within the corresponding haplotype blocks on 6q14, 19q13, 13q21, and 15q12 in which rs2874794, rs12462443, rs9599819 and rs1295534 are located (data not shown). However, there is a possibility of the existence of unknown mechanisms related to these regions. These loci may be critical for the development of AMD in combination with *LOC387715* (rs10490924) and/or *HTRA1* (rs11200638), and other behavioral, nutritional, and environmental factors. Further investigations are required of the individual regions to determine the molecular mechanisms related to the pathogenesis of AMD.

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Supplemental material

Supplemental Table 1

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Figure legends

Figure 1. Genome-wide association study for wet -type AMD susceptibility loci.

The analyseis compared 100 stage 5b AMD cases with 200 population-based controls (stage three analysis). The x-axis represents genomic locations, and the y-axis shows $-\log_{10}$ (genotypic *P*-value). All of the SNPs on autosomal chromosomes with genotypic *P* values < 0.01 are plotted.

Figure 2. Determination of statistical significant SNPs.

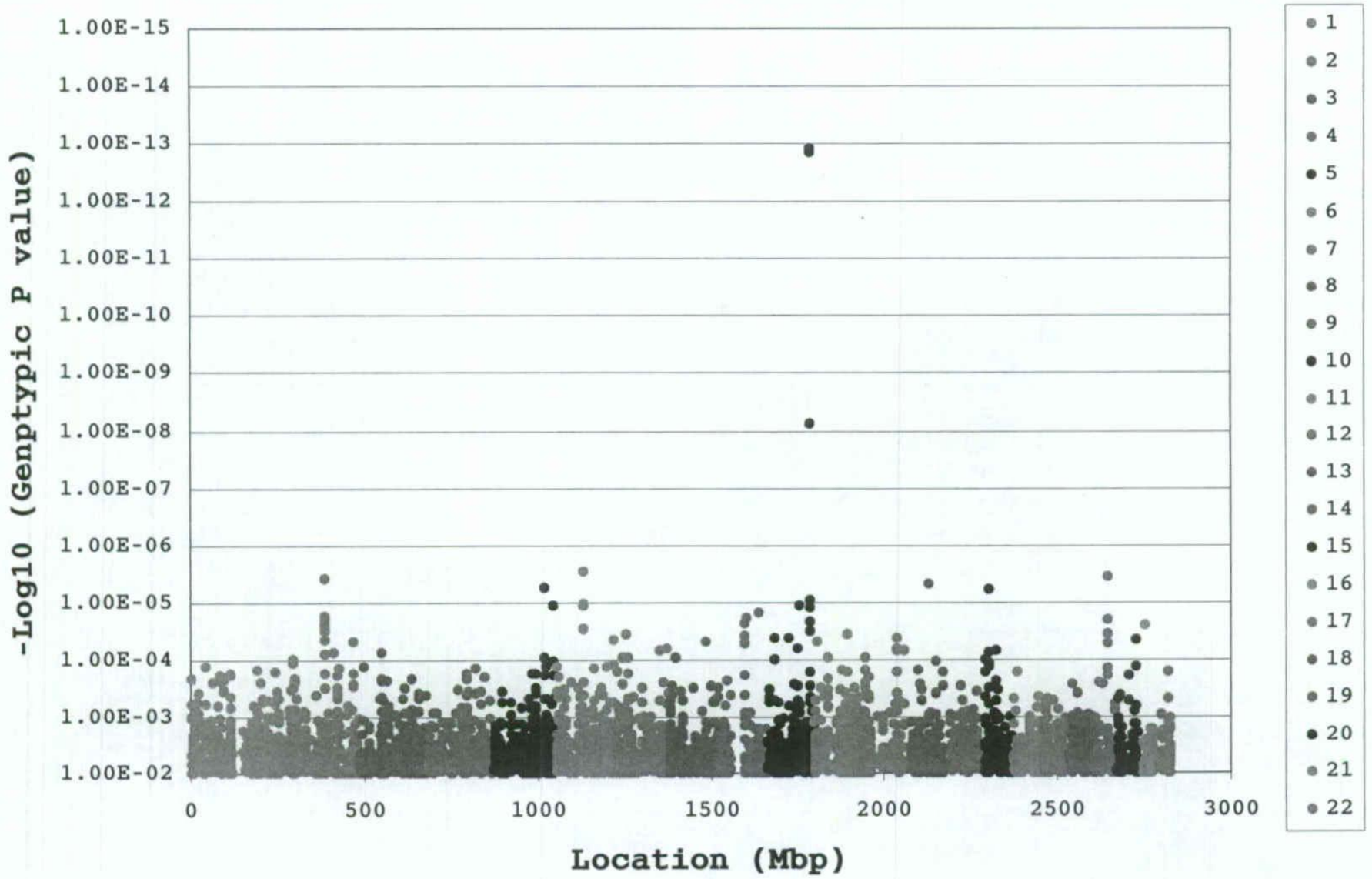
The Benjamini-Hochberg method to correct for multiple testing was used to identify SNPs significantly associated with AMD. A false discovery rate of 0.05 was used to determine statistical significance.

