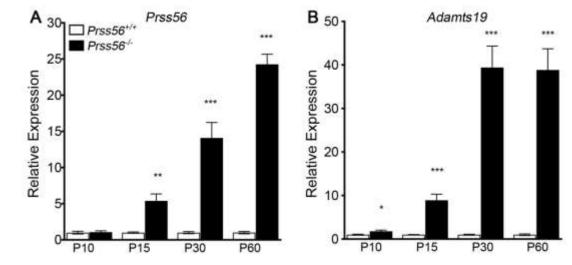
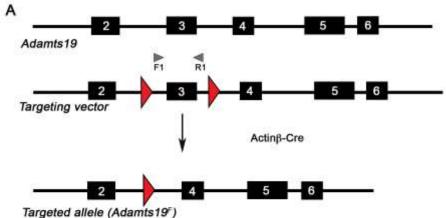
SUPPLEMENTAL FIGURES



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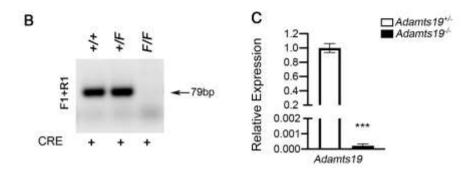
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Figure S1. *Prss56* and *Adamts19* expression in *Prss56^{-/-}* retina across ages. (A-B) 3 Graphs showing quantification of *Prss56* (A) and *Adamts19* (B) mRNA levels using qPCR 4 5 in wild-type and mutant retina at different developmental stages. A significant increase in 6 Adamts19 mRNA levels was detected as early as P10 in Prss56 mutant retina (B), while 7 upregulation in *Prss56* mRNA was first observed at P15 in the mutant retina (A). The 8 magnitude of the increase of both Prss56 and Adamts19 expression became more 9 pronounced with age in the mutant retina. Prss56 and Adamts19 expression were 10 normalized to the expression of three housekeeping genes (Hprt1, Actb1, and Mapk1). 11 Data are presented as fold expression relative to wild-type (mean ± SEM), N=4 to 6/group. 12 *p<0.05; **p<0.01; ***p<0.001, t-test. The *Prss56* qPCR data in **A** were previously 13 published in Figure 4 of Paylakhi et al. 2018 [13]. 14



Targeteu allele (Aualitis 15)

Adamts19 null allele generated by Cre-mediated recombination

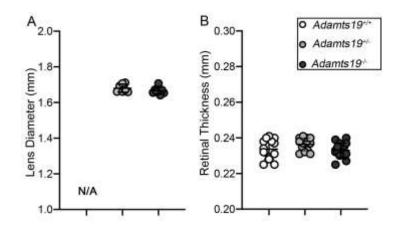


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17 Figure S2. Generation of *Adamts19* mutant mice allele.

(A) The LoxP site flanks the exon 3 of the Adamts19^F allele. In presence of Cre 18 recombinase, the Adamts19 exon is deleted resulting in a frameshift mutation and 19 20 premature stop codon, rendering the Adamts19 catalytically inactive. (B-C) Adamts19 21 exon 3 excisions was confirmed by PCR as well as qPCR. (B) PCR amplification of DNA 22 from wild-type (Adamts19^{+/+}, lane 1), heterozygous (Adamts19^{F/+,} lane 2), or homozygous (Adamts19^{F/F}) mice. PCR reactions were performed using primers amplifying regions of 23 intron 2 and exon 3. The deletion of exon 3 from the Adamts19^{F/F} allele gives no PCR 24 product. using primers amplifying a region of intron 2 and exon 3 gives no PCR product 25 from DNA from Adamts19^{F/F} mice. (C) qPCR analysis employing primers amplifying exon 26 3 of Adamts19 further confirm that Adamts19 transcript from Adamts19-/-; Prss56 -/- retina 27 28 lacks exon 3.

