SUPPL. TABLE 1. GENOTYPES Marker	Designation (Gene)	Allele 1	Allele 2	Genotypes Cases 11	12	22	MAF *	Genotypes Controls 11	12	22	MAF*	ATT ** P value
CFH gene												
rs800292	I62V (CFH)	G	A	84 75.0%	27 24.1%	1 8.9%	12.9%	38 56.7%	27 40.3%	2 3.0%	23.1%	0.009
rs1061170	Y402H (CFH)	T	C	20 17.9%	56 50.0%	36 32.1%	57.1%	27 40.3%	32 47.8%	8 11.9%	35.8%	<0.001
rs1048663	IVS 9 (CFH)	G	A	78 69.6%	32 28.6%	2 1.8%	16.1%	47 70.1%	16 23.9%	4 6.0%	17.9%	0.66
rs2274700	A473A (CFH)	G	A	71 63.3%	35 31.2%	6 5.4%	16.5%	21 31.3%	36 53.7%	10 14.9%	41.8%	<0.001
rs412852	IVS 15 (CFH)	A	G	16 14.3%	53 47.3%	43 38.4%	62.1%	23 34.3%	34 50.7%	10 14.9%	40.3%	<0.001
rs11582939	IVS 18 (CFH)	C	T	75 67.0%	35 31.2%	2 1.8%	17.4%	46 68.7%	17 25.4%	4 6.0%	18.7%	0.76
BF-C2 gene												
rs9332739	E318D (C2)	G	C	105 93.8%	7 6.3%	0 0.0%	3.1%	62 92.5%	5 7.5%	0 0.0%	3.7%	0.75
rs547154	IVS 10 (C2)	G	T	106 94.6%	6 5.4%	0 0.0%	2.7%	57 85.1%	10 14.9%	0 0.0%	7.5%	0.03
rs4151667	L9H (CFB)	T	A	105 93.8%	7 6.3%	0 0.0%	3.1%	62 92.5%	5 7.5%	0 0.0%	3.7%	0.75
rs12614	R32W (CFB)	C	T	88 78.6%	23 20.5%	1 0.9%	11.2%	60 89.6%	7 10.4%	0 0.0%	5.2%	0.05
rs641153	R32Q (CFB)	G	A	106 94.6%	6 5.4%	0 0.0%	2.7%	57 85.1%	10 14.9%	0 0.0%	7.5%	0.03
C3 gene												
rs2230199	R102G (C3)	G	C	68 60.7%	35 31.2%	9 8.0%	23.7%	50 74.6%	16 23.9%	1 1.5%	13.4%	0.03

* MAF, minor allele frequency; ** ATT, Armitage's trend test

SUPPLEMENTARY TABLE 2.
HAPLOTYPES AND THEIR FREQUENCIES IN THE CASE AND CONTROL POPULATION ESTIMATED BY FAMHAP.

Haplotype	Frequency	
	Cases (n = 112)	Controls (n = 67)
CFH gene		
A T G A A C	12.0%	23.1%
G C G G G C	56.7%	35.8%
G T A G A T	16.1%	17.9%
G T G A A C	8.1%	17.9%
G T G G G C	4.5%	4.5%
others	2.7%	0.7%
BF-C2 gene		
C G A C G	2.8%	2.4%
C T A C A	0.0%	1.3%
G G T C G	83.4%	85.3%
G G T T G	11.2%	4.8%
G T T C A	2.3%	5.7%
others	0.4%	0.4%

Supplementary Table 3: Retrospective Power Analysis

Marker	Designation (Gene)	Risk Allele Frequency	Heterozygotes Relative Risk	Homozygotes Relative Risk	Power
CFH gene					
rs800292	I62V (CFH)	0.769	2.00	4.42	0.942
rs1061170	Y402H (CFH)	0.358	2.36	6.08	0.999
rs1048663	IVS 9 (CFH)	0.821	4.00	3.32	0.050
rs2274700	A473A (CFH)	0.582	1.62	5.63	0.999
rs412852	IVS 15 (CFH)	0.403	2.24	6.18	0.999
rs11582939	IVS 18 (CFH)	0.813	4.12	3.26	0.053
CFB-C2 gene					
rs9332739	E318D (C2)	0.963	1.21	2.42 *	0.264
rs547154	IVS 10 (C2)	0.925	3.10	6.20 *	0.488
rs4151667	L9H (CFB)	0.963	1.21	2.42 *	0.264
rs12614	R32W (CFB)	0.052	2.24	4.48 *	0.716
rs641153	R32Q (CFB)	0.925	3.10	6.20 *	0.488
C3 gene					
rs2230199	R102G (C3)	0.134	1.61	6.62	0.723

* Because the homozygous risk genotype was not observed, the homozygous relative risk could not be calculated, and was therefore estimated as two times the risk of the heterozygotes.

The power calculations were performed for a two-sided level of $\alpha = 0.05$ and based on the prevalence of AMD according to van Leeuwen R, Klaver CC, Vingerling JR, Hofman A, de Jong PT (2003) Epidemiology of age-related maculopathy: a review. Eur J Epidemiol 18: 845-854.