SUPPLEMENTARY TABLES

Table 1. Case and control definition.

AMD Cases (n = 134)	Hospital-based controls (n = 134)
65 years or older.	65 years or older.
Any gender.	Any gender.
With or without a family history of AMD.	No family history of AMD.
AMD CARMS grades 4 or 5†.	No retinal changes suggestive of advanced AMD by fundoscopy.
No history of vitreoretinal procedures.	Drusen less than 65 μm in diameter by fundoscopy. #
No other concurrent retinal diseases.	

The presence of a few small hard drusen less than 65 μm in diameter is common and is no longer considered to be a risk factor for the development of age related maculopathy[31]

Table 2. Description of the sample by case/control status (n = 268).

Characteristic	Cases (n = 134)*	Controls (n = 134)*	p†
Age (years), mean ± SD	**76.7 ± 7.6**	**71.9 ± 8.1**	**<0.0001**
Age (years), n (%)			**<0.0001**
[50 – 60)	**0 (0.0)**	**7 (5.3)**	
[60 – 65)	**7 (5.2)**	**16 (12.0)**	
[65 – 70)	**18 (13.4)**	**28 (21.1)**	
[70 – 75)	**28 (20.9)**	**32 (24.1)**	
[75 – 80)	**30 (22.4)**	**29 (21.8)**	
≥ 80	**51 (38.1)**	**21 (15.8)**	
Sex, n (%)			0.098
Male	42 (31.3)	55 (41.0)	
Female	92 (68.7)	79 (59.0)	
Type 2 diabetes, n (%)	32 (24.4)	39 (30.5)	0.276
Hypertension, n (%)	73 (54.5)	61 (47.3)	0.244
Smoking history, n (%)			0.741
Never	106 (79.7)	96 (81.4)	
Former or current	27 (20.3)	22 (18.6)	

Stratified characteristics by case/control status. Statistically significant differences are shown in bold and were computed with Student's t-Test (Continuous variables) or χ^2 test (categorical variable). We excluded one subject from this analysis because of age (<50 years old).

* Numbers may not sum to totals due to missing data, and column percentages may not sum to 100% due to rounding.

† P-value for Student's t-test (continuous variable) or χ^2 test (categorical variable).

^ One subject was excluded because of being younger than 50 years old.

In bold significant characteristics at the 0.05 level.

Table 3. Unadjusted associations between study variables and age-related macular degeneration (n = 268).

Characteristic^	N* (% with AMD)	OR (95% CI)	p†
rs970476			
G/G	41 (30.6)	1.00	——
G/T	63 (47.0)	1.02 (0.59, 1.79)	NS
T/T	30 (22.4)	1.06 (0.54, 2.07)	NS
rs931798			
G/G	51 (38.1)	1.00	——
G/A	**70 (52.2)**	**1.74 (1.04, 2.90)**	**0.034**
A/A	13 (9.7)	1.22 (0.52, 2.83)	NS
rs140617			
A/A	97 (72.4)	1.00	——
G/A	31 (23.1)	0.80 (0.46, 1.40)	NS
G/G	6 (4.5)	1.42 (0.40, 5.78)	NS
rs140616			
T/T	34 (25.4)	1.00	——
T/C	70 (52.2)	1.01 (0.56, 1.82)	NS
C/C	30 (22.4)	0.86 (0.43, 1.70)	NS
Age(years)	**–**	**1.08 (1.05, 1.12)**	**<0.0001**
Sex			
Female	92 (68.7)	1.00	——
Male	42 (31.3)	0.66 (0.40, 1.08)	NS
Type 2 diabetes			
No	99 (75.6)	1.00	——
Yes	32 (24.4)	0.73 (0.42, 1.28)	NS
Hypertension			
No	61 (45.5)	1.00	——
Yes	73 (54.5)	1.33 (0.82, 2.17)	NS
Smoking history			
Never	106 (79.7)	1.00	——
Former or current	27 (20.3)	1.11 (0.60, 2.08)	NS

Bivariate associations between baseline characteristics and AMD diagnosis (0–No, 1–Yes AMD). For genetic data, we assumed a genotypic mode of inheritance. Such models follow: $\log(OR_{AMD}) \sim \text{SNP}\begin{pmatrix} AA_{00} \\ Aa_{01} \\ aa_{10} \end{pmatrix} + \in$ where: AA is the most frequent allele in our population, taken as reference. We considered statistically significant predictors of odds of disease those whose p-value < 0.05.

