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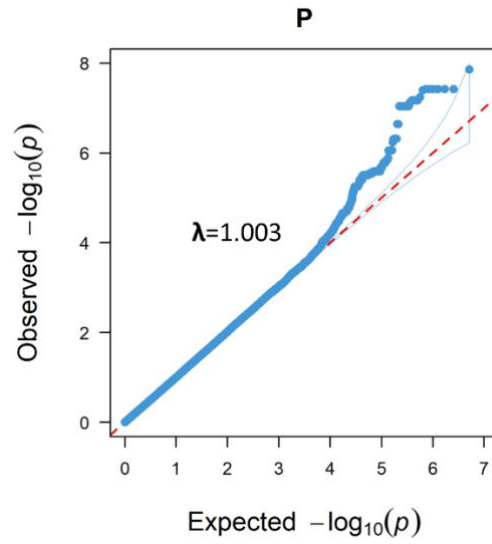


Fig. S1. Quantile-quantile plot of the association results of HKCES-1 and LAMP in the discovery stage. The red dashed line represents the null distribution. The observed $-\log_{10}(p)$ -values (blue dots) are plotted against the expected $-\log_{10}(p)$ -values under the null hypothesis of no association. The genomic inflation factor (λ) is 1.003, indicating little evidence of population stratification. HKCES, Hong Kong Children Eye Study; LAMP, Low Concentration Atropine for Myopia Progression Study. The figure was generated using R package (v. 3.4.2).

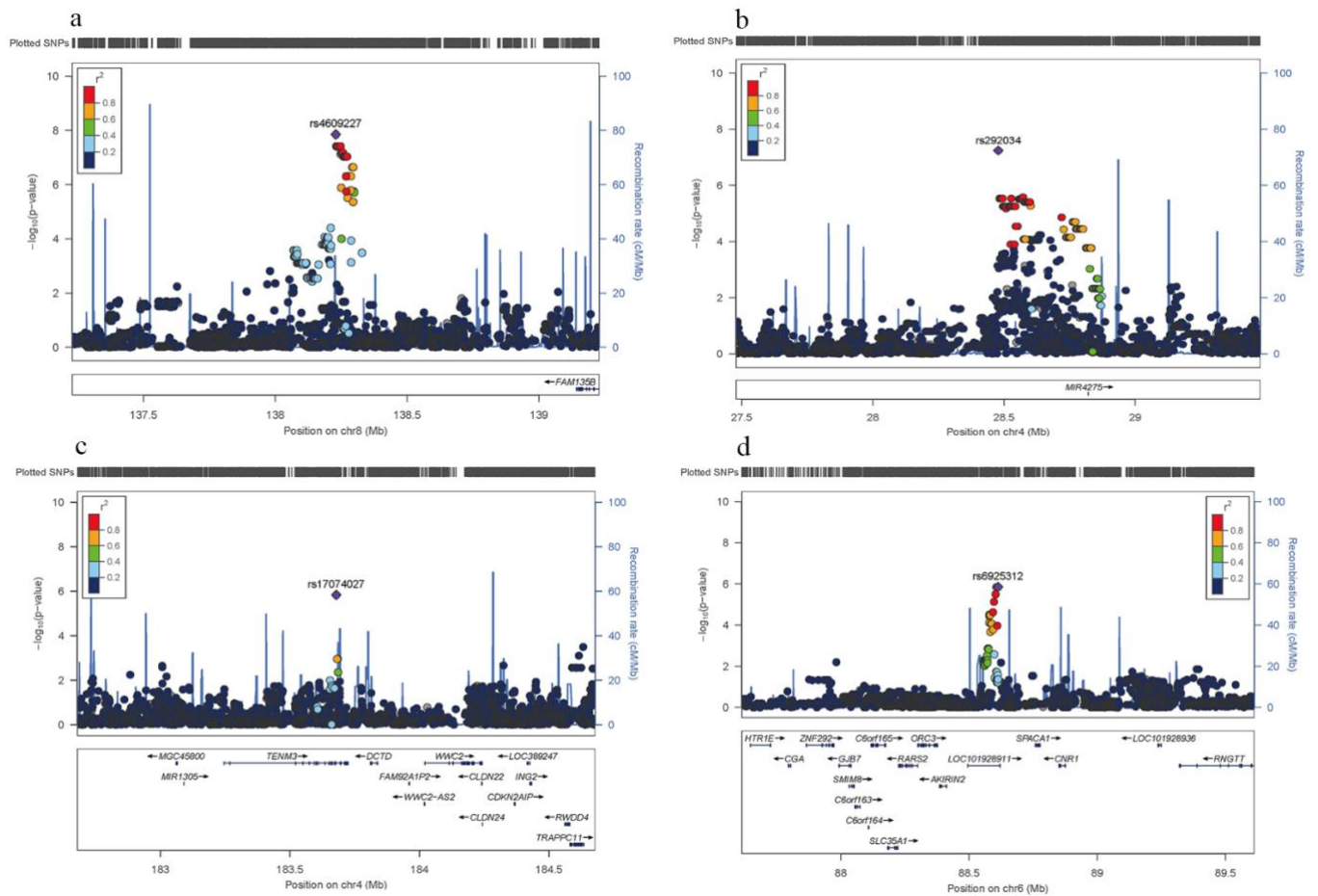


Fig. S2. Regional association plots of the 4 loci associated with spherical equivalent. Plots are shown for association in the Hong Kong children genome-wide association study discovery set at (a) *FAM135B* on 8q24.23; (b) *MIR4275* on 4p15.1; (c) *TENM3* on 4q34.3; (d) *LOC101928911* on 6q15. Genetic linkage disequilibrium (LD) in each region is estimated by r^2 . The figure was generated using LocusZoom version 1.4 (https://genome.sph.umich.edu/wiki/LocusZoom_Standalone).

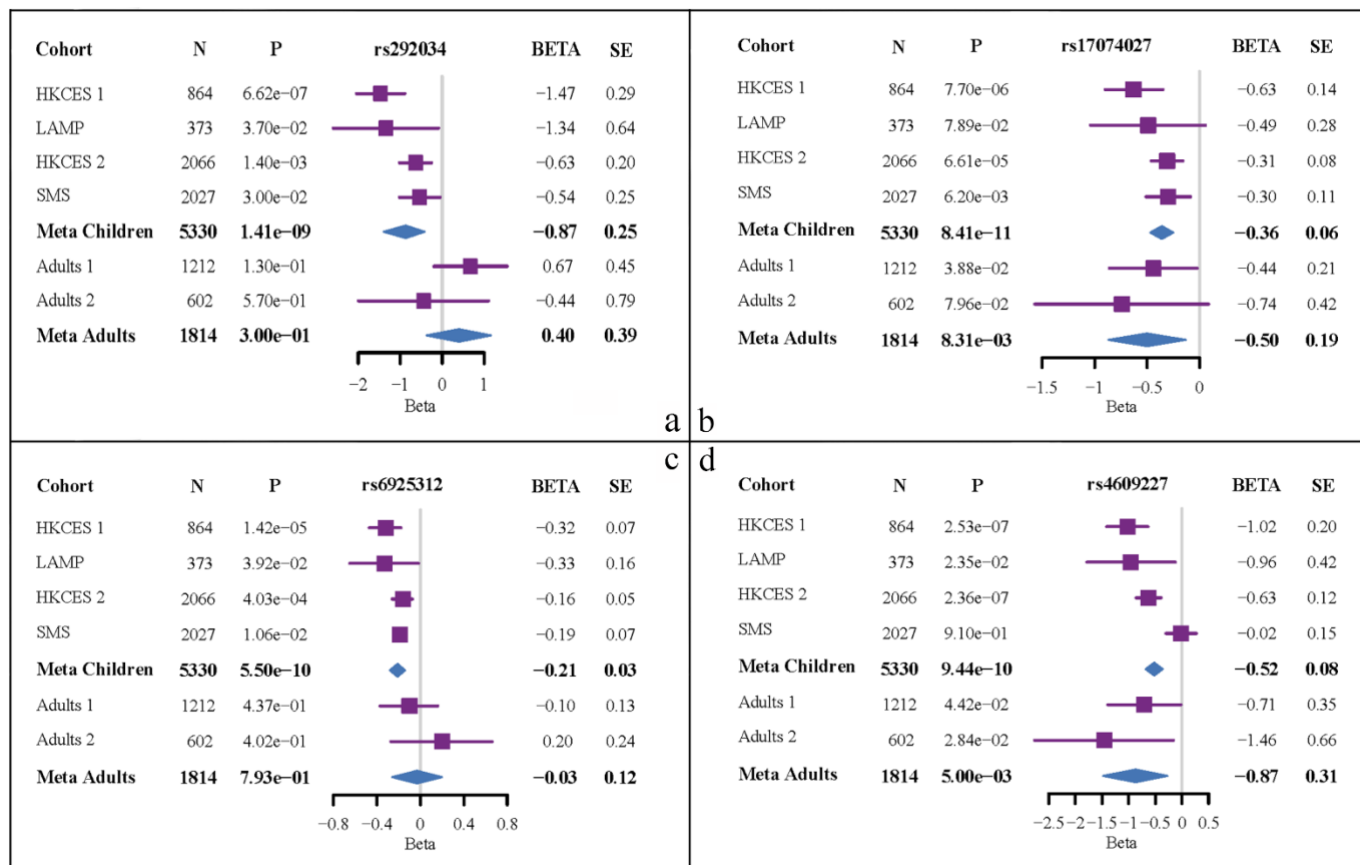


Fig. S3. Forest plot comparing associations between SNPs and spherical equivalent in children versus in adults. Each sub-figure represents a different SNP: (a) rs292034, (b) rs17074027, (c) rs6925312, and (d) rs4609227. The effect sizes (Beta) and standard errors (SE) are shown for each cohort. Meta-analysis was conducted using the Inverse Variance Weighted (IVW) fixed-effect model to combine the results from the different studies, with the summary effects presented for both children and adults. The horizontal lines indicate 95% confidence intervals. The figure was generated using R package (v. 3.4.2).

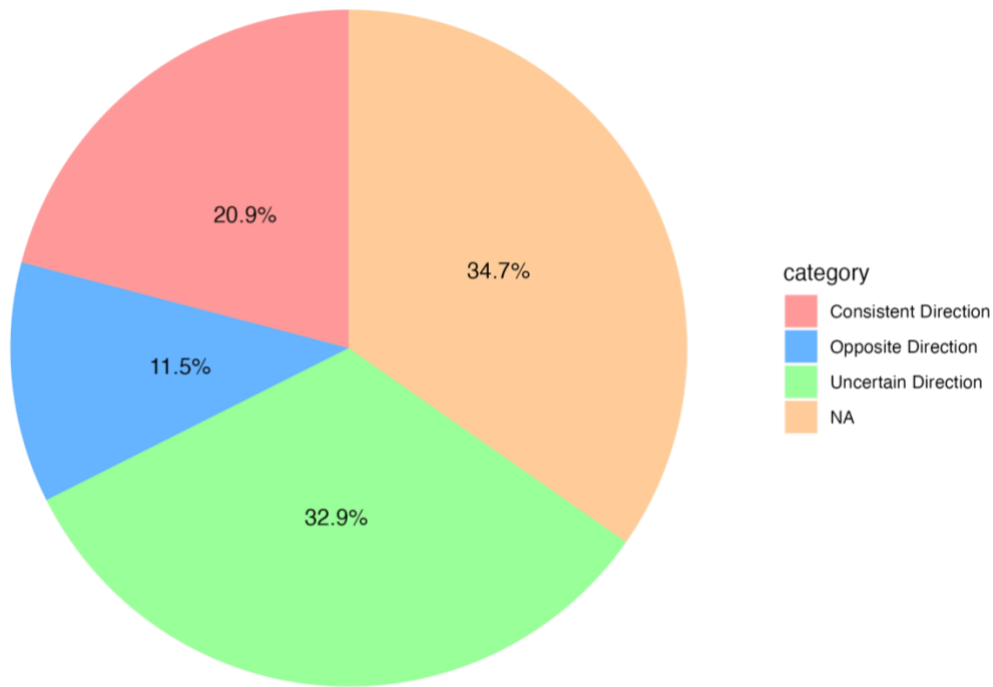


Fig. S4. Comparison of significant myopia loci between genome-wide association studies of European adults and our Chinese children. The orange part represents the percentage of SNPs that are not present in the GWAS of Chinese children; the red, blue, and green sections represent the percentages of SNPs showing consistent, opposite, and uncertain directions between the GWAS of European adults and Chinese children, respectively. The total number of 435 significant autosomal loci were from the study of Hysi et al. (Meta-analysis of 542,934 subjects of European ancestry identifies new genes and mechanisms predisposing to refractive error and myopia. *Nat Genet.* 2020 Apr;52(4):401-407). GWAS, genome-wide association studies; SNP, single nucleotide polymorphisms. The figure was generated using R package (v. 3.4.2).

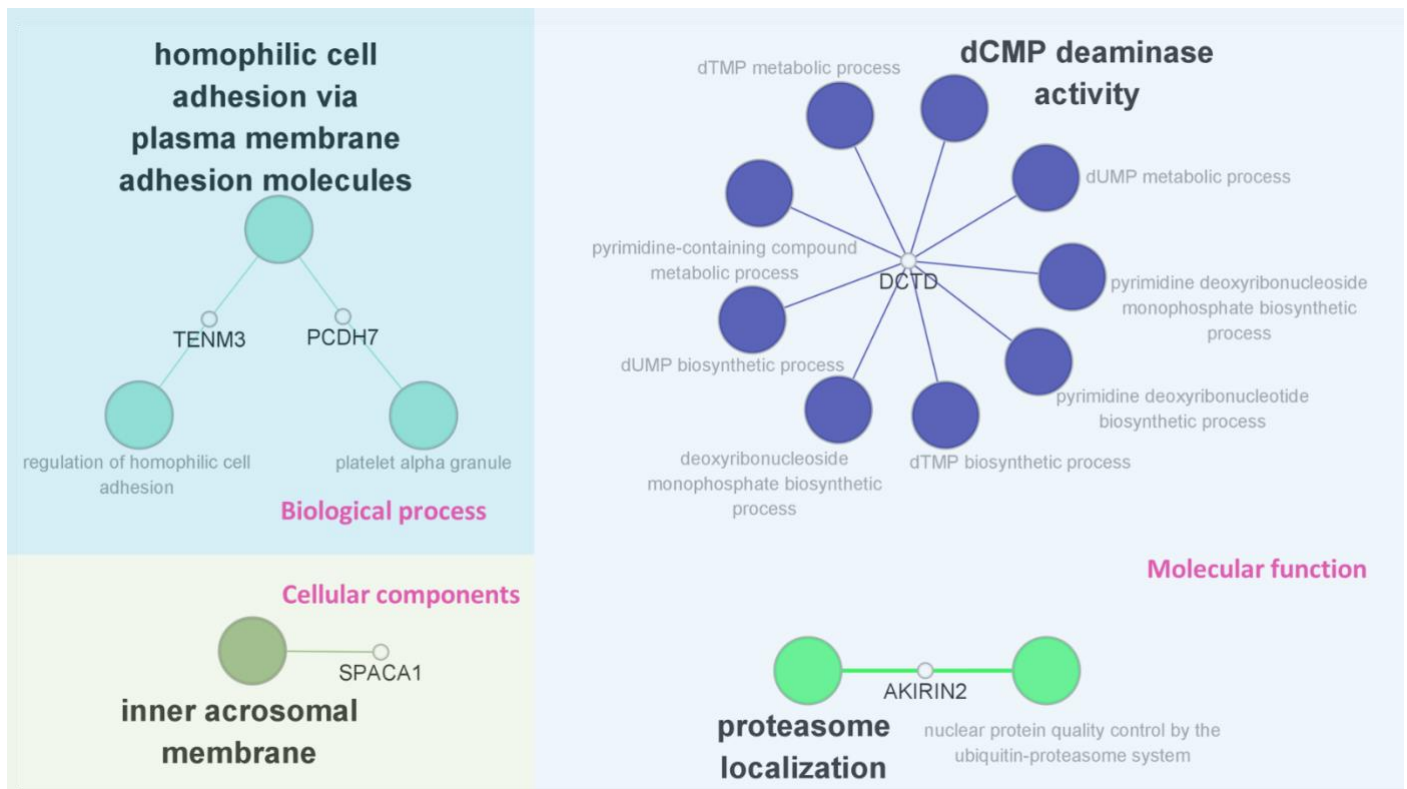


Fig. S5. Enrichment map showing the Gene Ontology (GO) terms identified in this study. Nodes represent GO terms. Important GO terms were shown in black bold. The map is categorized into three sections: biological processes, cellular components, and molecular functions. The figure was generated using ClueGo plugin in Cytoscape software (v. 3.9.1).

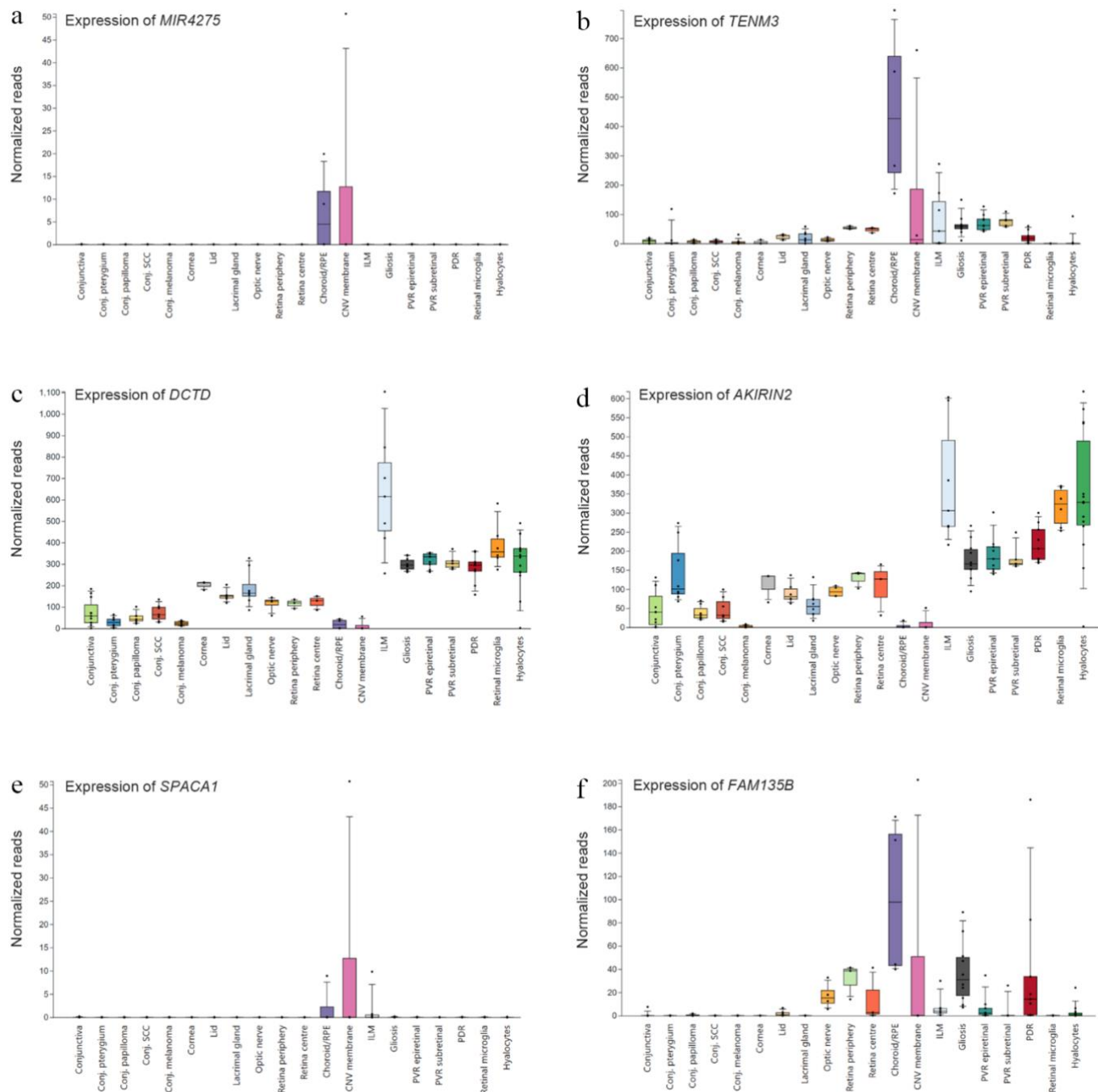


Fig. S6. Expression levels of genes nearby genome-wide significant SNPs predicted in ocular tissues by Human Eye Transcriptome Atlas. Normalized read counts are shown for (a) *MIR4275*, (b) *TENM3*, (c) *DCTD*, (d) *AKIRIN2*, (e) *SPACA1*, and (f) *FAM135B*. Each box plot represents the distribution of normalized reads, indicating the relative expression levels of the genes in different samples. Notable variations in expression can be observed in specific tissue or cell types for each gene. RPE, retinal pigment epithelium, ILM, internal limiting membrane; PVR, proliferative vitreoretinopathy; PDR, proliferative diabetic retinopathy. The figure was generated using Human Eye Transcriptome Atlas website (<https://www.eye-transcriptome.com/index.php>).

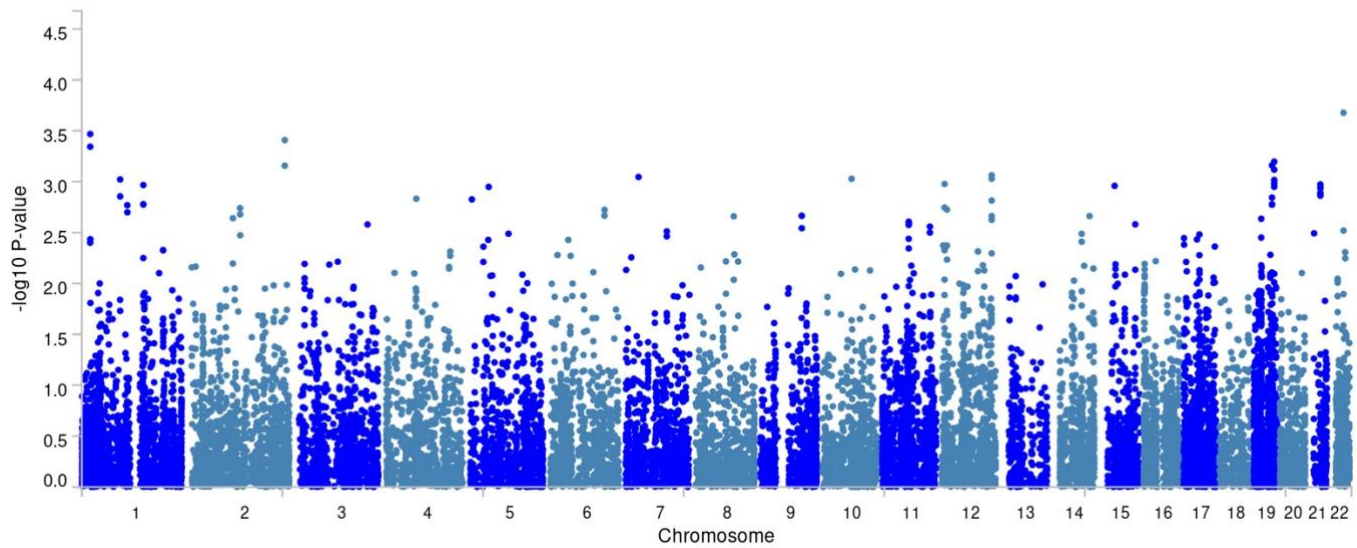


Fig. S7. Manhattan plot of gene-based test. The y axis is for the $-\log_{10} P$ values for association with spherical equivalent, the x axis is for chromosomes and base pair positions based on human genome build 37. $P < 2.60 \times 10^{-6}$ defines statistical significance. No genes reached the threshold for statistical significance in this analysis. The figure was generated using FUMA website (<https://fuma.ctglab.nl/>).

