

AMP-DCC Data Analysis Report

NUS

Phase 2

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This document was generated using Loamstream [18] and the AMP-DCC Data Analysis Pipeline [19]

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1 Data

In order to run the data we received through our analysis pipeline in an efficient manner, the genotype arrays were each given a short code name; DCSP21M, DCSP2610K, LBCHS, LBMAS, SCES, SIMES, and SINDI. In Table 1, we list the corresponding filename of the data set we received, the format of the file set (*note: 'bfile' refers to binary Plink format [1]*), and a liftOver [2] chain file if it was required to remap the variants to GRCh37 / hg19 coordinates.

See Figures 1 and 2 for intersection counts of samples and variants available for analysis. The counts for each genotype array have been broken down by inferred ancestry as well.

Table 1: Genotype array information

ID	Filename	Format	LiftOver
DCSP21M	DC_SP2-1M	bfile	N/A
DCSP2610K	DC_SP2-610	bfile	N/A
LBCHS	living_biobank-CHS.array.1263samples	bfile	N/A
LBMAS	living_biobank-MAS.array.1189samples	bfile	N/A
SCES	SCES-610	bfile	N/A
SIMES	SiMES	bfile	N/A
SINDI	SINDI	bfile	N/A

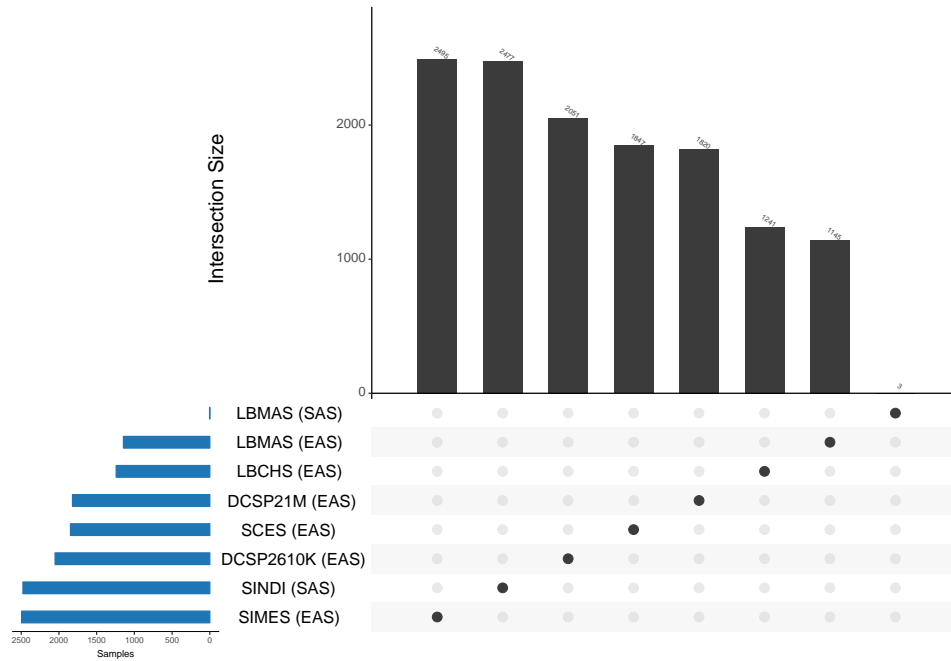


Figure 1: Samples remaining for analysis after quality control

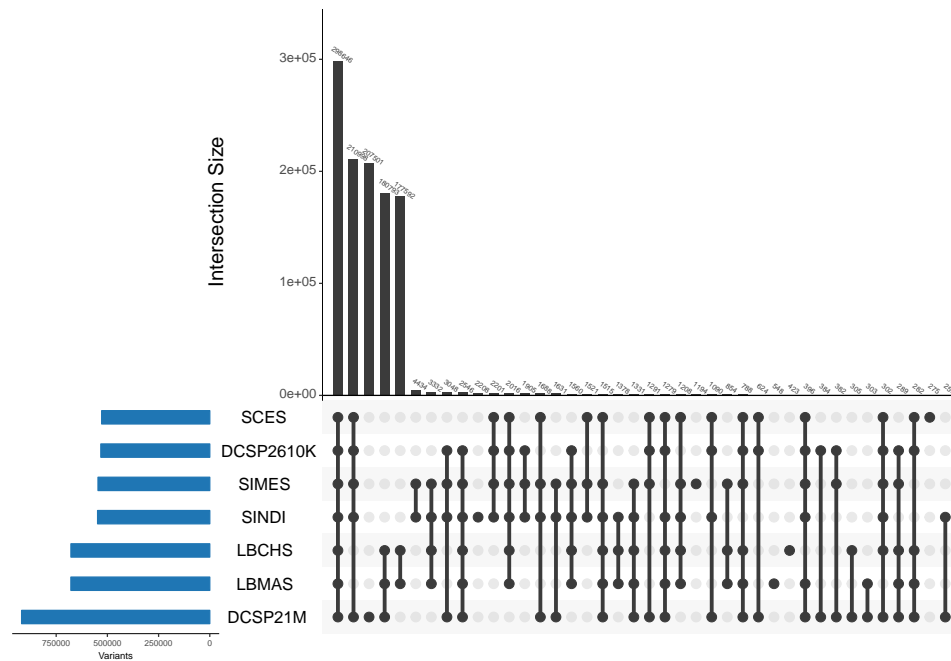


Figure 2: Variants remaining for analysis after quality control

2 Strategy

2.1 Sample structure and pipeline

The strategy we used to perform association testing can be found below. The 'ID' columns are the names used to identify each set of association test results in this document. The 'Report' columns indicate whether or not that particular set of association results will be presented in the tables and plots of the proceeding sections.

2.1.1 Cohort-level analysis

In Table 2, all of the cohorts available for analysis are defined. Each cohort was defined by a single array and one or more ancestral populations.

Table 2: Cohort-level analysis

ID	Array	Ancestry	Report
DCSP21M_EAS	DCSP21M	EAS	NO
DCSP2610K_EAS	DCSP2610K	EAS	NO
LBCHS_EAS	LBCHS	EAS	NO
LBMAS_EAS	LBMAS	EAS	NO
SCES_EAS	SCES	EAS	NO
SIMES_EAS	SIMES	EAS	NO
SINDI_SAS	SINDI	SAS	NO

2.1.2 Meta-analysis

Table 3 defines any meta-analyses performed on the cohorts. Each cohort that was included is detailed along with the number of samples removed prior to cohort-level association testing. In order to identify samples that needed to be removed due to relatedness across cohorts, the cohorts genotypes were first merged on common variants. Then, autosomal variants with $MAF \geq 0.01$ and $callrate \geq 0.98$ were extracted and kinship values were calculated using King [4] with the '--kinship' flag. The reference cohort, the first one listed, maintained all of its samples. Starting from the last listed cohort, any samples shown to have some relation ($kinship \geq 0.0884$) to a sample from any preceding cohort was removed. This was continued until all cohorts subsequent to the reference cohort had been processed.

Table 3: Meta-analysis

ID	Cohort	KinshipRemove	Report
META_NOLB			YES
	DCSP21M_EAS	0	
	DCSP2610K_EAS	0	
	SCES_EAS	78	
	SIMES_EAS	1	
	SINDI_SAS	9	
META_NOSEED			YES
	DCSP21M_EAS	0	
	DCSP2610K_EAS	0	
	LBCHS_EAS	53	
	LBMAS_EAS	5	
META_DCSP2			YES
	DCSP21M_EAS	0	
	DCSP2610K_EAS	0	
META			YES
	DCSP21M_EAS	0	
	DCSP2610K_EAS	0	
	LBCHS_EAS	53	
	LBMAS_EAS	5	
	SCES_EAS	93	
	SIMES_EAS	162	
	SINDI_SAS	15	

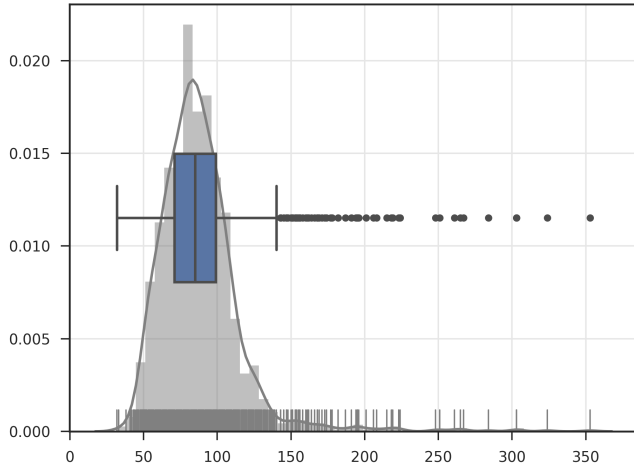
2.2 Ancestry Adjustment and Outlier Removal

Adjusting the statistical models for underlying ancestry is often crucial to reduce or eliminate Type 1 error. Often analysts include principal components of ancestry as covariates in their models as a matter of convention. In our case, we undertook a more nuanced approach. First, the top 10 PC's were calculated for each cohort using the PC-AiR method [3]. Then, the phenotype of interest was regressed on the covariates to be used in the model and all of the PC's. If the N th PC exhibited a statistically significant p -value ($p \leq 0.05$), we selected PC's $1 - N$ to be included in association testing. Once determined, any sample lying outside 6 standard deviations from the mean on any of the N PC's was marked as an outlier and removed from the sample set. This process

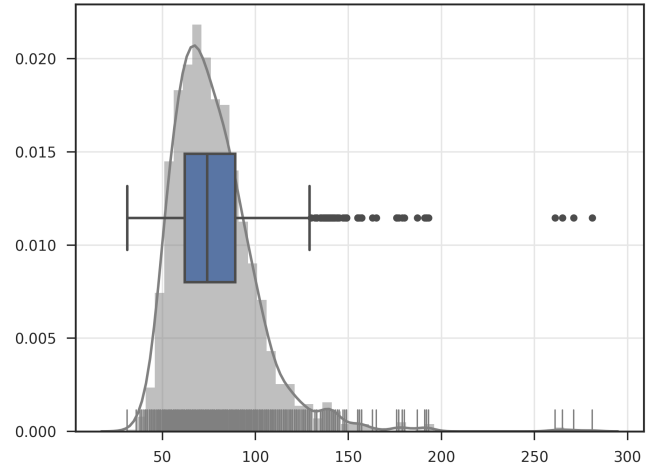
was repeated up to a maximum of ten times until no outliers were found, resulting in more homogeneous sample sets for each particular analysis. For this project, a hard minimum of 0 PC's to be included in analysis was set by the analyst.

3 Serum Creatinine (SERUM_CREATININE)

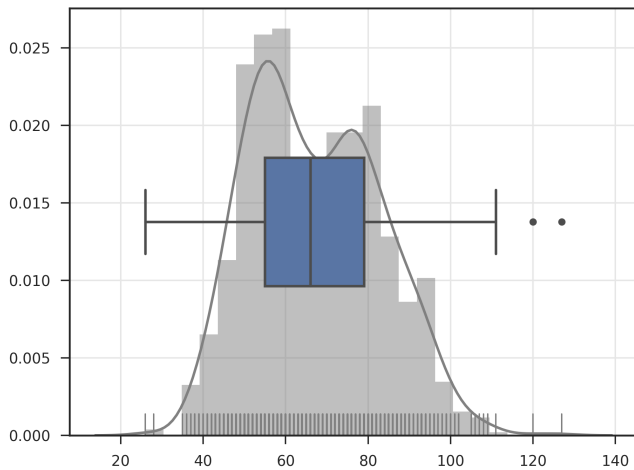
3.1 Summary



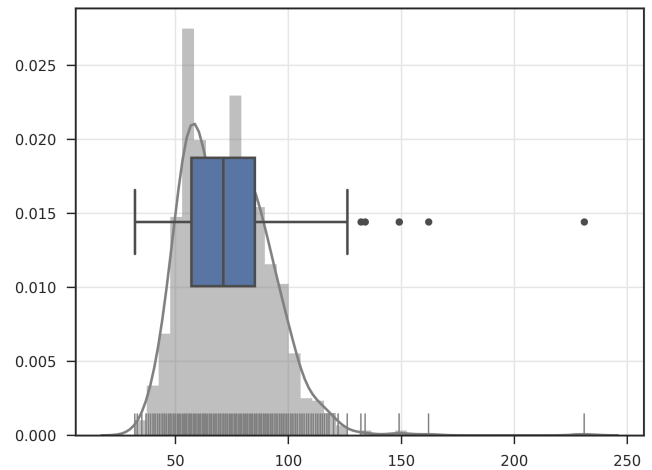
(a) DCSP21M_EAS



(b) DCSP2610K_EAS



(c) LBCHS_EAS



(d) LBMAS_EAS

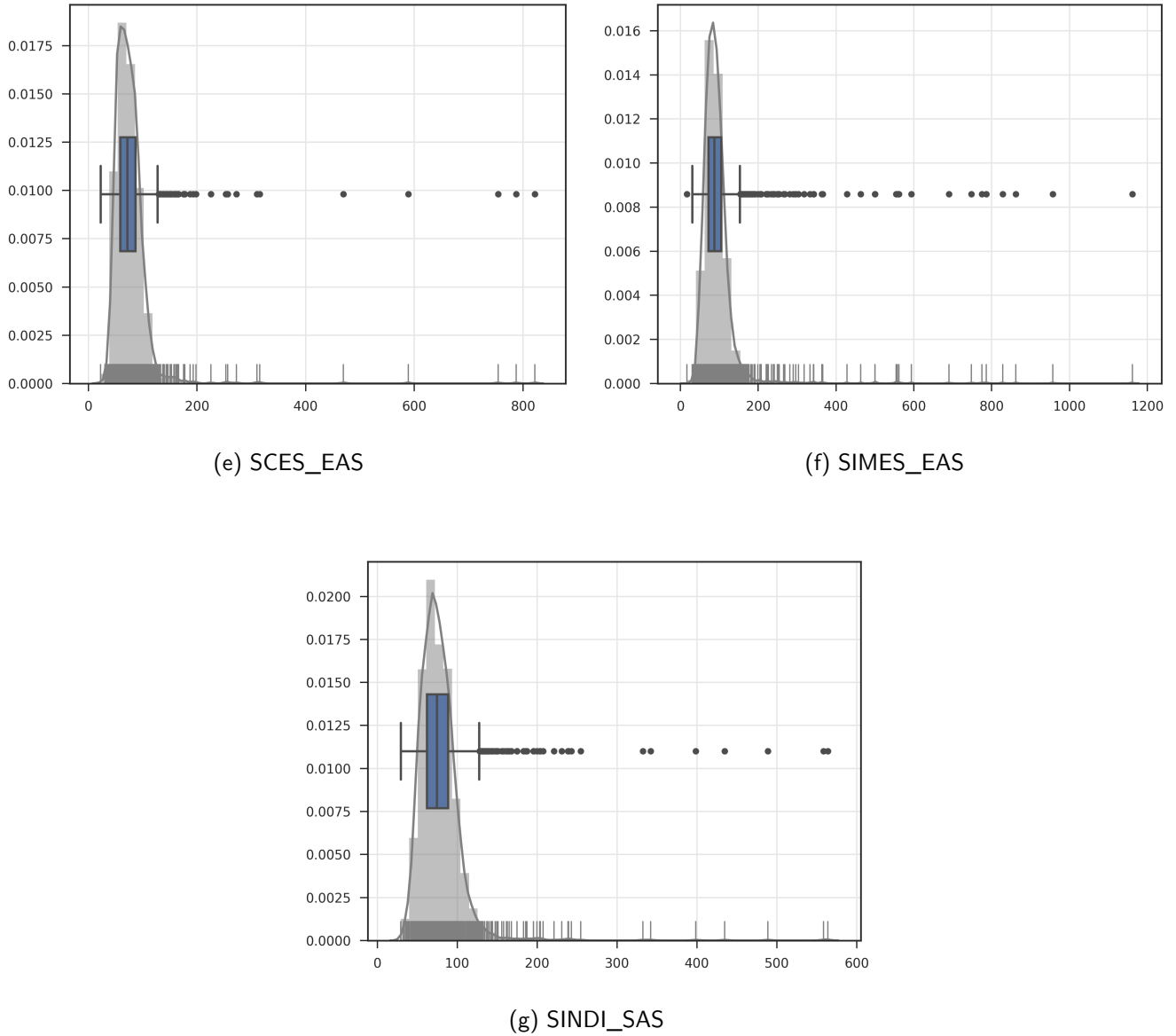


Figure 3: Distribution of SERUM_CREATININE in META by cohort

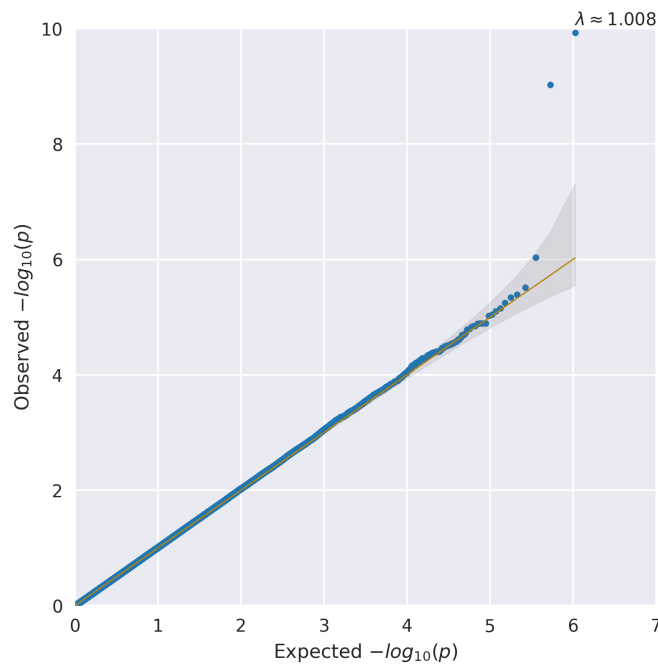
Table 4: Summary of samples removed from Serum Creatinine analysis by cohort and model

Cohort	Array	Ancestry	Trans	Covars	Total	-SampleQc	-KinshipCrossArray	-KinshipArray	-missObs	-PcOutlier
META DCSP21M_EAS	DCSP21M	EAS	invn	Age+SEX	1864	44	0	0	25	0
META DCSP2610K_EAS	DCSP2610K	EAS	invn	Age+SEX	2087	36	0	0	8	0
META LBCHS_EAS	LBCHS	EAS	invn	Age+SEX	1263	22	52	122	0	0
META LBMAS_EAS	LBMAS	EAS	invn	Age+SEX	1185	40	5	240	0	23
META SCES_EAS	SCES	EAS	invn	Age+SEX	1889	42	93	2	2	0
META SIMES_EAS	SIMES	EAS	invn	Age+SEX	2542	47	160	115	0	0
META SINDI_SAS	SINDI	SAS	invn	Age+SEX	2537	60	15	91	1	93

Table 5: Summary of samples remaining for Serum Creatinine analysis by cohort and model

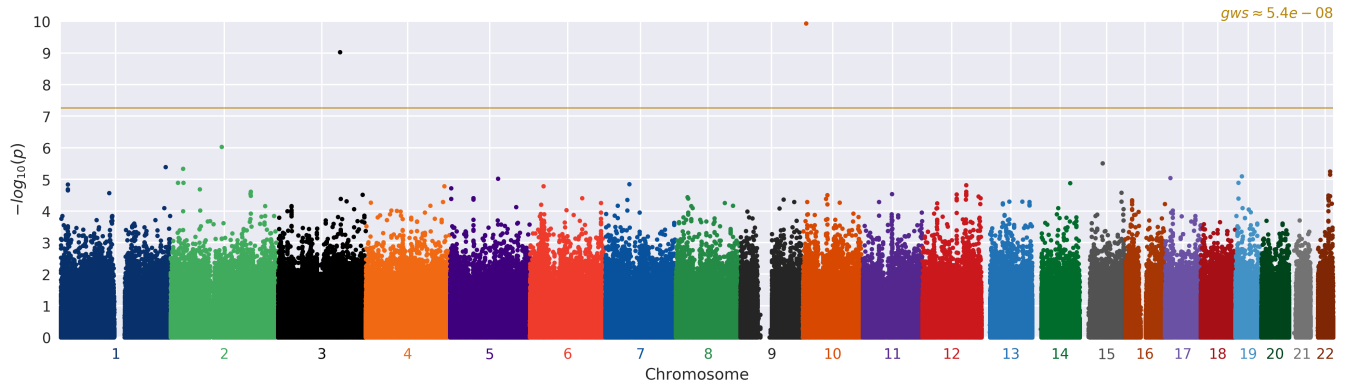
Cohort	Array	Ancestry	Trans	Covars	PCs	N	Male	Female	Max	Min	μ	\bar{x}	σ
META DCSP21M_EAS	DCSP21M	EAS	invn	Age+SEX	0	1795	1154	641	353.0	32.0	87.964	85.0	28.324
META DCSP2610K_EAS	DCSP2610K	EAS	invn	Age+SEX	0	2043	603	1440	281.0	31.0	78.039	74.0	23.493
META LBCHS_EAS	LBCHS	EAS	invn	Age+SEX	0	1067	531	536	127.0	26.0	67.158	66.0	15.633
META LBMAS_EAS	LBMAS	EAS	invn	Age+SEX	0	877	444	433	231.0	32.0	72.869	72.0	19.58
META SCES_EAS	SCES	EAS	invn	Age+SEX	0	1750	893	857	822.1	22.1	76.323	71.6	41.221
META SIMES_EAS	SIMES	EAS	invn	Age+SEX	0	2220	1117	1103	1161.6	16.8	95.006	86.6	59.73
META SINDI_SAS	SINDI	SAS	invn	Age+SEX	0	2277	1159	1118	564.0	29.2	77.695	74.3	30.382

3.2 Calibration



(a) invn Adjusted Age+SEX

Figure 4: QQ plots for SERUM_CREATININE in the META analysis



(a) invn Adjusted Age+SEX

Figure 5: Manhattan plots for SERUM_CREATININE in the META analysis

3.3 Top associations

Table 6: Top variants in the META invn Adjusted Age+SEX model (**bold** variants indicate previously identified associations)

CHR	POS	ID	EA	OA	GENE _{CLOSEST}	DIR	N	MALE	FEMALE	FREQ _{AVG}	FREQ _{MIN}	FREQ _{MAX}	EFFECT	STDERR	OR	ZSCORE	P
10	7401381	rs11255087	G	A	SFMBT2	xxxx+x	2,203	1,105	1,098	$2.18 \cdot 10^{-2}$	$2.18 \cdot 10^{-2}$	$2.18 \cdot 10^{-2}$	0.666	0.103	1.947	6.443	$1.17 \cdot 10^{-10}$
3	140253715	rs10513120	C	T	CLSTN2	xxxx+x	2,183	1,096	1,087	$2.22 \cdot 10^{-2}$	$2.22 \cdot 10^{-2}$	$2.22 \cdot 10^{-2}$	0.63	0.103	1.879	6.12	$9.37 \cdot 10^{-10}$
2	115305711	rs1430112	A	G	DPP10	++x+xxx	3,739	2,129	1,610	0.321	0.294	0.375	0.121	$2.46 \cdot 10^{-2}$	1.128	-4.905	$9.34 \cdot 10^{-7}$
15	51675625	rs2445738	C	T	GLDN	++xx+++	10,082	4,924	5,158	0.496	0.472	0.529	$6.56 \cdot 10^{-2}$	$1.41 \cdot 10^{-2}$	1.068	-4.665	$3.08 \cdot 10^{-6}$
1	237414375	rs888439	T	C	RYR2	++x+xxx	3,738	2,129	1,609	0.276	0.267	0.281	0.117	$2.55 \cdot 10^{-2}$	1.125	-4.607	$4.09 \cdot 10^{-6}$
2	27730940	rs1260326	C	T	GCKR	+++++++	12,028	5,901	6,127	0.594	0.512	0.798	$6.14 \cdot 10^{-2}$	$1.34 \cdot 10^{-2}$	1.063	4.583	$4.59 \cdot 10^{-6}$
22	44257056	rs8138048	A	G	SULT4A1	++x+xxx	3,739	2,129	1,610	$8.02 \cdot 10^{-3}$	$7.8 \cdot 10^{-3}$	$8.55 \cdot 10^{-3}$	0.589	0.13	1.803	-4.54	$5.62 \cdot 10^{-6}$
22	44276544	rs12485136	G	A	PNPLA5	++x+xxx	3,736	2,126	1,610	$8.3 \cdot 10^{-3}$	$7.99 \cdot 10^{-3}$	$8.55 \cdot 10^{-3}$	0.574	0.128	1.775	-4.492	$7.07 \cdot 10^{-6}$
19	15079104	rs11668879	A	G	SLC1A6	+xxxxxx	1,795	1,154	641	0.106	0.106	0.106	0.245	$5.48 \cdot 10^{-2}$	1.277	4.466	$7.96 \cdot 10^{-6}$
17	12394980	rs171084	G	A	MYOCD	++xx+++	10,080	4,925	5,155	$9.64 \cdot 10^{-2}$	$8.74 \cdot 10^{-2}$	0.102	0.106	$2.39 \cdot 10^{-2}$	1.112	4.438	$9.1 \cdot 10^{-6}$
5	108244804	rs10515395	T	C	FER	-xxx++	8,040	4,323	3,717	$2.1 \cdot 10^{-2}$	$2.79 \cdot 10^{-4}$	$6.28 \cdot 10^{-2}$	0.247	$5.58 \cdot 10^{-2}$	1.28	-4.429	$9.47 \cdot 10^{-6}$
2	28557080	rs1565326	T	C	BRE	++xx+++	10,080	4,923	5,157	0.95	0.869	0.978	0.144	$3.29 \cdot 10^{-2}$	1.155	4.365	$1.27 \cdot 10^{-5}$
2	16154226	rs13419529	T	C	MYCN	++xx+++	10,079	4,921	5,158	$9.29 \cdot 10^{-2}$	$6.49 \cdot 10^{-2}$	0.161	0.107	$2.45 \cdot 10^{-2}$	1.113	4.364	$1.28 \cdot 10^{-5}$
19	7547074	rs2303146	C	A	PEX11G	+++++++	12,023	5,898	6,125	0.411	0.376	0.494	$5.73 \cdot 10^{-2}$	$1.31 \cdot 10^{-2}$	1.059	4.363	$1.28 \cdot 10^{-5}$
14	85747008	rs17796723	A	G	FLRT2	+xxxxxx	1,795	1,154	641	0.267	0.267	0.267	0.163	$3.74 \cdot 10^{-2}$	1.177	-4.36	$1.3 \cdot 10^{-5}$
7	54394095	rs10253714	T	G	VSTM2A	++x+xxx	3,739	2,129	1,610	$9.03 \cdot 10^{-2}$	$7.72 \cdot 10^{-2}$	0.117	0.174	$4.01 \cdot 10^{-2}$	1.19	4.342	$1.42 \cdot 10^{-5}$
1	16277647	rs848189	T	C	ZBTB17	+++++++	12,024	5,898	6,126	0.179	0.139	0.212	$7.3 \cdot 10^{-2}$	$1.68 \cdot 10^{-2}$	1.076	4.339	$1.43 \cdot 10^{-5}$
12	98899329	rs4762492	A	C	TMPO	+++++++	12,012	5,890	6,122	0.464	0.208	0.559	$5.75 \cdot 10^{-2}$	$1.33 \cdot 10^{-2}$	1.059	4.326	$1.52 \cdot 10^{-5}$
4	178027773	rs2580061	C	T	NEIL3	++xx+++	10,085	4,926	5,159	0.206	0.114	0.444	$7.94 \cdot 10^{-2}$	$1.84 \cdot 10^{-2}$	1.083	-4.311	$1.62 \cdot 10^{-5}$
6	30931844	rs3131934	T	C	SFTA2	++x+xxx	3,738	2,128	1,610	$9.34 \cdot 10^{-2}$	$6.44 \cdot 10^{-2}$	0.181	0.171	$3.97 \cdot 10^{-2}$	1.186	-4.308	$1.65 \cdot 10^{-5}$

