genes were differentially expressed between temporal and nasal retina, suggesting that these two regions of the retina are molecularly indistinguishable using these criteria.

In the nasal vs. macular RPE/choroid comparison, 81 genes showed increased expression in the nasal RPE/choroid and 39 genes showed decreased expression (Table 4). When comparing temporal vs. macular RPE/choroid, 70 genes were increased in the temporal RPE/choroid and 44 genes were decreased (Table 5). In contrast to the retina, in which no gene expression differences between different peripheral regions met our criteria for differential expression, three genes (MPZ, VIP, and SCN7A) were increased in the nasal RPE/choroid and 11 were decreased when comparing temporal vs. nasal RPE/choroid (Table 6). Higher expression of neuroretinal genes (e.g., RHO, RCVRN, SAG) in the nasal RPE/choroid group as compared to the macular (Table 4) or temporal (Table 6) RPE/choroid groups is traceable to the slight but detectable neuroretinal contamination of the nasal RPE/choroid from donor 2.

We also performed comparisons between tissues within a region. We observed 2747 genes with increased expression and 2053 genes with decreased expression when comparing macular RPE/choroid vs. macular retina (Table 7). We observed 2842 genes with increased expression and 1935 genes with decreased expression when comparing nasal RPE/choroid vs. nasal retina (Table 8). We observed 2762 genes with increased expression and 1909
genes with decreased expression when comparing temporal RPE/choroid vs. temporal retina (Table 9). Figure 3 shows the overlaps between differentially expressed genes in these comparisons.

3.3 Regional expression differences for specific retinal cell-types

To explore regional differences in cell types in the retina, we mapped 92 genes identified by Siegert and coworkers as cell-type specific in mouse retina (Siegert et al., 2012) to 78 human genes in our dataset (we required genes with human homologs to be expressed above FPKM 0 in at least half of our human retina samples). As indicated in Figure 4, all four macula samples cluster together, while nasal and temporal samples are intermixed. All photoreceptor genes are enriched in the peripheral samples, whereas several genes of ganglion cell and amacrine cells are interleaved in a macula-enriched cluster.

3.4 RPE-specific and endothelium associated gene expression in the RPE/choroid

To compare cell populations in the RPE/choroid, we selected predefined RPE-specific and endothelium associated genes sets (Whitmore et al., 2013) and assessed trends in expression across temporal, macular, and nasal RPE/choroid punches (Figure 5). The RPE-specific set shows an overall lower expression in the macula while the endothelium associated set shows higher expression in the macula.

3.5 Intradonor variation in five regions of the retina

In a separate experiment, we took retinal punches from macula, superior, inferior, temporal, and nasal regions of a single human donor eye and performed pairwise correlation for all genes expressed above FPKM 1 in a least one punch. Macula as compared to any of the peripheral punches showed the greatest dispersion from the diagonal \((r\text{ from } 0.97-0.98;\) Figure 6). All peripheral vs. peripheral comparisons were also highly correlated, \((r = 0.99),\) with modest dispersion from the diagonal in the superior vs. nasal and nasal vs. inferior comparisons.

4. Discussion

Here we present the first RNA-Seq dataset to separately investigate gene expression in the macula, nasal, and temporal human retina and RPE/choroid. While intriguing differences between the peripheral and the macular tissues were found, we did not observe significant differences between nasal and temporal retina. Only a few genes were differentially expressed between nasal and temporal RPE/choroid. Thus, the use of either nasal or temporal retina as general surrogates of “peripheral” retina seems warranted based on these data.

4.1 Limitations of the current study

RNA-Seq provides a wealth of data from each sample but interpreting these data remains challenging. The most commonly used measurement of expression, fragments per kilobase mapped per million reads (FPKM), should not be interpreted as a straightforward reflection of the number of RNA molecules within a given cell or tissue punch. Moreover, as any RNA-Seq derived expression estimate is fundamentally based on digital read counts,
Gaussian models used for microarray analysis do not apply. To reduce false positives, we
selected stringent thresholds for calling a gene as differentially expressed, likely missing
some biologically relevant true positive events. Several neural retina genes, including \textit{RHO},
\textit{RCVRN}, and \textit{SAG}, showed increased expression in the nasal RPE/choroid. This is likely due
to incomplete separation of neural retina from the RPE during dissection, a problem widely
reported in previous studies of ocular gene expression. Moreover, a larger sample size may
provide enough power to detect transcriptome-level difference between nasal and temporal
retina. However, despite our sample size, our data showed strong rank correlations with
published FPKM values of peripheral and macular retina and RPE/choroid/sclera (Li et al.,
2014).

\subsection*{4.2 Molecular determinants of the macula}

Identifying the molecular determinants of the macular-peripheral distinction remains an
open challenge in vision research. We found several transcription factors that were
differentially expressed in the macula and periphery. For instance, \textit{FOXI3} was upregulated
in the nasal retina compared to the macular retina, whereas \textit{IRX2} was downregulated in this
comparison. \textit{SIX2} was upregulated in the temporal retina compared to the macular retina,
whereas \textit{POU4F1}, \textit{POU4F2}, \textit{IRX1}, and \textit{IRX2} were downregulated in this comparison.
\textit{POU4F1} and its target, \textit{RIT2} (Zhang et al., 2013), are enriched in retinal ganglion cells (Kim
et al., 2006), and both genes were significantly enriched in our macular retina samples. \textit{RIT2}
is also expressed in the mouse inner nuclear layer (Zhang et al., 2013).

\subsection*{4.3 Implications for vasculature in the retina and RPE/choroid}

We observed decreased expression of prolactin (\textit{PRL}) in the macular neuroretina as
compared to either peripheral region. Prolactin is anti-angiogenic in the retina (Aranda et al.,
2005), and systemic prolactin levels correlate with diabetic retinopathy (Arnold et al., 2010).
Previous studies in rats and green monkeys have shown that PRL is expressed throughout
the cell layers of the neural retina, and its receptor, PRLR, is expressed in photoreceptor
nuclei, inner nuclear layer, and ganglion cell layer (Rivera et al., 2008). To our knowledge,
this is the first dataset showing macular-peripheral differential expression of \textit{PRL} in the
retina. Distribution of \textit{PRL} and other regulators of angiogenesis may help to explain the
tendency of choroidal neovascular membranes to grow towards the fovea (Klein et al., 1989;
de Jong, 2006), particularly if the neovascular membrane had breached the RPE or if RPE
barrier function was compromised.

Of our predefined endothelium associated gene set, \textit{MGP} (matrix Gla protein) showed the
highest expression in the RPE/choroid, and was in the top 25 differentially expressed genes
in the nasal retina vs. nasal RPE/choroid comparison. \textit{MGP} may prevent calcification in the
choroidal stroma or in Bruch’s membrane (Booij et al., 2010). Recently, Gonzalez and
coworkers used the \textit{MGP} promoter to drive expression of \textit{β}-galactosidase in a gene vector in
anterior pole cultures of human donor eyes (Gonzalez et al., 2004). They observed localized
expression in the trabecular meshwork (Gonzalez et al., 2004). However, they did not
examine the tissues of the posterior pole. The Ocular Tissue Database (Wagner et al., 2013)
entry for \textit{MGP} (available at \url{https://genome.uiowa.edu/otdb/}) shows relatively high
expression in the RPE/choroid, on par with the trabecular meshwork, ciliary body, and iris,
and low expression in the retina, consistent with our findings. Further study will be needed to determine the extent to which MGP contributes to Bruch’s membrane and/or choroidal elasticity.

4.4 Comparison with previously published data

We also observed robust expression of TIMP3 in our dataset, compared to FPKM values of 0 in the RPE/choroid in that of Li et al. These authors noted that expression of TIMP3 was almost entirely limited to the retina. This result may be a side effect of the algorithm used by Cufflinks. When Cufflinks estimates FPKM values, it first computes “fragment bundles.” Extremely high bundle values can cause difficulty for the algorithm; thus, Cufflinks labels such genes as “HIDATA” and does not estimate FPKMs. In our initial analysis, we failed to detect RHO in both nasal and temporal retina. However, inspection of individual alignment files for these samples showed robust expression, with read counts in excess of 40,000 across the RHO transcript in temporal samples (Supplemental Figure S1). Further investigation revealed that identified expression of TTR also marked by the “HIDATA” criterion in the nasal RPE/choroid. Setting the “--max_bundle_frags” parameter for Cufflinks and cuffdiff to an arbitrarily high value (e.g., 20000000) removed the “HIDATA” label, resulting in FPKM estimates for RHO and TTR in all groups.