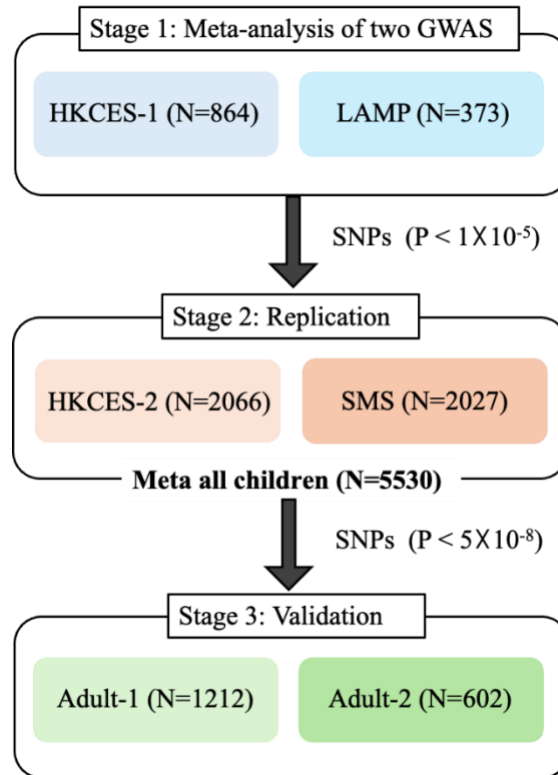


Fig. S8. Flowchart of the 3-stage study design. Stage 1 is a meta-analysis of two GWAS datasets from independent child cohorts: HKCES-1(N=864) and LAMP (N=373). Stage 2 is the replication of SNPs passing the preset significance threshold ($P \leq 1 \times 10^{-5}$) in another independent child cohorts: HKCES-2 (N=2066) and SMS (N=2027). A meta-analysis was then performed combining all child cohorts (total N=5530). Stage 3 is validation of SNPs reaching genome-wide significance ($P \leq 5 \times 10^{-8}$) in two independent adult cohorts: Adult-1 (N=1212) and Adult-2 (N=602). GWAS, genome-wide association studies; HKCES, Hong Kong Children Eye Study; LAMP, Low Concentration Atropine for Myopia Progression Study; SMS, Shantou Myopia Study. The figure was generated using Microsoft PowerPoint (v. 16.82).

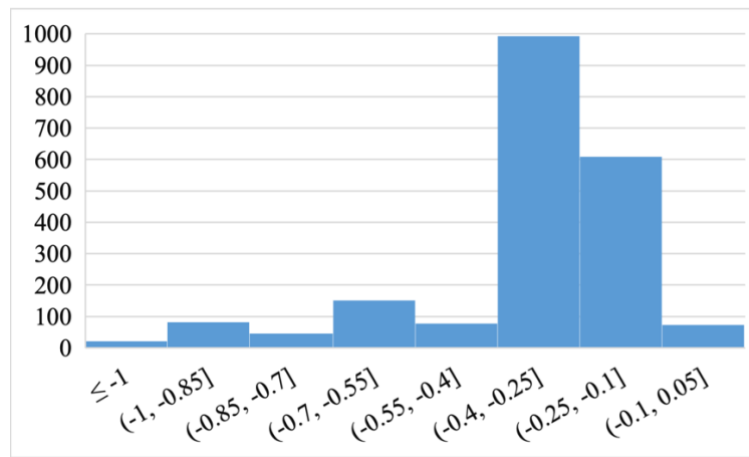


Fig. S9. Distribution of genetic risk scores. The x-axis represents the GRS score intervals, and the y-axis indicates the number of individuals within each interval. GRS, genetic risk score. The figure was generated using Microsoft Excel (v. 16.82).

Table S1. Results of the meta-GWAS of HKCES-1 and LAMP in the discovery stage

CHR	BP	SNP	EA	NEA	HKCES-1			LAMP			Meta-GWAS with age adjusted							Meta-GWAS with age2 adjusted						Nearby loci
					EAF	BETA	P	EAF	BETA	P	EAF	BETA ^a	P ^a	BETA.R. ^b	P.R. ^b	Q test	I ² (%)	BETA ^a	P ^a	BETA.R. ^b	P.R. ^b	Q test	I ² (%)	
1	242620371	rs75623525	A	G	0.064	-0.49	1.84E-04	0.062	-0.89	1.16E-03	0.063	-0.56	1.54E-06	-0.62	8.71E-04	0.19	42.74	-0.57	1.36E-06	-0.62	1.18E-03	0.17	46.38	PLD5
3	159168596	rs201346584	C	T	0.18	-0.29	5.97E-04	0.15	-0.56	2.00E-03	0.17	-0.34	9.09E-06	-0.38	3.13E-03	0.17	46.81	-0.34	8.45E-06	-0.38	4.24E-03	0.15	51.04	SCHIP1
4	28478119	rs292034	G	T	0.013	-1.47	6.62E-07	0.011	-1.34	3.69E-02	0.012	-1.45	5.72E-08	-1.45	5.72E-08	0.85	0	-1.44	5.91E-08	-1.44	5.908E-08	0.83	0	MIR4275
4	74640294	rs78130161	T	C	0.023	-0.85	5.81E-05	0.028	-0.75	6.27E-02	0.025	-0.83	8.71E-06	-0.83	8.71E-06	0.83	0	-0.83	9.03E-06	-0.83	0.000009032	0.81	0	CXCL8-CXCL6
4	183678700	rs17074027	G	T	0.058	-0.63	7.66E-06	0.06	-0.49	7.89E-02	0.059	-0.6	1.46E-06	-0.6	1.46E-06	0.66	0	-0.6	1.25E-06	-0.6	0.000001249	0.69	0	TENM3
6	88612769	rs6925312	G	A	0.77	-0.32	1.42E-05	0.75	-0.33	3.92E-02	0.76	-0.32	1.41E-06	-0.32	1.41E-06	1	0	-0.32	1.52E-06	-0.32	0.000001519	0.97	0	LOC101928911
8	65501179	rs149726960	T	C	0.018	-1.11	1.77E-06	0.02	-0.37	4.37E-01	0.019	-0.96	3.05E-06	-0.85	1.55E-02	0.16	49.66	-0.97	2.77E-06	-0.85	0.01535	0.16	50	CYP7B1
8	138229001	rs4609227	C	G	0.025	-1.02	2.53E-07	0.025	-0.96	2.35E-02	0.025	-1.01	1.40E-08	-1.01	1.40E-08	0.89	0	-1	1.58E-08	-1	1.584E-08	0.87	0	FAM135B
10	123023728	rs117198263	T	C	0.039	-0.72	1.68E-05	0.034	-0.55	1.39E-01	0.037	-0.69	5.22E-06	-0.69	5.22E-06	0.67	0	-0.7	4.83E-06	-0.7	0.000004833	0.66	0	FGFR2
14	94279274	rs75782951	T	A	0.033	0.77	9.67E-06	0.027	0.48	2.42E-01	0.031	0.72	5.07E-06	0.72	5.07E-06	0.53	0	0.73	4.82E-06	0.73	0.000004817	0.55	0	PRIMA1
15	32193644	rs6494040	T	C	0.29	-0.26	2.23E-04	0.31	-0.4	4.45E-03	0.30	-0.29	4.34E-06	-0.29	4.34E-06	0.36	0	-0.28	5.12E-06	-0.28	0.000005124	0.4	0	OTUD7A
17	33297065	rs1351554	T	C	0.11	-0.36	2.79E-04	0.14	-0.53	4.48E-03	0.12	-0.39	5.05E-06	-0.39	5.05E-06	0.41	0	-0.4	4.63E-06	-0.4	0.000004625	0.41	0	CCT6B
18	69708238	rs150547673	G	A	0.043	-0.55	4.14E-04	0.05	-0.92	3.51E-03	0.045	-0.63	7.38E-06	-0.64	3.71E-05	0.29	9.59	-0.62	9.51E-06	-0.62	0.00001341	0.31	1.91	CBLN2
20	22678410	rs2209794	C	T	0.16	0.29	6.47E-04	0.16	0.79	1.22E-05	0.16	0.39	5.77E-07	0.52	3.80E-02	0.011	84.4	0.38	6.51E-07	0.51	0.03719	0.012	84.05	LINC01747

^a Results were obtained using fixed-effect model; ^b results were obtained using random-effect model.

EA, effect allele; NEA, non-effect allele; EAF, effect allele frequency. I² (%), Heterogeneity.

Table S2. Results of the meta-GWAS of HKCES-1 and LAMP in the discovery stage

SNP	EA	EAF in HKCES 1	EAF in HKCES 2	EAF in LAMP	Original_P ^a	Bonferroni_P ^a	Original_P ^b	Bonferroni_P ^b
rs292034	T	0.013	0.011	0.011	0.54	1	1	1
rs17074027	T	0.058	0.076	0.06	0.02	0.06	1	1
rs6925312	A	0.78	0.78	0.76	0.24	0.97	1	1
rs4609227	G	0.025	0.025	0.025	0.99	1	1	1

The chi-square test is used to test the effect allele frequency between two cohorts; bonferroni test was used for multiple comparison.

^aComparisons between HKCES 1 and HKCES 2; ^bcomparisons between HKCES 1 and LAMP.

EA, effect allele; EAF, effect allele frequency.

Table S3. Associations between axial length and 4 SNPs identified in this study

CHR	SNP	BP ^a	Nearby Loci	Satge 1										Stage 2			Stage 3	
				EA	NEA	HKCES-1 (N=864)			LAMP (N=373)			Meta-GWAS (N=1237)		HKCES-2 (N=2066)			All cohorts (N=3303)	
						EAF	β	P	EAF	β	P	β ^b	P ^b	EAF	β	P	β ^c	P ^c
4	rs292034	28478119	MIR4275	G	T	0.013	0.68	3.31×10 ⁻⁴	0.011	0.32	0.28	0.58	2.88×10 ⁻⁴	0.011	0.35	4.76×10 ⁻³	0.43	8.37×10 ⁻⁶
4	rs17074027	183678700	TENM3	G	T	0.058	0.28	1.32×10 ⁻³	0.06	0.27	0.05	0.14	1.24×10 ⁻³	0.076	0.13	4.52×10 ⁻³	0.18	9.59×10 ⁻⁶
6	rs6925312	88612769	LOC101928911	G	A	0.78	0.16	5.32×10 ⁻⁴	0.76	0.1	0.23	0.15	3.09×10 ⁻³	0.78	0.09	1.07×10 ⁻³	0.11	1.89×10 ⁻⁶
8	rs4609227	138229001	FAM135B	C	G	0.025	0.55	8.49×10 ⁻⁶	0.025	0.076	0.71	0.31	5.15×10 ⁻⁶	0.025	0.29	1.49×10 ⁻⁴	0.34	5.03×10 ⁻⁸

CHR, chromosome; SNP, single nucleotide polymorphism; BP, base pair position; EA, effect allele; EAF, effect allele frequency; NEA, non-effect allele.

^a Position is based on NCBI human genome build 37.

^b Meta-analysis of AL used HKCES-1 and LAMP.

^c Meta-analysis of AL used HKCES-1, LAMP and HKCES-2.

Table S4. Association between rs292034 and different myopia severities

Cohort	EAF						EMM vs. Hyperopia		Myopia vs. NM		Mild myopia vs. NM		MH myopia vs. NM	
	Hyperopia	EMM	Myo	NM	Mild myopia	MH myopia	OR (95%CI)	P	OR (95%CI)	P	OR (95%CI)	P	OR (95%CI)	P
HKCES-1	0.0067	0.012	0.032	0.0087	0.021	0.093	1.72 (0.55, 5.42)	0.35	3.42 (1.42, 8.22)	6.01×10⁻³	2.39 (0.85, 6.68)	0.10	9.33 (2.77, 31.46)	3.16×10⁻⁴
HKCES-2	0.0052	0.016	0.014	0.0088	0.012	0.032	3.34 (1.59, 7.02)	1.50×10⁻³	1.72 (0.83, 3.57)	0.15	1.52 (0.69, 3.36)	0.30	4.41 (0.98, 19.88)	0.05
Shantou	0.031	0.0067	0.013	0.0084	0.011	0.019	0.22 (0.020, 2.38)	0.21	1.36 (0.48, 3.85)	0.57	1.20 (0.41, 3.51)	0.74	1.97 (0.64, 6.09)	0.24
Meta-all							2.33 (1.28, 4.27)	5.94×10⁻³	2.03 (1.24, 3.32)	5.06×10⁻³	1.62 (0.94, 2.79)	0.081	4.13 (2.0, 8.51)	1.30×10⁻⁴

EAF, effect allele frequency; Hyperopia ($SE \geq 0.5D$); EMM, emmetropia ($-0.5D < SE < 0.5D$); MH myopia, moderate and high myopia ($SE \leq -3.0D$); NM: no myopia (Hyperopia + EMM). The sample sizes for Hyperopia, EMM, Myo, NM, Mild myopia and MH myopia in HKCES-1 are 446, 246, 172, 692, 145 and 27; in HKCES-2 are 1140, 565, 361, 1705, 326 and 35; in Shantou are 17, 224, 1786, 241, 1257 and 529.

Table S5. Association between rs17074027 and different myopia severities

Cohort	EAF				EMM vs. Hyperopia				Myopia vs. NM		Mild myopia vs. NM		MH myopia vs. NM	
	Hyperopia	EMM	Myo	NM	Mild myopia	MH myopia	OR (95%CI)	P	OR (95%CI)	P	OR (95%CI)	P	OR (95%CI)	P
HKCES-1	0.047	0.045	0.1	0.046	0.093	0.17	0.91 (0.53, 1.57)	0.73	2.37 (1.49, 3.77)	2.81×10⁻⁴	2.10 (1.26, 3.47)	4.16×10⁻³	4.23 (1.77, 10.10)	1.15×10⁻³
HKCES-2	0.063	0.081	0.088	0.069	0.074	0.22	1.29 (0.97, 1.71)	0.077	1.27 (0.94, 1.71)	0.12	1.05 (0.75, 1.46)	0.77	3.88 (2.01, 7.50)	5.47×10⁻⁵
Shantou	0.029	0.051	0.076	0.05	0.075	0.079	1.84 (0.23, 14.69)	0.56	1.66 (1.07, 2.57)	0.025	1.59 (1.01, 2.51)	0.043	1.82 (1.12, 3.00)	0.016
Meta-all							1.20 (0.94, 1.55)	0.14	1.55 (1.25, 1.94)	7.99×10⁻⁵	1.37 (1.08, 1.74)	9.55×10⁻³	2.62 (1.84, 3.77)	1.24×10⁻⁷

EAF, effect allele frequency; Hyperopia ($SE \geq +0.5D$); EMM, emmetropia ($-0.5D < SE < 0.5D$); MH myopia, moderate and high myopia ($SE \leq -3.0D$); NM: no myopia (Hyperopia + EMM). The sample sizes for Hyperopia, EMM, Myo, NM, Mild myopia and MH myopia in HKCES-1 are 446, 246, 172, 692, 145 and 27; in HKCES-2 are 1140, 565, 361, 1705, 326 and 35; in Shantou are 17, 224, 1786, 241, 1257 and 529.

Table S6. Association between rs6925312 and different myopia severities

Cohort	EAF						EMM vs. Hyperopia		Myopia vs. NM		Mild myopia vs. NM		MH myopia vs. NM	
	Hyperopia	EMM	Myo	NM	Mild myopia	MH myopia	OR (95%CI)	P	OR (95%CI)	P	OR (95%CI)	P	OR (95%CI)	P
HKCES-1	0.74	0.77	0.83	0.75	0.81	0.93	1.23 (0.95, 1.62)	0.12	1.57 (1.14, 2.16)	5.66×10⁻³	1.39 (1, 1.93)	0.053	4.64 (1.61, 13.33)	4.37×10⁻³
HKCES-2	0.23	0.22	0.17	0.23	0.17	0.13	1.05 (0.88, 1.25)	0.56	1.44 (1.16, 1.78)	7.80×10⁻⁴	1.40 (1.13, 1.75)	2.60×10⁻³	1.88 (0.94, 3.77)	0.076
Shantou	0.82	0.75	0.79	0.76	0.79	0.81	0.74 (0.30, 1.84)	0.52	1.20 (0.96, 1.51)	0.11	1.17(0.93, 1.48)	0.18	1.32 (1.01, 1.73)	0.043
Meta-all							1.09 (0.94, 1.26)	0.22	1.37 (1.19, 1.57)	1.13×10⁻⁵	1.31 (1.13, 1.51)	2.63×10⁻⁴	1.48 (1.16, 1.88)	1.80×10⁻³

EAF, effect allele frequency; Hyperopia ($SE \geq +0.5D$); EMM, emmetropia ($-0.5D < SE < 0.5D$); MH myopia, moderate and high myopia ($SE \leq -3.0D$); NM: no myopia (Hyperopia + EMM). The sample sizes for Hyperopia, EMM, Myo, NM, Mild myopia and MH myopia in HKCES-1 are 446, 246, 172, 692, 145 and 27; in HKCES-2 are 1140, 565, 361, 1705, 326 and 35; in Shantou are 17, 224, 1786, 241, 1257 and 529.

Table S7. Association between rs4609227 and different myopia severities

Cohort	EAF				EMM vs. Hyperopia				Myopia vs. NM		Mild myopia vs. NM		MH myopia vs. NM	
	Hyperopia	EMM	Myo	NM	Mild myopia	MH myopia	OR (95%CI)	P	OR (95%CI)	P	OR (95%CI)	P	OR (95%CI)	P
HKCES-1	0.015	0.033	0.044	0.021	0.021	0.18	2.23 (1.05, 4.72)	0.037	1.74 (0.89, 3.39)	0.10	0.89 (0.36, 2.23)	0.80	8.85 (3.35, 23.35)	1.08×10⁻⁵
HKCES-2	0.018	0.023	0.05	0.02	0.046	0.11	1.24 (0.75, 2.06)	0.4	2.60 (1.68, 4.01)	1.62×10⁻⁵	2.37 (1.50, 3.73)	2.16×10⁻⁴	7.53 (2.64, 21.49)	1.59×10⁻⁴
Shantou	0.029	0.036	0.037	0.035	0.037	0.038	1.31 (0.16, 10.6)	0.8	1.05 (0.62, 1.79)	0.85	1.06 (0.62, 1.81)	0.84	1.06 (0.57, 1.97)	0.85
Meta-all							1.48 (0.98, 2.23)	0.061	1.79 (1.33, 2.42)	1.34×10⁻⁴	1.56 (1.13, 2.16)	7.46×10⁻³	2.55 (1.61, 4.09)	8.25×10⁻⁵

EAF, effect allele frequency; Hyperopia ($SE \geq +0.5D$); EMM, emmetropia ($-0.5D < SE < 0.5D$); MH myopia, moderate and high myopia ($SE \leq -3.0D$); NM: no myopia (Hyperopia + EMM). The sample sizes for Hyperopia, EMM, Myo, NM, Mild myopia and MH myopia in HKCES-1 are 446, 246, 172, 692, 145 and 27; in HKCES-2 are 1140, 565, 361, 1705, 326 and 35; in Shantou are 17, 224, 1786, 241, 1257 and 529.

Table S8. Associations between spherical equivalent and 4 SNPs in adults

CHR	SNP	BP	EA	NEA	Adult-1						Adult-2						Meta adult			
					EAF	BETA	SE	L95	U95	P	EAF	BETA	SE	L95	U95	P	BETA	P	Q test	I ²
4	rs292034	28478119	G	T	0.017	0.67	0.45	-0.2	1.55	0.13	0.017	-0.44	0.79	-1.99	1.10	0.57	0.40	0.30	0.22	34.11
4	rs17074027	183678700	G	T	0.077	-0.44	0.21	-0.86	-0.02	0.039	0.068	-0.74	0.42	-1.57	0.09	0.08	-0.50	0.0083	0.53	0
6	rs6925312	88612769	G	A	0.79	-0.10	0.13	-0.37	0.16	0.44	0.77	-0.2	0.24	-0.27	0.66	0.40	-0.031	0.79	0.27	19.25
8	rs4609227	138229001	C	G	0.028	-0.71	0.35	-1.39	-0.02	0.04	0.026	-1.46	0.66	-2.76	-0.16	0.028	-0.87	0.0051	0.32	0.45

EA, effect allele; NEA, non-effect allele; EAF, effect allele frequency. I², Heterogeneity.

Table S9. SNP×Age interaction analysis of 4 significant SNPs from GWAS of HKCES-1 cohort

	rs292034			rs17074027			rs6925312			rs4609227		
	β	Std.error	P	β	Std.error	P	β	Std.error	P	β	Std.error	P
Intercept	2.3	0.42	7.49E-08	2.41	0.44	6.26E-08	1.53	1.08	0.16	2.3	0.43	8.56E-08
Age	-0.32	0.05	7.55E-10	-0.33	0.05	1.94E-09	-0.16	0.14	0.27	-0.32	0.05	1.72E-09
SNP	4.07	2.51	0.1	0.04	1.27	0.97	0.62	0.65	0.34	1.97	1.64	0.23
SNP×Age	-0.66	0.31	0.036	-0.09	0.16	0.59	-0.13	0.09	0.14	-0.37	0.2	0.07
Sex	0.33	0.1	0.00058	0.32	0.1	0.00086	0.32	0.1	0.0009	0.32	0.1	0.001
PC1	0.66	3.14	0.83	-0.3	3.14	0.92	0.33	3.14	0.92	0.29	3.13	0.93
PC2	-3.44	5.14	0.5	-1.79	5.15	0.73	-3.07	5.15	0.55	-3.11	5.12	0.54
PC3	0.51	2.64	0.85	0.02	2.64	0.99	-0.05	2.64	0.98	0.33	2.63	0.9
PC4	1.75	1.49	0.24	2.22	1.5	0.14	1.78	1.49	0.23	1.67	1.48	0.26
PC5	-1.48	2.22	0.5	-2.09	2.22	0.35	-1.87	2.22	0.4	-1.51	2.21	0.5

SNP, single-nucleotide polymorphism; GWAS, genome-wide association study; HKCES, Hong Kong Children Eye Study; Std.error, standard error. PC, principal component.