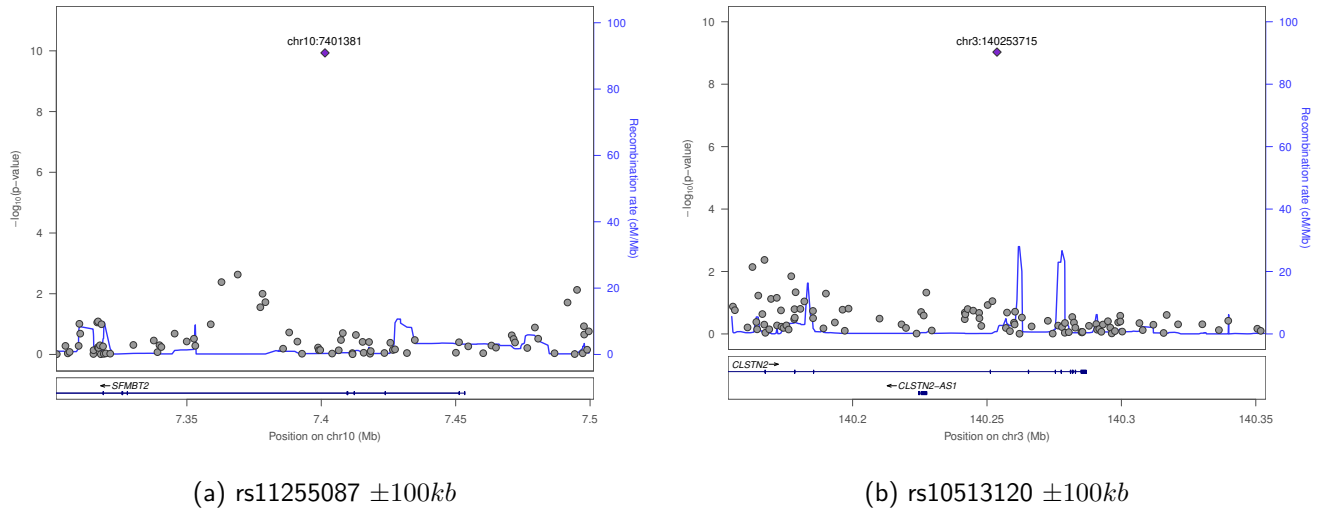


Figure 6: Regional plots for cohort META model invn Adjusted Age+SEX

3.4 Previously identified risk loci

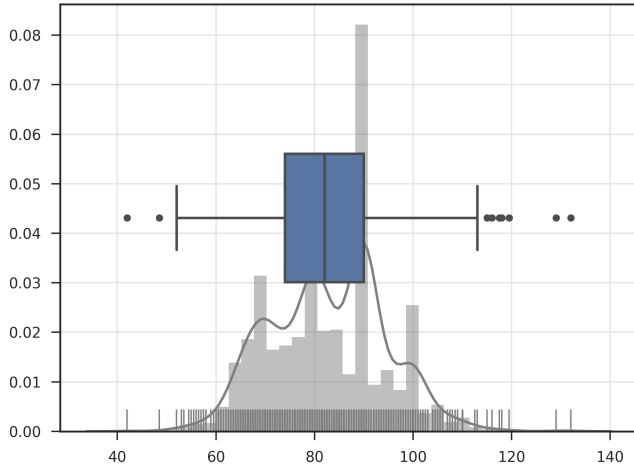
Table 7 shows statistics from the META cohort for 10 loci that were shown to be significantly associated with Serum Creatinine in the 2016 Nature Communications paper by Kettunen et al [8]. Where a previously reported variant was not genotyped in the study (indicated by $\bar{R}^2 < 1$), if available, a tagging variant in LD with the reported variant ($\bar{R}^2 \geq 0.7$ and within 250kb) was provided. Tags were identified using 1000 Genomes data. There are 4 variants that show at least nominal significance ($p < 0.05$) in this study. Out of the 9 variants in both studies, 9 exhibit the same direction of effect with the known result (binomial test $p = 0.00195$).

Table 7: Top known loci in META model invn Adjusted Age+SEX (**bold** variants indicate matching direction of effect)

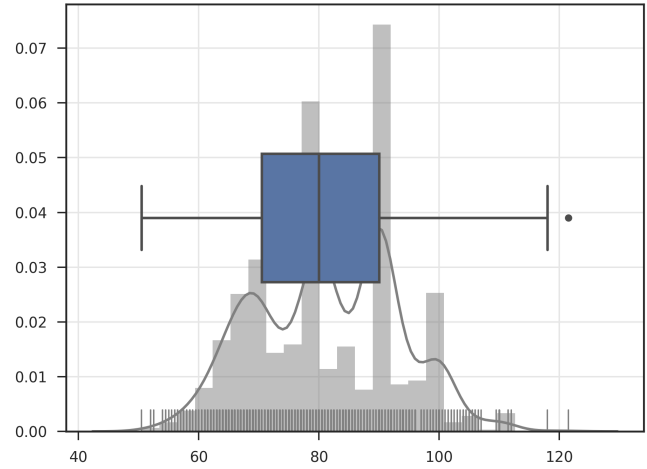
CHR	POS	ID	EA	OA	N	FREQ _{AVG}	FREQ _{MIN}	FREQ _{MAX}	EFFECT	STDERR	P	DIR	GENE _{CLOSEST}	R ²	ID _{KNOWN}	N _{KNOWN}	EFFECT _{KNOWN}	STDERR _{KNOWN}	P _{KNOWN}
15	45694516	rs1346266	T	G	1,795	0.829	0.829	0.829	6.46 · 10 ⁻²	4.45 · 10 ⁻²	0.147	+++++	SPATA5L1	1	rs1346266	24,925	8.06 · 10 ⁻²	1.03 · 10 ⁻²	6.29 · 10 ⁻¹⁵
15	45653592	rs1049508	G	A	3,737	0.813	0.743	0.841	8.04 · 10 ⁻²	2.99 · 10 ⁻²	7.23 · 10 ⁻³	+x++xxx	GATM	1	rs1049508	24,925	8 · 10 ⁻²	1.03 · 10 ⁻²	6.8 · 10 ⁻¹⁵
17	59465697	rs2079742	C	T	10,043	0.464	0.408	0.485	3.69 · 10 ⁻²	1.42 · 10 ⁻²	9.29 · 10 ⁻³	+++++	BCAS3	1	rs2079742	24,925	9.59 · 10 ⁻²	1.28 · 10 ⁻²	8.61 · 10 ⁻¹⁴
15	45609773	rs1719250	G	A	1,795	8.27 · 10 ⁻²	8.27 · 10 ⁻²	8.27 · 10 ⁻²	1.03 · 10 ⁻²	6.04 · 10 ⁻²	0.865	+++++	SLC28A2	1	rs1719250	24,925	6.51 · 10 ⁻²	9.52 · 10 ⁻³	8.52 · 10 ⁻¹²
15	45729123	rs1974981	G	A	1,942	0.677	0.61	0.732	3.36 · 10 ⁻²	3.51 · 10 ⁻²	0.339	xxx++xxx	C15orf48	1	rs1974981	24,925	7.03 · 10 ⁻²	1.03 · 10 ⁻²	9.04 · 10 ⁻¹²
4	77420784	rs1986734	T	C	12,023	0.552	0.41	0.607	9.02 · 10 ⁻³	1.31 · 10 ⁻²	0.49	+++++	SHROOM3	1	rs1986734	24,925	6.19 · 10 ⁻²	9.8 · 10 ⁻³	3.04 · 10 ⁻¹⁰
6	160693107	rs3119311	C	T	12,027	0.175	8.77 · 10 ⁻²	0.215	3.26 · 10 ⁻²	1.73 · 10 ⁻²	5.99 · 10 ⁻²	+++++	SLC22A2	1	rs3119311	24,925	9.08 · 10 ⁻²	1.55 · 10 ⁻²	5.29 · 10 ⁻⁹
17	59483766	rs8068318	C	T	1,942	0.331	0.322	0.339	6.47 · 10 ⁻²	3.39 · 10 ⁻²	5.62 · 10 ⁻²	xxx++xxx	TBX2	1	rs8068318	24,925	6.21 · 10 ⁻²	1.08 · 10 ⁻²	8.69 · 10 ⁻⁹
15	45801035	rs950027	C	T	1,943	0.885	0.824	0.936	0.104	5.13 · 10 ⁻²	4.2 · 10 ⁻²	xxx++xxx	SLC30A4	1	rs950027	24,925	5.28 · 10 ⁻²	9.32 · 10 ⁻³	1.59 · 10 ⁻⁸
7	151405818	rs10480299	C	T	12,023	1.53 · 10 ⁻²	4.7 · 10 ⁻¹	6.72 · 10 ⁻²	0.17	5.35 · 10 ⁻²	1.44 · 10 ⁻³	+++++	PRKAG2	0.871	rs10224002	24,925	7.07 · 10 ⁻²	1.11 · 10 ⁻²	1.89 · 10 ⁻¹⁰

4 Diastolic Blood Pressure (DBP10)

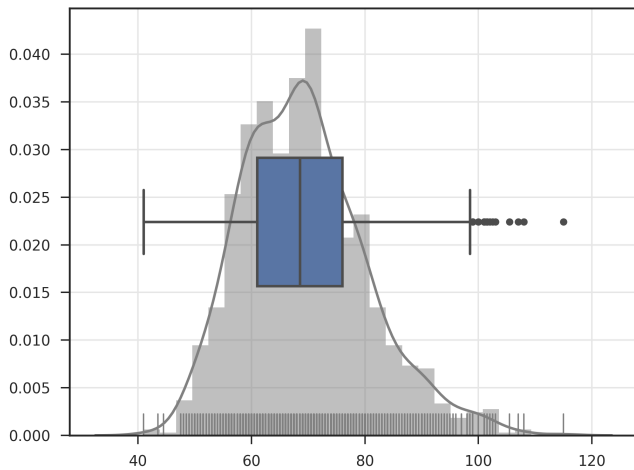
4.1 Summary



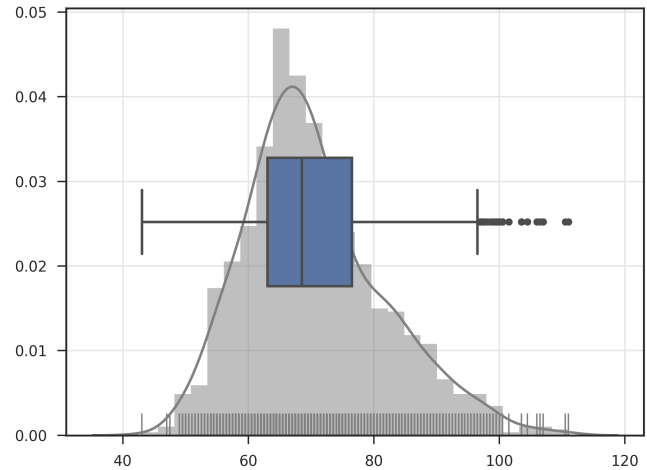
(a) DCSP21M_EAS



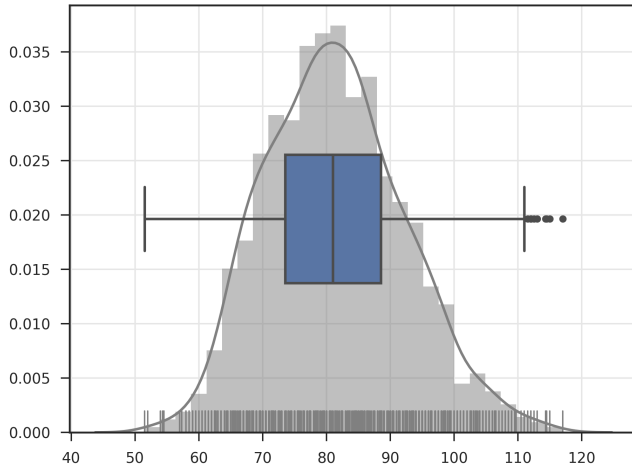
(b) DCSP2610K_EAS



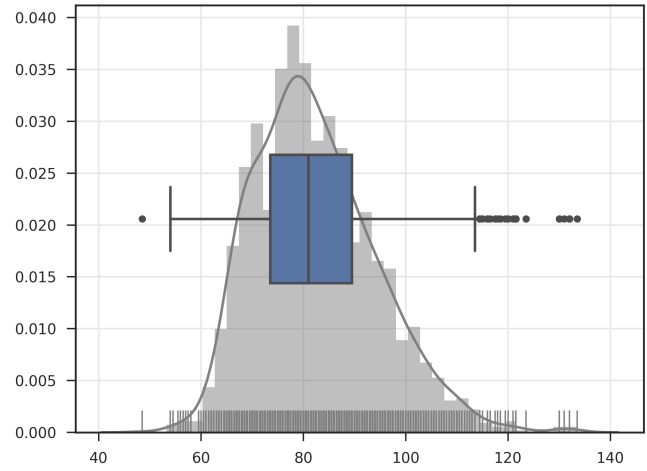
(c) LBCHS_EAS



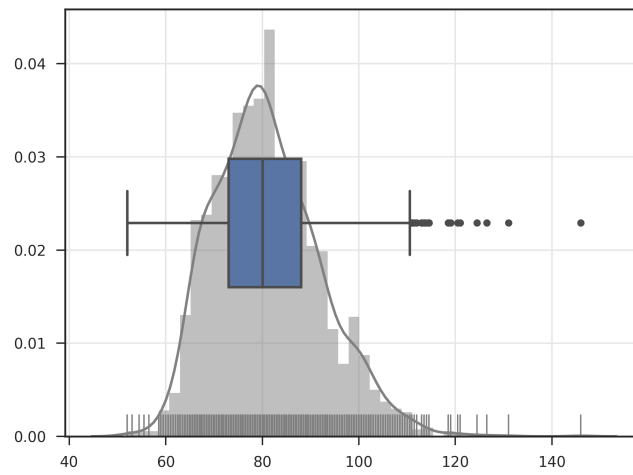
(d) LBMAS_EAS



(e) SCES_EAS



(f) SIMES_EAS



(g) SINDI_SAS

Figure 7: Distribution of DBP10 in META by cohort

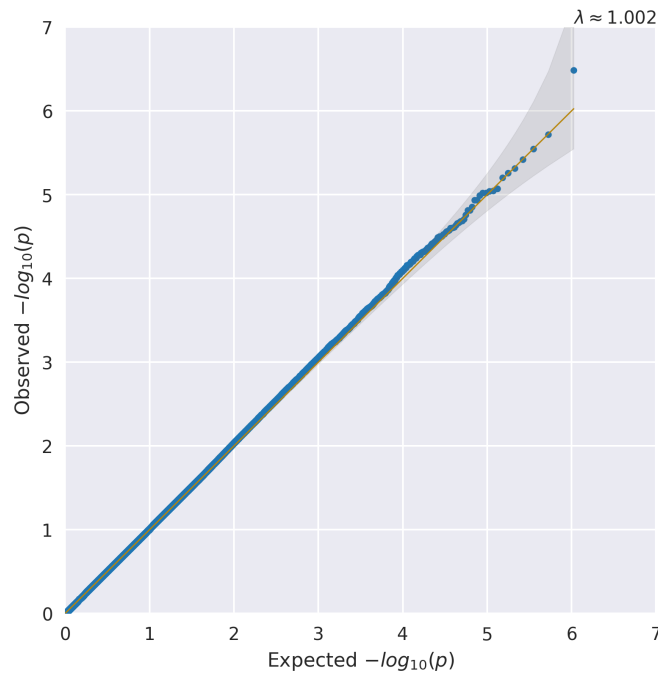
Table 8: Summary of samples removed from Diastolic Blood Pressure analysis by cohort and model

Cohort	Array	Ancestry	Trans	Covars	Total	-SampleQc	-KinshipCrossArray	-KinshipArray	-missObs	-PcOutlier
META DCSP21M_EAS	DCSP21M	EAS	invn	Age+Age2+SEX+BMI	1864	44	0	0	14	0
META DCSP2610K_EAS	DCSP2610K	EAS	invn	Age+Age2+SEX+BMI	2087	36	0	0	11	0
META LBCHS_EAS	LBCHS	EAS	invn	Age+Age2+SEX+BMI	1263	22	52	122	31	14
META LBMAS_EAS	LBMAS	EAS	invn	Age+Age2+SEX+BMI	1185	40	5	240	32	7
META SCES_EAS	SCES	EAS	invn	Age+Age2+SEX+BMI	1889	42	93	2	8	8
META SIMES_EAS	SIMES	EAS	invn	Age+Age2+SEX+BMI	2542	47	160	115	18	5
META SINDI_SAS	SINDI	SAS	invn	Age+Age2+SEX+BMI	2537	60	15	91	7	0

Table 9: Summary of samples remaining for Diastolic Blood Pressure analysis by cohort and model

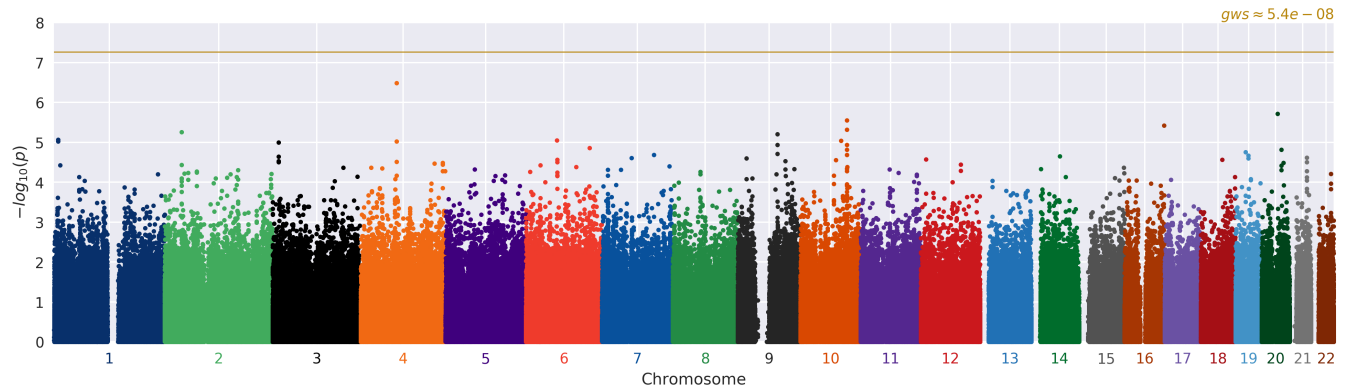
Cohort	Array	Ancestry	Trans	Covars	PCs	N	Male	Female	Max	Min	μ	\bar{x}	σ
META DCSP21M_EAS	DCSP21M	EAS	invn	Age+Age2+SEX+BMI	0	1806	1160	646	132.0	42.0	82.803	82.0	11.647
META DCSP2610K_EAS	DCSP2610K	EAS	invn	Age+Age2+SEX+BMI	0	2040	603	1437	121.5	50.5	81.386	80.0	11.831
META LBCHS_EAS	LBCHS	EAS	invn	Age+Age2+SEX+BMI	0	1022	506	516	115.0	41.0	69.315	69.0	10.99
META LBMAS_EAS	LBMAS	EAS	invn	Age+Age2+SEX+BMI	0	861	434	427	111.0	43.0	70.411	69.0	10.981
META SCES_EAS	SCES	EAS	invn	Age+Age2+SEX+BMI	0	1736	886	850	117.0	51.5	81.328	81.0	10.824
META SIMES_EAS	SIMES	EAS	invn	Age+Age2+SEX+BMI	4	2197	1109	1088	133.5	48.5	82.353	81.0	11.859
META SINDI_SAS	SINDI	SAS	invn	Age+Age2+SEX+BMI	0	2364	1204	1160	146.0	52.0	81.038	80.0	11.07

4.2 Calibration



(a) invn Adjusted Age+Age2+SEX+BMI

Figure 8: QQ plots for DBP10 in the META analysis



(a) invn Adjusted Age+Age2+SEX+BMI

Figure 9: Manhattan plots for DBP10 in the META analysis

4.3 Top associations

Table 10: Top variants in the META invn Adjusted Age+Age2+SEX+BMI model (**bold** variants indicate previously identified associations)