Figure 3. Haplotype block structure of the AMD-associated regions.

Squares shaded pink or red indicate significant linkage disequilibrium between SNP pairs (bright red indicates pairwise $D' = 1$), white squares indicate no evidence of significant linkage disequilibrium, and blue squares indicate pairwise $D' = 1$ without statistical significance. Locations of the regions on each chromosome are shown in scales above.

Genes within the views are shown by arrows. SNPs with a genotypic *P*- value < 10^{-6} in stage three analysis are indicated by open arrowheads. Haplotype block including these SNPs are surrounded with bold lines.

(A.) Haplotype block patterns on chromosome 10. rs10490924 and rs3750848 waere included in block two within the *LOC387715* gene region. rs2672587 is located between block two and three. rs10510110 is located on block one together with the *PLEKHA1* gene.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1.00E-13
1.00E-12
1.00E-11
1.00E-10
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1.00E-08
1.00E-07
1.00E-06
1.00E-05
1.00E-04
1.00E-03
1.00E-02
0
500
1000
1500
2000
2500
3000
Location (Mbp)
1
2
3
4
5
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7
8
9
10
11
12
13
14
15
16
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18
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20
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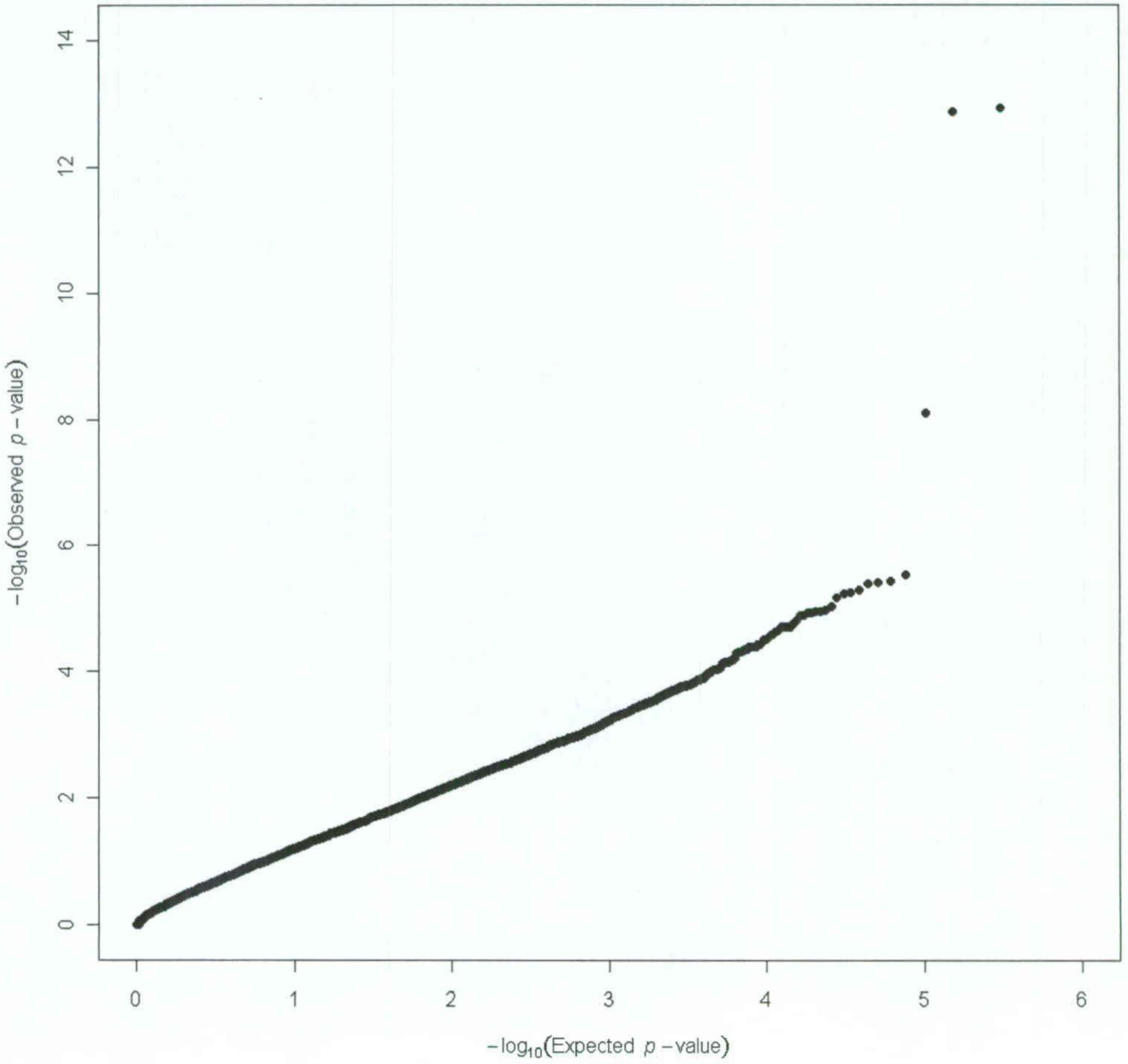
22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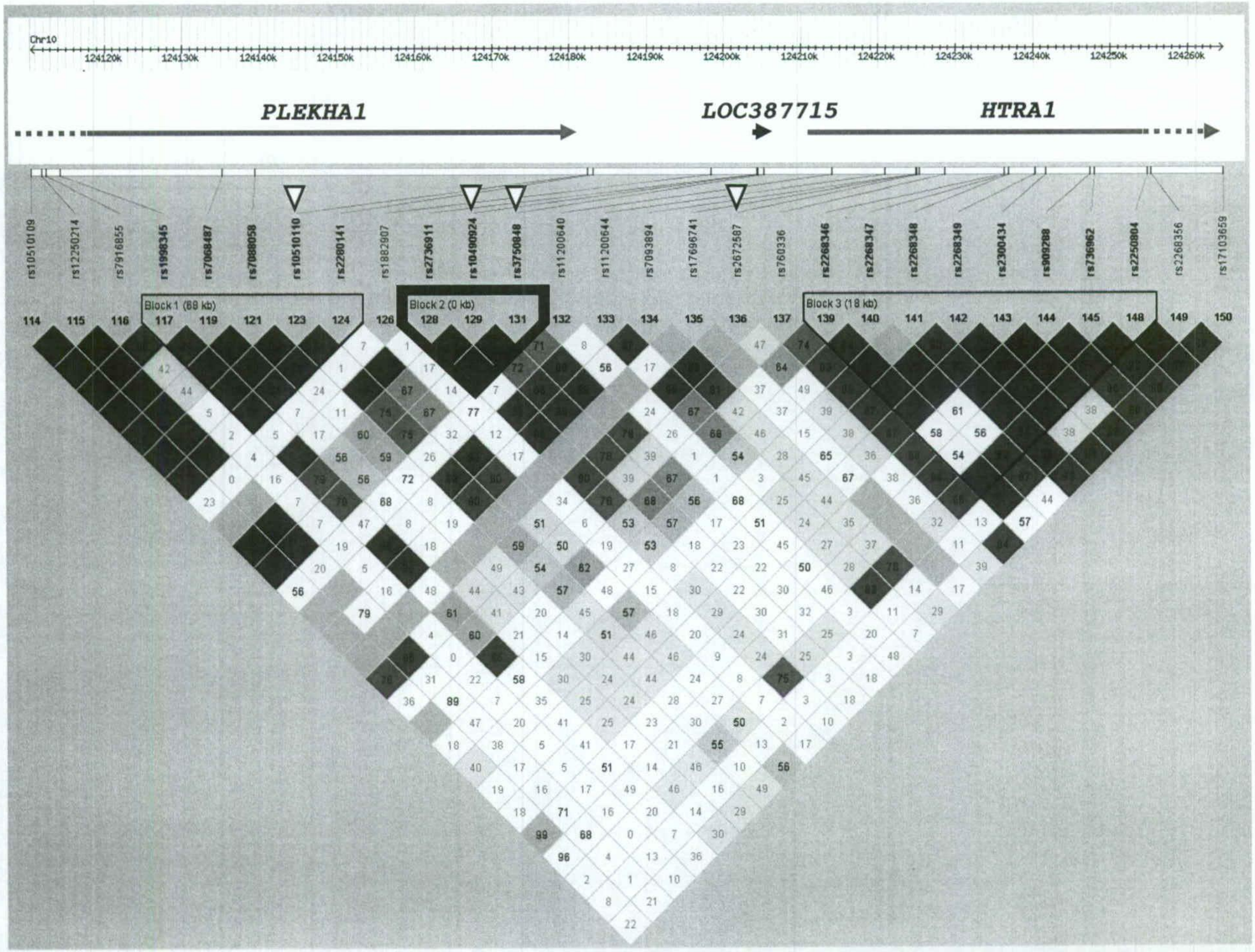
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LOC387715
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rs2268347
rs2268348
rs2268349
rs2300434
rs909288
rs736962
rs2250804
rs2268356
rs17103659
Block 1 (69 kb)
Block 2 (0 kb)
Block 3 (18 kb)