Table S10. SNP×Age interaction analysis of 4 significant SNPs in GWAS of LAMP cohort

	rs292034			rs17074027			rs6925312			rs4609227		
	β	Std.error	P	β	Std.error	P	β	Std.error	P	β	Std.error	P
(Intercept)	-2	0.52	0.00015	-1.74	0.54	0.0014	-1.18	1.48	0.43	-1.89	0.53	0.0004
Age	-0.2	0.06	0.00029	-0.22	0.06	0.00015	-0.24	0.17	0.16	-0.22	0.06	0.00017
SNP	-3.73	3.25	0.25	-1.65	1.53	0.28	-0.48	0.86	0.58	-1.85	1.76	0.29
SNP×Age	0.27	0.35	0.45	0.14	0.19	0.44	0.02	0.1	0.87	0.11	0.21	0.6
Sex	-0.15	0.19	0.44	-0.2	0.19	0.31	-0.17	0.19	0.37	-0.13	0.19	0.49
PC1	-0.65	1.79	0.72	-0.63	1.8	0.73	-0.59	1.8	0.74	-0.57	1.79	0.75
PC2	-3.52	1.78	0.05	-3.61	1.78	0.04	-3.97	1.79	0.03	-3.62	1.78	0.04
PC3	-0.86	1.79	0.63	-0.84	1.79	0.64	-0.83	1.79	0.64	-0.9	1.79	0.61
PC4	-1.39	1.78	0.44	-1.49	1.79	0.4	-1.21	1.82	0.51	-1.44	1.78	0.42
PC5	-5.08	1.79	0.0048	-4.99	1.79	0.01	-4.8	1.8	0.01	-4.97	1.79	0.01
PC6	0.09	1.82	0.96	0.28	1.82	0.88	0.23	1.82	0.9	0.28	1.82	0.88
PC7	-0.06	1.79	0.97	-0.22	1.79	0.9	0	1.8	1	-0.09	1.78	0.96

SNP, single-nucleotide polymorphism; GWAS, genome-wide association study; HKCES, Hong Kong Children Eye Study; Std.error, standard error. PC, principal component.

Table S11. Comparison of SNPs previously associated with myopia in European adults and their effects in our children cohorts

CHR	SNP	BP	Nearest genes	EA	NEA	Meta-GWAS of European adult cohorts ^a				Meta-GWAS of our Chinese children cohorts				
						EAF of European adults	P	Direction	Heterogeneity I ² (%)	EAF of HKCES	EAF of LAMP	P	Direction	Heterogeneity I ² (%)
1	rs6668720	2420913	<i>PLCH2</i>	A	G	0.37	2.81E-09	+?+++	13.9	0.19	0.21	4.27E-01	+-	0
1	rs902356	8432653	<i>RERE</i>	A	G	0.24	1.74E-08	+++++	35.7	0.77	0.74	1.77E-01	+-	86.31
1	rs11121599	10666735	<i>PEX14</i>	A	G	0.21	1.76E-09	+++++	59.8	NA	NA	NA	NA	NA
1	rs3013105	13802325	<i>LRRC38</i>	T	C	0.6	2.49E-09	-----	44.1	0.36	0.37	3.61E-01	++	0
1	rs10753502	20759231	<i>VWA5B1</i>	A	C	0.33	1.2E-09	+++++	2.8	0.46	0.48	5.26E-01	+-	0
1	rs10158878	23259421	<i>EPHB2</i>	C	G	0.74	5.16E-10	+++++	0	NA	NA	NA	NA	NA
1	rs3131703	40419681	<i>TRIT1</i>	A	G	0.41	4.09E-10	-----	2.9	NA	NA	NA	NA	NA
1	rs6670896	42334793	<i>HIVEP3</i>	A	G	0.68	5.21E-36	-----	75.3	0.42	0.43	1.81E-01	--	0
1	rs673253	44062154	<i>SZT2</i>	T	C	0.44	2.72E-13	-----	0	0.2	0.18	3.63E-01	++	0
1	rs12409365	48107910	<i>TRABD2B</i>	C	G	0.94	3.16E-10	-----	45.7	NA	NA	NA	NA	NA
1	rs72660683	54191811	<i>GLIS1</i>	T	C	0.78	7.2E-13	+++++	0	NA	NA	NA	NA	NA
1	rs556161	61324813	<i>NFIA</i>	A	G	0.36	1.96E-28	-----	69.5	0.52	0.52	1.11E-01	--	0
1	rs10493817	89126887	<i>PKN2</i>	T	G	0.62	3.35E-08	-----	0	0.65	0.66	2.22E-01	++	0
1	rs12568187	91193691	<i>BARHL2</i>	T	C	0.56	1.24E-30	+++++	27.1	0.6	0.6	5.58E-02	++	0
1	rs11165052	94444060	<i>FAM69A</i>	A	C	0.32	3.2E-10	+++++	39.7	0.17	0.16	5.13E-01	++	0
1	rs501057	108087825	<i>PRMT6</i>	A	G	0.5	7.17E-15	-----	56.3	0.59	0.57	7.87E-01	+-	0
1	rs4839270	113477320	<i>FAM19A3</i>	A	T	0.23	7.8E-20	-----	58.3	0.03	0.03	4.37E-02	--	74.09
1	rs942453	150257262	<i>OTUD7B</i>	A	G	0.87	2.93E-15	-----	0	NA	NA	NA	NA	NA
1	rs4845402	154977929	<i>FLAD1</i>	A	G	0.14	5.36E-13	-----	0	NA	NA	NA	NA	NA
1	rs17420551	158039425	<i>RRNAD1</i>	A	T	0.72	7.01E-38	+++++	0	0.96	0.96	3.93E-01	--	0
1	rs1556867	164213686	<i>PBX1</i>	T	C	0.24	9.45E-48	-----	74.9	0.67	0.71	2.78E-01	+-	67.04
1	rs10753823	170798444	<i>PRRX1</i>	A	G	0.68	2.78E-11	-----	0	0.45	0.46	5.67E-01	+-	0
1	rs505837	179871712	<i>TOR1AIP2</i>	A	G	0.64	3.09E-09	-----	41.4	0.74	0.75	6.13E-01	+-	68.8
1	rs12569272	192085298	<i>RGS18</i>	T	G	0.82	3.06E-08	+++++	8.7	0.38	0.38	6.66E-02	++	0
1	rs2808514	200343081	<i>PTPRC</i>	A	G	0.61	1.18E-52	+++++	26.9	0.91	0.88	8.89E-01	+-	0
1	rs7549293	205312280	<i>NUAK2</i>	C	G	0.41	7.79E-13	+++++	0	0.38	0.34	8.43E-01	+-	63.55
1	rs2017760	207455421	<i>SRGAP2</i>	T	G	0.31	2.17E-54	-----	3.7	0.68	0.66	4.50E-01	++	0
1	rs11119421	210321043	<i>SYT14</i>	A	G	0.69	1.49E-13	+++++	32.7	0.58	0.57	6.84E-01	+-	65.88
1	rs6700065	214135660	<i>RPS6KC1</i>	T	G	0.66	1.09E-10	-----	56.6	0.79	0.81	9.29E-01	--	0
1	rs11585774	217222415	<i>ESRRG</i>	A	G	0.2	2.56E-08	+++++	0	NA	NA	NA	NA	NA
1	rs7525202	219788519	<i>TGFB2</i>	A	G	0.45	1.2E-40	-----	15.6	0.72	0.73	2.38E-01	--	0
1	rs6667260	226923938	<i>ITPKB</i>	A	C	0.54	1.25E-12	+++++	0	0.34	0.34	2.79E-01	+-	0
1	rs1490276	238130842	<i>ZP4</i>	T	C	0.52	6.91E-10	+++++	17.7	0.51	0.51	5.84E-01	+-	0
2	rs300751	209063	<i>FAM110C</i>	A	C	0.5	6.45E-25	-----	80.2	0.7	0.71	4.33E-01	--	0
2	rs11675358	2919797	<i>TSSC1</i>	A	T	0.71	5.47E-10	+++++	0	0.73	0.72	7.07E-01	--	0
2	rs28495254	16226048	<i>MYCN</i>	T	C	0.91	1.56E-09	-----	41.3	0.96	0.97	1.14E-01	--	0
2	rs1260326	27730940	<i>SNX17</i>	T	C	0.4	4.73E-10	-----+	37.4	0.46	0.47	7.31E-01	--	0
2	rs11127261	30475153	<i>LBH</i>	A	G	0.28	2.05E-20	-----	79.6	NA	NA	NA	NA	NA

Table S11. Comparison of SNPs previously associated with myopia in European adults and their effects in our children cohorts

CHR	SNP	BP	Nearest genes	EA	NEA	Meta-GWAS of European adult cohorts ^a				Meta-GWAS of our Chinese children cohorts				
						EA of European adults	P	Direction	Heterogeneity I ² (%)	EA of HKCES	EA of LAMP	P	Direction	Heterogeneity I ² (%)
2	rs13409142	32666137	<i>YIPF4</i>	T	C	0.66	2.47E-09	----	0	NA	NA	NA	NA	NA
2	rs1558655	40586022	<i>SLC8A1</i>	A	T	0.43	5.99E-09	++++	5.2	0.66	0.63	5.53E-01	+-	0
2	rs17032696	45137870	<i>ABCG8</i>	A	C	0.81	2.6E-26	----	54.9	0.51	0.53	9.78E-01	+-	65.84
2	rs17817004	46735423	<i>EPAS1</i>	T	C	0.37	1.05E-11	++++	0.8	0.06	0.06	9.43E-01	+-	0
2	rs12475184	48293584	<i>FBXO11</i>	T	C	0.71	5.67E-09	++++	23.8	NA	NA	NA	NA	NA
2	rs9309272	56095366	<i>ASB3</i>	T	G	0.13	2.59E-34	----	0	NA	NA	NA	NA	NA
2	rs359260	60486936	<i>BCL11A</i>	T	G	0.63	1.54E-11	++++	13.6	0.84	0.8	6.98E-01	++	0
2	rs11555696	74588605	<i>SLC4A5</i>	A	G	0.03	2.01E-11	+?+++	0	NA	NA	NA	NA	NA
2	rs6547257	79918454	<i>CTNNA2</i>	A	T	0.67	3.37E-12	----	0	0.89	0.92	3.39E-01	--	32.63
2	rs2570495	104443942	<i>NA</i>	T	C	0.6	4.61E-15	++++	0	0.31	0.34	2.51E-01	+-	11.19
2	rs7584334	124950895	<i>CNTNAP5</i>	T	C	0.22	5.77E-10	-+---	35.1	NA	NA	NA	NA	NA
2	rs61049169	146888708	<i>ZEB2</i>	A	G	0.45	5.34E-69	++++	0	NA	NA	NA	NA	NA
2	rs7601475	148410887	<i>ACVR2A</i>	A	G	0.41	2.38E-10	++++	39.2	0.25	0.25	2.41E-01	++	0
2	rs57902545	153702724	<i>ARL6IP6</i>	T	C	0.61	6.17E-11	++++	0	0.95	0.95	8.93E-01	+-	0
2	rs192716	157376472	<i>GPD2</i>	C	G	0.71	1.28E-35	++++	50.2	0.81	0.79	1.31E-01	++	0
2	rs10174570	161305018	<i>BAZ2B</i>	A	G	0.24	7.72E-10	++++	0	NA	NA	NA	NA	NA
2	rs935402	166185721	<i>SCN2A</i>	A	C	0.74	1.1E-11	++++	47	0.62	0.64	3.95E-01	--	0
2	rs17428076	172851936	<i>DYNC1I2</i>	C	G	0.76	1.85E-39	----	25.7	0.94	0.94	7.12E-01	+-	51.97
2	rs2573081	178828507	<i>HNRNPA3</i>	C	G	0.53	1.12E-70	++++	51.2	0.57	0.53	7.52E-02	++	0
2	rs7602799	182260252	<i>ITGA4</i>	T	C	0.39	3.32E-08	++++	0	0.78	0.76	5.36E-01	+-	73.45
2	rs73042687	184351234	<i>NA</i>	T	G	0.22	7.53E-11	++++	42.7	0.54	0.57	4.42E-01	++	54.22
2	rs13027546	208359507	<i>CREB1</i>	C	G	0.18	2.01E-08	++++	30.3	NA	NA	NA	NA	NA
2	rs121908120	219755011	<i>ZNF142</i>	A	T	0.03	1.65E-17	----+	62.4	NA	NA	NA	NA	NA
2	rs7569375	228093172	<i>COL4A3</i>	T	C	0.62	1.14E-08	++++	39.8	0.97	0.96	9.15E-01	+-	0
2	rs1550094	233385396	<i>B3GNT7</i>	A	G	0.7	1.48E-123	+?+++	90.1	NA	NA	NA	NA	NA
2	rs7596847	239321118	<i>TRAF3IP1</i>	A	T	0.16	5.71E-16	----	36.1	0.19	0.18	7.85E-01	+-	0
3	rs795288	4204455	<i>LRRN1</i>	T	C	0.68	2.78E-16	++++	15.9	0.59	0.57	3.42E-01	+-	82.22
3	rs178597	8196941	<i>NA</i>	T	C	0.59	6.28E-48	++++	0	0.16	0.14	8.47E-01	+-	0
3	rs1568072	11041606	<i>SLC6A1</i>	A	G	0.23	1.57E-13	++++	0	0.24	0.26	8.73E-01	+-	0
3	rs13073161	16007825	<i>ANKRD28</i>	T	C	0.48	1.01E-17	----	42.5	NA	NA	NA	NA	NA
3	rs1700943	24231030	<i>NR1D2</i>	C	G	0.47	4.38E-34	----	18.6	NA	0.55	NA	NA-	NA
3	rs7427073	28163157	<i>CMC1</i>	A	C	0.71	9.76E-09	----	59.9	0.88	0.85	5.64E-02	++	0
3	rs4130686	29443963	<i>RBMS3</i>	C	G	0.65	2.54E-12	----	21.9	0.52	0.56	6.69E-01	++	0
3	rs6810039	33194990	<i>CRTAP</i>	A	C	0.4	2.01E-15	++++	0	NA	NA	NA	NA	NA
3	rs12492279	41289031	<i>EIF1B</i>	T	C	0.54	3.31E-27	++++	0	0.75	0.7	2.21E-01	+-	82.35
3	rs7634084	49949834	<i>LRRC2</i>	A	T	0.49	3.85E-14	----	23.8	0.86	0.86	9.77E-01	+-	0
3	rs78486117	51388394	<i>DOCK3</i>	C	G	0.08	7.77E-09	----	26	NA	NA	NA	NA	NA
3	rs14165	53847408	<i>TKT</i>	A	G	0.31	9.04E-24	++++	0	NA	NA	NA	NA	NA

Table S11. Comparison of SNPs previously associated with myopia in European adults and their effects in our children cohorts

CHR	SNP	BP	Nearest genes	EA	NEA	Meta-GWAS of European adult cohorts ^a				Meta-GWAS of our Chinese children cohorts				
						EA of European adults	P	Direction	Heterogeneity I ² (%)	EA of HKCES	EA of LAMP	P	Direction	Heterogeneity I ² (%)
3	rs1907462	56534434	<i>ERC2</i>	A	G	0.24	2.27E-10	+++++	44.6	0.46	0.46	3.52E-01	+-	0
3	rs7431936	58263847	<i>ABHD6</i>	A	G	0.92	4.93E-14	+++++	0	NA	NA	NA	NA	NA
3	rs1562523	60933802	<i>FHIT</i>	T	G	0.44	1.02E-08	+++++	0	NA	NA	NA	NA	NA
3	rs35667547	64547477	<i>THOC7</i>	C	G	0.13	4.6E-11	-?--+	67.9	NA	NA	NA	NA	NA
3	rs60743220	68945153	<i>FAM19A4</i>	T	C	0.84	6.73E-24	+++++	74.3	0.51	0.51	3.25E-01	+-	31.57
3	rs11928769	70985059	<i>FOXP1</i>	A	C	0.3	3.58E-08	+++++	0	NA	NA	NA	NA	NA
3	rs1045960	73117835	<i>PPP4R2</i>	T	C	0.4	3.32E-11	-----	36.9	0.09	0.08	6.96E-01	++	0
3	rs73117594	78593913	<i>ROBO1</i>	T	G	0.11	2.03E-09	+++++	0	NA	NA	NA	NA	NA
3	rs6549043	85632126	<i>CADM2</i>	A	T	0.37	3.59E-18	+++++	5.5	0.14	0.12	6.45E-01	++	0
3	rs9824877	98896242	<i>CPOX</i>	A	G	0.22	5.11E-25	-----	59.5	NA	NA	NA	NA	NA
3	rs7619476	107800880	<i>CD47</i>	A	G	0.55	3.64E-10	-----	29.2	NA	NA	NA	NA	NA
3	rs35867	118739836	<i>IGSF11</i>	T	C	0.39	5.78E-16	+++++	0	0.43	0.48	6.90E-01	+-	0
3	rs2124500	123093530	<i>ADCY5</i>	T	C	0.26	4.8E-08	+++++	8.9	NA	NA	NA	NA	NA
3	rs113761591	127305355	<i>KLF15</i>	T	C	0.2	9E-21	+++++	0	NA	NA	NA	NA	NA
3	rs10934960	130514936	<i>PIK3R4</i>	A	G	0.51	5.17E-11	+++++	0	0.49	0.48	9.36E-02	+-	24.67
3	rs3762672	132218623	<i>DNAJC13</i>	T	G	0.47	5.02E-09	+++++	6.5	0.88	0.87	5.32E-01	+-	52.45
3	rs6767786	141104180	<i>ZBTB38</i>	A	G	0.35	1.45E-57	+++++	53.4	NA	NA	NA	NA	NA
3	rs62273875	147707460	<i>ZIC1</i>	A	G	0.83	8.45E-12	-----	13.6	0.6	0.6	5.08E-01	--	0
3	rs41267883	150174658	<i>TSC22D2</i>	A	G	0.91	1.43E-10	+++++	64.6	0.92	0.93	5.06E-01	++	0
3	rs199771582	171989276	<i>FNDC3B</i>	T	G	0.81	1.89E-14	+++++	0	0.7	0.69	2.40E-01	++	0
3	rs9832291	178701523	<i>ZMAT3</i>	T	C	0.34	1.51E-09	-----	0	0.45	0.42	2.46E-01	+-	81.8
3	rs1863622	186396616	<i>HRG</i>	T	C	0.78	1.01E-08	++++-	54.3	NA	NA	NA	NA	NA
4	rs57829920	5783386	<i>EVC</i>	A	T	0.56	1.71E-09	-----	0	NA	NA	NA	NA	NA
4	rs3756171	8602225	<i>CPZ</i>	T	C	0.25	1.78E-08	+?+++	0	0.68	0.71	5.04E-01	+-	0
4	rs9968377	18185077	<i>LCORL</i>	T	C	0.62	3.92E-09	-----	36.1	0.8	0.8	5.62E-01	--	0
4	rs11734373	23939920	<i>PPARGC1A</i>	A	G	0.35	2.82E-11	-----	38.6	NA	NA	NA	NA	NA
4	rs6828872	30765027	<i>PCDH7</i>	C	G	0.53	3.47E-08	+?+++	33.5	0.36	0.38	6.64E-02	++	0
4	rs7691051	31993241	<i>NA</i>	A	T	0.33	4.27E-11	-----	5.2	0.31	0.29	5.29E-01	--	25.61
4	rs33998475	42200204	<i>BEND4</i>	A	G	0.1	3.51E-09	+++++	6	0.28	0.29	2.80E-01	+-	13.22
4	rs28526098	44933151	<i>GNPDA2</i>	A	C	0.88	5.08E-18	-----	56.4	0.63	0.62	9.38E-01	+-	50.86
4	rs10030755	62844408	<i>LPHN3</i>	A	C	0.8	1.55E-10	+++++	0	0.57	0.58	7.72E-01	--	0
4	rs28564890	72535505	<i>SLC4A4,GC</i>	T	C	0.9	8.38E-09	+++++	0	0.7	0.72	7.76E-01	+-	63.2
4	rs74764079	81952637	<i>ANXA3</i>	A	T	0.03	1.99E-65	-----	33.9	NA	NA	NA	NA	NA
4	rs3775228	87985166	<i>SLC10A6</i>	T	C	0.4	6.59E-12	+++++	56.4	0.39	0.39	1.36E-01	+-	67.02
4	rs59473955	89757082	<i>FAM13A</i>	T	C	0.76	6.17E-33	-----	72.7	NA	NA	NA	NA	NA
4	rs13107325	103188709	<i>BANK1</i>	T	C	0.07	4.03E-17	+++++	0	NA	NA	NA	NA	NA
4	rs9790778	112129355	<i>NA</i>	T	C	0.42	1.37E-08	+++++	0	0.22	0.22	3.15E-01	++	0
4	rs12511880	120901526	<i>MYOZ2</i>	A	T	0.39	5.13E-18	+++++	78.4	NA	NA	NA	NA	NA

Table S11. Comparison of SNPs previously associated with myopia in European adults and their effects in our children cohorts