* Numbers may not sum to total due to missing data.

† p-value for β significance

NS: not significant at the 0.05 level.

^We took the most common allele for each case and set it as reference. Effects displayed first as those of the intercept for each model.

~ One subject was excluded because of being younger than 50 years old.

In bold significant predictors at the 0.05 level.

Table 4. Unadjusted associations between study variables and age-related macular degeneration phenotype (n = 268).

Characteristic*	Geographic atrophy OR (95% CI)	p†	Neovascular OR (95% CI)	p†
rs931798^				
G/G	1.00	——	1.00	——
G/A	**1.82 (1.03, 3.21)**	**0.038**	1.41 (0.67, 2.98)	NS
A/A	1.27 (0.50, 3.22)	NS	1.13 (0.33, 3.86)	NS
Age(years)	**1.08 (1.04, 1.12)**	**<0.0001**	**1.09 (1.04, 1.14)**	**<0.0001**
Sex				
Female	1.00	——	1.00	——
Male	0.70 (0.40, 1.21)	NS	0.54 (0.25, 1.18)	NS
Type 2 diabetes				
No	1.00	——	1.00	——
Yes	0.65 (0.35, 1.22)	NS	0.86(0.39, 1.92)	NS
Hypertension				
No	1.00	——	1.00	——
Yes	1.39 (0.81, 2.38)	NS	1.23 (0.61, 2.5	NS
Smoking history				
Never	1.00	——	1.00	——
Former or current	1.32 (0.67, 2.56)	NS	0.77 (0.29, 2.04)	NS

Bivariate associations between baseline characteristics and AMD phenotype (either 1–GA, 0–else; or 1–NV, 0–else). For genetic data, we assumed a genotypic mode of inheritance. Such models follow: $\log(OR_{AMD\ phenotype}) \sim \mathrm{SNP}\begin{pmatrix} AA_{00} \\ Aa_{01} \\ aa_{10} \end{pmatrix} + \in$ where: AA is the most frequent allele in our population, taken as reference. We considered statistically significant predictors of odds of disease those whose p-value < 0.05.

† p-value for β significance

NS: not significant at the 0.05 level.

*Controls or non-diseased phenotype are set as reference for all multinomial logistic regression models.

^We took the most common allele and set it as reference.

In bold significant predictors at the 0.05 level.

Table 5. Unadjusted haplotypes of four SNPs with AMD (n = 268).

#	SNP 1	SNP 2	SNP 3	SNP 4	Pooled HF	Control HF	Case HF	OR (95% CI)	p†
1	**G**	**A**	**T**	**T**	**0.022**	**0.039**	**0.006**	**0.14 (0.02, 0.93)**	**0.011**
2	A	G	T	T	0.012	0.019	0.005	0.21 (0.02, 2.04)	0.216
3	G	A	C	T	0.099	0.107	0.089	0.82 (0.44, 1.51)	0.428
4	A	A	T	G	0.017	0.022	0.012	0.62 (0.16, 2.41)	0.530
5	G	A	T	G	0.022	0.022	0.021	1.00 (0.27, 3.75)	0.754
6	G	A	C	G	0.378	0.384	0.375	1.00 (NA, NA)	0.896
7	G	G	T	G	0.114	0.114	0.115	0.97 (0.52, 1.81)	0.956
8	G	G	T	T	0.025	0.023	0.027	1.84 (0.42, 7.98)	0.857
9	A	A	T	T	0.293	0.257	0.329	1.31 (0.84, 2.02)	0.084

Haplotype configurations of SNPs in the SGCD gene. We show their frequency (HF) in the full sample (Pooled HF) and stratified by case/control status. Also, bivariate associations between a haplotype configuration (#) and AMD diagnosis using logistic regression modeling.

SNP1: rs931798, SNP2: rs140617, SNP3: rs140616, SNP4: rs970476.
Four single-nucleotide polymorphism (SNP) haplotype configuration.
† p-value for haplotype $\chi 2$ test evaluated at the 0.05 level.
HF: Haplotype frequency among cases, controls, and full study sample (pooled).
NA: Not able to calculate by this method.
In bold significant haplotypes at the 0.05 level.