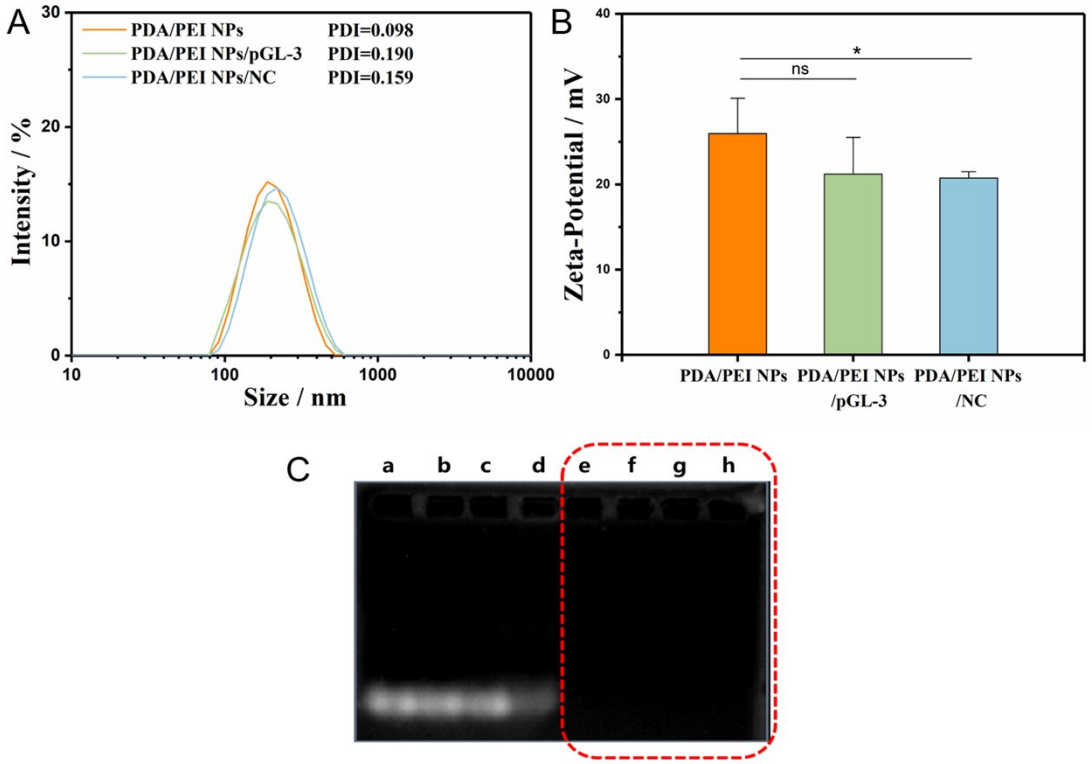
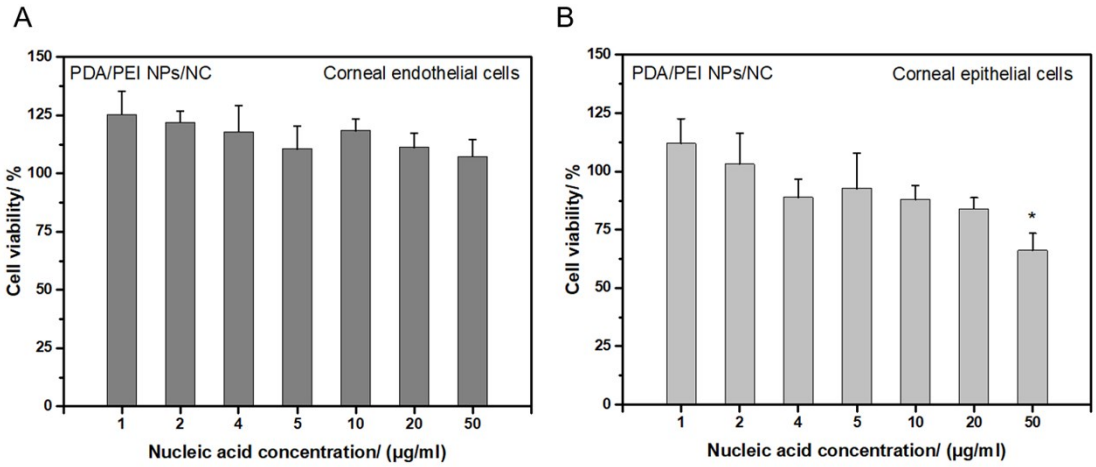
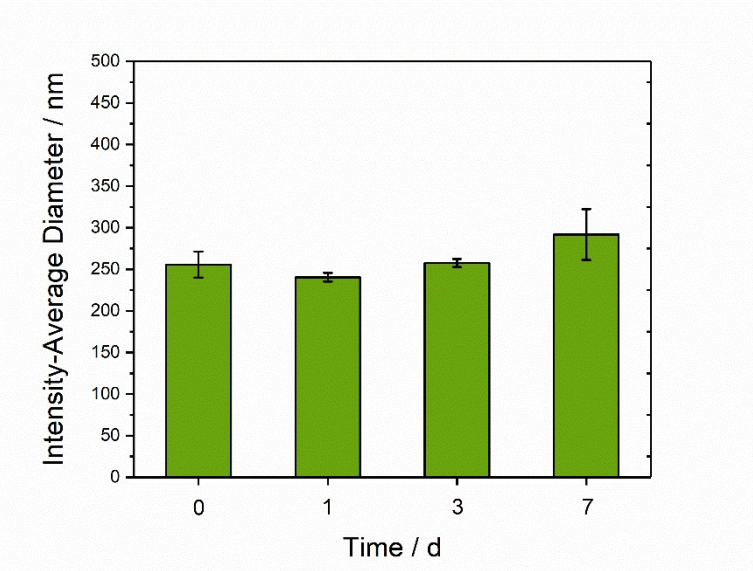
Supplementary information