CHR	SNP	BP	Nearest genes	EA	NEA	Meta-GWAS of European adult cohorts ^a				Meta-GWAS of our Chinese children cohorts				
						EAF of European adults	P	Direction	Heterogeneity I ² (%)	EAF of HKCES	EAF of LAMP	P	Direction	Heterogeneity I ² (%)
4	rs34687569	138497581	<i>PCDH18</i>	T	C	0.75	4.54E-11	+++++	32.7	0.47	0.44	1.56E-01	--	0
4	rs73858679	141918504	<i>RNF150</i>	A	C	0.06	1.75E-08	+++++	0	NA	NA	NA	NA	NA
4	rs6537315	145724712	<i>HHIP</i>	A	G	0.44	5.42E-09	+++++	0	NA	NA	NA	NA	NA
4	rs11940147	149974078	<i>NA</i>	T	G	0.25	6.55E-12	+++++	0	NA	NA	NA	NA	NA
4	rs2045629	166777051	<i>TLL1</i>	A	G	0.44	7.99E-11	+++++	0	0.84	0.82	6.71E-01	+-	0
4	rs147792504	174336590	<i>GALNT7</i>	A	T	0.02	2.01E-15	-?---	59.1	NA	NA	NA	NA	NA
4	rs35446926	183035265	<i>TENM3</i>	T	C	0.72	2.48E-11	-----	0	0.47	0.47	2.28E-01	--	0
5	rs4499830	11852047	<i>CTNND2</i>	T	C	0.67	3E-08	-----	0	NA	NA	NA	NA	NA
5	rs2910644	41265864	<i>C6</i>	A	G	0.14	2.13E-08	-----	0	0.27	0.28	5.30E-01	++	0
5	rs75150349	45491724	<i>FGF10</i>	T	G	0.13	1.45E-13	-----	0	NA	NA	NA	NA	NA
5	rs35567312	49626919	<i>EMB</i>	T	C	0.11	7.03E-10	-----	0	NA	NA	NA	NA	NA
5	rs12514897	52670974	<i>FST</i>	T	G	0.89	5.99E-12	+++++	22.7	NA	NA	NA	NA	NA
5	rs3936511	55860781	<i>MAP3K1</i>	A	G	0.81	6.34E-09	+++++	0	0.85	0.85	6.64E-01	+-	12.83
5	rs10223052	60800336	<i>ELOVL7</i>	A	G	0.36	8.83E-09	-----	0	NA	NA	NA	NA	NA
5	rs1309551	64288656	<i>CWC27</i>	T	G	0.55	1.84E-16	-----	60.9	0.62	0.67	7.41E-01	--	0
5	rs7730838	71708698	<i>MAP1B</i>	T	G	0.45	1.4E-12	+++++	60	0.88	0.87	3.45E-01	++	28.14
5	rs256438	79366249	<i>MTX3</i>	T	G	0.64	1.1E-12	+++++	12.9	0.77	0.81	2.18E-01	++	38.61
5	rs7737179	87795525	<i>TMEM161B</i>	A	G	0.23	3.25E-23	-----	1.9	NA	NA	NA	NA	NA
5	rs4242244	92546237	<i>NA</i>	T	G	0.58	5.68E-09	-+---	4.9	0.37	0.35	9.82E-01	+-	0
5	rs146172211	102620108	<i>PAM</i>	A	C	0.03	2.42E-10	++++-	59.5	NA	NA	NA	NA	NA
5	rs13189957	111836991	<i>EPB41L4A</i>	A	G	0.77	3.65E-08	-----	41.2	NA	NA	NA	NA	NA
5	rs10066524	123950880	<i>ZNF608</i>	A	G	0.21	4.14E-08	-----	13.7	0.41	0.44	5.93E-01	+-	0
5	rs6860901	127871750	<i>FBN2</i>	T	C	0.31	8.63E-11	+++++	44.5	0.17	0.15	1.45E-01	++	0
5	rs7732667	132070333	<i>IL4</i>	C	G	0.86	2.55E-10	+++++	14.8	0.2	0.19	9.29E-01	+-	32.18
5	rs246073	140317371	<i>CXXC5</i>	T	C	0.64	1.77E-14	+++++	0	0.41	0.42	9.03E-01	+-	0
5	rs6864640	143540718	<i>YIPF5</i>	T	C	0.21	1.95E-13	-----	0	0.18	0.19	1.88E-01	--	0
5	rs62385438	158497639	<i>EBF1</i>	T	C	0.68	8.63E-18	-----	21.3	0.81	0.78	7.22E-01	+-	0
5	rs10042371	165945863	<i>NA</i>	T	G	0.8	5.12E-12	+++++	0	0.81	0.8	6.15E-01	--	0
5	rs6875105	173054917	<i>BOD1</i>	T	C	0.62	7.52E-09	-----	40.1	NA	0.79	NA	NA-	NA
5	rs13190379	174697891	<i>DRD1</i>	A	T	0.41	4.51E-16	+++++	7.1	NA	NA	NA	NA	NA
5	rs12186577	178359989	<i>ZNF354B</i>	T	C	0.9	8.63E-17	+++++	47.4	0.88	0.87	6.17E-01	--	0
6	rs11758482	2438231	<i>MAS1L</i>	A	G	0.78	1.75E-20	+++++	44.5	0.58	0.55	1.33E-01	+-	0
6	rs9379066	6901856	<i>LY86</i>	T	C	0.64	1.01E-21	+++++	24	0.85	0.83	3.54E-02	++	63.8
6	rs115504329	11719478	<i>ADTRP</i>	C	G	0.06	3.23E-08	+++++	37.7	NA	NA	NA	NA	NA
6	rs4145443	22068174	<i>CDKAL1</i>	T	G	0.56	6.41E-38	-----	82.1	0.13	0.15	8.41E-01	+-	27.55
6	rs1150687	28162469	<i>LRRC16A</i>	T	C	0.61	4.32E-34	+++++	0	0.42	0.42	1.84E-01	++	0
6	rs4711751	43828582	<i>GLTSCR1L</i>	T	C	0.5	1.67E-12	-----	0	0.75	0.77	7.57E-01	--	0
6	rs2076309	50789451	<i>TFAP2D</i>	T	C	0.46	4.19E-37	+++++	26.7	NA	NA	NA	NA	NA

Table S11. Comparison of SNPs previously associated with myopia in European adults and their effects in our children cohorts

CHR	SNP	BP	Nearest genes	EA	NEA	Meta-GWAS of European adult cohorts ^a				Meta-GWAS of our Chinese children cohorts				
						EAF of European adults	P	Direction	Heterogeneity I ² (%)	EAF of HKCES	EAF of LAMP	P	Direction	Heterogeneity I ² (%)
6	rs7744813	73643289	<i>OGFRL1</i>	A	C	0.59	2.61E-205	----	91.5	0.78	0.82	5.51E-01	++	21.45
6	rs171835	82464987	<i>FAM46A</i>	A	G	0.24	5.7E-14	++++	42.3	0.27	0.22	7.25E-01	++	0
6	rs1118543	84380492	<i>PRSS35</i>	C	G	0.33	1.85E-26	++++	56.5	0.53	0.5	8.00E-01	++	0
6	rs1906252	98550289	<i>NA</i>	A	C	0.49	2.44E-15	----+	74.7	0.43	0.38	4.11E-01	--	0
6	rs9484245	100193003	<i>PRDM13</i>	A	C	0.79	1.54E-15	----	0	NA	NA	NA	NA	NA
6	rs11153164	109596309	<i>CCDC162P</i>	A	G	0.31	3.5E-08	----	0	0.39	0.38	8.00E-01	+-	78.72
6	rs4947120	111819044	<i>GTF3C6</i>	A	G	0.86	3.07E-10	----	61.5	NA	NA	NA	NA	NA
6	rs1064583	116446576	<i>FRK</i>	A	G	0.61	2.34E-36	++++	63.2	NA	NA	NA	NA	NA
6	rs9372732	123348147	<i>CLVS2</i>	T	C	0.35	4.11E-11	----	0	NA	NA	NA	NA	NA
6	rs12193446	129820038	<i>LAMA2</i>	A	G	0.91	0	----	93	NA	NA	NA	NA	NA
6	rs4896068	134834538	<i>SGK1</i>	A	G	0.44	6.39E-10	++++	52.4	0.78	0.78	3.38E-01	--	0
6	rs7756435	141335140	<i>NA</i>	C	G	0.23	7.91E-12	++++	0	0.37	0.37	7.34E-01	--	0
6	rs9497026	144950023	<i>UTRN</i>	T	G	0.18	6.15E-10	++++	0	0.07	0.06	9.46E-01	+-	0
6	rs4869965	151301241	<i>MTHFD1L</i>	A	G	0.3	5.14E-20	----	56.2	0.68	0.64	5.64E-01	+-	0
6	rs3127166	159248730	<i>SYTL3</i>	A	G	0.37	5.35E-09	++++	13.4	NA	NA	NA	NA	NA
6	rs880095	164249854	<i>QKI</i>	T	C	0.56	4.54E-12	+----	50.9	0.63	0.6	2.70E-01	++	0
7	rs4721135	1912222	<i>MAD1L1</i>	A	G	0.59	1.79E-15	-?---	7.6	0.51	0.51	5.92E-01	+-	0
7	rs7786560	7252249	<i>C1GALT1</i>	A	C	0.39	1.56E-17	++++	0	0.06	0.06	2.07E-01	--	0
7	rs2355125	11920805	<i>THSD7A</i>	A	G	0.37	3.97E-08	++++	0	0.24	0.22	3.94E-01	++	0
7	rs11772758	17079154	<i>AGR3</i>	A	G	0.22	8.61E-12	----	0	0.11	0.12	4.33E-01	++	0
7	rs7780001	19477981	<i>FERD3L</i>	A	T	0.87	2.31E-09	----	0	0.81	0.82	5.67E-01	--	0
7	rs2075822	30490760	<i>NOD1</i>	A	G	0.77	1.41E-08	++++	0	0.78	0.78	5.53E-01	+-	25.08
7	rs2726052	36199170	<i>EEPD1</i>	A	G	0.22	2.74E-08	++++	0	0.03	0.03	8.39E-01	+-	0
7	rs2696187	39043106	<i>POU6F2</i>	T	C	0.42	1.11E-11	----	0	NA	NA	NA	NA	NA
7	rs7793034	42115516	<i>GLI3</i>	A	G	0.49	1.27E-10	++++	3	0.45	0.42	4.59E-01	++	27.47
7	rs10258656	47763485	<i>PKD1L1</i>	A	C	0.22	1.17E-11	++++	61.6	0.29	0.31	6.69E-01	+-	0
7	rs12719025	51100190	<i>COBL</i>	A	G	0.54	3.11E-11	++++	52.8	0.81	0.79	6.92E-01	+-	0
7	rs7802500	69907025	<i>AUTS2</i>	A	G	0.21	1.97E-09	++++	31.3	0.22	0.23	7.79E-01	+-	0
7	rs2867673	71752652	<i>CALN1</i>	T	C	0.48	2E-09	----	0	0.45	0.43	6.26E-01	++	0
7	rs10260177	78075634	<i>MAGI2</i>	T	C	0.11	2.69E-17	----	0	NA	NA	NA	NA	NA
7	rs6954078	82435878	<i>PCLO</i>	T	G	0.5	9.58E-24	----	2.8	0.83	0.83	8.10E-01	+-	73.6
7	rs144137329	84150814	<i>SEMA3A</i>	T	C	0.78	6.71E-11	----+	42.8	0.83	0.85	4.76E-01	+-	0
7	rs7800245	86103733	<i>GRM3</i>	C	G	0.27	1.81E-16	----	48.8	0.26	0.3	2.15E-01	+-	61.58
7	rs854089	95303256	<i>PDK4</i>	A	T	0.3	8.04E-13	++++	46	0.32	0.29	1.37E-01	+-	0
7	rs6946168	99598286	<i>OR2AE1</i>	T	C	0.29	3.38E-16	----	21.8	0.22	0.24	6.62E-01	++	0
7	rs2708597	112056230	<i>DOCK4</i>	C	G	0.13	2.98E-11	++++	38.9	0.19	0.16	2.62E-01	+-	0
7	rs2024211	116153025	<i>CAV2</i>	A	C	0.73	5.9E-10	++++	52.4	NA	NA	NA	NA	NA
7	rs148101639	124531504	<i>GPR37</i>	A	G	0.01	4.35E-08	-?--+	18.7	NA	NA	NA	NA	NA

Table S11. Comparison of SNPs previously associated with myopia in European adults and their effects in our children cohorts

CHR	SNP	BP	Nearest genes	EA	NEA	Meta-GWAS of European adult cohorts ^a				Meta-GWAS of our Chinese children cohorts				
						EA of European adults	P	Direction	Heterogeneity I ² (%)	EA of HKCES	EA of LAMP	P	Direction	Heterogeneity I ² (%)
7	rs17150996	127174679	<i>GCC1</i>	A	G	0.36	3.96E-08	+++++	49.7	0.74	0.75	9.39E-01	+-	0
7	rs62468101	131550503	<i>MKLN1</i>	T	C	0.76	1.4E-11	----	0	0.97	0.96	2.13E-01	--	0
7	rs1646555	137604835	<i>CREB3L2</i>	A	T	0.37	2.09E-09	----+	48.1	NA	NA	NA	NA	NA
7	rs58287690	151122699	<i>WDR86</i>	T	G	0.87	1.04E-20	+?+++	0	0.95	0.94	7.42E-01	++	0
7	rs12234576	158928375	<i>PTPRN2</i>	A	G	0.18	1.79E-37	+++++	0	0.16	0.13	2.18E-02	++	0
8	rs4875839	2490537	<i>CSMD1</i>	C	G	0.64	6.73E-10	+++++	0	0.39	0.4	6.67E-02	--	0
8	rs10100265	10633159	<i>SGK223</i>	A	C	0.39	1E-24	+++++	0	0.65	0.64	3.77E-01	+-	86.54
8	rs1905014	13407297	<i>DLC1</i>	T	C	0.57	1.41E-08	----	49.7	0.62	0.61	4.52E-01	--	0
8	rs11781149	22473158	<i>DOK2</i>	T	C	0.33	2.39E-17	----	0	NA	NA	NA	NA	NA
8	rs1532276	27466157	<i>CLU</i>	T	C	0.4	3.35E-16	----	69.8	0.24	0.25	2.62E-01	--	0
8	rs16890057	40726582	<i>ZMAT4</i>	A	G	0.21	1.99E-81	+++++	73.8	0.1	0.08	1.11E-01	++	0
8	rs1371951	53385818	<i>ST18</i>	C	G	0.14	7.08E-25	----	49.6	NA	NA	NA	NA	NA
8	rs61334940	57072570	<i>LYN</i>	T	C	0.81	1.14E-19	----	0	0.92	0.94	5.20E-01	+-	0
8	rs72621438	60178580	<i>TOX</i>	C	G	0.65	1E-153	----	65.9	0.55	0.59	4.07E-01	--	0
8	rs1425598	64753446	<i>NA</i>	T	C	0.71	3.5E-10	+++++	0	NA	NA	NA	NA	NA
8	rs4738094	71423744	<i>NCOA2</i>	A	G	0.65	1.21E-26	----	60.8	NA	NA	NA	NA	NA
8	rs10112386	74281152	<i>RDH10</i>	T	C	0.83	8E-12	+?+++	64	NA	NA	NA	NA	NA
8	rs9650252	75731730	<i>PII5</i>	T	C	0.07	1.71E-13	+++++	0	0.02	0.01	1.29E-02	++	0
8	rs6995342	78951749	<i>NA</i>	A	T	0.63	3.57E-18	----	10.3	0.49	0.48	5.03E-01	++	0
8	rs13268738	87673711	<i>CNGB3</i>	T	C	0.42	1.01E-14	+++++	0	NA	NA	NA	NA	NA
8	rs7816934	89312391	<i>MMP16</i>	T	C	0.9	1.15E-10	+++++	36.4	NA	NA	NA	NA	NA
8	rs2575725	97610840	<i>SDC2</i>	A	G	0.51	4.46E-09	+++++	0	NA	NA	NA	NA	NA
8	rs4133395	108314971	<i>ANGPT1</i>	T	G	0.61	2.72E-08	+?+++	42.3	0.86	0.86	6.48E-01	++	0
8	rs6988919	121630740	<i>SNTB1</i>	C	G	0.62	3.09E-27	+++++	11.3	0.26	0.24	2.18E-01	+-	58.69
8	rs1158569	131331012	<i>ASAP1</i>	A	C	0.49	3.48E-09	+++++	41.4	0.39	0.38	9.29E-01	+-	0
8	rs1865249	142215982	<i>DENND3</i>	A	C	0.4	4.98E-10	-?---	8.9	0.17	0.2	3.43E-01	+-	36.43
9	rs7048915	4206388	<i>GLIS3</i>	A	G	0.26	3.94E-09	----	0	NA	NA	NA	NA	NA
9	rs62538956	12679244	<i>TYRP1</i>	T	C	0.88	1.18E-11	+++++	58.1	0.98	0.98	9.09E-01	+-	66.56
9	rs1340044	18362105	<i>ADAMTSL1</i>	A	T	0.53	3.92E-51	----	27.9	NA	NA	NA	NA	NA
9	rs7855188	20032153	<i>SLC24A2</i>	A	T	0.56	1.22E-13	----	29.8	NA	NA	NA	NA	NA
9	rs1823289	22792513	<i>NA</i>	C	G	0.41	1.17E-09	----+	22	NA	NA	NA	NA	NA
9	rs855719	33817617	<i>PRSS3</i>	T	C	0.42	4E-13	----	0	0.27	0.29	9.72E-01	+-	0
9	rs11145461	71766119	<i>FXN</i>	T	C	0.22	3.41E-39	----	84.1	NA	0.99	NA	NA+	NA
9	rs7042950	77149837	<i>TMC1</i>	A	G	0.78	6E-36	+++++	75.4	0.2	0.19	1.10E-01	--	0
9	rs1961952	86325806	<i>IDNK</i>	A	G	0.61	5.7E-10	----	0	NA	NA	NA	NA	NA
9	rs7849438	92038144	<i>SEMA4D</i>	T	C	0.67	2.62E-08	----	11.7	0.92	0.92	1.98E-01	+-	0
9	rs13301794	100193001	<i>TDRD7</i>	A	G	0.52	4.79E-08	+++++	3.5	NA	NA	NA	NA	NA
9	rs1571590	101883808	<i>TGFBR1</i>	A	G	0.8	6.91E-25	+++++	47.5	NA	NA	NA	NA	NA

Table S11. Comparison of SNPs previously associated with myopia in European adults and their effects in our children cohorts

CHR	SNP	BP	Nearest genes	EA	NEA	Meta-GWAS of European adult cohorts ^a				Meta-GWAS of our Chinese children cohorts				
						EAF of European adults	P	Direction	Heterogeneity I ² (%)	EAF of HKCES	EAF of LAMP	P	Direction	Heterogeneity I ² (%)
9	rs3764523	109765215	<i>ZNF462</i>	A	G	0.88	1.41E-15	+++++	55.2	NA	NA	NA	NA	NA
9	rs10980037	112544024	<i>PALM2</i>	T	C	0.76	4.44E-09	-----	4.4	0.7	0.71	7.49E-01	+-	0
9	rs41305473	116346118	<i>RGS3</i>	A	G	0.1	4.17E-08	+++++	0	NA	NA	NA	NA	NA
9	rs2072438	123651301	<i>PHF19</i>	T	C	0.44	1.65E-11	-----	0	0.5	0.52	5.95E-01	++	0
9	rs10122788	129206832	<i>SCAI</i>	A	G	0.57	1.1E-13	+++++	0	0.73	0.72	6.62E-01	-+	81.54
9	rs943423	137437183	<i>RXRA</i>	A	G	0.7	4.56E-12	+?+++	0	NA	NA	NA	NA	NA
9	rs11103381	139097773	<i>LHX3</i>	A	C	0.68	1.37E-14	-?----	81.2	NA	NA	NA	NA	NA
10	rs12762379	21559884	<i>NEBL</i>	T	C	0.08	4.59E-09	-----	10.6	NA	NA	NA	NA	NA
10	rs10829282	27873025	<i>RAB18</i>	A	T	0.49	1.37E-08	+++++	55.9	0.23	0.22	7.84E-01	--	0
10	rs3739996	30316872	<i>NA</i>	T	C	0.61	3.79E-19	+++++	12.8	0.8	0.8	2.10E-01	++	1.97
10	rs10793568	45415209	<i>TMEM72</i>	A	G	0.29	1.09E-14	-----	0	NA	0.53	NA	NA-	NA
10	rs56036047	49405013	<i>ANXA8</i>	T	C	0.73	1.98E-49	+++++	0	0.93	0.93	3.63E-01	--	0
10	rs2842083	60329230	<i>TFAM</i>	A	C	0.46	1.87E-44	-----	0	0.47	0.5	8.07E-01	+-	0
10	rs1599166	62163729	<i>ANK3</i>	A	G	0.78	3.41E-18	+++++	1.9	NA	NA	NA	NA	NA
10	rs4262652	74127853	<i>ANAPC16</i>	A	G	0.64	1.83E-17	+++++	0	0.14	0.12	5.78E-01	++	0
10	rs7073435	75886512	<i>VCL</i>	T	C	0.27	2.42E-09	+++++	0	0.65	0.65	5.41E-01	+-	13.56
10	rs7895108	79061458	<i>KCNMA1</i>	T	G	0.37	2.96E-69	-----	76.7	0.14	0.15	NA	-NA	NA
10	rs4517452	86021024	<i>GHITM</i>	T	C	0.63	9.53E-71	+++++	63.7	0.7	0.7	NA	+NA	NA
10	rs10887652	88511237	<i>BMPRI1A</i>	C	G	0.63	3.22E-08	-----	0	0.27	0.27	4.45E-01	--	0
10	rs3781196	90042154	<i>RNLS</i>	T	G	0.23	4.6E-32	+++++	0	0.17	0.16	8.03E-02	+-	0
10	rs4933627	92712252	<i>ANKRD1</i>	A	G	0.42	2E-08	+++++	0	NA	NA	NA	NA	NA
10	rs12778014	94950273	<i>EXOC6</i>	A	G	0.34	2.77E-23	+++++	51.1	0.07	0.08	3.68E-01	+-	0
10	rs807037	102824349	<i>ERLIN1</i>	C	G	0.66	3.07E-22	-----	0	0.43	0.43	2.68E-03	--	0
10	rs2501571	111855439	<i>XPNPEP1</i>	T	G	0.18	2.04E-14	+++++	31.5	NA	NA	NA	NA	NA
10	rs56299331	114788436	<i>VTG1A</i>	T	C	0.2	9.38E-46	-----	70.8	NA	NA	NA	NA	NA
10	rs11196996	116694631	<i>TRUB1</i>	T	C	0.41	2.36E-08	-----	0	0.03	0.04	8.64E-01	-+	48.92
10	rs3750847	124215421	<i>PLEKHAI</i>	T	C	0.22	5.72E-23	-----	43.2	0.6	0.56	7.89E-01	++	0
10	rs1152698	126807285	<i>CTBP2</i>	C	G	0.17	8.33E-17	-----	16.4	NA	NA	NA	NA	NA
11	rs113626448	589392	<i>PHRF1</i>	T	G	0.95	9.54E-09	-?----	0	NA	NA	NA	NA	NA
11	rs10839545	1744093	<i>MOB2</i>	A	G	0.46	3.68E-13	+++++	17.9	NA	NA	NA	NA	NA
11	rs12291662	14342949	<i>SPON1</i>	T	C	0.65	3.38E-11	-----	0	0.63	0.61	3.30E-01	-+	0
11	rs1550870	18751041	<i>IGSF22</i>	T	C	0.47	2.02E-27	+++++	61.8	NA	NA	NA	NA	NA
11	rs6484385	28668416	<i>METTL15</i>	T	C	0.63	6.6E-16	+++++	12.9	0.21	0.2	NA	+NA	NA
11	rs511217	30029948	<i>KCNA4</i>	A	T	0.74	2.3E-49	-----	0	0.69	0.73	7.04E-01	++	0
11	rs11606250	40149300	<i>LRRC4C</i>	A	G	0.17	1.38E-175	-----	88.6	0.28	0.33	7.01E-02	--	0
11	rs11037404	43296794	<i>API5</i>	T	C	0.38	2.37E-24	+++++	31.5	0.28	0.26	3.24E-01	+-	18.82
11	rs55681357	45687366	<i>CHST1</i>	T	C	0.36	1.4E-10	-----	58.9	0.16	0.16	3.29E-01	+-	34.1
11	rs7928419	47392114	<i>DDB2</i>	A	G	0.67	1.94E-14	-----	38.4	NA	NA	NA	NA	NA

Table S11. Comparison of SNPs previously associated with myopia in European adults and their effects in our children cohorts

