Genome-wide analysis of multiethnic cohorts identifies new loci influencing intraocular pressure and susceptibility to glaucoma

Supplementary Information and Note

Contents

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Supplementary Information

Supplementary Table 1. Summary of the demographic and phenotypic characteristics of the cohorts

Abbreviation used in article	Cohort name	N	Mean age (SD)	% males	Mean mmHg IOP (SD)	IOP measurement method	Genotyping Platform(s)	Imputation Method
ALIENOR	Antioxydants, Lipides Essentiels, Nutrition et maladies OculaiRes	939	80.20 (4.44)	38.02	14.21 (2.72)	Non contact tonometer (Kowa KT800)	Illumina Human 610-Quad BeadChip	
BATS	Brisbane Adolescent Twins Study	1152	20.10 (0.08)	46	15.78(2.88)	TONO-PEN XL (Reichert, Inc. New York, USA)	Illumina 610/660 Quad Array	Mach
BES	Beijing Eye Study	805	60.42(10.04)	40.4	15.73 (3.03)	Non-contact pneumotonometer	Illumina Human Quad 610 chip	IMPUTE
BMES	Blue Mountains Eye Study	1667	66.19(9.77)	57	16.04(2.63)		Illumina Human 660W Quad	IMPUTE
ERF	Erasmus Rucphen Family Study	2591	49.05(14.31)	45	15.09(3.00)	Goldmann applanation tonometry (Haag-Streit, Bern, Switzerland)	Illumina 6K, Illumina 318K, Illumina 370K, Affymetrix 250K	Mach
Framingham	Framingham Eye Study	2455	57.38 (12.39)	44.8	13.6 (3.32)	Goldmann applanation tonometry	Affymetrix 250k_Nsp 250k_Sty HuGeneFocused50K	Mach
GHS I	Gutenberg Health Study I	2727	55.9(10.9)	52	14.19(2.81)	Non-contact tonometer	Affymetrix Genome-Wide Human SNP 6.0 Array	IMPUTE
GHS II	Gutenberg Health Study II	1130	55.10(10.90)	49.6	13.90(2.7)	Non-contact tonometer	Affymetrix Genome-Wide Human SNP 6.0 Array	IMPUTE
ORCADES	Orkney Complex Disease Study	474	56.5(14.5)	38	15.38(2.80)	Tono-Pen	Illumina HumanHap 300v2 and 370CNV-Quad arrays	Mach
RAINE	Western Australian Pregnancy (Raine) Cohort 20 year follow up Eye Study	1025	20.0 (0.43)	51	15.42(3.21)	Icare TAO1i Tonometer, Icare Finland Oy, Helsinki, Finland	Illumina 660 Quad Array	Mach

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Abbreviation used in article	Cohort name	N	Mean age (SD)	% males	Mean mmHg IOP (SD)	IOP measurement method	Genotyping Platform(s)	Imputation Method
RS-I	Rotterdam Study-I	5782	68.76(8.92)	41	14.72(3.34)	Goldmann applanation tonometry (Haag-Streit, Bern, Switzerland)	Illumina Infinium II HumanHap500chip v3.0 array	Mach
RS-II	Rotterdam Study-II	2116	64.81(7.91)	46	14.2(3.1)	Goldmann applanation tonometry (Haag-Streit, Bern, Switzerland)	HumanHap550 Duo Arrays + Human610-Quad Arrays Illumina	Mach
RS-III	Rotterdam Study-III	2038	56.15(5.81)	44	13.61(2.96)	Goldmann applanation tonometry (Haag-Streit, Bern, Switzerland)	Human 610 Quad Arrays Illumina	Mach
SCES	Singapore Chinese Eye Study	1884	58.51 (9.53)	51	14.60 (3.21)	Goldmann Tonometry	Illumina Human Quad 610 chip	IMPUTE
SIMES	Singapore Malay Eye Study	2537	59.09 (11.04)	49	15.42 (3.76)	Goldmann Tonometry	Illumina Human Quad 610 chip	IMPUTE
SINDI	Singapore Indian Eye Study	2535	58.04 (10.01)	51	15.84 (2.87)	Goldmann Tonometry	Illumina Human Quad 610 chip	IMPUTE
TEST	Twins Eye Study in Tasmania	663	25.64(18.80)	40	15.84(3.12)	TONO-PEN XL (Reichert, Inc. New York, USA)	Illumina 610/660 Quad Array	Mach
TwinsUK	Twins UK Cohort Study	2776	56.46 (11.83)	2	15.55 (3.18)	Ocular Response Analyser	300K Duo, HumanHap610-Quad array	IMPUTE

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Supplementary Table 2. Genomic Inflation factors (λ) observed in individual cohorts' IOP analyses

Cohort	Lambda
ALIENOR	1.008
BATS	0.999
BES	0.992
BMES	0.999
ERF	1.043
Framingham	1.011
GHS I	1.016
GHS II	1.004
ORCADES	0.999
RAINE	0.996
RS-I	1.024
RS-II	1.008
RS-III	1.011
SCES	0.998
SIMES	1.002
SINDI	0.996
TEST	1.009
TwinsUK	1.033

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Supplementary Table 3. Significant association ($p<5x10^{-08}$)in the IOP meta-analysis.

chr	position	SNP	A1	A2	beta	se	p-value	heterogeneity p-value	I2
1	165670957	rs1547725	T	C	0.226	0.041	4.41E-08	0.652	0.000
1	165684706	rs6426936	T	C	0.230	0.041	1.81E-08	0.711	0.000
1	165687204	rs4656461	G	A	0.228	0.039	6.51E-09	0.460	0.000
1	165694896	rs7524755	T	C	0.232	0.039	3.71E-09	0.541	0.000
1	165695854	rs6660601	T	C	-0.234	0.039	2.78E-09	0.575	0.000
1	165718978	rs7555523	C	A	0.235	0.039	2.19E-09	0.553	0.000
1	165732660	rs4657476	T	C	-0.235	0.039	2.48E-09	0.570	0.000
1	165736879	rs7518099	T	C	-0.234	0.039	2.72E-09	0.631	0.000
1	165737703	rs2790053	G	C	-0.233	0.039	3.24E-09	0.551	0.000
1	165738310	rs2251768	T	A	-0.233	0.041	9.04E-09	0.412	0.036
1	165738462	rs2790052	G	C	0.239	0.040	2.19E-09	0.529	0.000
1	165739597	rs2814471	T	C	-0.233	0.039	3.23E-09	0.554	0.000
3	171992386	rs6445055	G	A	0.177	0.030	4.19E-09	0.168	0.242
3	171995604	rs4894535	T	C	-0.175	0.031	9.18E-09	0.139	0.271
7	116144903	rs10253097	T	C	-0.176	0.033	9.29E-08	0.994	0.000
7	116146073	rs8940	G	C	0.177	0.033	6.12E-08	0.993	0.000
7	116150094	rs10258482	C	A	-0.196	0.029	1.87E-11	0.810	0.000
7	116150951	rs10262524	C	A	-0.186	0.029	9.69E-11	0.667	0.000
7	116151337	rs10281637	T	C	-0.184	0.029	1.3E-10	0.716	0.000
7	116153024	rs2024211	C	A	0.184	0.029	1.09E-10	0.731	0.000
7	116154830	rs6969706	T	G	0.179	0.029	3.92E-10	0.802	0.000
7	116161946	rs10227696	G	A	-0.181	0.033	3.38E-08	0.998	0.000
7	116162728	rs4236601	G	A	-0.182	0.028	1.58E-10	0.735	0.000
7	116175710	rs10256914	T	C	-0.165	0.029	1.15E-08	0.779	0.000
7	116180849	rs4730751	C	A	-0.160	0.029	3.13E-08	0.807	0.000
9	107695352	rs2472496	G	A	0.153	0.024	2.31E-10	0.0001	0.642
9	107695847	rs2472493	G	A	0.159	0.024	2.8E-11	4.84E-05	0.657
9	136131187	rs8176749	T	C	0.260	0.039	3.94E-11	0.520	0.000
9	136131314	rs8176747	G	C	0.252	0.039	1.15E-10	0.696	0.000
9	136131321	rs8176746	T	G	0.260	0.039	3.68E-11	0.516	0.000
9	136131414	rs8176743	T	C	0.261	0.039	3.08E-11	0.527	0.000
9	136131591	rs7853989	G	C	-0.221	0.037	2.04E-09	0.626	0.000
9	136132524	rs8176730	T	C	-0.215	0.037	5.96E-09	0.608	0.000
9	136132616	rs8176725	G	A	-0.209	0.036	5.86E-09	0.712	0.000
9	136132753	rs8176722	C	A	-0.213	0.037	7.11E-09	0.592	0.000
9	136137656	rs8176693	T	C	0.257	0.039	6.39E-11	0.533	0.000
11	47404313	rs11828339	G	A	-0.185	0.033	1.68E-08	0.464	0.000
11	47410165	rs11821917	T	A	-0.183	0.033	2.46E-08	0.458	0.000
11	47411735	rs11824864	G	A	0.181	0.033	2.79E-08	0.481	0.000

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chr	position	SNP	A1	A2	beta	se	p-value	heterogeneity p-value	I2
11	47431528	rs753812	G	A	-0.189	0.033	8.21E-09	0.398	0.048
11	47441663	rs2242511	T	C	0.190	0.035	8.14E-08	0.313	0.122
11	47447201	rs17790804	T	C	-0.188	0.035	9.69E-08	0.297	0.137
11	47447954	rs7948705	G	C	0.147	0.026	2.66E-08	0.727	0.000
11	47449543	rs7105122	T	C	0.146	0.026	2.68E-08	0.742	0.000
11	47450317	rs7105907	T	A	0.147	0.026	2.46E-08	0.729	0.000
11	47454700	rs10742805	G	A	-0.147	0.026	2.36E-08	0.721	0.000
11	47456201	rs4282946	G	A	0.147	0.026	2.32E-08	0.720	0.000
11	47456225	rs10742806	T	A	0.147	0.026	2.43E-08	0.728	0.000
11	47460305	rs7126210	G	A	-0.147	0.026	2.62E-08	0.746	0.000
11	47464518	rs3847503	G	A	-0.190	0.033	6.16E-09	0.404	0.043
11	47465954	rs4752837	G	A	0.146	0.026	2.77E-08	0.719	0.000
11	47468544	rs12419342	T	C	-0.153	0.026	4.77E-09	0.745	0.000
11	47468568	rs3824867	G	A	-0.147	0.026	2.6E-08	0.663	0.000
11	47468819	rs3740684	T	C	-0.145	0.026	3.51E-08	0.701	0.000
11	47469438	rs7111873	G	A	-0.147	0.026	2.36E-08	0.723	0.000
11	47477848	rs17198158	G	A	0.189	0.033	6.73E-09	0.473	0.000
11	47487739	rs1044269	G	A	0.191	0.033	5.23E-09	0.474	0.000
11	47495201	rs4752839	G	A	-0.193	0.033	3.46E-09	0.509	0.000
11	47531883	rs4752843	T	G	-0.192	0.033	3.92E-09	0.559	0.000
11	47539207	rs11819955	G	A	0.199	0.033	2.44E-09	0.564	0.000
11	47540006	rs9666924	T	C	-0.189	0.033	6.99E-09	0.456	0.000
11	47558219	rs4752783	G	A	-0.206	0.037	3.34E-08	0.341	0.098
11	47605426	rs4147730	G	A	-0.194	0.033	2.83E-09	0.466	0.000
11	47606983	rs10742816	T	C	-0.193	0.033	3.5E-09	0.470	0.000
11	47628535	rs4752786	T	C	0.193	0.033	3.8E-09	0.478	0.000
11	47632706	rs1474056	G	A	-0.192	0.033	4.6E-09	0.475	0.000
11	47633505	rs7931089	G	A	-0.193	0.033	3.74E-09	0.466	0.000
11	47702394	rs7120737	G	A	0.194	0.033	3.51E-09	0.376	0.067
11	47727589	rs17791016	C	A	0.199	0.033	2.01E-09	0.282	0.144
11	47736022	rs4752791	T	C	-0.201	0.033	1.32E-09	0.239	0.180
11	47829344	rs6485783	T	C	-0.207	0.033	4.74E-10	0.275	0.149
11	47857167	rs2305982	G	A	0.207	0.033	4.46E-10	0.287	0.139
11	47858754	rs2305983	T	C	0.183	0.030	7.8E-10	0.661	0.000
11	47868473	rs7942031	T	C	-0.182	0.030	9.37E-10	0.693	0.000
11	47873882	rs6485788	G	A	0.180	0.030	1.59E-09	0.652	0.000
11	47886164	rs4752877	C	A	-0.212	0.034	5.59E-10	0.202	0.212
11	47893119	rs7924699	T	A	0.184	0.030	7.56E-10	0.712	0.000
11	47901268	rs1872167	T	C	0.210	0.033	2.65E-10	0.251	0.170
11	47940924	rs747782	T	C	-0.204	0.030	1.04E-11	0.924	0.000
11	47969151	rs1681630	T	C	0.144	0.026	1.69E-08	0.601	0.000

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chr	position	SNP	A1	A2	beta	se	p-value	heterogeneity p-value	I2
11	47999217	rs1017875	T	C	0.196	0.031	1.68E-10	0.797	0.000
11	48004368	rs7946766	T	C	0.230	0.035	2.71E-11	0.351	0.087
11	48013483	rs7123436	G	A	-0.197	0.031	1.22E-10	0.842	0.000
11	48028342	rs17198607	T	G	0.238	0.036	3.06E-11	0.508	0.000
11	48050994	rs7130876	G	A	0.180	0.031	4.13E-09	0.631	0.000
11	48145165	rs2270993	G	A	-0.203	0.034	2.99E-09	0.185	0.227
11	48150575	rs7129364	G	A	-0.203	0.034	2.9E-09	0.180	0.232
11	48168663	rs3741410	T	G	-0.186	0.034	3.28E-08	0.198	0.216
11	48183564	rs17198985	T	C	-0.209	0.034	8.02E-10	0.086	0.331
11	48199226	rs7952205	G	A	0.211	0.034	6.59E-10	0.084	0.333
11	48207258	rs11039571	G	A	-0.211	0.034	6.6E-10	0.106	0.306
11	48234679	rs12289516	G	A	-0.208	0.034	1.11E-09	0.114	0.298
11	48238879	rs10838833	T	C	0.213	0.034	3.8E-10	0.066	0.359
11	48246456	rs10838835	G	A	0.211	0.034	4.77E-10	0.148	0.262
11	48266735	rs7120775	G	C	0.213	0.034	4.1E-10	0.083	0.335
11	48279795	rs1316604	G	A	-0.207	0.034	1E-09	0.087	0.330
11	48285905	rs16905753	T	C	0.208	0.034	8.07E-10	0.089	0.327
11	48346201	rs7949865	T	G	0.211	0.035	1.08E-09	0.090	0.340
11	48365756	rs7945174	T	C	-0.207	0.035	2.25E-09	0.099	0.329
11	48387274	rs10838881	T	C	-0.208	0.035	1.89E-09	0.104	0.323
11	48388393	rs2200183	G	A	-0.205	0.035	6.07E-09	0.082	0.350
11	48455030	rs6485831	T	A	0.207	0.035	2.55E-09	0.095	0.333
11	48458360	rs7102865	C	A	0.208	0.035	2.96E-09	0.084	0.348
11	48485876	rs9667626	T	C	-0.199	0.035	1.11E-08	0.058	0.386
11	48515429	rs10769370	G	A	0.190	0.034	3.73E-08	0.062	0.364
11	48520269	rs7942042	G	A	0.194	0.034	1.71E-08	0.060	0.367
11	48520423	rs7942284	T	C	0.195	0.034	1.49E-08	0.057	0.372
11	48541516	rs6485848	T	G	0.192	0.034	1.83E-08	0.050	0.384
11	48556297	rs6485856	G	C	-0.194	0.034	1.51E-08	0.056	0.374
11	48556318	rs7924372	T	A	-0.213	0.038	2.49E-08	0.022	0.464
11	48588533	rs7104642	T	C	0.195	0.034	1.27E-08	0.057	0.372
11	48589191	rs7928243	T	A	0.196	0.034	1.16E-08	0.060	0.367
11	48590677	rs7950737	T	G	-0.199	0.034	7.18E-09	0.047	0.389
11	48592509	rs10769383	G	C	-0.196	0.034	1.11E-08	0.038	0.407
11	48630322	rs7478904	T	C	0.228	0.039	4.6E-09	0.028	0.445
11	48650490	rs12281162	T	C	-0.197	0.035	1.34E-08	0.050	0.383
11	48652197	rs6485908	G	A	0.196	0.035	1.61E-08	0.049	0.386
11	48703441	rs10839007	C	A	0.201	0.035	1.19E-08	0.052	0.396
11	48931738	rs7929225	G	C	-0.200	0.035	1.55E-08	0.077	0.358
11	48984317	rs7125913	G	A	-0.199	0.035	1.91E-08	0.076	0.359
11	49004024	rs1847640	G	A	-0.198	0.033	3.28E-09	0.327	0.110

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chr	position	SNP	A1	A2	beta	se	p-value	heterogeneity p-value	I2
11	49011008	rs2202454	T	C	-0.213	0.036	3.13E-09	0.114	0.311
11	49068144	rs10839217	C	A	-0.204	0.036	1.47E-08	0.204	0.219
11	49080564	rs7932738	C	A	0.204	0.036	1.54E-08	0.204	0.220
11	49121751	rs913894	G	C	-0.193	0.035	5.46E-08	0.159	0.252
11	49131994	rs11040255	T	C	0.196	0.036	3.57E-08	0.153	0.257
11	49156038	rs11040261	T	C	-0.191	0.035	5.22E-08	0.223	0.193
11	49156751	rs11040263	G	A	-0.191	0.035	5.12E-08	0.216	0.200
11	49159222	rs6485963	C	A	0.191	0.035	5.13E-08	0.221	0.195
11	49165239	rs10839230	G	C	0.189	0.035	6.82E-08	0.221	0.195
11	49373689	rs11040348	T	G	-0.198	0.035	1.93E-08	0.260	0.162
11	49381197	rs7929980	G	A	-0.196	0.036	4.13E-08	0.308	0.127
11	49387336	rs10839270	C	A	0.186	0.035	8.51E-08	0.382	0.061
11	49493735	rs11040387	G	A	-0.210	0.036	4.31E-09	0.331	0.107
11	49505174	rs11040392	T	C	0.183	0.034	9.19E-08	0.389	0.055
11	49506589	rs10839288	G	C	0.184	0.034	7.25E-08	0.385	0.059
11	49517159	rs3862347	T	C	0.193	0.035	2.72E-08	0.447	0.004
11	49546907	rs12098986	T	C	0.196	0.035	1.79E-08	0.490	0.000
11	49555760	rs1827012	T	G	-0.194	0.035	2.53E-08	0.468	0.000
11	49615515	rs7925397	C	A	0.191	0.035	3.45E-08	0.391	0.055
11	49675011	rs12223469	T	C	0.188	0.035	5.91E-08	0.405	0.042
11	50367358	rs7103246	T	C	-0.207	0.038	5.81E-08	0.042	0.414
17	10031089	rs12150284	T	C	-0.175	0.026	1.68E-11	0.0004	0.621
17	10031182	rs9913911	G	A	-0.179	0.026	1.03E-11	0.0004	0.616
17	10033678	rs11656696	C	A	0.154	0.025	1.15E-09	8.89E-05	0.654

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Supplementary Table 4. Association between the strength of SNPs' effect on IOP levels and their strength on the risk of POAG

Dependent outcome variable	Independent variable	Beta	SE	95% CI	P value
$Beta_{POAG}$	$Beta_{IOP}$	0.788	0.264	0.109 - 1.148	0.031

$Beta_{POAG}$: the effect size of the association of a given SNP with POAG, log(OR), from the meta-analysis of the four case-control panels

$Beta_{IOP}$: the effect size of the association of a given SNP with IOP from the meta-analysis of the 18 discovery cohorts

The following independent IOP-associated SNPs were used in the linear regression analysis: rs7555523 (*TMCO1*), rs6445055 (*FNDC3B*), rs10258482 (*CAV1*), rs2472493 (*ABCA1*), rs8176743 (*ABO*), rs747782 (*NUP160-PTPRJ*), rs9913911 (*GAS7*).