CHR	POS	ID	EA	OA	GENE _{CLOSEST}	DIR	N	MALE	FEMALE	FREQ _{AVG}	FREQ _{MIN}	FREQ _{MAX}	EFFECT	STDERR	OR	ZSCORE	P
4	81164723	rs1458038	T	C	FGF5	+++++++	12,025	5,902	6,123	0.423	0.288	0.489	$6.76 \cdot 10^{-2}$	$1.32 \cdot 10^{-2}$	1.07	5.107	$3.27 \cdot 10^{-7}$
20	35502240	rs1291117	A	G	TLDC2	x+xx+++	8,337	3,802	4,535	$1.86 \cdot 10^{-2}$	$2.88 \cdot 10^{-4}$	$5.94 \cdot 10^{-2}$	0.278	$5.83 \cdot 10^{-2}$	1.32	-4.763	$1.91 \cdot 10^{-6}$
10	104591393	rs17115100	G	T	CYP17A1	+++++++	12,025	5,902	6,123	0.297	0.249	0.342	$6.63 \cdot 10^{-2}$	$1.41 \cdot 10^{-2}$	1.069	-4.683	$2.83 \cdot 10^{-6}$
16	88738964	rs4074632	C	T	SNAI3	+++++++	12,023	5,900	6,123	0.715	0.477	0.8	$6.84 \cdot 10^{-2}$	$1.48 \cdot 10^{-2}$	1.071	4.621	$3.82 \cdot 10^{-6}$
10	104614350	rs3824754	C	T	BORCS7-ASMT	+++xxxx	10,143	4,962	5,181	0.283	0.216	0.341	$7.15 \cdot 10^{-2}$	$1.56 \cdot 10^{-2}$	1.074	-4.571	$4.86 \cdot 10^{-6}$
2	38066683	rs17411119	C	T	RMDN2	+++++++	12,022	5,901	6,121	0.172	0.124	0.336	$7.95 \cdot 10^{-2}$	$1.75 \cdot 10^{-2}$	1.083	4.544	$5.51 \cdot 10^{-6}$
9	89481996	rs1169848	G	T	GAS1	-+++++++	12,024	5,901	6,123	0.289	0.275	0.318	$6.43 \cdot 10^{-2}$	$1.42 \cdot 10^{-2}$	1.066	-4.516	$6.29 \cdot 10^{-6}$
1	9860050	rs4585981	C	A	CLSTN1	+xxxxxx	1,806	1,160	646	0.962	0.962	0.962	0.389	$8.74 \cdot 10^{-2}$	1.476	-4.452	$8.52 \cdot 10^{-6}$
6	70108848	rs1328729	C	T	ADGRB3	+++++++	12,023	5,899	6,124	$4.55 \cdot 10^{-2}$	$1.02 \cdot 10^{-2}$	0.163	0.142	$3.2 \cdot 10^{-2}$	1.153	-4.441	$8.95 \cdot 10^{-6}$
10	91343607	rs3824603	G	A	PANK1	xxxxx+	2,360	1,202	1,158	0.301	0.301	0.301	0.138	$3.11 \cdot 10^{-2}$	1.148	-4.439	$9.05 \cdot 10^{-6}$
3	13305930	rs648445	C	T	NUP210	xx+++xx	1,883	940	943	0.9	0.854	0.939	0.24	$5.45 \cdot 10^{-2}$	1.272	4.414	$1.02 \cdot 10^{-5}$
6	142949260	rs9373355	T	C	HIVEP2	+x+++xx	3,685	2,100	1,585	0.423	0.417	0.426	0.103	$2.37 \cdot 10^{-2}$	1.108	-4.345	$1.39 \cdot 10^{-5}$
20	44130596	rs1883519	G	A	SPINT3	+++++++	12,020	5,898	6,122	$4.9 \cdot 10^{-2}$	$9.8 \cdot 10^{-4}$	0.22	0.139	$3.22 \cdot 10^{-2}$	1.15	-4.324	$1.54 \cdot 10^{-5}$
19	22846788	rs11672238	C	A	ZNF492	+x+++xx	3,683	2,098	1,585	0.128	$9.53 \cdot 10^{-2}$	0.141	0.149	$3.47 \cdot 10^{-2}$	1.161	-4.296	$1.74 \cdot 10^{-5}$
10	104685299	rs12411886	C	A	CNNM2	+x+++xx	10,119	4,949	5,170	0.247	0.207	0.285	$6.93 \cdot 10^{-2}$	$1.63 \cdot 10^{-2}$	1.072	-4.259	$2.05 \cdot 10^{-5}$
7	116901160	rs6958283	T	C	WNT2	xx+++xx	1,882	939	943	0.735	0.732	0.739	0.156	$3.67 \cdot 10^{-2}$	1.169	-4.258	$2.07 \cdot 10^{-5}$
19	29150490	rs2215191	G	A	UQCRF51	+xxxxxx	1,805	1,160	645	0.201	0.201	0.201	0.176	$4.15 \cdot 10^{-2}$	1.193	-4.248	$2.16 \cdot 10^{-5}$
14	63759190	rs2012961	C	T	RHOJ	+++++++	12,026	5,902	6,124	0.675	0.617	0.826	$5.88 \cdot 10^{-2}$	$1.39 \cdot 10^{-2}$	1.061	4.242	$2.21 \cdot 10^{-5}$
21	38727277	rs12106331	A	G	DYRK1A	+x+++xx	3,689	2,100	1,589	0.362	0.301	0.388	0.103	$2.44 \cdot 10^{-2}$	1.109	-4.22	$2.44 \cdot 10^{-5}$
7	66877880	rs4266531	C	T	TYW1	-----+	12,022	5,899	6,123	$8.69 \cdot 10^{-3}$	$2.77 \cdot 10^{-4}$	$3.7 \cdot 10^{-2}$	0.294	$6.98 \cdot 10^{-2}$	1.342	-4.218	$2.46 \cdot 10^{-5}$

4.4 Previously identified risk loci

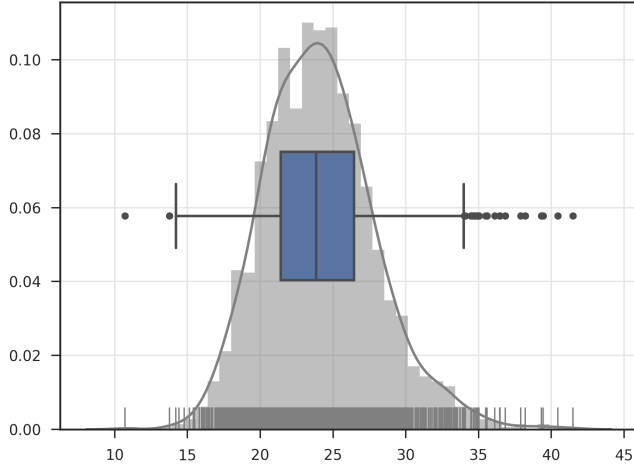
Table 11 shows statistics from the META cohort for 27 loci that were shown to be significantly associated with Diastolic Blood Pressure in the 2011 Nature paper by Ehret et al [10]. Where a previously reported variant was not genotyped in the study (indicated by $\bar{R}^2 < 1$), if available, a tagging variant in LD with the reported variant ($\bar{R}^2 \geq 0.7$ and within 250kb) was provided. Tags were identified using 1000 Genomes data. There are 8 variants that show at least nominal significance ($p < 0.05$) in this study. Out of the 25 variants in both studies, 13 exhibit the same direction of effect with the known result (binomial test $p = 0.5$).

Table 11: Top known loci in META model invn Adjusted Age+Age2+SEX+BMI (**bold** variants indicate matching direction of effect)

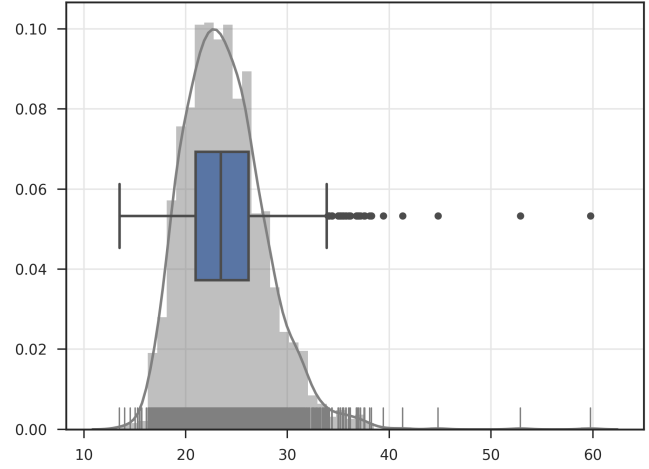
CHR	POS	ID	EA	OA	N	FREQ _{AVG}	FREQ _{MIN}	FREQ _{MAX}	EFFECT	STDERR	P	DIR	GENE _{CLOSEST}	R ²	ID _{KNOWN}	N _{KNOWN}	EFFECT _{KNOWN}	STDERR _{KNOWN}	P _{KNOWN}
12	112007756	rs653178	T	C	8,405	0.983	0.946	1	0.131	6.12 · 10 ⁻²	3.22 · 10 ⁻²	++xxx++	ATXN2	1	rs653178	2 · 10 ⁵	0.48	6.26 · 10 ⁻²	1.64 · 10 ⁻¹⁴
12	111884608	rs3184504	C	T	8,407	0.983	0.946	1	0.128	6.11 · 10 ⁻²	3.67 · 10 ⁻²	++xxx++	SH2B3	1	rs3184504	2 · 10 ⁵	-0.48	6.29 · 10 ⁻²	2.33 · 10 ⁻¹⁴
4	81164723	rs1458038	T	C	12,026	0.423	0.288	0.489	6.78 · 10 ⁻²	1.32 · 10 ⁻²	3.08 · 10 ⁻⁷	+++++++	FGF5	1	rs1458038	2 · 10 ⁵	0.503	7.02 · 10 ⁻²	7.91 · 10 ⁻¹³
12	112591686	rs17630235	G	A	1,806	2.77 · 10 ⁻⁴	2.77 · 10 ⁻⁴	2.77 · 10 ⁻⁴	0.377	1	0.706	+xxxxxx	TRAFD1	1	rs17630235	2 · 10 ⁵	0.447	6.4 · 10 ⁻²	2.92 · 10 ⁻¹²
12	112610714	rs11066188	G	A	8,406	1.38 · 10 ⁻²	2.77 · 10 ⁻⁴	4.38 · 10 ⁻²	0.138	6.75 · 10 ⁻²	4.09 · 10 ⁻²	++xxx++	HECTD4	1	rs11066188	2 · 10 ⁵	0.447	6.41 · 10 ⁻²	3.06 · 10 ⁻¹²
15	75077367	rs1378942	C	A	10,143	0.175	0.153	0.19	2.54 · 10 ⁻²	1.84 · 10 ⁻²	0.167	++xxx++	CSK	1	rs1378942	2 · 10 ⁵	0.445	6.4 · 10 ⁻²	3.47 · 10 ⁻¹²
12	112906415	rs11066320	G	A	10,275	0.987	0.952	1	0.124	6.35 · 10 ⁻²	5.03 · 10 ⁻²	+++x+++	PTPN11	1	rs11066320	2 · 10 ⁵	0.413	6.32 · 10 ⁻²	6.32 · 10 ⁻¹¹
15	75057203	rs4886406	T	G	12,026	0.668	0.606	0.774	3.16 · 10 ⁻³	1.38 · 10 ⁻²	0.819	+++++	CYP1A2	1	rs4886406	2 · 10 ⁵	0.426	6.85 · 10 ⁻²	4.83 · 10 ⁻¹⁰
15	75125645	rs6495122	A	C	12,023	0.175	0.116	0.206	3.99 · 10 ⁻²	1.7 · 10 ⁻²	1.85 · 10 ⁻²	+++++++	CPLX3	1	rs6495122	2 · 10 ⁵	-0.383	6.23 · 10 ⁻²	8.41 · 10 ⁻¹⁰
15	75115895	rs7162232	A	G	3,689	0.658	0.623	0.764	3.03 · 10 ⁻²	2.44 · 10 ⁻²	0.214	+x+++xx	LMAN1L	1	rs7162232	2 · 10 ⁵	-0.416	6.89 · 10 ⁻²	1.58 · 10 ⁻⁹
7	2512545	rs2969070	G	A	10,142	0.807	0.722	0.855	1.02 · 10 ⁻²	1.79 · 10 ⁻²	0.569	-xxx++	GRIFIN	1	rs2969070	2 · 10 ⁵	0.386	6.47 · 10 ⁻²	2.57 · 10 ⁻⁹
12	90008959	rs2681472	A	G	12,021	0.289	0.206	0.325	5.9 · 10 ⁻²	1.43 · 10 ⁻²	3.8 · 10 ⁻⁵	+++++++	ATP2B1	1	rs2681472	2 · 10 ⁵	-0.492	8.36 · 10 ⁻²	3.9 · 10 ⁻⁹
15	75140854	rs3765066	A	G	3,685	0.531	0.476	0.558	2.97 · 10 ⁻²	2.3 · 10 ⁻²	0.197	+x+++xx	SCAMP2	1	rs3765066	2 · 10 ⁵	-0.382	6.51 · 10 ⁻²	4.17 · 10 ⁻⁹
1	11883731	rs12567136	T	C	3,689	0.148	0.123	0.225	1.72 · 10 ⁻³	3.26 · 10 ⁻²	0.958	-x+++xx	CLCN6	1	rs12567136	2 · 10 ⁵	0.488	8.56 · 10 ⁻²	1.15 · 10 ⁻⁸
1	11862778	rs17367504	A	G	12,019	0.169	0.121	0.232	3.62 · 10 ⁻²	1.73 · 10 ⁻²	3.64 · 10 ⁻²	+++++++	MTHFR	1	rs17367504	2 · 10 ⁵	-0.49	8.61 · 10 ⁻²	1.29 · 10 ⁻⁸
10	63507669	rs10509158	T	C	12,024	0.174	0.145	0.212	2.16 · 10 ⁻³	1.7 · 10 ⁻²	0.899	+++++	C10orf107	1	rs10509158	2 · 10 ⁵	0.43	7.63 · 10 ⁻²	1.74 · 10 ⁻⁸
12	89942390	rs11105328	A	G	3,684	0.186	0.174	0.205	2.48 · 10 ⁻²	2.97 · 10 ⁻²	0.403	+x+++xx	POC1B-GALNT4	1	rs11105328	2 · 10 ⁵	-0.487	8.66 · 10 ⁻²	1.83 · 10 ⁻⁸
15	75129594	rs2290573	G	A	1,806	0.179	0.179	0.179	2.49 · 10 ⁻²	4.37 · 10 ⁻²	0.569	+xxxxxx	ULK3	1	rs2290573	2 · 10 ⁵	0.361	6.42 · 10 ⁻²	1.85 · 10 ⁻⁸
12	111798553	rs3742004	A	G	12,027	0.704	0.392	0.846	2.39 · 10 ⁻²	1.54 · 10 ⁻²	0.12	+++++++	FAM109A	1	rs3742004	2 · 10 ⁵	-0.429	7.66 · 10 ⁻²	2.15 · 10 ⁻⁸
15	75234610	rs11072518	C	T	12,027	0.433	0.251	0.521	1.57 · 10 ⁻²	1.32 · 10 ⁻²	0.236	+++++++	COX5A	1	rs11072518	2 · 10 ⁵	-0.355	6.45 · 10 ⁻²	3.78 · 10 ⁻⁸
6	26107463	rs198846	A	G	3,689	0.97	0.97	0.97	2.62 · 10 ⁻²	6.78 · 10 ⁻²	0.699	-x+++xx	HIST1H1T	1	rs198846	2 · 10 ⁵	-0.487	8.85 · 10 ⁻²	3.8 · 10 ⁻⁸
6	26091179	rs1799945	G	C	3,886	2.43 · 10 ⁻²	2.19 · 10 ⁻²	3.14 · 10 ⁻²	5.12 · 10 ⁻²	7.54 · 10 ⁻²	0.497	-x+++xx	HFE	1	rs1799945	2 · 10 ⁵	0.482	8.82 · 10 ⁻²	4.78 · 10 ⁻⁸
12	111788402	rs10219736	C	T	9,829	0.585	0.287	0.724	1.36 · 10 ⁻²	1.56 · 10 ⁻²	0.386	+++++++	CUX2	1	rs10219736	2 · 10 ⁵	-0.414	7.58 · 10 ⁻²	4.88 · 10 ⁻⁸
15	75185670	rs7495739	G	A	1,805	0.218	0.218	0.218	1.75 · 10 ⁻²	4 · 10 ⁻²	0.662	+xxxxxx	MPI	1	rs7495739	2 · 10 ⁵	0.335	6.15 · 10 ⁻²	5.02 · 10 ⁻⁸
6	26107463	rs198846	A	G	3,689	0.97	0.97	0.97	2.62 · 10 ⁻²	6.78 · 10 ⁻²	0.699	-x+++xx	HIST1H2BC	1	rs198833	2 · 10 ⁵	-0.485	8.88 · 10 ⁻²	4.58 · 10 ⁻⁸
12	112591686	rs17630235	G	A	1,806	2.77 · 10 ⁻⁴	2.77 · 10 ⁻⁴	2.77 · 10 ⁻⁴	0.377	1	0.706	+xxxxxx	NAA25	0.922	rs17696736	2 · 10 ⁵	0.422	6.34 · 10 ⁻²	2.8 · 10 ⁻¹¹
12	112007756	rs653178	T	C	8,405	0.983	0.946	1	0.131	6.12 · 10 ⁻²	3.22 · 10 ⁻²	++xxx++	BRAP	0.811	rs11065987	2 · 10 ⁵	-0.449	6.46 · 10 ⁻²	3.43 · 10 ⁻¹²

5 Body Mass Index (BMI)

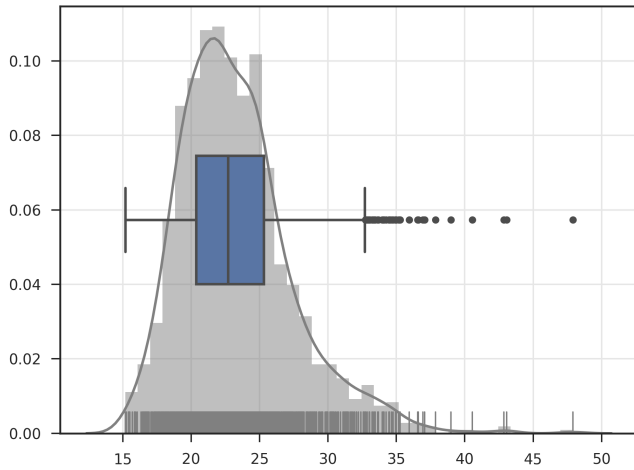
5.1 Summary



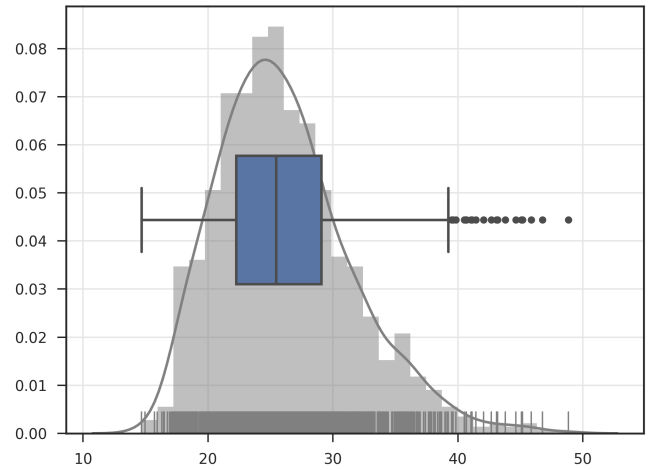
(a) DCSP21M_EAS



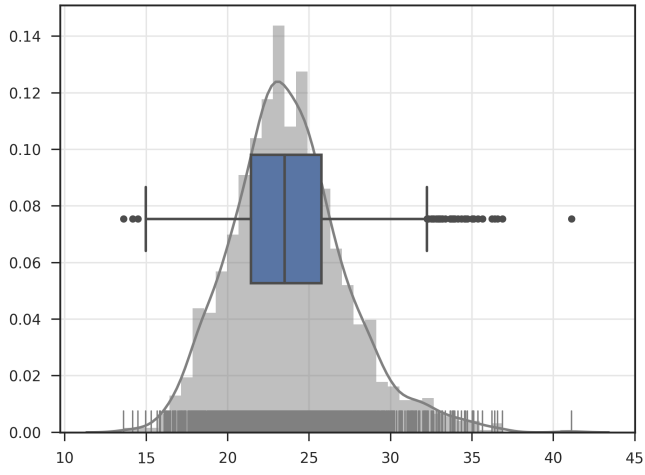
(b) DCSP2610K_EAS



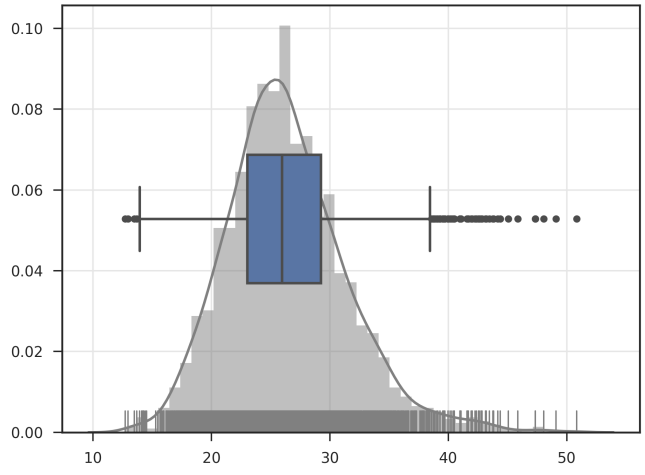
(c) LBCHS_EAS



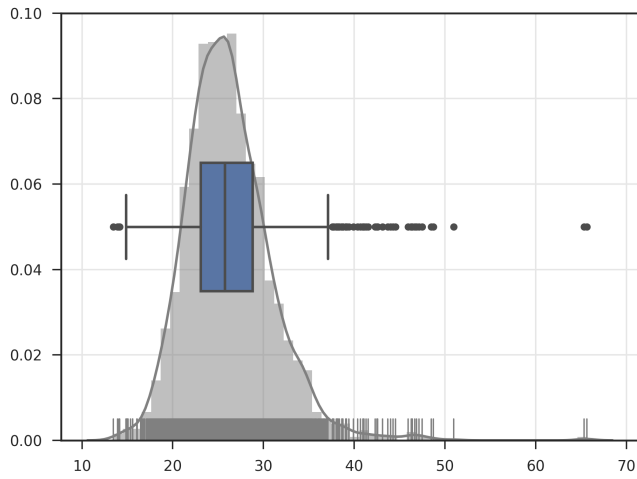
(d) LBMAS_EAS



(e) SCES_EAS



(f) SIMES_EAS



(g) SINDI_SAS

Figure 10: Distribution of BMI in META by cohort

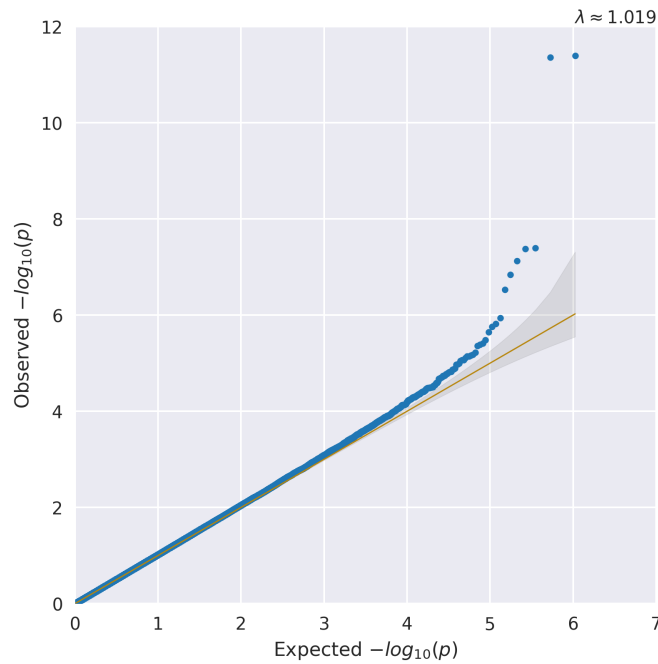
Table 12: Summary of samples removed from Body Mass Index analysis by cohort and model

Cohort	Array	Ancestry	Trans	Covars	Total	-SampleQc	-KinshipCrossArray	-KinshipArray	-missObs	-PcOutlier
META DCSP21M_EAS	DCSP21M	EAS	invn	Age+Age2+SEX	1864	44	0	0	14	0
META DCSP2610K_EAS	DCSP2610K	EAS	invn	Age+Age2+SEX	2087	36	0	0	8	10
META LBCHS_EAS	LBCHS	EAS	invn	Age+Age2+SEX	1263	22	52	122	0	15
META LBMAS_EAS	LBMAS	EAS	invn	Age+Age2+SEX	1185	40	5	240	0	0
META SCES_EAS	SCES	EAS	invn	Age+Age2+SEX	1889	42	93	2	8	11
META SIMES_EAS	SIMES	EAS	invn	Age+Age2+SEX	2542	47	160	115	16	7
META SINDI_SAS	SINDI	SAS	invn	Age+Age2+SEX	2537	60	15	91	7	49

Table 13: Summary of samples remaining for Body Mass Index analysis by cohort and model

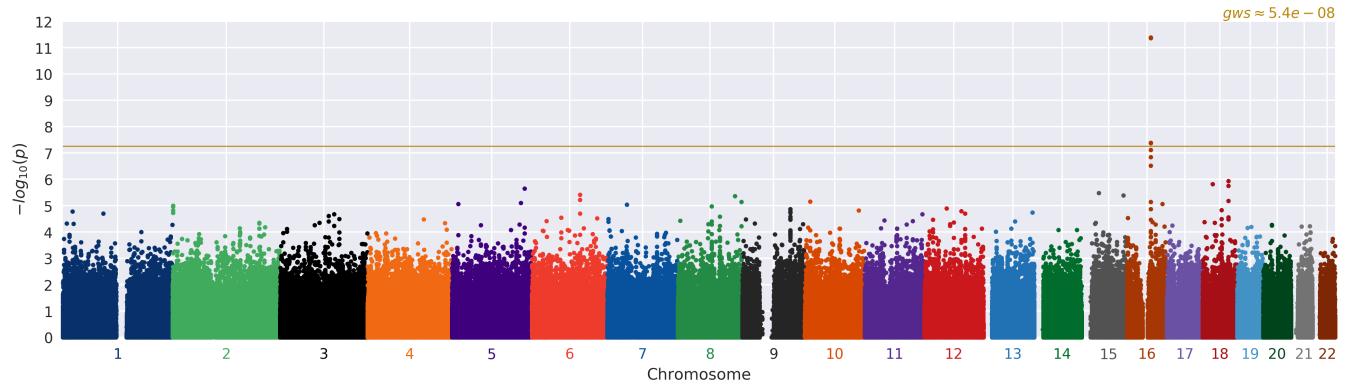
Cohort	Array	Ancestry	Trans	Covars	PCs	N	Male	Female	Max	Min	μ	\bar{x}	σ
META DCSP21M_EAS	DCSP21M	EAS	invn	Age+Age2+SEX	0	1806	1160	646	41.484	10.714	24.092	23.836	3.83
META DCSP2610K_EAS	DCSP2610K	EAS	invn	Age+Age2+SEX	2	2033	596	1437	59.766	13.51	23.836	23.448	4.094
META LBCHS_EAS	LBCHS	EAS	invn	Age+Age2+SEX	7	1052	522	530	47.899	15.178	23.377	22.745	4.179
META LBMAS_EAS	LBMAS	EAS	invn	Age+Age2+SEX	1	900	455	445	48.849	14.684	26.136	25.449	5.458
META SCES_EAS	SCES	EAS	invn	Age+Age2+SEX	10	1733	885	848	41.119	13.615	23.747	23.479	3.536
META SIMES_EAS	SIMES	EAS	invn	Age+Age2+SEX	5	2197	1108	1089	50.844	12.719	26.396	25.967	5.097
META SINDI_SAS	SINDI	SAS	invn	Age+Age2+SEX	0	2315	1176	1139	65.636	13.438	26.208	25.789	4.77