CHR	SNP	BP	Nearest genes	EA	NEA	Meta-GWAS of European adult cohorts ^a				Meta-GWAS of our Chinese children cohorts				
						EAF of European adults	P	Direction	Heterogeneity I ² (%)	EAF of HKCES	EAF of LAMP	P	Direction	Heterogeneity I ² (%)
11	rs198443	61505696	<i>SLC15A3</i>	T	G	0.44	2.18E-24	-----	71.4	0.79	0.81	8.93E-01	++	0
11	rs620088	65508986	<i>SLC25A45</i>	A	G	0.35	3.21E-11	+++++	36.1	0.25	0.22	5.52E-01	+-	10.26
11	rs2276118	67288594	<i>RPS6KB2</i>	T	C	0.56	2.93E-13	+++++	0	0.69	0.69	8.65E-01	+-	29.66
11	rs493786	69329674	<i>CCND1</i>	T	C	0.33	5.45E-09	+++++	0	NA	NA	NA	NA	NA
11	rs1278092	73233855	<i>P2RY6</i>	T	C	0.39	1.4E-13	-----	0	NA	NA	NA	NA	NA
11	rs2155413	84634790	<i>ANKRD42</i>	A	C	0.47	1.97E-53	-----	85.7	NA	NA	NA	NA	NA
11	rs535888	92407574	<i>FAT3</i>	T	C	0.49	2.86E-10	+++++	19.5	0.39	0.4	1.20E-01	+-	74.76
11	rs4753693	95293753	<i>KDM4E</i>	A	T	0.51	2.85E-10	-----	0	NA	NA	NA	NA	NA
11	rs10895869	105600358	<i>GRIA4</i>	A	C	0.37	4.28E-39	-----	66.2	0.33	0.38	4.16E-02	--	66.02
11	rs2028155	108267430	<i>CUL5</i>	A	G	0.45	3.53E-19	-----	46.8	0.6	0.62	1.65E-01	++	51.28
11	rs7947524	117671091	<i>APOC3</i>	T	C	0.5	2.95E-34	-----	8.9	0.31	0.27	2.00E-01	-+	0
11	rs1029278	123421402	<i>GRAMD1B</i>	A	G	0.34	4.57E-21	-----	0	NA	NA	NA	NA	NA
11	rs6590199	126235667	<i>ST3GAL4</i>	A	G	0.16	6.21E-09	-----	0	0.3	0.29	3.62E-01	--	45.98
11	rs10219187	129103092	<i>ETS1</i>	T	C	0.68	1.17E-17	-----	0	0.71	0.69	3.95E-01	--	0
11	rs1790165	131928971	<i>NTM</i>	A	C	0.42	7.47E-29	+++++	75.4	0.19	0.17	1.28E-01	++	0
12	rs10848650	377207	<i>SLC6A13</i>	C	G	0.59	1.55E-08	-----	0	0.17	0.14	6.10E-01	--	0
12	rs6489568	4930100	<i>KCNA6</i>	A	G	0.21	1.61E-08	-----	0	0.37	0.4	8.80E-01	-+	0
12	rs5442	6954864	<i>GNB3</i>	A	G	0.07	2.64E-62	-?----	84.7	NA	NA	NA	NA	NA
12	rs10842971	9303296	<i>A2ML1</i>	A	T	0.69	1.34E-40	+++++	0	0.92	0.91	6.98E-01	-+	14.42
12	rs7966177	10879132	<i>YBX3</i>	T	C	0.47	5.05E-09	-----	42.7	0.23	0.2	8.33E-02	++	85.43
12	rs17834080	14039124	<i>GPR19</i>	T	G	0.27	4.43E-34	-----	0	NA	NA	NA	NA	NA
12	rs6487108	20736762	<i>PDE3A</i>	A	G	0.29	2.95E-08	-----	62	0.19	0.19	9.09E-01	+-	71.88
12	rs144311425	22555028	<i>ST8SIA1</i>	T	C	0.09	8.8E-26	-----	40.7	0.05	0.04	2.61E-01	--	8.48
12	rs4964008	26776560	<i>ITPR2</i>	C	G	0.66	2.44E-13	-----	10	NA	NA	NA	NA	NA
12	rs1489081	29063122	<i>FAR2</i>	A	G	0.47	2.98E-14	-----	53.6	0.34	0.37	5.27E-01	--	0
12	rs7311970	31746047	<i>DENND5B</i>	A	C	0.62	8.09E-10	-----	0	0.58	0.61	4.09E-01	-+	65.5
12	rs11181913	43574200	<i>GXYLT1</i>	A	G	0.91	2.75E-11	+++++	0	0.93	0.92	9.17E-01	+-	66.46
12	rs1468993	46155145	<i>ARID2</i>	T	C	0.49	2.42E-29	+++++	68.5	NA	NA	NA	NA	NA
12	rs3138142	56115585	<i>CBX5</i>	T	C	0.23	5.71E-174	+++++	86.2	0.15	0.11	4.68E-01	++	0
12	rs11178450	71233908	<i>PTPRR</i>	T	C	0.22	5.12E-26	+++++	55.8	0.43	0.4	6.46E-02	++	0
12	rs1280632	91622254	<i>DCN</i>	T	C	0.89	3.67E-09	+++++	0	NA	NA	NA	NA	NA
12	rs117821803	96194586	<i>NTN4</i>	T	C	0.19	1.2E-19	+++++	0	0.03	0.03	1.71E-01	-+	0
12	rs7136446	102838515	<i>NUP37</i>	T	C	0.59	2.54E-10	-----	0	0.82	0.84	7.79E-01	-+	9.32
12	rs17218455	106716441	<i>CKAP4</i>	T	C	0.17	1.14E-12	-----	12.5	0.02	0.02	6.31E-01	--	0
12	rs7315286	108979990	<i>TMEM119</i>	A	G	0.55	1.51E-08	+++++	26.1	0.13	0.16	NA	+NA	NA
12	rs1732579	115716844	<i>NA</i>	A	G	0.65	3.85E-09	-----	0	0.96	0.98	3.72E-01	-+	82.04
12	rs4766878	118236577	<i>KSR2</i>	T	C	0.45	8.41E-14	-----	56.5	0.73	0.73	5.99E-01	+-	0
12	rs11065286	121271734	<i>COQ5</i>	T	C	0.45	8.47E-11	-----	0	NA	NA	NA	NA	NA

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CHR	SNP	BP	Nearest genes	EA	NEA	Meta-GWAS of European adult cohorts ^a				Meta-GWAS of our Chinese children cohorts				
						EAF of European adults	P	Direction	Heterogeneity I ² (%)	EAF of HKCES	EAF of LAMP	P	Direction	Heterogeneity I ² (%)
12	rs7307053	124494540	<i>ZNF664</i>	T	C	0.32	3.74E-08	----	0	0.07	0.07	5.73E-01	--	0
12	rs12308700	131157564	<i>RIMBP2</i>	A	G	0.42	1.24E-13	----	71.2	0.31	0.32	8.60E-02	--	0
12	rs905224	133684321	<i>ANKLE2</i>	T	G	0.56	1.33E-12	----	0	NA	NA	NA	NA	NA
13	rs587289	21596183	<i>LATS2</i>	A	G	0.28	9.68E-12	++++	0	NA	NA	NA	NA	NA
13	rs34961350	28991902	<i>FLT1</i>	C	G	0.79	4.13E-32	----	0	0.72	0.72	6.50E-01	+-	28.23
13	rs4769824	30883339	<i>KATNAL1</i>	T	C	0.44	1.32E-11	----	0	0.13	0.13	5.84E-01	++	0
13	rs353	32454349	<i>EEF1DP3</i>	A	G	0.94	9.73E-13	++++	0	NA	NA	NA	NA	NA
13	rs45502300	36246512	<i>MIR548F5</i>	A	G	0.97	2.17E-23	++++	0	NA	NA	NA	NA	NA
13	rs9526001	45339106	<i>TSC22D1</i>	T	C	0.27	5E-09	----	1.1	0.36	0.37	6.63E-01	+-	0
13	rs9535263	50137363	<i>SETDB2</i>	A	T	0.7	1.08E-36	----	13.6	0.65	0.65	2.79E-01	++	0
13	rs9526736	51799497	<i>GUCY1B2</i>	T	C	0.57	9.23E-09	++++	4.7	0.83	0.82	2.86E-01	--	0
13	rs36080062	67726830	<i>PCDH9</i>	C	G	0.2	7.14E-13	----	0	NA	NA	NA	NA	NA
13	rs75012440	74631240	<i>KLF12</i>	A	G	0.14	6.22E-10	----	50.6	0.06	0.07	6.27E-01	++	0
13	rs4052505	80512487	<i>NA</i>	T	C	0.19	8.13E-20	----	23.7	0.32	0.34	9.35E-02	--	0
13	rs9547035	85573496	<i>NA</i>	T	G	0.73	7.12E-32	++++	59.8	0.59	0.59	8.55E-01	+-	0
13	rs1328371	93912785	<i>GPC6</i>	T	C	0.49	3.59E-23	----	0	NA	NA	NA	NA	NA
13	rs9562057	96897856	<i>HS6ST3</i>	T	C	0.1	6.06E-09	----	0	0.32	0.29	1.44E-02	--	0
13	rs724154	100673616	<i>SLC15A1</i>	A	G	0.45	1.92E-76	----	71	0.18	0.2	2.97E-01	++	0
13	rs9521975	111539925	<i>ANKRD10</i>	A	G	0.41	5.56E-09	----	0	0.14	0.14	1.84E-01	--	20.8
14	rs4981370	21779495	<i>RPGRIP1</i>	A	G	0.49	5.67E-09	-+---	43.9	0.47	0.43	4.67E-01	+-	72.04
14	rs34354104	24707479	<i>NEDD8-MDPI</i>	A	G	0.05	4.84E-10	++++	0	NA	NA	NA	NA	NA
14	rs12883788	33303540	<i>AKAP6</i>	T	C	0.45	2.11E-33	++++	0	0.28	0.27	4.29E-01	--	0
14	rs34217772	42273570	<i>LRFN5</i>	C	G	0.81	1.18E-39	++++	74	NA	0.99	NA	NA+	NA
14	rs9788504	51270267	<i>SAV1</i>	C	G	0.59	1.07E-11	++++	32.4	NA	NA	NA	NA	NA
14	rs2855530	54421917	<i>BMP4</i>	C	G	0.5	1.92E-59	----	56.4	0.47	0.47	2.98E-01	--	39.67
14	rs928109	57279583	<i>OTX2</i>	T	C	0.48	6.15E-11	----	0	0.36	0.36	7.50E-01	+-	0
14	rs1254314	60896434	<i>PPM1A</i>	C	G	0.29	1.98E-40	----	60.5	0.69	0.72	4.04E-01	+-	72.37
14	rs34096978	63784378	<i>GPHB5</i>	A	G	0.04	1.03E-11	++++	0	NA	NA	NA	NA	NA
14	rs3211166	69703158	<i>TMEM229B</i>	A	G	0.69	6.16E-11	++++	0	NA	NA	NA	NA	NA
14	rs73294488	74949801	<i>DPF3</i>	T	C	0.99	6.52E-25	-?---	56.6	NA	NA	NA	NA	NA
14	rs56284621	89429230	<i>TTC8</i>	T	C	0.8	2.82E-19	++++	62.5	0.62	0.63	2.17E-01	+-	9.97
14	rs12896393	92625903	<i>TRIP11</i>	A	G	0.84	4.49E-24	----	75.9	0.49	0.49	7.18E-01	+-	0
14	rs7144361	96103184	<i>GLRX5</i>	T	C	0.08	9.31E-11	++++	0	0.11	0.11	1.74E-01	++	0
14	rs4905998	101181781	<i>WDR25</i>	A	G	0.32	3.19E-10	++++	25.4	0.6	0.59	9.75E-01	+-	0
14	rs35337422	104407243	<i>ZNF839</i>	A	C	0.86	9.67E-21	++++	53.8	NA	NA	NA	NA	NA
15	rs11161294	26607405	<i>ATP10A3</i>	A	G	0.13	4.18E-11	++++	25.6	0.18	0.2	9.88E-01	+-	0
15	rs79406658	27988096	<i>OCA2</i>	A	C	0.43	1.37E-15	++++	0	0.04	0.05	4.58E-01	--	0
15	rs3784589	31294714	<i>TRPM1</i>	A	C	0.05	4.74E-10	++++	64.6	NA	NA	NA	NA	NA

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CHR	SNP	BP	Nearest genes	EA	NEA	Meta-GWAS of European adult cohorts ^a				Meta-GWAS of our Chinese children cohorts				
						EAF of European adults	P	Direction	Heterogeneity I ² (%)	EAF of HKCES	EAF of LAMP	P	Direction	Heterogeneity I ² (%)
15	rs524952	35005886	<i>GOLGA8B</i>	A	T	0.49	2.49E-245	-----	94.1	0.56	0.52	3.65E-02	++	0
15	rs35636169	36594557	<i>NA</i>	T	C	0.63	3.33E-09	-----	14.4	0.77	0.76	8.50E-01	+-	60.39
15	rs1058734	40862064	<i>BAHD1</i>	T	C	0.46	2.83E-11	+++++	50.9	0.09	0.1	2.30E-01	+-	48.17
15	rs2017765	48749703	<i>FBN1</i>	T	C	0.13	3.3E-24	+++++	25.1	NA	NA	NA	NA	NA
15	rs8042462	51045616	<i>USP50</i>	A	G	0.03	5.53E-12	+++++	35.7	NA	NA	NA	NA	NA
15	rs1912409	56158495	<i>NEDD4</i>	T	C	0.6	1.72E-09	-----	0	0.51	0.52	7.02E-01	+-	71.62
15	rs55870008	61489314	<i>RORA</i>	A	G	0.45	5.55E-09	+++++	50.6	0.68	0.64	4.26E-01	++	33.76
15	rs7162310	63571234	<i>TPM1</i>	T	C	0.21	5.98E-36	+++++	68.1	0.47	0.46	4.93E-01	-+	74.98
15	rs8042545	66992821	<i>LCTL</i>	A	G	0.25	2.04E-12	-----	61	0.05	0.06	1.96E-01	++	0
15	rs28588430	74223430	<i>LOXL1</i>	C	G	0.49	1.61E-18	+++++	30.7	0.1	0.09	5.53E-02	++	0
15	rs4886850	77404160	<i>PEAK1</i>	C	G	0.76	1.08E-09	-----	44.6	NA	NA	NA	NA	NA
15	rs1961579	79380516	<i>CHRNA3</i>	A	G	0.42	7.72E-84	-----	79.2	0.51	0.53	1.03E-01	--	0
15	rs8039459	82320426	<i>MEX3B</i>	C	G	0.31	2.52E-27	+++++	0	0.52	0.53	1.75E-01	--	0
15	rs12440698	85825906	<i>AKAP13</i>	A	G	0.88	4.69E-08	-----	0	NA	NA	NA	NA	NA
15	rs4502168	93744204	<i>SLCO3A1</i>	T	C	0.28	5.67E-12	+++++	0	0.27	0.28	6.30E-01	-+	0
15	rs10520789	96141867	<i>MCTP2</i>	A	G	0.12	1E-11	+++++	31.9	0.02	0.02	9.27E-01	-+	0
15	rs2654980	99504843	<i>IGFIR</i>	T	C	0.25	3.71E-08	+++++	0	0.03	0.02	9.00E-01	+-	0
16	rs710902	1376510	<i>AXIN1</i>	T	C	0.13	6.4E-18	+?+++	0	NA	NA	NA	NA	NA
16	rs17648524	7459683	<i>RBFOX1</i>	C	G	0.37	1.35E-180	-----	86.8	0.07	0.07	1.15E-01	--	53.65
16	rs1868289	10215813	<i>GRIN2A</i>	T	G	0.68	1.13E-17	-----	50.6	0.55	0.53	7.00E-01	--	0
16	rs2606558	18821191	<i>RPS15A</i>	C	G	0.46	8.96E-10	-----	0.3	NA	NA	NA	NA	NA
16	rs497523	28577931	<i>GSG1L</i>	T	C	0.65	3E-09	+++--	74.6	NA	NA	NA	NA	NA
16	rs62026817	55492932	<i>IRX5</i>	A	G	0.23	7.43E-10	-+---	60.8	0.18	0.17	6.70E-01	-+	66.32
16	rs255049	68013471	<i>SLC9A5</i>	T	C	0.81	2.45E-14	+++++	58.7	0.9	0.93	8.40E-01	--	0
16	rs28533147	73195849	<i>MARVELD3</i>	T	G	0.82	4.38E-10	+++++	46.3	NA	NA	NA	NA	NA
16	rs13339407	78156295	<i>WWOX</i>	A	G	0.69	9.45E-10	-----	0	NA	NA	NA	NA	NA
16	rs4635359	80537760	<i>MAF</i>	A	C	0.74	1.71E-28	-----	0	0.41	0.47	6.10E-01	--	0
16	rs1054521	87436720	<i>MAP1LC3B</i>	T	G	0.94	5.53E-09	+?+++	75.1	NA	NA	NA	NA	NA
17	rs9892466	3969527	<i>ATP2A3</i>	A	T	0.33	6.47E-14	-----	0	0.16	0.16	3.29E-01	++	65.99
17	rs9217	7363088	<i>NLGN2</i>	T	C	0.64	3E-22	-----	72.6	0.79	0.81	3.76E-01	++	0
17	rs2908972	11407259	<i>SHISA6</i>	A	T	0.4	3.71E-84	-----	77.3	0.54	0.58	1.26E-01	++	0
17	rs115152181	14136125	<i>COX10</i>	A	T	0.43	3.96E-27	-----	25.9	NA	NA	NA	NA	NA
17	rs62070229	31227593	<i>MYO1D</i>	A	G	0.81	7.04E-44	+++++	68.7	NA	NA	NA	NA	NA
17	rs35497503	37620627	<i>STAC2</i>	T	C	0.75	1.11E-24	+++++	21.6	0.68	0.68	7.71E-01	-+	27.39
17	rs76324150	43973233	<i>ARHGAP27</i>	T	C	0.22	8.24E-16	+++++	33.5	NA	NA	NA	NA	NA
17	rs7222840	47280915	<i>B4GALNT2</i>	T	C	0.32	1.27E-44	+++++	74.4	NA	NA	NA	NA	NA
17	rs8075811	54735307	<i>NOG</i>	A	G	0.36	7.34E-42	+++++	76.4	0.35	0.31	4.71E-01	++	55.1
17	rs3785837	59468942	<i>BCAS3</i>	A	G	0.77	3.36E-21	-?---	0	NA	NA	NA	NA	NA

Table S11. Comparison of SNPs previously associated with myopia in European adults and their effects in our children cohorts

CHR	SNP	BP	Nearest genes	EA	NEA	Meta-GWAS of European adult cohorts ^a				Meta-GWAS of our Chinese children cohorts				
						EAF of European adults	P	Direction	Heterogeneity I ² (%)	EAF of HKCES	EAF of LAMP	P	Direction	Heterogeneity I ² (%)
17	rs1991401	62502435	<i>KCNH6</i>	A	G	0.68	1.81E-13	+++++	20.4	0.6	0.59	8.80E-01	+-	0
17	rs9895291	63550797	<i>AXIN2</i>	A	C	0.16	1.4E-08	----	27.6	0.08	0.08	5.32E-01	+-	0
17	rs62084693	66036110	<i>BPTF</i>	T	C	0.75	7.11E-12	----	0	0.28	0.28	6.21E-01	--	0
17	rs4793501	68718734	<i>NA</i>	T	C	0.58	2.57E-24	----	83.3	0.39	0.4	6.27E-01	+-	78.24
17	rs448203	75495065	<i>MGAT5B</i>	T	C	0.6	4.35E-14	+++++	12.9	0.07	0.05	3.86E-01	+-	0
17	rs9747347	79606820	<i>TMEM105</i>	T	C	0.36	2.22E-50	----	86.1	NA	NA	NA	NA	NA
18	rs11659457	6461151	<i>L3MBTL4</i>	A	G	0.41	3.63E-14	+++++	19.9	0.51	0.53	4.56E-01	-+	0
18	rs11564403	25662803	<i>CDH2</i>	A	T	0.28	2.48E-15	----	39.1	NA	NA	NA	NA	NA
18	rs1427039	35347100	<i>CELF4</i>	T	C	0.66	1.49E-08	----	0	NA	0.7	NA	NA-	NA
18	rs10163854	39162524	<i>NA</i>	C	G	0.9	5.7E-12	----	32.4	0.99	0.98	6.13E-01	-+	0
18	rs16978339	42886236	<i>SETBP1</i>	T	G	0.84	2.88E-36	----	0	0.88	0.89	4.37E-01	--	0
18	rs12965607	47391025	<i>DYM</i>	T	G	0.85	3.89E-60	+++++	2.9	NA	NA	NA	NA	NA
18	rs41396445	53242137	<i>TCF4</i>	A	C	0.35	4.14E-12	++++-	66.8	0.4	0.37	9.82E-01	+-	13.53
18	rs9646588	62990567	<i>NA</i>	A	G	0.37	9.42E-12	----	0	0.45	0.46	1.25E-01	--	61.54
18	rs734559	72179579	<i>CNDP2</i>	A	G	0.23	2.41E-14	+++++	80.1	0.3	0.29	2.37E-01	-+	54.83
18	rs72973714	74076020	<i>ZNF516</i>	T	C	0.07	3.06E-08	+++++	0	NA	NA	NA	NA	NA
18	rs8096658	77156537	<i>NEATC1</i>	C	G	0.51	5.19E-10	-?---	49.8	0.63	0.65	8.65E-01	++	0
19	rs123698	807442	<i>PPAP2C</i>	C	G	0.6	1.19E-11	+?+++	0	NA	NA	NA	NA	NA
19	rs75488612	4037322	<i>PIAS4</i>	A	G	0.1	1.7E-09	-?---	0	NA	NA	NA	NA	NA
19	rs10416763	8232734	<i>FBN3</i>	T	C	0.45	3.8E-16	+++++	0	0.45	0.43	1.40E-02	++	8.38
19	rs113628353	13201606	<i>NFIX,LYL1</i>	A	G	0.11	1.93E-11	+++++	0	NA	NA	NA	NA	NA
19	rs75452709	17455453	<i>ANO8</i>	C	G	0.5	3.9E-08	+?+++	0	NA	NA	NA	NA	NA
19	rs2074302	19381728	<i>REFANK</i>	C	G	0.16	3.99E-29	----	0	0.02	0.02	NA	-NA	NA
19	rs73035723	31779696	<i>TSHZ3</i>	A	G	0.11	1.32E-10	----	71.4	NA	NA	NA	NA	NA
19	rs807479	36253317	<i>UPK1A</i>	T	C	0.47	1.2E-10	-?---	45.7	0.46	0.45	7.38E-01	-+	0
19	rs57654288	38078771	<i>ZNF793</i>	A	G	0.38	7.04E-09	+++++	0	0.08	0.06	3.49E-01	--	76.44
19	rs429358	45411941	<i>PVRL2</i>	T	C	0.85	3.03E-17	----	59.7	0.91	0.92	2.54E-01	+-	29.21
19	rs75601727	48531806	<i>CCDC9</i>	A	G	0.1	1.11E-27	+++++	0	0.05	0.05	2.15E-01	++	0
20	rs11087326	2127684	<i>STK35</i>	T	C	0.25	1.01E-12	----	53.6	0.93	0.94	9.44E-01	-+	0
20	rs41281858	3209083	<i>LZTS3</i>	A	G	0.13	5.81E-11	+++++	37	NA	NA	NA	NA	NA
20	rs7272323	4756691	<i>RASSF2</i>	C	G	0.6	9.41E-11	+++++	0	0.27	0.24	5.26E-01	++	20.99
20	rs235770	6761765	<i>BMP2</i>	T	C	0.39	3.9E-31	----	13.4	0.29	0.31	3.86E-01	--	0
20	rs6136407	18529855	<i>DZANK1</i>	A	C	0.61	2.14E-08	+++++	25.1	0.87	0.86	2.30E-02	++	0
20	rs6137371	21485247	<i>NKX2-2</i>	T	C	0.58	2.68E-09	+++++	0	0.53	0.57	6.89E-01	-+	21.05
20	rs6050351	25118271	<i>VSX1</i>	T	C	0.18	4.59E-08	+++++	7.2	0.42	0.42	5.76E-02	--	0
20	rs2378078	32714728	<i>CHMP4B</i>	T	C	0.64	4.84E-19	----	58.6	NA	NA	NA	NA	NA
20	rs6120993	34185161	<i>GDF5</i>	T	G	0.14	1.59E-20	----	30.8	0.15	0.19	6.25E-01	+-	0
20	rs6102322	39872768	<i>TOP1</i>	T	C	0.31	7.27E-10	----	0	0.78	0.82	1.17E-01	--	10.4

Table S11. Comparison of SNPs previously associated with myopia in European adults and their effects in our children cohorts

CHR	SNP	BP	Nearest genes	EA	NEA	Meta-GWAS of European adult cohorts ^a				Meta-GWAS of our Chinese children cohorts				
						EAF of European adults	P	Direction	Heterogeneity I ² (%)	EAF of HKCES	EAF of LAMP	P	Direction	Heterogeneity I ² (%)
20	rs8121964	42489757	<i>TOX2</i>	A	G	0.25	1.45E-08	-----	0	NA	NA	NA	NA	NA
20	rs6099283	55375861	<i>TFAP2C</i>	A	G	0.25	3.06E-09	-----	0	0.35	0.33	3.53E-01	++	1.53
20	rs6070941	58354388	<i>PHACTR3</i>	C	G	0.83	1.55E-10	+++++	0	0.75	0.76	5.86E-01	-+	42.36
20	rs2259858	62346459	<i>BHLHE23</i>	A	T	0.75	1.03E-14	+++++	51.4	0.41	0.37	1.13E-01	+-	48.4
21	rs2229741	16340289	<i>NRIP1</i>	T	C	0.42	1.34E-29	-----	43.4	0.79	0.81	4.63E-01	+-	53.05
21	rs117123217	30910628	<i>GRIK1</i>	A	G	0.04	1.35E-10	-----	7.9	NA	NA	NA	NA	NA
21	rs74848904	36612241	<i>RUNX1</i>	A	C	0.1	1.66E-08	+++++	0	NA	NA	NA	NA	NA
21	rs2212597	39983404	<i>ERG</i>	T	C	0.82	5.49E-11	-----	3.3	0.72	0.69	4.06E-01	--	0
21	rs7277023	41915359	<i>DSCAM</i>	A	G	0.98	4.63E-08	-----	9.8	0.9	0.91	9.05E-02	--	0
21	rs11700909	45118701	<i>HSF2BP</i>	C	G	0.59	2.56E-10	+++++	52.7	NA	NA	NA	NA	NA
21	rs73157695	47371947	<i>PCBP3</i>	A	G	0.3	1.91E-36	-----	30.6	0.17	0.2	8.07E-01	+-	40.62
22	rs9608575	27486722	<i>MNI</i>	A	G	0.67	2.32E-11	----+	28.2	NA	NA	NA	NA	NA
22	rs2097352	30236444	<i>ASCC2</i>	A	T	0.75	2.46E-09	+++++	0	0.86	0.89	2.26E-02	++	0
22	rs9606973	32900527	<i>BPIFC</i>	A	T	0.21	5.91E-13	-----	0	0.14	0.12	9.97E-02	--	0
22	rs13056506	38580917	<i>CARD10</i>	T	G	0.6	2.46E-13	-----	0	0.74	0.78	6.19E-01	+-	0
22	rs6519240	41416557	<i>CACNA1I</i>	T	C	0.24	1.83E-27	-----	0	0.27	0.24	8.87E-01	+-	0
22	rs73175083	46383612	<i>WNT7B</i>	T	C	0.32	1.42E-26	-?---	71.3	NA	NA	NA	NA	NA

^aThe results were from Hysi PG, et al. Meta-analysis of 542,934 subjects of European ancestry identifies new genes and mechanisms predisposing to refractive error and myopia. Nat Genet. 2020 Apr;52(4):401-407. doi: 10.1038/s41588-020-0599-0. Epub 2020 Mar 30. I² (%), Heterogeneity. EA, effect allele; NEA, non-effect allele; EAF, effect allele frequency.