4.5 Utility of ophthalmic expression datasets

Linkage studies have identified many disease loci in families affected by macular dystrophies or other eye diseases (see examples at RetNet [https://sph.uth.edu/retnet/] and Online Mendelian Inheritance in Man [http://omim.org/]). Causative mutations have yet to be pinpointed within several of these loci, which cover megabases of the genome and contain dozens of genes. Multi-tissue regional ophthalmic datasets, such as we present here, may help reduce the search space for candidate genes, especially for diseases with region-specific or tissue-specific phenotypes.

Moreover, as more Mendelian diseases with coding mutations are solved, identifying silent mutations and changes in regulatory regions is the remaining frontier for molecular genetics. For instance, in 2002 Schulz and coworkers examined NPVF (formerly C7orf9) for coding sequence changes that could explain Cystoid Macular Edema (chr7:7,300,000 - 28,800,000; OMIM 153880). They found no deleterious SNPs in the coding sequence of NPVF, but they acknowledged that the promoter sequence may harbor the causative mutation (Schulz et al., 2002). In our data, we observe significant macular enrichment of NPVF as compared to both nasal and temporal retina, suggesting that promoter changes could alter the region-specific expression of NPVF in the retina.

MAK-related RP (OMIM 614181) tends to spare the temporal retina while damaging the inferior and nasal retina (Stone et al., 2011; Tucker et al., 2011). While we observed lower expression of MAK in the macula (Figure 7A), similar to many other photoreceptor cell specific genes (Figure 4), differences in peripheral regions of the retina were not detected. This suggests that the regional degeneration observed in MAK-related RP is likely due to the distribution of substrates or factors regulating MAK function rather than differences in gene expression across retinal topography.
*BEST1*, the gene mutated in Best vitelliform macular dystrophy (OMIM 153700), has previously been shown to be expressed at lower levels in the macular RPE/choroid than in the periphery by immunohistochemistry, quantitative PCR, and proteomics (Mullins et al., 2007; Skeie and Mahajan, 2014). We observed a similar pattern of expression in our data (Figure 5, 7B). However, comparable profiles were seen for many other RPE-specific genes, including *RPE65*, a gene previously shown to have relatively equal abundance between macular and peripheral RPE/choroid (Kociok and Joussen, 2007). One implication of these findings, as depicted in Figure 5, is that normalization should be performed using cell-type specific genes with relatively consistent expression across anatomic regions.

### 4.6 Conclusion

We have presented a comprehensive, transcriptome-wide view of gene expression across the neural retina and RPE/choroid in three regions of the retina. Gene expression in the retina correlates with the anatomic distribution of rod photoreceptors and ganglion cells in the macula and periphery. RPE-specific and endothelium associated gene expression in the RPE/choroid appear inversely related, with RPE-specific genes expressed at a lower level in the macula than at the periphery, whereas endothelium associated genes show slightly higher expression in the macula than in the periphery. Additional RNA-Seq datasets for ophthalmic tissues will facilitate more complex analyses, including mapping retina-specific transcriptional regulatory circuits and identifying lowly expressed exons.

Both analyses will facilitate the search for novel disease causing mutations. For example, we previously used the five-region RNA-Seq data to identify rare alternative exons in *ABCA4*, screened a cohort of patients with clinical evidence of *ABCA4* disease for variants in these exons, and identified novel splice-site mutations not found in controls (Braun et al., 2013). To advance similar studies, we are making our samples available on the database of Genotypes and Phenotypes (dbGAP).

### Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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Figure 1. Hierarchical clustering on expressed isoforms based on Spearman's correlation
Figure 2. Comparison of GWAS associated gene sets with data published by Li et al. (2014)
The previously published dataset included sclera in the RPE/choroid punches, likely accounting for the number of genes in RPE/choroid below the diagonal. Spearman rank correlation coefficient shown ($r$).
Figure 3. Intersection between differentially expressed genes sets
(A) Regional pairwise comparisons in the retina. (B) Regional pairwise comparisons in the RPE/choroid. (C) RPE/choroid compared to retina for each region without respect to direction of fold change.
Figure 4. Clustering of cell-type specific genes in the retina
Lighter shading indicates higher expression while darker shading indicates lower expression (FPKM values after row scaling). Hierarchical clustering was performed with complete linking on Spearman rank correlation distance.
Figure 5. Expression of RPE-specific and endothelium associated gene sets across regions of the RPE/choroid
Figure 6. Intradonor region variability across five regions of the retina
Figure 7. Expression of MAK (retina) and BEST1 (RPE/choroid) across regions
Mean indicated by (×). Error bars denote 95% confidence intervals for abundance as calculated by Cuffdiff.
Table 1

Donor information. Samples marked by asterisks (*) were analyzed for differential expression in Cuffdiff. Library prep involved poly-A selection.

| Donor | Eye | Sex | Age | Cause of death     | Death-to-preservation (h) | Retina | RPE/choroid | Library prep. |
|-------|-----|-----|-----|-------------------|--------------------------|--------|-------------|--------------|
| 1*    | OS  | F   | 82  | Respiratory failure | < 4                      | M, N, T| M, N, T     | stranded     |
| 2*    | OD  | M   | 77  | Congestive heart failure | < 5                      | M, N, T| M, N, T     | stranded     |
| 3*    | OD  | F   | 89  | Pneumonia          | 3-4.5                    | M, N, T| M, N, T     | stranded     |
| 4*    | OS  | M   | 91  | Pneumonia          | 5-6                      | M, N, T| M, N, T     | stranded     |
| 5     | OD  | F   | 91  | Unknown            | < 6                      | M, N, T,S, I| —           | unstranded   |

Abbreviations: M – macula; N – nasal; T – temporal; S – superior; I – inferior.
Table 2

Top 40 differentially expressed genes between nasal retina vs. macular retina with q-value < 0.001 and absolute log₂(fold-change) ≥ 1.

| Symbol | Description | Chromosome | Start | Stop | Macular Retina (FPKM) | Nasal Retina (FPKM) | Log2(FC) | P-value | Q-value |
|--------|-------------|------------|-------|------|-----------------------|---------------------|----------|---------|---------|
| HSD17B2 | hydroxysteroid (17-beta) dehydrogenase 2 | chr16 | 82056731 | 82132139 | 1.29 | 9.55 | 2.88 | 5.00E-05 | 2.86E-04 |
| CYP26B1 | cytochrome P450, family 26, subfamily B, polypeptide 1 | chr2 | 72356363 | 72375687 | 0.41 | 2.77 | 2.75 | 5.00E-05 | 2.86E-04 |
| COL2A1 | collagen, type II, alpha 1 | chr12 | 48366747 | 48398285 | 1.56 | 9.98 | 2.68 | 5.00E-05 | 2.86E-04 |
| STEAP4 | STEAP family member 4 | chr7 | 87900209 | 87936319 | 0.31 | 1.89 | 2.58 | 5.00E-05 | 2.86E-04 |
| FOXI3 | forkhead box 13 | chr2 | 88744347 | 88752197 | 0.49 | 1.89 | 2.58 | 5.00E-05 | 2.86E-04 |
| OXTR | oxytocin receptor | chr3 | 8792094 | 8811460 | 0.49 | 1.91 | 1.96 | 5.00E-05 | 2.86E-04 |
| NPVF | neuropeptide VF precursor | chr7 | 25264190 | 25268105 | 29.12 | 106.31 | 1.87 | 5.00E-05 | 2.86E-04 |
| ZIC1 | Zic family member 1 | chr3 | 147103834 | 147134784 | 1.24 | 4.25 | 1.78 | 5.00E-05 | 2.86E-04 |
| PRL | prolactin | chr6 | 22287472 | 22303082 | 4.48 | 15.15 | 1.76 | 5.00E-05 | 2.86E-04 |
| LOXL4 | lysyl oxidase-like 4 | chr10 | 100007442 | 100028007 | 0.98 | 3.20 | 1.71 | 1.00E-04 | 5.49E-04 |
| FXYD2 | a FXYD domain containing ion transport regulator 2 | chr11 | 25264190 | 25268105 | 12.05 | 35.28 | 1.55 | 5.00E-05 | 2.86E-04 |
| KRT39 | keratin 39 | chr17 | 23884420 | 23886285 | 17.01 | 48.24 | 1.50 | 5.00E-05 | 2.86E-04 |
| EGR1 | early growth response 1 | chr1 | 23884420 | 23886285 | 17.01 | 48.24 | 1.50 | 5.00E-05 | 2.86E-04 |
| HTR1F | 5-hydroxytryptamine (serotonin) receptor 1F, G protein-coupled | chr6 | 147103834 | 147134784 | 1.24 | 4.25 | 1.78 | 5.00E-05 | 2.86E-04 |
| CSRP2 | cysteine and glycine-rich protein 2 | chr10 | 55595934 | 55612148 | 16.89 | 41.31 | 1.29 | 5.00E-05 | 2.86E-04 |
| CYR61 | cysteine-rich, angiogenic inducer, 61 | chr1 | 86046443 | 86049648 | 11.76 | 29.12 | 1.31 | 5.00E-05 | 2.86E-04 |
| LGALS3 | lectin, galactoside-binding, soluble, 3 | chr5 | 137801180 | 137805004 | 15.34 | 39.41 | 1.36 | 5.00E-05 | 2.86E-04 |
| C4A | complement component 4A (Rodgers blood group) | chr3 | 88744347 | 88752197 | 0.49 | 1.89 | 2.58 | 5.00E-05 | 2.86E-04 |
| NR4A1 | nuclear receptor subfamily 4, group A, member 1 | chr12 | 22287472 | 22303082 | 4.48 | 15.15 | 1.76 | 5.00E-05 | 2.86E-04 |
| KCNC2 | potassium voltage-gated channel, Shaw-related subfamily, member 2 | chr12 | 77252493 | 77272799 | 19.34 | 48.16 | 1.32 | 5.00E-05 | 2.86E-04 |
| TRPM2 | transient receptor potential cation channel, subfamily M, member 2 | chr17 | 39113368 | 39143387 | 3.43 | 10.02 | 1.55 | 5.00E-05 | 2.86E-04 |
| RIT2 | Ras-like without CAAX 2 | chr17 | 39113368 | 39143387 | 3.43 | 10.02 | 1.55 | 5.00E-05 | 2.86E-04 |
| ISLR2 | immunoglobulin superfamily containing leucine-rich repeat 2 | chr17 | 39113368 | 39143387 | 3.43 | 10.02 | 1.55 | 5.00E-05 | 2.86E-04 |
| AHNAK2 | AHNAK nucleoprotein 2 | chr14 | 105371613 | 105444694 | 84.49 | 25.19 | −1.69 | 5.00E-05 | 2.86E-04 |