5.2 Calibration



(a) invn Adjusted Age+Age2+SEX

Figure 11: QQ plots for BMI in the META analysis



(a) invn Adjusted Age+Age2+SEX

Figure 12: Manhattan plots for BMI in the META analysis

5.3 Top associations

Table 14: Top variants in the META invn Adjusted Age+Age2+SEX model (**bold** variants indicate previously identified associations)

CHR	POS	ID	EA	OA	GENE _{CLOSEST}	DIR	N	MALE	FEMALE	FREQ _{AVG}	FREQ _{MIN}	FREQ _{MAX}	EFFECT	STDERR	OR	ZSCORE	P
16	53816275	rs8050136	A	C	FTO	+++++++	12,034	5,901	6,133	0.209	0.121	0.33	0.112	$1.62 \cdot 10^{-2}$	1.119	6.935	$4.05 \cdot 10^{-12}$
18	57962862	rs9963410	T	G	MC4R	+++++++	12,033	5,901	6,132	0.164	$8.95 \cdot 10^{-2}$	0.384	$8.8 \cdot 10^{-2}$	$1.81 \cdot 10^{-2}$	1.092	4.865	$1.15 \cdot 10^{-6}$
18	22781850	rs4131454	C	T	ZNF521	+x++xxx	3,749	2,133	1,616	0.139	0.134	0.149	0.161	$3.35 \cdot 10^{-2}$	1.175	-4.811	$1.5 \cdot 10^{-6}$
5	164448888	rs6892131	T	C	MAT2B	+++++++	12,015	5,889	6,126	0.835	0.546	0.946	$8.85 \cdot 10^{-2}$	$1.87 \cdot 10^{-2}$	1.092	-4.728	$2.26 \cdot 10^{-6}$
15	38482004	rs970498	G	A	SPRED1	+++++++	12,034	5,901	6,133	0.631	0.591	0.657	$6.17 \cdot 10^{-2}$	$1.33 \cdot 10^{-2}$	1.064	-4.653	$3.27 \cdot 10^{-6}$
6	108815553	rs12526579	G	A	LACE1	+++++++	12,029	5,900	6,129	0.387	0.291	0.662	$6.33 \cdot 10^{-2}$	$1.37 \cdot 10^{-2}$	1.065	-4.618	$3.88 \cdot 10^{-6}$
15	93970984	rs901966	A	G	AC112693	xx++xxx	1,952	977	975	0.166	0.123	0.202	0.197	$4.27 \cdot 10^{-2}$	1.217	-4.607	$4.08 \cdot 10^{-6}$
8	129012574	rs10087240	C	T	TMEM75	+++++	12,033	5,899	6,134	0.538	0.478	0.59	$5.93 \cdot 10^{-2}$	$1.29 \cdot 10^{-2}$	1.061	-4.593	$4.36 \cdot 10^{-6}$
10	11831111	rs17150863	G	A	ECHDC3	+++++++	12,031	5,898	6,133	0.279	0.172	0.364	$6.51 \cdot 10^{-2}$	$1.45 \cdot 10^{-2}$	1.067	4.497	$6.9 \cdot 10^{-6}$
8	143838062	rs7813604	G	A	LYPD2	+xxxxxx	1,806	1,160	646	0.332	0.332	0.332	0.158	$3.52 \cdot 10^{-2}$	1.171	-4.487	$7.23 \cdot 10^{-6}$
5	155741238	rs7737496	G	A	SGCG	xx++xxx	1,951	977	974	$3.79 \cdot 10^{-2}$	$2.85 \cdot 10^{-2}$	$4.89 \cdot 10^{-2}$	0.374	$8.37 \cdot 10^{-2}$	1.454	-4.472	$7.73 \cdot 10^{-6}$
5	13954951	rs173090	G	A	DNAH5	+++++++	12,035	5,901	6,134	0.623	0.33	0.713	$6.24 \cdot 10^{-2}$	$1.4 \cdot 10^{-2}$	1.064	4.45	$8.58 \cdot 10^{-6}$
16	79722913	rs11865979	T	C	MAF	xx++xxx	1,949	976	973	$6.39 \cdot 10^{-2}$	$4.33 \cdot 10^{-2}$	$8.15 \cdot 10^{-2}$	0.291	$6.53 \cdot 10^{-2}$	1.337	-4.449	$8.62 \cdot 10^{-6}$
7	44231216	rs3757840	G	T	GCK	+++++++	12,023	5,894	6,129	0.478	0.45	0.513	$5.7 \cdot 10^{-2}$	$1.28 \cdot 10^{-2}$	1.059	4.441	$8.97 \cdot 10^{-6}$
2	638144	rs4854344	T	G	TMEM18	+++++++	12,000	5,882	6,118	0.918	0.868	0.936	0.104	$2.35 \cdot 10^{-2}$	1.109	4.417	$1 \cdot 10^{-5}$
8	76532640	rs1839330	T	A	HNF4G	++xx++x	7,756	3,742	4,014	0.408	0.379	0.446	$7.18 \cdot 10^{-2}$	$1.63 \cdot 10^{-2}$	1.074	4.408	$1.05 \cdot 10^{-5}$
12	50319086	rs297941	A	G	FAIM2	+++++++	12,034	5,900	6,134	0.526	0.423	0.568	$5.63 \cdot 10^{-2}$	$1.29 \cdot 10^{-2}$	1.058	-4.366	$1.27 \cdot 10^{-5}$
9	107988197	rs446641	T	C	SLC44A1	+++++++	12,036	5,902	6,134	0.103	0.119	0.119	$9.16 \cdot 10^{-2}$	$2.1 \cdot 10^{-2}$	1.096	4.352	$1.35 \cdot 10^{-5}$
18	42812895	rs1903647	G	A	SLC14A2	+++xxxx	10,082	4,923	5,159	0.17	0.145	0.202	$8.17 \cdot 10^{-2}$	$1.89 \cdot 10^{-2}$	1.085	4.331	$1.49 \cdot 10^{-5}$
10	121876520	rs10788038	C	T	SEC23IP	+++++++	12,032	5,900	6,132	0.843	0.676	0.892	$7.86 \cdot 10^{-2}$	$1.82 \cdot 10^{-2}$	1.082	4.329	$1.5 \cdot 10^{-5}$

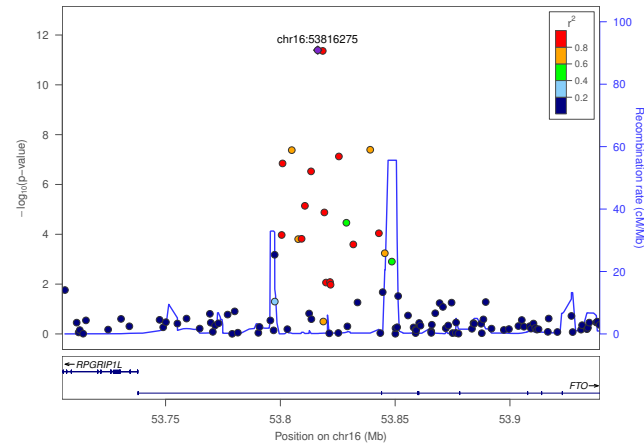


Figure 13: Regional plot for cohort META model invn Adjusted Age+Age2+SEX: rs8050136 $\pm 100kb$

5.4 Previously identified risk loci

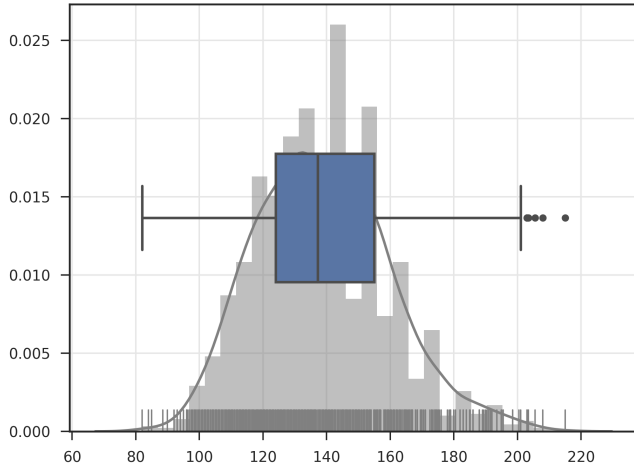
Table 15 shows statistics from the META cohort for 50 loci that were shown to be significantly associated with Body Mass Index in the 2015 Nature paper by Locke et al [13]. Where a previously reported variant was not genotyped in the study (indicated by $\bar{R}^2 < 1$), if available, a tagging variant in LD with the reported variant ($\bar{R}^2 \geq 0.7$ and within 250kb) was provided. Tags were identified using 1000 Genomes data. There are 14 variants that show at least nominal significance ($p < 0.05$) in this study. Out of the 50 variants in both studies, 38 exhibit the same direction of effect with the known result (binomial test $p = 0.000153$).

Table 15: Top known loci in META model invn Adjusted Age+Age2+SEX (**bold** variants indicate matching direction of effect)

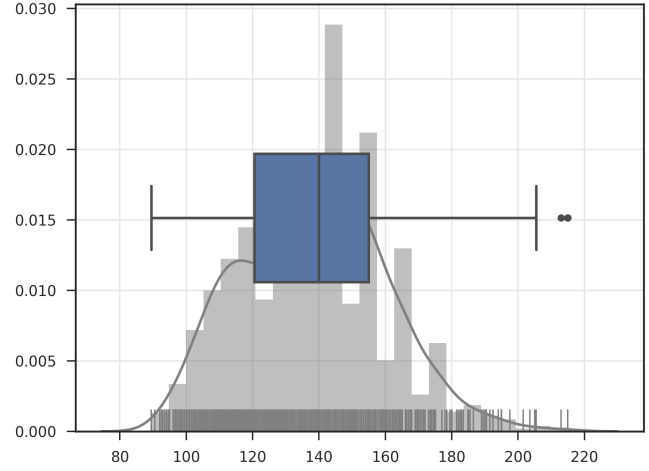
Table with 19 columns: CHR, POS, ID, EA, OA, N, FREQ_AVG, FREQ_MIN, FREQ_MAX, EFFECT, STDERR, P, DIR, GENE_CLOSEST, R^2, ID_KNOWN, N_KNOWN, EFFECT_KNOWN, STDERR_KNOWN, P_KNOWN. The table lists various SNPs across chromosomes 1-11, including IDs like rs1421085, rs6567160, rs1320338, etc., and associated gene names like FTO, MC4R, TMEM18, etc.

6 Systolic Blood Pressure (SBP15)

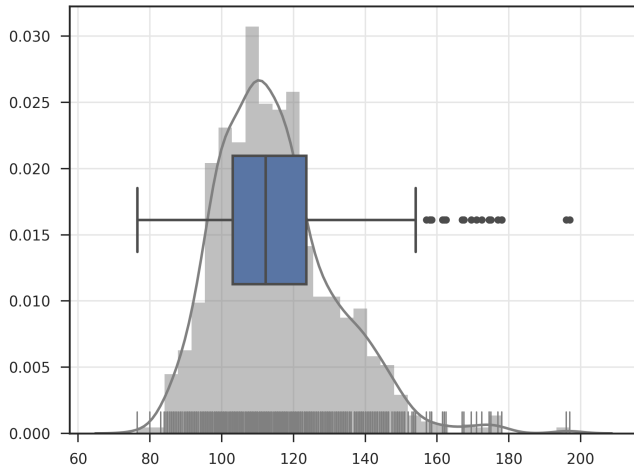
6.1 Summary



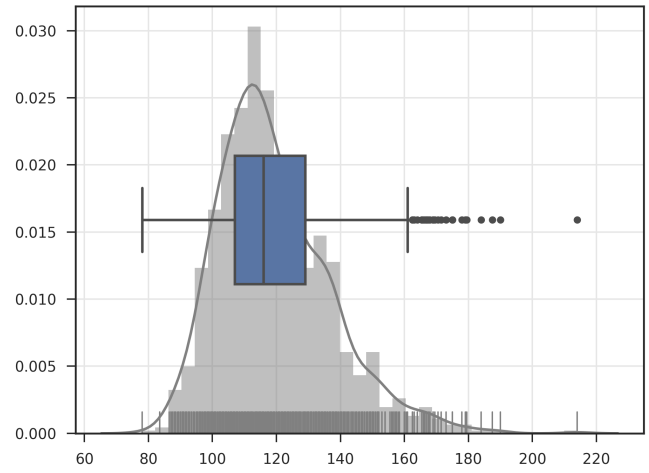
(a) DCSP21M_EAS



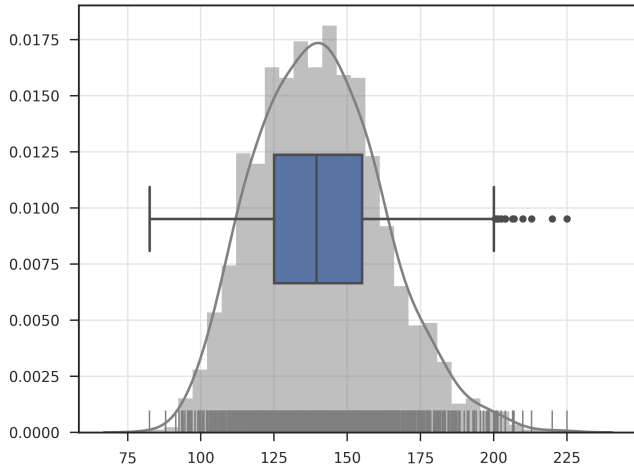
(b) DCSP2610K_EAS



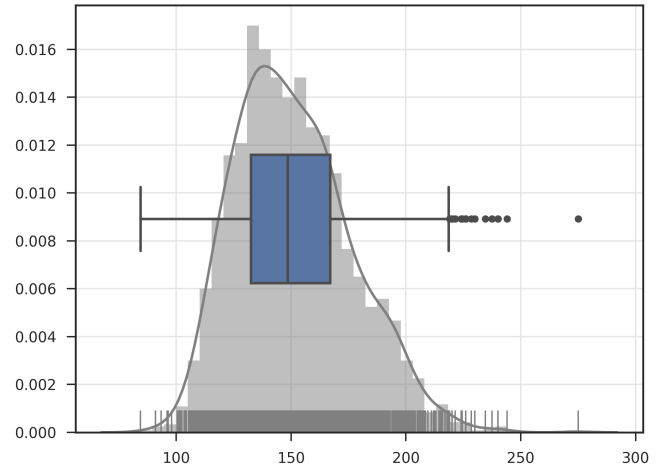
(c) LBCHS_EAS



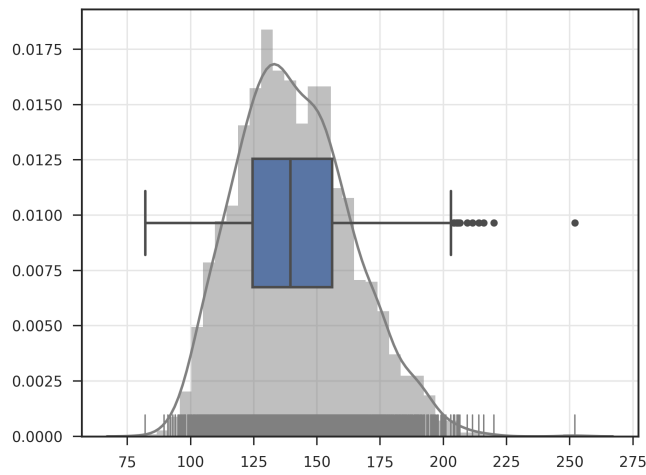
(d) LBMAS_EAS



(e) SCES_EAS



(f) SIMES_EAS



(g) SINDI_SAS

Figure 14: Distribution of SBP15 in META by cohort

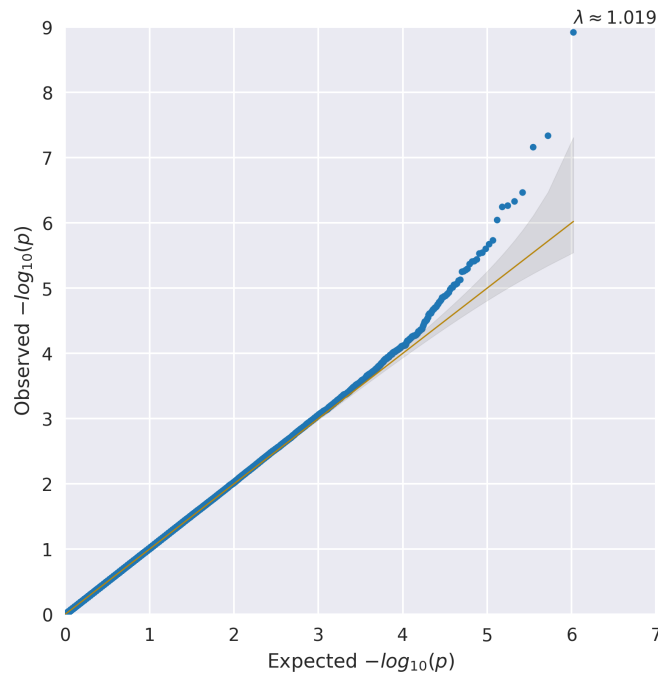
Table 16: Summary of samples removed from Systolic Blood Pressure analysis by cohort and model

Cohort	Array	Ancestry	Trans	Covars	Total	-SampleQc	-KinshipCrossArray	-KinshipArray	-missObs	-PcOutlier
META DCSP21M_EAS	DCSP21M	EAS	invn	Age+Age2+SEX+BMI	1864	44	0	0	14	0
META DCSP2610K_EAS	DCSP2610K	EAS	invn	Age+Age2+SEX+BMI	2087	36	0	0	11	10
META LBCHS_EAS	LBCHS	EAS	invn	Age+Age2+SEX+BMI	1263	22	52	122	4	15
META LBMAS_EAS	LBMAS	EAS	invn	Age+Age2+SEX+BMI	1185	40	5	240	17	0
META SCES_EAS	SCES	EAS	invn	Age+Age2+SEX+BMI	1889	42	93	2	8	0
META SIMES_EAS	SIMES	EAS	invn	Age+Age2+SEX+BMI	2542	47	160	115	18	32
META SINDI_SAS	SINDI	SAS	invn	Age+Age2+SEX+BMI	2537	60	15	91	7	49

Table 17: Summary of samples remaining for Systolic Blood Pressure analysis by cohort and model

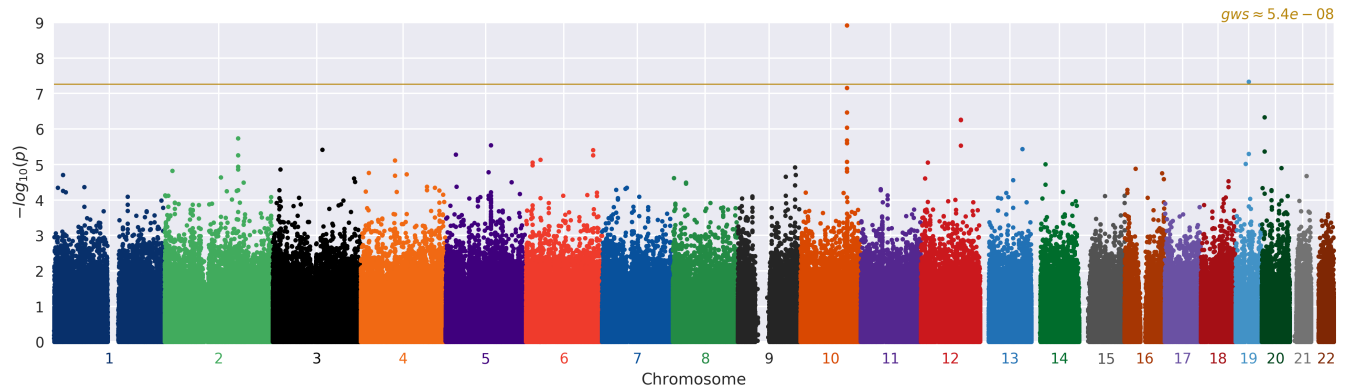
Cohort	Array	Ancestry	Trans	Covars	PCs	N	Male	Female	Max	Min	μ	\bar{x}	σ
META DCSP21M_EAS	DCSP21M	EAS	invn	Age+Age2+SEX+BMI	0	1806	1160	646	215.0	82.0	138.9	137.25	20.772
META DCSP2610K_EAS	DCSP2610K	EAS	invn	Age+Age2+SEX+BMI	0	2030	596	1434	215.0	89.5	138.6	140.0	21.896
META LBCHS_EAS	LBCHS	EAS	invn	Age+Age2+SEX+BMI	0	1048	522	526	197.0	76.5	114.626	112.0	16.392
META LBMAS_EAS	LBMAS	EAS	invn	Age+Age2+SEX+BMI	0	883	446	437	190.0	78.0	118.922	116.0	17.27
META SCES_EAS	SCES	EAS	invn	Age+Age2+SEX+BMI	0	1744	892	852	225.0	82.5	140.613	139.5	21.755
META SIMES_EAS	SIMES	EAS	invn	Age+Age2+SEX+BMI	0	2170	1096	1074	275.0	84.5	150.909	148.0	25.2
META SINDI_SAS	SINDI	SAS	invn	Age+Age2+SEX+BMI	0	2315	1176	1139	252.0	82.0	140.943	139.0	22.498

6.2 Calibration



(a) invn Adjusted Age+Age2+SEX+BMI

Figure 15: QQ plots for SBP15 in the META analysis



(a) invn Adjusted Age+Age2+SEX+BMI

Figure 16: Manhattan plots for SBP15 in the META analysis

6.3 Top associations

Table 18: Top variants in the META invn Adjusted Age+Age2+SEX+BMI model (**bold** variants indicate previously identified associations)