Table S12. Frequency distribution in our study and the 1000Genome Project

SNP	Gene	EA	Frequency of EA in our study							Frequency of EA in 1000 Genome Project					
			HKCES-1 (N=864)	LAMP (N=373)	HKCES-2 (N=2066)	SMS (N=2027)	HKCES_all (N=2930)	Adult-1 (N=1212)	Adult-2 (N=602)	Global (N=2504)	AFR (N=661)	AMR (N=347)	EAS (N=504)	EUR (N=503)	SAS (N=489)
rs292034	<i>MIR4275</i>	G	0.013	0.011	0.011	0.013	0.012	0.017	0.017	0.15	0.19	0.15	0.01	0.27	0.11
rs17074027	<i>TENM3</i>	G	0.058	0.06	0.076	0.073	0.071	0.077	0.068	0.09	0.08	0.08	0.09	0.06	0.15
rs6925312	<i>LOC101928911</i>	G	0.78	0.76	0.78	0.790	0.780	0.79	0.77	0.47	0.26	0.51	0.76	0.42	0.47
rs4609227	<i>FAM135B</i>	C	0.025	0.025	0.03	0.037	0.025	0.028	0.026	0.10	0.08	0.07	0.05	0.11	0.14

EA, effect allele; AFR, Africa; AMR, America; EAS, East Asia; EUR, Europe; SAS, South Asia.

Table S13. Interactions between genetic risk score strata of spherical equivalent and diopter-hours and outdoor time

	Marginal effect model ^a			Interaction effect model ^b			Interaction effect model ^c		
	β	Std.Error	P	β	Std.Error	P	β	Std.Error	P
GRS	1.02	0.13	2.14x10⁻¹⁵	-	-	-	-	-	-
Diopter-hours	-0.032	0.0078	3.49x10⁻⁵	-	-	-	-	-	-
Outdoor time	0.23	0.048	1.76x10⁻⁶	-	-	-	-	-	-
GRS:Diopter-hours	-	-	-	0.14	0.038	0.0003	-	-	-
GRS:Outdoor time	-	-	-	-	-	-	-0.0031	0.2	0.99

^a The marginal model was adjusted for age and sex.

^b In the interaction model, multiplicative interaction effect was estimated as the product of the individual effects of GRS and diopter-hours with age, sex and outdoor time adjusted.

^c In the interaction model, multiplicative interaction effect was estimated as the product of the individual effects of GRS and outdoor time with age, sex and diopter-hours adjusted.

Toal of 2057 children in HKCES-2 with data of diopter-hours and outdoor time are used for analysis in each model.

Table S14. Associations of strata of genetic risk score and diopter-hours in relation to myopia status

Strata of diopter-hours	GRS strata	Control (N=1628)	Case (N=429)	OR (95%CI)	P
Q1 (0.4 to < 7.0 diopter-hours/day)	Low	148	23	1	-
	Moderate	196	34	1.1 (0.62, 1.98)	0.74
	High	79	12	0.95 (0.43, 2)	0.90
P for trend	0.95				
Q2 (7.0 to < 9.0 diopter-hours/day)	Low	135	19	0.91 (0.47, 1.74)	0.77
	Moderate	158	31	1.07 (0.60, 1.94)	0.83
	High	94	25	1.54 (0.82, 2.91)	0.18
P for trend	0.07				
Q3 (9.0 to < 12.0 diopter-hours/day)	Low	136	23	1.03 (0.55, 1.94)	0.91
	Moderate	177	47	1.6 (0.93, 2.82)	0.10
	High	70	32	2.81 (1.64, 5.6)	0.00044
P for trend	0.00039				
Q4 (≥ 12.0 diopter-hours/day)	Low	155	47	1.78 (1.03, 3.14)	0.04
	Moderate	31	12	1.95 (0.77, 4.96)	0.15
	High	249	124	3.01 (1.73, 4.71)	4.70E-05
P for trend	0.011				

Multivariable model with further adjustment for age, sex and outdoor time.

Myopia is defined as $\leq -0.5D$.

Total of 2057 children in HKCES-2 with data of diopter-hours and outdoor time are used for analysis.

Table S15. Functional prediction of 4 genome-wide significance SNPs

Roadmap Epigenomics Project					Encyclopedia of DNA Elements Project		
SNP	CHR	Feature Type Class	Feature Type	Epigenome	Feature Type Class	Feature Type	Epigenome
rs292034	4	Histone	H3K9me3	Placenta	Histone	H3K9me3	HepG2
			H3K14ac	IMR90			
			H3K36me3	Neural stem progenitor cell, H1 hESC, HUES64		H3K36me3	Bipolar neuron, SK N SH
			H3K36me3, H3K4me1	Neuron			
rs17074027	4	Histone	H3K27me3	T cells	Histone	H3K9me3	Bipolar neuron
			H3K79me1	IMR90			
			H3K4me1	H1 hESC, HUES64, iPS 20b, HUES48		H3K27me3	PC9, A549
			H2BK20ac	H9			
rs6925312	6	Histone	H3K4me1	Neutrophil, Monocytes-CD14+ (PB), HUES64, iPS 20b, HUES48, neuron, iPS 15b, neural stem progenitor cell, HUES6, endodermal cell, H1 hESC	Histone	H3K4me1	Bipolar neuron, monocytes-CD14+, GM12878, Karpas 42, MM 1S
			H3K27ac	Spleen			
			H3K4me3	CD4 positive CD25 positive alpha beta regulatory T cell		H3K36me3	Bipolar neuron
			H3K27me3	IMR90		H3K27me3	HSMMtube, myotube, NH-A, DND-41, astrocyte, skeletal muscle myoblast, HSMM
rs4609227	8	Histone		Endodermal cell, HUES64, HUES48, HUES6, fetal muscle Leg, iPS 20b, H1 hESC, IMR 90, monocytes-CD14+, placenta, kidney	Histone	H3K9me3	Bipolar neuron, HepG2, HCT116, HeLa-S3
			H3K9me3			H3K4me1	PC3, HeLa-S3
						Open Chromatin	DNase1
							PC3
			H2BK12ac, H3K14ac, H2AK5ac	H1-trophoblast	Transcription Factor	JunD	HeLa-S3

IMR90: human lung fibroblast cell line IMR90; H1 hESC: H1 human embryonic stem cells; HUES: homo sapiens embryonic stem cell; iPS: induced pluripotent stem cell; SK N SH: human neuroblastoma cell line; PC9: human non-small cell lung cancer (NSCLC) cell line; A549: adenocarcinomic human alveolar basal epithelial cell line; GM12878: lymphoblastoid cell line; MM 1S: multiple myeloma cell line; HSMM: skeletal muscle myoblasts; NH-A: normal human astrocytes; DND-41: T cell leukemia cell line; HCT116: human colon cancer cell line; HeLa-S3: human cervical epithelioid carcinoma cell line; PC3: human prostate cancer cell line; DNase1: deoxyribonuclease I.

Annotations are available at SNPnexus <https://www.snp-nexus.org/v4/>.

Table S16. Gene Ontology Terms Significantly Enriched among Candidate Genes

Gene Ontology Identification	Gene Ontology Term	Category, Level	Gene Set Size	Candidate Genes Contained ^a	P Value	q Value
GO:0007156	Homophilic cell adhesion via plasma membrane adhesion molecules	BP, 5	169	<i>TENM3</i> ; <i>PCDH7</i>	0.00073	0.00073
GO:0098742	Cell-cell adhesion via plasma-membrane adhesion molecules	BP, 4	275	<i>TENM3</i> ; <i>PCDH7</i>	0.0019	0.015
GO:0030667	Secretory granule membrane	CC, 3	306	<i>SPACA1</i> ; <i>PCDH7</i>	0.0024	0.024
GO:0042802	Identical protein binding	MF, 3	1948	<i>TENM3</i> ; <i>DCTD</i> ; <i>AKIRIN2</i>	0.0085	0.017

GO, Gene ontology; BP,Biological process; CC, Cellular components; MF, Molecular function.

^a The nearby coding gene *PCDH7* (1.9Mpb downstream of *MIR4275*), *AKIRIN2* (82.6Kbp upstream of *LOC101928911*) and *SPACA1* (136 Kbp downstream of *LOC101928911*) and *DCTD* (87 Kbp downstream of *TENM3*) were additionally included in the GO analysis.

Table S17. Credible set of SNPs identified using CAVIAR

CHR	BP	SNP	A1	A2	Prob_in_pCausalSet	Causal_Post_Prob	r2
4	28478119	rs292034	G	T	0.050	0.097	1.00
4	28482974	rs55684803	T	A	0.006	0.011	1.00
4	28484234	rs569100	C	T	0.006	0.011	1.00
4	28484389	rs567993	G	T	0.006	0.011	1.00
4	28488065	rs292085	A	G	0.006	0.011	1.00
4	28489008	rs292084	C	T	0.006	0.011	1.00
4	28489163	rs1402670715	A	T	0.005	0.009	0.97
4	28490381	rs292082	C	T	0.006	0.011	1.00
4	28493198	rs292079	G	A	0.006	0.011	1.00
4	28493840	rs292078	C	G	0.006	0.011	1.00
4	28494313	rs292076	A	G	0.006	0.011	1.00
4	28496256	rs292072	A	G	0.004	0.008	0.97
4	28497583	rs292065	T	C	0.004	0.008	0.97
4	28498910	rs292063	G	A	0.004	0.008	0.97
4	28499782	rs292062	G	A	0.004	0.008	0.97
4	28500681	rs292060	A	C	0.004	0.008	0.97
4	28503151	rs292057	T	C	0.004	0.008	0.97
4	28506937	rs28645352	T	G	0.004	0.008	0.97
4	28507244	rs1303819	G	A	0.004	0.008	0.97
4	28507335	rs1303818	G	A	0.004	0.008	0.97
4	28507573	rs1303817	T	C	0.004	0.008	0.97
4	28507739	rs1303816	A	G	0.004	0.008	0.94
4	28509079	rs13147296	A	C	0.004	0.008	0.97
4	28518533	rs13123915	G	C	0.004	0.008	0.97
4	28519470	rs673272	G	A	0.004	0.008	0.97
4	28520773	rs893217957	C	A	0.003	0.007	0.94
4	28521854	rs292053	G	T	0.004	0.008	0.97
4	28522519	rs292052	C	T	0.004	0.008	0.97
4	28524559	rs611376	T	C	0.004	0.008	0.97
4	28525051	rs292049	T	C	0.001	0.002	0.88

Table S17. Credible set of SNPs identified using CAVIAR

CHR	BP	SNP	A1	A2	Prob_in_pCausalSet	Causal_Post_Prob	r2
4	28527304	rs167106	C	A	0.004	0.008	0.97
4	28527537	rs292047	T	G	0.006	0.012	0.84
4	28528060	rs10517147	C	T	0.004	0.008	0.97
4	28532565	rs638223	C	T	0.004	0.008	0.97
4	28538250	rs292038	G	C	0.004	0.008	0.97
4	28538736	rs1510712	G	A	0.004	0.008	0.97
4	28539924	rs687535	A	G	0.001	0.002	0.88
4	28540930	rs13125329	C	A	0.004	0.008	0.97
4	28542348	rs542264	G	C	0.004	0.008	0.97
4	28542928	rs292014	A	G	0.004	0.008	0.97
4	28545048	rs167104	G	A	0.002	0.004	0.94
4	28547108	rs557255	T	C	0.002	0.004	0.94
4	28557165	rs2458606	G	A	0.006	0.011	0.83
4	28558043	rs2458607	G	A	0.006	0.011	0.83
4	28560540	rs2458608	A	G	0.006	0.011	0.83
4	28561303	rs2995111	A	G	0.006	0.011	0.83
4	28561374	rs2960592	T	C	0.006	0.011	0.83
4	28562034	rs2471721	C	T	0.006	0.011	0.83
4	28563166	rs2471720	A	G	0.006	0.011	0.83
4	28563313	rs2458613	A	G	0.006	0.011	0.83
4	28563413	rs2471719	C	T	0.006	0.011	0.83
4	28563455	rs2458614	G	A	0.006	0.011	0.83
4	28565123	rs2458616	A	C	0.006	0.011	0.83
4	28565233	rs2471718	G	A	0.006	0.011	0.83
4	28566571	rs2458617	C	T	0.006	0.011	0.83
4	28566686	rs2458618	T	G	0.006	0.011	0.83
4	28568637	rs2943155	C	T	0.006	0.011	0.83
4	28568717	rs2943156	C	G	0.006	0.011	0.83
4	28569819	rs2471717	T	G	0.006	0.011	0.83
4	28570278	rs2471715	T	G	0.006	0.011	0.83

Table S17. Credible set of SNPs identified using CAVIAR

CHR	BP	SNP	A1	A2	Prob_in_pCausalSet	Causal_Post_Prob	r2
4	28571563	rs12505899	C	T	0.006	0.012	0.65
4	28571606	rs12501893	T	C	0.006	0.012	0.65
4	28571640	rs2943157	T	C	0.006	0.012	0.65
4	28571652	rs2943158	G	T	0.006	0.012	0.65
4	28571988	rs1514126	G	A	0.006	0.012	0.65
4	28572095	rs1514128	C	T	0.006	0.012	0.65
4	28572856	rs2458624	A	G	0.006	0.012	0.65
4	28575113	rs2471710	T	C	0.001	0.002	0.57
4	28575292	rs2471709	T	C	0.001	0.002	0.57
4	28575709	rs2458626	C	A	0.001	0.002	0.57
4	28576379	rs2458627	C	A	0.001	0.002	0.57
4	28577504	rs1514129	G	C	0.005	0.01	0.64
4	28579020	rs2458628	T	C	0.001	0.002	0.57
4	28580184	rs2458629	G	A	0.001	0.002	0.57
4	28581335	rs2471707	A	C	0.001	0.002	0.57
4	28581431	rs2458630	A	T	0.005	0.01	0.64
4	28583060	rs2471705	A	G	0.005	0.01	0.64
4	28584417	rs2471703	A	G	0.005	0.01	0.64
4	28587846	rs1168693995	G	C	0.005	0.01	0.64
4	28589079	rs2471711	T	C	0.005	0.01	0.64
4	28589619	rs2248575	A	G	0.005	0.01	0.64
4	28591924	rs2458619	A	G	0.005	0.01	0.64
4	28593164	rs2471685	C	T	0.005	0.01	0.64
4	28593978	rs2471687	C	T	0.005	0.01	0.64
4	28594111	rs2471688	A	G	0.005	0.01	0.64
4	28595064	rs2471689	G	A	0.005	0.01	0.64
4	28596316	rs2471690	C	T	0.005	0.01	0.64
4	28597991	rs2471691	C	T	0.005	0.01	0.64
4	28598358	rs2471692	C	T	0.005	0.01	0.64
4	28600877	rs2458621	C	G	0.004	0.008	0.62

Table S17. Credible set of SNPs identified using CAVIAR

CHR	BP	SNP	A1	A2	Prob_in_pCausalSet	Causal_Post_Prob	r2
4	28604977	rs9790405	C	T	0.0002	0.0003	0.24
4	28678144	rs1267296960	T	A	0.002	0.004	0.61
4	28719509	rs1493159	C	T	0.003	0.005	0.58
4	28727427	rs2087875	A	G	0.002	0.003	0.54
4	28735828	rs28793586	T	C	0.002	0.003	0.54
4	28736038	rs55869607	A	G	0.001	0.002	0.50
4	28736971	rs28704662	A	T	0.001	0.002	0.50
4	28737112	rs67524851	C	T	0.001	0.002	0.50
4	28738088	rs10001415	C	T	0.001	0.002	0.50
4	28740012	rs36071950	A	C	0.001	0.002	0.50
4	28741919	rs1491311167	T	A	0.001	0.002	0.50
4	28745163	rs77075089	A	G	0.001	0.002	0.50
4	28747310	rs10001616	A	G	0.001	0.002	0.50
4	28748805	rs71596161	A	G	0.001	0.002	0.50
4	28748810	rs28401471	T	C	0.001	0.002	0.50
4	28748871	rs28362049	C	T	0.001	0.002	0.50
4	28749863	rs7695442	T	A	0.001	0.002	0.50
4	28750665	rs13102811	T	C	0.001	0.002	0.50
4	28754779	rs7693339	T	A	0.001	0.002	0.50
4	28761781	rs6851565	A	G	0.002	0.004	0.51
4	28762951	rs34024932	T	C	0.002	0.004	0.51
4	28767776	rs11737432	A	G	0.002	0.004	0.51
4	28771767	rs73215498	A	T	0.002	0.004	0.51
4	28774747	rs73219413	A	G	0.002	0.003	0.50
4	28775853	rs73219415	G	A	0.002	0.003	0.50
4	28779671	rs66528608	A	G	0.002	0.003	0.50
4	28781817	rs73219418	T	A	0.002	0.003	0.50
4	28788513	rs13144199	A	T	0.002	0.003	0.50
4	28791121	rs13113800	C	T	0.002	0.003	0.50
4	28792788	rs1353049	C	T	0.002	0.003	0.50

Table S17. Credible set of SNPs identified using CAVIAR

CHR	BP	SNP	A1	A2	Prob_in_pCausalSet	Causal_Post_Prob	r2
4	28793330	rs35538171	A	G	0.002	0.003	0.50
4	28795187	rs67741650	T	C	0.002	0.003	0.50
4	28798954	rs67753751	C	A	0.002	0.003	0.50
4	28799742	rs13140136	C	T	0.002	0.003	0.50
4	28801221	rs34072092	C	T	0.002	0.003	0.50
4	28812966	rs34575420	A	T	0.001	0.002	0.53
4	28813116	rs34231546	A	C	0.001	0.002	0.53
4	28813302	rs13118585	T	C	0.001	0.002	0.53
4	28816220	rs7349599	A	G	0.001	0.002	0.53
4	28820334	rs35351681	T	C	0.001	0.002	0.53
4	28827186	rs35168262	T	C	0.001	0.002	0.53
4	28827190	rs2309887	T	G	0.0004	0.001	0.47
4	28829722	rs71596163	A	G	0.001	0.002	0.53
4	28831118	rs67012720	C	G	0.001	0.002	0.53
4	28832740	rs17653404	G	A	0.001	0.002	0.53
4	28836491	rs541307772	C	T	0.0002	0.0004	0.47
4	28838463	rs13125283	C	T	0.0002	0.0004	0.47
4	28841728	rs36008028	A	G	0.0002	0.0004	0.47
4	28842321	rs13127063	A	G	0.0002	0.0004	0.47
4	28848518	rs11730630	C	T	0.0002	0.0004	0.47
4	28851739	rs34940643	G	A	0.0002	0.0004	0.47
4	28853720	rs75924892	A	G	0.0002	0.0004	0.47
4	28854021	rs111923755	T	C	0.0003	0.001	0.42
4	28854081	rs35875568	C	T	0.0003	0.001	0.42
4	28854365	rs13124043	G	A	0.0003	0.001	0.42
4	28855098	rs4450915	C	T	0.0003	0.001	0.42
4	28855370	rs10021028	C	T	0.0003	0.001	0.42
4	28855708	rs10011877	C	G	0.0003	0.001	0.42
4	28855799	rs145797021	T	G	0.0003	0.001	0.42
4	28856428	rs4467552	A	G	0.0003	0.001	0.42