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| Symbol | Description | Chromosome | Start | Stop | Macular Retina (FPKM) | Nasal Retina (FPKM) | Log2(FC) | P-value | Q-value |
|--------|-------------|------------|-------|------|-----------------------|---------------------|----------|---------|---------|
| IRX2   | iroquois homeobox 2 | chr5       | 2745916 | 2751769 | 14.95 | 4.34 | −1.78 | 5.00E-05 | 2.86E-04 |
| CPNE9  | copine family member IX | chr3       | 9745509 | 9771592 | 5.89 | 1.70 | −1.79 | 5.00E-05 | 2.86E-04 |
| TTC39A | tetrasricopeptide repeat domain 39A | chr1       | 51752172 | 51810785 | 22.16 | 6.24 | −1.83 | 5.00E-05 | 2.86E-04 |
| HTR1B  | 5-hydroxytryptamine (serotonin) receptor 1B, G protein-coupled | chr6       | 78168875 | 78174100 | 3.40 | 0.95 | −1.84 | 1.50E-04 | 8.01E-04 |
| PHOSPHO1 | phosphatase, orphan 1 | chr17      | 47300731 | 47308128 | 6.47 | 1.81 | −1.84 | 5.00E-05 | 2.86E-04 |
| FABP3  | fatty acid binding protein 3, muscle and heart (mammary-derived growth inhibitor) | chr1       | 31769837 | 31846528 | 131.10 | 35.95 | −1.87 | 5.00E-05 | 2.86E-04 |
| PTH1R  | parathyroid hormone 1 receptor | chr3       | 46761072 | 46945351 | 11.74 | 3.18 | −1.88 | 1.00E-04 | 5.49E-04 |
| LCP1   | lymphocyte cytosolic protein 1 (L-plastin) | chr13      | 46700056 | 46785977 | 7.48 | 1.94 | −1.95 | 5.00E-05 | 2.86E-04 |
| SLN    | sarcolipin | chr11      | 107578100 | 107582787 | 42.78 | 10.92 | −1.97 | 5.00E-05 | 2.86E-04 |
| MCTP1  | multiple C2 domains, transmembrane 1 | chr5        | 94036882 | 94620279 | 3.33 | 0.84 | −2.00 | 5.00E-05 | 2.86E-04 |
| MRGPRE | MAS-related GPR, member E | chr11      | 3246156 | 3254111 | 12.08 | 2.58 | −2.22 | 5.00E-05 | 2.86E-04 |
| RASGRP3 | RAS guanyl releasing protein 3 (calcium and DAG-regulated) | chr2       | 33630960 | 33792285 | 5.84 | 1.09 | −2.42 | 5.00E-05 | 2.86E-04 |
| C1orf170 | chromosome 1 open reading frame 170 | chr1       | 901876 | 917673 | 8.05 | 1.37 | −2.55 | 5.00E-05 | 2.86E-04 |
| PRPH   | peripherin | chr12      | 49686760 | 49692481 | 55.03 | 8.39 | −2.71 | 5.00E-05 | 2.86E-04 |

*a* FXYD2, FXYD6, and FXYD6-FXYD2 (readthrough) were reported as a single transcriptional locus by Cufflinks.

*b* KRT39 and KRT40 were reported as a single transcriptional locus by Cufflinks.

*c* C4A and C4B_2 were reported as a single transcriptional locus by Cufflinks.
### Table 3

Top 40 differentially expressed genes between temporal retina vs. macular retina with q-value < 0.001 and absolute log2(fold-change) ≥1.