CHR	POS	ID	EA	OA	GENE _{CLOSEST}	DIR	N	MALE	FEMALE	FREQ _{AVG}	FREQ _{MIN}	FREQ _{MAX}	EFFECT	STDERR	OR	ZSCORE	P
10	104591393	rs17115100	G	T	CYP17A1	+++++++	11,995	5,888	6,107	0.296	0.246	0.343	$8.61 \cdot 10^{-2}$	$1.42 \cdot 10^{-2}$	1.09	-6.081	$1.2 \cdot 10^{-9}$
19	29633225	rs11668428	T	C	UQCRFS1	+xxxxxx	1,806	1,160	646	0.854	0.854	0.854	0.256	$4.68 \cdot 10^{-2}$	1.291	-5.467	$4.58 \cdot 10^{-8}$
10	104614350	rs3824754	C	T	BORCS7-ASMT	+++xxxx	10,065	4,920	5,145	0.283	0.213	0.342	$8.47 \cdot 10^{-2}$	$1.57 \cdot 10^{-2}$	1.088	-5.394	$6.9 \cdot 10^{-8}$
20	6322657	rs6139969	A	G	FERMT1	+++++++	11,991	5,885	6,106	0.557	0.283	0.673	$6.81 \cdot 10^{-2}$	$1.35 \cdot 10^{-2}$	1.071	5.04	$4.67 \cdot 10^{-7}$
12	90013089	rs2681492	T	C	ATP2B1	+++++++	11,982	5,883	6,099	0.289	0.206	0.329	$7.2 \cdot 10^{-2}$	$1.44 \cdot 10^{-2}$	1.075	-5.01	$5.44 \cdot 10^{-7}$
2	165004476	rs1446477	G	T	GRB14	+++xxxx	10,064	4,919	5,145	0.317	0.236	0.355	$7.19 \cdot 10^{-2}$	$1.51 \cdot 10^{-2}$	1.075	-4.772	$1.83 \cdot 10^{-6}$
10	104685299	rs12411886	C	A	CNNM2	+++xxxx	10,042	4,907	5,135	0.247	0.205	0.285	$7.75 \cdot 10^{-2}$	$1.63 \cdot 10^{-2}$	1.081	-4.743	$2.11 \cdot 10^{-6}$
5	101819981	rs981988	T	C	SLCO6A1	+++xxxx	11,092	5,431	5,661	0.349	0.262	0.43	$6.68 \cdot 10^{-2}$	$1.43 \cdot 10^{-2}$	1.069	-4.681	$2.86 \cdot 10^{-6}$
13	94568278	rs12855484	A	C	GPC6	+++++++	11,993	5,886	6,107	0.303	0.251	0.472	$6.56 \cdot 10^{-2}$	$1.42 \cdot 10^{-2}$	1.068	-4.632	$3.63 \cdot 10^{-6}$
3	111257405	rs1391361	G	T	CD96	+++++++	11,995	5,887	6,108	0.936	0.847	0.96	0.124	$2.67 \cdot 10^{-2}$	1.132	4.62	$3.83 \cdot 10^{-6}$
6	150931131	rs1492577	C	T	PLEKHG1	+++++++	11,993	5,887	6,106	0.135	0.103	0.161	$8.75 \cdot 10^{-2}$	$1.89 \cdot 10^{-2}$	1.091	4.617	$3.89 \cdot 10^{-6}$
5	23000050	rs13154490	T	C	CDH12	xxx+xxx	1,919	963	956	0.301	0.292	0.308	0.16	$3.51 \cdot 10^{-2}$	1.173	4.555	$5.25 \cdot 10^{-6}$
6	32804414	rs241427	G	A	TAP2	+++++++	11,989	5,885	6,104	0.704	0.629	0.783	$6.35 \cdot 10^{-2}$	$1.42 \cdot 10^{-2}$	1.066	4.483	$7.36 \cdot 10^{-6}$
4	77204500	rs1542096	C	T	FAM47E	+++++++	11,995	5,888	6,107	0.719	0.625	0.753	$6.44 \cdot 10^{-2}$	$1.44 \cdot 10^{-2}$	1.067	-4.476	$7.6 \cdot 10^{-6}$
6	14522827	rs9370746	T	C	CD83	xxx+xxx	1,931	968	963	0.284	0.274	0.293	0.158	$3.56 \cdot 10^{-2}$	1.171	4.446	$8.76 \cdot 10^{-6}$
12	16285538	rs17352791	T	C	SLC15A5	+++++++	11,962	5,873	6,089	0.172	0.153	0.216	$7.64 \cdot 10^{-2}$	$1.72 \cdot 10^{-2}$	1.079	-4.444	$8.82 \cdot 10^{-6}$
19	22846788	rs11672238	C	A	ZNF492	+x+++xx	3,731	2,126	1,605	0.128	$9.58 \cdot 10^{-2}$	0.141	0.153	$3.45 \cdot 10^{-2}$	1.165	-4.426	$9.62 \cdot 10^{-6}$
14	31844402	rs10134212	A	T	HEATR5A	+xxxxxx	1,806	1,160	646	0.161	0.161	0.161	0.201	$4.56 \cdot 10^{-2}$	1.223	4.422	$9.79 \cdot 10^{-6}$
9	128746044	rs7868608	A	G	PBX3	+++++++	11,974	5,879	6,095	0.734	0.646	0.771	$6.37 \cdot 10^{-2}$	$1.45 \cdot 10^{-2}$	1.066	-4.377	$1.2 \cdot 10^{-5}$
20	44130596	rs1883519	G	A	SPINT3	+++++++	11,990	5,884	6,106	$4.8 \cdot 10^{-2}$	$9.85 \cdot 10^{-4}$	0.218	0.142	$3.26 \cdot 10^{-2}$	1.153	-4.369	$1.25 \cdot 10^{-5}$

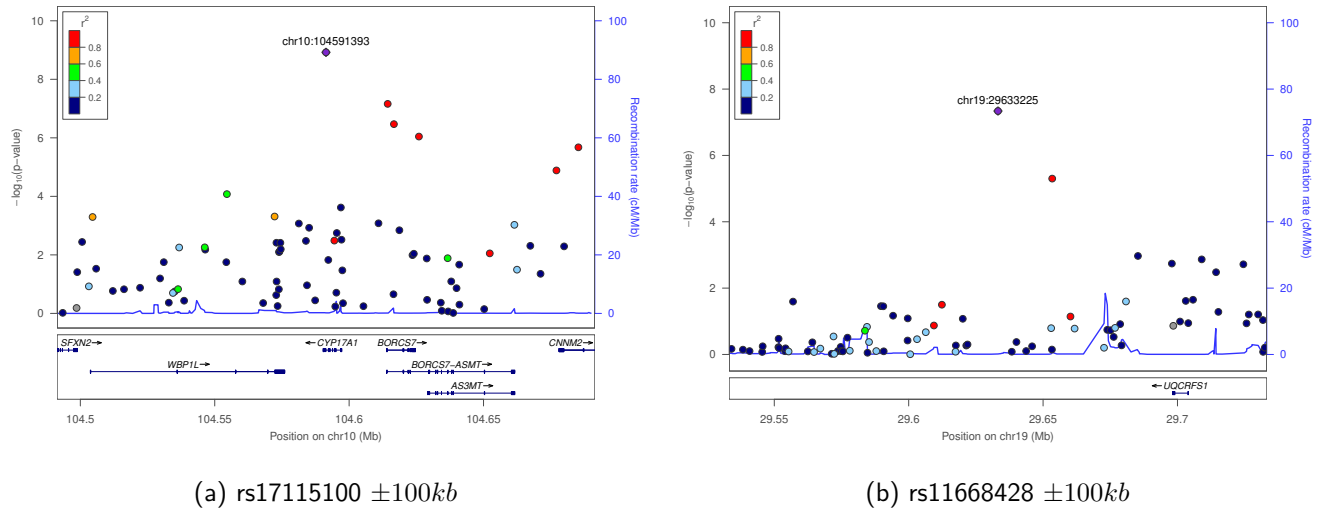


Figure 17: Regional plots for cohort META model invn Adjusted Age+Age2+SEX+BMI

6.4 Previously identified risk loci

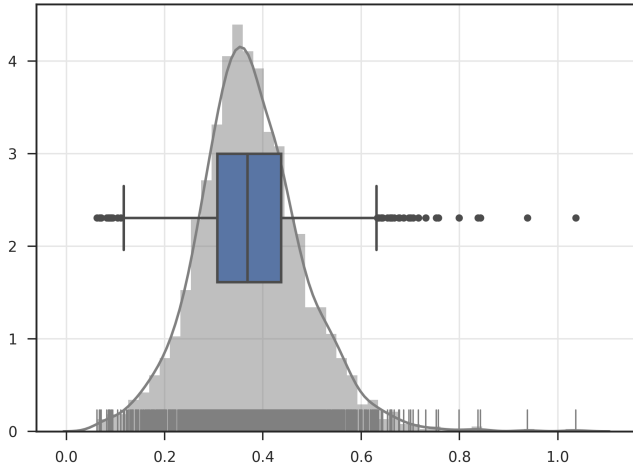
Table 19 shows statistics from the META cohort for 21 loci that were shown to be significantly associated with Systolic Blood Pressure in the 2011 Nature paper by Ehret et al [17]. Where a previously reported variant was not genotyped in the study (indicated by $\bar{R}^2 < 1$), if available, a tagging variant in LD with the reported variant ($\bar{R}^2 \geq 0.7$ and within 250kb) was provided. Tags were identified using 1000 Genomes data. There are 8 variants that show at least nominal significance ($p < 0.05$) in this study. Out of the 19 variants in both studies, 10 exhibit the same direction of effect with the known result (binomial test $p = 0.5$).

Table 19: Top known loci in META model invn Adjusted Age+Age2+SEX+BMI (**bold** variants indicate matching direction of effect)

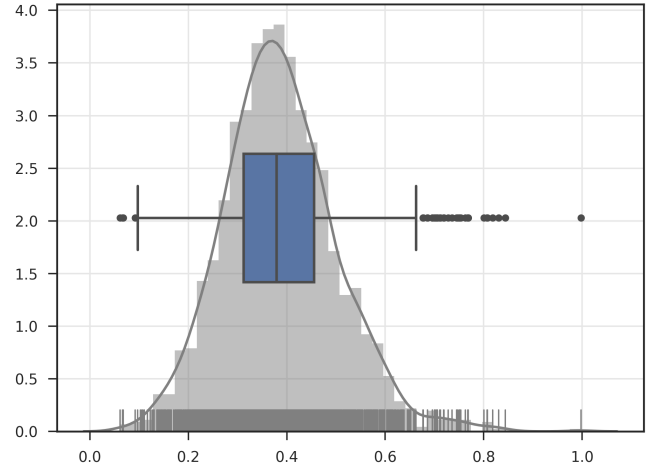
CHR	POS	ID	EA	OA	N	FREQ _{AVG}	FREQ _{MIN}	FREQ _{MAX}	EFFECT	STDERR	P	DIR	GENE _{CLOSEST}	R ²	ID _{KNOWN}	N _{KNOWN}	EFFECT _{KNOWN}	STDERR _{KNOWN}	P _{KNOWN}
12	90008959	rs2681472	A	G	11,990	0.289	0.205	0.324	7.19 · 10 ⁻²	1.43 · 10 ⁻²	5.34 · 10 ⁻⁷	++++++	ATP2B1	1	rs2681472	2 · 10 ⁵	-0.946	0.133	1.32 · 10 ⁻¹²
1	11862778	rs17367504	A	G	11,988	0.169	0.121	0.23	3.1 · 10 ⁻²	1.74 · 10 ⁻²	7.44 · 10 ⁻²	++++++	MTHFR	1	rs17367504	2 · 10 ⁵	-0.861	0.136	2.11 · 10 ⁻¹⁰
1	11883731	rs12567136	C	T	7,377	0.148	0.123	0.221	1.9 · 10 ⁻²	3.24 · 10 ⁻²	0.557	+x+++x	CLCN6	1	rs12567136	2 · 10 ⁵	-0.847	0.135	3.41 · 10 ⁻¹⁰
15	75077367	rs1378942	C	A	10,064	0.175	0.153	0.189	1.99 · 10 ⁻²	1.85 · 10 ⁻²	0.282	+x+++	CSK	1	rs1378942	2 · 10 ⁵	0.632	0.101	3.43 · 10 ⁻¹⁰
10	104939215	rs11191593	T	C	1,806	0.272	0.272	0.272	0.108	3.78 · 10 ⁻²	4.49 · 10 ⁻³	+xxxxxxx	NT5C2	1	rs11191593	2 · 10 ⁵	1.075	0.173	5.43 · 10 ⁻¹⁰
10	104594507	rs1004467	A	G	1,805	0.344	0.344	0.344	0.104	3.52 · 10 ⁻²	3.25 · 10 ⁻³	+xxxxxxx	CYP17A1	1	rs1004467	2 · 10 ⁵	-1.01	0.164	6.61 · 10 ⁻¹⁰
12	112007756	rs653178	T	C	8,319	0.983	0.946	1	9.19 · 10 ⁻²	6.16 · 10 ⁻²	0.136	+xxxx++	ATXN2	1	rs653178	2 · 10 ⁵	0.605	9.88 · 10 ⁻²	9.3 · 10 ⁻¹⁰
10	104614350	rs3824754	C	T	10,065	0.283	0.213	0.342	8.44 · 10 ⁻²	1.57 · 10 ⁻²	7.58 · 10 ⁻⁸	+xxxx++	BORCS7-ASMT	1	rs3824754	2 · 10 ⁵	-0.997	0.163	9.75 · 10 ⁻¹⁰
12	89942390	rs11105328	A	G	3,732	0.185	0.173	0.205	2.65 · 10 ⁻²	2.96 · 10 ⁻²	0.371	+x+++x	POC1B-GALNT4	1	rs11105328	2 · 10 ⁵	-0.838	0.137	1.08 · 10 ⁻⁹
10	104773364	rs11191514	C	T	7,375	0.262	0.209	0.285	0.118	2.65 · 10 ⁻²	8.41 · 10 ⁻⁶	+x+++x	CNNM2	1	rs11191514	2 · 10 ⁵	-1.056	0.174	1.24 · 10 ⁻⁹
12	111884608	rs3184504	C	T	8,321	0.983	0.946	1	9.91 · 10 ⁻²	6.16 · 10 ⁻²	0.107	+xxxx++	SH2B3	1	rs3184504	2 · 10 ⁵	-0.598	9.93 · 10 ⁻²	1.69 · 10 ⁻⁹
4	81164723	rs1458038	T	C	11,995	0.423	0.289	0.489	5.29 · 10 ⁻²	1.32 · 10 ⁻²	6.59 · 10 ⁻⁵	++++++	FGF5	1	rs1458038	2 · 10 ⁵	0.662	0.111	2.12 · 10 ⁻⁹
11	16902268	rs381815	T	C	1,930	0.158	0.163	0.163	1.98 · 10 ⁻²	4.46 · 10 ⁻²	0.657	x++-xxx	PLEKHA7	1	rs381815	2 · 10 ⁵	0.655	0.11	2.45 · 10 ⁻⁹
10	104546284	rs486955	T	C	3,737	0.586	0.55	0.688	6.68 · 10 ⁻²	2.41 · 10 ⁻²	5.51 · 10 ⁻³	+x+++x	WBP1L	1	rs486955	2 · 10 ⁵	0.895	0.156	9.47 · 10 ⁻⁹
12	112591686	rs17630235	G	A	1,806	2.77 · 10 ⁻⁴	2.77 · 10 ⁻⁴	2.77 · 10 ⁻⁴	0.503	1	0.615	+xxxxxxx	TRAFD1	1	rs17630235	2 · 10 ⁵	0.569	0.1	1.45 · 10 ⁻⁸
12	112610714	rs11066188	G	A	8,320	1.38 · 10 ⁻²	2.77 · 10 ⁻⁴	4.41 · 10 ⁻²	0.119	6.79 · 10 ⁻²	7.98 · 10 ⁻²	+xxxx++	HECTD4	1	rs11066188	2 · 10 ⁵	0.567	0.101	1.72 · 10 ⁻⁸
15	75107880	rs7176022	C	A	1,805	0.627	0.627	0.627	1.88 · 10 ⁻²	3.4 · 10 ⁻²	0.58	+xxxxxxx	LMAN1L	1	rs7176022	2 · 10 ⁵	0.602	0.107	2.11 · 10 ⁻⁸
15	75057203	rs4886406	T	G	11,995	0.667	0.605	0.773	1.2 · 10 ⁻²	1.37 · 10 ⁻²	0.381	++++++	CYP1A2	1	rs4886406	2 · 10 ⁵	0.599	0.108	3.06 · 10 ⁻⁸
10	104652323	rs11191447	C	T	1,797	0.273	0.273	0.273	9.78 · 10 ⁻²	3.74 · 10 ⁻²	8.87 · 10 ⁻³	+xxxxxxx	AS3MT	1	rs3740390	2 · 10 ⁵	-1.005	0.172	4.61 · 10 ⁻⁹
12	112591686	rs17630235	G	A	1,806	2.77 · 10 ⁻⁴	2.77 · 10 ⁻⁴	2.77 · 10 ⁻⁴	0.503	1	0.615	+xxxxxxx	NAA25	0.922	rs17696736	2 · 10 ⁵	0.549	9.96 · 10 ⁻²	3.43 · 10 ⁻⁸
12	112007756	rs653178	T	C	8,319	0.983	0.946	1	9.19 · 10 ⁻²	6.16 · 10 ⁻²	0.136	+xxxx++	BRAP	0.811	rs11065987	2 · 10 ⁵	-0.57	0.102	2.12 · 10 ⁻⁸

7 Estimated Glomerular Filtration Rate (eGFR)

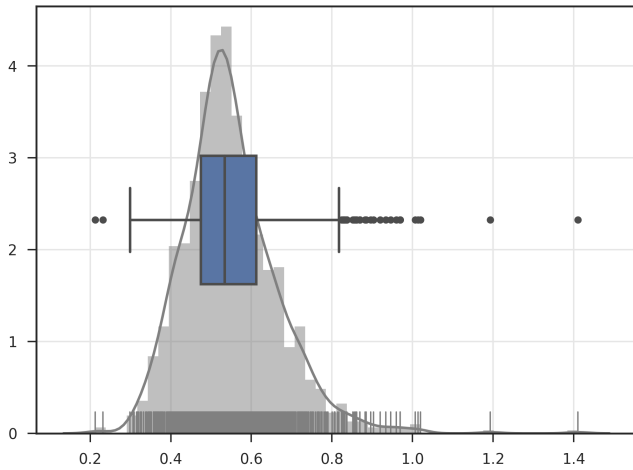
7.1 Summary



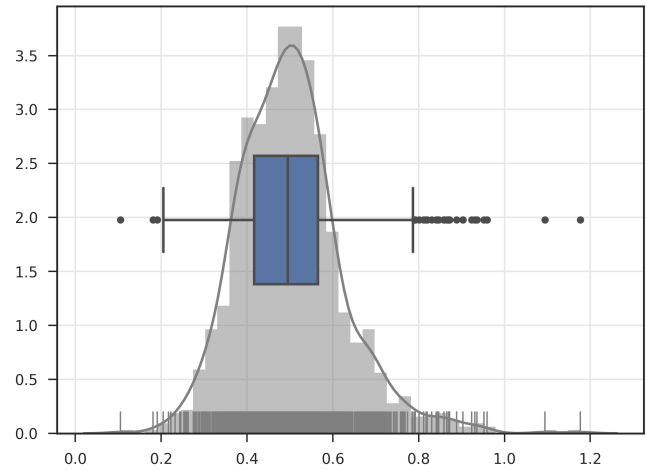
(a) DCSP21M_EAS



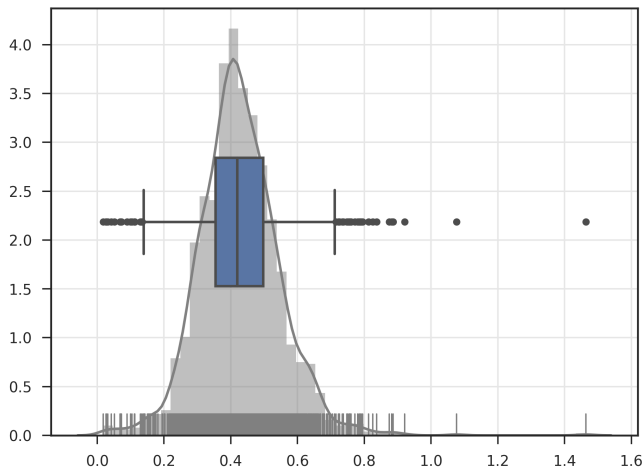
(b) DCSP2610K_EAS



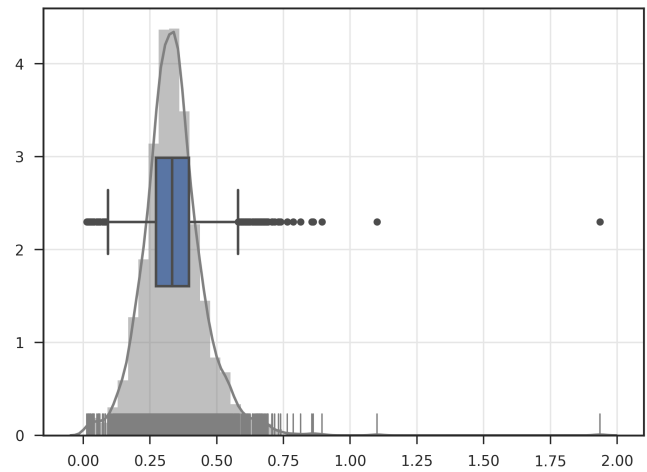
(c) LBCHS_EAS



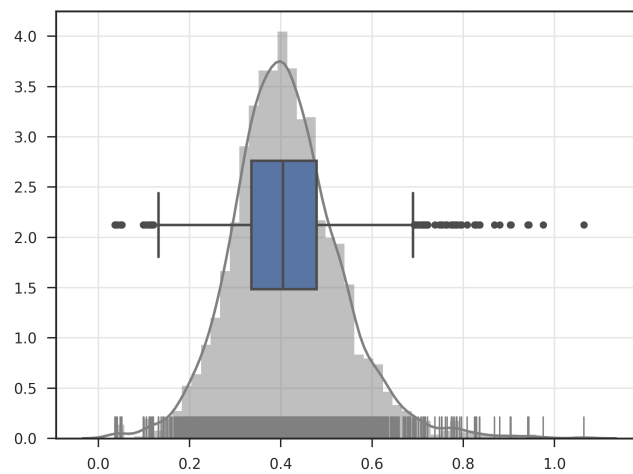
(d) LBMAS_EAS



(e) SCES_EAS



(f) SIMES_EAS



(g) SINDI_SAS

Figure 18: Distribution of eGFR in META by cohort

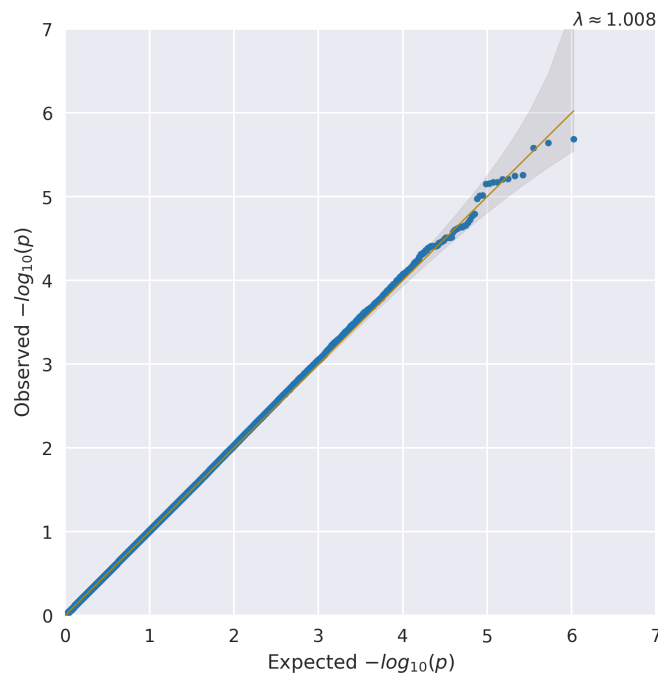
Table 20: Summary of samples removed from Estimated Glomerular Filtration Rate analysis by cohort and model

Cohort	Array	Ancestry	Trans	Covars	Total	-SampleQc	-KinshipCrossArray	-KinshipArray	-missObs	-PcOutlier
META DCSP21M_EAS	DCSP21M	EAS	invn		1864	44	0	0	25	5
META DCSP2610K_EAS	DCSP2610K	EAS	invn		2087	36	0	0	8	9
META LBCHS_EAS	LBCHS	EAS	invn		1263	22	52	122	0	12
META LBMAS_EAS	LBMAS	EAS	invn		1185	40	5	240	0	0
META SCES_EAS	SCES	EAS	invn		1889	42	93	2	2	4
META SIMES_EAS	SIMES	EAS	invn		2542	47	160	115	0	6
META SINDI_SAS	SINDI	SAS	invn		2537	60	15	91	1	0

Table 21: Summary of samples remaining for Estimated Glomerular Filtration Rate analysis by cohort and model

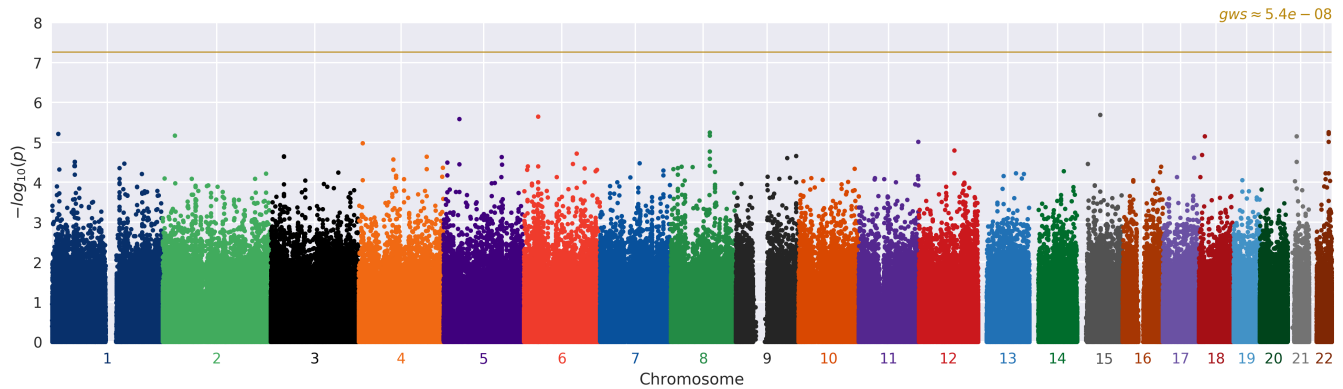
Cohort	Array	Ancestry	Trans	Covars	PCs	N	Male	Female	Max	Min	μ	\bar{x}	σ
META DCSP21M_EAS	DCSP21M	EAS	invn		4	1790	0	0	1.037	0.063	0.374	0.368	0.109
META DCSP2610K_EAS	DCSP2610K	EAS	invn		4	2034	0	0	0.997	0.061	0.387	0.379	0.115
META LBCHS_EAS	LBCHS	EAS	invn		0	1055	0	0	1.41	0.213	0.547	0.532	0.116
META LBMAS_EAS	LBMAS	EAS	invn		0	900	0	0	1.177	0.105	0.5	0.495	0.125
META SCES_EAS	SCES	EAS	invn		0	1746	0	0	1.464	0.018	0.427	0.419	0.12
META SIMES_EAS	SIMES	EAS	invn		6	2214	0	0	1.936	0.014	0.339	0.333	0.117
META SINDI_SAS	SINDI	SAS	invn		0	2370	0	0	1.065	0.036	0.412	0.405	0.119