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Supplementary Table 5:

Table 5A. Results of the eQTL analyses for the GWAS-significant level SNPs.

PROBE	Gene	SNP	eQTL p-value(fat)	eQTL p-value (LCL)	eQTL pvalue (skin)
ILMN_2263333	RXRG	rs2814471	0.1957	0.3273	0.0235
ILMN_2263333	RXRG	rs2251768	0.1942	0.3296	0.0257
ILMN_2263333	RXRG	rs2790053	0.1934	0.3302	0.0268
ILMN_2263333	RXRG	rs7524755	0.2066	0.301	0.0279
ILMN_2263333	RXRG	rs6660601	0.2081	0.295	0.0287
ILMN_2263333	RXRG	rs4657476	0.1929	0.3311	0.0276
ILMN_2263333	RXRG	rs4656461	0.1712	0.2939	0.0355
ILMN_2263333	RXRG	rs7518099	0.1934	0.3306	0.028
ILMN_2263333	RXRG	rs7555523	0.1974	0.3342	0.0273
ILMN_1761804	ALDH9A1	rs6660601	0.4092	1.89E-04	0.0277
ILMN_1761804	ALDH9A1	rs7555523	0.3859	1.24E-04	0.0486
ILMN_1761804	ALDH9A1	rs2814471	0.378	1.21E-04	0.0513
ILMN_1761804	ALDH9A1	rs7524755	0.4064	2.02E-04	0.0285
ILMN_1761804	ALDH9A1	rs2251768	0.3782	1.25E-04	0.0514
ILMN_1761804	ALDH9A1	rs2790053	0.3785	1.27E-04	0.0514
ILMN_1761804	ALDH9A1	rs4657476	0.3785	1.29E-04	0.0512
ILMN_1761804	ALDH9A1	rs7518099	0.3892	1.27E-04	0.0551
ILMN_1761804	ALDH9A1	rs4656461	0.3643	3.99E-04	0.0203
ILMN_1793829	TMCO1	rs4656461	0.0039	0.1177	0.0031
ILMN_1793829	TMCO1	rs7555523	0.009	0.1487	0.0021
ILMN_1793829	TMCO1	rs6660601	0.0079	0.1668	0.0023
ILMN_1793829	TMCO1	rs2814471	0.0094	0.1538	0.0021
ILMN_1793829	TMCO1	rs2251768	0.0093	0.1558	0.0021
ILMN_1793829	TMCO1	rs2790053	0.0093	0.1566	0.0022
ILMN_1793829	TMCO1	rs4657476	0.0093	0.1573	0.0022
ILMN_1793829	TMCO1	rs7524755	0.008	0.1702	0.0024
ILMN_1793829	TMCO1	rs7518099	0.0095	0.1563	0.0024
ILMN_1749960	FAM78B	rs2814471	0.0258	0.3097	0.4651
ILMN_1749960	FAM78B	rs2251768	0.0259	0.3189	0.4582
ILMN_1749960	FAM78B	rs7555523	0.0259	0.3227	0.4542
ILMN_1749960	FAM78B	rs2790053	0.0259	0.3228	0.4561
ILMN_1749960	FAM78B	rs4657476	0.0259	0.3259	0.4535
ILMN_1749960	FAM78B	rs7518099	0.0265	0.3384	0.4619
ILMN_1749960	FAM78B	rs6660601	0.0281	0.3673	0.4176
ILMN_1749960	FAM78B	rs7524755	0.0301	0.3666	0.4128
ILMN_1662681	AMBRA1	rs9666924	0.6793	0.0448	0.6623
ILMN_2163051	HARBI1	rs4752839	0.1257	0.3048	0.0148
ILMN_2163051	HARBI1	rs3847503	0.1057	0.4655	0.0123

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PROBE	Gene	SNP	eQTL p-value(fat)	eQTL p-value (LCL)	eQTL pvalue (skin)
ILMN_2163051	HARBI1	rs17198158	0.1353	0.4173	0.0138
ILMN_2163051	HARBI1	rs1044269	0.1493	0.3842	0.0136
ILMN_2163051	HARBI1	rs753812	0.1296	0.5213	0.0127
ILMN_2163051	HARBI1	rs4752843	0.1663	0.4744	0.0164
ILMN_2163051	HARBI1	rs9666924	0.1702	0.3865	0.0202
ILMN_2163051	HARBI1	rs4147730	0.1351	0.4243	0.0236
ILMN_2163051	HARBI1	rs4752786	0.1325	0.4257	0.0269
ILMN_2163051	HARBI1	rs10742816	0.137	0.426	0.0263
ILMN_2163051	HARBI1	rs11819955	0.1387	0.4488	0.0281
ILMN_2163051	HARBI1	rs7931089	0.1426	0.4519	0.0296
ILMN_2163051	HARBI1	rs1474056	0.1449	0.4597	0.0293
ILMN_1759828	HARBI1	rs12419342	0.5313	0.0326	0.8936
ILMN_1732060	ARHGAP1	rs1044269	0.1638	0.0332	0.0549
ILMN_1732060	ARHGAP1	rs17198158	0.1972	0.0312	0.0494
ILMN_1732060	ARHGAP1	rs3847503	0.2461	0.0337	0.0415
ILMN_1732060	ARHGAP1	rs9666924	0.1678	0.03	0.0722
ILMN_1732060	ARHGAP1	rs4752843	0.316	0.0248	0.0667
ILMN_1732060	ARHGAP1	rs1474056	0.2188	0.0297	0.0837
ILMN_1732060	ARHGAP1	rs7120737	0.2169	0.0104	0.2422
ILMN_1732060	ARHGAP1	rs4147730	0.249	0.0311	0.0763
ILMN_1732060	ARHGAP1	rs11819955	0.2396	0.0297	0.0846
ILMN_1732060	ARHGAP1	rs10742816	0.2244	0.0331	0.0852
ILMN_1732060	ARHGAP1	rs7931089	0.2423	0.0299	0.0898
ILMN_1732060	ARHGAP1	rs4752786	0.2436	0.0348	0.0901
ILMN_1732060	ARHGAP1	rs753812	0.3474	0.0604	0.0421
ILMN_1732060	ARHGAP1	rs4752839	0.2392	0.0367	0.1341
ILMN_1675268	LRP4	rs12419342	0.3256	0.0433	0.905
ILMN_1769250	ARFGAP2	rs17198985	0.927	6.72E-04	0.8109
ILMN_1769250	ARFGAP2	rs17198607	0.9212	0.0016	0.6627
ILMN_1769250	ARFGAP2	rs7946766	0.9523	0.0019	0.6169
ILMN_1769250	ARFGAP2	rs2270993	0.9034	0.0029	0.5508
ILMN_1769250	ARFGAP2	rs7129364	0.8973	0.003	0.5564
ILMN_1769250	ARFGAP2	rs3741410	0.9794	0.0021	0.9041
ILMN_1769250	ARFGAP2	rs4752877	0.8398	0.0068	0.6558
ILMN_1769250	ARFGAP2	rs3847503	0.6549	0.0105	0.7398
ILMN_1769250	ARFGAP2	rs7120737	0.8531	0.0071	0.8889
ILMN_1769250	ARFGAP2	rs4752843	0.8043	0.0093	0.7817
ILMN_1769250	ARFGAP2	rs4752791	0.9321	0.0075	0.8895
ILMN_1769250	ARFGAP2	rs17791016	0.9352	0.0072	0.9653
ILMN_1769250	ARFGAP2	rs1872167	0.9664	0.0077	0.9098
ILMN_1769250	ARFGAP2	rs17198158	0.615	0.0141	0.8251

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PROBE	Gene	SNP	eQTL p-value(fat)	eQTL p-value (LCL)	eQTL pvalue (skin)
ILMN_1769250	ARFGAP2	rs6485783	0.9879	0.0088	0.9386
ILMN_1769250	ARFGAP2	rs2305982	0.9942	0.0088	0.9329
ILMN_1769250	ARFGAP2	rs11819955	0.7185	0.0145	0.8412
ILMN_1769250	ARFGAP2	rs753812	0.544	0.0176	0.9308
ILMN_1769250	ARFGAP2	rs4147730	0.7224	0.015	0.826
ILMN_1769250	ARFGAP2	rs7931089	0.7342	0.0146	0.8521
ILMN_1769250	ARFGAP2	rs4752786	0.7565	0.0144	0.8397
ILMN_1769250	ARFGAP2	rs1044269	0.6682	0.016	0.9163
ILMN_1769250	ARFGAP2	rs10742816	0.7707	0.0148	0.8676
ILMN_1769250	ARFGAP2	rs7130876	0.397	0.0298	0.8383
ILMN_1769250	ARFGAP2	rs1474056	0.748	0.0171	0.869
ILMN_1769250	ARFGAP2	rs9666924	0.7289	0.0169	0.9562
ILMN_1769250	ARFGAP2	rs4752839	0.5976	0.0264	0.7528
ILMN_1769250	ARFGAP2	rs7123436	0.4215	0.0404	0.966
ILMN_1769250	ARFGAP2	rs1017875	0.4214	0.0436	0.9656
ILMN_1682957	PACSIN3	rs12419342	0.6082	0.4142	6.31E-04
ILMN_1682957	PACSIN3	rs1681630	0.1803	0.5662	0.0035
ILMN_1660817	DDB2	rs1017875	0.9151	0.0301	0.3952
ILMN_1660817	DDB2	rs7123436	0.9233	0.0314	0.398
ILMN_1660817	DDB2	rs7130876	0.9425	0.0426	0.4336
ILMN_1660817	DDB2	rs7942031	0.774	0.0377	0.6175
ILMN_1660817	DDB2	rs6485788	0.7796	0.0381	0.6213
ILMN_1660817	DDB2	rs2305983	0.7735	0.0385	0.6221
ILMN_1660817	DDB2	rs7924699	0.7863	0.0391	0.6096
ILMN_2104830	ACP2	rs9666924	0.6572	0.0278	0.2026
ILMN_2104830	ACP2	rs1044269	0.6047	0.0388	0.2195
ILMN_2104830	ACP2	rs10742816	0.7482	0.0329	0.2598
ILMN_2104830	ACP2	rs1474056	0.7155	0.0374	0.2826
ILMN_2104830	ACP2	rs4147730	0.7304	0.0358	0.2898
ILMN_2104830	ACP2	rs4752786	0.7143	0.0365	0.2927
ILMN_2104830	ACP2	rs17198158	0.5389	0.0494	0.3336
ILMN_2104830	ACP2	rs7931089	0.7165	0.0417	0.3019
ILMN_2104830	ACP2	rs11819955	0.7156	0.0416	0.3083
ILMN_2104830	ACP2	rs4752877	0.5054	0.0478	0.4203
ILMN_2104830	ACP2	rs7120737	0.8701	0.0346	0.373
ILMN_1814022	NR1H3	rs753812	0.2587	0.0166	0.0795
ILMN_1814022	NR1H3	rs4752843	0.2064	0.0279	0.0976
ILMN_1814022	NR1H3	rs3847503	0.2512	0.0261	0.0932
ILMN_1814022	NR1H3	rs17198158	0.1635	0.0394	0.0965
ILMN_1814022	NR1H3	rs1044269	0.1613	0.0374	0.1263
ILMN_1814022	NR1H3	rs10838833	0.5515	0.0056	0.2823

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PROBE	Gene	SNP	eQTL p-value(fat)	eQTL p-value (LCL)	eQTL pvalue (skin)
ILMN_1814022	NR1H3	rs10838835	0.4787	0.0067	0.3175
ILMN_1814022	NR1H3	rs1316604	0.4062	0.0067	0.3761
ILMN_1814022	NR1H3	rs7120775	0.4313	0.0071	0.3807
ILMN_1814022	NR1H3	rs9666924	0.1684	0.0453	0.1553
ILMN_1814022	NR1H3	rs12289516	0.5802	0.0067	0.3078
ILMN_1814022	NR1H3	rs4147730	0.2412	0.0362	0.1434
ILMN_1814022	NR1H3	rs11819955	0.236	0.0394	0.1414
ILMN_1814022	NR1H3	rs16905753	0.4451	0.0082	0.3641
ILMN_1814022	NR1H3	rs1474056	0.2341	0.0365	0.1612
ILMN_1814022	NR1H3	rs7931089	0.2413	0.0386	0.1527
ILMN_1814022	NR1H3	rs10742816	0.2437	0.0387	0.1529
ILMN_1814022	NR1H3	rs4752786	0.2444	0.0402	0.1495
ILMN_1814022	NR1H3	rs2270993	0.6592	0.0124	0.2193
ILMN_1814022	NR1H3	rs4752839	0.2062	0.0423	0.2179
ILMN_1814022	NR1H3	rs7129364	0.6597	0.0133	0.2192
ILMN_1814022	NR1H3	rs11039571	0.5022	0.0146	0.2682
ILMN_1814022	NR1H3	rs7952205	0.5193	0.0152	0.2692
ILMN_1814022	NR1H3	rs12419342	0.395	0.0109	0.5247
ILMN_1814022	NR1H3	rs7120737	0.4278	0.028	0.2179
ILMN_1814022	NR1H3	rs17791016	0.4511	0.0453	0.1403
ILMN_1814022	NR1H3	rs17198985	0.7125	0.0141	0.3134
ILMN_1814022	NR1H3	rs4752877	0.6059	0.0469	0.1709
ILMN_1814022	NR1H3	rs17198607	0.9689	0.0197	0.258
ILMN_1814022	NR1H3	rs7946766	0.995	0.0227	0.2253
ILMN_1814022	NR1H3	rs3741410	0.7702	0.0416	0.4176
ILMN_1696463	SPI1	rs1681630	0.006	2.72E-10	0.0015
ILMN_1696463	SPI1	rs12419342	0.0023	4.32E-08	3.00E-04
ILMN_1696463	SPI1	rs4752839	0.1859	5.95E-06	0.037
ILMN_1696463	SPI1	rs7130876	0.1603	1.14E-05	0.032
ILMN_1696463	SPI1	rs753812	0.3096	5.25E-06	0.0359
ILMN_1696463	SPI1	rs7123436	0.2278	1.30E-05	0.0461
ILMN_1696463	SPI1	rs3847503	0.3071	9.83E-06	0.0479
ILMN_1696463	SPI1	rs2270993	0.2215	1.51E-05	0.045
ILMN_1696463	SPI1	rs17198158	0.2337	1.41E-05	0.0463
ILMN_1696463	SPI1	rs1017875	0.2411	1.47E-05	0.0494
ILMN_1696463	SPI1	rs7129364	0.2305	1.66E-05	0.0473
ILMN_1696463	SPI1	rs4147730	0.2632	1.85E-05	0.0533
ILMN_1696463	SPI1	rs11819955	0.2703	1.93E-05	0.0509
ILMN_1696463	SPI1	rs7931089	0.2667	2.06E-05	0.0494
ILMN_1696463	SPI1	rs1474056	0.2732	2.43E-05	0.0434
ILMN_1696463	SPI1	rs1044269	0.2562	1.77E-05	0.065

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PROBE	Gene	SNP	eQTL p-value(fat)	eQTL p-value (LCL)	eQTL pvalue (skin)
ILMN_1696463	SPI1	rs4752843	0.43	1.46E-05	0.0613
ILMN_1696463	SPI1	rs4752786	0.2704	2.41E-05	0.0593
ILMN_1696463	SPI1	rs10742816	0.2842	2.36E-05	0.0628
ILMN_1696463	SPI1	rs9666924	0.2579	2.61E-05	0.0717
ILMN_1696463	SPI1	rs6485788	0.3606	2.92E-05	0.0837
ILMN_1696463	SPI1	rs7924699	0.3498	3.19E-05	0.0842
ILMN_1696463	SPI1	rs7942031	0.3574	3.07E-05	0.0911
ILMN_1696463	SPI1	rs2305983	0.3632	3.37E-05	0.0906
ILMN_1696463	SPI1	rs17198607	0.2148	9.34E-05	0.0872
ILMN_1696463	SPI1	rs17198985	0.1819	1.85E-04	0.0557
ILMN_1696463	SPI1	rs7952205	0.1711	3.38E-04	0.0796
ILMN_1696463	SPI1	rs3741410	0.1946	2.38E-04	0.0997
ILMN_1696463	SPI1	rs7946766	0.2652	1.72E-04	0.1263
ILMN_1696463	SPI1	rs11039571	0.1865	3.90E-04	0.0921
ILMN_1696463	SPI1	rs7120737	0.4423	1.47E-04	0.1301
ILMN_1696463	SPI1	rs4752791	0.3666	2.38E-04	0.1122
ILMN_1696463	SPI1	rs17791016	0.3904	2.18E-04	0.1337
ILMN_1696463	SPI1	rs4752877	0.275	5.10E-04	0.1239
ILMN_1696463	SPI1	rs12289516	0.301	5.76E-04	0.1036
ILMN_1696463	SPI1	rs6485783	0.3931	4.25E-04	0.1798
ILMN_1696463	SPI1	rs2305982	0.3997	4.30E-04	0.1812
ILMN_1696463	SPI1	rs1872167	0.394	4.42E-04	0.1988
ILMN_1696463	SPI1	rs10838833	0.3112	9.38E-04	0.136
ILMN_1696463	SPI1	rs10838835	0.3105	0.0012	0.1431
ILMN_1696463	SPI1	rs2200183	0.3583	0.0012	0.1505
ILMN_1696463	SPI1	rs10838881	0.363	0.0016	0.1212
ILMN_1696463	SPI1	rs1316604	0.363	0.0016	0.1212
ILMN_1696463	SPI1	rs7120775	0.3567	0.0016	0.1295
ILMN_1696463	SPI1	rs7945174	0.3687	0.0015	0.1454
ILMN_1696463	SPI1	rs7949865	0.3725	0.0015	0.1521
ILMN_1696463	SPI1	rs16905753	0.3656	0.0017	0.1425
ILMN_2392043	SPI1	rs10838833	0.63	0.9743	0.0325
ILMN_2392043	SPI1	rs12289516	0.6492	0.9879	0.0361
ILMN_2392043	SPI1	rs10838835	0.6286	0.955	0.0452
ILMN_2392043	SPI1	rs7949865	0.6902	0.8554	0.0474
ILMN_2392043	SPI1	rs7945174	0.6959	0.8838	0.0484
ILMN_2392043	SPI1	rs2270993	0.7447	0.9303	0.044
ILMN_2392043	SPI1	rs7129364	0.7507	0.9475	0.0432
ILMN_2392043	SPI1	rs7942031	0.8897	0.8779	0.043
ILMN_2392043	SPI1	rs2305983	0.8949	0.8808	0.0436
ILMN_2392043	SPI1	rs7924699	0.8937	0.8875	0.0449