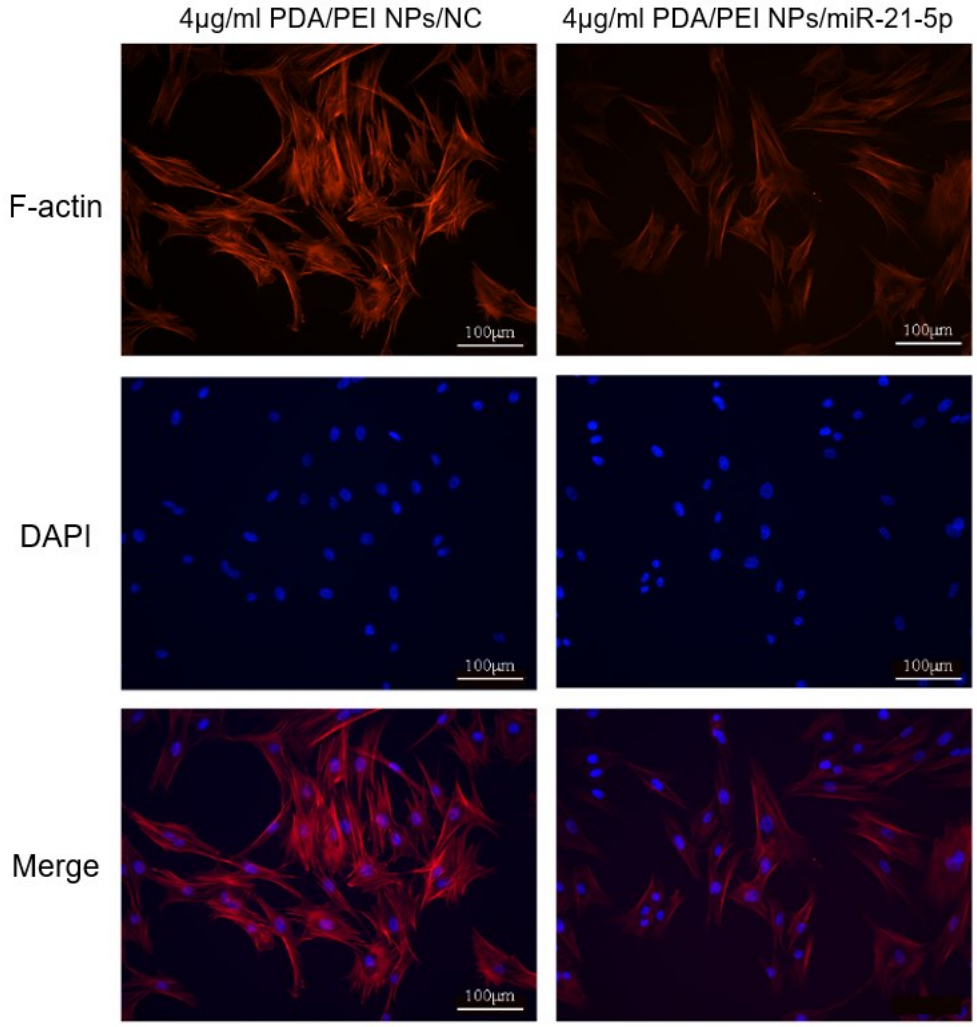
Supplementary figure S1. a) size distributions and b) Zeta-potentials of PDA/PEI NPs, PDA/PEI NPs/pGL-3, and PDA/PEI NPs/ NC complexes. The mass ratio of PDA/PEI NPs and nucleic acids in those complexes was 10. Data were presented as mean ± standard deviation, student t-test, * indicates $p<0.05$, ns denotes non-significance ($p>0.05$). c) Gel separation of PDA/PEI NPs-nucleic acid complexes. The ratios of PDA/PEI NPs-to-nucleic acid were a: 0; b: 0.1; c: 0.2; d: 0.5; e: 1; f: 2; g: 5 and h: 8.