7.2 Calibration



(a) invn Unadjusted

Figure 19: QQ plots for eGFR in the META analysis



(a) invn Unadjusted

Figure 20: Manhattan plots for eGFR in the META analysis

7.3 Top associations

Table 22: Top variants in the META invn Unadjusted model (**bold** variants indicate previously identified associations)

CHR	POS	ID	EA	OA	GENE _{CLOSEST}	DIR	N	MALE	FEMALE	FREQ _{AVG}	FREQ _{MIN}	FREQ _{MAX}	EFFECT	STDERR	OR	ZSCORE	P
15	51675625	rs2445738	T	C	GLDN	++xxxx+	10,151	4,961	5,190	0.495	0.472	0.528	$6.65 \cdot 10^{-2}$	$1.4 \cdot 10^{-2}$	1.069	4.748	$2.05 \cdot 10^{-6}$
6	31946614	rs6941112	A	G	STK19	+++++++	12,107	5,941	6,166	0.237	0.173	0.279	$7.1 \cdot 10^{-2}$	$1.5 \cdot 10^{-2}$	1.074	4.727	$2.28 \cdot 10^{-6}$
5	35031048	rs465974	A	G	AGXT2	+++++++	12,106	5,941	6,165	0.813	0.789	0.879	$7.75 \cdot 10^{-2}$	$1.65 \cdot 10^{-2}$	1.081	4.699	$2.61 \cdot 10^{-6}$
22	44195967	rs764310	C	A	EFCAB6	++x+xxx	3,735	2,131	1,604	0.992	0.991	0.993	0.58	0.128	1.785	-4.545	$5.49 \cdot 10^{-6}$
8	87614243	rs1441249	T	C	CNGB3	+++++++	12,106	5,943	6,163	0.275	0.261	0.309	$6.5 \cdot 10^{-2}$	$1.43 \cdot 10^{-2}$	1.067	-4.539	$5.66 \cdot 10^{-6}$
1	14496787	rs12568548	G	A	KAZN	+++++++	12,107	5,941	6,166	0.301	0.188	0.342	$6.35 \cdot 10^{-2}$	$1.41 \cdot 10^{-2}$	1.066	-4.522	$6.13 \cdot 10^{-6}$
22	44257056	rs8138048	G	A	SULT4A1	++x+xxx	3,745	2,132	1,613	$8.14 \cdot 10^{-3}$	$7.82 \cdot 10^{-3}$	$8.89 \cdot 10^{-3}$	0.581	0.129	1.788	4.52	$6.17 \cdot 10^{-6}$
2	27730940	rs1260326	T	C	GCKR	+++++++	12,108	5,943	6,165	0.596	0.512	0.8	$6.02 \cdot 10^{-2}$	$1.34 \cdot 10^{-2}$	1.062	-4.502	$6.73 \cdot 10^{-6}$
8	87578131	rs7000333	C	T	CPNE3	++xx++	10,153	4,963	5,190	0.323	0.266	0.47	$6.8 \cdot 10^{-2}$	$1.51 \cdot 10^{-2}$	1.07	-4.502	$6.74 \cdot 10^{-6}$
18	13890906	rs12954832	C	T	MC2R	+xxxx++	6,371	3,474	2,897	$1.62 \cdot 10^{-2}$	$5.59 \cdot 10^{-4}$	$3.93 \cdot 10^{-2}$	0.321	$7.14 \cdot 10^{-2}$	1.378	4.494	$6.98 \cdot 10^{-6}$
21	20204620	rs2825191	A	C	TMPRSS15	+++++++	12,052	5,915	6,137	0.953	0.847	0.987	0.14	$3.11 \cdot 10^{-2}$	1.15	-4.492	$7.07 \cdot 10^{-6}$
11	133796676	rs11223625	C	A	IGSF9B	xx+xxx	1,955	980	975	$9.1 \cdot 10^{-2}$	$7.63 \cdot 10^{-2}$	0.108	0.249	$5.62 \cdot 10^{-2}$	1.282	4.425	$9.65 \cdot 10^{-6}$
22	44276544	rs12485136	A	G	PNPLA5	++x+xxx	3,742	2,129	1,613	$8.42 \cdot 10^{-3}$	$8.08 \cdot 10^{-3}$	$8.89 \cdot 10^{-3}$	0.56	0.127	1.751	4.423	$9.72 \cdot 10^{-6}$
4	8593744	rs3756176	T	G	CPZ	+xxxxxx	1,790	1,152	638	0.351	0.351	0.351	0.151	$3.44 \cdot 10^{-2}$	1.164	-4.405	$1.06 \cdot 10^{-5}$
12	79804808	rs1405497	T	C	SYT1	++xx+++	10,153	4,962	5,191	0.286	0.269	0.307	$6.69 \cdot 10^{-2}$	$1.55 \cdot 10^{-2}$	1.069	4.314	$1.61 \cdot 10^{-5}$
6	118157833	rs4946293	A	C	SLC35F1	xx+xxx	1,955	980	975	0.167	0.134	0.196	0.182	$4.26 \cdot 10^{-2}$	1.2	4.277	$1.89 \cdot 10^{-5}$
18	7276969	rs10853347	G	A	LRRRC30	+++++++	12,099	5,938	6,161	0.504	0.43	0.654	$5.53 \cdot 10^{-2}$	$1.3 \cdot 10^{-2}$	1.057	-4.26	$2.05 \cdot 10^{-5}$
9	135658564	rs2809249	G	T	AK8	+xxxxxx	1,770	1,135	635	0.807	0.807	0.807	0.18	$4.24 \cdot 10^{-2}$	1.197	-4.244	$2.2 \cdot 10^{-5}$
3	29851445	rs7651843	G	A	RBMS3	++xx+++	10,153	4,962	5,191	0.125	$8.13 \cdot 10^{-2}$	0.225	$9.03 \cdot 10^{-2}$	$2.13 \cdot 10^{-2}$	1.095	-4.24	$2.23 \cdot 10^{-5}$
4	152557786	rs12651635	T	C	FAM160A1	xx+xxx	1,945	977	968	0.178	0.139	0.21	0.177	$4.18 \cdot 10^{-2}$	1.194	4.234	$2.3 \cdot 10^{-5}$

7.4 Previously identified risk loci

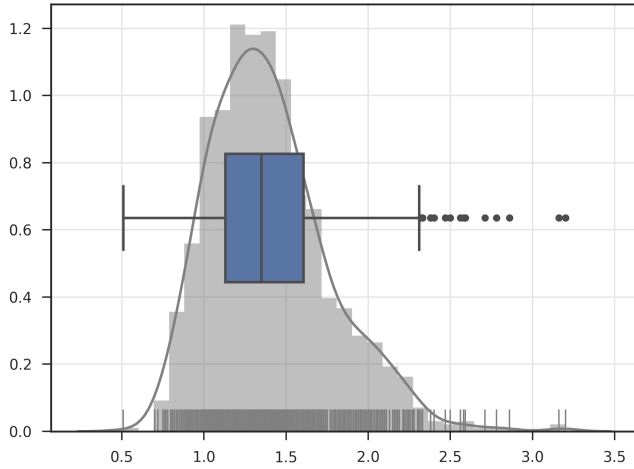
Table 23 shows statistics from the META cohort for 50 loci that were shown to be significantly associated with Estimated Glomerular Filtration Rate in the 2016 Nature Communications paper by Pattaro et al [12]. Where a previously reported variant was not genotyped in the study (indicated by $\bar{R}^2 < 1$), if available, a tagging variant in LD with the reported variant ($\bar{R}^2 \geq 0.7$ and within 250kb) was provided. Tags were identified using 1000 Genomes data. There are 15 variants that show at least nominal significance ($p < 0.05$) in this study. Out of the 50 variants in both studies, 42 exhibit the same direction of effect with the known result (binomial test $p = 5.82e - 07$).

Table 23: Top known loci in META model invn Unadjusted (**bold** variants indicate matching direction of effect)

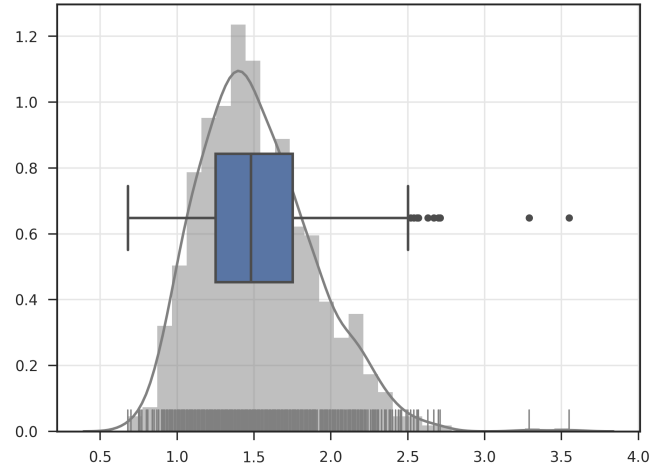
CHR	POS	ID	EA	OA	N	FREQ _{AVG}	FREQ _{MIN}	FREQ _{MAX}	EFFECT	STDERR	P	DIR	GENE _{CLOSEST}	R ²	ID _{KNOWN}	N _{KNOWN}	EFFECT _{KNOWN}	STDERR _{KNOWN}	P _{KNOWN}
15	45683795	rs1145077	G	T	1,790	0.915	0.915	0.915	0.103	5.98 · 10 ⁻²	8.59 · 10 ⁻²	+xxxxxxx	SPATA5L1	1	rs1145077	1.33 · 10 ⁵	1.2 · 10 ⁻²	9.2 · 10 ⁻⁴	3.5 · 10 ⁻⁴²
15	45640627	rs2461700	T	C	12,111	0.826	0.615	0.921	4.97 · 10 ⁻²	1.78 · 10 ⁻²	5.22 · 10 ⁻³	++++++++	GATM	1	rs2461700	1.33 · 10 ⁵	1.2 · 10 ⁻²	9.2 · 10 ⁻⁴	5 · 10 ⁻⁴²
16	20359831	rs13335818	C	T	3,745	2.22 · 10 ⁻²	1.14 · 10 ⁻²	5.5 · 10 ⁻²	1.73 · 10 ⁻²	7.86 · 10 ⁻²	0.826	-xxxxxxxx	UMOD	1	rs13335818	1.33 · 10 ⁵	-1.5 · 10 ⁻²	1.1 · 10 ⁻³	2 · 10 ⁻⁴¹
4	77410318	rs4859682	C	A	12,112	0.196	0.134	0.232	6.84 · 10 ⁻²	1.63 · 10 ⁻²	2.71 · 10 ⁻⁵	+xxxxxxxx	SHROOM3	1	rs4859682	1.33 · 10 ⁵	1.1 · 10 ⁻²	9.2 · 10 ⁻⁴	1.2 · 10 ⁻³⁶
5	45723983	rs1547487	A	G	3,744	0.785	0.659	0.83	6.82 · 10 ⁻²	2.85 · 10 ⁻²	1.67 · 10 ⁻²	+x-xxxxx	C15orf48	1	rs1547487	1.33 · 10 ⁵	1.1 · 10 ⁻²	9.2 · 10 ⁻⁴	2 · 10 ⁻³²
16	20400839	rs11864909	T	C	12,112	0.15	0.116	0.276	4.73 · 10 ⁻²	1.81 · 10 ⁻²	8.89 · 10 ⁻³	+xxxxxxxx	PDILT	1	rs11864909	1.33 · 10 ⁵	1.2 · 10 ⁻²	1 · 10 ⁻³	1 · 10 ⁻³⁰
7	151407801	rs7805747	G	A	10,154	1.8 · 10 ⁻²	4.92 · 10 ⁻⁴	6.77 · 10 ⁻²	0.127	5.34 · 10 ⁻²	1.73 · 10 ⁻²	+xxxx+++	PRKAG2	1	rs7805747	1.33 · 10 ⁵	1.3 · 10 ⁻²	1.1 · 10 ⁻³	8 · 10 ⁻²⁹
15	45609773	rs1719250	A	G	1,790	8.21 · 10 ⁻²	8.21 · 10 ⁻²	8.21 · 10 ⁻²	0.119	6.06 · 10 ⁻²	5 · 10 ⁻²	+xxxxxxxx	SLC28A2	1	rs1719250	1.33 · 10 ⁵	1 · 10 ⁻²	9.2 · 10 ⁻⁴	4.5 · 10 ⁻²⁷
15	45801035	rs950027	T	C	1,954	0.885	0.824	0.937	5.8 · 10 ⁻²	5.13 · 10 ⁻²	0.258	xxx+xxxx	SLC30A4	1	rs950027	1.33 · 10 ⁵	8.8 · 10 ⁻³	9.2 · 10 ⁻⁴	8.1 · 10 ⁻²³
5	176817636	rs6420094	A	G	10,153	0.217	0.158	0.318	5.02 · 10 ⁻²	1.71 · 10 ⁻²	3.38 · 10 ⁻³	+xxxxxxxx	SLC3A4	1	rs6420094	1.33 · 10 ⁵	9.6 · 10 ⁻³	1 · 10 ⁻³	4.9 · 10 ⁻²²
5	176801131	rs10866705	A	C	12,103	0.812	0.749	0.859	3.92 · 10 ⁻²	1.66 · 10 ⁻²	1.81 · 10 ⁻²	-+++++	RGS14	1	rs10866705	1.33 · 10 ⁵	9.9 · 10 ⁻³	1 · 10 ⁻³	1.2 · 10 ⁻²¹
2	211543055	rs715	T	C	1,790	0.188	0.188	0.188	4.62 · 10 ⁻²	4.3 · 10 ⁻²	0.282	+xxxxxxxx	CPS1	1	rs715	1.33 · 10 ⁵	9.6 · 10 ⁻³	1 · 10 ⁻³	2.3 · 10 ⁻²¹
17	59450441	rs9905274	C	T	1,953	0.501	0.494	0.507	9.16 · 10 ⁻³	3.15 · 10 ⁻²	0.771	x-xxxxx	BCAS3	1	rs9905274	1.33 · 10 ⁵	1.1 · 10 ⁻²	1.2 · 10 ⁻³	1.4 · 10 ⁻²⁰
5	39368176	rs700237	A	G	1,790	5.25 · 10 ⁻²	5.25 · 10 ⁻²	5.25 · 10 ⁻²	0.112	7.55 · 10 ⁻²	0.138	+xxxxxxxx	C9	1	rs700237	1.33 · 10 ⁵	8.2 · 10 ⁻³	9.2 · 10 ⁻⁴	2.3 · 10 ⁻²⁰
5	39381357	rs835223	C	T	10,158	0.138	4.23 · 10 ⁻²	0.37	4.02 · 10 ⁻²	2.21 · 10 ⁻²	6.93 · 10 ⁻²	+xxxxxxxx	DAB2	1	rs835223	1.33 · 10 ⁵	8.1 · 10 ⁻³	9.2 · 10 ⁻⁴	4.1 · 10 ⁻²⁰
2	73679280	rs6546838	G	A	12,108	2.89 · 10 ⁻²	3.14 · 10 ⁻³	0.119	2.87 · 10 ⁻²	3.92 · 10 ⁻²	0.463	+xxxxxxxx	ALMS1	1	rs6546838	1.33 · 10 ⁵	9.3 · 10 ⁻³	1 · 10 ⁻³	7.7 · 10 ⁻²⁰
4	77296600	rs1876535	T	C	10,156	9.6 · 10 ⁻²	5.11 · 10 ⁻²	0.122	4.85 · 10 ⁻²	2.38 · 10 ⁻²	4.17 · 10 ⁻²	+xxxxxxxx	CCDC158	1	rs1876535	1.33 · 10 ⁵	8.1 · 10 ⁻³	9.2 · 10 ⁻⁴	8.9 · 10 ⁻²⁰
4	77208837	rs12506745	T	G	3,743	0.127	8.4 · 10 ⁻²	0.143	8.75 · 10 ⁻²	3.46 · 10 ⁻²	1.13 · 10 ⁻²	+x-xxxxx	FAM47E-STBD1	1	rs12506745	1.33 · 10 ⁵	8 · 10 ⁻³	9.2 · 10 ⁻⁴	3.7 · 10 ⁻¹⁹
6	160675764	rs316009	T	C	12,111	0.946	0.87	0.973	3.81 · 10 ⁻²	2.87 · 10 ⁻²	0.184	+xxxx+	SLC22A2	1	rs316009	1.33 · 10 ⁵	1.3 · 10 ⁻²	1.4 · 10 ⁻³	4.4 · 10 ⁻¹⁹
11	30749090	rs963837	C	T	10,154	0.348	0.274	0.387	3.01 · 10 ⁻²	1.48 · 10 ⁻²	4.2 · 10 ⁻²	+xxxxxxxx	DCDC1	1	rs963837	1.33 · 10 ⁵	7.8 · 10 ⁻³	9.2 · 10 ⁻⁴	5.7 · 10 ⁻¹⁸
4	77228724	rs3796491	C	A	3,738	0.784	0.758	0.796	2.76 · 10 ⁻²	2.76 · 10 ⁻²	0.316	+x-xxxxx	STBD1	1	rs3796491	1.33 · 10 ⁵	-7.2 · 10 ⁻³	9.2 · 10 ⁻⁴	1.9 · 10 ⁻¹⁵
8	23728271	rs6999484	A	G	3,743	0.291	0.277	0.333	4.96 · 10 ⁻³	2.55 · 10 ⁻²	0.846	+xxxxxxx	STC1	1	rs6999484	1.33 · 10 ⁵	-7.1 · 10 ⁻³	9.2 · 10 ⁻⁴	1.9 · 10 ⁻¹⁵
15	53960628	rs17549749	G	A	12,113	0.489	0.43	0.654	1.05 · 10 ⁻²	1.31 · 10 ⁻²	0.423	-+++++	WDR72	1	rs17549749	1.33 · 10 ⁵	7.7 · 10 ⁻³	1 · 10 ⁻³	5.6 · 10 ⁻¹⁵
6	43806609	rs881858	G	A	1,955	0.779	0.772	0.786	3.88 · 10 ⁻²	3.79 · 10 ⁻²	0.305	xxx+xxxxx	VEGFA	1	rs881858	1.33 · 10 ⁵	8.1 · 10 ⁻³	1 · 10 ⁻³	7.5 · 10 ⁻¹⁵
9	71433212	rs1556751	G	A	12,107	0.671	0.607	0.769	2.37 · 10 ⁻²	1.38 · 10 ⁻²	0.986	+-----	PIP5K1B	1	rs1556751	1.33 · 10 ⁵	-7 · 10 ⁻³	9.2 · 10 ⁻⁴	9.9 · 10 ⁻¹⁵
17	37525274	rs6503507	T	C	1,789	0.299	0.299	0.299	4.03 · 10 ⁻²	3.68 · 10 ⁻²	0.274	+xxxxxxxx	FBXL20	1	rs6503507	1.33 · 10 ⁵	7.6 · 10 ⁻³	1 · 10 ⁻³	1.5 · 10 ⁻¹⁴
17	37665554	rs12936996	G	A	1,787	0.702	0.702	0.702	4.54 · 10 ⁻²	3.68 · 10 ⁻²	0.217	+xxxxxxxx	CDK12	1	rs12936996	1.33 · 10 ⁵	7.6 · 10 ⁻³	1 · 10 ⁻³	2.4 · 10 ⁻¹⁴
2	27730940	rs1260326	T	C	12,112	0.596	0.512	0.8	6 · 10 ⁻²	1.34 · 10 ⁻²	7.2 · 10 ⁻⁶	+xxxxxxxx	GCKR	1	rs1260326	1.33 · 10 ⁵	6.8 · 10 ⁻³	9.2 · 10 ⁻⁴	3.4 · 10 ⁻¹⁴
17	37576417	rs7501488	T	G	1,789	0.703	0.703	0.703	4.69 · 10 ⁻²	3.68 · 10 ⁻²	0.202	+xxxxxxxx	MED1	1	rs7501488	1.33 · 10 ⁵	7.5 · 10 ⁻³	1 · 10 ⁻³	3.8 · 10 ⁻¹⁴
9	71397747	rs2017	C	T	3,745	0.567	0.541	0.646	1.47 · 10 ⁻²	2.36 · 10 ⁻²	0.535	+x-xxxxx	FAM122A	1	rs2017	1.33 · 10 ⁵	6.8 · 10 ⁻³	9.2 · 10 ⁻⁴	4.7 · 10 ⁻¹⁴
2	73878352	rs6759452	T	C	3,744	4.41 · 10 ⁻³	1.42 · 10 ⁻³	1.28 · 10 ⁻²	0.137	0.17	0.423	+x-xxxxx	NAT8	1	rs6759452	1.33 · 10 ⁵	9 · 10 ⁻³	1.2 · 10 ⁻³	4.7 · 10 ⁻¹⁴
15	76159893	rs1394125	G	A	12,113	0.106	6.62 · 10 ⁻³	0.207	1.96 · 10 ⁻²	2.11 · 10 ⁻²	0.354	+-----	UBE2Q2	1	rs1394125	1.33 · 10 ⁵	7.3 · 10 ⁻³	1 · 10 ⁻³	5.5 · 10 ⁻¹⁴
6	160735281	rs3125056	C	T	10,155	3.62 · 10 ⁻²	9.08 · 10 ⁻³	5.63 · 10 ⁻²	2.29 · 10 ⁻²	3.77 · 10 ⁻²	0.543	+xxxx++	SLC22A3	1	rs3125056	1.33 · 10 ⁵	-1 · 10 ⁻²	1.3 · 10 ⁻³	8.6 · 10 ⁻¹⁴
17	37739274	rs1619021	G	A	1,790	0.701	0.701	0.701	5.15 · 10 ⁻²	3.68 · 10 ⁻²	0.162	+xxxxxxxx	NEUROD2	1	rs1619021	1.33 · 10 ⁵	7.4 · 10 ⁻³	1 · 10 ⁻³	1.3 · 10 ⁻¹³
3	141812759	rs9877817	G	A	10,155	0.805	0.763	0.862	1.37 · 10 ⁻²	1.78 · 10 ⁻²	0.442	+xxxx++	TFDP2	1	rs9877817	1.33 · 10 ⁵	7.2 · 10 ⁻³	1 · 10 ⁻³	1.4 · 10 ⁻¹³
15	76304503	rs10851885	A	G	10,361	3.16 · 10 ⁻²	2.46 · 10 ⁻⁴	0.123	4.13 · 10 ⁻²	4.12 · 10 ⁻²	0.315	---xxxx	NRG4	1	rs10851885	1.33 · 10 ⁵	7.5 · 10 ⁻³	1 · 10 ⁻³	2.5 · 10 ⁻¹³
15	59483766	rs8068318	T	C	1,953	0.332	0.325	0.339	3.2 · 10 ⁻²	3.38 · 10 ⁻²	0.343	xxx+xxxx	TBX2	1	rs8068318	1.33 · 10 ⁵	7.6 · 10 ⁻³	1 · 10 ⁻³	3 · 10 ⁻¹³
4	77198986	rs6812193	C	T	12,110	0.118	7.63 · 10 ⁻²	0.272	2.51 · 10 ⁻²	2.04 · 10 ⁻²	0.99	+xxxx+	FAM47E	1	rs6812193	1.33 · 10 ⁵	-6.6 · 10 ⁻³	9.2 · 10 ⁻⁴	4.1 · 10 ⁻¹³
20	52732362	rs17216707	C	T	1,790	3.83 · 10 ⁻²	3.83 · 10 ⁻²	3.83 · 10 ⁻²	0.121	8.79 · 10 ⁻²	0.169	+xxxxxxxx	CYP24A1	1	rs17216707	1.33 · 10 ⁵	8.4 · 10 ⁻³	1.1 · 10 ⁻³	6 · 10 ⁻¹³
19	33364628	rs8101881	T	C	12,111	0.38	0.29	0.538	2.73 · 10 ⁻³	1.34 · 10 ⁻²	0.839	+xxxx++	CEP89	1	rs8101881	1.33 · 10 ⁵	-6.4 · 10 ⁻³	9.2 · 10 ⁻⁴	8.1 · 10 ⁻¹²
5	176755841	rs6860069	T	C	1,787	7.19 · 10 ⁻²	7.19 · 10 ⁻²	7.19 · 10 ⁻²	1.74 · 10 ⁻²	6.58 · 10 ⁻²	0.792	+xxxxxxxx	LMAN2	1	rs6860069	1.33 · 10 ⁵	-6.8 · 10 ⁻³	9.2 · 10 ⁻⁴	8.2 · 10 ⁻¹²
7	77463843	rs11772392	C	T	10,156	0.198	0.135	0.335	5.16 · 10 ⁻²	1.78 · 10 ⁻²	3.81 · 10 ⁻³	+xxxx++	PHF2	1	rs11772392	1.33 · 10 ⁵	7.1 · 10 ⁻³	1 · 10 ⁻³	8.8 · 10 ⁻¹²
7	77423152	rs1045463	C	T	3,744	0.149	0.136	0.181	5.23 · 10 ⁻²	3.18 · 10 ⁻²	0.1	+x-xxxxx	TMEM60	1	rs1045463	1.33 · 10 ⁵	7 · 10 ⁻³	1 · 10 ⁻³	1.1 · 10 ⁻¹²
1	150040625	rs267738	G	T	12,113	2.8 · 10 ⁻²	8.8												