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PROBE	Gene	SNP	eQTL p-value(fat)	eQTL p-value (LCL)	eQTL pvalue (skin)
ILMN_2392043	SPI1	rs6485788	0.8956	0.8447	0.0477
ILMN_2392043	SPI1	rs1017875	0.9881	0.9898	0.0391
ILMN_2392043	SPI1	rs7123436	0.9913	0.998	0.0432
ILMN_1809010	PSMC3	rs1681630	0.0051	0.2064	0.8298
ILMN_1809010	PSMC3	rs12419342	0.0085	0.3437	0.9783
ILMN_1668000	KBTBD4	rs12419342	0.3238	0.0018	0.6251
ILMN_1668000	KBTBD4	rs1681630	0.7003	0.0081	0.986
ILMN_1668000	KBTBD4	rs9666924	0.7091	0.0133	0.7751
ILMN_1668000	KBTBD4	rs17198158	0.7364	0.0127	0.8081
ILMN_1668000	KBTBD4	rs1044269	0.7069	0.0145	0.7622
ILMN_1668000	KBTBD4	rs4752786	0.7699	0.013	0.8908
ILMN_1668000	KBTBD4	rs4752839	0.7313	0.013	0.984
ILMN_1668000	KBTBD4	rs10742816	0.78	0.014	0.8666
ILMN_1668000	KBTBD4	rs7931089	0.7822	0.014	0.8893
ILMN_1668000	KBTBD4	rs11819955	0.7779	0.0144	0.8856
ILMN_1668000	KBTBD4	rs3847503	0.8395	0.0151	0.8341
ILMN_1668000	KBTBD4	rs10769370	0.4753	0.042	0.5328
ILMN_1668000	KBTBD4	rs4147730	0.7622	0.0162	0.8629
ILMN_1668000	KBTBD4	rs1474056	0.833	0.0148	0.905
ILMN_1668000	KBTBD4	rs753812	0.9661	0.0158	0.7694
ILMN_1668000	KBTBD4	rs7104642	0.512	0.0359	0.6408
ILMN_1668000	KBTBD4	rs7928243	0.5121	0.0359	0.6407
ILMN_1668000	KBTBD4	rs10769383	0.5197	0.0385	0.6453
ILMN_1668000	KBTBD4	rs7924699	0.8401	0.0473	0.3279
ILMN_1668000	KBTBD4	rs6485788	0.8238	0.0492	0.3253
ILMN_1668000	KBTBD4	rs6485856	0.5216	0.0394	0.6435
ILMN_1668000	KBTBD4	rs7942031	0.8185	0.0487	0.335
ILMN_1668000	KBTBD4	rs7952205	0.557	0.0295	0.8499
ILMN_1668000	KBTBD4	rs7942284	0.5455	0.0415	0.6376
ILMN_1668000	KBTBD4	rs7942042	0.5456	0.0415	0.6377
ILMN_1668000	KBTBD4	rs3741410	0.7692	0.0223	0.8461
ILMN_1668000	KBTBD4	rs7120737	0.7441	0.0348	0.5619
ILMN_1668000	KBTBD4	rs6485831	0.5127	0.0401	0.7079
ILMN_1668000	KBTBD4	rs11039571	0.5527	0.0313	0.8414
ILMN_1668000	KBTBD4	rs4752843	0.7538	0.0222	0.8753
ILMN_1668000	KBTBD4	rs6485848	0.5993	0.0406	0.6022
ILMN_1668000	KBTBD4	rs7945174	0.5659	0.0354	0.7363
ILMN_1668000	KBTBD4	rs7950737	0.5849	0.0413	0.623
ILMN_1668000	KBTBD4	rs7102865	0.5278	0.0435	0.6728
ILMN_1668000	KBTBD4	rs7949865	0.5772	0.0358	0.748
ILMN_1668000	KBTBD4	rs7120775	0.5839	0.0363	0.7344

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PROBE	Gene	SNP	eQTL p-value(fat)	eQTL p-value (LCL)	eQTL pvalue (skin)
ILMN_1668000	KBTBD4	rs2200183	0.5352	0.0399	0.758
ILMN_1668000	KBTBD4	rs7130876	0.8943	0.0401	0.4557
ILMN_1668000	KBTBD4	rs17198985	0.6132	0.0322	0.8312
ILMN_1668000	KBTBD4	rs10838881	0.5741	0.0387	0.7472
ILMN_1668000	KBTBD4	rs1316604	0.5741	0.0387	0.7472
ILMN_1668000	KBTBD4	rs16905753	0.59	0.038	0.7447
ILMN_1668000	KBTBD4	rs10838835	0.626	0.0365	0.7322
ILMN_1668000	KBTBD4	rs10838833	0.6126	0.0371	0.7534
ILMN_1668000	KBTBD4	rs7123436	0.8634	0.0468	0.4407
ILMN_1668000	KBTBD4	rs12289516	0.5358	0.044	0.7571
ILMN_1668000	KBTBD4	rs1017875	0.8651	0.0478	0.4455
ILMN_1668000	KBTBD4	rs7129364	0.9806	0.0234	0.9703
ILMN_1668000	KBTBD4	rs2270993	0.9955	0.023	0.9759
ILMN_1756355	NDUFS3	rs12419342	0.4264	0.0216	0.5511
ILMN_1756355	NDUFS3	rs1681630	0.5688	0.0218	0.7284
ILMN_2195462	C1QTNF4	rs12419342	0.0013	0.942	0.0312
ILMN_2195462	C1QTNF4	rs1681630	1.41E-04	0.8618	0.3328
ILMN_2195462	C1QTNF4	rs4752839	0.3016	0.5608	0.0014
ILMN_2195462	C1QTNF4	rs3847503	0.2595	0.551	0.0029
ILMN_2195462	C1QTNF4	rs1044269	0.3794	0.5245	0.0025
ILMN_2195462	C1QTNF4	rs11819955	0.2469	0.4342	0.0048
ILMN_2195462	C1QTNF4	rs753812	0.2956	0.5902	0.003
ILMN_2195462	C1QTNF4	rs4752843	0.2605	0.4028	0.005
ILMN_2195462	C1QTNF4	rs7931089	0.2464	0.4374	0.0049
ILMN_2195462	C1QTNF4	rs17198158	0.3079	0.5471	0.0032
ILMN_2195462	C1QTNF4	rs10742816	0.2659	0.4413	0.0047
ILMN_2195462	C1QTNF4	rs4147730	0.2569	0.4586	0.0049
ILMN_2195462	C1QTNF4	rs9666924	0.3636	0.4582	0.0035
ILMN_2195462	C1QTNF4	rs1474056	0.2634	0.4633	0.005
ILMN_2195462	C1QTNF4	rs4752786	0.251	0.4576	0.0055
ILMN_2195462	C1QTNF4	rs7120737	0.2971	0.5021	0.0082
ILMN_2195462	C1QTNF4	rs17791016	0.1817	0.7119	0.0099
ILMN_2195462	C1QTNF4	rs4752791	0.1583	0.8016	0.0102
ILMN_2195462	C1QTNF4	rs1872167	0.1598	0.8329	0.0119
ILMN_2195462	C1QTNF4	rs6485783	0.1613	0.8377	0.0118
ILMN_2195462	C1QTNF4	rs2305982	0.1602	0.8354	0.012
ILMN_2195462	C1QTNF4	rs4752877	0.1622	0.9554	0.0134
ILMN_2195462	C1QTNF4	rs17198985	0.2948	0.8445	0.0148
ILMN_2195462	C1QTNF4	rs3741410	0.3639	0.8134	0.014
ILMN_2195462	C1QTNF4	rs7946766	0.267	0.6481	0.0242
ILMN_2195462	C1QTNF4	rs17198607	0.3034	0.7607	0.0184

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PROBE	Gene	SNP	eQTL p-value(fat)	eQTL p-value (LCL)	eQTL pvalue (skin)
ILMN_2195462	C1QTNF4	rs2270993	0.3211	0.9655	0.02
ILMN_2195462	C1QTNF4	rs7129364	0.3386	0.9565	0.0199
ILMN_2195462	C1QTNF4	rs7952205	0.3683	0.9671	0.0229
ILMN_2195462	C1QTNF4	rs11039571	0.3838	0.9746	0.0249
ILMN_2195462	C1QTNF4	rs12289516	0.3335	0.9651	0.0338
ILMN_2195462	C1QTNF4	rs7924372	0.2797	0.9649	0.0471
ILMN_2195462	C1QTNF4	rs10838833	0.3625	0.9983	0.0383
ILMN_2195462	C1QTNF4	rs10838835	0.4375	0.9806	0.0454
ILMN_1785218	MTCH2	rs2305983	0.0126	6.22E-04	0.0025
ILMN_1785218	MTCH2	rs7942031	0.0132	5.77E-04	0.0026
ILMN_1785218	MTCH2	rs6485788	0.013	6.99E-04	0.0027
ILMN_1785218	MTCH2	rs7924699	0.0148	6.11E-04	0.0028
ILMN_1785218	MTCH2	rs7130876	0.0614	4.04E-04	0.0255
ILMN_1785218	MTCH2	rs1017875	0.0791	4.00E-04	0.0202
ILMN_1785218	MTCH2	rs7123436	0.0821	3.76E-04	0.0207
ILMN_1785218	MTCH2	rs12419342	0.733	0.1165	1.20E-04
ILMN_1785218	MTCH2	rs1681630	0.0093	0.0767	0.8751
ILMN_1785218	MTCH2	rs10769370	0.0465	0.2001	0.4969
ILMN_1785218	MTCH2	rs10838833	0.0499	0.3344	0.3536
ILMN_1688627	AGBL2	rs2305982	0.5748	1.67E-05	0.0015
ILMN_1688627	AGBL2	rs1872167	0.5791	1.74E-05	0.0015
ILMN_1688627	AGBL2	rs6485783	0.5788	1.75E-05	0.0016
ILMN_1688627	AGBL2	rs17791016	0.6888	2.31E-05	0.0017
ILMN_1688627	AGBL2	rs4752791	0.6779	2.09E-05	0.0021
ILMN_1688627	AGBL2	rs4752877	0.5642	2.40E-05	0.0028
ILMN_1688627	AGBL2	rs7120737	0.8634	5.21E-05	0.0019
ILMN_1688627	AGBL2	rs7946766	0.6626	2.02E-05	0.0066
ILMN_1688627	AGBL2	rs4752839	0.8732	3.09E-05	0.0035
ILMN_1688627	AGBL2	rs1044269	0.9779	2.22E-05	0.0051
ILMN_1688627	AGBL2	rs17198158	0.9638	3.07E-05	0.0043
ILMN_1688627	AGBL2	rs9666924	0.9242	2.39E-05	0.0063
ILMN_1688627	AGBL2	rs17198607	0.5217	3.12E-05	0.0139
ILMN_1688627	AGBL2	rs753812	0.8793	9.81E-05	0.0049
ILMN_1688627	AGBL2	rs11819955	0.8192	1.03E-04	0.0056
ILMN_1688627	AGBL2	rs7931089	0.823	1.05E-04	0.0056
ILMN_1688627	AGBL2	rs10742816	0.8249	9.95E-05	0.0062
ILMN_1688627	AGBL2	rs4752786	0.8415	1.05E-04	0.0059
ILMN_1688627	AGBL2	rs4147730	0.7949	1.04E-04	0.0069
ILMN_1688627	AGBL2	rs1474056	0.8266	1.19E-04	0.0061
ILMN_1688627	AGBL2	rs7478904	0.9122	9.21E-06	0.0756
ILMN_1688627	AGBL2	rs3847503	0.9537	1.26E-04	0.0055

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PROBE	Gene	SNP	eQTL p-value(fat)	eQTL p-value (LCL)	eQTL pvalue (skin)
ILMN_1688627	AGBL2	rs7924372	0.955	9.24E-06	0.0774
ILMN_1688627	AGBL2	rs7952205	0.633	4.61E-05	0.0291
ILMN_1688627	AGBL2	rs11039571	0.657	4.42E-05	0.0304
ILMN_1688627	AGBL2	rs4752843	0.7348	1.41E-04	0.0096
ILMN_1688627	AGBL2	rs10769370	0.5862	3.53E-05	0.0759
ILMN_1688627	AGBL2	rs12289516	0.499	1.05E-04	0.0438
ILMN_1688627	AGBL2	rs17198985	0.4784	1.88E-04	0.0281
ILMN_1688627	AGBL2	rs3741410	0.7769	2.17E-04	0.0158
ILMN_1688627	AGBL2	rs9667626	0.6134	1.36E-04	0.0341
ILMN_1688627	AGBL2	rs7129364	0.5864	1.13E-04	0.0504
ILMN_1688627	AGBL2	rs2270993	0.5912	1.18E-04	0.0514
ILMN_1688627	AGBL2	rs16905753	0.6624	9.42E-05	0.0574
ILMN_1688627	AGBL2	rs2200183	0.6082	9.33E-05	0.064
ILMN_1688627	AGBL2	rs10839007	0.651	8.49E-05	0.0666
ILMN_1688627	AGBL2	rs10838835	0.6277	1.15E-04	0.0515
ILMN_1688627	AGBL2	rs6485908	0.636	8.71E-05	0.0678
ILMN_1688627	AGBL2	rs12281162	0.6351	8.74E-05	0.0679
ILMN_1688627	AGBL2	rs10838833	0.5763	1.53E-04	0.0438
ILMN_1688627	AGBL2	rs7949865	0.6572	1.06E-04	0.0576
ILMN_1688627	AGBL2	rs6485831	0.6036	1.03E-04	0.0659
ILMN_1688627	AGBL2	rs7945174	0.646	1.10E-04	0.0588
ILMN_1688627	AGBL2	rs7120775	0.6569	1.12E-04	0.0594
ILMN_1688627	AGBL2	rs7102865	0.5837	1.07E-04	0.0706
ILMN_1688627	AGBL2	rs7928243	0.6158	1.10E-04	0.0727
ILMN_1688627	AGBL2	rs7104642	0.6159	1.10E-04	0.0727
ILMN_1688627	AGBL2	rs10838881	0.6501	1.28E-04	0.0625
ILMN_1688627	AGBL2	rs1316604	0.6501	1.28E-04	0.0625
ILMN_1688627	AGBL2	rs10769383	0.6009	1.17E-04	0.0751
ILMN_1688627	AGBL2	rs7942042	0.5942	1.15E-04	0.0774
ILMN_1688627	AGBL2	rs7942284	0.5943	1.15E-04	0.0774
ILMN_1688627	AGBL2	rs6485856	0.599	1.23E-04	0.0759
ILMN_1688627	AGBL2	rs6485848	0.6178	1.28E-04	0.0732
ILMN_1688627	AGBL2	rs7950737	0.5815	1.58E-04	0.1021
ILMN_1688627	AGBL2	rs6485788	0.6918	0.0195	0.0221
ILMN_1688627	AGBL2	rs7942031	0.6903	0.0198	0.0222
ILMN_1688627	AGBL2	rs2305983	0.6986	0.0202	0.0222
ILMN_1688627	AGBL2	rs7924699	0.6925	0.0219	0.0225
ILMN_1688627	AGBL2	rs7123436	0.7525	0.0349	0.0642
ILMN_1688627	AGBL2	rs1017875	0.7538	0.0357	0.0638
ILMN_1688627	AGBL2	rs7130876	0.6838	0.0464	0.1175
ILMN_2108938	FNBP4	rs7120737	0.0321	0.2146	0.2634

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PROBE	Gene	SNP	eQTL p-value(fat)	eQTL p-value (LCL)	eQTL pvalue (skin)
ILMN_2108938	FNBP4	rs17791016	0.0436	0.2815	0.3124
ILMN_2108938	FNBP4	rs1872167	0.0391	0.3534	0.2779
ILMN_2108938	FNBP4	rs2305982	0.0408	0.3374	0.2906
ILMN_2108938	FNBP4	rs6485783	0.041	0.3361	0.291
ILMN_1731589	PTPRJ	rs12419342	0.3511	0.0267	0.8828
ILMN_2150123	OR4B1	rs1681630	0.018	0.1518	0.3333
ILMN_2150123	OR4B1	rs7952205	0.0226	0.7396	0.0748
ILMN_2150123	OR4B1	rs11039571	0.0236	0.7444	0.0738
ILMN_2150123	OR4B1	rs17198607	0.0206	0.5145	0.1227
ILMN_2150123	OR4B1	rs7946766	0.0214	0.4663	0.154
ILMN_2150123	OR4B1	rs9666924	0.0213	0.5925	0.1544
ILMN_2150123	OR4B1	rs2270993	0.0208	0.9925	0.1024
ILMN_2150123	OR4B1	rs4752791	0.0202	0.967	0.109
ILMN_2150123	OR4B1	rs7129364	0.0212	0.9903	0.1049
ILMN_2150123	OR4B1	rs2305982	0.0222	0.8912	0.1261
ILMN_2150123	OR4B1	rs6485783	0.0222	0.8936	0.1268
ILMN_2150123	OR4B1	rs1872167	0.0203	0.9104	0.1373
ILMN_2150123	OR4B1	rs17791016	0.0234	0.9318	0.1225
ILMN_2150123	OR4B1	rs17198985	0.0301	0.7481	0.1288
ILMN_1756038	OR4B1	rs1847640	0.0421	0.7799	0.0916
ILMN_2150123	OR4B1	rs1044269	0.0249	0.6561	0.1869
ILMN_2150123	OR4B1	rs17198158	0.0251	0.701	0.1896
ILMN_2150123	OR4B1	rs12419342	0.0188	0.421	0.4595
ILMN_2150123	OR4B1	rs2200183	0.0317	0.8044	0.1428
ILMN_2150123	OR4B1	rs4752877	0.0233	0.9958	0.1575
ILMN_2150123	OR4B1	rs10838835	0.0392	0.8126	0.117
ILMN_2150123	OR4B1	rs10838833	0.0443	0.7899	0.1077
ILMN_2150123	OR4B1	rs10742816	0.0308	0.6218	0.2023
ILMN_2150123	OR4B1	rs4147730	0.0281	0.6315	0.2186
ILMN_2150123	OR4B1	rs7949865	0.0369	0.8113	0.1297
ILMN_2150123	OR4B1	rs12289516	0.0416	0.8563	0.1119
ILMN_2150123	OR4B1	rs11819955	0.0307	0.6461	0.2073
ILMN_2150123	OR4B1	rs7945174	0.0377	0.8128	0.1348
ILMN_2150123	OR4B1	rs4752786	0.0341	0.6209	0.1972
ILMN_2150123	OR4B1	rs16905753	0.0441	0.8263	0.1159
ILMN_2150123	OR4B1	rs6485831	0.0308	0.7787	0.1788
ILMN_2150123	OR4B1	rs7931089	0.0333	0.6459	0.2005
ILMN_2150123	OR4B1	rs1474056	0.0379	0.635	0.1873
ILMN_2150123	OR4B1	rs10838881	0.0437	0.8315	0.1282
ILMN_2150123	OR4B1	rs1316604	0.0437	0.8315	0.1282
ILMN_2150123	OR4B1	rs7120775	0.0454	0.8189	0.1259

