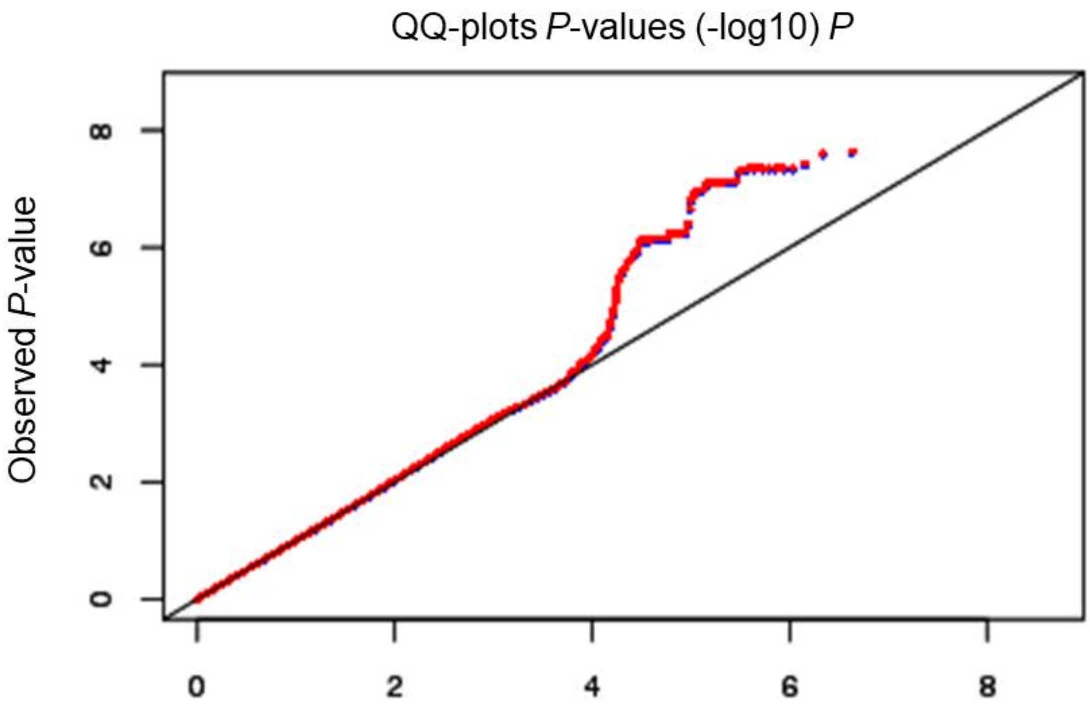
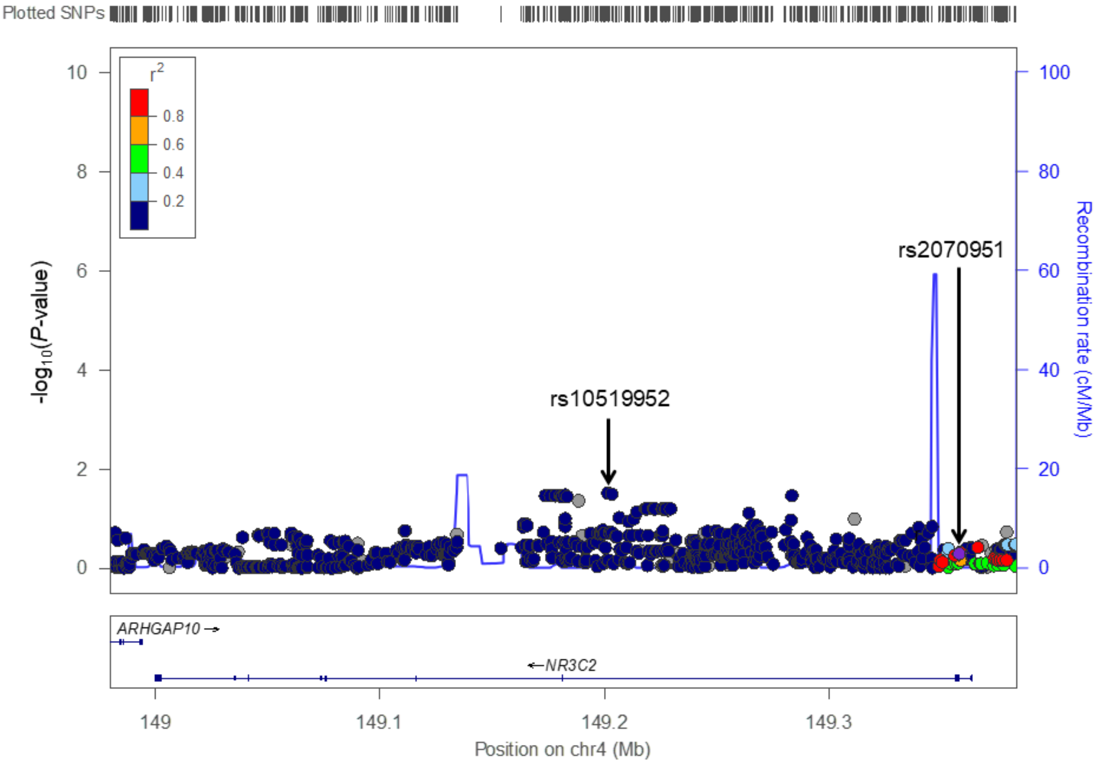
Supplementary Figure 1: Quantile-quantile (QQ) plots from the discovery stage. QQ plots for association between all analyzed single nucleotide polymorphisms and choroidal thickness in the discovery stage. Each blue dot represents an observed statistic (defined as the -log10(*P*-value)) versus the corresponding expected statistic before genomic control, whereas each red dot represents the observed statistic versus the corresponding expected statistic after genomic control. The black line corresponds to the null distribution.