8 HDL Cholesterol (HDL)

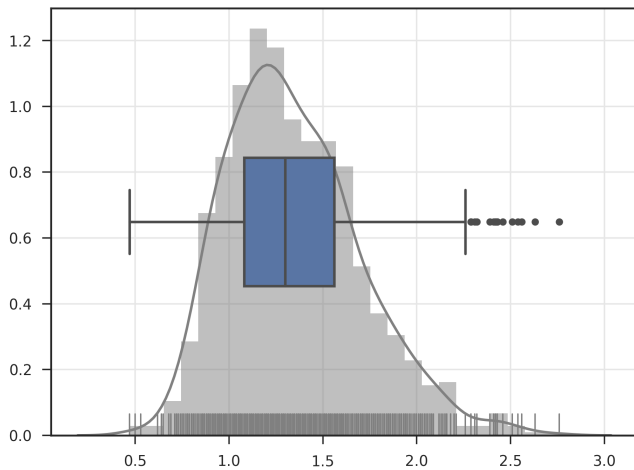
8.1 Summary



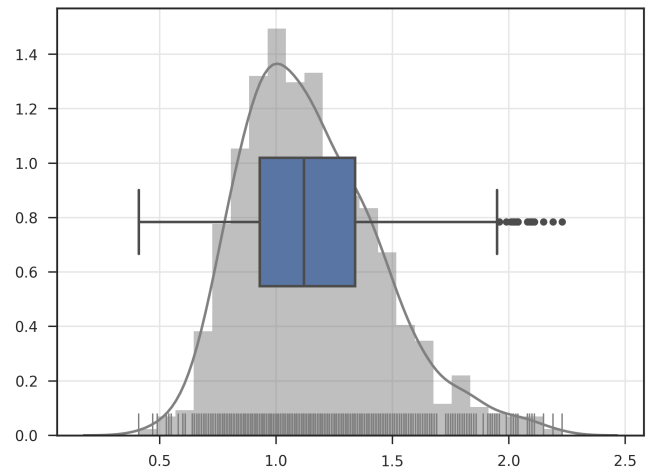
(a) DCSP21M_EAS



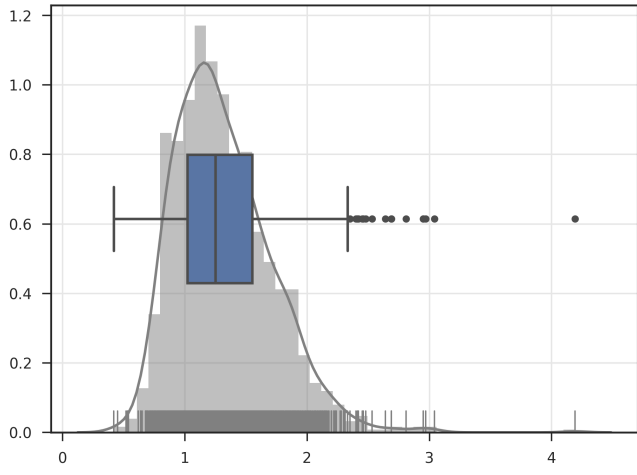
(b) DCSP2610K_EAS



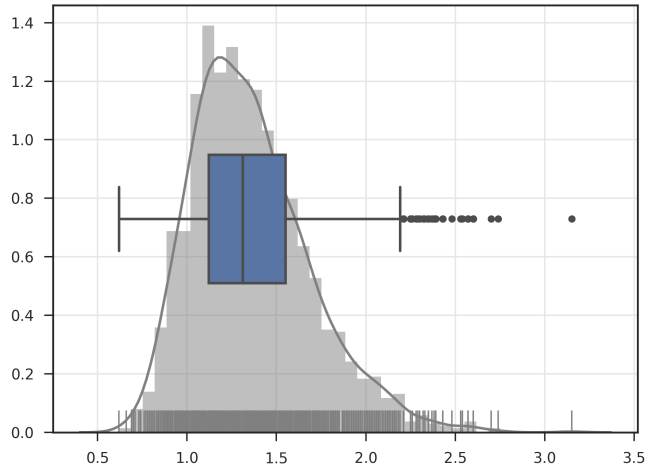
(c) LBCHS_EAS



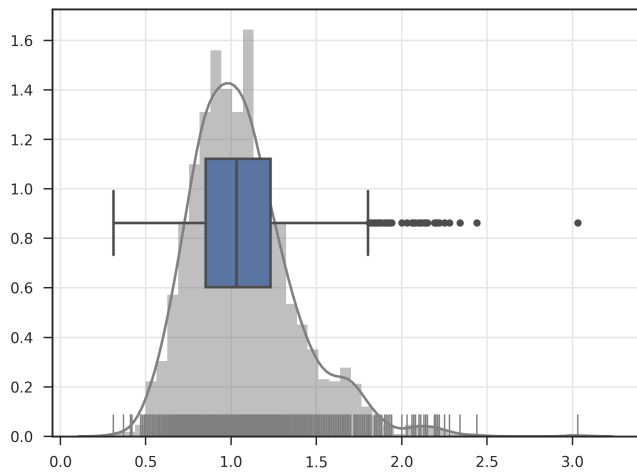
(d) LBMAS_EAS



(e) SCES_EAS



(f) SIMES_EAS



(g) SINDI_SAS

Figure 21: Distribution of HDL in META by cohort

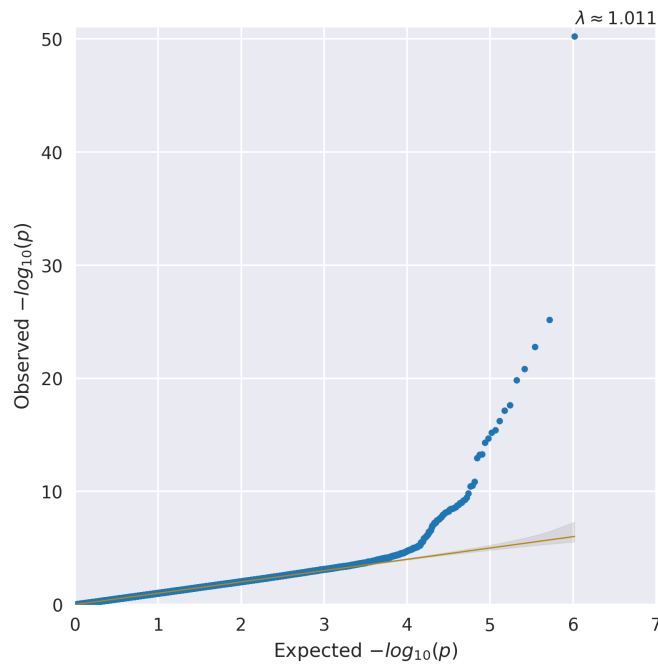
Table 24: Summary of samples removed from HDL Cholesterol analysis by cohort and model

Cohort	Array	Ancestry	Trans	Covars	Total	-SampleQc	-KinshipCrossArray	-KinshipArray	-missObs	-PcOutlier
META DCSP21M_EAS	DCSP21M	EAS	invn	Age+Age2+SEX+BMI	1864	44	0	0	765	2
META DCSP2610K_EAS	DCSP2610K	EAS	invn	Age+Age2+SEX+BMI	2087	36	0	0	909	0
META LBCHS_EAS	LBCHS	EAS	invn	Age+Age2+SEX+BMI	1263	22	52	122	33	12
META LBMAS_EAS	LBMAS	EAS	invn	Age+Age2+SEX+BMI	1185	40	5	240	42	0
META SCES_EAS	SCES	EAS	invn	Age+Age2+SEX+BMI	1889	42	93	2	416	0
META SIMES_EAS	SIMES	EAS	invn	Age+Age2+SEX+BMI	2542	47	160	115	279	0
META SINDI_SAS	SINDI	SAS	invn	Age+Age2+SEX+BMI	2537	60	15	91	718	78

Table 25: Summary of samples remaining for HDL Cholesterol analysis by cohort and model

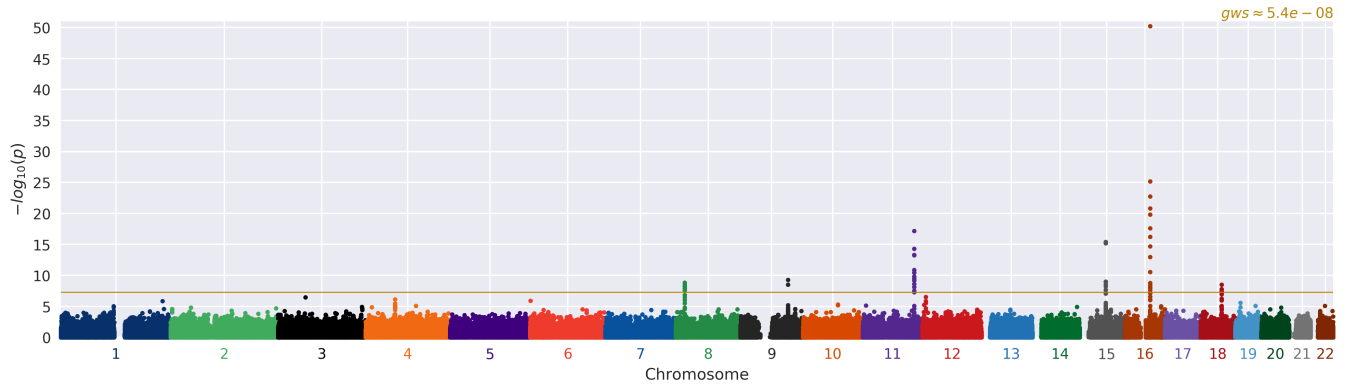
Cohort	Array	Ancestry	Trans	Covars	PCs	N	Male	Female	Max	Min	μ	\bar{x}	σ
META DCSP21M_EAS	DCSP21M	EAS	invn	Age+Age2+SEX+BMI	2	1053	686	367	3.2	0.51	1.401	1.35	0.369
META DCSP2610K_EAS	DCSP2610K	EAS	invn	Age+Age2+SEX+BMI	1	1142	258	884	3.55	0.68	1.519	1.48	0.371
META LBCHS_EAS	LBCHS	EAS	invn	Age+Age2+SEX+BMI	0	1022	504	518	2.76	0.47	1.345	1.3	0.358
META LBMAS_EAS	LBMAS	EAS	invn	Age+Age2+SEX+BMI	0	858	433	425	2.23	0.41	1.156	1.12	0.301
META SCES_EAS	SCES	EAS	invn	Age+Age2+SEX+BMI	0	1336	676	660	4.19	0.42	1.315	1.25	0.394
META SIMES_EAS	SIMES	EAS	invn	Age+Age2+SEX+BMI	0	1941	978	963	3.15	0.62	1.357	1.31	0.332
META SINDI_SAS	SINDI	SAS	invn	Age+Age2+SEX+BMI	2	1575	789	786	3.03	0.31	1.064	1.02	0.31

8.2 Calibration



(a) invn Adjusted Age+Age2+SEX+BMI

Figure 22: QQ plots for HDL in the META analysis



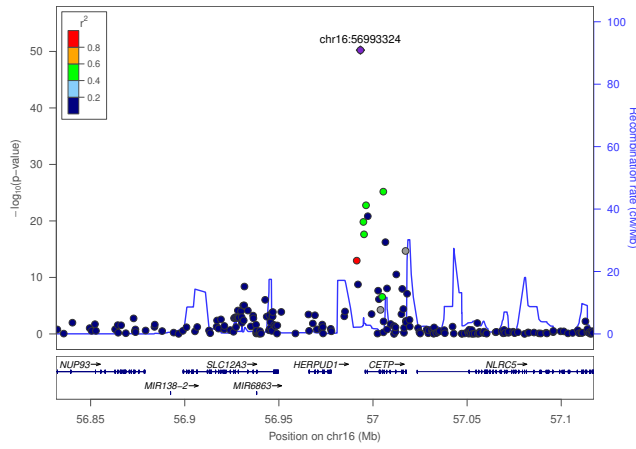
(a) invn Adjusted Age+Age2+SEX+BMI

Figure 23: Manhattan plots for HDL in the META analysis

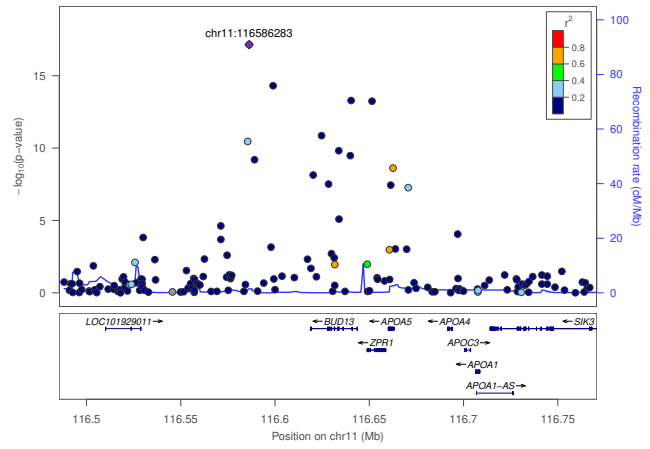
8.3 Top associations

Table 26: Top variants in the META invn Adjusted Age+Age2+SEX+BMI model (**bold** variants indicate previously identified associations)

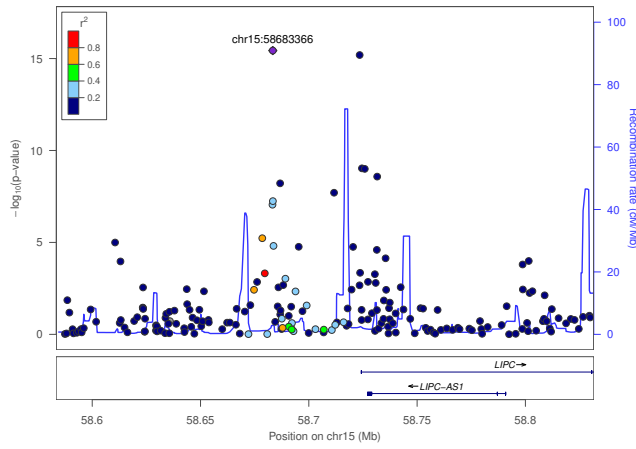
CHR	POS	ID	EA	OA	GENE _{CLOSEST}	DIR	N	MALE	FEMALE	FREQ _{AVG}	FREQ _{MIN}	FREQ _{MAX}	EFFECT	STDERR	OR	ZSCORE	P
16	56993324	rs3764261	A	C	CETP	+++++++	8,925	4,322	4,603	0.175	0.134	0.283	0.29	1.93 · 10 ⁻²	1.337	15.014	5.9 · 10 ⁻⁵¹
11	116586283	rs7350481	C	T	BUD13	+++xxxx	7,044	3,385	3,659	0.748	0.712	0.773	0.166	1.93 · 10 ⁻²	1.181	8.613	7.11 · 10 ⁻¹⁸
15	58683366	rs1532085	A	G	LIPC	+++++++	8,913	4,318	4,595	0.514	0.444	0.574	0.121	1.49 · 10 ⁻²	1.129	-8.149	3.68 · 10 ⁻¹⁶
11	116651463	rs1942478	G	T	ZPR1	+++++++	8,927	4,324	4,603	0.293	0.276	0.3	0.123	1.64 · 10 ⁻²	1.131	7.515	5.71 · 10 ⁻¹⁴
9	107665739	rs2575876	G	A	ABCA1	+++++++	8,926	4,323	4,603	0.287	0.229	0.421	0.103	1.66 · 10 ⁻²	1.109	-6.211	5.27 · 10 ⁻¹⁰
8	19871637	rs2410629	C	T	LPL	+++++++	8,911	4,318	4,593	0.198	0.145	0.314	0.114	1.89 · 10 ⁻²	1.121	6.044	1.5 · 10 ⁻⁹
11	116662579	rs651821	T	C	APOA5	+x++xxx	2,930	1,621	1,309	0.728	0.72	0.736	0.175	2.93 · 10 ⁻²	1.191	5.968	2.4 · 10 ⁻⁹
18	47179516	rs1943973	A	G	LIPG	+++++++	8,919	4,320	4,599	0.828	0.802	0.897	0.118	2 · 10 ⁻²	1.126	5.917	3.27 · 10 ⁻⁹
16	56931704	rs7187932	G	A	SLC12A3	+++++++	8,927	4,324	4,603	0.313	0.269	0.384	9.45 · 10 ⁻²	1.61 · 10 ⁻²	1.099	-5.881	4.07 · 10 ⁻⁹
12	7729433	ss1388044986	G	A	APOBEC1	+++xxxx	7,041	3,385	3,656	0.326	0.148	0.414	9.39 · 10 ⁻²	1.83 · 10 ⁻²	1.099	5.127	2.95 · 10 ⁻⁷
3	61368839	rs12636375	T	C	FHIT	+xxxxxx	1,053	686	367	0.311	0.311	0.311	0.248	4.87 · 10 ⁻²	1.282	5.095	3.49 · 10 ⁻⁷
4	66280171	rs2305351	T	C	EPHA5	+++++++	8,924	4,323	4,601	0.266	0.211	0.298	8.37 · 10 ⁻²	1.69 · 10 ⁻²	1.087	4.963	6.93 · 10 ⁻⁷
6	1488725	rs7762812	G	A	FOXF2	xx+++xxx	1,880	937	943	0.975	0.975	0.976	0.501	0.103	1.651	-4.845	1.26 · 10 ⁻⁶
1	230168963	rs4847027	G	A	GALNT2	+++++++	8,913	4,316	4,597	0.43	0.309	0.473	7.28 · 10 ⁻²	1.51 · 10 ⁻²	1.076	-4.835	1.33 · 10 ⁻⁶
15	58557062	rs17821159	A	G	ALDH1A2	+++++++	8,920	4,322	4,598	0.116	5.75 · 10 ⁻²	0.234	0.113	2.4 · 10 ⁻²	1.119	-4.709	2.49 · 10 ⁻⁶
19	11347493	rs737337	T	C	DOCK6	+++++++	8,927	4,324	4,603	0.196	0.11	0.277	8.95 · 10 ⁻²	1.91 · 10 ⁻²	1.094	-4.697	2.64 · 10 ⁻⁶
12	7727544	ss1388044932	T	C	CD163	+++xxxx	7,044	3,385	3,659	0.615	0.573	0.693	8.1 · 10 ⁻²	1.73 · 10 ⁻²	1.084	-4.67	3.01 · 10 ⁻⁶
10	79378558	rs1878001	C	T	KCNMA1	+++++++	8,927	4,324	4,603	0.17	0.151	0.222	9.06 · 10 ⁻²	1.98 · 10 ⁻²	1.095	-4.565	5 · 10 ⁻⁶
12	4158184	rs10492325	A	C	PARP11	+++xxxx	7,047	3,387	3,660	4.42 · 10 ⁻²	3.37 · 10 ⁻²	6 · 10 ⁻²	0.186	4.1 · 10 ⁻²	1.204	-4.539	5.66 · 10 ⁻⁶
11	7272026	rs2055708	C	T	SYT9	+++++++	8,922	4,322	4,600	0.738	0.696	0.776	7.59 · 10 ⁻²	1.69 · 10 ⁻²	1.079	-4.485	7.31 · 10 ⁻⁶



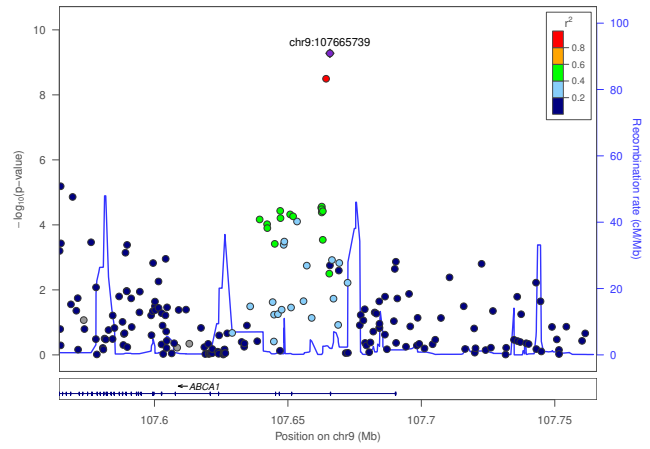
(a) rs3764261 ±100kb



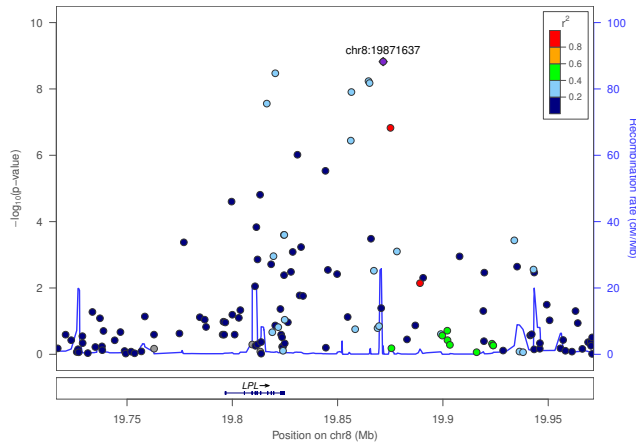
(b) rs7350481 ±100kb



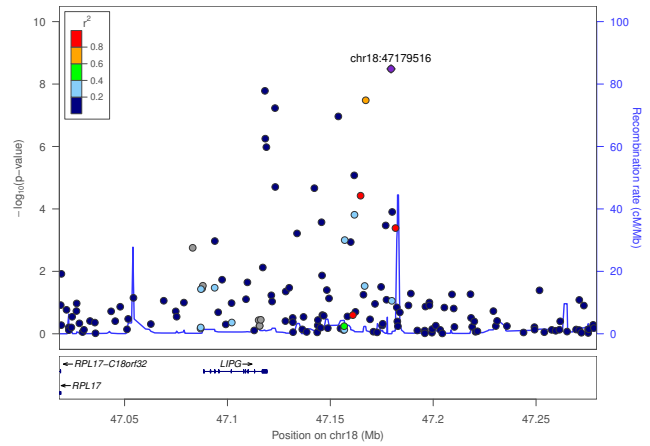
(c) rs1532085 ±100kb



(d) rs2575876 ±100kb



(e) rs2410629 ±100kb



(f) rs1943973 ±100kb

Figure 24: Regional plots for cohort META model invn Adjusted Age+Age2+SEX+BMI

8.4 Previously identified risk loci

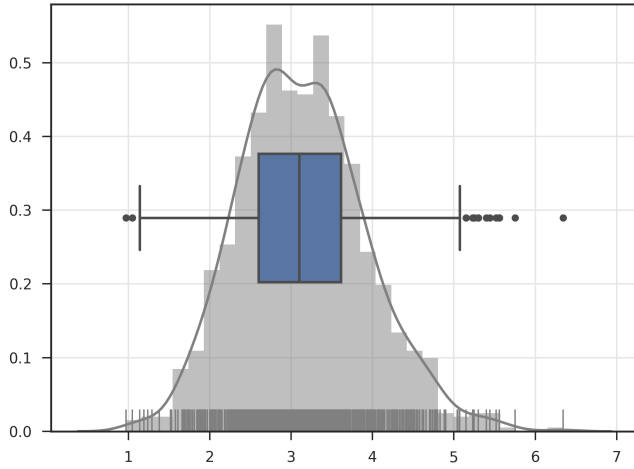
Table 27 shows statistics from the META cohort for 50 loci that were shown to be significantly associated with HDL Cholesterol in the 2013 Nature Genetics paper by Willer et al [11]. Where a previously reported variant was not genotyped in the study (indicated by $\bar{R}^2 < 1$), if available, a tagging variant in LD with the reported variant ($\bar{R}^2 \geq 0.7$ and within 250kb) was provided. Tags were identified using 1000 Genomes data. There are 17 variants that show at least nominal significance ($p < 0.05$) in this study. Out of the 50 variants in both studies, 44 exhibit the same direction of effect with the known result (binomial test $p = 1.62e - 08$).