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PROBE	Gene	SNP	eQTL p-value(fat)	eQTL p-value (LCL)	eQTL pvalue (skin)
ILMN_2150123	OR4B1	rs7478904	0.0295	0.9075	0.1805
ILMN_2150123	OR4B1	rs10769370	0.0307	0.6309	0.2498
ILMN_2150123	OR4B1	rs4752843	0.0483	0.4768	0.212
ILMN_2150123	OR4B1	rs7924372	0.0305	0.8977	0.1815
ILMN_2150123	OR4B1	rs7102865	0.0329	0.7624	0.1983
ILMN_2150123	OR4B1	rs7120737	0.039	0.9761	0.1393
ILMN_2150123	OR4B1	rs2202454	0.047	0.6631	0.2078
ILMN_2150123	OR4B1	rs3847503	0.0347	0.7914	0.2466
ILMN_2150123	OR4B1	rs10839007	0.0394	0.7919	0.2252
ILMN_2150123	OR4B1	rs6485908	0.0422	0.7829	0.2209
ILMN_2150123	OR4B1	rs12281162	0.0424	0.7816	0.2212
ILMN_2150123	OR4B1	rs6485856	0.0457	0.7848	0.2376
ILMN_2150123	OR4B1	rs10769383	0.0458	0.7899	0.2394
ILMN_2150123	OR4B1	rs7942042	0.0492	0.7912	0.2235
ILMN_2150123	OR4B1	rs7942284	0.0492	0.7914	0.2235
ILMN_2150123	OR4B1	rs9667626	0.0475	0.8061	0.2275
ILMN_2150123	OR4B1	rs7104642	0.0467	0.79	0.2371
ILMN_2150123	OR4B1	rs7928243	0.0468	0.7901	0.2372
ILMN_1688825	OR4X2	rs1681630	0.2718	0.3658	0.0439
ILMN_1688825	OR4X2	rs1017875	0.0207	0.8031	0.6308
ILMN_1688825	OR4X2	rs7123436	0.0212	0.7901	0.6383
ILMN_1688825	OR4X2	rs7130876	0.0216	0.7857	0.6745
ILMN_1764512	OR4X1	rs4752877	0.0736	6.21E-04	0.5807
ILMN_1764512	OR4X1	rs1872167	0.0911	0.001	0.4774
ILMN_1764512	OR4X1	rs2305982	0.0891	0.0011	0.4629
ILMN_1764512	OR4X1	rs6485783	0.0891	0.0011	0.4629
ILMN_1764512	OR4X1	rs4752791	0.1071	9.96E-04	0.4373
ILMN_1764512	OR4X1	rs2305983	0.2392	3.44E-04	0.6031
ILMN_1764512	OR4X1	rs7942031	0.2425	3.45E-04	0.5966
ILMN_1764512	OR4X1	rs7924699	0.2437	3.54E-04	0.5939
ILMN_1764512	OR4X1	rs6485788	0.2504	3.60E-04	0.6045
ILMN_1764512	OR4X1	rs17791016	0.1057	0.0015	0.4337
ILMN_1764512	OR4X1	rs4752843	0.0944	0.0037	0.3031
ILMN_1764512	OR4X1	rs1044269	0.1199	0.003	0.3166
ILMN_1764512	OR4X1	rs17198158	0.1179	0.0037	0.289
ILMN_1764512	OR4X1	rs7931089	0.1288	0.0034	0.2915
ILMN_1764512	OR4X1	rs1474056	0.1215	0.0038	0.2861
ILMN_1764512	OR4X1	rs753812	0.1317	0.0027	0.3727
ILMN_1764512	OR4X1	rs4752786	0.1264	0.0034	0.3088
ILMN_1764512	OR4X1	rs10742816	0.1296	0.0032	0.3206
ILMN_1764512	OR4X1	rs11819955	0.1339	0.0034	0.297

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PROBE	Gene	SNP	eQTL p-value(fat)	eQTL p-value (LCL)	eQTL pvalue (skin)
ILMN_1764512	OR4X1	rs9666924	0.1152	0.0034	0.3584
ILMN_1764512	OR4X1	rs3847503	0.1392	0.0038	0.273
ILMN_1764512	OR4X1	rs4147730	0.1336	0.0039	0.3092
ILMN_1764512	OR4X1	rs4752839	0.1615	0.0047	0.3188
ILMN_1764512	OR4X1	rs2270993	0.1161	0.0079	0.309
ILMN_1764512	OR4X1	rs1017875	0.5095	0.0014	0.4005
ILMN_1764512	OR4X1	rs7120737	0.1277	0.0055	0.409
ILMN_1764512	OR4X1	rs7129364	0.1156	0.0084	0.3067
ILMN_1764512	OR4X1	rs7123436	0.5102	0.0015	0.4095
ILMN_1764512	OR4X1	rs17198985	0.1376	0.0151	0.2112
ILMN_1764512	OR4X1	rs17198607	0.2684	0.0057	0.3232
ILMN_1764512	OR4X1	rs7946766	0.321	0.0055	0.3082
ILMN_1764512	OR4X1	rs7130876	0.4399	0.0029	0.4448
ILMN_1764512	OR4X1	rs7952205	0.1285	0.025	0.1798
ILMN_1764512	OR4X1	rs11039571	0.1359	0.0291	0.169
ILMN_1764512	OR4X1	rs7950737	0.2389	0.0318	0.0924
ILMN_1764512	OR4X1	rs7478904	0.3173	0.0402	0.0779
ILMN_1764512	OR4X1	rs7924372	0.3151	0.0407	0.0775
ILMN_1764512	OR4X1	rs7929225	0.2619	0.0295	0.1364
ILMN_1764512	OR4X1	rs7125913	0.2638	0.0294	0.1371
ILMN_1764512	OR4X1	rs10769370	0.2714	0.0449	0.0874
ILMN_1764512	OR4X1	rs6485848	0.2629	0.0364	0.1156
ILMN_1764512	OR4X1	rs12289516	0.2296	0.0326	0.1636
ILMN_1764512	OR4X1	rs10839007	0.2929	0.0337	0.1281
ILMN_1764512	OR4X1	rs6485908	0.2866	0.0347	0.1278
ILMN_1764512	OR4X1	rs11040263	0.3606	0.0208	0.1696
ILMN_1764512	OR4X1	rs7942042	0.2764	0.038	0.1213
ILMN_1764512	OR4X1	rs7942284	0.2764	0.038	0.1213
ILMN_1764512	OR4X1	rs12281162	0.2863	0.0349	0.1277
ILMN_1764512	OR4X1	rs11040261	0.3598	0.021	0.1702
ILMN_1764512	OR4X1	rs10838833	0.2148	0.0414	0.1456
ILMN_1764512	OR4X1	rs2202454	0.2715	0.0358	0.1393
ILMN_1764512	OR4X1	rs3741410	0.1232	0.0288	0.3876
ILMN_1764512	OR4X1	rs10838835	0.2466	0.0403	0.1416
ILMN_1764512	OR4X1	rs7928243	0.2847	0.0396	0.1252
ILMN_1764512	OR4X1	rs7104642	0.2849	0.0396	0.1252
ILMN_1764512	OR4X1	rs6485856	0.2845	0.0396	0.1275
ILMN_1764512	OR4X1	rs10769383	0.2809	0.0405	0.1271
ILMN_1764512	OR4X1	rs16905753	0.2773	0.0432	0.1318
ILMN_1764512	OR4X1	rs6485963	0.3931	0.0226	0.1819
ILMN_1764512	OR4X1	rs10839230	0.3932	0.0226	0.182

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PROBE	Gene	SNP	eQTL p-value(fat)	eQTL p-value (LCL)	eQTL pvalue (skin)
ILMN_1764512	OR4X1	rs598841	0.3928	0.0227	0.182
ILMN_1764512	OR4X1	rs913894	0.3984	0.0219	0.1887
ILMN_1764512	OR4X1	rs11040255	0.3983	0.0226	0.1867
ILMN_1764512	OR4X1	rs10839217	0.3892	0.0239	0.1864
ILMN_1764512	OR4X1	rs7949865	0.2741	0.0455	0.1401
ILMN_1764512	OR4X1	rs7932738	0.3939	0.0227	0.1975
ILMN_1764512	OR4X1	rs7120775	0.2821	0.0446	0.1413
ILMN_1764512	OR4X1	rs7945174	0.2804	0.0469	0.1466
ILMN_1764512	OR4X1	rs10838881	0.2783	0.048	0.1445
ILMN_1764512	OR4X1	rs1316604	0.2783	0.048	0.1445
ILMN_1764512	OR4X1	rs9667626	0.3416	0.0438	0.1319
ILMN_1764512	OR4X1	rs7102865	0.3085	0.0448	0.1428
ILMN_1764512	OR4X1	rs6485831	0.3076	0.0473	0.1481
ILMN_1764512	OR4X1	rs2200183	0.3072	0.0492	0.1547
ILMN_1764512	OR4X1	rs1847640	0.4711	0.045	0.1455
ILMN_1670149	OR4S1	rs7932738	0.5818	0.5115	0.0449
ILMN_1670149	OR4S1	rs913894	0.5711	0.5452	0.0459
ILMN_1670149	OR4S1	rs10839217	0.6162	0.4926	0.0477
ILMN_1670149	OR4S1	rs11040255	0.5604	0.5531	0.0471
ILMN_1670149	OR4S1	rs6485963	0.5587	0.5724	0.0499
ILMN_1670149	OR4S1	rs11040263	0.5776	0.5813	0.0496
ILMN_1670149	OR4S1	rs11040261	0.5793	0.5838	0.0499
ILMN_1777706	OR4C12	rs2202454	0.7445	0.0433	0.0315
ILMN_1777706	OR4C12	rs1847640	0.5294	0.0323	0.0617
ILMN_1777706	OR4C12	rs7932738	0.7127	0.0521	0.0437
ILMN_1777706	OR4C12	rs10839217	0.7195	0.0539	0.046
ILMN_1777706	OR4C12	rs913894	0.7788	0.0592	0.0442
ILMN_1777706	OR4C12	rs11040255	0.853	0.0708	0.0484
ILMN_2381468	TFEC	rs10256914	0.9481	0.7188	0.0021
ILMN_2381468	TFEC	rs4730751	0.9728	0.7416	0.0027
ILMN_2381468	TFEC	rs10262524	0.8762	0.7302	0.0038
ILMN_2381468	TFEC	rs10281637	0.8762	0.7302	0.0038
ILMN_2381468	TFEC	rs6969706	0.876	0.7304	0.0038
ILMN_2381468	TFEC	rs4236601	0.876	0.7306	0.0038
ILMN_2381468	TFEC	rs2024211	0.8783	0.7289	0.004
ILMN_2360730	CAV2	rs4730751	0.0188	N/S	N/S
ILMN_2360730	CAV2	rs2024211	0.026	N/S	N/S
ILMN_2360730	CAV2	rs4236601	0.0262	N/S	N/S
ILMN_2360730	CAV2	rs6969706	0.0264	N/S	N/S
ILMN_2360730	CAV2	rs10281637	0.0265	N/S	N/S
ILMN_2360730	CAV2	rs10262524	0.0266	N/S	N/S

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PROBE	Gene	SNP	eQTL p-value(fat)	eQTL p-value (LCL)	eQTL pvalue (skin)
ILMN_2360730	CAV2	rs10256914	0.0268	N/S	N/S
ILMN_1658835	CAV2	rs2024211	0.0318	0.2675	4.09E-04
ILMN_1658835	CAV2	rs6969706	0.0313	0.2698	4.13E-04
ILMN_1658835	CAV2	rs10281637	0.0313	0.27	4.13E-04
ILMN_1658835	CAV2	rs10262524	0.0313	0.2701	4.13E-04
ILMN_1658835	CAV2	rs4236601	0.0314	0.2695	4.13E-04
ILMN_1658835	CAV2	rs4730751	0.0352	0.2292	0.0012
ILMN_1658835	CAV2	rs10256914	0.0353	0.2298	0.0012
ILMN_1735220	CAV2	rs10256914	0.711	0.0485	0.9973
ILMN_1735220	CAV2	rs4730751	0.7838	0.0455	0.9707
ILMN_1687583	CAV1	rs2024211	5.43E-16	8.00E-05	3.84E-13
ILMN_1687583	CAV1	rs10262524	5.79E-16	8.54E-05	3.91E-13
ILMN_1687583	CAV1	rs10281637	5.79E-16	8.53E-05	3.92E-13
ILMN_1687583	CAV1	rs6969706	5.79E-16	8.54E-05	3.94E-13
ILMN_1687583	CAV1	rs4236601	5.79E-16	8.54E-05	3.95E-13
ILMN_1687583	CAV1	rs4730751	1.69E-14	3.37E-04	8.28E-13
ILMN_1687583	CAV1	rs10256914	1.69E-14	3.86E-04	1.60E-12
ILMN_1694011	WNT2	rs10262524	0.543	0.2649	0.0416
ILMN_1694011	WNT2	rs10281637	0.5431	0.265	0.0417
ILMN_1694011	WNT2	rs6969706	0.5433	0.2653	0.0418
ILMN_1694011	WNT2	rs4236601	0.5435	0.2655	0.0419
ILMN_1694011	WNT2	rs2024211	0.5428	0.2654	0.0423
ILMN_1694011	WNT2	rs4730751	0.4953	0.2926	0.0455
ILMN_1694011	WNT2	rs10256914	0.5107	0.3733	0.0479
ILMN_1782246	ASZ1	rs4730751	0.0445	0.2063	N/S
ILMN_1739763	OR13C4	rs2472493	0.9919	0.1788	0.0317
ILMN_1766054	ABCA1	rs2472493	0.1863	3.67E-05	0.3569
ILMN_1677572	FSD1CL	rs2472493	0.043	0.5806	0.4816
ILMN_1784156	FKTN	rs2472493	0.7047	0.4151	0.0461
ILMN_1676864	DDX31	rs7853989	0.8887	0.0385	0.1496
ILMN_1676864	DDX31	rs8176730	0.8943	0.0376	0.1544
ILMN_1676864	DDX31	rs8176725	0.8987	0.0383	0.1588
ILMN_1676864	DDX31	rs8176722	0.8977	0.0402	0.1761
ILMN_1754871	TSC1	rs8176747	0.2117	0.0725	0.0132
ILMN_1754871	TSC1	rs8176749	0.3425	0.1243	0.0132
ILMN_1754871	TSC1	rs8176693	0.3203	0.0898	0.0196
ILMN_1754871	TSC1	rs8176746	0.4743	0.094	0.0132
ILMN_2246510	TSC1	rs8176747	0.5623	0.3916	0.0374
ILMN_1678947	CELP	rs8176725	0.7844	0.0299	0.0097
ILMN_1678947	CELP	rs8176722	0.7786	0.0313	0.0096
ILMN_1678947	CELP	rs8176730	0.7961	0.0324	0.0093

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PROBE	Gene	SNP	eQTL p-value(fat)	eQTL p-value (LCL)	eQTL pvalue (skin)
ILMN_1678947	CELP	rs7853989	0.8143	0.0306	0.0098
ILMN_1678947	CELP	rs8176747	0.8083	0.1386	0.0117
ILMN_1678947	CELP	rs8176749	0.8984	0.1496	0.0176
ILMN_1678947	CELP	rs8176746	0.884	0.1547	0.0176
ILMN_1678947	CELP	rs8176693	0.9163	0.1899	0.0178
ILMN_2093072	FAM163B	rs8176749	0.7501	0.0556	0.0313
ILMN_2093072	FAM163B	rs8176746	0.8758	0.064	0.0313
ILMN_2093072	FAM163B	rs8176693	0.7702	0.0561	0.0424
ILMN_2093072	FAM163B	rs8176747	0.6474	0.1459	0.0399
ILMN_1737087	WDR5	rs8176725	0.8383	0.0336	0.2364
ILMN_1737087	WDR5	rs8176730	0.8557	0.0329	0.2381
ILMN_1737087	WDR5	rs7853989	0.8602	0.0336	0.2372
ILMN_1737087	WDR5	rs8176722	0.7877	0.0379	0.2632
ILMN_1813837	C9orf9	rs8176722	0.0293	0.2636	0.1549
ILMN_1813837	C9orf9	rs8176725	0.0342	0.3008	0.1312
ILMN_1813837	C9orf9	rs7853989	0.037	0.293	0.1272
ILMN_1813837	C9orf9	rs8176730	0.0352	0.3123	0.1286
ILMN_1813837	C9orf9	rs8176747	0.0377	0.826	0.1933
ILMN_1813837	C9orf9	rs8176693	0.0252	0.7595	0.4886
ILMN_1813837	C9orf9	rs8176746	0.0423	0.9983	0.2822

Table 5B. Strongest eQTL effects were observed for the genes in Table 1 for any of the available SNPs.

Chr	PROBE	Gene	SNP	A1	Fat p	LCL p	Skin p	IOP GWAS p-value
1	ILMN_1761804	ALDH9A1	rs12408101	T	0.06	3.41E-10	0.0097	0.067
1	ILMN_1793829	TMCO1	rs6426936	T	0.001	0.262	0.0034	1.81E-08
7	ILMN_1687583	CAV1	rs1049337	T	2.65E-64	6.31E-17	1.55E-53	0.0045
9	ILMN_1766054	ABCA1	rs2487050	C	0.8	1.13E-20	0.8819	0.015
9	ILMN_1678947	CELP	rs5320	G	0.02	0.0046	9.86E-05	0.1
9	ILMN_1797367	TSC1	rs2519154	T	0.0213	0.1375	7.13E-04	0.16
11	ILMN_1688627	AGBL2	rs2305982	G	0.5748	1.67E-05	0.0015	4.46E-10
11	ILMN_1785218	MTCH2	rs11605061	T	3.34E-10	2.75E-07	6.37E-09	0.39
11	ILMN_1696463	SPI1	rs11605672	G	1.15E-08	1.08E-43	1.82E-16	9.84E-05

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Table 6: The expression of twenty-five nearest genes in adult human eye tissues.

Chromosome	Nearest Gene	Expression in 5 adult eye tissues[1]						The Ocular Tissue Database[2]						EyeSAGE[3,4]			
		Probe ID	Sclera	Cornea	Optic Nerve	Retina	RPE	Probe ID	Sclera	Cornea	Optic Nerve	TM	Retina				
			avg sig(*p*-val)	avg sig(*p*-val)	avg sig(*p*-val)	avg sig(*p*-val)	avg sig(*p*-val)		PLIER	PLIER	PLIER	PLIER	PLIER	TM	MAC	RPE MAC	RPE Peri
1	TMCO1	1470209	442.35(0)	1150.70 (0)	291.67 (0)	1415.48 (0)	667.48(0)	2422722	7	48.67	33.6	129.42	20.54	+	+	+	+
3	FNDC3B	4250736	557.93 (0)	615.6 (0)	148.3(0)	175.32 (0)	308.22(0)	2652410	112.57	79.98	46.5	69.84	47.15	+	+	+	+
7	CAV1	1070215	494.12(0)	594.05 (0)	316.75 (0)	606.35 (0)	165.4 (0.01)	3020302	48.39	68.62	37.6	98.42	35.3	+	+	+	+
7	CAV2	620360	78.82 (0)	165.12 (0)	76.75 (0)	277.07(0)	50.47(0.13)	3020273	23.71	30.32	19.5	39.83	20.39	+	+	+	+
9	ABCA1	4060358	330.12 (0)	258.17(0)	213.05 (0)	189.23 (0)	568.05(0)	3164914	na	na	33.31	na	na	+	+	+	+
9	ABO	not found	na	na	na	na	na	3292561	5.84	11.29	4.64	2.81	9.38	+	na	na	na
11	AGBL2	4890338	14.43(0.25)	8.45 (0.13)	5.52(0.26)	18.02(0.23)	19.22 (0.12)	not found	na	na	na	na	na	na	na	na	na
11	CUGBP1	1580133	58.97(0)	46.42 (0)	41.48 (0)	176.65(0)	58.78 (0.01)	3372896	32.17	23.95	164.64	28.79	22.58	+	+	+	+
11	FOLH1	4830086	11.22(0.38)	7.07 (0.19)	44.38 (0)	27.67(0.08)	10.95 (0.44)	not found	na	na	na	na	na	na	+	+	+
11	LOC732416	5080092	10.73(0.38)	8.38 (0.12)	7.70(0.16)	20.23(0.13)	22.22 (0.13)	3372368	81.35	153.17	139.11	147.73	118.05	na	na	na	na
11	MTCH2	70689	na	38.13 (0)	22.3(0.01)	na	na	3329904	134.79	na	219.09	289.26	178.56	+	+	+	+
11	NDUFS3	1710168	450.22(0)	1124.35 (0)	638.18 (0)	1914.48 (0)	1270.7 (0)	3371986	17.15	29.048	26.11	na	26.99	+	+	+	+
11	NUP160	5050670	91.67(0.01)	145.13 (0)	56.18 (0)	270.23 (0)	70.58 (0.07)	not found	na	na	na	na	na	+	+	+	+
11	OR4A47	5700193	8.80 (0.47)	-1.12 (0.52)	0.57(0.36)	14.30(0.27)	10.57 (0.49)	3329983	34.88	28.11	34.64	55.81	na	na	na	na	na
11	OR4B1	6420678	9.02 (0.13)	1.50 (0.42)	3.15(0.26)	20.05(0.12)	20.88 (0.09)	3330131	na	51.77	83.6	50.02	70.29	na	na	na	na
11	OR4C3	5700632	15.98(0.17)	3.33 (0.25)	4.82(0.19)	16.42(0.27)	16.18 (0.20)	3330137	16	12.98	7.57	14.78	11.82	na	na	na	na
11	OR4X2	4480239	5.88(0.64)	-5.08 (0.75)	-5.65(0.70)	6.18 (0.61)	4.88 (0.68)	3330131	13.88	17.08	11.84	5.89	12.47	na	na	na	na
11	PSMC3	6960315	312.38 (0)	394.65 (0)	242.5 (0)	620.2 (0)	888.98 (0)	3372209	104.04	100.36	84.61	131.58	71.45	+	+	+	+
11	PTPRJ	4210253	17.93(0.11)	2.78 (0.31)	5.37 (0.16)	22.12(0.11)	22.97 (0.13)	3329983	34.88	28.11	34.64	55.81	34.34	+	+	+	+
11	RAPSN	4780370	13.15(0.29)	6.62 (0.21)	2.92 (0.25)	25.03(0.08)	28.45 (0.12)	3372235	63.67	72.82	71.53	na	55.84	na	na	na	na
11	SLC39A13	1190706	19.20(0.09)	12.87(0.03)	10.63(0.05)	23.93(0.14)	17.85 (0.25)	3329793	42.48	30.78	38.89	46.23	36.9	+	na	na	na
11	SPI1	5810398	19.82 (0.2)	10.25(0.04)	42.22(0.01)	23.08 (0.1)	88.05 (0)	3372174	33.4	6.64	23.27	23.06	22.29	+	+	+	-
11	SSSCA1	6480605	14.92(0.24)	46.23 (0)	9.23 (0.1)	25.38(0.12)	23.77 (0.18)	3335327	18.51	23.21	6.37	9.23	18.41	na	+	+	+
11	TYRL	not found	na	na	na	na	na	3343832	20.77	13.77	11.7	38.81	11.53	na	na	na	na
17	GAS7	1070435	190.93(0)	22.73(0.01)	533.02 (0)	595.18 (0)	298.15 (0)	3744965	77.2	19.7	219.09	127.97	102.89	na	+	+	+

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In the adult human eye tissues[1], the avg sig represents the gene expression. The avg sig is the average of detected signals of all probes for each single gene on the Illumina HumanHT-12-v4 Expression BeadChips after background noise subtraction. The signal detection *p*-val (*p*-val<0.05) defines the gene expression. Avg sig of 28 is the background expression signal; avg sig >40 is a strong expression signal. A complete description of this work can be found elsewhere[1].