| Symbol       | Description                                                                 | Chromosome | Start          | Stop           | Macular Retina (FPKM) | Temporal Retina (FPKM) | Log2(FC) | P-value | Q-value |
|--------------|-----------------------------------------------------------------------------|------------|----------------|----------------|-----------------------|------------------------|-----------|---------|---------|
| MIR1247      | microRNA 1247                                                              | chr14      | 102023301      | 102026828      | 0.30                  | 4.16                   | 3.77      | 5.00E-05| 2.86E-04|
| CYP26B1      | cytochrome P450, family 26, subfamily B, polypeptide 1                     | chr2       | 72356363       | 72375687       | 0.41                  | 4.68                   | 3.51      | 5.00E-05| 2.86E-04|
| HSD17B2      | hydroxysteroid (17-beta) dehydrogenase 2                                   | chr16      | 82056731       | 82132139       | 1.29                  | 10.96                  | 3.08      | 5.00E-05| 2.86E-04|
| PRL          | prolactin                                                                  | chr6       | 22287472       | 22303082       | 4.48                  | 29.37                  | 2.71      | 5.00E-05| 2.86E-04|
| COL2A1       | collagen, type II, alpha 1                                                 | chr12      | 48366747       | 48398285       | 1.56                  | 9.42                   | 2.59      | 5.00E-05| 2.86E-04|
| ZIC1         | Zic family member 1                                                         | chr3       | 147103834      | 147134784      | 1.24                  | 6.24                   | 2.33      | 5.00E-05| 2.86E-04|
| NDUFA4L2     | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4-like 2               | chr12      | 57623324       | 57634949       | 42.98                 | 162.00                 | 1.91      | 1.00E-04| 5.49E-04|
| FAM46B       | family with sequence similarity 46, member B                               | chr1       | 27331510       | 27339333       | 0.96                  | 3.61                   | 1.91      | 5.00E-05| 2.86E-04|
| LOXL4        | lysyl oxidase-like 4                                                        | chr10      | 100007442      | 100028007      | 0.98                  | 3.65                   | 1.90      | 1.00E-04| 5.49E-04|
| FXYD2        | FXYD domain containing ion transport regulator 2                            | chr11      | 117690789      | 117748201      | 12.05                 | 43.78                  | 1.86      | 5.00E-05| 2.86E-04|
| ATP1A2       | ATPase, Na+/K+ transporting, alpha 2 polypeptide                            | chr1       | 160085519      | 160113374      | 17.41                 | 57.10                  | 1.71      | 5.00E-05| 2.86E-04|
| SIX2         | SIX homeobox 2                                                              | chr2       | 45232323       | 45236563       | 2.44                  | 7.92                   | 1.70      | 5.00E-05| 2.86E-04|
| GPR124       | G protein-coupled receptor 124                                              | chr8       | 37654400       | 37707431       | 4.99                  | 15.61                  | 1.65      | 5.00E-05| 2.86E-04|
| ADSSL1       | adenylosuccinate synthase like 1                                            | chr1        | 105190533      | 105213663      | 5.25                  | 15.63                  | 1.57      | 5.00E-05| 2.86E-04|
| HTR1F        | 5-hydroxytryptamine (serotonin) receptor 1F, G protein-coupled             | chr3        | 87841874       | 88049226       | 0.78                  | 2.31                   | 1.56      | 5.00E-05| 2.86E-04|
| ATOH8        | atonal homolog 8 (Drosophila)                                               | chr2        | 85978936       | 86018506       | 1.13                  | 3.20                   | 1.50      | 5.00E-05| 2.86E-04|
| NPFV         | neuropeptide VF precursor                                                  | chr7        | 25264190       | 25268105       | 29.12                 | 81.63                  | 1.49      | 5.00E-05| 2.86E-04|
| PPP1R3C      | protein phosphatase 1, regulatory subunit 3C                               | chr10       | 93379047       | 93392858       | 14.02                 | 38.45                  | 1.46      | 5.00E-05| 2.86E-04|
| CLEC4F       | C-type lectin domain family 4, member F                                    | chr2        | 71035775       | 71047732       | 2.07                  | 5.67                   | 1.45      | 1.00E-04| 5.49E-04|
| CD4          | CD4 molecule                                                                | chr12       | 6898637       | 6929977        | 5.55                  | 14.99                  | 1.43      | 5.00E-05| 2.86E-04|
| POU4F2       | POU class 4 homeobox 2                                                      | chr4        | 147560044      | 147563263      | 11.13                 | 1.98                   | −2.49     | 5.00E-05| 2.86E-04|
| NEFM         | neurofilament, medium polypeptide                                           | chr8        | 24771273       | 24776612       | 544.29                | 94.76                  | −2.52     | 5.00E-05| 2.86E-04|
| SLC17A6      | solute carrier family 17 (vesicular glutamate transporter), member 6       | chr11      | 22355132       | 22401046       | 43.08                 | 7.44                   | −2.53     | 5.00E-05| 2.86E-04|
| TTC39A       | tetraicopeptide repeat domain 39A                                          | chr1        | 51752172       | 51810785       | 22.16                 | 3.76                   | −2.56     | 5.00E-05| 2.86E-04|
| ISLR2        | immunoglobulin superfamily containing leucine-rich repeat 2               | chr15       | 74418236       | 74429152       | 15.76                 | 2.61                   | −2.59     | 5.00E-05| 2.86E-04|
| POU4F1       | POU class 4 homeobox 1                                                      | chr13       | 78628989       | 79233323       | 23.65                 | 3.84                   | −2.62     | 5.00E-05| 2.86E-04|
| AHNAK2       | AHNAK nucleoprotein 2                                                       | chr14       | 105371613      | 105444694      | 84.49                 | 13.65                  | −2.63     | 5.00E-05| 2.86E-04|
| IRX1         | iroquois homeobox 1                                                         | chr5        | 3596054       | 3601517        | 5.55                  | 0.88                   | −2.66     | 5.00E-05| 2.86E-04|
| IRX2         | iroquois homeobox 2                                                         | chr5        | 2745916       | 2751769        | 14.95                 | 2.34                   | −2.67     | 5.00E-05| 2.86E-04|
| Symbol | Description                                                                 | Chromosome | Start   | Stop    | Macular Retina (FPKM) | Temporal Retina (FPKM) | Log2(FC) | P-value     | Q-value     |
|--------|-----------------------------------------------------------------------------|------------|---------|---------|-----------------------|------------------------|----------|-------------|-------------|
| HTR1B  | 5-hydroxytryptamine (serotonin) receptor 1B, G protein-coupled              | chr6       | 78168875| 78174100| 3.40                  | 0.51                   | −2.74    | 5.00E-05    | 2.86E-04    |
| MCTP1  | multiple C2 domains, transmembrane 1                                        | chr5       | 94036882| 94620279| 3.33                  | 0.50                   | −2.75    | 5.00E-05    | 2.86E-04    |
|        | potentially novel                                                            | chr6       | 11374551| 11375504| 3.32                  | 1.90                   | −2.81    | 5.00E-05    | 2.86E-04    |
| CPNE9  | copine family member IX                                                      | chr3       | 9745509 | 9771592 | 5.89                  | 0.83                   | −2.83    | 5.00E-05    | 2.86E-04    |
| MRGPRE | MAS-related GPR, member E                                                   | chr11      | 3246156 | 3254111 | 12.08                 | 1.55                   | −2.96    | 5.00E-05    | 2.86E-04    |
| ABO    | ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase; transferase B, alpha 1-3-galactosyltransferase) | chr9       | 136099931| 136151454| 3.68                  | 0.44                   | −3.07    | 5.00E-05    | 2.86E-04    |
|        | potentially novel                                                            | chr12      | 108203132| 108258620| 3.78                  | 0.45                   | −3.08    | 5.00E-05    | 2.86E-04    |
| RASGRP3| RAS guanyl releasing protein 3 (calcium and DAG-regulated)                   | chr2       | 33630960| 33792285| 5.84                  | 0.62                   | −3.24    | 5.00E-05    | 2.86E-04    |
| C3orf55| chromosome 3 open reading frame 55                                          | chr3       | 157260745| 157395552| 6.11                  | 0.60                   | −3.34    | 5.00E-05    | 2.86E-04    |
| PRPH   | peripherin                                                                  | chr12      | 49686760| 49692481| 55.03                 | 5.00                   | −3.46    | 5.00E-05    | 2.86E-04    |
| C1orf170| chromosome 1 open reading frame 170                                          | chr1       | 901876 | 917673 | 8.05                  | 0.66                   | −3.60    | 5.00E-05    | 2.86E-04    |

\(^{a}\)FXYD2, FXYD6, and FXYD6-FXYD2 (readthrough) were reported as a single transcriptional locus by Cufflinks.
### Table 4

Top 40 differentially expressed genes between nasal RPE/choroid vs. macular RPE/choroid with q-value < 0.001 and absolute log$_2$(fold-change) ≥ 1.