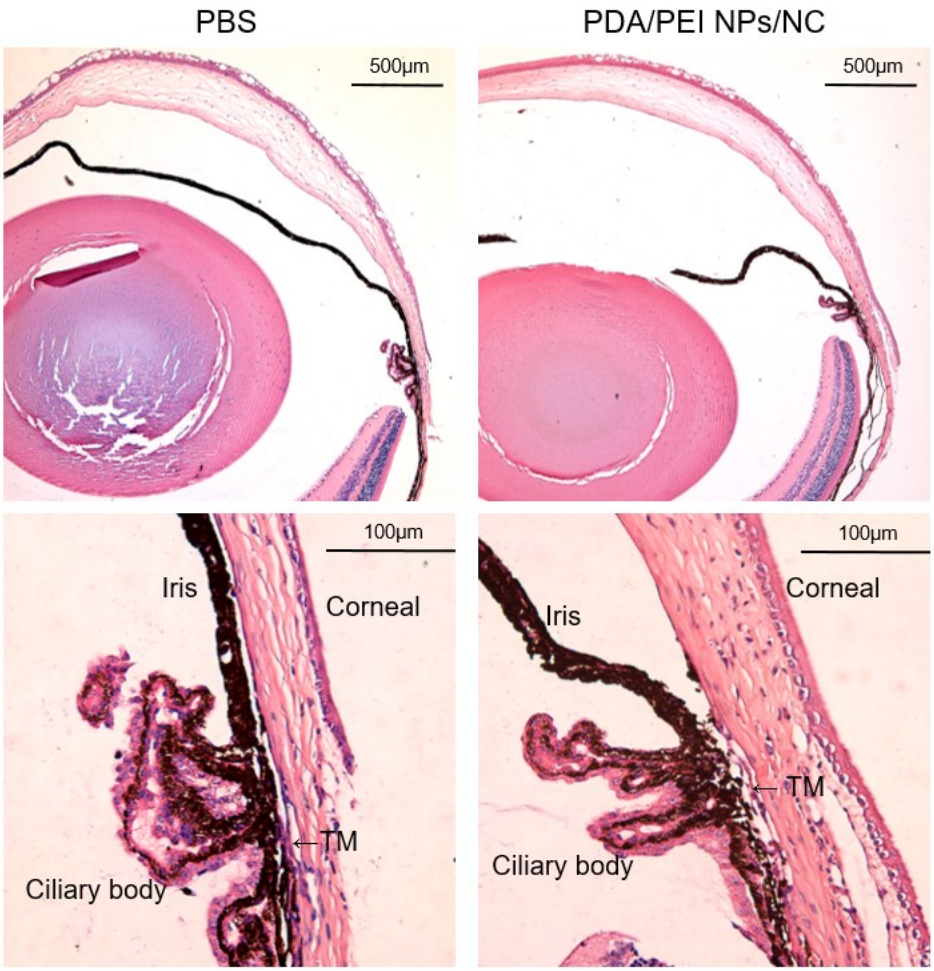
Supplementary figure S2. Cell viability of a) corneal endothelial cells and b) epithelial cells after treated with PDA/PEI NPs/NC complexes at various concentrations. Data were presented as mean ± standard deviation, one-way ANOVA, * indicates $p<0.05$.



Supplementary figure S3. Stability test of PDA/PEI NPs/nucleic acid complexes in various days after complexes preparation DLS.



