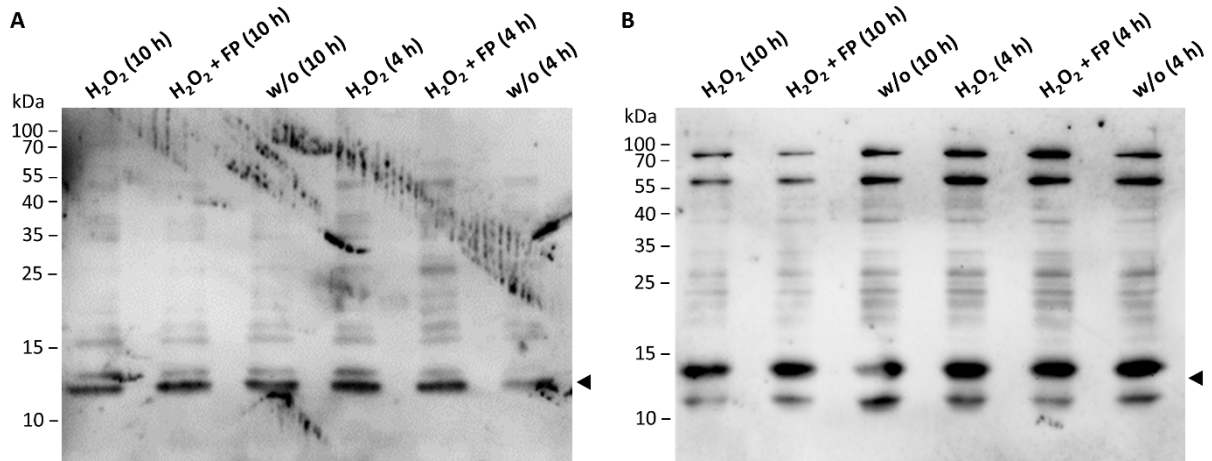


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Figure S1. *Ex vivo* cultivated human hprPE cells show RPE-specific markers. (A–D) hprPE were pigmented and vital for 14 days on transwell filters. Shown are the cells of donor 2 at day (A) 2, (B) 4, (C) 10 and (D) 14 as an example. Scale bars 400 μ m. Magnification 10x. (E–F) hprPE were positive for (E) *RPE65* mRNA and (F) RPE65 protein in immunostainings. (G–H) hprPE were positive for (G) Bestrophin (*BEST*) mRNA and (H) bestrophin protein in immunostainings. (E, H) Shown are representative examples after 10 days in culture. Scale bars 100 μ m. Magnification 100x. (I, J) Marker for epithelial–mesenchymal transition (I) mRNA *SMA1* and (J) mRNA *VIM* were partly increased after properdin treatment of stressed hprPE cells.

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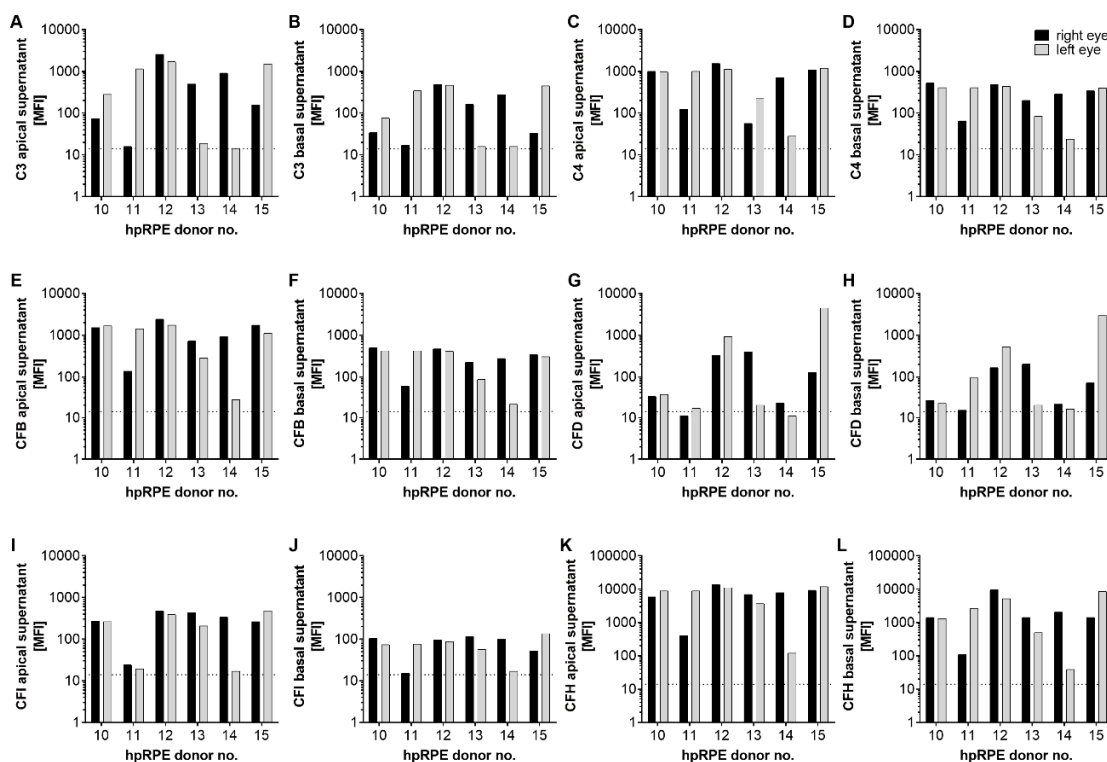
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Figure S2. Western Blots of C3a and C5a in hpRPE cells. **(A)** C3a was detected in 5 h and 10 h stressed (H₂O₂, H₂O₂ + FP) and unstressed (w/o) hpRPE cells at approx. 12 kDa (arrow). Exemplarily shown for donor 6. **(B)** C5a was detected as double band in 5 h and 10 h stressed (H₂O₂, H₂O₂ + FP) and unstressed (w/o) hpRPE cells between 10 – 15 kDa (arrow). Exemplarily shown for donor 5. FP - properdin. Reduced conditions.

