

Supplementary Table S1. Distribution of baseline characteristics for study population

	N or mean (\pmSD)	%
Number of progressors		
Subjects	616/2941	
Eyes	948/5421	17.5
Follow up time (years)		
Eyes that progressed	6.4 (\pm 3.0)	
All eyes	9.6 (\pm 2.4)	
Age at baseline		
	68.8 (\pm 5.0)	
<65	555	18.9
65- <75	1916	65.2
75+	470	16.0
Demographic		
male	1291	43.9
white	2835	96.4
> high school	1950	66.3
Behavioral		
Smoking status		
Never smoker	1385	47.1
Current smoker	180	6.1
Past smoker	1376	46.8
BMI category		
BMI <25	963	32.7
BMI 25-29	1248	42.4
BMI \geq 30	730	24.8
Baseline Severity Scale (per eye)		
1	2304	42.5
2	748	13.8
3	307	5.7
4	577	10.6
5	361	6.7
6	463	8.5
7	479	8.8
8	182	3.4
Genetic variants		
Complement pathway		
<i>CFH</i> Y402H: rs1061170		
TT	891	30.3
CT	1345	45.7

CC	705	24.0
<i>CFH</i> : rs1410996		
TT	382	13.0
CT	1199	40.8
CC	1360	46.2
<i>CFH</i> R1210C: rs121913059		
CC	2928	99.6
CT	13	0.4
<i>C2</i> E318D: rs9332739		
GG	2738	93.1
CG/CC	203	6.9
<i>CFB</i> R32Q: rs641153		
CC	2530	86.0
TC/TT	411	14.0
<i>CFI</i> : rs10033900		
CC	754	25.6
CT	1437	48.9
TT	750	25.5
<i>C3</i> R102G: rs2230199		
CC	1713	58.3
CG	1066	36.3
GG	162	5.5
<i>C3</i> K155Q: rs147859257		
TT	2882	98.0
GT	59	2.0
<i>C9</i> P167S: rs34882957		
GG	2874	97.7
AG	67	2.3
<i>CFH</i> N1050Y: rs35274867		
AA	2872	97.7
TA	66	2.2
TT	3	0.1
Angiogenesis pathway		
<i>VEGFA</i> : rs943050		
CC	639	21.7
CT	1492	50.7
TT	810	27.5
<i>TGFBR1</i> : rs334353		
TT	1715	58.3
GT	1048	35.6
GG	178	6.1
Lipid pathway		
<i>LIPC</i> : rs10468017		

CC	1548	52.6
TC	1183	40.2
TT	210	7.1
<i>ABCA1: rs1883025</i>		
CC	1633	55.5
TC	1131	38.5
TT	177	6.0
<i>CETP: rs3764261</i>		
CC	1273	43.3
AC	1332	45.3
AA	336	11.4
<i>APOC1/APOE: rs4420638</i>		
AA	2104	71.5
GA	837	28.5
<i>APOH: rs1801689</i>		
AA	2756	93.7
AC	184	6.3
CC	1	0.0
Immune/inflammatory pathway		
<i>ARMS2/HTRA1: rs10490924</i>		
GG	1487	50.6
TG	1141	38.8
TT	313	10.6
<i>PEL13: rs145732233</i>		
CC	2918	99.2
TC	23	0.8
<i>TNFRSF10A: rs13278062</i>		
TT	821	27.9
GT	1474	50.1
GG	646	22.0
<i>SLC16A8: rs8135665</i>		
CC	1862	63.3
TC	950	32.3
TT	129	4.4
<i>PILRB/PILRA: rs11769700</i>		
TT	1849	62.9
CT	975	33.2
CC	117	4.0
<i>TMEM97/VTN: rs704</i>		
AA	693	23.6
AG	1456	49.5
GG	792	26.9

Extracellular matrix

<i>COL8A1: rs13095226</i>		
TT	2358	80.2
CT	548	18.6
CC	35	1.2
<i>COL4A3: rs11884770</i>		
CC	1558	53.0
TC	1159	39.4
TT	224	7.6
<i>CTRB1: rs8056814</i>		
GG	2440	83.0
AG	473	16.1
AA	28	1.0
<i>ADAMTS9: rs6795735</i>		
CC	881	30.0
TC	1421	48.3
TT	639	21.7
<i>TIMP3: rs9621532</i>		
AA	2653	90.2
CA/CC	288	9.8
DNA repair/protein binding		
<i>RAD51B: rs8017304</i>		
AA	1210	41.1
GA	1349	45.9
GG	382	13.0
<i>NPLOC4/TSPAN10:</i>		
rs9895741		
GG	1226	41.7
AG	1311	44.6
AA	404	13.7
<i>HSPH1/B3GALTL: rs9542236</i>		
TT	960	32.6
CT	1418	48.2
CC	563	19.1