| Symbol | Description | Chromosome | Start | Stop | Macular RPE/Choroid (FPKM) | Nasal RPE/Choroid (FPKM) | Log2(FC) | P-value | Q-value |
|--------|-------------|------------|-------|------|-----------------------------|---------------------------|----------|---------|---------|
| SCG5   | secretogranin V (7B2 protein) | chr15     | 32933669 | 32989298 | 8.80                       | 117.88                    | 3.74     | 5.00E-05 | 2.86E-04 |
| TFPI2  | tissue factor pathway inhibitor 2 | chr7      | 93514708 | 93545731 | 1.87                       | 23.83                     | 3.67     | 5.00E-05 | 2.86E-04 |
| FHT    | fragile histidine triad | chr3      | 59733016 | 61237133 | 14.79                      | 115.57                    | 2.97     | 5.00E-05 | 2.86E-04 |
| RHO    | rhodopsin | chr3      | 129247481 | 129254187 | 9.49                       | 73.90                     | 2.96     | 5.00E-05 | 2.86E-04 |
| MT1G   | metallothionein 1G | chr16     | 56700645 | 56701980 | 61.09                      | 468.12                    | 2.94     | 5.00E-05 | 2.86E-04 |
| GNAT1  | guanine nucleotide binding protein (G protein), alpha transducing activity polypeptide 1 | chr3 | 50229042 | 50235129 | 2.34                       | 16.38                     | 2.81     | 5.00E-05 | 2.86E-04 |
| AIPL1  | aryl hydrocarbon receptor interacting protein-like 1 | chr17     | 6327058 | 6338519 | 2.44                       | 16.67                     | 2.77     | 5.00E-05 | 2.86E-04 |
| TF     | transferrin | chr3      | 133426380 | 133497850 | 6.84                       | 46.00                     | 2.75     | 5.00E-05 | 2.86E-04 |
| PRSS33 | protease, serine, 33 | chr16     | 2833938 | 2837578 | 1.83                       | 11.43                     | 2.64     | 5.00E-05 | 2.86E-04 |
| COL9A2 | collagen, type IX, alpha 2 | chr1   | 40766086 | 40782939 | 3.20                       | 19.90                     | 2.64     | 5.00E-05 | 2.86E-04 |
| ATP10B | ATPase, class V, type 10B | chr5      | 159990126 | 160365633 | 31.64                      | 191.17                    | 2.60     | 5.00E-05 | 2.86E-04 |
| RCVRN  | recoverin | chr17     | 9801026 | 9808684 | 5.57                       | 31.88                     | 2.52     | 5.00E-05 | 2.86E-04 |
| SAG    | S-antigen; retina and pineal gland (arrestin) | chr2     | 234210734 | 234255703 | 9.56                      | 53.93                     | 2.50     | 5.00E-05 | 2.86E-04 |
| KCNV2  | potassium channel, subfamily V, member 2 | chr9     | 2717525 | 2730037 | 1.88                       | 10.23                     | 2.44     | 5.00E-05 | 2.86E-04 |
| SLC4A10| solute carrier family 4, sodium bicarbonate transporter, member 10 | chr2    | 162480844 | 162841786 | 1.33                       | 6.97                      | 2.39     | 5.00E-05 | 2.86E-04 |
| ALDH1A3| aldehyde dehydrogenase 1 family, member A3 | chr15    | 101420008 | 101456897 | 18.69                      | 96.70                     | 2.37     | 5.00E-05 | 2.86E-04 |
| ECEL1  | endothelin converting enzyme-like 1 | chr2      | 233344356 | 233362207 | 1.43                       | 6.55                      | 2.20     | 5.00E-05 | 2.86E-04 |
| SFRP1  | secreted frizzled-related protein 1 | chr8      | 41119475 | 41166990 | 13.15                      | 60.45                     | 2.20     | 5.00E-05 | 2.86E-04 |
| AKR7A3 | aldo-keto reductase family 7, member A3 (aflatoxin aldehyde reductase) | chr1 | 19592475 | 19616124 | 0.98                       | 4.06                      | 2.06     | 1.50E-04 | 8.01E-04 |
| NRN1   | neuritin 1 | chr6     | 5998227 | 60080788 | 11.86                      | 4.36                      | −1.44    | 5.00E-05 | 2.86E-04 |
| Symbol | Description | Chromosome | Start | Stop | Macular RPE/Choroid (FPKM) | Nasal RPE/Choroid (FPKM) | Log2(FC) | P-value | Q-value |
|--------|-------------|------------|-------|------|---------------------------|--------------------------|----------|---------|---------|
| PRIMA1 | proline rich membrane anchor 1 | chr14 | 94184643 | 94255079 | 11.83 | 4.13 | −1.52 | 5.00E-05 | 2.86E-04 |
| CXCL14 | chemokine (C-X-C motif) ligand 14 | chr5 | 134906370 | 134914969 | 21.66 | 7.49 | −1.53 | 5.00E-05 | 2.86E-04 |
| SCN7A  | sodium channel, voltage-gated, type VII, alpha subunit | chr2 | 167260082 | 167350946 | 9.90 | 3.33 | −1.57 | 5.00E-05 | 2.86E-04 |
| C1QL1  | complement component 1, q subcomponent-like 1 | chr17 | 43036339 | 43046605 | 11.94 | 3.90 | −1.62 | 1.50E-04 | 8.01E-04 |
| TRDN   | triadin | chr6 | 123537304 | 123958601 | 24.71 | 7.99 | −1.63 | 5.00E-05 | 2.86E-04 |
| PKHD1L1| polycystic kidney and hepatic disease 1 (autosomal recessive)-like 1 | chr8 | 110374702 | 110549447 | 9.90 | 3.33 | −1.57 | 5.00E-05 | 2.86E-04 |
| GABRE  | gamma-aminobutyric acid (GABA) A receptor, epsilon | chrX | 151121595 | 151143206 | 6.17 | 1.98 | −1.64 | 5.00E-05 | 2.86E-04 |
| RGS7BP | regulator of G-protein signaling 7 binding protein | chr5 | 63801626 | 63910486 | 6.04 | 1.92 | −1.65 | 5.00E-05 | 2.86E-04 |
| EPHA3  | EPH receptor A3 | chr3 | 89155673 | 89531390 | 11.95 | 3.72 | −1.59 | 5.00E-05 | 2.86E-04 |
| CRHBP  | corticotropin releasing hormone binding protein | chr5 | 76248679 | 76276815 | 6.58 | 1.97 | −1.74 | 5.00E-05 | 2.86E-04 |
| CCL14c | chemokine (C-C motif) ligand 14 | chr17 | 34310691 | 34329084 | 208.78 | 62.35 | −1.74 | 5.00E-05 | 2.86E-04 |
| CPAMD8 | C3 and PZP-like, alpha-2-macroglobulin domain containing 8 | chr19 | 17003760 | 17137625 | 12.55 | 3.69 | −1.77 | 5.00E-05 | 2.86E-04 |
| AQP7P1 | aquaporin 7 pseudogene 1 | chr9 | 67269284 | 67289625 | 14.91 | 4.37 | −1.77 | 5.00E-05 | 2.86E-04 |
| LOC100507387 | | chr5 | 175542798 | 175554408 | 11.01 | 2.77 | −1.99 | 5.00E-05 | 2.86E-04 |
| POSTN | peristin, osteoblast specific factor | chr13 | 38136718 | 38172981 | 5.91 | 1.45 | −2.02 | 5.00E-05 | 2.86E-04 |
| NRXN1  | neurexin 1 | chr2 | 50145624 | 51259674 | 4.18 | 1.00 | −2.06 | 5.00E-05 | 2.86E-04 |
| SULT1E1| sulfotransferase family 1E, estrogen-prefering, member 1 | chr4 | 70706929 | 70725870 | 8.30 | 1.82 | −2.19 | 5.00E-05 | 2.86E-04 |
| WFDC1  | WAP four-disulfide core domain 1 | chr16 | 84303639 | 84363457 | 154.28 | 33.71 | −2.19 | 5.00E-05 | 2.86E-04 |
| TBX15  | T-box 15 | chr1 | 119425665 | 119543988 | 5.11 | 1.08 | −2.24 | 5.00E-05 | 2.86E-04 |

\[a\] ATP10B and LOC285629 were reported as a single transcriptional locus by Cufflinks.

\[b\] AKR7A3 and AKR7L were reported as a single transcriptional locus by Cufflinks.

\[c\] CCL14, CCL15, CCL15-CCL14 (readthrough) were reported as a single transcriptional locus by Cufflinks.
Table 5
Top 40 differentially expressed genes between temporal RPE/choroid vs. macular RPE/choroid with q-value < 0.001 and absolute log2(fold-change) ≥ 1.