In the Ocular Tissue Database[2] (OTDB), the gene expression is indicated as Affymetrix Probe Logarithmic Intensity Error (PLIER) number. The PLIER numbers were calculated by GC-background correction, PLIER normalization, log transformation and *z*-score calculation. The OTDB is also available at https://genome.uiowa.edu/otdb/.

In the EyeSAGE[3,4] datasets from NEIBank, the gene expression is determined by tag counts in the Serial Analysis of Gene Expression (SAGE). We summarized all counts for each gene per tissue and put '+' to indicate the expression; put '-' to label the no expression while the counts are 0. The EyeSAGE is publicly available at the http://neibank.nei.nih.gov/EyeSAGE/index.shtml.

Abbreviations: avg sig, average signal; p-val, p-value; RPE, retinal pigment epithelium; TM, trabecular meshwork; MAC, retina macular; RPE Peri, RPE peripheral; na, not applicable.

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Supplementary Table 7. VEGAS gene based output results with gene empirical p-value <2.88×10^{-6}.

Gene	Chr	Start Position (build 36)	Stop Position (build 36)	Gene-based empirical p-value		
				European ancestry cohort	ASIAN ancestry cohort	Combined P
SLC39A13	11	47386626	47394623	2.61×10^{-06}	0.00389	2.48×10^{-07}
PSMC3	11	47396895	47404600	1.66×10^{-06}	0.00373	1.55×10^{-07}
RAPSN	11	47415890	47427306	1.14×10^{-06}	0.00493	1.39×10^{-07}
CUGBP1	11	47446520	47531264	3.80×10^{-07}	0.00961	8.77×10^{-08}
PTPMT1	11	47543704	47549944	7.80×10^{-07}	0.00969	1.77×10^{-07}
MYBPC3	11	47309532	47330829	5.97×10^{-06}	0.00686	9.16×10^{-07}
SPI1	11	47332984	47356703	5.97×10^{-06}	0.00379	5.36×10^{-07}
KBTBD4	11	47550325	47557101	4.66×10^{-06}	0.00821	8.49×10^{-07}
NDUFS3	11	47557207	47562690	8.31×10^{-06}	0.00748	1.36×10^{-06}
C1QTNF4	11	47567791	47572537	2.16×10^{-05}	0.00556	2.59×10^{-06}

Supplementary Table 8. Top 5 pathways from Pathway-VEGAS results.

GO_ID	GO_Term	No. of Genes	CEU-EmpP	ASIA-EmpP	Combined EmpP
GO:0005581	Collagen	28	0.045	1.82×10^{-4}	1.22×10^{-4}
GO:0010576	metalloenzyme regulator activity	9	0.199	9.40×10^{-5}	2.14×10^{-4}
GO:0048551	metalloenzyme inhibitor activity	9	0.173	1.2×10^{-4}	2.42×10^{-4}
GO:0008191	metalloendopeptidase inhibitor activity	9	0.186	1.36×10^{-4}	2.88×10^{-4}
GO:0031116	positive regulation of microtubule polymerization	6	7.80×10^{-5}	0.627	3.63×10^{-4}
GO:0005578	proteinaceous extracellular matrix	233	0.0105	0.0025	3.92×10^{-4}
GO:0031112	positive regulation of microtubule polymerization or depolymerization	7	1.06×10^{-4}	0.573	4.66×10^{-4}
GO:0031012	extracellular matrix	256	0.0133	0.0027	5.19×10^{-4}
GO:0031113	regulation of microtubule polymerization	7	1.14×10^{-4}	0.727	5.5×10^{-4}
GO:0051495	positive regulation of cytoskeleton organization	36	1.14×10^{-4}	0.856	5.75×10^{-4}

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Supplementary Table 9. Comparison of analyses adjusted and non-adjusted for Central Corneal Thickness (CCT) *

					Unadjusted for CCT (N=19563)			Adjusted for CCT (N=19,563)			Whole sample unadjusted (N=35296)		
Chr.	position	SNP_ID	A1	A2	beta	se	p-value	beta	se	p-value	beta	se	p-value
1	165687205	rs4656461	G	A	0.216	0.045	1.65E-06	0.239	0.052	3.78E-06	0.228	0.039	$6.51x10^{-09}$
1	165718979	rs7555523	C	A	0.229	0.045	3.98E-07	0.254	0.052	9.18E-07	0.235	0.039	$2.19x10^{-09}$
3	171992387	rs6445055	A	G	-0.177	0.034	1.30E-07	-0.121	0.037	9.87E-04	-0.177	0.03	$4.19x10^{-08}$
7	116150095	rs10258482	A	C	0.188	0.033	1.89E-08	0.178	0.038	3.68E-06	0.196	0.029	$1.87x10^{-11}$
7	116150952	rs10262524	A	C	0.181	0.033	3.74E-08	0.170	0.038	7.08E-06	0.186	0.029	$9.69x10^{-11}$
7	116153025	rs2024211	C	A	0.180	0.033	4.05E-08	0.168	0.038	7.62E-06	0.184	0.029	$1.09x10^{-10}$
9	107695353	rs2472496	G	A	0.183	0.027	1.46E-11	0.165	0.030	3.86E-08	0.153	0.024	$2.31x10^{-10}$
9	107695848	rs2472493	G	A	0.189	0.027	1.91E-12	0.168	0.030	1.74E-08	0.159	0.024	$2.80x10^{-11}$
9	136131415	rs8176743	T	C	0.265	0.043	6.82E-10	0.244	0.045	6.92E-08	0.261	0.039	$3.08x10^{-11}$
9	136131592	rs7853989	C	G	0.220	0.041	6.51E-08	0.214	0.043	6.73E-07	0.221	0.037	$2.04x10^{-09}$
9	136137657	rs8176693	T	C	0.267	0.043	5.67E-10	0.246	0.045	6.24E-08	0.257	0.039	$6.39x10^{-11}$
11	47468545	rs12419342	C	T	0.160	0.029	5.38E-08	0.109	0.033	8.83E-04	0.153	0.026	$4.77x10^{-09}$
11	47857168	rs2305982	G	A	0.207	0.036	1.33E-08	0.173	0.040	1.73E-05	0.207	0.033	$4.46x10^{-10}$
11	47886165	rs4752877	A	C	0.209	0.037	2.23E-08	0.173	0.041	2.54E-05	0.211	0.034	$5.59x10^{-10}$
11	47893120	rs7924699	T	A	0.193	0.033	6.86E-09	0.138	0.037	1.77E-04	0.184	0.03	$7.56x10^{-10}$
11	47940925	rs747782	C	T	0.215	0.033	9.16E-11	0.158	0.037	1.91E-05	0.203	0.03	$1.13x10^{-11}$
11	47969152	rs1681630	T	C	0.149	0.029	2.01E-07	0.088	0.032	0.005466	0.144	0.026	$1.69x10^{-08}$
11	48004369	rs7946766	T	C	0.238	0.038	4.96E-10	0.192	0.043	9.39E-06	0.23	0.035	$2.71x10^{-11}$
17	10031090	rs12150284	T	C	-0.180	0.028	1.41E-10	-0.151	0.031	1.47E-06	-0.175	0.026	$1.68x10^{-11}$
17	10031183	rs9913911	G	A	-0.184	0.028	8.83E-11	-0.154	0.032	1.22E-06	-0.179	0.026	$1.03x10^{-11}$

* The three columns under “Unadjusted for CCT” heading show the beta coefficient of linear regression, standard error and p-values respectively for regression of IOP adjusted for age and sex only in the subsample for which CCT was available, the columns under “Adjusted for CCT” are as per the previous three but the analyses were adjusted for age, sex and CCT and the last three columns under “Whole sample unadjusted” for the initial GWAS using the whole sample and adjusted for age and sex only.

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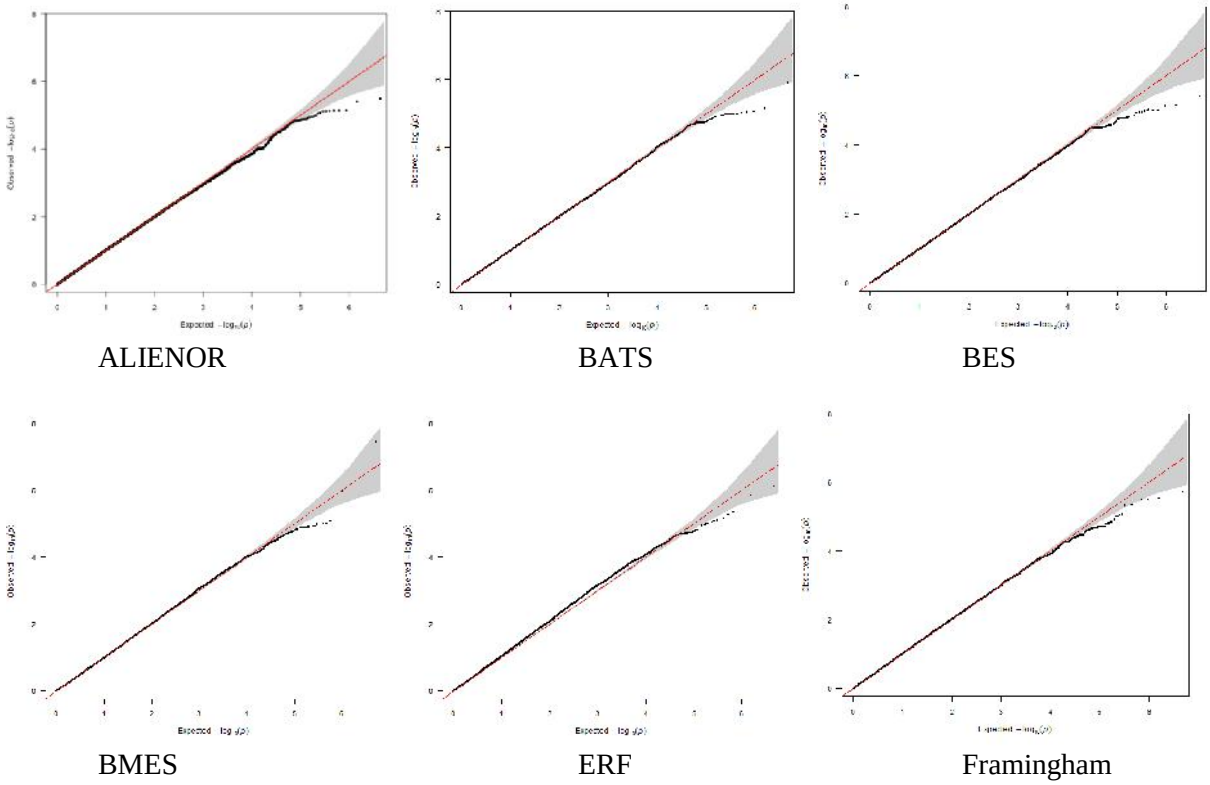
Supplementary Table 10. POAG variance explained by the SNPs showing strongest association with IOP.

IOP GWAS probability for which SNPs were selected	R^2 (variance explained)	p-value for R^2
p<0.000001	0.0068	4.33E-05
p<0.00001	0.0047	0.00069
p<0.0001	0.0041	0.0015
p<0.001	0.0035	0.0033
p<0.01	0.0055	0.0002
p<0.1	0.0046	0.0008
p<0.5	0.0044	0.001

Supplementary Figure 1: Quantile-quantile plots of the analysis IOP regression analysis results for each cohort.



ALIENOR BATS BES

BMES ERF Framingham

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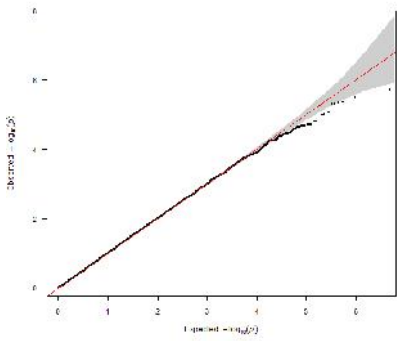
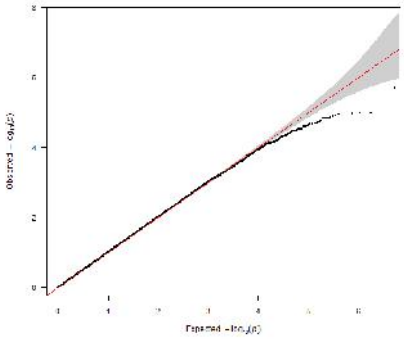


GHS I



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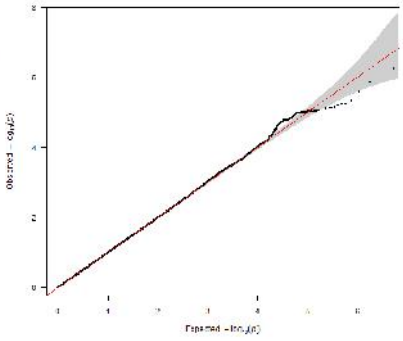
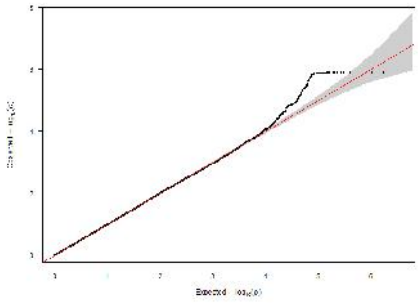


ORCADES



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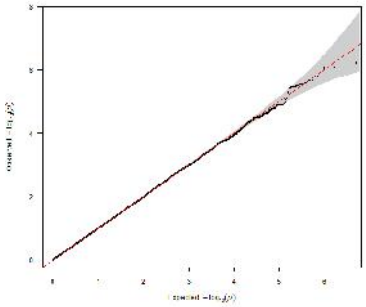

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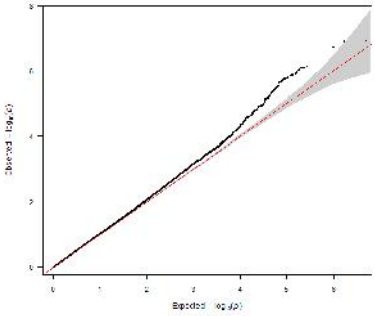

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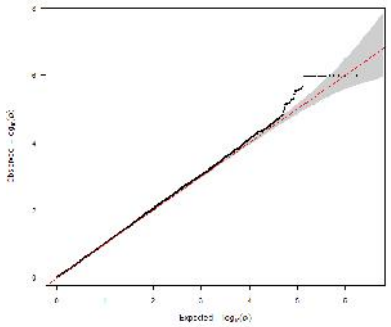

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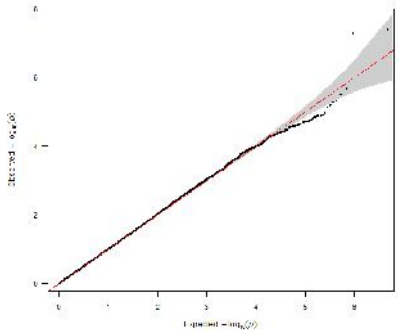

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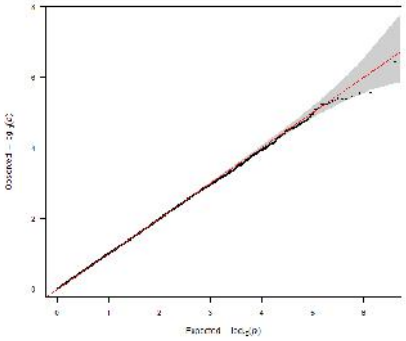

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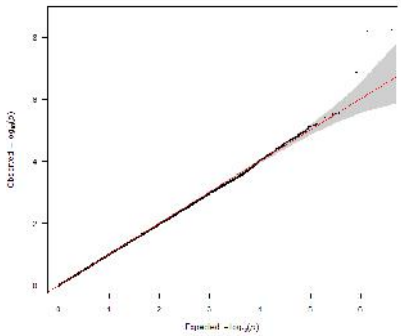

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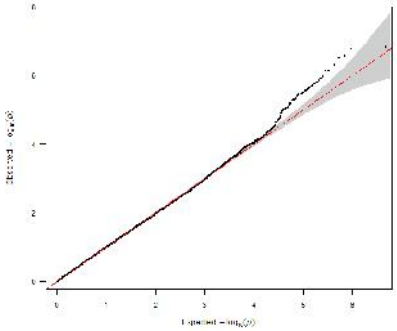

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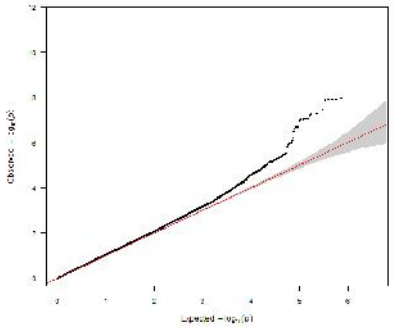

