Supplementary Tables:

Supplementary Table S1. Primer sequences

Supplementary Table S2A. MicroRNAs in Retina.

Supplementary Table S2B. MicroRNAs in RPE/choroid.

Supplementary Table S3A. snoRNAs in Retina.

Supplementary Table S3B. snoRNAs in RPE/choroid.

Supplementary. Table S3C. Polycistronic snoRNA cluster from which sno-RNAs are derived.

Supplementary Table S4. Expression of novel microRNAs in other mouse tissues and cells.

Supplementary Table S5A. Predicted significantly altered pathways for highly expressed, retina-enriched microRNAs by DIANAmiRPath V2.0.

Supplementary Table S5B. Predicted significantly altered pathways for highly expressed, RPE/choroid-enriched microRNAs by DIANAmiRPath V2.0.

Supplementary Table S6A. Predicted target genes for canonical and isomiR sequence of miR-183-5p.

Supplementary Table S6B. Predicted target genes for canonical and isomiR sequence of miR-133a-1-3p.
Supplementary Figure S1. A) Length distribution of sequence reads from retina; most reads were between 21-23 nt. B) Pie charts indicating the percentages of unique sequences or total raw reads mapping to different classes of ncRNAs. Although only a quarter of the unique sequences mapped to microRNAs, these accounted for 81% of the total number of reads, meaning that microRNAs are generally represented by more reads (ie. expressed at a higher level) than the other RNA species in our libraries.
Supplementary Figure S2. RT-qPCR validation of microRNA expression. Quantitative RT-qPCR was performed upon equal quantities of RNA from retina and RPE/choroid to measure the relative expression of miR-182-5p; miR-183-5p; miR-181a-5p; miR-143-3p; miR-22-3p; and miR-133a-3p. A) Ct values were analysed using REST2009 software (miR-99b-5p which was shown by deep sequencing to have similar expression in retina and RPE/choroid was used as a reference). The relative expression of the microRNAs in the original retina and RPE/choroid RNA samples matched the pattern determined by deep sequencing. The expression was remarkably consistent in a set of biological replicates (retina: n=3; RPE/choroid=3). (* p<0.05; ** p<0.01). B) Normalisation of the RT-qPCR data to account for apparently lower efficiency of amplification in the RPE/choroid samples highlights the similarity with the relative microRNA expression values detected by deep sequencing.
Supplementary Figure S3. The frequencies of individual isomiRs of miR-182-5p differed between retina and RPE/choroid.

**Suppl. Fig. S4**

Supplementary Figure S4. Alignment of sequences detected in both retina and RPE/choroid (seq1-3) with primate miR-1260 orthologs and mouse tRNA_leu.
**Suppl. Fig. S5**

A) **Sno_Retina1-5p** ATTTTCCTTGGCTATTCTGATA  **Sno_Retina1-3p** TTAGTTTTAAGTCATGGGTTTGT

(reads: 30)

Minimum free energy -20.01 kcal/mol.

B) **Sno RPE1-5p** CCTCACAGGGTTGGGACTTTTGCA  **Sno_RPE1-3p** AACTATGGGGTGCAGCTGGGTGCTGAG

(reads: 75)

Minimum free energy -33.69 kcal/mol.
Supplementary Figure S5. Two putative novel microRNAs overlapped snoRNAs (Sno_Retina1 and Sno_RPE1). Mapping to the mouse genome showed conservation among mammalian species. The putative pre-miRs have stable predicted secondary structures.