| Symbol     | Description                        | Chromosome | Start     | Stop      | Macular RPE/Choroid (FPKM) | Temporal RPE/Choroid (FPKM) | Log2(FC) | P-value       | Q-value       |
|------------|------------------------------------|------------|-----------|-----------|-----------------------------|------------------------------|----------|---------------|---------------|
| TFPI2      | tissue factor pathway inhibitor 2  | chr7       | 93514708  | 93545731  | 1.87                        | 82.08                        | 5.45     | 5.00E-05      | 2.86E-04      |
| SCG5       | secretorgrammin V (7B2 protein)    | chr15      | 32933869  | 32989298  | 8.80                        | 118.78                       | 3.75     | 5.00E-05      | 2.86E-04      |
| FHIT       | fragile histidine triad            | chr3       | 59733016  | 61237133  | 14.79                       | 194.50                       | 3.72     | 5.00E-05      | 2.86E-04      |
| COL9A2     | collagen, type IX, alpha 2         | chr1       | 40766086  | 40789299  | 3.20                        | 25.78                        | 3.01     | 5.00E-05      | 2.86E-04      |
| ALDH1A3    | aldehyde dehydrogenase 1 family,  | chr15      | 101420008 | 101456897 | 18.69                       | 139.08                       | 2.90     | 5.00E-05      | 2.86E-04      |
| SFRP1      | secreted frizzled-related protein  | chr8       | 41119475  | 41166990  | 13.15                       | 91.25                        | 2.79     | 5.00E-05      | 2.86E-04      |
| ATP10Ba    | ATPase, class V, type 10B          | chr5       | 159990126 | 160365633 | 31.64                       | 181.87                       | 2.52     | 5.00E-05      | 2.86E-04      |
| PRSS33     | protease, serine, 33              | chr16      | 28339383  | 2837578   | 1.83                        | 9.95                         | 2.44     | 5.00E-05      | 2.86E-04      |
| ECEL1      | endothelin converting enzyme-like 1| chr2       | 23334536  | 233362207 | 1.43                        | 7.16                         | 2.33     | 5.00E-05      | 2.86E-04      |
| VIP        | vasoactive intestinal peptide      | chr6       | 153054002 | 153080902 | 1.91                        | 9.35                         | 2.29     | 5.00E-05      | 2.86E-04      |
| MT1G       | metallothionein 1G                 | chr16      | 56700645  | 56701980  | 61.09                       | 287.71                       | 2.24     | 5.00E-05      | 2.86E-04      |
| PCOLCE2    | procollagen C-endopeptidase enhancer 2| chr3 | 142536701 | 142608045 | 2.57                        | 12.07                        | 2.23     | 5.00E-05      | 2.86E-04      |
| SFRP4      | secreted frizzled-related protein 4| chr7       | 37945553  | 37956525  | 30.86                       | 125.85                       | 2.03     | 5.00E-05      | 2.86E-04      |
| DCN        | decorin                            | chr12      | 91539034  | 91576806  | 102.16                      | 403.72                       | 1.98     | 5.00E-05      | 2.86E-04      |
| TMEM151A   | transmembrane protein 151A         | chr11      | 66059344  | 66068063  | 1.65                        | 6.39                         | 1.95     | 5.00E-05      | 2.86E-04      |
| RD3        | retinal degeneration 3             | chr1       | 211649102 | 211667124 | 1.39                        | 5.29                         | 1.93     | 5.00E-05      | 2.86E-04      |
| FABP4      | fatty acid binding protein 4, adipocyte | chr8 | 82390731      | 82395473  | 8.71                        | 32.59                        | 1.90     | 5.00E-05      | 2.86E-04      |
| FXYD3      | FXYD domain containing ion transport regulator 3 | chr19 | 35606414 | 35615228  | 24.91                       | 88.14                        | 1.82     | 5.00E-05      | 2.86E-04      |
| PKP1       | plakophilin                         | chr1       | 201252579 | 201302121 | 3.18                        | 10.93                        | 1.78     | 5.00E-05      | 2.86E-04      |
| AQP1b      | aquaporin 1 (Colton blood group)   | chr7       | 30791750  | 30965131  | 142.63                      | 50.74                        | 1.49     | 5.00E-05      | 2.86E-04      |
| NMNAT2     | nicotinamide nucleotide adenylyltransferase 2 | chr1 | 183217073        | 183387634 | 6.38                        | 2.19                         | 1.54     | 5.00E-05      | 2.86E-04      |
| KCNA1      | potassium voltage-gated channel, shaker-related subfamily, beta member 1 | chr3 | 155838336         | 156256927 | 11.14                       | 3.80                         | 1.55     | 5.00E-05      | 2.86E-04      |
| IGJ        | immunoglobulin J polypeptide, linker protein for immunoglobulin alpha and mu polypeptides | chr4 | 71521257        | 71532652  | 70.78                       | 23.84                        | 1.57     | 5.00E-05      | 2.86E-04      |
| ITGA8      | integrin, alpha 8                  | chr10      | 15555950  | 15762323  | 45.26                       | 15.18                        | 1.58     | 5.00E-05      | 2.86E-04      |
| POSTN      | peristin, osteoblast specific factor | chr13 | 38136718        | 38172981  | 5.91                        | 1.94                         | 1.60     | 5.00E-05      | 2.86E-04      |
| LOC100507387 | non-coding RNA                     | chr5       | 175542798 | 175554408 | 11.01                       | 3.40                         | 1.70     | 5.00E-05      | 2.86E-04      |
| Symbol     | Description                                                                 | Chromosome | Start       | Stop        | Macular RPE/Choroid (FPKM) | Temporal RPE/Choroid (FPKM) | Log2(FC) | P-value       | Q-value       |
|------------|------------------------------------------------------------------------------|------------|-------------|-------------|----------------------------|----------------------------|----------|---------------|---------------|
| RGS7BP     | regulator of G-protein signaling 7 binding protein                          | chr5       | 63801626    | 63910486    | 1.82                       | −1.73                     | 5.00E-05 | 2.86E-04      |
| TBX15      | T-box 15                                                                     | chr1       | 119425665   | 119543988   | 1.53                       | −1.74                     | 5.00E-05 | 2.86E-04      |
| CPAMD8     | C3 and PZP-like, alpha-2-macroglobulin domain containing 8                  | chr19      | 17003760    | 17137625    | 3.68                       | −1.77                     | 5.00E-05 | 2.86E-04      |
| PKD1L2     | polycystic kidney disease 1-like 2                                           | chr16      | 81134483    | 81253975    | 1.64                       | −1.78                     | 5.00E-05 | 2.86E-04      |
| SULT1E1    | sulfotransferase family 1E, estrogen-prefering, member 1                    | chr4       | 70706929    | 70725870    | 2.35                       | −1.82                     | 5.00E-05 | 2.86E-04      |
| TMEM132C   | transmembrane protein 132C                                                   | chr12      | 128751947   | 129192460   | 2.35                       | −1.90                     | 5.00E-05 | 2.86E-04      |
| EPHA3      | EPH receptor A3                                                              | chr3       | 89156673    | 89531390    | 2.77                       | −2.11                     | 5.00E-05 | 2.86E-04      |
| CRHBP      | corticotropin releasing hormone binding protein                              | chr5       | 76248679    | 76276815    | 1.45                       | −2.18                     | 5.00E-05 | 2.86E-04      |
| CXCL14     | chemokine (C-X-C motif) ligand 14                                             | chr5       | 134906370   | 134914969   | 4.45                       | −2.28                     | 5.00E-05 | 2.86E-04      |
| CALCB      | calcitonin-related polypeptide beta                                          | chr11      | 15095145    | 15100177    | 0.99                       | −2.97                     | 5.00E-05 | 2.86E-04      |
| WFDCL1     | WAP four-disulfide core domain 1                                             | chr16      | 84303639    | 84363457    | 14.90                      | −3.37                     | 5.00E-05 | 2.86E-04      |
| TRDN       | triadin                                                                      | chr6       | 123537304   | 123958601   | 2.33                       | −3.41                     | 5.00E-05 | 2.86E-04      |

\(^a\) ATP10B and LOC285629 were reported as a single transcriptional locus by Cufflinks.

\(^b\) AQP1, FAM188B, INMT, and INMT-FAM188B (readthrough) were reported as a single transcriptional locus by Cufflinks.
Table 6

All differentially expressed genes between temporal RPE/choroid vs. nasal RPE/choroid with q-value < 0.001 and absolute log$_2$(fold-change) ≥ 1.

| Symbol | Description                                           | Chromosome | Start   | Stop     | Nasal RPE/Choroid (FPKM) | Temporal RPE/Choroid (FPKM) | Log2(FC) | P-value   | Q-value       |
|--------|-------------------------------------------------------|------------|---------|----------|--------------------------|-----------------------------|----------|-----------|---------------|
| MPZ    | myelin protein zero                                   | chr1       | 161274410 | 161279793 | 5.28                     | 40.31                       | 2.93     | 5.00E-05  | 2.86E-04      |
| VIP    | vasoactive intestinal peptide                        | chr6       | 153054002 | 153080902 | 2.62                     | 9.35                        | 1.84     | 5.00E-05  | 2.86E-04      |
| SCN7A  | sodium channel, voltage-gated, type VII, alpha subunit| chr2       | 167260082  | 167350946 | 3.33                     | 6.72                        | 1.01     | 1.50E-04 | 8.01E-04      |
| WFDC1  | WAP four-disulfide core domain 1                     | chr16      | 84303639  | 84363457  | 33.71                    | 14.90                       | -1.18    | 5.00E-05  | 2.86E-04      |
| HBA2   | hemoglobin, alpha 2                                   | chr16      | 222845    | 223709    | 139.35                   | 56.67                       | -1.30    | 5.00E-05  | 2.86E-04      |
| TRDN   | triadin                                               | chr6       | 123537304 | 123958601 | 7.99                     | 2.33                        | -1.78    | 5.00E-05  | 2.86E-04      |
| TULP1  | tubby like protein 1                                  | chr6       | 35465650  | 35480663  | 7.68                     | 2.21                        | -1.80    | 5.00E-05  | 2.86E-04      |
| TF     | transferrin                                           | chr3       | 133426380 | 133497850 | 46.00                    | 12.52                       | -1.88    | 1.00E-04 | 5.49E-04      |
| GUCA1B | guanylate cyclase activator 1B (retina)              | chr6       | 42151021  | 42168689  | 7.48                     | 1.62                        | -2.21    | 5.00E-05  | 2.86E-04      |
| RCVRN  | recoverin                                             | chr17      | 9801026   | 9808864   | 31.88                    | 4.18                        | -2.93    | 5.00E-05  | 2.86E-04      |
| SAG    | S-antigen; retina and pineal gland (arrestin)         | chr2       | 234210734 | 234255703 | 53.93                    | 6.09                        | -3.15    | 5.00E-05  | 2.86E-04      |
| GNAT1  | guanine nucleotide binding protein (G protein), alpha transducing activity polypeptide 1 | chr3 | 50229042 | 50235129 | 16.38 | 1.54 | -3.41 | 5.00E-05 | 2.86E-04 |
| AIPL1  | aryl hydrocarbon receptor interacting protein-like 1  | chr17      | 6327058   | 6338519   | 16.67                    | 1.53                        | -3.44    | 5.00E-05  | 2.86E-04      |
| RHO    | rhodopsin                                             | chr3       | 129247481 | 129254187 | 73.90                    | 6.61                        | -3.48    | 5.00E-05  | 2.86E-04      |