Table 1. Characteristics of AMD cases and control subjects in this study

Characteristic (AMD)					
Sex -no. (%)					
Male	73 (73.00)				
Female	27 (27.00)				
Mean age at recruitment- yr (SE)					
Total	74.56 (0.88)				
Male	73.64 (0.99)				
Female	77.04 (1.83)				
Age distribution - no. (%)					
	50s	60s	70s	80s	90s
Total	7 (7.00)	24 (24.00)	34 (34.00)	34 (34.00)	1 (1.00)
Male	6 (8.22)	17 (23.29)	29 (39.72)	20 (27.40)	1 (1.37)
Female	1 (3.70)	7 (25.93)	5 (18.52)	14 (51.85)	0 (0.00)

Characteristic (Control)						
Sex - no. (%)						
Male	91 (45.5)					
Female	109 (54.5)					
Mean age at recruitment - yr (SE)						
Total	71.00 (0.75)					
Male	71.00 (1.09)					
Female	71.00 (1.03)					
Age distribution - no. (%)						
	30s	40s	50s	60s	70s	80s
Total	3 (1.5))	4 (2.00))	18 (9.00)	43 (21.50)	96 (48.00)	36 (18.00)
Male	0 (0.00)	2 (2.20)	9 (9.89)	19 (20.88)	45 (49.45)	16 (17.58)
Female	3 (2.75)	2 (1.83)	9 (8.26)	24 (22.02)	51 (46.79)	20 (18.35)

Table 2. Summary of ten SNPs analyzed in this study

SNP	Nearest gene	Location		*P* value OR (95%CI)
rs10490924	*LOC387715*	10q26	Allele	9.70×10^{-15} 4.00 (2.79-5.74)
			Genotype	2.41×10^{-13}
			Heterozygote	6.11×10^{-6} 3.61 (2.02-6.46)
			Homozygote	1.19×10^{-13} 8.29 (4.62-14.89)
rs3750848	*LOC387715*	10q26	Allele	1.65×10^{-14} 3.97 (2.77-5.69)
			Genotype	3.39×10^{-13}

			Heterozygote	1.38×10^{-13}
				3.57 (1.99-6.39)
			Homozygote	6.48×10^{-6}
				8.24 (4.59-14.80)
rs2672587	*HTRA1*	10q26	Allele	1.67×10^{-10}
				3.14 (2.20-4.48)
			Genotype	8.02×10^{-9}
			Heterozygote	1.08×10^{-5}
				3.73 (2.01-6.92)
			Homozygote	2.91×10^{-8}
				4.63 (2.68-7.98)
rs2874794	*SH3BGRL2*	6q14	Allele	5.56×10^{-6}
				2.23 (1.58-3.17)
			Genotype	6.46×10^{-6}

			Heterozygote	3.05×10^{-6}
				2.21 (1.22-3.99)
			Homozygote	0.0087
				3.93 (2.22-6.96)
rs12462443	*ZNF507*	19q13	Allele	0.00016
				1.96 (1.39-2.76)
			Genotype	1.53×10^{-5}
			Heterozygote	3.70×10^{-6}
				3.94 (2.12-7.30)
			Homozygote	0.15
				1.60 (0.87-2.95)
rs2714212	*LRP1B*	2q22	Allele	0.0084
				1.87 (1.17-2.99)
			Genotype	4.04×10^{-6}

			Heterozygote	1.68×10^{-4}
				0.32 (0.088-1.16)
			Homozygote	0.089
				2.88 (1.65-5.05)
rs9599819	*DACH1*	13q21	Allele	0.61
				1.11 (0.75-1.65)
			Genotype	5.08×10^{-6}
			Heterozygote	5.77×10^{-4}
				1.73 (1.06-2.81)
			Homozygote	0.034
rs3763022	*SH2TC2*	5q33	Allele	2.18×10^{-6}
				6.44 (2.53-16.36)
			Genotype	1.78×10^{-5}
			Heterozygote	0.17

			Homozygote	5.59×10^{-6}
				6.62 (2.54-17.22)
rs12595534	TRPM1	15q13	Allele	4.26×10^{-5}
				2.13 (1.48-3.08)
			Genotype	1.10×10^{-5}
			Heterozygote	0.011
				8.91 (2.69-29.52)
			Homozygote	5.98×10^{-6}
				1.94 (1.19-3.16)
rs10510110	*PLEKHA1*	10q26	Allele	4.93×10^{-6}
				2.35 (1.62-3.43)
			Genotype	2.07×10^{-5}
			Heterozygote	9.50×10^{-6}
				2.92 (1.25-6.81)