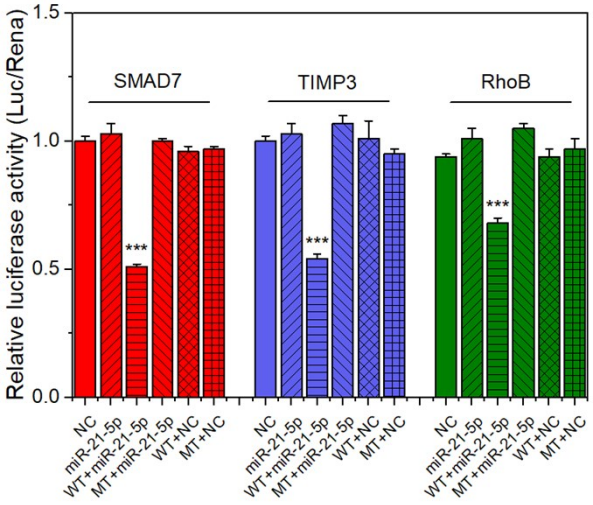
Supplementary figure S4. Immunocytochemistry staining of f-actin skeleton. AAP cells were pretreated PDA/PEI NPs/miR-21-5p or PDA/PEI NPs/NC for 24 hours. Shown were representative images of 5 replicates.



Supplementary figure S5. Hematoxylin-eosin (HE) staining of eyes that injected with sterile PBS or PDA/PEI NPs/NC at 24 hours. The gross morphology could be observed without obvious inflammation infiltration. The representative images of three replicates were shown. Scale bar 500μm (upper panel), 100 μm (lower panel).

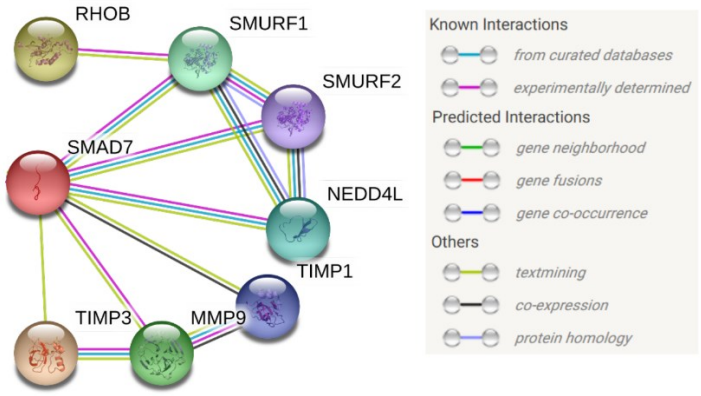
Target genes	Representative transcript	Cumulative weighted context++ score	Previous TargetScan publication(s)
SMAD7	ENST00000262158.2	-0.46	2005, 2007, 2009, 2011
TIMP3	ENST00000266085.6	-0.46	2005, 2007, 2009, 2011
RHOB	ENST00000272233.4	-0.12	2005, 2007, 2009, 2011

Supplementary table S6. Predicted target genes of miR-21-5p from TargetScan. After searching for the publications of glaucoma pathological researches, RhoB, SMAD7, and TIMP3 were selected and presented from 384 target genes of miR-21-5p. The cumulative weighted context++ score, which is a scoring method of predicted efficacy of targeting of the sites (Agarwal et al., 2015), was listed for reference.

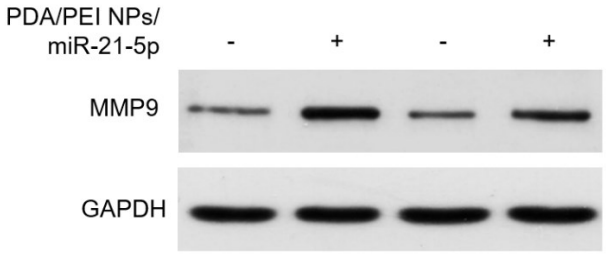


Supplementary figure S7. Dual-luciferase reporter assay verification of target genes of miR-21-5p. The relative luciferase activity was significantly decreased in the presence

of wild type (WT) 3’ untranslated region, and then restored in mutant type (MT) constructs. (n=3, *** p<0.001, student t-test)



Supplementary figure S8. The proteins interaction network of the miR-21-5p targets. The network of protein-protein interaction for the three genes (RhoB, SMAD7, and TIMP3) protein products was constructed according to the STRING database (https://string-db.org/).



Supplementary figure S9. The expression of MMP9 in outflow tissue. The protein level of MMP9 was significantly increased in outflow tissue.