Supplementary Information

Supplementary Table S1. Instrument for measuring corneal curvature.

Study	Instrument
ALSPAC	IOLmaster
BMES	IOLmaster
EPIC	IOLmaster V.4
FITSA	IOLmaster
GenerationR	IOLmaster
GHS 1	Lenstar LS 900
GHS 2	Lenstar LS 900
RAINE	IOLmaster
Rotterdam-I	Javal Keratometer/Lenstar LS 900
Rotterdam-II	Javal Keratometer/Lenstar LS 900
Rotterdam-III	Javal Keratometer/Lenstar LS 900
OGP-A	IOLmaster
OGP-B	IOLmaster
TwinsUK	Visionix VX-120
BES-610K	Lenstar LS 900
BES-OmniE	Lenstar LS 900
SCES-610K	IOLmaster
SCES-OmniE	IOLmaster
SCORM	Canon RK-5
SIMES	IOLmaster
SINDI	IOLmaster
STARS	IOLmaster

Supplementary Table S2. Most strongly associated marker in each region in the GWAS meta-analysis of all Europeans aged >25 years.
EAF = effect allele frequency, OR = odds ratio.

SNP	Chr	Pos	Effect allele	Other allele	EAF	OR (95%CI)	P-value	Nearest gene
rs1620100	2	36179888	T	C	0.41	0.91 (0.87-0.94)	1.14×10^{-6}	MRPL50P1
rs138222255	4	113801232	A	T	0.89	0.82 (0.76-0.89)	2.52×10^{-6}	ANK2
rs73076614	12	22633729	T	C	0.95	1.24 (1.13-1.36)	3.32×10^{-6}	C2CD5
rs10187347	2	227348324	T	C	0.47	0.91 (0.88-0.95)	3.58×10^{-6}	MIR5702
rs11183146	12	46024937	A	G	0.54	0.84 (0.78-0.90)	3.82×10^{-6}	LINC00938
rs4804959	19	31803331	T	C	0.61	1.12 (1.07-1.17)	3.95×10^{-6}	TSHZ3
rs9393856	6	27767825	T	G	0.08	0.82 (0.75-0.89)	4.37×10^{-6}	TRNAQ10
rs2184695	10	89890390	A	C	0.53	0.91 (0.87-0.95)	4.66×10^{-6}	MED6P1
rs35587414	1	153174958	T	C	0.15	1.15 (1.08-1.23)	4.84×10^{-6}	LELP1
rs5806282	13	102849565	I	R	0.75	1.12 (1.07-1.17)	5.41×10^{-6}	FGF14

Supplementary Table S3. Most strongly associated marker in each region in the GWAS meta-analysis of all Europeans aged <25 years.
EAF = effect allele frequency, OR = odds ratio.

SNP	Chr	Pos	Effect allele	Other allele	EAF	OR (95%CI)	P-value	Nearest gene
rs6005414	22	27783185	A	G	0.53	0.80 (0.74-0.87)	5.83×10^{-8}	LINC02554
rs17056435	5	158453783	A	G	0.05	2.19 (1.64-2.92)	1.14×10^{-7}	EBF1
rs2596618	3	24221506	A	G	0.11	1.38 (1.22-1.57)	3.16×10^{-7}	THRB
rs12859952	13	26381179	A	G	0.77	0.77 (0.69-0.85)	3.61×10^{-7}	ATP8A2
rs9652372	14	75377345	T	C	0.09	0.70 (0.61-0.81)	7.43×10^{-7}	RPS6KL1
rs139812140	8	118821440	D	R	0.16	0.75 (0.67-0.85)	1.34×10^{-6}	EXT1
rs7702605	5	2653180	C	G	0.88	0.75 (0.67-0.85)	1.66×10^{-6}	IRX2
rs12130807	1	82036836	A	C	0.09	0.71 (0.61-0.82)	3.43×10^{-6}	ADGRL2
rs202172201	4	40109940	I	R	0.09	1.41 (1.22-1.62)	3.79×10^{-6}	N4BP2
rs9581136	13	19639265	T	C	0.06	0.65 (0.54-0.78)	4.20×10^{-6}	GTF2IP3

Supplementary Table S4. Most strongly associated marker in each region in the GWAS meta-analysis of all Asians aged >25 years. EAF = effect allele frequency, OR = odds ratio.