TwinsUK

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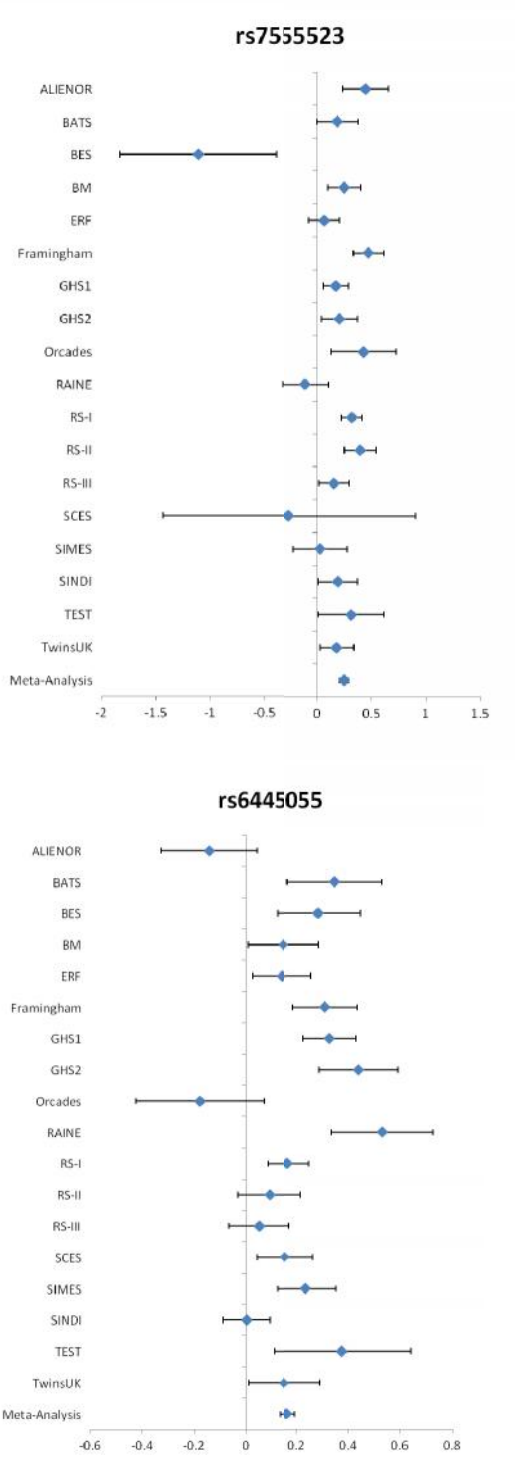
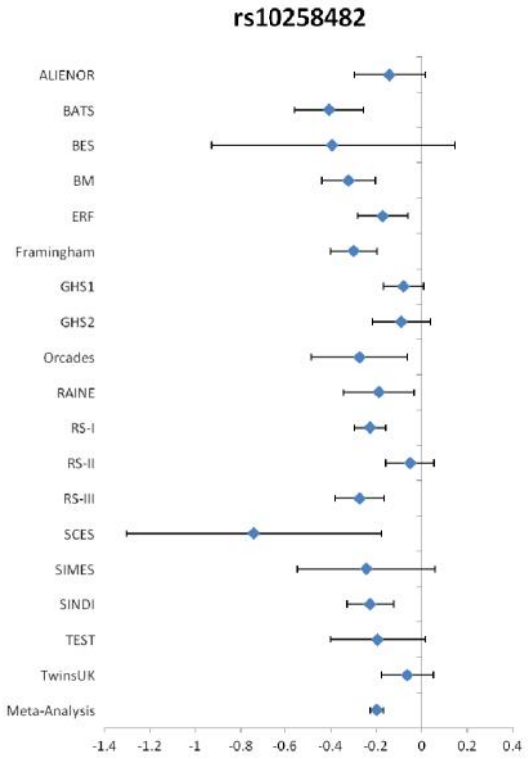
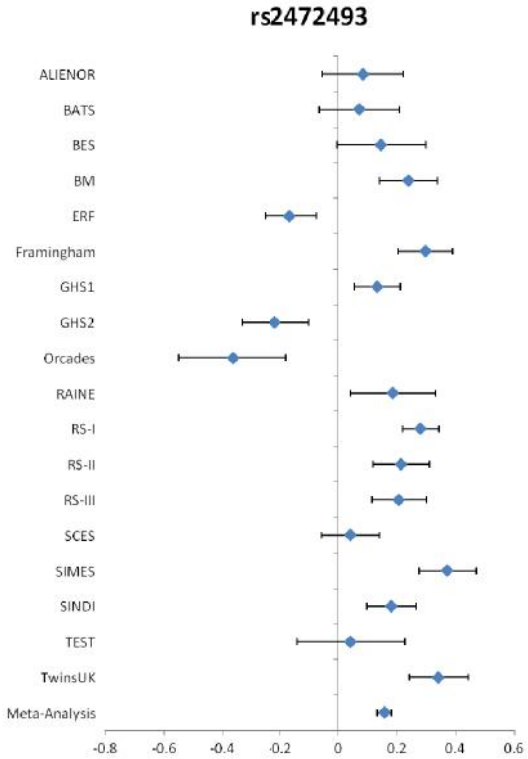
Supplementary Figure 2. Association forest plots for a selection of some of the strongest associated SNPs.

Effect sizes (beta regression coefficients) are shown by the diamond symbol, standard errors with bars.

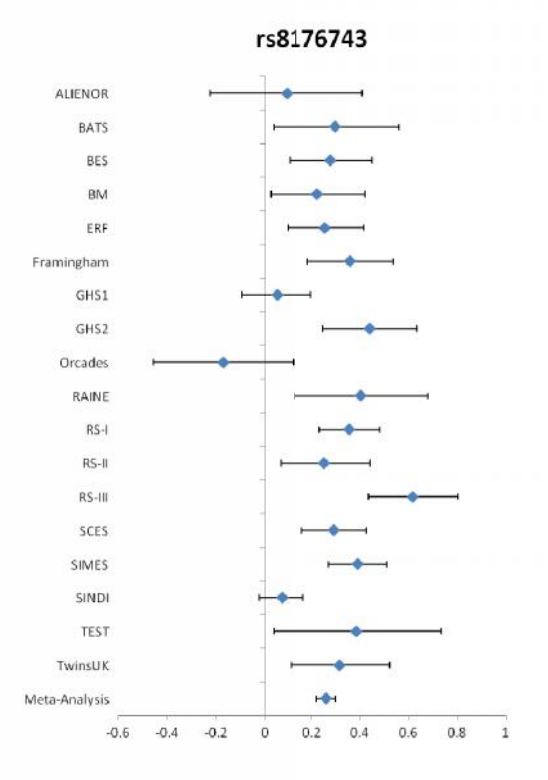


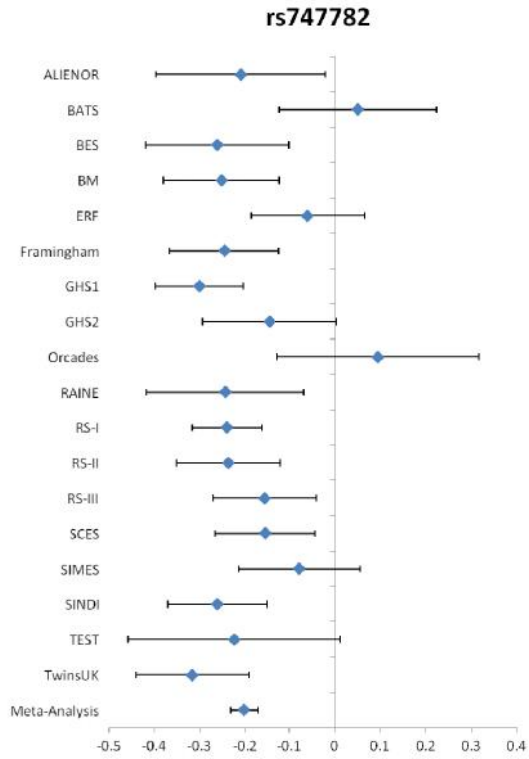
Nature Genetics: doi:10.1038/ng.3087



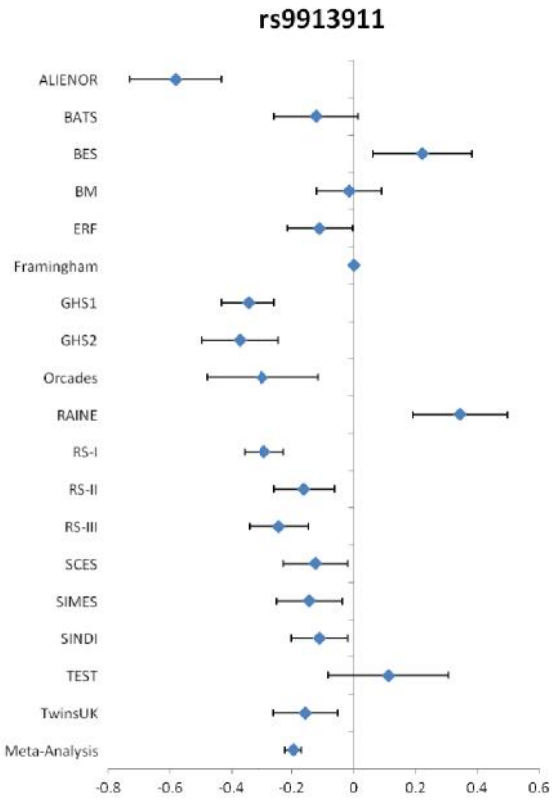


Nature Genetics: doi:10.1038/ng.3087





Nature Genetics: doi:10.1038/ng.3087



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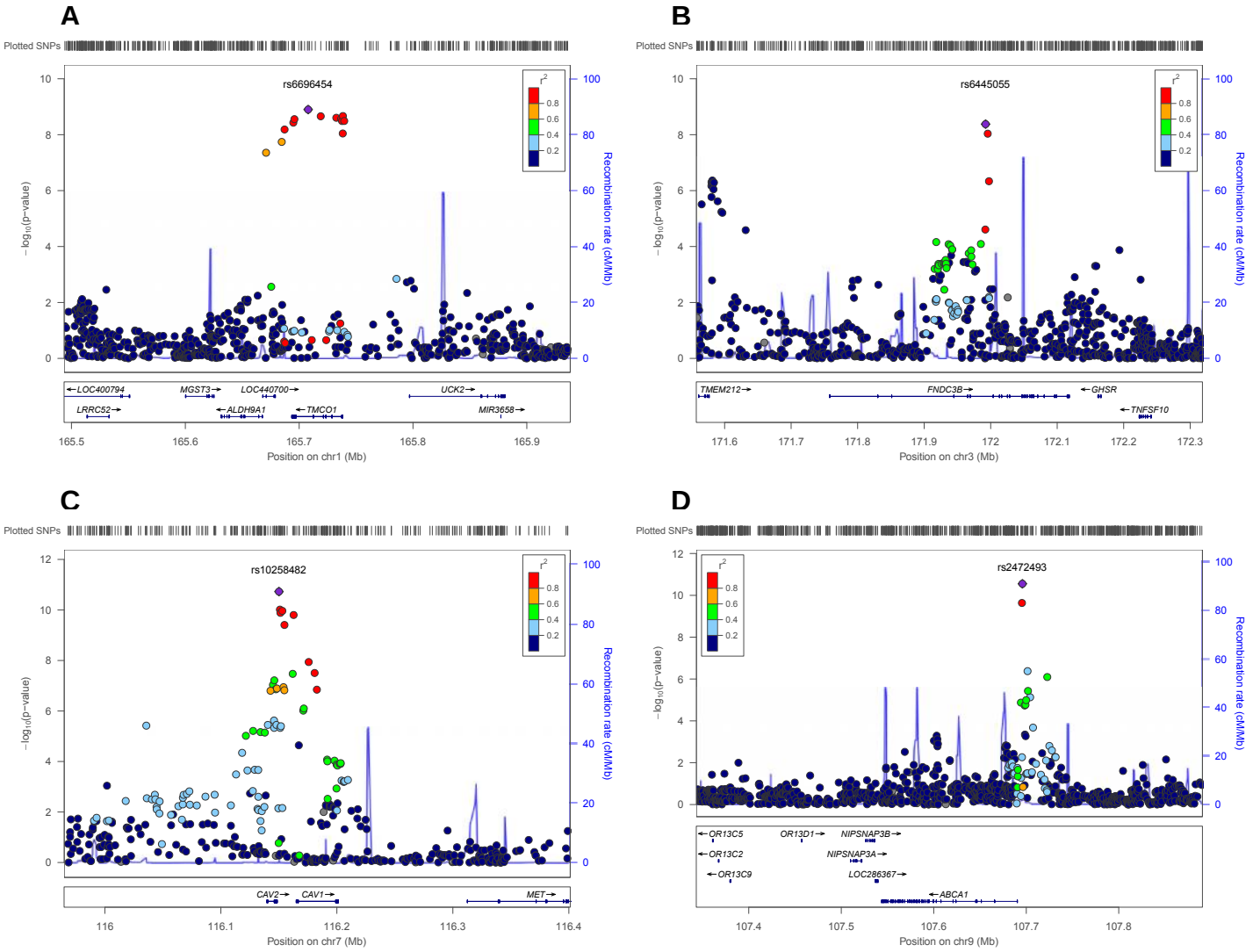
Supplementary Figure 3. Regional association plots and recombination rates of the loci associated with intraocular pressure.

Data are shown for association at (**A**) *TMCO1*, (**B**) *FNDC3B*, (**C**) *CAV1/CAV2*, (**D**) *ABCA1*, (**E**) *ABO*, (**F**) chromosome 11p11.2, and (**G**) GAS7. Data of both directly genotyped and imputed SNPs are presented. In each panel, the genotyped SNP with the most significant association is denoted with a purple diamond. The color coding of all other SNPs indicates LD with the lead SNP, estimated by CEU r^2 from phase II HapMap: red, $r^2 \geq 0.8$; yellow, $0.6 \leq r^2 < 0.8$; green, $0.4 \leq r^2 < 0.6$; cyan, $0.2 \leq r^2 < 0.4$; blue, $r^2 < 0.2$; and gray, r^2 unknown. The left *y* axis represents $-\log_{10} P$ values for association with axial length, the right *y* axis represents the recombination rate, estimated from the International HapMap Project[5], and the *x* axis represents base-pair positions along the chromosome based on human genome build 37. Gene annotations are taken from the University of California Santa Cruz (UCSC) genome browser. The plots were created using LocusZoom[6].



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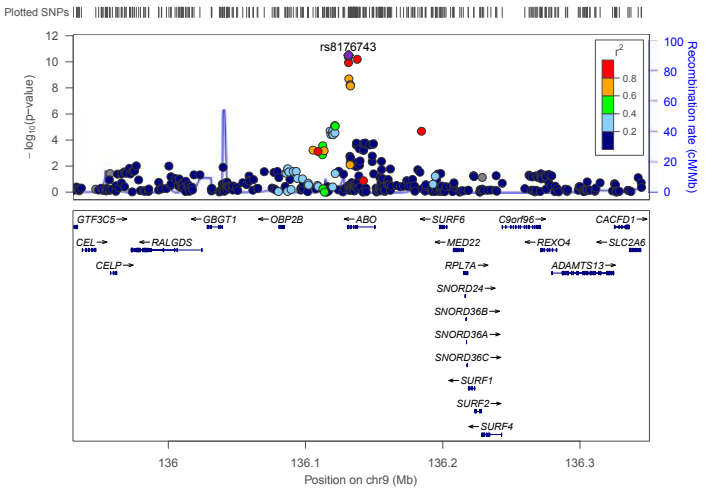
E



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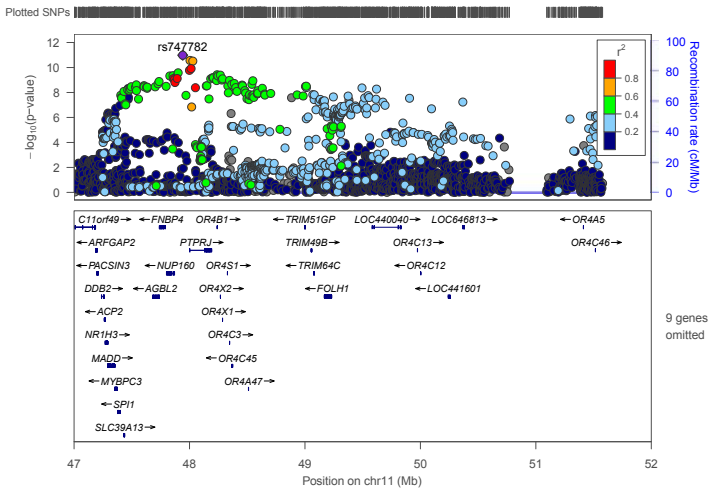

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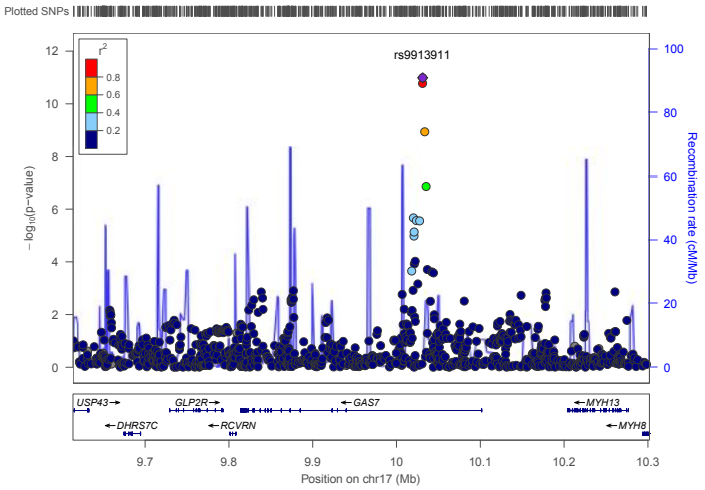

Nature Genetics: doi:10.1038/ng.3087

References

1. Young, T. et al. Whole Genome Expression Profiling of Normal Human Fetal and Adult Ocular Tissues. Experimental Eye Research http://dx.doi.org/10.1016/j.exer.2013.08.009(2013).
2. Wagner, A.H. et al. Exon-level expression profiling of ocular tissues. Exp Eye Res 111, 105-11 (2013).
3. Bowes Rickman, C. et al. Defining the human macula transcriptome and candidate retinal disease genes using EyeSAGE. Invest Ophthalmol Vis Sci 47, 2305-16 (2006).
4. Liu, Y. et al. Serial analysis of gene expression (SAGE) in normal human trabecular meshwork. Mol Vis 17, 885-93 (2011).
5. The International HapMap Project. Nature 426, 789-96 (2003).
6. Pruim, R.J. et al. LocusZoom: regional visualization of genome-wide association scan results. Bioinformatics 26, 2336-7 (2010).

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Supplementary Note

Consortia membership lists

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Wellcome Trust Case Control Consortium 2 (WTCCC2)

WTCCC2 members

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Description of participating cohorts – IOP meta-analysis cohorts

ALIENOR

The Alienor study is a population-based study in residents of Bordeaux, France[7]. The 963 participants, aged 73 years or more, were recruited from an ongoing population-based study (3C Study)[8]. They underwent an ophthalmological examination, including a recording of ophthalmological history, measures of visual acuity, refraction, two 45° non mydriatic colour retinal photographs (one centred on the macula, the other centred on the optic disc), measures of intraocular pressure and central corneal thickness and break-up time test. Intraocular pressure was measured using a non contact tonometer (KT800, Kowa, Japan). Central corneal thickness was measured using Pachpen (Accutome Inc., Malvern Pa, USA). This research followed the tenets of the Declaration of Helsinki. Participants gave written consent for the participation in the study. The design of this study has been approved by the Ethical Committee of Bordeaux (Comité de Protection des Personnes Sud-Ouest et Outre-Mer III) in May 2006.
There were 939 individuals with IOP phenotype, among which 805 were genotyped at the French national centre for genotyping (CNG) using Illumina Human 610-Quad BeadChip. Among them, 748 individuals have good genotype QC and have imputation data. 57 individuals were excluded (for non-European ancestry, related with other individuals or missingness > 5%). Imputation was performed using Hapmap2 CEU release 22 as reference panel. Imputation was performed in two steps: pre-phasing with SHAPEIT (v1), followed by imputation with IMPUTE2. SNPs are used in the imputation process if call rate > 98%, HWE pvalue > 1e-6, MAF> 1% (in the whole Alzheimer GWAS data). For genotyped SNPs, sporadic missing data are imputed during the pre-phasing step, hence there is no missing data. However, only genotyped SNPs with missingness lower than 2% are included in the imputation process. Linear regression was performed on untransformed IOP, under an additive genetic model, using the score test as implemented in SNPTEST(v2.4.1), which allows to take into account uncertainty in imputed data. Covariates were included as required in the analysis plan. Analysis was not adjusted on principal components. As a post-analysis QC, two qqplots for each GWAS analysis were generated showing the lambda (first plot generated on all SNPs with imputation quality > 0.4 and second plot generated on all SNPs with imputation quality > 0.8). Statistics do not seem to be inflated, suggesting it is correct not to adjust the analysis on PC.