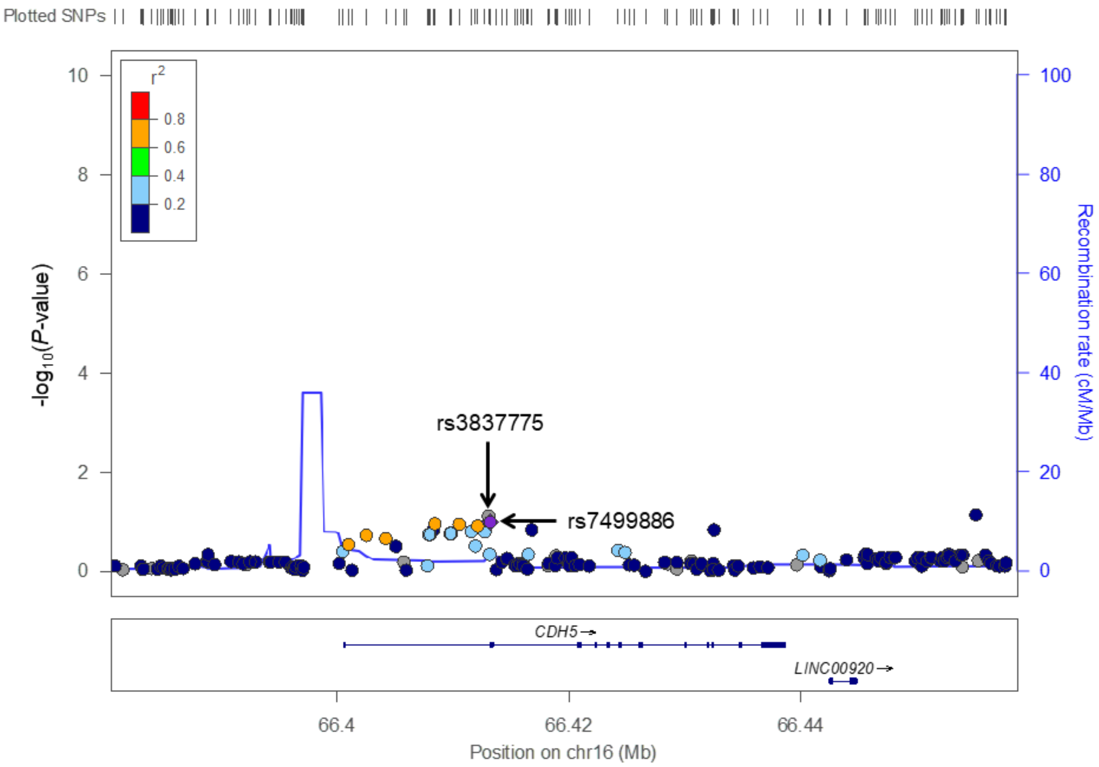


www.pnas.org/cgi/doi/10.1073/pnas.1802212115

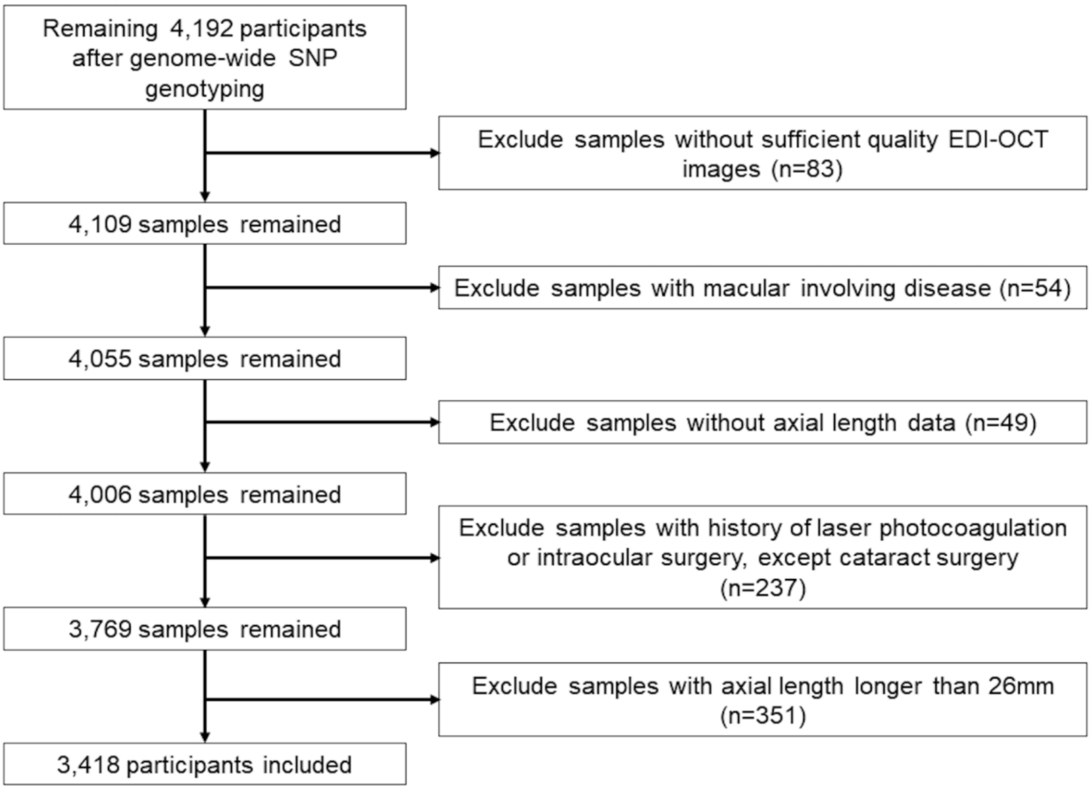
Supplementary Figure 2: Regional association plots for genotyped single nucleotide polymorphisms in the *NR3C2* region. Plots represented using the -log10(*P*-values) obtained from the first-stage genome-wide association study. Each *P*-value was calculated by age-, sex-, axial length and the first principal component-adjusted quantitative trait locus analysis.



Supplementary Figure 3: Regional association plots for genotyped single nucleotide polymorphisms in the *CDH5* region. Plots represented using the -log10(*P*-values) obtained from the first-stage genome-wide association study. Each *P*-value was calculated by age-, sex-, axial length and the first principal component-adjusted quantitative trait locus analysis.



Supplementary Figure 4: Flow diagram summarizing the participants included in the discovery GWAS. SNP, single nucleotide polymorphism; EDI, enhanced depth imaging; OCT, optical coherence tomogramphy.



Supplementary Table 1. Description of the cohort

Stage	N	Female (%)	Age (years)	SFCT (μm)	AL (mm)
Discovery	3,418	2,373 (69.4)	57.8 ± 13.1	296.2 ± 100.5	23.79 ± 1.02
Replication	2,692	1,847 (68.6)	59.9 ± 12.0	293.0 ± 98.6	23.72 ± 1.02