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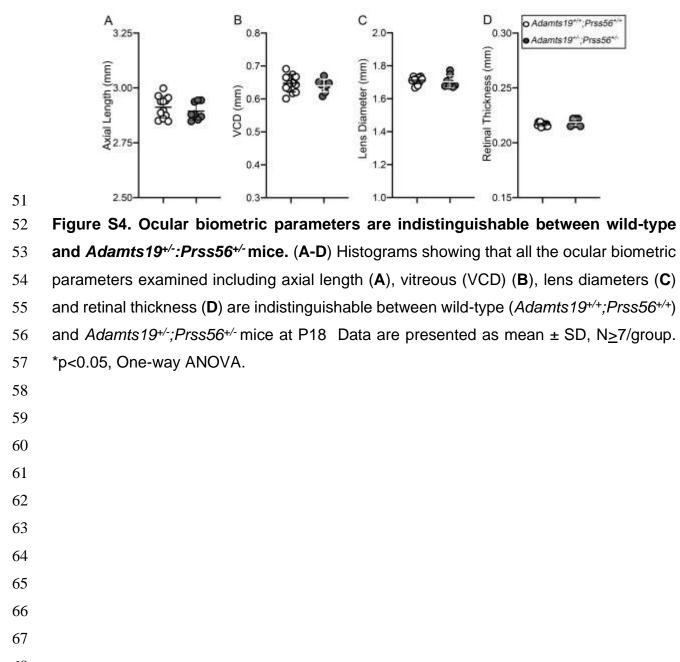
32 Figure S3. Ocular biometric analysis in *Adamts19* mutant mice

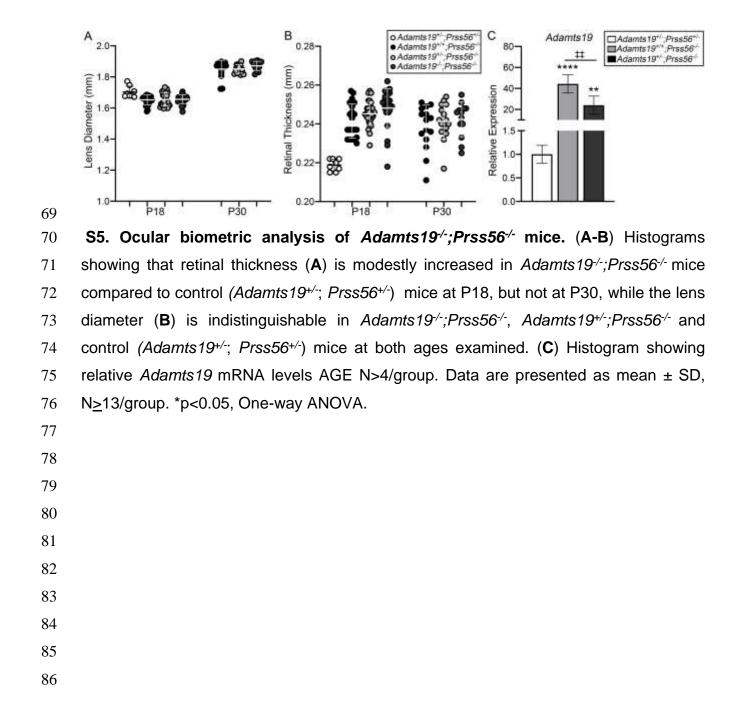
33 Histograms showing that ocular the lens diameter (A) and retinal thickness (B) were

34 indistinguishable in *Adamts19^{-/-};Prss56^{-/-}*, *Adamts19^{+/-};Prss56^{-/-}* and control *Adamts19^{+/-};*

35 Prss56^{+/-} mice. Data are presented as mean ± SD, N≥7/group. *p<0.05, One-way

- 36 ANOVA.





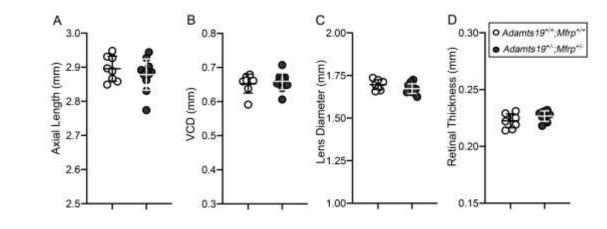
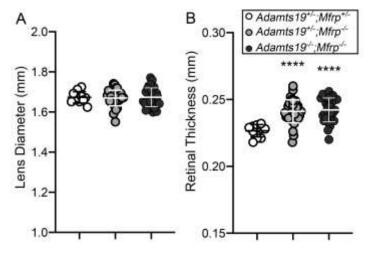