SNP	Chr	Pos	Effect allele	Other allele	EAF	OR (95%CI)	P-value	Nearest gene
rs16875983	8	108285287	T	G	0.25	1.22 (1.13-1.32)	2.14×10^{-7}	ANGPT1
rs67687099	3	152747454	D	R	0.20	1.37 (1.22-1.55)	3.25×10^{-7}	HMGN2P13
rs35026266	15	48769044	T	C	0.31	0.84 (0.79-0.91)	2.52×10^{-6}	FBN1
rs10809667	9	1209532	A	T	0.23	1.20 (1.11-1.30)	3.37×10^{-6}	RPS27AP14
rs56738713	5	29586419	A	G	0.08	1.37 (1.20-1.57)	5.17×10^{-6}	UBL5P1
rs3924436	1	24908959	A	G	0.41	0.86 (0.81-0.92)	5.42×10^{-6}	NCMAP
rs1687660	16	86416646	C	G	0.52	0.86 (0.81-0.92)	6.11×10^{-6}	LINC00917
rs58435984	4	55127990	T	C	0.78	0.84 (0.77-0.90)	8.58×10^{-6}	PDGFRA
rs141310268	18	45633672	D	R	0.14	0.80 (0.72-0.88)	9.87×10^{-6}	ZBTB7C
rs817755	7	98202672	A	C	0.91	1.42 (1.21-1.65)	1.00×10^{-5}	NPTX2

Supplementary Table S5. Most strongly associated marker in each region in the GWAS meta-analysis of all Asians aged <25 years. EAF = effect allele frequency, OR = odds ratio.

SNP	Chr	Pos	Effect allele	Other allele	EAF	OR (95%CI)	P-value	Nearest gene
rs72971923	18	69822333	A	G	0.15	0.32 (0.21-0.50)	2.68×10^{-7}	LOC101927537
rs2069368	5	162870726	C	G	0.94	7.30 (3.28-16.26)	1.14×10^{-6}	CCNG1
rs7905017	10	92868457	A	G	0.62	1.98 (1.50-2.62)	1.63×10^{-6}	LINC00502
rs11079429	17	59472403	A	G	0.29	0.48 (0.35-0.65)	2.23×10^{-6}	BCAS3
rs9957	5	179290154	C	G	0.74	1.92 (1.47-2.53)	2.48×10^{-6}	TBC1D9B
rs17072824	18	62003510	A	G	0.10	0.35 (0.23-0.54)	2.80×10^{-6}	LINC01924
rs779593	3	118029874	T	C	0.69	1.81 (1.41-2.32)	2.95×10^{-6}	LOC101926968
rs143004236	7	135420794	A	G	0.05	0.13 (0.06-0.31)	3.00×10^{-6}	FAM180A
rs11085245	19	18859757	A	G	0.83	0.45 (0.32-0.63)	3.31×10^{-6}	CRTC1
rs12144639	1	213817311	A	G	0.22	0.53 (0.40-0.70)	4.75×10^{-6}	PROX1-AS1

Supplementary Table S6. Top 10 genes from VEGAS2 gene-based association test with ±50kb buffers for all Europeans. Start and stop positions listed include ±50kb buffers. nSNPs: number of variants included in gene region. Test Statistic: gene-based χ^2 test statistic to *nSNPs* degrees of freedom. P-value: obtained from Test Statistic and adjusting for LD between variants. FDR: false discovery rate (likelihood of gene association being a false positive result). Top SNP: variant within gene locus with strongest association signal from previous SNP-based association test. Genes shown in bold were also identified with MAGMA (Table S7).