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## Table 7

Top 40 differentially expressed genes between macular RPE/choroid vs. macular retina with q-value < 0.001 and absolute log₂(fold-change) ≥1

| Symbol | Description                                                                 | Chromosome | Start      | Stop       | Macular RPE/Choroid (FPKM) | Macular RPE/Choroid (FPKM) | Log2(FC) | P-value   | Q-value        |
|--------|-----------------------------------------------------------------------------|------------|------------|------------|-----------------------------|-----------------------------|----------|-----------|----------------|
| PRRX2  | paired related homeobox 2                                                  | chr9       | 132427911  | 132484952  | 0.00                        | 322.59                      | Inf      | Inf       | 5.00E-05       |
| PITX1  | paired-like homeodomain 1                                                  | chr5       | 134363350  | 134370461  | 0.00                        | 60.99                       | Inf      | Inf       | 5.00E-05       |
| ABCB5  | ATP-binding cassette, subfamily B (MDR/TAP), member 5                       | chr7       | 20655244   | 20796642   | 0.00                        | 21.83                       | Inf      | Inf       | 5.00E-05       |
| CCL23  | chemokine (C-C motif) ligand 2                                             | chr17      | 34340096   | 34345026   | 0.00                        | 21.39                       | Inf      | Inf       | 5.00E-05       |
| CPXM1  | carboxypeptidase X (M14 family), member 1                                   | chr20      | 2774714    | 2781292    | 0.00                        | 19.60                       | Inf      | Inf       | 5.00E-05       |
| LOC340357 | long non-coding RNA                                                            | chr8      | 12623570   | 12675830   | 0.00                        | 14.19                       | Inf      | Inf       | 5.00E-05       |
| GZMK   | granzyme K (granzyme 3; tryptase II)                                       | chr5       | 54320106   | 54329960   | 0.00                        | 9.88                        | Inf      | Inf       | 5.00E-05       |
| SULT1E1 | sulfotransferase family 1E, estrogen-preferring, member 1                  | chr4       | 70706929   | 70725870   | 0.00                        | 8.30                        | Inf      | Inf       | 5.00E-05       |
| CD3E   | CD3e molecule, epsilon (CD3-TCR complex)                                   | chr11      | 118175294  | 118186890  | 0.00                        | 7.73                        | Inf      | Inf       | 5.00E-05       |
| KCNK17 | potassium channel, subfamily K, member 17                                   | chr6       | 39266776   | 39282237   | 0.00                        | 5.88                        | Inf      | Inf       | 5.00E-05       |
| LINC00226 | long intergenic non-protein coding RNA 226                               | chr14      | 106573231  | 106791526  | 0.00                        | 4.93                        | Inf      | Inf       | 5.00E-05       |
| CTSG   | cathepsin G                                                                 | chr14      | 25042723   | 25045466   | 0.00                        | 4.32                        | Inf      | Inf       | 5.00E-05       |
| DEFB131 | defensin, beta 131                                                        | chr4       | 9446259    | 9452240    | 3.61                        | 0.00                        | −Inf     | Inf       | 5.00E-05       |
| LRTM2  | leucine-rich repeats and transmembrane domains 2                            | chr12      | 2032895    | 2032895    | 4.46                        | 0.00                        | −Inf     | 1.00E-04  | 5.49E-04       |

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| Symbol | Description                                                          | Chromosome | Start (FPKM) | Stop (FPKM) | Log2(FC) | P-value  | Q-value  |
|--------|---------------------------------------------------------------------|------------|--------------|-------------|----------|----------|----------|
| DSCR8  | Down syndrome critical region gene 8                               | chr21      | 3940544      | 39528605    | 5.99     | 0.00     | -Inf     |
|        |                                                                    |            |              |             |          |          |          |
| TRPC7  | transient receptor potential cation channel, subfamily C, member 7 | chr5       | 135548424    | 135732845   | 7.25     | 0.00     | -Inf     |
|        |                                                                    |            |              |             |          |          |          |
| CCDC172| coiled-coil domain containing 172                                  | chr10      | 118083939    | 118139551   | 7.56     | 0.00     | -Inf     |
|        | potentially novel                                                   | chr8       | 55506068     | 55508509    | 8.16     | 0.00     | -Inf     |
|        |                                                                    | chr1       | 23280951     | 23299340    | 9.02     | 0.00     | -Inf     |
| FEZF2  | FEZ family zinc finger 2                                            | chr3       | 62355295     | 62360692    | 9.07     | 0.00     | -Inf     |
|        | potentially novel                                                   | chr18      | 5847207      | 5876306     | 9.92     | 0.00     | -Inf     |
| POU4F2 | POU class 4 homeobox 2                                              | chr4       | 147560044    | 147563623   | 11.13    | 0.00     | -Inf     |
|        | potentially novel                                                   | chr5       | 178422323    | 178423333   | 12.42    | 0.00     | -Inf     |
| CACNG3 | calcium channel, voltage-dependent, gamma subunit 3                | chr16      | 24266873     | 24373737    | 16.08    | 0.00     | -Inf     |
|        | potentially novel                                                   | chr12      | 9727536      | 9728249     | 30.87    | 0.00     | -Inf     |
Table 8

Top 40 differentially expressed genes between nasal RPE/choroid vs. nasal retina with q-value < 0.001 and absolute log2(fold-change) ≥ 1.

| Symbol | Description | Chromosome | Start | Stop | Nasal Retina (FPKM) | Nasal RPE/Choroid (FPKM) | Log2(FC) | P-value | Q-value |
|--------|-------------|-------------|-------|------|---------------------|--------------------------|----------|---------|---------|
| PITX1  | paired-like homeodomain 1 | chr5 | 134363350 | 134370461 | 0.00 | 19.53 | Inf | 5.00E-05 | 2.86E-04 |
| LOC340357 | long non-coding RNA | chr8 | 12623570 | 12675830 | 0.00 | 10.88 | Inf | 5.00E-05 | 2.86E-04 |
| GZMK  | granzyme K (granzyme 3; tryptase II) | chr5 | 54320106 | 54329960 | 0.00 | 8.65 | Inf | 5.00E-05 | 2.86E-04 |
| KCNK17 | potassium channel, subfamily K, member 17 | chr6 | 39266776 | 39282237 | 0.00 | 8.45 | Inf | 5.00E-05 | 2.86E-04 |
| CCL23 | chemokine (C-C motif) ligand 23 | chr17 | 34340096 | 34345026 | 0.00 | 7.03 | Inf | 5.00E-05 | 2.86E-04 |
| TEX41  | testis expressed 41 (non-protein coding) | chr2 | 145245533 | 146021001 | 0.00 | 5.35 | Inf | 5.00E-05 | 2.86E-04 |
| KLKB1 | killer cell lectin-like receptor subfamily B, member 1 | chr12 | 9747869 | 9760497 | 0.00 | 3.53 | Inf | 5.00E-05 | 2.86E-04 |
| CCL13 | chemokine (C-C motif) ligand 13 | chr17 | 32683470 | 32685629 | 0.00 | 3.52 | Inf | 5.00E-05 | 2.86E-04 |
| LMX1B | LIM homeobox transcription factor 1, beta | chr9 | 129376673 | 129463311 | 0.00 | 2.93 | Inf | 5.00E-05 | 2.86E-04 |
| SLAMF7 | SLAM family member 7 | chr1 | 160709032 | 160725021 | 0.00 | 1.57 | Inf | 5.00E-05 | 2.86E-04 |
| ZG16B | zymogen granule protein 16B | chr16 | 2880172 | 2882285 | 0.00 | 1.53 | Inf | 5.00E-05 | 2.86E-04 |
| SAA1  | serum amyloid A1 | chr11 | 18287807 | 18291523 | 0.45 | 2255.58 | 12.30 | 5.00E-05 | 2.86E-04 |
| PLAG2A | phospholipase A2, group IIA (platelets, synovial fluid) | chr1 | 20301923 | 20306932 | 0.27 | 553.86 | 11.01 | 5.00E-05 | 2.86E-04 |
| ABCB5 | ATP-binding cassette, sub-family B (MDR/TAP), member 5 | chr7 | 20655244 | 20796642 | 0.01 | 18.83 | 10.65 | 1.50E-04 | 8.01E-04 |
| PLVAP | plasmalemma vesicle associated protein | chr19 | 17462251 | 17488137 | 0.09 | 122.71 | 10.47 | 5.00E-05 | 2.86E-04 |
| KCNC2 | potassium voltage-gated channel, Shaw-related subfamily, member 2 | chr12 | 75433857 | 7560328 | 17.88 | 0.18 | −6.60 | 5.00E-05 | 2.86E-04 |
| NEFM  | neurofilament, medium polypeptide | chr8 | 24771273 | 24776612 | 169.15 | 1.71 | −6.63 | 5.00E-05 | 2.86E-04 |
| CNGA3 | cyclic nucleotide gated channel alpha 3 | chr2 | 98703294 | 99013798 | 4.16 | 0.04 | −6.67 | 5.00E-05 | 2.86E-04 |
| RASGRF1 | Ras protein-specific guanine nucleotide-releasing factor 1 | chr15 | 79252288 | 79383265 | 14.36 | 0.14 | −6.69 | 5.00E-05 | 2.86E-04 |
| CACNG5 | calcium channel, voltage-dependent, gamma subunit 5 | chr17 | 64831229 | 64898071 | 19.03 | 0.18 | −6.72 | 5.00E-05 | 2.86E-04 |
| ABL4  | ATP/GTP binding protein-like 4 | chr1 | 48998369 | 50489626 | 2.06 | 0.02 | −6.76 | 5.00E-05 | 2.86E-04 |
| CRYAA | crystallin, alpha A | chr21 | 44570160 | 44592913 | 318.89 | 1.65 | −7.59 | 5.00E-05 | 2.86E-04 |
| C6orf7 | chromosome 6 open reading frame 7 | chr6 | 80472023 | 80580137 | 2.24 | 0.01 | −8.22 | 5.00E-05 | 2.86E-04 |