Figure S6. Ocular biometric parameters are indistinguishable between wild-type and *Adamts19*^{+/-}:*Mfrp*^{+/-} mice. (A-D) Histograms showing that all the ocular biometric parameters examined including axial length (A), vitreous (VCD) (B), lens diameters (C), and retinal thickness (D) are indistinguishable between wild-type (*Adamts19*^{+/+};*Mfrp*^{+/+}) and *Adamts19*^{+/-};*Mfrp*^{+/-} mice at P18. Data are presented as mean \pm SD, N \geq 7/group. *p<0.05, One-way ANOVA.

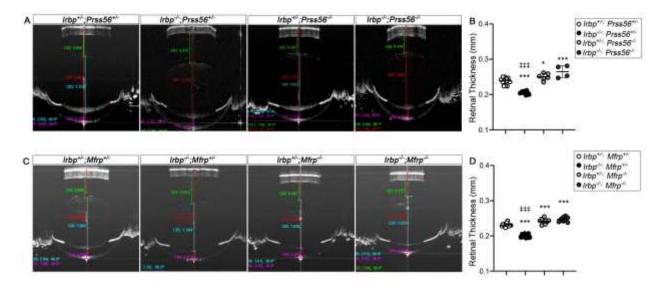
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Figure S7. Ocular biometric analysis of Adamts19^{-/-};*Mfrp*^{-/-} mice. (A-C) Histograms showing that the lens diameter (A) are indistinguishable in Adamts19^{+/-}; *Mfrp*^{-/-}, Adamts1⁻ $^{/-}$; *Mfrp*^{-/-}, and control (Adamts19^{+/-}; *Mfrp*^{+/-}) mice, while the retinal thickness (B) is increased in both Adamts19^{+/-}; *Mfrp*^{-/-} and Adamts1^{-/-};*Mfrp*^{-/-} mice compared to control Adamts19^{+/-}; *Mfrp*^{+/-} mice at P18. Data are presented as mean ± SD, N≥11/group. *****p<0.0001, One-way ANOVA.

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119 Figure S8.

120 Ocular biometric analysis of *Irbp* mutant mice following *Prss56* inactivation

(A) Representative OCT images showing that ocular axial length (quantified in Fig. 6A) 121 122 and VCD (quantified in Fig. 6 B) are increased in *Irpb* mutant mice (*Irpb*^{-/-}; *Prss56*^{+/-}) and reduced in *Prss56* mutant mice compared to control *Irpb+/-; Prss56+/-* control mice at P18. 123 124 In contrast, retinal thickness (**B**) were reduced in *Irpb* mutant mice (*Irpb^{-/-}: Prss56^{+/-}*) and 125 retinal thickness was increased in Prss56 mutant and Irbp;Prss56 double mutant mice 126 (Irpb+/-: Prss56-/- and Irbp-/-: Prss56-/-, respectively) compared to control Irpb+/-: Prss56+/mice. Data are presented as mean ± SD, N>4/group. **p<0.01; ***p<0.0001 (compared 127 to controls); ^{‡‡‡}p<0.001 (compared to double mutant *Irpb*^{-/-};*Prss56*^{-/-} mice), One-way 128 129 Anova.

130 Biometric analysis of *Irbp* mutant mice following *Mfrp* inactivation (C) 131 Representative OCT images showing that ocular axial length (quantified in Fig. 6 C) and 132 vitreous chamber depth (VCD, quantified in Fig. 6 D) are increased in Irpb mutant mice (Irpb-/-: Mfrp+/-) and reduced in Mfrp mutant and Irbp:Mfrp double mutant mice (Irpb+/-: 133 *Mfrp^{-/-}* and *Irbp^{-/-}*; *Mfrp^{-/-}*, respectively) compared to control *Irpb^{+/-}*; *Mfrp^{+/-}* mice at P18. In 134 135 contrast, and retinal thickness (**D**) were reduced in *Irpb* mutant mice (*Irpb*^{-/-}; *Mfrp*^{+/-}) and retinal thickness was increased in *Mfrp* mutant and *Irbp;Mfrp* double mutant mice (*Irpb*^{+/-} 136 ; Mfrp^{-/-} and Irbp^{-/-}; Mfrp^{-/-}, respectively) compared to control Irpb^{+/-}; Mfrp^{+/-} mice. Data are 137 138 presented as mean ± SD. N>8/group. **p<0.01: ***p<0.0001 (compared to controls): ^{‡‡‡}p<0.001 (compared to double mutant *Irpb^{-/-}*; *Mfrp^{-/-}* mice), One-way Anova. 139