Table S17. Credible set of SNPs identified using CAVIAR

CHR	BP	SNP	A1	A2	Prob_in_pCausalSet	Causal_Post_Prob	r2
4	28856499	rs4461513	C	A	0.0003	0.001	0.42
4	28856694	rs4459975	A	G	0.0003	0.001	0.42
4	28856766	rs4459978	C	T	0.0003	0.001	0.42
4	28856826	rs146120146	T	A	0.0003	0.001	0.42
4	28856930	rs141149319	G	A	0.0003	0.001	0.42
4	28858062	rs28876111	G	A	0.0002	0.0005	0.40
4	28858325	rs28857240	A	G	0.0002	0.0005	0.38
4	28858542	rs28798375	A	C	0.0002	0.0005	0.40
4	28858558	rs28876079	T	C	0.0002	0.0005	0.40
4	28858575	rs1202616961	A	G	0.0002	0.0005	0.40
4	28858578	rs28868298	A	G	0.0002	0.0005	0.40
4	28858857	rs6828321	G	A	0.0002	0.0005	0.40
4	28858875	rs6828839	A	G	0.0002	0.0005	0.40
4	28858917	rs13120881	T	C	0.0002	0.0004	0.44
4	28859001	rs6828537	G	A	0.0002	0.0005	0.40
4	28859077	rs6829283	A	G	0.0002	0.0005	0.40
4	28859332	rs73221285	G	A	0.0002	0.0005	0.40
4	28859532	rs28419219	A	G	0.0002	0.0005	0.40
4	28859561	rs28508131	G	A	0.0002	0.0005	0.40
4	28859652	rs28674090	G	A	0.0002	0.0005	0.40
4	28859923	rs28710451	C	G	0.0002	0.0005	0.40
4	28859955	rs28532690	G	A	0.0002	0.0005	0.40
4	28860189	rs13129333	C	G	0.0002	0.0005	0.40
4	28860282	rs13129541	C	G	0.0002	0.0004	0.44
4	28860291	rs10025076	T	G	0.0002	0.0005	0.40
4	28860599	rs9992199	A	T	0.0002	0.0005	0.40
4	28861789	rs11736200	T	C	0.0002	0.0005	0.40
4	28861911	rs10008384	G	A	0.0002	0.0005	0.40
4	28862413	rs10031220	T	C	0.0002	0.0005	0.40
4	28862538	rs4280718	G	A	0.0002	0.0005	0.40

Table S17. Credible set of SNPs identified using CAVIAR

CHR	BP	SNP	A1	A2	Prob_in_pCausalSet	Causal_Post_Prob	r2
4	28862780	rs73221298	T	C	0.0002	0.0004	0.44
4	28863159	rs7698028	G	A	0.0002	0.0005	0.40
4	28863746	rs7682215	C	T	0.0002	0.0005	0.40
4	28863905	rs12331292	A	T	0.0002	0.0005	0.40
4	28863907	rs12330987	A	C	0.0002	0.0005	0.40
4	28864153	rs7439579	C	T	0.0002	0.0005	0.40
4	28864709	rs3924142	T	C	0.0002	0.0005	0.40
4	28865223	rs34939094	A	G	0.0002	0.0005	0.40
4	28865703	rs28544086	T	C	0.0002	0.0005	0.40
4	28867318	rs67583658	A	C	0.0002	0.0003	0.37
4	28867795	rs6853736	G	A	0.0002	0.0003	0.37
4	28868305	rs10033285	T	C	0.0002	0.0003	0.37
4	28868349	rs7356502	G	A	0.0002	0.0003	0.37
4	28868389	rs10000627	A	T	0.0002	0.0003	0.37
4	28868549	rs979446864	G	T	0.0002	0.0003	0.37
4	28868688	rs34723504	T	C	0.0002	0.0003	0.37
4	28869631	rs35412443	A	G	0.0002	0.0003	0.37
4	28871596	rs13146956	A	T	0.0002	0.0004	0.38
4	28871862	rs28633494	G	A	0.0002	0.0004	0.38
4	28873007	rs73222920	G	A	0.0002	0.0004	0.38
4	rs118081337	183654119	A	G	0.0018	0.0032	0.31
4	rs118081337	183654119	A	G	0.002	0.003	0.31
4	rs11938233	183605088	A	G	0.00052	0.00094	0.16
4	rs13435237	183654099	G	A	0.0011	0.0021	0.26
4	rs13435237	183654099	G	A	0.001	0.002	0.26
4	rs17074027	183678700	G	T	0.22	0.4	1.00
4	rs17074036	183685402	A	G	0.003	0.005	0.55
4	rs17074036	183685402	A	G	0.0027	0.0048	0.55
4	rs4862091	183684204	C	T	0.006	0.01	0.37
4	rs4862091	183684204	C	T	0.0055	0.01	0.37

Table S17. Credible set of SNPs identified using CAVIAR

CHR	BP	SNP	A1	A2	Prob_in_pCausalSet	Causal_Post_Prob	r2
4	rs6552604	183663607	T	C	0.0012	0.0022	0.29
4	rs6552604	183663607	T	C	0.001	0.002	0.29
4	rs6829132	183681725	C	A	0.006	0.01	0.59
4	rs6829132	183681725	C	A	0.0055	0.01	0.59
4	rs7691449	183660235	G	A	0.001	0.003	0.27
4	rs7691449	183660235	G	A	0.0014	0.0025	0.27
4	rs9993361	183671543	G	A	0.0012	0.0022	0.31
4	rs9993361	183671543	G	A	0.001	0.002	0.31
6	88546326	rs2499497	T	C	0.0003	0.001	0.22
6	88547515	rs2787913	A	G	0.0003	0.001	0.21
6	88549795	rs718220	G	A	0.0003	0.001	0.23
6	88550425	rs2499495	T	G	0.0003	0.001	0.23
6	88550917	rs2477310	C	T	0.0003	0.001	0.23
6	88555067	rs1324688	T	C	0.001	0.002	0.45
6	88556885	rs1324689	T	C	0.001	0.002	0.48
6	88559273	rs9344734	T	G	0.001	0.001	0.47
6	88559472	rs9344735	A	G	0.001	0.002	0.48
6	88559495	rs9344736	A	G	0.001	0.002	0.48
6	88560207	rs9342126	A	G	0.001	0.001	0.47
6	88562207	rs373513473	A	G	0.001	0.002	0.48
6	88562282	6:88562282:TAA	T	TAAC	0.001	0.001	0.48
6	88562327	rs574644780	CT	C	0.001	0.001	0.43
6	88563032	rs6454654	T	C	0.001	0.002	0.48
6	88563240	rs1222677393	A	AT	0.001	0.001	0.46
6	88563303	rs6415023	C	G	0.001	0.002	0.48
6	88563547	rs6454655	G	A	0.001	0.002	0.48
6	88564756	rs9353509	T	C	0.001	0.002	0.48
6	88566365	rs9351134	A	T	0.001	0.002	0.48
6	88568988	rs56071491	T	C	0.001	0.002	0.49
6	88569002	rs55764175	G	A	0.001	0.002	0.49

Table S17. Credible set of SNPs identified using CAVIAR

CHR	BP	SNP	A1	A2	Prob_in_pCausalSet	Causal_Post_Prob	r2
6	88569098	rs6939791	A	G	0.001	0.002	0.49
6	88569317	6:88569317:CT:C	C	CT	0.001	0.002	0.49
6	88569662	rs6940862	A	G	0.001	0.002	0.49
6	88569807	rs73752066	A	G	0.001	0.002	0.48
6	88570008	rs7770681	G	T	0.001	0.002	0.48
6	88571034	rs4615355	T	G	0.001	0.002	0.52
6	88571289	rs77565838	G	C	0.001	0.002	0.48
6	88571309	rs6454657	A	G	0.001	0.002	0.52
6	88571437	rs6454658	A	G	0.001	0.002	0.52
6	88571803	rs1327051952	G	C	0.003	0.006	0.55
6	88571968	rs9450817	A	G	0.002	0.004	0.55
6	88575196	rs4298315	G	C	0.002	0.004	0.55
6	88575620	rs9362457	G	T	0.002	0.004	0.55
6	88575716	rs9344737	T	C	0.002	0.003	0.47
6	88577883	rs3923216	A	G	0.008	0.016	0.66
6	88578195	rs6415024	T	C	0.014	0.026	0.70
6	88578373	rs4320331	T	C	0.013	0.024	0.74
6	88578393	rs4389736	G	A	0.013	0.024	0.74
6	88579382	rs4537110	G	A	0.013	0.024	0.75
6	88579560	rs4129674	A	G	0.013	0.024	0.74
6	88579705	rs4129673	C	G	0.013	0.024	0.74
6	88580664	rs4506018	A	G	0.013	0.025	0.74
6	88582415	rs9294392	T	A	0.013	0.025	0.79
6	88582598	rs9344738	T	C	0.005	0.009	0.70
6	88584710	rs1464272840	C	CAAA	0.009	0.016	0.80
6	88585489	rs9444561	T	C	0.008	0.015	0.73
6	88588004	rs9784861	A	G	0.008	0.015	0.73
6	88592819	rs4519980	G	A	0.016	0.03	0.83
6	88593579	rs9359760	T	C	0.006	0.01	0.73
6	88596854	rs4485983	A	G	0.030	0.056	0.85

Table S17. Credible set of SNPs identified using CAVIAR

CHR	BP	SNP	A1	A2	Prob_in_pCausalSet	Causal_Post_Prob	r2
6	88603026	rs9359761	G	A	0.049	0.09	0.91
6	88605297	6:88605297:TG:T	T	TG	0.015	0.027	0.80
6	88606134	rs9450821	A	G	0.076	0.14	0.91
6	88608343	rs9450823	G	C	0.001	0.003	0.21
6	88609397	rs9362458	A	G	0.007	0.013	0.86
6	88609933	rs5878052	C	CT	0.001	0.003	0.21
6	88610137	rs4235834	T	G	0.001	0.003	0.21
6	88611793	rs6918951	C	T	0.001	0.003	0.21
6	88611850	rs6903270	T	C	0.001	0.003	0.21
6	88612769	rs6925312	A	G	0.079	0.15	1.00
8	138068064	rs36014845	G	A	0.0002	0.0005	0.20
8	138068934	rs34063731	C	T	0.001	0.001	0.25
8	138069118	rs35628260	AC	A	0.001	0.001	0.26
8	138069364	rs11984900	T	G	0.001	0.001	0.25
8	138070221	rs34266606	C	T	0.001	0.001	0.25
8	138070877	rs11997096	G	A	0.001	0.001	0.25
8	138071307	rs72736397	T	C	0.001	0.001	0.25
8	138071531	rs78342455	T	G	0.001	0.001	0.25
8	138073544	rs34164683	G	A	0.001	0.001	0.25
8	138073934	rs13267873	T	C	0.001	0.001	0.25
8	138075582	rs116713894	A	G	0.001	0.001	0.25
8	138077925	rs111833581	G	T	0.001	0.001	0.25
8	138079129	rs1012244813	T	TA	0.001	0.001	0.25
8	138079747	rs34948159	T	G	0.001	0.001	0.25
8	138080449	rs13260461	A	G	0.001	0.001	0.25
8	138081290	rs4295697	G	A	0.001	0.001	0.25
8	138082238	rs34065840	T	G	0.0005	0.001	0.26
8	138083152	rs71532111	T	G	0.001	0.001	0.27
8	138083408	rs71532112	C	G	0.0005	0.001	0.26
8	138085350	rs71532113	T	G	0.0005	0.001	0.26

Table S17. Credible set of SNPs identified using CAVIAR

CHR	BP	SNP	A1	A2	Prob_in_pCausalSet	Causal_Post_Prob	r2
8	138085500	rs71532114	A	T	0.0005	0.001	0.26
8	138086085	rs35498675	GT	G	0.0005	0.001	0.26
8	138087924	rs76844363	G	A	0.0005	0.001	0.26
8	138088089	rs35725671	T	G	0.0005	0.001	0.26
8	138088503	rs36074855	T	C	0.0005	0.001	0.26
8	138090760	rs35926600	A	G	0.0005	0.001	0.26
8	138092136	rs35253257	T	G	0.0005	0.001	0.26
8	138095097	rs4366109	A	G	0.0005	0.001	0.26
8	138097325	rs2076987	G	C	0.0005	0.001	0.26
8	138099701	rs1009752441	C	A	0.0004	0.001	0.26
8	138100124	rs13250544	G	A	0.0005	0.001	0.26
8	138100641	rs4401897	A	G	0.0005	0.001	0.26
8	138102948	rs12375407	C	T	0.0005	0.001	0.26
8	138103238	rs12375349	G	C	0.0005	0.001	0.26
8	138104714	rs13255859	T	C	0.0005	0.001	0.26
8	138105391	rs35409626	A	C	0.0005	0.001	0.26
8	138105486	rs12375361	C	T	0.0005	0.001	0.26
8	138110330	rs34101782	C	G	0.0005	0.001	0.26
8	138110428	rs36103261	A	G	0.0005	0.001	0.26
8	138113906	rs13266672	A	T	0.0004	0.001	0.26
8	138114639	rs16906760	C	T	0.0005	0.001	0.26
8	138114990	rs9657449	A	G	0.0005	0.001	0.26
8	138116658	rs16906762	T	C	0.0005	0.001	0.26
8	138118015	rs16906764	G	A	0.0005	0.001	0.26
8	138119182	8:138119182:TG:T	T	TG	0.0003	0.001	0.26
8	138123015	rs36076245	C	G	0.0003	0.001	0.28
8	138123150	rs35201079	C	T	0.0003	0.001	0.28
8	138124046	rs34561439	T	A	0.0003	0.001	0.28
8	138125859	8:138125859:A:<(<CN0>	A	A	0.0003	0.001	0.28
8	138132057	rs13266810	A	G	0.0003	0.001	0.28

Table S17. Credible set of SNPs identified using CAVIAR

CHR	BP	SNP	A1	A2	Prob_in_pCausalSet	Causal_Post_Prob	r2
8	138133781	rs13278930	A	G	0.0003	0.001	0.28
8	138134249	rs34802845	C	T	0.0003	0.001	0.28
8	138139421	rs79537912	C	G	0.0003	0.001	0.28
8	138139430	rs77164139	A	G	0.0003	0.0005	0.27
8	138140306	rs71532115	G	T	0.0003	0.001	0.28
8	138140402	rs71532116	T	G	0.0003	0.001	0.28
8	138141732	rs79603374	G	A	0.0003	0.001	0.28
8	138143836	rs13257805	T	C	0.0003	0.001	0.28
8	138143957	8:138143957:AC:.A	AC	AC	0.0003	0.001	0.28
8	138144251	rs35406480	C	T	0.0003	0.001	0.28
8	138145168	rs35204735	G	C	0.0003	0.001	0.28
8	138145866	rs13261322	G	A	0.0003	0.001	0.28
8	138147898	rs1395122747	C	T	0.0003	0.001	0.28
8	138148461	rs35751459	T	C	0.0003	0.001	0.28
8	138150662	rs146391199	C	T	0.0003	0.001	0.28
8	138150772	rs35123521	C	T	0.0003	0.001	0.28
8	138152537	rs71532118	A	G	0.0003	0.001	0.28
8	138159522	rs13275346	G	C	0.0003	0.001	0.28
8	138163740	rs34250776	T	A	0.0004	0.001	0.33
8	138165302	rs34679127	TA	T	0.0005	0.001	0.33
8	138176986	rs71532119	A	G	0.001	0.001	0.38
8	138178588	rs2091923	G	A	0.001	0.001	0.38
8	138184366	rs34797832	C	T	0.001	0.001	0.38
8	138186519	rs13266366	A	C	0.001	0.002	0.37
8	138186852	rs13276198	C	T	0.001	0.001	0.38
8	138190742	rs36036943	A	G	0.001	0.001	0.38
8	138190839	rs71532120	T	G	0.001	0.001	0.38
8	138191583	rs57275182	A	G	0.001	0.001	0.38
8	138193581	rs13263868	A	G	0.001	0.001	0.38
8	138193884	rs34229947	A	G	0.001	0.002	0.37

Table S17. Credible set of SNPs identified using CAVIAR

CHR	BP	SNP	A1	A2	Prob_in_pCausalSet	Causal_Post_Prob	r2
8	138194801	rs34136532	T	C	0.001	0.002	0.37
8	138195417	rs35601795	C	G	0.001	0.001	0.38
8	138195423	rs34164159	G	A	0.001	0.002	0.37
8	138196442	rs539732750	TA	T	0.001	0.002	0.37
8	138196686	rs35469155	T	C	0.001	0.002	0.38
8	138198353	rs13260372	A	G	0.001	0.002	0.38
8	138198722	rs71532121	T	C	0.001	0.002	0.38
8	138201893	rs36041928	T	A	0.001	0.001	0.38
8	138203722	rs35284528	G	A	0.001	0.001	0.38
8	138204086	rs56034364	G	A	0.001	0.001	0.38
8	138204459	rs6993267	C	G	0.001	0.001	0.38
8	138205679	rs1327465202	T	C	0.001	0.001	0.38
8	138205739	rs7825732	C	A	0.001	0.001	0.38
8	138206529	rs13255582	G	A	0.001	0.001	0.38
8	138206735	rs35116705	A	T	0.001	0.001	0.38
8	138207554	rs60849715	A	G	0.0004	0.001	0.36
8	138207778	rs1466052925	A	AACAC	0.001	0.001	0.38
8	138207845	rs1201942664	T	TAA	0.001	0.001	0.38
8	138207850	rs34923526	G	A	0.001	0.001	0.38
8	138207967	rs35624484	A	G	0.0004	0.001	0.36
8	138207978	rs34352107	C	T	0.0004	0.001	0.36
8	138208072	rs34796536	AT	A	0.0004	0.001	0.36
8	138208097	rs10109188	A	G	0.0004	0.001	0.36
8	138208193	rs10096608	C	A	0.0004	0.001	0.36
8	138208196	rs10096609	G	A	0.0004	0.001	0.36
8	138209031	rs7822935	T	C	0.0004	0.001	0.36
8	138209049	rs7840717	G	A	0.0004	0.001	0.36
8	138209669	rs7012808	G	A	0.001	0.002	0.40
8	138209837	rs6982911	C	T	0.001	0.001	0.38
8	138209903	rs532615715	GA	G	0.001	0.001	0.37

Table S17. Credible set of SNPs identified using CAVIAR

CHR	BP	SNP	A1	A2	Prob_in_pCausalSet	Causal_Post_Prob	r2
8	138210656	rs28622139	C	G	0.001	0.001	0.36
8	138229001	rs4609227	C	G	0.043	0.083	1.00
8	138230558	rs28403940	C	G	0.025	0.048	0.97
8	138234249	rs80211230	A	G	0.025	0.048	0.97
8	138235253	rs10112576	G	A	0.024	0.046	0.97
8	138237837	rs75806625	A	G	0.025	0.048	0.97
8	138244924	rs6984969	C	G	0.025	0.048	0.97
8	138247025	rs146779024	CA	C	0.017	0.033	0.95
8	138247237	rs11166694	T	A	0.025	0.048	0.97
8	138247238	rs11166695	A	C	0.025	0.048	0.97
8	138249581	rs11985863	G	A	0.004	0.007	0.81
8	138250392	rs74886588	A	G	0.001	0.001	0.70
8	138251017	rs11998305	T	C	0.018	0.035	0.95
8	138252239	rs73389879	G	A	0.018	0.035	0.95
8	138255624	rs10094379	G	A	0.018	0.035	0.95
8	138256100	rs57442651	C	T	0.018	0.035	0.95
8	138257593	rs59661752	T	C	0.0001	0.0003	0.21
8	138257675	rs58693023	G	A	0.0001	0.0003	0.21
8	138258042	rs144388387	T	G	0.015	0.03	0.94
8	138258220	rs7829774	C	A	0.0001	0.0003	0.21
8	138259895	rs927781987	AT	A	0.0001	0.0003	0.21
8	138260171	rs11780629	A	G	0.0001	0.0003	0.21
8	138260456	rs10113847	G	A	0.015	0.03	0.94
8	138261877	rs7813071	G	A	0.0001	0.0003	0.21
8	138263163	rs9886630	A	C	0.015	0.03	0.94
8	138265199	rs4301477	T	C	0.015	0.03	0.94
8	138265859	rs10088225	A	T	0.015	0.03	0.94
8	138266983	rs4634676	A	G	0.0001	0.0003	0.21
8	138267262	rs77674621	T	C	0.015	0.03	0.94
8	138267684	rs78339783	G	T	0.006	0.012	0.89

Table S17. Credible set of SNPs identified using CAVIAR

CHR	BP	SNP	A1	A2	Prob_in_pCausalSet	Causal_Post_Prob	r2
8	138268297	rs57391177	A	T	0.006	0.012	0.89
8	138268600	rs61548155	G	C	0.015	0.03	0.94
8	138268930	rs56907949	G	T	0.003	0.006	0.88
8	138268994	rs58971409	C	T	0.015	0.03	0.94
8	138271518	rs7002431	A	G	0.015	0.03	0.94
8	138273862	rs10505672	A	G	0.003	0.005	0.76
8	138275567	rs6986961	T	C	0.007	0.013	0.78
8	138278430	rs7817282	C	T	0.0001	0.0003	0.21
8	138280386	rs36031258	CAT	C	0.005	0.01	0.69
8	138282708	rs777367903	A	T	0.001	0.002	0.70
8	138284752	rs10094924	C	T	0.004	0.007	0.77
8	138285722	rs4338139	A	G	0.004	0.007	0.77
8	138286203	rs933952236	A	C	0.004	0.007	0.77
8	138286211	rs10090816	A	G	0.007	0.013	0.78
8	138286232	rs7000198	T	C	0.004	0.007	0.77
8	138286602	rs139017414	TA	T	0.007	0.013	0.78
8	138287048	rs117105019	A	G	0.001	0.001	0.65
8	138287175	rs117497573	T	C	0.0004	0.001	0.33
8	138291867	rs6992584	T	G	0.010	0.019	0.77
8	138297674	rs11774124	T	C	0.004	0.007	0.67
8	138298903	rs56200536	G	C	0.003	0.007	0.66
8	138328409	rs78507288	A	T	0.0004	0.001	0.47

Table S18. Significant eQTL results

UniqID	CHR	BP	Database	Tissue	Gene	Symbol	Tested_allele	Signed_stats	P	FDR
4:28470936:A:G	4	28470936	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	G	-0.32	2.83E-22	1.83E-19
4:28472221:A:T	4	28472221	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	-0.31	7.26E-22	4.57E-19
4:28473625:G:T	4	28473625	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	T	-0.31	1.05E-21	6.57E-19
4:28473922:C:T	4	28473922	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	C	-0.31	2.36E-21	1.44E-18
4:28474937:C:G	4	28474937	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	C	-0.31	1.33E-19	7.14E-17
4:28476701:A:G	4	28476701	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	-0.31	1.28E-19	6.88E-17
4:28476726:A:G	4	28476726	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	-0.31	1.24E-19	6.65E-17
4:28476895:A:G	4	28476895	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	G	-0.31	1.31E-19	7.03E-17
4:28482974:A:T	4	28482974	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	T	-0.29	9.09E-18	4.24E-15
4:28484234:C:T	4	28484234	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	C	-0.29	3.69E-18	1.77E-15
4:28484389:G:T	4	28484389	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	G	-0.29	3.67E-18	1.76E-15
4:28488065:A:G	4	28488065	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	-0.29	1.57E-17	7.17E-15
4:28490381:C:T	4	28490381	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	C	-0.29	1.87E-17	8.50E-15
4:28493198:A:G	4	28493198	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	G	-0.29	5.89E-18	2.78E-15
4:28493840:C:G	4	28493840	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	C	-0.29	6.21E-18	2.93E-15
4:28494313:A:G	4	28494313	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	-0.29	6.53E-18	3.08E-15
4:28496256:A:G	4	28496256	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	-0.29	7.56E-18	3.55E-15
4:28497583:C:T	4	28497583	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	T	-0.28	3.70E-17	1.64E-14
4:28498910:A:G	4	28498910	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	G	-0.29	1.06E-17	4.90E-15
4:28499782:A:G	4	28499782	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	G	-0.29	1.20E-17	5.53E-15
4:28503151:C:T	4	28503151	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	T	-0.29	6.80E-18	3.20E-15
4:28506937:G:T	4	28506937	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	T	-0.27	7.11E-17	3.09E-14
4:28507335:A:G	4	28507335	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	G	-0.29	8.30E-18	3.88E-15
4:28507573:C:T	4	28507573	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	T	-0.29	8.32E-18	3.89E-15
4:28507739:A:G	4	28507739	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	-0.27	7.34E-17	3.19E-14
4:28509079:A:C	4	28509079	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	-0.29	9.10E-18	4.24E-15
4:28518533:C:G	4	28518533	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	G	-0.29	1.71E-17	7.81E-15
4:28519470:A:G	4	28519470	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	G	-0.29	1.88E-17	8.53E-15
4:28520773:A:C	4	28520773	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	C	-0.29	8.90E-18	4.16E-15
4:28522519:C:T	4	28522519	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	C	-0.28	3.79E-17	1.68E-14
4:28524559:C:T	4	28524559	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	T	-0.28	4.18E-17	1.85E-14
4:28524852:A:G	4	28524852	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	G	0.18	8.97E-11	2.17E-08
4:28527861:A:G	4	28527861	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	G	0.18	8.49E-11	2.06E-08
4:28528060:C:T	4	28528060	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	C	-0.28	7.15E-17	3.10E-14
4:28528234:A:T	4	28528234	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	-0.19	1.27E-11	3.40E-09
4:28532565:C:T	4	28532565	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	C	-0.28	2.02E-16	8.46E-14
4:28538250:C:G	4	28538250	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	G	-0.28	1.07E-16	4.57E-14
4:28538736:A:G	4	28538736	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	G	-0.28	2.60E-16	1.08E-13

