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## Supplementary Information

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<b>Index</b>		<b>Page</b>
Table S1.	Instrument for measuring corneal curvature.	S2
Table S2.	Most strongly associated marker in each region in the GWAS meta-analysis of all Europeans aged >25 years.	S3
Table S3.	Most strongly associated marker in each region in the GWAS meta-analysis of all Europeans aged <25 years.	S3
Table S4.	Most strongly associated marker in each region in the GWAS meta-analysis of all Asians aged >25 years.	S4
Table S5.	Most strongly associated marker in each region in the GWAS meta-analysis of all Asians aged <25 years.	S4
Table S6.	Top 10 genes from VEGAS2 gene-based association test with $\pm 50$ kb buffers for all Europeans.	S5
Table S7.	Top 10 genes from MAGMA gene-based association test with $\pm 50$ kb buffers for all Europeans.	S6
Figure S1.	Manhattan plots for the separate ancestry/age strata fixed effects meta-analyses.	S7
Figure S2.	Quantile-quantile plots for the separate ancestry/age strata fixed effects meta-analyses.	S8

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**Supplementary Table S1. Instrument for measuring corneal curvature.**

<i>Study</i>	<i>Instrument</i>
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.

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

**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.

<i>SNP</i>	<i>Chr</i>	<i>Pos</i>	<i>Effect allele</i>	<i>Other allele</i>	<i>EAf</i>	<i>OR (95%CI)</i>	<i>P-value</i>	<i>Nearest gene</i>
rs6005414	22	27783185	A	G	0.53	0.80 (0.74-0.87)	5.83 x 10 <sup>-8</sup>	<i>LINC02554</i>
rs17056435	5	158453783	A	G	0.05	2.19 (1.64-2.92)	1.14 x 10 <sup>-7</sup>	<i>EBF1</i>
rs2596618	3	24221506	A	G	0.11	1.38 (1.22-1.57)	3.16 x 10 <sup>-7</sup>	<i>THR3</i>
rs12859952	13	26381179	A	G	0.77	0.77 (0.69-0.85)	3.61 x 10 <sup>-7</sup>	<i>ATP8A2</i>
rs9652372	14	75377345	T	C	0.09	0.70 (0.61-0.81)	7.43 x 10 <sup>-7</sup>	<i>RPS6KL1</i>
rs139812140	8	118821440	D	R	0.16	0.75 (0.67-0.85)	1.34 x 10 <sup>-6</sup>	<i>EXT1</i>
rs7702605	5	2653180	C	G	0.88	0.75 (0.67-0.85)	1.66 x 10 <sup>-6</sup>	<i>IRX2</i>
rs12130807	1	82036836	A	C	0.09	0.71 (0.61-0.82)	3.43 x 10 <sup>-6</sup>	<i>ADGRL2</i>
rs202172201	4	40109940	I	R	0.09	1.41 (1.22-1.62)	3.79 x 10 <sup>-6</sup>	<i>N4BP2</i>
rs9581136	13	19639265	T	C	0.06	0.65 (0.54-0.78)	4.20 x 10 <sup>-6</sup>	<i>GTF2IP3</i>

**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.

<b>SNP</b>	<b>Chr</b>	<b>Pos</b>	<b>Effect allele</b>	<b>Other allele</b>	<b>EAF</b>	<b>OR (95%CI)</b>	<b>P-value</b>	<b>Nearest gene</b>
rs16875983	8	108285287	T	G	0.25	1.22 (1.13-1.32)	2.14 x 10 <sup>-7</sup>	ANGPT1
rs67687099	3	152747454	D	R	0.20	1.37 (1.22-1.55)	3.25 x 10 <sup>-7</sup>	HMG2P13
rs35026266	15	48769044	T	C	0.31	0.84 (0.79-0.91)	2.52 x 10 <sup>-6</sup>	FBN1
rs10809667	9	1209532	A	T	0.23	1.20 (1.11-1.30)	3.37 x 10 <sup>-6</sup>	RPS27AP14
rs56738713	5	29586419	A	G	0.08	1.37 (1.20-1.57)	5.17 x 10 <sup>-6</sup>	UBL5P1
rs3924436	1	24908959	A	G	0.41	0.86 (0.81-0.92)	5.42 x 10 <sup>-6</sup>	NCMAP
rs1687660	16	86416646	C	G	0.52	0.86 (0.81-0.92)	6.11 x 10 <sup>-6</sup>	LINC00917
rs58435984	4	55127990	T	C	0.78	0.84 (0.77-0.90)	8.58 x 10 <sup>-6</sup>	PDGFRA
rs141310268	18	45633672	D	R	0.14	0.80 (0.72-0.88)	9.87 x 10 <sup>-6</sup>	ZBTB7C
rs817755	7	98202672	A	C	0.91	1.42 (1.21-1.65)	1.00 x 10 <sup>-5</sup>	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.

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

**Supplementary Table S6. Top 10 genes from VEGAS2 gene-based association test with  $\pm 50\text{kb}$  buffers for all Europeans.** Start and stop positions listed include  $\pm 50\text{kb}$  buffers.

nSNPs: number of variants included in gene region. Test Statistic: gene-based  $\chi^2$  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).