Gene	Chr	Start	Stop	nSNPs	Test Statistic	P-value	FDR	Top SNP
ACP2	11	47210852	47320457	175	1680.63	1.00×10^{-5}	0.097	rs3758670
MADD	11	47240926	47401582	271	2472.89	1.10×10^{-5}	0.097	rs2697920
NR1H3	11	47219850	47340584	191	1929.38	1.20×10^{-5}	0.097	rs3758670
DDB2	11	47186492	47310769	193	1638.98	2.00×10^{-5}	0.097	rs3758670
CLDN7	17	7113221	7216512	123	980.06	2.00×10^{-5}	0.097	rs222836
CTDNEP1	17	7096905	7205259	114	1013.67	2.90×10^{-5}	0.111	rs222836
ELP5	17	7105371	7213259	123	1012.32	3.20×10^{-5}	0.111	rs222836
GABARAP	17	7093737	7195753	96	952.50	4.10×10^{-5}	0.118	rs222836
TYR	11	88861039	89078927	402	3017.77	4.40×10^{-5}	0.118	rs12808354
PHF23	17	7088346	7192825	104	903.47	7.90×10^{-5}	0.174	rs222836

Supplementary Table S7. Top 10 genes from MAGMA gene-based association test with ±50kb buffers for all Europeans. Start and stop positions listed include ±50kb buffers. nSNPs: number of variants included in gene region. Z Statistic: gene-based test statistic. P-value: obtained from *Z Statistic* under the assumption of a normally distributed model. FDR: false discovery rate (likelihood of gene association being a false positive result). Genes shown in bold were also identified with VEGAS2 (Table S6).

Gene	Chr	Start	Stop	nSNPs	Z Statistic	P-value	FDR	Bonferroni Adjusted P
ELP5	17	7105372	7213259	123	4.71	1.23×10^{-6}	0.009	0.023
CLDN7	17	7113222	7216863	124	4.69	1.39×10^{-6}	0.009	0.026
CTDNEP1	17	7096906	7205259	114	4.67	1.50×10^{-6}	0.009	0.028
TNFAIP8L3	15	51298798	51447473	212	4.59	2.26×10^{-6}	0.009	0.042
ACP2	11	47210853	47320457	175	4.56	2.52×10^{-6}	0.009	0.046
GABARAP	17	7093738	7195753	96	4.45	4.23×10^{-6}	0.013	0.078
PHF23	17	7088347	7192825	104	4.36	6.59×10^{-6}	0.017	0.121
DVL2	17	7078661	7187867	112	4.27	9.80×10^{-6}	0.021	0.181
SLC2A4	17	7134986	7241367	155	4.22	1.21×10^{-5}	0.021	0.223
ACADVL	17	7070444	7178586	104	4.22	1.22×10^{-5}	0.021	0.224

