

Appendix 4. Risk of AMD (subgroup) cases for *SLC2A1* SNP rs4660687 in five replication populations

| | No AMD | | Early AMD | | GA | | CNV | | CNV + Mixed cases | | Mixed AMD | |
|---------------------------------|-------------|------------|-------------------------|-----------|------------|------------------|-------|------------|-------------------|-----------|-----------|-------------------------|
| The Rotterdam study | | | | | | | | | | | | |
| | N=2221 | | N=894 | | N=72 | | N=64 | | N=103 | | N=39 | |
| <i>Rs4660687</i> | No. (%) | No. (%) | OR (95% CI) | | No. (%) | OR (95% CI) | | No. (%) | OR (95% CI) | | No. (%) | OR (95% CI) |
| Genotype | | | | | | | | | | | | |
| Noncarrier (AA) | 772 (34.8) | 279 (31.2) | 1 | 24 (33.3) | 1 | 23 (35.9) | 1 | 37 (35.9) | 1 | 14 (35.9) | 1 | |
| Heterozygous (Aa) | 1091 (49.1) | 436 (48.8) | 1.14 (0.95-1.36) | | 34 (47.2) | 1.04 (0.61-1.79) | | 47 (45.6) | 0.90 (0.58-1.40) | | 16 (41.0) | 0.91 (0.44-1.90) |
| Homozygous (aa) | 358 (16.1) | 179 (20.0) | 1.42 (1.13-1.78) | | 14 (19.4) | 1.28 (0.65-2.53) | | 10 (15.6) | 0.93 (0.44-2.00) | | 9 (23.1) | 1.47 (0.62-3.50) |
| m.a.f(%) | 40.7 | 44.4 | | 43.0 | | 39.8 | | 41.3 | | 43.6 | | |
| The Franconian AMD study | | | | | | | | | | | | |
| | N=608 | | N=86 | | N=162 | | N=419 | | N=545 | | N=126 | |
| <i>Rs4660687</i> | No(%) | No(%) | OR (95% CI) | | No(%) | OR (95% CI) | | No(%) | OR (95% CI) | | No(%) | OR (95% CI) |
| Genotype | | | | | | | | | | | | |
| Noncarrier (AA) | 212 (34.9) | 34 (39.5) | 1 | 62 (38.3) | 1 | 152 (36.3) | 1 | 211 (38.7) | 1 | 59 (46.8) | 1 | |
| Heterozygous (Aa) | 296 (48.7) | 41 (47.7) | 0.86 (0.53-1.41) | | 79 (48.8) | 0.91 (0.63-1.33) | | 205 (48.9) | 0.88 (0.68-1.13) | | 54 (42.9) | 0.66 (0.44-0.99) |
| Homozygous (aa) | 100 (16.4) | 11 (12.8) | 0.69 (0.33-1.41) | | 21 (12.9) | 0.72 (0.41-1.24) | | 62 (14.8) | 0.75 (0.53-1.07) | | 13 (10.3) | 0.47 (0.24-0.89) |
| m.a.f(%) | 40.8 | 36.6 | | 37.3 | | 39.3 | | 37.5 | | 31.7 | | |
| AREDS | | | | | | | | | | | | |
| | N=206 | | N=246 | | N=167 | | N=312 | | N=488 | | N=176 | |
| <i>Rs4660687</i> | No(%) | No(%) | OR (95% CI) | | No(%) | OR (95% CI) | | No(%) | OR (95% CI) | | No. (%) | OR (95% CI) |
| Genotype | | | | | | | | | | | | |
| Noncarrier (AA) | 73 (35.4) | 91 (37.0) | 1 | 65 (38.9) | 1 | 113 (36.2) | 1 | 174 (35.7) | 1 | 61 (34.7) | 1 | |
| Heterozygous (Aa) | 90 (43.7) | 109 (44.3) | 0.97 (0.64-1.47) | | 76 (45.5) | 0.95 (0.60-1.49) | | 132 (42.3) | 0.95 (0.64-1.41) | | 83 (47.2) | 1.10 (0.70-1.73) |
| Homozygous (aa) | 43 (20.9) | 46 (18.7) | 0.86 (0.51-1.44) | | 26 (15.6) | 0.68 (0.38-1.22) | | 67 (21.5) | 1.01 (0.62-1.63) | | 32 (18.2) | 0.89 (0.50-1.57) |
| m.a.f(%) | 42.7 | 40.8 | | 38.3 | | 42.6 | | 42.3 | | 41.8 | | |
| Columbia university | | | | | | | | | | | | |
| | N=363 | | N=362 | | N=208 | | N=519 | | | | | |
| <i>Rs4660687</i> | No(%) | No(%) | OR (95% CI) | | No(%) | OR (95% CI) | | No(%) | OR (95% CI) | | | |
| Genotype | | | | | | | | | | | | |
| Noncarrier (AA) | 133 (36.6) | 119 (32.9) | 1 | 72 (34.6) | 1 | | N.P | 169 (32.6) | 1 | | N.P | |
| Heterozygous (Aa) | 174 (47.9) | 181 (50.0) | 1.16 (0.84-1.61) | | 110 (52.9) | 1.17 (0.80-1.70) | | 257 (49.5) | 1.16 (0.86-1.57) | | | |
| Homozygous (aa) | 56 (15.4) | 62 (17.1) | 1.24 (0.80-1.92) | | 26 (12.5) | 0.86 (0.50-1.48) | | 93 (17.9) | 1.31 (0.87-1.95) | | | |
| m.a.f(%) | 39.4 | 42.1 | | 38.9 | | | 42.7 | | | | | |
| The university of Iowa | | | | | | | | | | | | |
| | N=379 | | N=312 | | N=77 | | N=632 | | N=669 | | N=37 | |
| <i>Rs4660687</i> | No(%) | No(%) | OR (95% CI) | | No(%) | OR (95% CI) | | No(%) | OR (95% CI) | | No. (%) | OR (95% CI) |
| Genotype | | | | | | | | | | | | |
| Noncarrier (AA) | 127 (33.5) | 95 (30.4) | 1 | 27 (35.1) | 1 | 205 (32.4) | 1 | 216 (32.2) | 1 | 11 (29.7) | 1 | |
| Heterozygous (Aa) | 191 (50.4) | 158 (50.6) | 1.11 (0.79-1.55) | | 38 (49.4) | 0.93 (0.54-1.61) | | 324 (51.2) | 1.05 (0.79-1.40) | | 22 (59.4) | 1.33 (0.62-2.84) |
| Homozygous (aa) | 61 (16.1) | 59 (18.9) | 1.29 (0.83-2.02) | | 12 (15.5) | 0.92 (0.44-1.95) | | 103 (16.3) | 1.05 (0.71-1.54) | | 4 (10.8) | 0.76 (0.23-2.47) |
| m.a.f(%) | 41.3 | 44.2 | | 40.3 | | 41.9 | | 41.8 | | 40.5 | | |

AMD = age-related macular degeneration; CI = confidence interval; OR = odds ratio; SNP = single nucleotide polymorphism; m.a.f = minor allele frequency; GA= geographic atrophy; CNV = choroidal neovascularization; Mixed AMD = combination of GA + CNV; N.P = not performed. "A" indicates common allele, "a" minor allele. Percentages not always 100% because of rounding. ORs are estimated with logistic regression analysis. Adjustment for age and gender only in the Rotterdam study.