SUPPLEMENTARY DATA

Supplementary Figure 1. Distributions of lncRNA expression profiling in mouse ocular tissues at birth and in 8-week-old adult mice. After the normalization, the distributions of log2-signal value among different samples were shown. The box plots consist of boxes with a central line and two tails. The central line represents the median of the data, whereas the tails represent the upper and lower quartiles.

Supplementary Figure 2. Number of the up-regulated and down-regulated differentially expressed lncRNAs (adult vs P0) in each developing ocular tissue. Red columns indicated the up-regulated lncRNAs in adult (≥ 2-fold compared to P0). Green columns represent the down-regulated lncRNAs in adult (≤ 0.5-fold compared to P0).
Supplementary Figure 3. Heat map of protein-coding gene clusters across 12 ocular tissues. These genes were selected on the basis of a difference in expression of ≥2-fold (relative to expression in all other subsets) from newborn and adult mice, respectively. Order of lows and columns represent gene clusters resulting from K-means clustering; color intensity (key) indicates z-score log₂-normalized raw counts; gradual color columns on the right represent samples as shown in Fig. 1A; numbers at top left indicate percent assigned to specific clusters.

Supplementary Figure 4. Ratio of the average expression level of tissue-specific lncRNAs compared to that of protein-coding genes in each ocular tissue subset.
Supplementary Figure 5. GO enrichment analysis of protein-coding genes proximal to lncRNA signatures in mouse ocular tissues. Here are shown fifteen of the most significant overrepresented GO biological process terms in the cornea (A), lens (B), RPE (C), choroid (D) and sclera (E). Blue bars (extreme left) represent terms enriched among protein-coding genes proximal to distinctive lncRNA signatures in maturing tissues. Green bars (middle) illustrate enriched terms among genes proximal to retina-specific lncRNAs from newborn (P0) whereas pink (right) shows terms for targets proximal to retina-specific lncRNAs from normal adult mice. Abbreviations are used as follows: “RO” is “Regulation Of”, “PRO” is “Positive Regulation Of”, “NRO” is “Negative Regulation Of”, “FGFR” is “Fibroblast Growth Factor Receptor”, “ILGFR” is “Insulin-Like Growth Factor Receptor”, “PDGFR” is “Platelet-Derived Growth Factor Receptor”, “VEGFR” is “Vascular Endothelial Growth Factor Receptor”, “TGFBR” is “Transforming Growth Factor Beta Receptor”, “CDPS” is
“Cyclin-Dependent Protein Serine”, “TKA” is “Threonine Kinase Activity”, “RPP” is “RNA Polymerase II Promoter”, “CRTC3” is “Cellular Response To Chemical Stimulus”, “PMCAM” is “Plasma Membrane Cell Adhesion Molecules”, “CRTGS” is “Cellular Response To Glucose Stimulus” and “TRPTK” is “Transmembrane Receptor Protein Tyrosine Kinase”.

Supplementary Table 1. RNA samples for the microarray experiments.

Supplementary Table 2. Primers used in quantitative PCR.

Supplementary Table 3. The top thirty of the most highly expressed lncRNAs in each ocular tissue subset.

Supplementary Table 4. Tissue-specific lncRNA signatures in six murine ocular tissues.