141 Table S1. List of genotyping primers

Allele (mouse strain)	Primer name	Primer sequence
Prss56 ^{g/cr4} (C57BL/6.Cq-Prss56 glcr4/SjJ)	Prss56 glcr4 F1	5' TGGCTCCAGAAACCAAAGCCGGAA GAGCGCCCGGAAACAAAGAGT 3'
	Prss56 glcr4 F2 Prss56 glcr4 R	5' GCGGCGCCCGGAAACAAAAGGA 3' 5' TCCTGGAAGAGAGGGAGTGA 3'
Prss56 ^{cre} (C57BI/6.Cg-Prss56tm)	Prss56 Cre F Prss56 Cre R WT Prss56 Cre R Cre	5' CAG GGC ATC GTT TCC CTG AG 3' 5' GAC AGG CGC GTG TAC AGT GG 3' 5' CCA TGA GTG AAC GAA CCT GG 3'
<i>Egr1</i> ≁ (C57BL/6. Egr1tm1Jmi/J)	EGR1 common R EGR1 MUT F EGR1 WT F	5' GGG CAC AGG GGA TGG GAA3 5' AAC CGG CCC AGC AAG ACA 3' 5' CTC GTG CTT TAC GGT ATC G 3'
<i>Adamts19[≁]</i> (Adamts19tm4a(EUCOMM)Wtsi)	Adamts19_244_F Adamts19_244_R CAS_R1_Term	5' AGA AGG GAA CAA ACA CAA CAA GTG 3' 5' AGT TAG CCT GAG CCT GTG TGG 3' 5' TCG TGG TAT CGT TAT GCG GCC 3'
<i>Mfrp[≁]</i> (B6.C3Ga-Mfrprd6/J)	Mfrp F Mfrp R	5' CAC TAC CAC CCC AGC AAG GAC 3' 5' CTT CTC CAG AGA GTG CCC TTG 3'
<i>lrbp[≁]</i> (B6.129P2-Rbp3tm1Gil/J)	Common IRBP MF IRBP WT IRBP	5' CAT ATC CAC ACC TGC CAA CA 3' 5' GCT ACT TCC ATT TGT CAC GTC C 3' 5' GGA CCC ACA CCT GAA GAC AG3'
Ubc-Cre (C57Bl/6.Cg-Tg(UBC-Cre/ERT2)1Ejb)	Cr1 Cr2	5' TGA TGA GGT TCG CAA GAA CC 3' 5' CCA TGA GTG AAC GAA CCT GG 3'

148 Table S2. List of qPCR primers

Gene	Forward Primer	Reverse Primer
House Keeping Genes		
Actb	5' CCCTGAGGAGCACCCTGTGC 3'	5' GGCTGGGGTGTTGAAGGTCT 3'
Hprt1	5' TGCCGAGGATTTGGAAAAAGTGT 3'	5' GTGATGGCCTCCCATCTCCT 3'
Mapk1	5' TTGAACAGGCTCTGGCCCAC 3'	5' TGAATGGCGCTTCAGCAATGG 3'
Genes of Interest		
Prss56	5' ACCTGGACGCCCTAGACCTC 3'	5' TGTTGGCAACGCCTTGATGT 3'
Adamts19	5' `TGCTGAAGACAACGGCCTGA 3'	5' CAGCACAGGATGGGTGGTCA 3'
Adamts19 Ex3	5' GAGGACTTCCTATTCATTGAGCCA 3'	5' CCTGTATAAACGGTGCGGGT 3'