Australian Twin Studies (BATS and TEST)

The Australian Twin Eye Study comprises participants examined as part of the Twins Eye Study in Tasmania (TEST) or the Brisbane Adolescent Twins Study (BATS). This study was approved by the human ethics committees of the University of Tasmania, Royal Victorian Eye and Ear Hospital, and Queensland Institute of Medical Research. Informed consent was obtained from parents with the child's assent or from adult participants. In most participants, the IOP was measured with the TONO-PEN XL (Reichert, Inc. New York, USA) as outlined in Mackey et al[9]. The Australian cohorts were genotyped on the Illumina Human Hap610W Quad array, with part of the sample typed alongside the TwinsUK cohort and the remainder typed as a separate

contract with DeCODE genetics. The inclusion criteria for the SNPs were a minor allele frequency >0.01, Hardy-Weinberg equilibrium $p \geq 10^{-6}$, and a SNP call rate >95% or Illumina Beadstudio Gencall Score ≥0.7, resulting in 543,862 SNPs. Imputation was done with reference to HapMap release 22 CEU using MACH (http://www.sph.umich.edu/csg/abecasis/MACH/). In BATS data from 1,152 people, from 517 families, were included in the analyses. For TEST, 686 individuals from 350 families were included. The mean IOP of both eyes was used as outcome variable. Association analyses were performed in Merlin (http://www.sph.umich.edu/csg/abecasis/merlin/) by using the –fastassoc option. Age, sex and measurement technique (tonopen or Goldmann applanation tonometry) were fitted as covariates. Ancestry, initially determined through self-reporting, was verified through Principal Component decomposition.

Beijing Eye Study

The Beijing Eye Study (BES) is a population-based cohort of Han Chinese in the rural region and in the urban region of Beijing in North China[10]. The Medical Ethics Committee of the Beijing Tongren Hospital approved the study protocol and all participants gave informed consent, according to the Declaration of Helsinki. At baseline in 2001, 4,439 individuals out of 5,324 eligible individuals aged 40 years or older participated (response rate: 83.4%). In the year 2006, the study was repeated by re-inviting all participants from the survey from 2001 to be re-examined. Out of the 4,439 subjects examined in 2001, 3,251 (73.2%) subjects returned for the follow-up examination in 2006.

All study participants underwent an ophthalmic examination including refractometry, pneumotonometry, slit-lamp biomicroscopy, and photography of the cornea, lens, optic disk, and macula. Intraocular pressure (IOP) was measured using a non-contact pneumotonometer (CT-60 computerized tonometer, Topcon Ltd., Japan) by an experienced technician. Three measurements were taken, and the mean of the three measurements was taken for further statistical analysis. If the measurements were higher than 25 mmHg, tonometry was repeated. Central corneal thickness (CCT) was measured by slit-lamp mounted optical coherence tomography (Heidelberg Engineering Co. Heidelberg, Germany) for the right eye only in study participants. A questionnaire included questions for self-reported diseases, including topical anti-glaucomatous medications, and previous ocular surgery. The systolic and diastolic BP was measured in a seated position using the Riva-Rocci method. The study participants rested for approximately 10 minutes before BP was measured. In these 10 minutes, participants were advised to refrain from caffeine intake, smoking, or exercise. Only right eye was included in the statistical analysis as CCT was measured in the right eye.

Blood samples were taken from 2,929 (90.1%), and DNA was extracted from blood leucocytes according to standard procedures. We performed genotyping using Illumina Human610-Quad BeadChip in 988 subjects[11,12]. 151 individuals with cryptic relatedness were excluded during sample QC procedure. After the removal of samples, SNPs were excluded based on (i) high rates of missingness (>5%); (ii) monomorphism; (iii) gross departure from HWE of $p<10^{-6}$. Imputation was performed using IMPUTE v2.2.2 [13] on post-QC SNPs. The HapMap Phase II panel (build36, release 22 db126 JPT+CHB HapMap panel) was used for the imputation. A total of 805 individuals with both complete post-QC GWAS data and IOP measurements on the right

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eye, and did not have prior glaucoma laser or surgery, were included in the analysis.

Blue Mountains Eye Study

Participants are part of the Blue Mountains Eye Study (BMES), a population-based eye disease survey in individuals living in the Blue Mountains region, west of Sydney, Australia. The study complied with recommendations of the Helsinki Declaration and was approved by the Sydney West Area Health Service Human Research Ethics Committee. Written informed consent was obtained from all participants.
Samples were genotyped on the Human660W-Quad. Imputation was performed with IMPUTE2 which adopts a two-stage approach using both haploid and diploid reference panels. 1000 Genome pilot data was used as reference panel. The SNPs considered in this study were those present also in HapMap2.
Intraocular pressure (IOP) was measured by applanation tonometry using a Goldmann tonometer (Haag-Streit, Bern, Switzerland). Vertical disc and cup diameter were obtained after pupil dilation from 30º colour stereoscopic optic disc photographs taken with a 99 Zeiss FF3 fundus camera (Carl Zeiss Meditec, Dublin, CA). Vertical cup-to-disc ratio (VCDR) was calculated by the vertical disc and cup measurements. Central corneal thickness, CCT, was measured using ultrasonic pachymetry.
The number of participants in the Blue Mountain Eye Study in the baseline is 3654 (57%males, 43% females), 2303 of them have imputed genotyping data available. The age range is 49-97 with mean 66.19 (±9.77) Intraocular pressure data and GWASs data are available for 1667 individuals with mean 16.04 mmHg (±2.63) and range 8.00-34.50 mmHg. 961 individuals have both IOP and CCT available. 1672 of the people with IOP have blood pressure measurements available. Information on IOP-lowering therapies and surgery for glaucoma are accessible and 10 individuals were deleted for ocular surgery.

Erasmus Rucphen Family Study (ERF)

The Erasmus Rucphen Family (ERF) Study is a family-based cohort in a genetically isolated population in the southwest of the Netherlands with over 3,000 participants aged between 18 and 86 years. The rationale and study design of this study have been described elsewhere[14,15]. Cross-sectional examination took place between 2002 and 2005. The IOP was measured with Goldmann applanation tonometry (Haag-Streit, Bern, Switzerland). IOP was measured twice per eye. If the two measurements in one eye differed, a third measurement was performed, and the median value was recorded. All measurements in these studies were conducted after the Medical Ethics Committee of the Erasmus University had approved the study protocols and all participants had given a written informed consent in accordance with the Declaration of Helsinki. DNA was genotyped on one of four different platforms (Illumina 610k, Illumina 300K, Illumina 370K and Affymetrix 250K). Samples with low call rate (<90%), with excess autosomal heterozygosity (fdr <1%), with sex-mismatch and ethnic outliers were excluded, as were outliers identified by the identity-by-state clustering analysis (outliers were defined as having identity-by-state probabilities >95%). A set of genotyped input SNPs with call rate >95% and with Hardy-Weinberg P value $>10^{-6}$ were included. After quality control, the different platforms were

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merged and imputation was done. For phasing, we used the Markov Chain Haplotyping (MaCH) package version 1.0.18.c software and for imputations minimac version 2011.10.27 to impute to the plus strand of NCBI build 36 with the Hapmap release #22 as a reference. For each imputed SNP, a reliability of imputation was estimated as the ratio of the empirically observed dosage variance to the expected binomial dosage variance (O/E ratio). GWAS analyses were performed using the ProbABEL package. Mmscore models were used to correct for family structure.

Framingham Eye Study

The Framingham Eye Study[16] (FES) was nested within the Framingham Heart Study (FHS, http://www.framinghamheartstudy.org), which began its first round of extensive physical examinations in 1948 by recruiting 5,209 men and women from the town of Framingham, MA, USA. Surviving participants from the original cohort returned for biennial exams, which continue to the present. A total of 2675 FHS participants were also examined as part of the FES between 1973 and 1975. The FES was designed to evaluate ocular characteristics of examinees such as: senile cataract; age-related macular disease; glaucoma; and retinopathy. Between 1989 and 1991, 1603 offspring of original cohort participants also received ocular examinations. All data--including refractive error, demographics and genotypes--were retrieved from the database of Genotypes and Phenotypes (dbGaP, http://www.ncbi.nlm.nih.gov/gap) after approval for controlled access to individual-level data. All study protocols are in compliance with the World Medical Association Declaration of Helsinki. Since 1971, written consent has been obtained from participants before each examination. The research protocols of the Framingham Heart Study are reviewed annually by the Institutional Review Board of the Boston University Medical Center and by the Observational Studies Monitoring Board of the National Heart, Lung and Blood Institute.

Genotyping was conducted as part of the NHLBI Framingham SNP Health Association Resource (SHARe). This sub-study contains genotype data for approximately 550000 SNPs (Affymetrix 500K mapping arrays [Mapping250k_Nsp and Mapping250K_Sty] plus Affymetrix 50K supplemental human gene-focused array) in over 9200 FHS participants. Samples were chosen based on pedigree information and genotyping quality; Samples with a genotypic call rate below 95% were not chosen for analysis. The mean call rate for analyzed samples was 99.2% (SD=0.4%). Genotype data cleaning was carried-out in several steps. The final marker list contained 436,494 high-quality SNPs with a minor-allele frequency >= 0.01, a Mendelian error rate below 2% across all pedigrees, a genotype call rate above 95%, and whose distribution was consistent with Hardy-Weinberg expectations (P>0.0001). Genotype imputation to the HapMap-II reference panel (CEU population release 22, NCBI build 36) was carried out in a two-step process using the Markov Chain Haplotyping (MACH version 1.0.16.a) software. First, crossover and error-rate maps were built using 400 unrelated individuals (200 male and 200 female) sampled from FHS subjects. Second, genotype imputations of approximately 2.5 million autosomal HapMap-II SNPs were carried out on the entire FHS dataset using parameters estimated from step 1.

IOP Measuremements were taken using Goldmann Applanation Tonometry (GAT) or (rarely) using Schiotz tonometry in non-ambulatory participants. IOP was taken under topical anesthesia with one drop of a combined proparacaine and fluorescein ophthalmic solution. Only GAT measurements were considered in the analyses. IOP measurements were taken three times and

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each reading was rated as 'reliable' or 'unreliable' by the examiner. A detailed description of the IOP measurement procedure can be found in the original published FES protocol[12]. The protocol for the Framingham Offspring eye study in unavailable. This study also used GAT and the protocol appears to have been based on the original FES.

The final unilateral IOPs were coded as the mean of all reliable readings in each eye, in millimeters of mercury (mmHg). Unilateral IOPs were truncated (Winsorized) at 40 mmHg. The mean of both unilateral IOPs were used in the analyses. Individual eyes were excluded if: all readings were unreliable; there was a history or evidence of previous intraocular surgery (including cataract surgery); best-corrected monocular distance visual acuity was 20/200 or worse; and/or if stromal corneal opacities were present. In addition, one participant was excluded because of extreme IOP measurements (76 mmHg) which were subject to the range limitations of GAT.

Gutenberg Health Study (GHS I, GHS II)

The GHS is a population-based, prospective, observational cohort study in the Rhine-Main Region in midwestern Germany with a total of 15,010 participants and follow-up after five years. The study sample is recruited from subjects aged between 35 and 74 years at the time of the exam. The sample was drawn randomly from local governmental registry offices and stratified by gender, residence (urban and rural) and decade of age. Exclusion criteria were insufficient knowledge of the German language to understand explanations and instructions, and physical or psychic inability to participate in the examinations in the study center. The study was approved by the Medical Ethics Committee of the University Medical Center Mainz and by the local and federal data safety commissioners. According to the tenets of the Declaration of Helsinki, written informed consent was obtained from all participants prior to entering the study.
Within GHS, DNA was extracted from buffy-coats from EDTA blood samples as described in Zeller *et al*.[17]. Genetic analysis was conducted in the first 5,000 study participants. For these, 3,463 individuals were genotyped in 2008 (GHS I) and further 1,439 individuals in 2009 (GHS II). Genotyping was performed for GHS I and GHS II using the Affymetrix Genome-Wide Human SNP Array 6.0. Genotypes were called using the Affymetrix Birdseed-V2 calling algorithm. Individuals with a call rate below 97% or a too high autosomal heterozygosity (3 SD from mean) and sex-mismatches were excluded. After applying standard quality criteria (MAF >1%, genotype call rate >98% and *P*-value of deviation from HWE of $>10^{-4}$), 675,350 SNPs in 2750 individuals from GHS I and 673,914 SNPs in 1,143 individuals from GHS II remained for analysis. Imputation of missing genotypes was performed using IMPUTE software v2.1.0[18] and HapMap release 24, NCBI Build 36.
All participants underwent an ophthalmological investigation of 25 minutes' duration taking place between 11:00 a.m. and 8:00 p.m. The IOP measurement was performed with a non-contact tonometer with automatic airpuff control (Nidek NT-2000™, Nidek Co., Japan). The mean of three measurements within a range of 3 mmHg was obtained for each eye. Central corneal thickness was measured by optical pachymetry (Scheimpflug imaging with the Pachycam™, Oculus, Wetzlar, Germany*).* The measurement with the best quality (at least above 90%) per eye was selected for analysis.

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Orkney Complex Disease Study (ORCADES)

The Orkney Complex Disease Study (ORCADES) is a population-based, cross-sectional study in the Scottish archipelago of Orkney, including 1,285 individuals with eye measurements. The study received approval from relevant ethics committees in Scotland and followed the tenets of the Declaration of Helsinki. Informed consent and blood samples were provided by Orcadian volunteers.
IOP was measured with a tonopen.
Measures on eyes with a history of trauma were removed and the analysis was done on the average of both eye measures, or on one eye measure only when the fellow-eye measurement was missing. 474 individuals which had been genotyped and had IOP measurements were used in this analysis. Genome-wide association analysis was performed using the "mmscore" function of ProbABEL under an additive model for the SNP allelic effect. This score test for family based association takes into account relationship structure and allowed unbiased estimations of SNP allelic effect when relatedness is present between examinees. The relationship matrix used in this analysis was generated by the "ibs" function of GenABEL (using weight= "freq" option), which uses genomic data to estimate the realized pair-wise kinship coefficients.
Genotypes were generated using HumanHap 300v2 or 370CNV-Quad Illumina SNP arrays. Genotypes were determined using the Illumina BeadStudio software following the manufacturer's standard recommendations. Samples with a call rate below 97% (for SNPs with call rates above 98%, a minor allele frequency below 1% and p-value for Fisher's exact test of Hardy Weinberg equilibrium (HWE)>10-6), potentially mixed samples with excess autosomal heterozygosity or gender discrepancy (based on the genotyped sex chromosomes), and ethnic outliers (based on principal components analysis of genotypic data), were excluded from the analysis using the quality control algorithm implemented in GenABEL.
Principal components of ancestry were obtained by multidimentional scaling of the population-specific identity-by-state (IBS) derived distances matrix obtained using the ibs function in GenABEL.
Imputation of allele dosage for over 2 million SNPs on the 22 autosomal chromosomes with reference to HapMap CEU build 36 release 22 was performed using the software MACH v1.0.15.

RAINE (Western Australian Pregnancy Cohort 20 year follow up Eye Study)

The Western Australian Pregnancy Cohort (Raine) Study is an ongoing prospective cohort study of pregnancy, childhood, adolescence and young adulthood in Perth, Western Australia[19]. At the initiation of the study, 2,900 pregnant women were recruited at 16-18 weeks' gestation from the state's largest public women's hospital and surrounding private practices for a randomized clinical trial investigating effects of intensive ultrasound and Doppler studies in pregnancy outcomes. Following this study, the offspring of the recruited individuals have been evaluated in detail during childhood and adolescence. At the 20-year review of the cohort, Raine participants underwent a comprehensive ocular examination for the first time[20]. As part of this examination, IOP was measured using an Icare TAO1i Tonometer (Icare Finland Oy, Helsinki, Finland) and CCT was obtained from the Pupil Center Pachymetry readout obtained by anterior segment

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tomography of each dilated eye taken with an Oculus Pentacam (Optikgerate GmbH, Wetzlar, Germany). DNA samples and consents for GWAS studies were available from the previous assessments. Genotype data was generated using the genome-wide Illumina 660 Quad Array at the Centre for Applied Genomics (Toronto, Ontario, Canada). As part of quality control (QC), we investigated for any individuals who were related with a $\pi > 0.1875$ (second or third degree relatives) and excluded the individuals with the higher proportion of missing data. We also excluded people who had a high degree of missing genotyping data (> 3%). The data was filtered for a Hardy-Weinberg equilibrium p-value > 5.7x10-7, SNP call rate >95%, and a minor allele frequency >0.01. We performed the GWAS imputation in the MACH v1.0.16 (http://www.sph.umich.edu/csg/yli/mach/index.html) software using the CEU samples from HapMap phase2 build 36 release 22 (http://hapmap.ncbi.nlm.nih.gov/index.html.en). This study was approved by the Human Research Ethics Committee of the University of Western Australia. The study was conducted in accordance with the Declaration of Helsinki and informed consent was obtained from all participants.

Rotterdam Study (RS-I, RS-II, RS-III)

The Rotterdam Study is a prospective population-based cohort study in the elderly living in Ommoord, a suburb of Rotterdam, the Netherlands. Details of the study are described elsewhere[21]. In brief, the Rotterdam Study consists of 3 independent cohorts: RSI, RS-II, and RS-III. Participants underwent multiple physical examinations with regular intervals from 1991 to present. The IOP was measured with Goldmann applanation tonometry (Haag-Streit, Bern, Switzerland). IOP was measured twice per eye. If the two measurements in one eye differed, a third measurement was performed, and the median value was recorded. All measurements in RS-I, RS-II and RS-III were conducted after the Medical Ethics Committee of the Erasmus University had approved the study protocols and all participants had given a written informed consent in accordance with the Declaration of Helsinki.
DNA was extracted from blood leucocytes according to standard procedures. Genotyping of SNPs was performed using the Illumina Infinium II HumanHap550 chip v3.0 array (RS-I); the HumanHap550 Duo Arrays and the Illumina Human610-Quad Arrays (RS-II), and the Human 610 Quad Arrays Illumina (RS-III). Samples with low call rate (<97.5%), with excess autosomal heterozygosity (>0.336), or with sex-mismatch were excluded, as were outliers identified by the identity-by-state clustering analysis (outliers were defined as being >3 s.d. from population mean or having identity-by-state probabilities >97%). We used genomic control to obtain optimal and unbiased results and applied the inverse variance method of each effect size estimated for both autosomal SNPs that were genotyped and imputed in both cohorts. A set of genotyped input SNPs with call rate >98%, with minor allele frequency >0.01, and with Hardy-Weinberg P value $>10^{-6}$ was used for imputation. We used the Markov Chain Haplotyping (MACH) package version 1.0.15 software (Rotterdam, The Netherlands; imputed to plus strand of NCBI build 36, HapMap release #22) for the analyses. For each imputed SNP, a reliability of imputation was estimated as the ratio of the empirically observed dosage variance to the expected binomial dosage variance (O/E ratio). GWAS analyses were performed using GRIMP[22].