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| Symbol | Description                          | Chromosome | Start      | Stop        | Log2(FC) | P-value | Q-value | Nasal Retina (FPKM) | Nasal RPE/Choroid (FPKM) |
|--------|-------------------------------------|------------|------------|-------------|----------|---------|---------|---------------------|---------------------------|
|        | potentially novel                    | chr6       | 89881239   | 89881908    | 1.30     | −Inf    | 5.00E-05 | 2.86E-04            |                           |
| LEMD1  | LEM domain containing 1             | chr1       | 205342379  | 205436588   | 1.54     | −Inf    | 5.00E-05 | 2.86E-04            |                           |
|        | potentially novel                    | chr9       | 32865800   | 32909556    | 2.00     | −Inf    | 5.00E-05 | 2.86E-04            |                           |
|        | potentially novel                    | chr17      | 5000474    | 5000915     | 2.59     | −Inf    | 5.00E-05 | 2.86E-04            |                           |
|        | potentially novel                    | chr11      | 35999999   | 3602427     | 2.82     | −Inf    | 5.00E-05 | 2.86E-04            |                           |
|        | potentially novel                    | chr1       | 10873924   | 10874785    | 3.12     | −Inf    | 5.00E-05 | 2.86E-04            |                           |
|        | potentially novel                    | chr16      | 84273764   | 84281615    | 3.15     | −Inf    | 5.00E-05 | 2.86E-04            |                           |
| C1orf141| chromosome 1 open reading frame 141| chr1       | 67557494   | 67607567    | 3.55     | −Inf    | 5.00E-05 | 2.86E-04            |                           |
|        | potentially novel                    | chr10      | 81657061   | 81657275    | 3.67     | −Inf    | 5.00E-05 | 2.86E-04            |                           |
|       | defensin, beta 131                  | chr4       | 9446259    | 9452240     | 4.55     | −Inf    | 5.00E-05 | 2.86E-04            |                           |
Table 9

Top 40 differentially expressed genes between temporal RPE/choroid vs. temporal retina with q-value < 0.001 and absolute log2(fold-change) ≥ 1.

| Symbol     | Description                                                                 | Chromosome | Start  | Stop   | Temporal Retina (FPKM) | Temporal RPE/Choroid (FPKM) | Log2(FC) | P-value | Q-value |
|------------|------------------------------------------------------------------------------|------------|--------|--------|------------------------|------------------------------|----------|---------|---------|
| PITX1      | paired-like homeodomain 1                                                   | chr5       | 134363350 | 134370461 | 0.00 | 19.83 | Inf | 5.00E-05 | 2.86E-04 |
| LOC340357  | long non-coding RNA                                                         | chr8       | 12623570 | 12675830 | 0.00 | 14.87 | Inf | 5.00E-05 | 2.86E-04 |
| PAX3       | paired box 3                                                                 | chr2       | 223064605 | 223169936 | 0.00 | 13.21 | Inf | 5.00E-05 | 2.86E-04 |
| AKR1B10    | aldo-keto reductase family 1, member B10 (aldose reductase)                  | chr7       | 134200788 | 134226166 | 0.00 | 8.67  | Inf | 5.00E-05 | 2.86E-04 |
| GZMK       | granzyme K (granzyme 3; trypase II)                                          | chr5       | 543201066 | 543299600 | 0.00 | 8.60  | Inf | 5.00E-05 | 2.86E-04 |
|            | potentially novel                                                             | chr1       | 170632134 | 170633074 | 0.00 | 8.30  | Inf | 5.00E-05 | 2.86E-04 |
| FOXD3      | forkhead box D3                                                              | chr1       | 63786575  | 63790797 | 0.00 | 6.14  | Inf | 5.00E-05 | 2.86E-04 |
| TEX41      | testis expressed 41 (non-protein coding)                                     | chr2       | 145425533 | 146021001 | 0.00 | 5.47  | Inf | 5.00E-05 | 2.86E-04 |
| CLEC10A    | C-type lectin domain family 10, member A                                     | chr17      | 6977855   | 6983826  | 0.00 | 4.53  | Inf | 5.00E-05 | 2.86E-04 |
| LCK        | LCK proto-oncogene, Src family tyrosine kinase                               | chr1       | 32716839  | 32751766 | 0.00 | 3.57  | Inf | 5.00E-05 | 2.86E-04 |
| LMX1B      | LIM homeobox transcription factor 1, beta                                    | chr9       | 129376673 | 129463311 | 0.00 | 3.50  | Inf | 5.00E-05 | 2.86E-04 |
| S1PR5      | sphingosine-1-phosphate receptor 5                                           | chr19      | 10623417 | 10628668 | 0.00 | 3.27  | Inf | 5.00E-05 | 2.86E-04 |
| CLIC3      | chloride intracellular channel 3                                             | chr9       | 139889059 | 139891024 | 0.00 | 3.18  | Inf | 5.00E-05 | 2.86E-04 |
| CCL13      | chemokine (C-C motif) ligand 13                                              | chr17      | 32683470  | 32685629 | 0.00 | 2.56  | Inf | 5.00E-05 | 2.86E-04 |
| C1orf141   | chromosome 1 open reading frame 141                                          | chr1       | 67557494  | 67607567 | 3.83  | 0.00  | −Inf | 5.00E-05 | 2.86E-04 |
| NAT16      | N-acetyltransferase 16 (GCN5-related, putative)                              | chr7       | 100813667 | 100823557 | 4.36  | 0.00  | −Inf | 5.00E-05 | 2.86E-04 |
| C1orf11    | chromosome 16 open reading frame 11                                          | chr16      | 610179    | 615529   | 4.39  | 0.00  | −Inf | 5.00E-05 | 2.86E-04 |
| DEFB131    | defensin, beta 131                                                          | chr4       | 9446259   | 9452240  | 5.46  | 0.00  | −Inf | 5.00E-05 | 2.86E-04 |
| Symbol | Description       | Chromosome | Start      | Stop       | Temporal Retina (FPKM) | Temporal RPE/Choroid (FPKM) | Log2(FC) | P-value    | Q-value    |
|--------|-------------------|------------|------------|------------|------------------------|----------------------------|----------|------------|------------|
|        | potentially novel | chr7       | 21181327   | 21253288   | 6.30                   | 0.00                       | −Inf     | 5.00E-05   | 2.86E-04   |
|        | potentially novel | chr1       | 23280951   | 23299340   | 6.93                   | 0.00                       | −Inf     | 5.00E-05   | 2.86E-04   |
| MIR124-3 | microRNA 124-3   | chr20      | 61808787   | 61813324   | 6.97                   | 0.00                       | −Inf     | 5.00E-05   | 2.86E-04   |
|        | potentially novel | chr20      | 61785077   | 61787572   | 9.70                   | 0.00                       | −Inf     | 5.00E-05   | 2.86E-04   |
|        | potentially novel | chr8       | 55506068   | 55508509   | 11.21                  | 0.00                       | −Inf     | 5.00E-05   | 2.86E-04   |
|        | potentially novel | chr5       | 178422323  | 178423333  | 11.40                  | 0.00                       | −Inf     | 5.00E-05   | 2.86E-04   |
|        | potentially novel | chr9       | 2734043    | 2734455    | 16.22                  | 0.00                       | −Inf     | 5.00E-05   | 2.86E-04   |
| DEFB119 | defensin, beta 119 | chr20    | 29964965   | 29978452   | 56.91                  | 0.00                       | −Inf     | 5.00E-05   | 2.86E-04   |
|        | potentially novel | chr12      | 9727536    | 9728249    | 58.97                  | 0.00                       | −Inf     | 5.00E-05   | 2.86E-04   |