Supplementary Figure S1. Manhattan plots for the separate ancestry/age strata fixed effects meta-analyses. Y-axes show negative $\log_{10}$ p-values and X-axes show genomic position. Red line corresponds to $P = 5 \times 10^{-8}$, blue line corresponds to $P = 1 \times 10^{-5}$. Panel A, European ancestry, aged >25 years; B, European ancestry, aged <25 years; C, Asian ancestry, aged >25 years; D, Asian ancestry, aged <25 years.
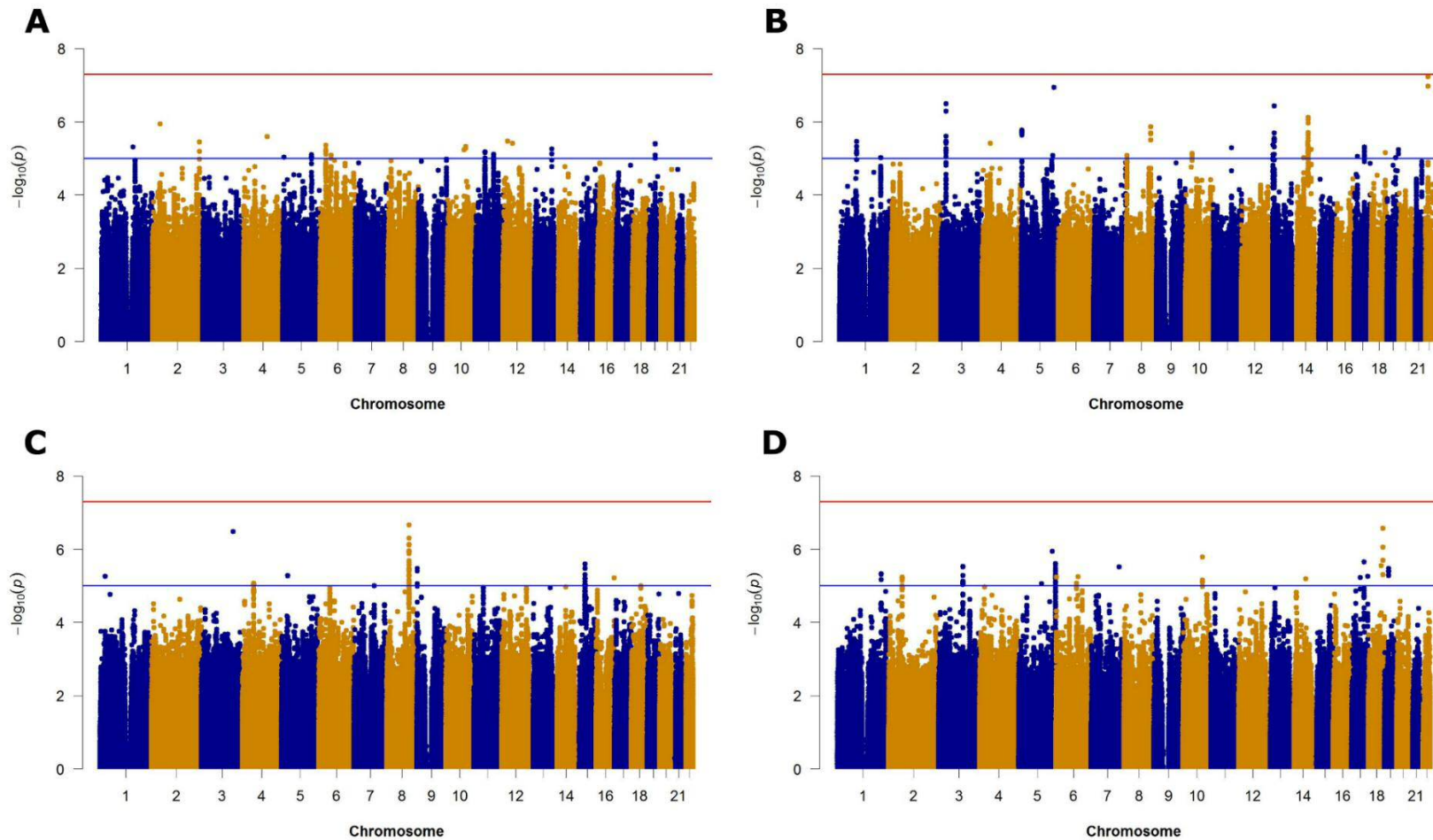
Supplementary Figure S2. Quantile-quantile plots for the separate ancestry/age strata fixed effects meta-analyses. Y-axes show observed negative $\log_{10}$ p-values and X-axes show expected negative $\log_{10}$ p-values according to the null hypothesis of no genetic association. Red line is the line of unity (y = x). Panel **A**, European ancestry, aged >25 years; **B**, European ancestry, aged <25 years; **C**, Asian ancestry, aged >25 years; **D**, Asian ancestry, aged <25 years.