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Singapore cohorts (SIMES, SINDI, SCES)

Singapore Malay Eye Study (SiMES)

SiMES is a population-based prevalence survey of Malay adults aged 40 to 79 years living in Singapore that was conducted between August of 2004 and June of 2006[23]. From a Ministry of Home Affairs random sample of 16,069 Malay adults in the Southwestern area, an age-stratified random sampling strategy was used in selecting 1400 from each decade from age 40 years onward (40–49, 50–59, 60–69, and 70–79 years).The 4,168 eligible participants from the sampling frame, while 3280 (78.7%) participated. Genome-wide genotyping was performed in 3,072 individuals[24,25].

A total of 3,072 DNA samples were genotyped using the Illumina Human 610 Quad Beadchips[25,26]. Using the same quality control criteria, we omitted a total of 530 individuals including those of subpopulation structure (n=170), cryptic relatedness (n=279), excessive heterozygosity or high missingness rate > 5% (n=37), and gender discrepancy (n=44). After the removal of the samples, SNP QC was then applied on a total of 579,999 autosomal SNPs for the 2,542 post-QC samples. SNPs were excluded based on (i) high rates of missingness (> 5%) ; (ii) monomorphism or MAF < 1% ; or (iii) genotype frequencies deviated from HWE ($p < 1 \times 10^{-6}$).

Singapore Indian Eye Study (SINDI)

SINDI is a population-based survey of major eye diseases[27] in ethnic Indians aged 40 to 80 years living in the South-Western part of Singapore and was conducted from August 2007 to December 2009. In brief, 4,497 Indian adults were eligible and 3,400 participated. Genome-wide genotyping was performed in 2,953 individuals[26].

The Illumina Human610 Quad Beadchips was used for genotyping all DNA samples from SINDI (n=2,593). We excluded 415 subjects from the total of 2,953 genotyped samples based on: excessive heterozygosity or high missingness rate > 5% (n=34) , cryptic relatedness (n=326), issues with population structure ascertainment (n=39) and gender discrepancies (n=16). This left a total of 2,538 individuals with 579,999 autosomal SNPs. During SNP QC procedure. SNPs were excluded based on (i) high rates of missingness (> 5%) ; (ii) monomorphism or MAF < 1% ; or (iii) genotype frequencies deviated from HWE ($p < 1 \times 10^{-6}$).

Singapore Chinese Eye Study (SCES)

Similar to SINDI, the Singapore Chinese Eye Study (SCES) is a population-based cross-sectional study of eye diseases in Chinese adults 40 years of age or older residing in the southwestern part of Singapore. The methodology of the SCES study has been described in details previously. Between 2009 and 2011, 3,353 (72.8%) of 4,605 eligible individuals underwent a comprehensive ophthalmologic examination, using the same protocol as SINDI[23]. Genome-wide genotyping using was done in a subset of 1,952 SCES participants using Illumina Human610-Quad BeadChip[24] The same QC methods used for SiMES and SINDI were applied to the SCES genotyping samples: samples were excluded if they showed evidence of admixture, cryptic relatedness, high heterogeneity and gender discrepancies. From a starting number of 1,952 individuals, three samples had per-sample call rate of <95% and were removed from analysis. A total of 21 individuals showed evidence of admixture and were consequently excluded. Biological relationship verification revealed a total of 29 sample pairs with cryptic relatedness. For these, the sample with the lower call rate was removed. In addition, further 14

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samples with impossible biological sharing or heterogeneity, probably because of contamination, were removed, as well as two individuals who were removed due to gender discrepancies. PC analysis of the remaining individuals for SCES against the HapMap CHB (Han Chinese) reference populations did not show the cohort to be dissimilar in ancestry, and therefore no PCs were used to correct for any underlying population substructure in the analysis performed. After phenotype and genotype QC, 1,723 individuals were left for the analysis.

All three studies (SiMES, SINDI and SCES) adhere to the Declaration of Helsinki. Ethics approvals have been obtained from the Institutional Review Boards of the Singapore Eye Research Institute, Singapore General hospital, National University of Singapore and National Healthcare Group, Singapore. In all cohorts, participants provided written, informed consent at the recruitment into the studies.

TwinsUK

For this analysis, 2774 participants (95% female and all of Caucasian ancestry) within the TwinsUK adult twin registry based at St. Thomas' Hospital in London were analyzed for whom both genotype and IOP information was available. Twins largely volunteered unaware of the eye studies interests at the time of enrolment and gave fully informed consent under a protocol reviewed by the St. Thomas' Hospital Local Research Ethics Committee. Exclusion criteria included any form of glaucoma surgery such as trabeculectomy or laser surgery that could alter IOP.

We measured IOP with a non-contact air-puff tonometer. The Ocular Response Analyser (ORA, Reichert®, Buffalo, NY) ejects an air impulse in order to flatten the cornea, which is detected by an electro-optical collimation system. The mean IOP was calculated from 4 readings (2 from each eye) for each participant. IOP for subjects receiving IOP-lowering medications (26 out of 2774) was imputed by increasing the measured value by 30%, based on efficacy data from commonly prescribed therapies. CCT was measured using an ultrasound pachymetry device provided with the ORA instrument.

Subjects were genotyped in two different batches of approximately the same size, using two genotyping platforms from Illumina: 300K Duo for and HumanHap610-Quad arrays. Whole genome imputation of the genotypes was performed using HapMap2 (www.hapmap.org) haplotypes.

Stringent quality control (QC) measures were implemented, including minimum genotyping success rate (>95%), Hardy-Weinberg equilibrium ($P>10^{-6}$), minimum MAF (>1%) and imputation quality score (>0.7). Subjects of non Caucasian ancestry were excluded from the analysis.

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POAG case-control cohorts

ANZRAG

The Australian & New Zealand Registry of Advanced Glaucoma (ANZRAG) recruits cases of advanced glaucoma Australia-wide through ophthalmologist referral. The cohort also included participants enrolled in the Glaucoma Inheritance Study in Tasmania (GIST) that met the criteria for ANZRAG. This case cohort has been previously described[28]. Advanced Primary Open Angle Glaucoma was defined as best-corrected visual acuity worse than 6/60 due to primary open angle glaucoma, or a reliable 24-2 Visual Field with a mean deviation of worse than -22db or at least 2 out of 4 central fixation squares affected with a Pattern Standard Deviation of < 0.5%. The less severely affected eye was also required to have signs of glaucomatous disc damage. Worst ever recorded intraocular pressure was obtained from the patient's medical record. Due to the advanced nature of the glaucoma, all participants were on medical treatment to lower intraocular pressure and/or had undergone surgery for the same. Clinical exclusion criteria included: i) pseudoexfoliation or pigmentary glaucoma; ii) angle closure or mixed mechanism glaucoma; iii) secondary glaucoma due to aphakia, rubella, rubeosis or inflammation; iv) infantile glaucoma, v) glaucoma in the presence of a known associated syndrome vii) mutation in the MYOC gene (by direct sequencing of exon 3). All participants provided written informed consent. Approval was obtained from the Human Research Ethics Committees of Southern Adelaide Health Service/Flinders University, University of Tasmania and Royal Victorian Eye and Ear Hospital. DNA extracted from peripheral whole blood was genotyped on Illumina Human1M-Omni or OmniExpress arrays. SNPs with a mean BeadStudio GenCall score <0.7 were excluded. All samples had successful genotypes for >95% of SNPs. Controls used for this analysis were historic, primarily unexamined controls, from several sources. The Blue Mountains Eye Study (described above) were included. Known cases of glaucoma were excluded from this dataset. Additional controls from the Wellcome Trust Case Control Consortium 1958 British Birth Cohort genotyped on Illumina arrays and Caucasian samples from the Illumina iControl datasets were utilized. Data were downloaded from each source with appropriate permissions and merged with the other control and case data to generate a panel of SNPs common to all arrays utilized. SNPs with call rates <0.90, Hardy-Weinberg equilibrium in controls $P<10^{-6}$, and/or MAF <0.01 were excluded. Cryptic relatedness was identified through the production of a full identity by state matrix and first degree relatives removed. Ancestry outliers were identified by principal component (PC) analysis using the EIGENSOFT package. Individuals lying ≥ 6 standard deviations from the mean PC1 and PC2 scores were removed. Following this data cleaning, 1090 cases, 7173 controls were included in the final analysis. Imputation was calculated with reference to HapMap release 22 CEU using MACH. Association analysis was conducted in PLINK.

deCode

The Icelandic primary open angle glaucoma (POAG) cases were identified from a list of participants in the Reykjavik Eye Study[29] and from a list compiled by Icelandic

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ophthalmologists in 2008 that included patients 55-86 years old at the time of diagnosis, all meeting either structural (glaucomatous optic neuropathy) or functional (glaucomatous visual field defects) criteria of glaucoma or both. For visual fields measurements, Octopus 123 perimeter (Haag-Streit AG, Koniz Switzerland) was used. Intra ocular pressure (IOP) was not a part of the definition. On gonioscopy the angles were found to be open and normal in appearance. The combined list includes 598 individuals, 290 men and 308 women with POAG. The diagnosis of exfoliation syndrome (XFS) was specifically evaluated and if detected the participant was excluded from the study. The control group included 98,670 Icelandic individuals without know history of glaucoma. 533 of the POAG samples and 85,689 of the controls samples were assayed with the Illumina HumanHap300, HumanCNV370, HumanHap610, HumanHap1M, HumanHap660, Omni-1, Omni 2.5 or Omni Express bead chips at deCODE genetics and genotypes for about 34 million sequence variants were imputed into the chip typed individuals based on a training set of 2,230 whole genome sequenced Icelanders using methods previously described [30]. The case-control association analysis was done on the imputed genotypes, including in addition 65 cases and 12,981controls that were not chip typed but for which genotype probabilities were imputed using methods of familial imputation. For the risk score analysis only chip typed individuals were used. The study was approved by the Icelandic National Bioethics Committee and by the Icelandic Data Protection Authority. Informed consent was obtained from all participants. The study was conducted in accordance with revised Declaration of Helsinki.

MEEI

491 cases and 351 controls collected from the Massachusetts Eye and Ear Infirmary glaucoma clinic and comprehensive ophthalmology clinics were recruited for this study. All cases and controls were residents of the continental United States and were of mainly European ancestry, which was confirmed by both self-identification and genetic markers. All participants gave informed and formal consent prior to enrollment. The institutional review boards of the Massachusetts Eye and Ear Infirmary, Harvard School of Public Health, the Brigham and Women's Hospital, University of Pittsburgh, Johns Hopkins University, Duke University, University of West Virginia, University of Miami, University of Michigan, Stanford University, Marshfield Clinic, and the University of California, San Diego approved the MEEI and NEIGHBOR studies.
Primary open angle glaucoma (POAG) cases were defined as individuals for whom reliable visual field (VF) tests show characteristic VF defects consistent with glaucomatous optic neuropathy. Individuals were classified as affected if the VF defects were reproduced on a subsequent test or if a single qualifying VF was accompanied by a cup-disc ratio (CDR) of 0.7 or more in at least one eye. The examination of the ocular anterior segment did not show signs of secondary causes for elevated IOP such as exfoliation syndrome or pigment dispersion syndrome and the filtration structures were deemed to be open based on clinical measures. Elevation of IOP was not a criterion for inclusion; however, 67% of cases did have a history of elevated IOP (≥22 mm Hg) measured in a clinical setting (typically between the hours of 8AM and 5PM) and were classified as high-pressure glaucoma (HPG).
Genotyping was performed using the Illumina Human660W_Quad_v1 array and 495,132 SNPs passed quality control filters. Illumina‟s BeadStudio and GenomeStudio and Autocall software

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along with genotype cluster definitions based on study samples were used to generate genotyping calls. SNPs with a GenTrain score <0.6, cluster separation score <0.4 and call rate <97% were considered technical failures at the genotyping center and were automatically deleted before release for further quality control. Subsequent data quality control measures consisted of identifying and removing samples with gender misidentification, unexpected duplicates and unexpected relatedness. Analysis of connectivity removed samples that appeared to be related to other samples and/or suggestive of contamination. Any SNP with missing call rate >2% or with Hardy Weinberg p-value < 10-4 in the control population was excluded. Imputation was performed with IMPUTE2 using the March 2012 1000 genomes as a reference panel.

Logistic regression using a model included age, gender, DNA source, DNA extraction method and 3 eigenvectors (EV1, 2 and 6) was to assess the association between individual SNPs and POAG was done using PLINK v1.07.

NEIGHBOR

2,170 cases and 2,347 controls collected from 12 sites throughout the United States were genotyped for the NEIGHBOR study. All participants gave informed formal consent prior to enrollment and ethical approval was obtained as specified above for the MEEI cohort. Primary open angle glaucoma (POAG) cases were defined as individuals for whom reliable visual field (VF) tests show characteristic VF defects consistent with glaucomatous optic neuropathy. Individuals were classified as affected if the VF defects were reproduced on a subsequent test or if a single qualifying VF was accompanied by a cup-disc ratio (CDR) of 0.7 or more in at least one eye. The examination of the ocular anterior segment did not show signs of secondary causes for elevated IOP such as exfoliation syndrome or pigment dispersion syndrome and the filtration structures were deemed to be open based on clinical measures. Elevation of IOP was not a criterion for inclusion; however, 67% of cases did have a history of elevated IOP (≥22 mm Hg) measured in a clinical setting (typically between the hours of 8AM and 5PM) and were classified as high-pressure glaucoma (HPG).
Genotyping was performed using the Illumina Human660W_Quad_v1 array and 523,528 SNPs passed quality control filters. Allele cluster definitions for each SNP were determined using Illumina GenomeStudio Genotyping Module version 1.7.4, GenTrain version 1.0 and the combined intensity data from 99.9% of the samples. The resulting cluster definitions were used on all samples. Genotypes were not called if the quality threshold (Gencall score) was below 0.15. Genotypes were released by CIDR for 557,029 SNPs (99.58% of attempted). Genotypes were not released for SNPs that had call rates less than 85%, more than 1 HapMap replicate error, cluster separation less than 0.2, more than a 3% (autosomal) or 2.2% (X chromosome) difference in call rate between genders, more than 0.4% (X chromosome) male heterozygosity, or more than a 8% (autosomal) difference in AB frequency.
Imputation was performed with IMPUTE2 using the March 2012 1000 genomes as a reference panel.
Logistic regression using a model included age, gender, study site and 2 eigenvectors (EV1 and 2) was to assess the association between individual SNPs and POAG was done using PLINK v1.07

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ALIENOR

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ANZRAG

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Beijing Eye Study

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BATS/TEST

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deCode

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References:

1. Young, T. *et al.* Whole Genome Expression Profiling of Normal Human Fetal and Adult Ocular Tissues. *Experimental Eye Research* **http://dx.doi.org/10.1016/j.exer.2013.08.009**(2013).
2. Wagner, A.H. *et al.* Exon-level expression profiling of ocular tissues. *Exp Eye Res* **111**, 105-11 (2013).
3. Bowes Rickman, C. *et al.* Defining the human macula transcriptome and candidate retinal disease genes using EyeSAGE. *Invest Ophthalmol Vis Sci* **47**, 2305-16 (2006).
4. Liu, Y. *et al.* Serial analysis of gene expression (SAGE) in normal human trabecular meshwork. *Mol Vis* **17**, 885-93 (2011).
5. The International HapMap Project. *Nature* **426**, 789-96 (2003).
6. Pruim, R.J. *et al.* LocusZoom: regional visualization of genome-wide association scan results. *Bioinformatics* **26**, 2336-7 (2010).
7. Delcourt, C. *et al.* Nutrition and age-related eye diseases: the Alienor (Antioxydants, Lipides Essentiels, Nutrition et maladies OculaiRes) Study. *J Nutr Health Aging* **14**, 854-61 (2010).
8. Vascular factors and risk of dementia: design of the Three-City Study and baseline characteristics of the study population. *Neuroepidemiology* **22**, 316-25 (2003).
9. Mackey, D.A. *et al.* Twins eye study in Tasmania (TEST): rationale and methodology to recruit and examine twins. *Twin Res Hum Genet* **12**, 441-54 (2009).
10. Xu, L. *et al.* Intraocular pressure in Northern China in an urban and rural population: the Beijing eye study. *Am J Ophthalmol* **140**, 913-5 (2005).
11. Cornes, B.K. *et al.* Identification of four novel variants that influence central corneal thickness in multi-ethnic Asian populations. *Human molecular genetics* **21**, 437-45 (2012).
12. Xu, L., Zhang, H., Wang, Y.X. & Jonas, J.B. Central corneal thickness and glaucoma in adult Chinese: the Beijing Eye Study. *J Glaucoma* **17**, 647-53 (2008).
13. Marchini, J., Howie, B., Myers, S., McVean, G. & Donnelly, P. A new multipoint method for genome-wide association studies by imputation of genotypes. *Nat Genet* **39**, 906-13 (2007).
14. Aulchenko, Y.S. *et al.* Linkage disequilibrium in young genetically isolated Dutch population. *Eur J Hum Genet* **12**, 527-34 (2004).
15. Pardo, L.M., MacKay, I., Oostra, B., van Duijn, C.M. & Aulchenko, Y.S. The effect of genetic drift in a young genetically isolated population. *Ann Hum Genet* **69**, 288-95 (2005).
16. Leibowitz, H.M. *et al.* The Framingham Eye Study monograph: An ophthalmological and epidemiological study of cataract, glaucoma, diabetic retinopathy, macular degeneration, and visual acuity in a general population of 2631 adults, 1973-1975. *Surv Ophthalmol* **24**, 335-610 (1980).
17. Zeller, T. *et al.* Genetics and beyond--the transcriptome of human monocytes and disease susceptibility. *PLoS One* **5**, e10693 (2010).
18. Howie, B.N., Donnelly, P. & Marchini, J. A flexible and accurate genotype imputation method for the next generation of genome-wide association studies. *PLoS Genet* **5**, e1000529 (2009).

19. McKnight, C.M. *et al.* Birth of a cohort--the first 20 years of the Raine study. *Med J Aust* **197**, 608-10 (2012).
20. Yazar, S. *et al.* Raine Eye Health Study: Design, Methodology and Baseline Prevalence of Ophthalmic Disease in a Birth-cohort Study of Young Adults. *Ophthalmic Genet* (2013).
21. Hofman, A. *et al.* The Rotterdam Study: 2012 objectives and design update. *Eur J Epidemiol* **26**, 657-86 (2011).
22. Estrada, K. *et al.* GRIMP: a web- and grid-based tool for high-speed analysis of large-scale genome-wide association using imputed data. *Bioinformatics* **25**, 2750-2 (2009).
23. Foong, A.W. *et al.* Rationale and methodology for a population-based study of eye diseases in Malay people: The Singapore Malay eye study (SiMES). *Ophthalmic Epidemiol* **14**, 25-35 (2007).
24. Cornes, B.K. *et al.* Identification of four novel variants that influence central corneal thickness in multi-ethnic Asian populations. *Hum Mol Genet* **21**, 437-45 (2012).
25. Vithana, E.N. *et al.* Collagen-related genes influence the glaucoma risk factor, central corneal thickness. *Hum Mol Genet* **20**, 649-58 (2011).
26. Khor, C.C. *et al.* Genome-wide association studies in Asians confirm the involvement of ATOH7 and TGFBR3, and further identify CARD10 as a novel locus influencing optic disc area. *Hum Mol Genet* **20**, 1864-72 (2011).
27. Lavanya, R. *et al.* Methodology of the Singapore Indian Chinese Cohort (SICC) eye study: quantifying ethnic variations in the epidemiology of eye diseases in Asians. *Ophthalmic Epidemiol* **16**, 325-36 (2009).
28. Burdon, K.P. *et al.* Genome-wide association study identifies susceptibility loci for open angle glaucoma at TMCO1 and CDKN2B-AS1. *Nat Genet* **43**, 574-8 (2011).
29. Jonasson, F. *et al.* Prevalence of open-angle glaucoma in Iceland: Reykjavik Eye Study. *Eye (Lond)* **17**, 747-53 (2003).
30. Styrkarsdottir, U. *et al.* Nonsense mutation in the LGR4 gene is associated with several human diseases and other traits. *Nature* **497**, 517-20 (2013).