Table S18. Significant eQTL results

UniqID	CHR	BP	Database	Tissue	Gene	Symbol	Tested_allele	Signed_stats	P	FDR
4:28539924:A:G	4	28539924	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	-0.19	9.36E-11	2.26E-08
4:28540930:A:C	4	28540930	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	C	-0.28	2.56E-16	1.06E-13
4:28542348:C:G	4	28542348	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	G	-0.28	4.51E-16	1.84E-13
4:28542928:A:G	4	28542928	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	-0.28	1.77E-16	7.46E-14
4:28545048:A:G	4	28545048	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	G	-0.27	1.23E-15	4.84E-13
4:28557165:A:G	4	28557165	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	G	-0.27	1.42E-15	5.54E-13
4:28558043:A:G	4	28558043	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	G	-0.27	7.34E-16	2.94E-13
4:28560540:A:G	4	28560540	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	-0.27	7.39E-16	2.96E-13
4:28561303:A:G	4	28561303	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	-0.27	1.28E-15	5.00E-13
4:28561374:C:T	4	28561374	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	T	-0.27	7.37E-16	2.95E-13
4:28562034:C:T	4	28562034	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	C	-0.27	7.40E-16	2.96E-13
4:28563166:A:G	4	28563166	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	-0.27	7.40E-16	2.96E-13
4:28563313:A:G	4	28563313	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	-0.27	7.42E-16	2.97E-13
4:28563413:C:T	4	28563413	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	C	-0.27	7.42E-16	2.97E-13
4:28565123:A:C	4	28565123	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	-0.27	7.40E-16	2.96E-13
4:28565233:A:G	4	28565233	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	G	-0.27	7.39E-16	2.96E-13
4:28566571:C:T	4	28566571	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	C	-0.27	7.33E-16	2.93E-13
4:28566686:G:T	4	28566686	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	T	-0.27	7.32E-16	2.93E-13
4:28568637:C:T	4	28568637	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	C	-0.27	6.83E-16	2.74E-13
4:28568717:C:G	4	28568717	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	C	-0.27	8.73E-16	3.47E-13
4:28569819:G:T	4	28569819	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	T	-0.28	5.84E-16	2.36E-13
4:28570278:G:T	4	28570278	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	T	-0.28	5.40E-16	2.19E-13
4:28571606:C:T	4	28571606	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	T	-0.28	4.81E-16	1.95E-13
4:28571640:C:T	4	28571640	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	T	-0.28	6.62E-16	2.66E-13
4:28571652:G:T	4	28571652	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	G	-0.27	1.54E-15	5.98E-13
4:28571988:A:G	4	28571988	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	G	-0.28	4.54E-16	1.85E-13
4:28572856:A:G	4	28572856	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	-0.28	4.24E-16	1.73E-13
4:28575113:C:T	4	28575113	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	T	-0.15	9.01E-06	0.001
4:28575292:C:T	4	28575292	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	T	-0.15	8.81E-06	0.001
4:28575709:A:C	4	28575709	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	C	-0.15	8.81E-06	0.001
4:28576379:A:C	4	28576379	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	C	-0.15	8.82E-06	0.001
4:28577504:C:G	4	28577504	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	G	-0.22	4.28E-09	8.39E-07
4:28581335:A:C	4	28581335	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	-0.15	9.41E-06	0.001
4:28581431:A:T	4	28581431	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	-0.25	8.66E-10	1.86E-07
4:28583060:A:G	4	28583060	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	-0.22	4.22E-09	8.27E-07
4:28584417:A:G	4	28584417	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	-0.22	8.51E-09	1.60E-06
4:28587846:C:G	4	28587846	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	G	-0.22	1.42E-08	2.58E-06
4:28589079:C:T	4	28589079	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	T	-0.25	1.04E-09	2.20E-07

Table S18. Significant eQTL results

UniqID	CHR	BP	Database	Tissue	Gene	Symbol	Tested_allele	Signed_stats	P	FDR
4:28589619:A:G	4	28589619	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	-0.25	1.04E-09	2.22E-07
4:28591924:A:G	4	28591924	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	-0.25	1.10E-09	2.33E-07
4:28593164:C:T	4	28593164	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	C	-0.25	1.12E-09	2.36E-07
4:28593978:C:T	4	28593978	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	C	-0.25	1.10E-09	2.34E-07
4:28594111:A:G	4	28594111	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	-0.25	1.10E-09	2.33E-07
4:28595064:A:G	4	28595064	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	G	-0.25	1.10E-09	2.33E-07
4:28596316:C:T	4	28596316	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	C	-0.25	1.10E-09	2.33E-07
4:28597991:C:T	4	28597991	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	C	-0.22	1.41E-08	2.57E-06
4:28598358:C:T	4	28598358	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	C	-0.25	1.10E-09	2.33E-07
4:28600877:C:G	4	28600877	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	C	-0.25	1.10E-09	2.33E-07
4:28616198:A:G	4	28616198	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	G	0.25	1.74E-09	3.59E-07
4:28617013:C:G	4	28617013	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	C	0.13	5.15E-05	0.0047
4:28618060:G:T	4	28618060	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	G	0.25	1.73E-09	3.56E-07
4:28620849:A:T	4	28620849	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	0.14	3.40E-05	0.0033
4:28621704:C:T	4	28621704	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	C	0.25	1.77E-09	3.65E-07
4:28623448:A:G	4	28623448	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	0.25	1.75E-09	3.61E-07
4:28623645:G:T	4	28623645	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	G	0.25	1.75E-09	3.61E-07
4:28624594:G:T	4	28624594	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	G	0.25	1.71E-09	3.53E-07
4:28626286:A:C	4	28626286	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	C	0.25	1.60E-09	3.31E-07
4:28629058:C:G	4	28629058	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	C	0.25	1.48E-09	3.07E-07
4:28629539:C:T	4	28629539	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	C	0.25	1.45E-09	3.01E-07
4:28631217:A:G	4	28631217	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	0.25	1.41E-09	2.94E-07
4:28633364:G:T	4	28633364	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	G	0.25	1.33E-09	2.78E-07
4:28633813:C:T	4	28633813	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	C	0.25	1.02E-09	2.17E-07
4:28651223:A:G	4	28651223	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	G	0.25	8.95E-10	1.92E-07
4:28651305:C:T	4	28651305	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	T	0.25	8.96E-10	1.92E-07
4:28652801:C:T	4	28652801	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	T	0.25	9.01E-10	1.93E-07
4:28653531:C:T	4	28653531	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	C	0.25	9.00E-10	1.93E-07
4:28656016:A:C	4	28656016	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	0.25	8.72E-10	1.87E-07
4:28656017:G:T	4	28656017	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	T	0.25	8.72E-10	1.87E-07
4:28662735:C:T	4	28662735	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	C	0.25	1.30E-09	2.73E-07
4:28663069:C:G	4	28663069	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	C	0.25	1.12E-09	2.38E-07
4:28666576:A:G	4	28666576	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	0.25	1.06E-09	2.25E-07
4:28666876:C:G	4	28666876	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	G	0.25	1.05E-09	2.23E-07
4:28671928:A:G	4	28671928	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	0.25	9.70E-10	2.07E-07
4:28673636:A:C	4	28673636	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	0.13	6.80E-05	0.006
4:28676223:C:T	4	28676223	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	C	0.25	9.00E-10	1.93E-07
4:28676642:A:G	4	28676642	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	0.25	8.94E-10	1.91E-07

Table S18. Significant eQTL results

UniqID	CHR	BP	Database	Tissue	Gene	Symbol	Tested_allele	Signed_stats	P	FDR
4:28681385:G:T	4	28681385	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	G	0.25	8.38E-10	1.80E-07
4:28686903:A:G	4	28686903	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	0.25	8.11E-10	1.75E-07
4:28687841:C:T	4	28687841	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	C	0.25	8.12E-10	1.75E-07
4:28690532:G:T	4	28690532	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	T	0.19	3.86E-07	5.58E-05
4:28692671:A:G	4	28692671	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	G	0.25	8.89E-10	1.90E-07
4:28696268:A:G	4	28696268	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	G	0.25	9.83E-10	2.09E-07
4:28696850:A:T	4	28696850	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	T	0.24	2.36E-09	4.79E-07
4:28698177:C:T	4	28698177	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	C	0.25	1.03E-09	2.18E-07
4:28699965:C:T	4	28699965	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	C	0.25	1.09E-09	2.30E-07
4:28701658:C:G	4	28701658	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	C	0.25	1.14E-09	2.41E-07
4:28710551:A:T	4	28710551	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	T	0.25	1.08E-09	2.29E-07
4:28712457:A:G	4	28712457	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	0.25	1.20E-09	2.52E-07
4:28714432:A:T	4	28714432	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	T	0.25	1.11E-09	2.34E-07
4:28717531:A:G	4	28717531	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	G	0.25	1.20E-09	2.53E-07
4:28719509:C:T	4	28719509	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	T	0.24	3.24E-09	6.44E-07
4:28720102:A:G	4	28720102	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	G	0.24	3.25E-09	6.47E-07
4:28720915:A:G	4	28720915	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	G	0.25	1.14E-09	2.41E-07
4:28721385:C:T	4	28721385	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	C	0.24	3.15E-09	6.28E-07
4:28722300:A:G	4	28722300	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	G	0.25	8.91E-10	1.91E-07
4:28723616:G:T	4	28723616	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	G	0.25	1.07E-09	2.28E-07
4:28724974:A:G	4	28724974	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	0.25	9.96E-10	2.12E-07
4:28727427:A:G	4	28727427	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	-0.24	1.90E-07	2.89E-05
4:28735828:C:T	4	28735828	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	T	-0.25	1.10E-07	1.74E-05
4:28736036:A:C	4	28736036	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	-0.15	3.21E-05	0.0031
4:28736038:A:G	4	28736038	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	-0.25	1.46E-07	2.27E-05
4:28736971:A:T	4	28736971	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	-0.15	2.72E-05	0.0027
4:28737112:C:T	4	28737112	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	C	-0.25	1.12E-07	1.78E-05
4:28740012:A:C	4	28740012	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	-0.26	6.46E-08	1.06E-05
4:28747310:A:G	4	28747310	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	-0.17	1.29E-06	0.00017
4:28748805:A:G	4	28748805	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	-0.26	7.51E-08	1.22E-05
4:28749863:A:T	4	28749863	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	T	-0.18	4.47E-07	6.38E-05
4:28750665:C:T	4	28750665	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	T	-0.25	7.74E-08	1.26E-05
4:28754779:A:T	4	28754779	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	T	-0.21	7.91E-09	1.49E-06
4:28761781:A:G	4	28761781	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	-0.23	4.90E-09	9.52E-07
4:28762951:C:T	4	28762951	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	T	-0.26	3.29E-08	5.66E-06
4:28767776:A:G	4	28767776	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	-0.26	3.53E-08	6.04E-06
4:28771767:A:T	4	28771767	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	-0.26	3.72E-08	6.36E-06
4:28774747:A:G	4	28774747	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	-0.26	4.03E-08	6.84E-06

Table S18. Significant eQTL results

UniqID	CHR	BP	Database	Tissue	Gene	Symbol	Tested_allele	Signed_stats	P	FDR
4:28775853:A:G	4	28775853	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	G	-0.26	5.25E-08	8.75E-06
4:28779671:A:G	4	28779671	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	-0.26	4.00E-08	6.80E-06
4:28781817:A:T	4	28781817	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	T	-0.26	5.41E-08	9.00E-06
4:28788513:A:T	4	28788513	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	-0.26	4.48E-08	7.55E-06
4:28791121:C:T	4	28791121	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	C	-0.27	2.70E-08	4.71E-06
4:28792788:C:T	4	28792788	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	C	-0.27	2.63E-08	4.60E-06
4:28793330:A:G	4	28793330	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	-0.27	2.12E-08	3.75E-06
4:28795187:C:T	4	28795187	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	T	-0.27	1.87E-08	3.34E-06
4:28799742:C:T	4	28799742	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	C	-0.16	2.75E-05	0.0027
4:28801221:C:T	4	28801221	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	C	-0.27	1.39E-08	2.53E-06
4:28812966:A:T	4	28812966	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	-0.28	2.97E-08	5.15E-06
4:28813116:A:C	4	28813116	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	-0.28	2.84E-08	4.93E-06
4:28813302:C:T	4	28813302	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	T	-0.28	2.93E-08	5.08E-06
4:28820334:C:T	4	28820334	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	T	-0.27	1.26E-08	2.30E-06
4:28827186:C:T	4	28827186	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	T	-0.28	3.54E-08	6.07E-06
4:28829722:A:G	4	28829722	PsychENCODE	Brain_Cortex	ENSG00000250064	RP11-123O22.1	A	-0.28	3.42E-08	5.87E-06
4:28466655:A:ATAT	4	28466655	GTEEx/v8	Brain_Cortex	ENSG00000249228	RP11-769N22.1	A	-0.45	3.15E-06	0.00014
4:28473922:C:T	4	28473922	GTEEx/v8	Brain_Cortex	ENSG00000249228	RP11-769N22.1	C	-0.43	5.98E-05	0.00014

Table S19. Association between *MIR4275* rs292034 and spherical power in children

CHR	SNP	BP	EA	NEA	HKCES 1						HKCES 2						Meta children			
					EAF	BETA	SE	L95	U95	P ^a	EAF	BETA	SE	L95	U95	P ^a	BETA	P	Q test	I ² (%)
4	rs292034	28478119	G	T	0.013	-1.43	0.32	-2.06	-0.81	8.29×10 ⁻⁶	0.011	-0.59	0.2	-0.99	-0.19	0.0037	-0.83	1.18×10 ⁻⁶	0.02	79

^aResults were adjusted for age and sex. I² (%), Heterogeneity.

Table S20. Association between *MIR4275* rs292034 and corneal astigmatism in children

CHR	SNP	BP	EA	NEA	HKCES 1						HKCES 2						Meta children			
					EA F	OR	SE	L95	U95	P ^a	EA F	OR	SE	L95	U95	P ^a	OR	P	Q test	I ² (%)
4	rs292034	28478119	G	T	0.013	1.64	0.46	0.66	4.06	0.29	0.011	2.1	0.34	1.09	4.05	0.027	1.93	0.016	0.66	0

^aResults were adjusted for age, sex and spherical equivalent. I² (%), Heterogeneity.
Corneal astigmatism was expressed using positive notation and defined as astigmatism of 1.0 D or greater.

Table S21. Study cohorts description**Hong Kong Children Eye Study (HKCES)¹**

HKCES is an ongoing population-based study focusing on eye conditions in primary school children in Hong Kong. All subjects recruited in this study were based on a stratified protocol which stratified all 571 primary schools registered with the Education Bureau into the 7 cluster regions used by the Hospital Authority Services in Hong Kong. All children were cycloplegic for comprehensive ocular examinations and to answer standardized questionnaires according to the unified protocol. The discovery set was randomly selected from each age strata and the rest of subjects were used as replication set.

Low concentration atropine for myopia progression (LAMP) study²

LAMP is a randomized, placebo-controlled, double-masked trial, which aims to evaluate the efficacy and safety of low-concentration atropine eye drops at different concentrations. This study was conducted from January 2016 to November 2017 at the CUHK Eye Centre of the Chinese University of Hong Kong, Hong Kong, China. Children enrolled in this study were aged from 4 to 12 with myopic refraction of at least 1.0 D in both eyes, astigmatism of less than 2.5D, and documented myopic progression of at least 0.5D in the past 1 year. Written informed consent was obtained from parents or guardians, and verbal consent was obtained from the participants. The ocular examinations and cycloplegic regimen is the same with that in HKCES.

Shantou Myopia Study (SMS)^{3,4}

The SMS was a long-term, city-wide, population-based programme which was mainly carried out by the technical institution Joint Shantou International Eye Center (JSIEC). All schoolchildren from all primary, junior high and senior high schools in Shantou undertake vision screening once a year. The details of data collection procedures of this study can be obtained from previous study.^{3,4} The subjects used in current study were aged from 6-12.

Adult-1⁵

All study subjects were Chinese adults recruited from the Chinese University of Hong Kong (CUHK) Eye Centre, Hong Kong, between 2015 to 2018. All subjects underwent detailed ophthalmic assessments, including visual acuity and noncycloplegic refraction, slit lamp examination, ocular motility by Zeiss IOL Master (Carl Zeiss Meditec, Dublin, CA). We excluded those who had prior ocular surgery, or had other major eye diseases that might affect the accuracy of refraction, such as strabismus, corneal scar, keratoconus and cataract.

Adult-2

This is a myopia cohort recruited from the CUHK Eye Centre, Hong Kong, between January 2016 to 2017. This cohort include myopic subjects from mild to extreme ($<-10D$) myopia. Non-myopic controls had SE between $+0.50D$ and $-0.50D$. All participants were free of any major eye diseases, such as keratoconus, cataract, glaucoma and age-related macular degeneration at the recruitment.

1. Yam JC, Tang SM, Kam KW, et al. High prevalence of myopia in children and their parents in Hong Kong Chinese Population: the Hong Kong Children Eye Study. *Acta Ophthalmol.* 2020 Aug;98(5):e639-e648. doi: 10.1111/aos.14350.
2. Yam JC, Jiang Y, Tang SM, et al. Low-Concentration Atropine for Myopia Progression (LAMP) Study: A Randomized, Double-Blinded, Placebo-Controlled Trial of 0.05%, 0.025%, and 0.01% Atropine Eye Drops in Myopia Control. *Ophthalmology.* 2019 Jan;126(1):113-124. doi: 10.1016/j.ophtha.2018.05.029.
3. Wang H, Li Y, Qiu K, et al. Prevalence of myopia and uncorrected myopia among 721 032 schoolchildren in a city-wide vision screening in southern China: the Shantou Myopia Study. *Br J Ophthalmol.* 2023 Nov 22;107(12):1798-1805. doi: 10.1136/bjo-2021-320940.
4. Huang Y, Huang C, Li L, et al. Corneal biomechanics, refractive error, and axial length in Chinese primary school children. *Invest Ophthalmol Vis Sci.* 2011 Jul 1;52(7):4923-8. doi: 10.1167/iovs.10-6211.
5. Tang SM, Li FF, Lu SY, et al. Association of the ZC3H11B, ZFHX1B and SNTB1 genes with myopia of different severities. *Br J Ophthalmol.* 2020 Oct;104(10):1472-1476. doi: 10.1136/bjophthalmol-2019-314203.

Table S22. Demographics of study cohorts

	Discovery set		Replication set			
	HKCES-1	LAMP Study	HKCES-2	SMS	Adult-1	Adult-2
N	864	373	2066	2027	1212	602
Men (%)	449 (52)	207 (55)	1116 (54)	1065 (52.5)	452 (37.29)	301 (50)
Mean age (range, years)	7.54 (6-9)	8.38 (4-12)	7.58 (5-10)	9.63 (6-12)	40.69 (24-69)	43 (29-68)
Average SE (SD, D)	0.32 (1.47)	-3.94 (1.83)	0.43 (1.56)	-2.20 (1.77)	-2.79 (2.77)	-4.09 (3.47)
Average AL (SD, mm)	23.05 (0.92)	24.84 (0.93)	23.02 (0.94)	-	-	-

HKCES, Hong Kong children eye study; LAMP, low concentration atropine for myopia progression; SMS, Shantou Myopia Study; Adult-1, parents of children from HKCES; Adult-2, parents of children from LAMP; SE, spherical equivalent; AL, axial length; SD, standard deviation.

Table S23. The results of Tracy-Widom test in HKCES-1 and LAMP Study for principal component adjustment

No.	HKCES				LAMP			
	Eigenvalue	Difference	Twstat	P	Eigenvalue	Difference	Twstat	P
1	2.03	NA	0.53	0.09	2.06	NA	-2.53	0.85
2	2.01	-0.013	2.41	0.005	2.03	-0.027	-2.12	0.76
3	1.98	-0.036	4.47	7.77E-05	2.02	-0.009	-1.02	0.42
4	1.97	-0.004	10.26	2.37E-11	2	-0.027	-0.19	0.21
5	1.7	-0.269	7.06	1.17E-07	1.98	-0.015	1.46	0.02
6	1.59	-0.115	-1.68	0.63	1.94	-0.039	3.18	0.001
7	1.58	-0.011	-2.06	0.74	1.94	-0.005	8.48	5.87E-09
8	1.56	-0.016	-3.58	0.98	1.62	-0.314	0.27	0.12
9	1.56	-0.004	-3.3	0.96	1.6	-0.027	-1.74	0.65
10	1.55	-0.002	-2.55	0.86	1.59	-0.003	-0.58	0.3
11	1.54	-0.01	-3.08	0.94	1.58	-0.014	-1.04	0.43
12	1.54	-0.007	NA	NA	1.57	-0.01	NA	NA
13	1.53	-0.005	NA	NA	1.56	-0.01	NA	NA
14	1.53	-0.003	NA	NA	1.55	-0.009	NA	NA
15	1.52	-0.01	NA	NA	1.54	-0.008	NA	NA
16	1.52	-0.003	NA	NA	1.54	-0.005	NA	NA
17	1.51	-0.006	NA	NA	1.53	-0.01	NA	NA
18	1.5	-0.013	NA	NA	1.51	-0.013	NA	NA
19	1.47	-0.029	NA	NA	1.51	-0.006	NA	NA
20	1.46	-0.009	NA	NA	1.5	-0.005	NA	NA

No., the component number; Eigenvalue, the eigenvalue corresponding to each principal component. It represents the amount of variance explained by that principal component; Difference, the difference between consecutive eigenvalues. This difference is used to evaluate the relative importance of each principal component; Twstat (Tracy-Widom Statistic) is based on the Tracy-Widom distribution and is used to evaluate the significance of the eigenvalue.