AL, axial length; SFCT, subfoveal choroidal thickness. Data are expressed as mean ± standard deviation.

Supplementary Table 2. Associations between *NR3C2* and *CDH5* with choroidal thickness in the discovery stage

SNP	Gene	CHR	Position	N	Effect allele (indel)	β	Standard error	MAF	P^a
rs10519952	*NR3C2*	4	149201414	3,418	G	-5.701	2.633	0.196	**0.030**[b]
rs2070951	*NR3C2*	4	149358014	3,418	G	-1.628	2.457	0.252	0.51
rs3837775	*CDH5*	16	66413050	3,418	CG	3.741	2.122	0.470	0.076
rs7499886	*CDH5*	16	66413195	3,418	G	3.473	2.119	0.467	0.10

CHR, chromosome; MAF, minor allele frequency; SNP, single nucleotide polymorphism.

[a] *P*-values derived using linear regression.

[b] *P*-values in bold are statistically significant.

Supplementary Table 3. Associations between *NR3C2* and *CDH5* with CSC

			Minor allele frequency			
Variant	Gene	Major/minor allele (indel)	Controls N = 3,418	CSC N = 250	Odds ratio (95% CI)	*P*[a]
rs10519952	*NR3C2*	A/G	0.196	0.19	0.96 (0.76-1.21)	0.73
rs2070951	*NR3C2*	C/G	0.252	0.238	0.93 (0.75-1.15)	0.50
rs3837775	*CDH5*	C/CG	0.470	0.466	0.98 (0.82-1.18)	0.86
rs7499886	*CDH5*	A/G	0.467	0.466	1.00 (0.83-1.19)	0.96

CSC, central serous chorioretinopathy; CI, confidence interval.

[a] *P*-values derived using chi-squared test.

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