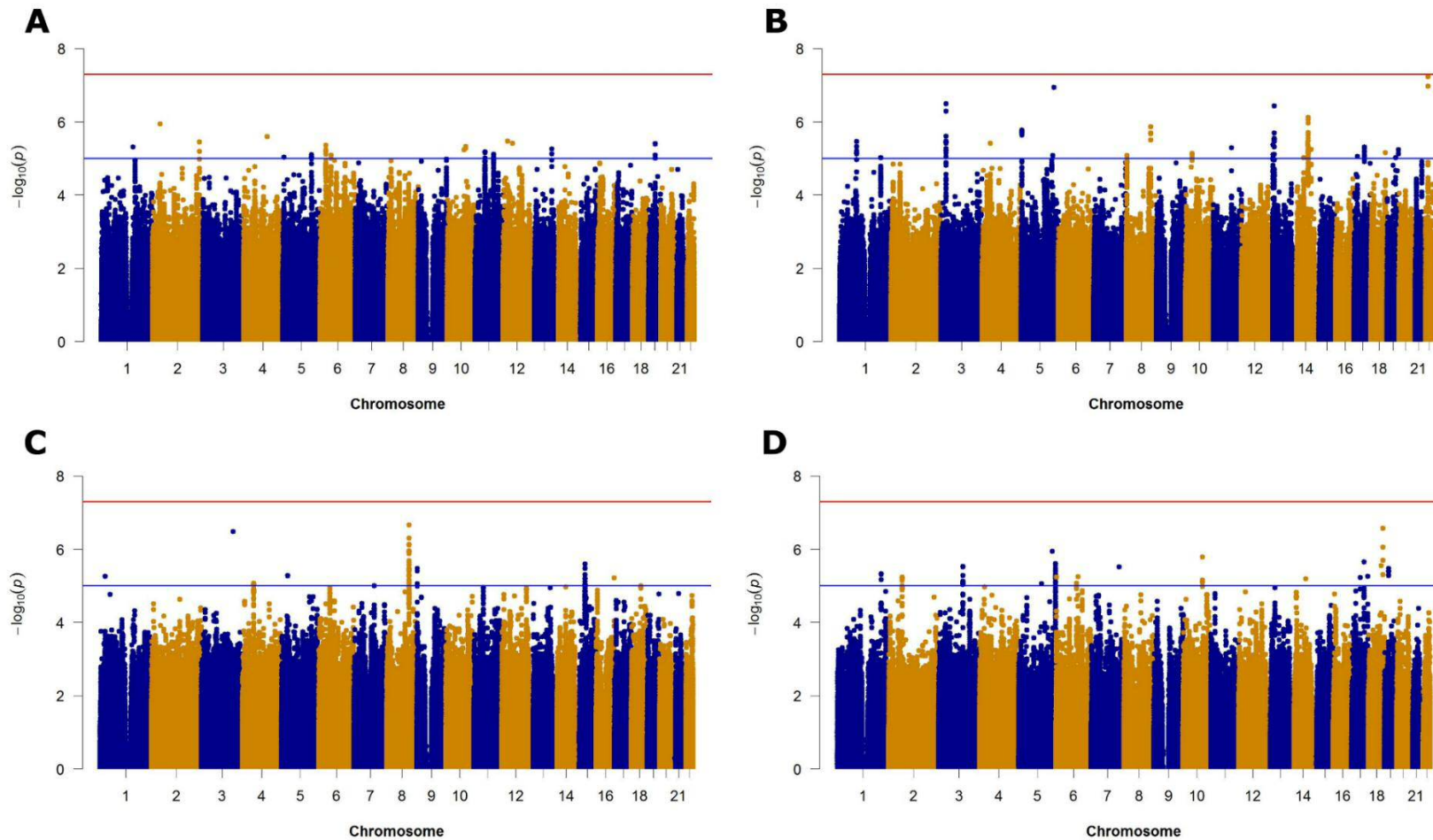
Gene	Chr	Start	Stop	nSNPs	Test Statistic	P-value	FDR	Top SNP
<b>ACP2</b>	11	47210852	47320457	175	1680.63	$1.00 \times 10^{-5}$	0.097	rs3758670
<i>MADD</i>	11	47240926	47401582	271	2472.89	$1.10 \times 10^{-5}$	0.097	rs2697920
<i>NR1H3</i>	11	47219850	47340584	191	1929.38	$1.20 \times 10^{-5}$	0.097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

**Supplementary Table S7. Top 10 genes from MAGMA gene-based association test with  $\pm 50\text{kb}$  buffers for all Europeans.** Start and stop positions listed include  $\pm 50\text{kb}$  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
<b>ELP5</b>	17	7105372	7213259	123	4.71	$1.23 \times 10^{-6}$	0.009	0.023
<b>CLDN7</b>	17	7113222	7216863	124	4.69	$1.39 \times 10^{-6}$	0.009	0.026
<b>CTDNEP1</b>	17	7096906	7205259	114	4.67	$1.50 \times 10^{-6}$	0.009	0.028
<i>TNFAIP8L3</i>	15	51298798	51447473	212	4.59	$2.26 \times 10^{-6}$	0.009	0.042
<b>ACP2</b>	11	47210853	47320457	175	4.56	$2.52 \times 10^{-6}$	0.009	0.046
<b>GABARAP</b>	17	7093738	7195753	96	4.45	$4.23 \times 10^{-6}$	0.013	0.078
<b>PHF23</b>	17	7088347	7192825	104	4.36	$6.59 \times 10^{-6}$	0.017	0.121
<i>DVL2</i>	17	7078661	7187867	112	4.27	$9.80 \times 10^{-6}$	0.021	0.181
<i>SLC2A4</i>	17	7134986	7241367	155	4.22	$1.21 \times 10^{-5}$	0.021	0.223
<i>ACADVL</i>	17	7070444	7178586	104	4.22	$1.22 \times 10^{-5}$	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.