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Figure S3. Complement component secretion is different in hpRPE cells from left and right donor eyes. Complement secretion of (A, B) C3, (C, D) C4, (E, F) CFB, (G, H) CFD, (I, J) CFI and (K, L) CFH was increased at the (A, C, E, G, I, K) apical compared to the (B, D, F, H, J, L) basal side. hpRPE isolated from the right eye (black) showed different complement component secretion activity than hpRPE from the left eye (grey). Dotted line shows blank control.

Table S1. In-house designed PCR primers.

transcript	gene accession number	name of sequence	application
<i>ARMS_375</i>	NG_011725	fw: CATTCTAATATCAAATCAAACATTCAT rv: CCTGGGGCTCTGTTTGAATTG	
<i>C2_116</i>	NG_011730	fw: AGCACCATCTACACTTCGCC rv: CATGGCCCTTACCTCGACAT	
<i>C2_144</i>	NG_011730	fw: CAGGGGGAGATCAGAATCGTC rv: GTGGGGGCAGGGAAATTCTTT	
<i>C3_147</i>	NG_009557	fw: TTGCTCTCCTAAGCCTGTG rv: GGCTAGGGTCTCACGAGG	
<i>C3_223_2</i>	NG_009557	fw: CTGGATGAAGAGGTACCCGC rv: CTTGGAACAGACCCCTGACA	
<i>C9_623</i>	NG_009894	fw: TCTGTGACAATGGCAGACAAT rv: TTTATTCCCCACTCTCTGTTATCTT	
<i>CFH_106</i>	NG_007259	fw: CCTTTGTTAGTAACTTTAGTTCGTCTT rv: GGAGTAGGAGACCAGCCATTC	hpRPE genotyping (2.2; Tab. 1)
<i>CFH_109</i>	NG_007259	fw: AGTCTACCTTGCTAACGGTTC rv: CCTTCTAGATTGTAGTACCTGTTGCT	
<i>CFH_121</i>	NG_007259	fw: CAGATCCGTGTGTAATATCCCGA rv: TAAGAAGAGAGCCACCGGTCTCA	
<i>CFH_570</i>	NG_007259	fw: AGTGGTGAGGAAAAATGTAGAATGT rv: CATCTCCATCTTTCTTAAATTCTGTGA	
<i>CFH_618*</i>	NG_007259	fw: GTGCATTACAGGGGCATATTC rv: CCTGAAGACACAAATCTCACTGG	
<i>CFI_100</i>	NG_007569	fw: CCTGCAGTGTGGTCTGTGAG rv: CCAGTGCTACAAGGTGGGAA	
<i>CFI_141</i>	NG_007569	fw: ATCCACTGATACAAGCGCTCA rv: TTAAAATCGTCATGATGTTCAAAGC	
<i>IL1B</i>	NG_008851	fw: CTCGCCAGTGAAATGATGGCT rv: GTCGGAGATTCGTAGCTGGAT	PCR (2.2/3; Fig. 5A) and RT-qPCR (2.3; Fig. 5B, C)
<i>SMA1</i>	NG_006672	fw: GCCTTGGTGTGTGACAATGG rv: AAAACAGCCCTGGGAGCAT	qPCR (2.3; Fig. S1)
<i>VIM</i>	NG_012413	fw: TGTCCAAATCGATGTGGATGTTTC rv: TTGTACCATTCTTCTGCCTCCTG	

*transcript refers to SNP *CFHR3/1_618*

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29**Table S2** QuantiTect PrimerAssays (Qiagen)

mRNA transcript	gene accession number	PrimerAssay name	catalogue number
<i>GAPDH</i>	NG_007073	Hs_GAPDH_1_SG	QT00079247
<i>C1Q</i>	NG_007283	Hs_C1QB_1_SG	QT00003493
<i>C3</i>	NG_009557	Hs_C3_1_SG	QT00089698
<i>C4A</i>	NG_011638	Hs_C4A_1_SG	QT00237160
<i>C4B</i>	NG_011639	Hs_C4B_1_SG	QT00237167
<i>C5</i>	NG_007364	Hs_C5_1_SG	QT00088011
<i>CFB</i>	NG_008191	Hs_BF_1_SG	QT00012138
<i>CFD</i>	NG_007274	Hs_CFD_1_SG	QT00212191
<i>CFI</i>	NG_007569	Hs_CFI_1_SG	QT00213794
<i>CFH</i>	NG_007259	Hs_CFH_1_SG	QT00001624
<i>CFP</i>	NG_009893	Hs_CFP_1_SG	QT00010514
<i>CD46</i>	NG_009296	Hs_MCP_1_SG	QT00073689
<i>CD59</i>	NG_008057	Hs_CD59_1_SG	QT00035952
<i>C3AR</i>	NG_050736	Hs_C3AR1_1_SG	QT00090398
<i>C5AR1</i>	NM_001736.4	Hs_C5R1_1_SG	QT00997766
<i>CD11B</i>	NG_011719	Hs_ITGAM_1_SG	QT00031500
<i>NLRP3</i>	NG_007509	Hs_NLRP3_1_SG	QT00029771
<i>RPE65</i>	NG_008472	Hs_RPE65_1_SG	QT00001351
<i>BEST</i>	NG_009033	Hs_BEST1_1_SG	QT00023282

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