Table 27: Top known loci in META model invn Adjusted Age+Age2+SEX+BMI (**bold** variants indicate matching direction of effect)

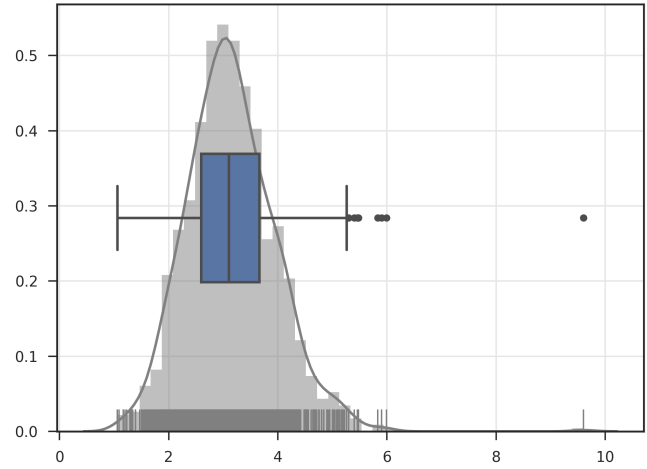
CHR	POS	ID	EA	OA	N	FREQ _{AVG}	FREQ _{MIN}	FREQ _{MAX}	EFFECT	STDERR	P	DIR	GENE _{CLOSEST}	R ²	ID _{KNOWN}	N _{KNOWN}	EFFECT _{KNOWN}	STDERR _{KNOWN}	P _{KNOWN}
16	57005479	rs1532624	A	C	7.044	0.332	0.278	0.477	0.188	1.79 · 10 ⁻²	6.3 · 10 ⁻²⁶	++xxxx+	CETP	1	rs1532624	94,595	0.204	3.5 · 10 ⁻³	0
16	56985139	rs9989419	G	A	7.044	0.719	0.619	0.768	7.25 · 10 ⁻²	1.86 · 10 ⁻²	9.91 · 10 ⁻⁵	+x-xxx	HERPUD1	1	rs9989419	94,595	0.147	3.6 · 10 ⁻³	0
15	58678512	rs10468017	T	C	7.045	0.18	0.168	0.189	9.76 · 10 ⁻²	2.17 · 10 ⁻²	6.6 · 10 ⁻⁶	++++xxx	LIPC	1	rs10468017	94,595	0.118	3.8 · 10 ⁻³	1.21 · 10 ⁻¹⁸⁸
8	19824492	rs13702	C	T	2.933	0.184	0.163	0.194	0.123	3.36 · 10 ⁻²	2.51 · 10 ⁻⁴	++x++xxx	LPL	1	rs13702	94,595	0.106	3.8 · 10 ⁻³	1.28 · 10 ⁻¹⁶⁰
8	19928582	rs9644568	A	G	1.052	0.124	0.124	0.124	1.96 · 10 ⁻²	6.71 · 10 ⁻²	0.77	+xxxxxxx	SLC18A1	1	rs9644568	94,595	0.127	5.4 · 10 ⁻³	4.07 · 10 ⁻¹¹⁰
18	47167214	rs4939883	C	T	7.046	0.826	0.807	0.862	0.122	2.21 · 10 ⁻²	3.75 · 10 ⁻⁸	+xxxxxxx	LIPG	1	rs4939883	94,595	7.99 · 10 ⁻²	4.5 · 10 ⁻³	1.8 · 10 ⁻⁶⁶
9	107664301	rs1883025	C	T	2.933	0.256	0.233	0.312	0.177	2.99 · 10 ⁻²	3.19 · 10 ⁻⁹	+x++xxx	ABCA1	1	rs1883025	94,595	6.98 · 10 ⁻²	4.1 · 10 ⁻³	1.5 · 10 ⁻⁶⁵
16	56866196	rs2241770	T	C	8.925	0.164	7.46 · 10 ⁻²	0.247	4.46 · 10 ⁻²	2.05 · 10 ⁻²	2.94 · 10 ⁻²	++++xxx	NUP93	1	rs2241770	94,595	9.89 · 10 ⁻²	5.7 · 10 ⁻³	6.78 · 10 ⁻⁶⁰
2	21231524	rs676210	A	G	8.925	0.694	0.61	0.733	3.02 · 10 ⁻²	1.64 · 10 ⁻²	6.49 · 10 ⁻²	++++xxx	APOB	1	rs676210	94,595	6.6 · 10 ⁻²	4 · 10 ⁻³	2.35 · 10 ⁻⁵⁴
16	67928042	rs16942887	A	G	2.933	2.93 · 10 ⁻²	1.8 · 10 ⁻²	5.48 · 10 ⁻²	1.17 · 10 ⁻²	7.74 · 10 ⁻²	0.88	+x++xxx	PSKH1	1	rs16942887	94,595	8.31 · 10 ⁻²	5.1 · 10 ⁻³	8.28 · 10 ⁻⁵⁴
16	67897487	rs1124324	T	C	2.932	2.88 · 10 ⁻²	1.71 · 10 ⁻²	5.48 · 10 ⁻²	1.16 · 10 ⁻³	7.81 · 10 ⁻²	0.988	+x++xxx	NUTF2	1	rs1124324	94,595	8.28 · 10 ⁻²	5.1 · 10 ⁻³	1.82 · 10 ⁻⁵³
16	67879400	rs3809630	A	G	2.933	2.86 · 10 ⁻²	1.8 · 10 ⁻²	5.24 · 10 ⁻²	3.2 · 10 ⁻²	7.82 · 10 ⁻²	0.682	+x++xxx	CENPT	1	rs3809630	94,595	8.28 · 10 ⁻²	5.1 · 10 ⁻³	2.05 · 10 ⁻⁵³
16	67985706	rs2292318	T	C	1.053	0.104	0.104	0.104	7.89 · 10 ⁻²	7.28 · 10 ⁻²	0.279	+xxxxxxx	SLC12A4	1	rs2292318	94,595	8.05 · 10 ⁻²	5 · 10 ⁻³	3.3 · 10 ⁻⁵²
16	67758778	rs4474673	T	C	2.933	2.73 · 10 ⁻²	1.85 · 10 ⁻²	4.72 · 10 ⁻²	3.52 · 10 ⁻²	8.02 · 10 ⁻²	0.661	+x++xxx	RANBP10	1	rs4474673	94,595	8.46 · 10 ⁻²	5.3 · 10 ⁻³	9.34 · 10 ⁻⁵²
16	56926195	rs13306677	A	G	7.044	7.03 · 10 ⁻²	4.65 · 10 ⁻²	9.02 · 10 ⁻²	0.102	3.25 · 10 ⁻²	1.7 · 10 ⁻³	++++xxx	SLC12A3	1	rs13306677	94,595	9 · 10 ⁻²	5.7 · 10 ⁻³	1.35 · 10 ⁻⁵⁰
11	116648917	rs964184	C	G	1.052	0.793	0.793	0.793	0.136	5.32 · 10 ⁻²	1.05 · 10 ⁻²	+xxxxxxx	ZPRI	1	rs964184	94,595	0.107	7.1 · 10 ⁻³	6.09 · 10 ⁻⁴⁸
11	116637146	rs12294259	C	T	1.052	4.75 · 10 ⁻⁴	4.75 · 10 ⁻⁴	4.75 · 10 ⁻⁴	0.267	1.001	0.79	+xxxxxxx	BUD13	1	rs12294259	94,595	0.106	7.1 · 10 ⁻³	7.22 · 10 ⁻⁴⁷
16	68039850	rs16957696	T	C	2.933	9.07 · 10 ⁻²	7.05 · 10 ⁻²	0.107	1.87 · 10 ⁻²	4.61 · 10 ⁻²	0.686	+x-xxx	DPEP2	1	rs16957696	94,595	7.45 · 10 ⁻²	4.9 · 10 ⁻³	1.31 · 10 ⁻⁴⁶
16	68099821	rs7201742	G	T	2.932	9.14 · 10 ⁻²	7.17 · 10 ⁻²	0.107	1.43 · 10 ⁻²	4.59 · 10 ⁻²	0.756	+x-xxx	DUS2	1	rs7201742	94,595	7.36 · 10 ⁻²	4.8 · 10 ⁻³	5.13 · 10 ⁻⁴⁶
16	68150527	rs12447640	G	A	2.921	9.16 · 10 ⁻²	7.22 · 10 ⁻²	0.106	1.58 · 10 ⁻²	4.59 · 10 ⁻²	0.731	+x-xxx	NFATC3	1	rs12447640	94,595	7.3 · 10 ⁻²	4.9 · 10 ⁻³	5.07 · 10 ⁻⁴⁵
2	21123352	rs6711016	A	C	1.053	0.55	0.55	0.55	2.35 · 10 ⁻²	4.47 · 10 ⁻²	0.599	+xxxxxxx	LDHA	1	rs6711016	94,595	5.69 · 10 ⁻²	4 · 10 ⁻³	9.32 · 10 ⁻⁴³
8	9185146	rs2126259	C	T	7.045	0.965	0.922	0.992	0.159	4.6 · 10 ⁻²	5.52 · 10 ⁻⁴	-xxx+++	PPP1R3B	1	rs2126259	94,595	7.52 · 10 ⁻²	5.4 · 10 ⁻³	1.53 · 10 ⁻⁴²
16	67967878	rs7187289	C	A	2.932	0.101	8.62 · 10 ⁻²	0.113	6.5 · 10 ⁻²	4.4 · 10 ⁻²	0.139	+x++xxx	PSMB10	1	rs7187289	94,595	6.42 · 10 ⁻²	4.4 · 10 ⁻³	6.51 · 10 ⁻⁴²
8	19746876	rs17482310	T	G	1.879	9.69 · 10 ⁻²	9.56 · 10 ⁻²	9.79 · 10 ⁻²	6.89 · 10 ⁻²	5.54 · 10 ⁻²	0.213	xx++xxx	INTS10	1	rs17482310	94,595	6.36 · 10 ⁻²	4.6 · 10 ⁻³	1.01 · 10 ⁻⁴⁰
16	67911517	rs8060686	C	T	8.919	0.118	5.96 · 10 ⁻²	0.286	3.04 · 10 ⁻²	2.39 · 10 ⁻²	0.204	++++xxx	EDC4	1	rs8060686	94,595	6.3 · 10 ⁻²	4.4 · 10 ⁻³	1.32 · 10 ⁻⁴⁰
15	58579956	rs2899624	A	G	8.924	0.119	8.16 · 10 ⁻²	0.146	9.49 · 10 ⁻²	2.32 · 10 ⁻²	4.29 · 10 ⁻⁵	++++xxx	ALDH1A2	1	rs2899624	94,595	7.14 · 10 ⁻²	4.9 · 10 ⁻³	1.39 · 10 ⁻⁴⁰
16	68280317	rs3826164	A	G	1.053	0.103	0.103	0.103	7.58 · 10 ⁻²	7.3 · 10 ⁻²	0.299	+xxxxxxx	PLA2G15	1	rs3826164	94,595	7.34 · 10 ⁻²	5.2 · 10 ⁻³	2.56 · 10 ⁻⁴⁰
1	230294916	rs2144300	T	C	1.880	0.239	0.195	0.292	6.77 · 10 ⁻²	3.8 · 10 ⁻²	7.47 · 10 ⁻²	xx++xxx	GALNT2	1	rs2144300	94,595	4.74 · 10 ⁻²	3.5 · 10 ⁻³	4 · 10 ⁻⁴⁰
16	68268836	rs8057119	T	C	1.052	0.103	0.103	0.103	7.63 · 10 ⁻²	7.3 · 10 ⁻²	0.296	+xxxxxxx	ESRP2	1	rs8057119	94,595	7.2 · 10 ⁻²	5.1 · 10 ⁻³	5.21 · 10 ⁻⁴⁰
20	44554015	rs6065906	C	T	2.471	2.29 · 10 ⁻²	2.15 · 10 ⁻²	2.4 · 10 ⁻²	3.28 · 10 ⁻³	9.45 · 10 ⁻²	0.972	x++xxx	PCIF1	1	rs6065906	94,595	-5.94 · 10 ⁻²	4.4 · 10 ⁻³	5.34 · 10 ⁻⁴⁰
16	67922342	rs10468274	A	G	8.925	8.08 · 10 ⁻²	2.06 · 10 ⁻²	0.285	4.67 · 10 ⁻²	2.94 · 10 ⁻²	0.112	++++xxx	NRN1L	1	rs10468274	94,595	6.39 · 10 ⁻²	4.6 · 10 ⁻³	2.39 · 10 ⁻³⁹
11	47294626	rs10501321	C	T	1.053	0.726	0.726	0.726	6.76 · 10 ⁻²	4.87 · 10 ⁻²	0.165	+xxxxxxx	MADD	1	rs10501321	94,595	4.83 · 10 ⁻²	3.6 · 10 ⁻³	3.54 · 10 ⁻³⁸
16	67708897	rs12449157	G	A	8.924	8.29 · 10 ⁻²	2.06 · 10 ⁻²	0.29	5.5 · 10 ⁻²	2.9 · 10 ⁻²	5.8 · 10 ⁻²	++++xxx	GFOD2	1	rs12449157	94,595	6.19 · 10 ⁻²	4.6 · 10 ⁻³	7.85 · 10 ⁻³⁷
11	47354787	rs1052373	T	C	2.931	0.701	0.681	0.719	4.35 · 10 ⁻³	2.83 · 10 ⁻²	0.878	+x++xxx	MYBPC3	1	rs1052373	94,595	4.78 · 10 ⁻²	3.7 · 10 ⁻³	1.55 · 10 ⁻³⁶
16	67699948	rs7187476	C	T	5.378	2.8 · 10 ⁻²	2.1 · 10 ⁻²	6.17 · 10 ⁻²	3.57 · 10 ⁻²	5.82 · 10 ⁻²	0.54	+++xxx	ENK1	1	rs7187476	94,595	6.46 · 10 ⁻²	4.8 · 10 ⁻³	2.17 · 10 ⁻³⁶
20	44547068	rs17447545	A	G	1.874	4.75 · 10 ⁻²	2.94 · 10 ⁻²	6.91 · 10 ⁻²	5.87 · 10 ⁻²	7.7 · 10 ⁻²	0.446	xx++xxx	PLTP	1	rs17447545	94,595	5.62 · 10 ⁻²	4.4 · 10 ⁻³	3.98 · 10 ⁻³⁶
11	116660686	rs2266788	A	G	2.933	0.788	0.759	0.806	0.104	3.18 · 10 ⁻²	1.05 · 10 ⁻³	+x++xxx	APOA5	1	rs2266788	94,595	9.22 · 10 ⁻²	6.8 · 10 ⁻³	1.19 · 10 ⁻³⁵
11	47259668	rs326222	T	C	1.053	0.229	0.229	0.229	2.24 · 10 ⁻²	5.12 · 10 ⁻²	0.662	+xxxxxxx	DOB2	1	rs326222	94,595	4.76 · 10 ⁻²	3.7 · 10 ⁻³	2.48 · 10 ⁻³⁵
18	47243912	rs6507945	A	C	2.933	0.414	0.407	0.421	3.04 · 10 ⁻³	2.6 · 10 ⁻²	0.907	+x++xxx	ACA2	1	rs6507945	94,595	-4.41 · 10 ⁻²	3.4 · 10 ⁻³	1.33 · 10 ⁻³⁴
20	43042364	rs1800961	C	T	8.923	1.52 · 10 ⁻²	9.79 · 10 ⁻³	2.79 · 10 ⁻²	7.3 · 10 ⁻²	6.15 · 10 ⁻²	0.236	++++xxx	HNF4A	1	rs1800961	94,595	0.127	9.9 · 10 ⁻³	1.64 · 10 ⁻³⁴
16	68013471	rs255049	C	T	8.906	0.135	8.67 · 10 ⁻²	0.289	7.17 · 10 ⁻²	2.25 · 10 ⁻²	1.47 · 10 ⁻³	++++xxx	DPEP3	1	rs255049	94,595	5.64 · 10 ⁻²	4.4 · 10 ⁻³	2.26 · 10 ⁻³⁴
11	47275064	rs10838681	G	A	1.878	0.654	0.563	0.731	6.54 · 10 ⁻²	3.46 · 10 ⁻²	5.87 · 10 ⁻²	xx++xxx	NR1H3	1	rs10838681	94,595	-4.8 · 10 ⁻²	3.8 · 10 ⁻³	1.72 · 10 ⁻³³
12	125261813	rs838882	T	C	1.053	0.844	0.844	0.844	9.86 · 10 ⁻²	5.97 · 10 ⁻²	0.869	+xxxxxxx	SCARB1	1	rs838882	94,595	-4.92 · 10 ⁻²		

9 LDL Cholesterol (LDL_MERGED)

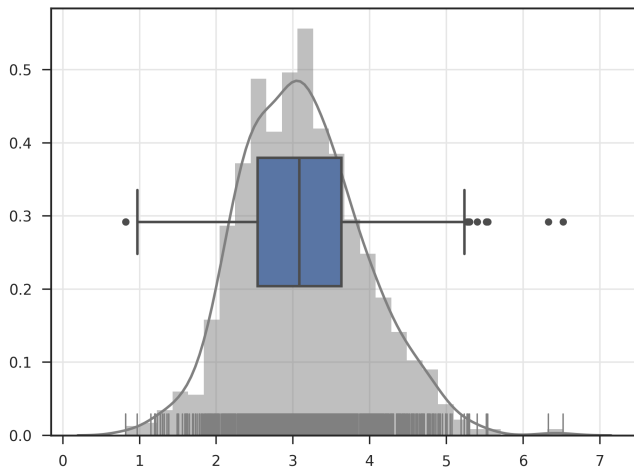
9.1 Summary



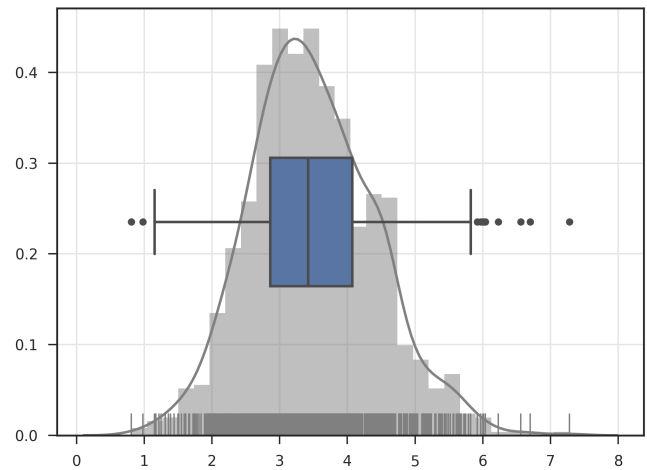
(a) DCSP21M_EAS



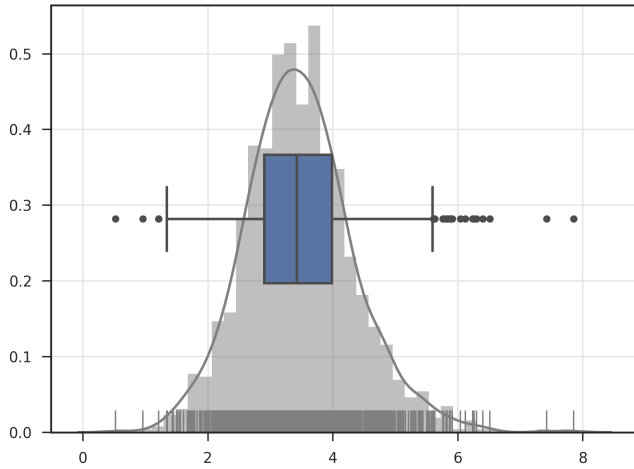
(b) DCSP2610K_EAS



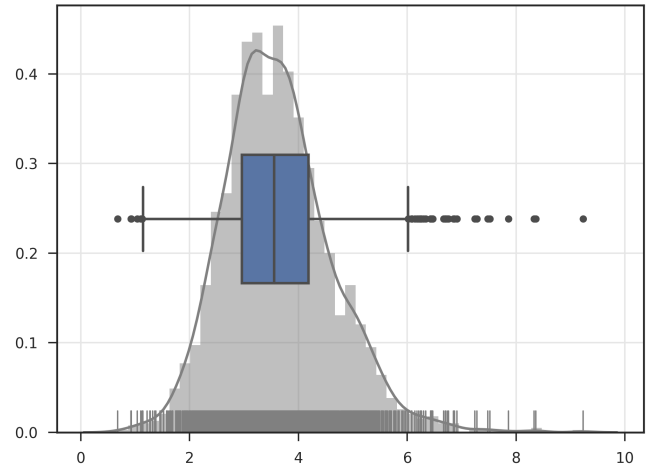
(c) LBCHS_EAS



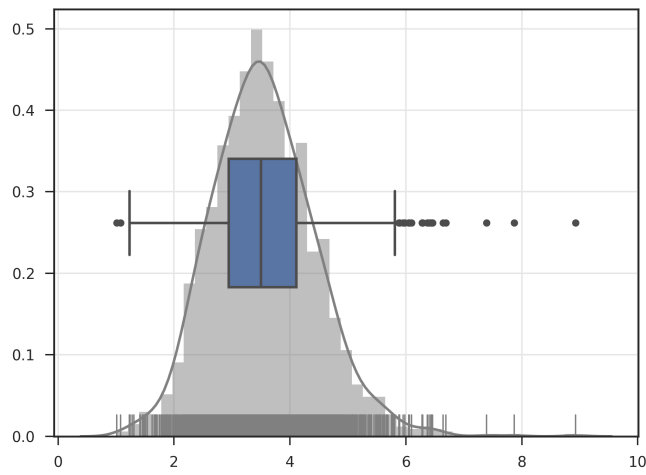
(d) LBMAS_EAS



(e) SCES_EAS



(f) SIMES_EAS



(g) SINDI_SAS

Figure 25: Distribution of LDL_MERGED in META by cohort

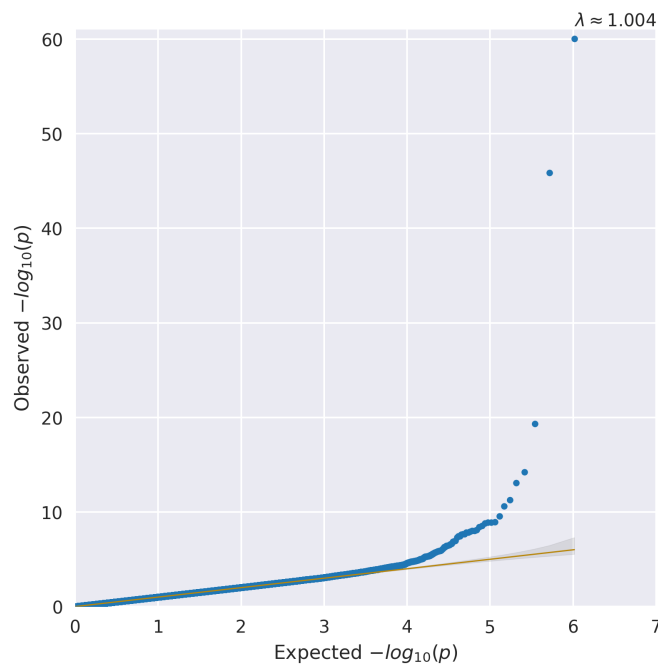
Table 28: Summary of samples removed from LDL Cholesterol analysis by cohort and model

Cohort	Array	Ancestry	Trans	Covars	Total	-SampleQc	-KinshipCrossArray	-KinshipArray	-missObs	-PcOutlier
META DCSP21M_EAS	DCSP21M	EAS	invn	Age+Age2+SEX+BMI	1864	44	0	0	775	0
META DCSP2610K_EAS	DCSP2610K	EAS	invn	Age+Age2+SEX+BMI	2087	36	0	0	915	0
META LBCHS_EAS	LBCHS	EAS	invn	Age+Age2+SEX+BMI	1263	22	52	122	33	7
META LBMAS_EAS	LBMAS	EAS	invn	Age+Age2+SEX+BMI	1185	40	5	240	42	5
META SCES_EAS	SCES	EAS	invn	Age+Age2+SEX+BMI	1889	42	93	2	416	5
META SIMES_EAS	SIMES	EAS	invn	Age+Age2+SEX+BMI	2542	47	160	115	280	35
META SINDI_SAS	SINDI	SAS	invn	Age+Age2+SEX+BMI	2537	60	15	91	718	106

Table 29: Summary of samples remaining for LDL Cholesterol analysis by cohort and model

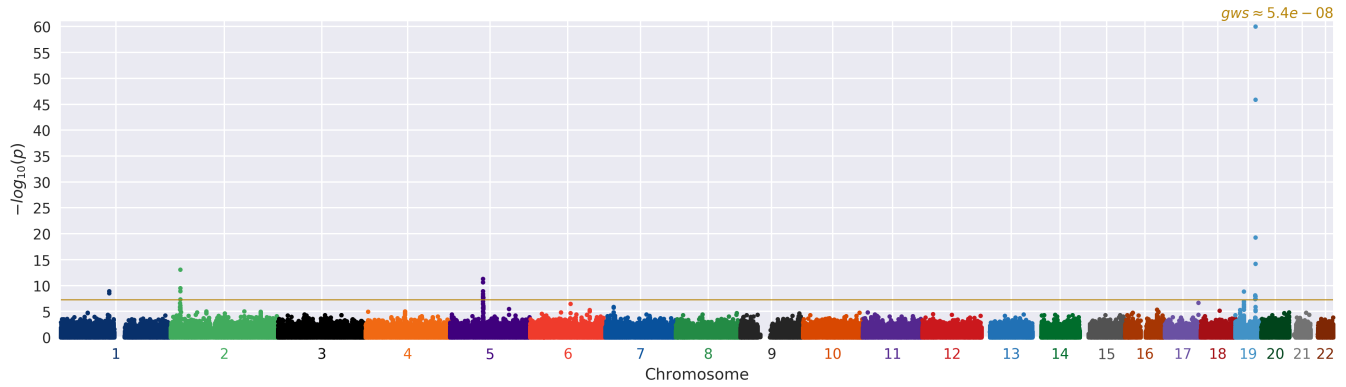
Cohort	Array	Ancestry	Trans	Covars	PCs	N	Male	Female	Max	Min	μ	\bar{x}	σ
META DCSP21M_EAS	DCSP21M	EAS	invn	Age+Age2+SEX+BMI	0	1045	679	366	6.34	0.97	3.136	3.1	0.776
META DCSP2610K_EAS	DCSP2610K	EAS	invn	Age+Age2+SEX+BMI	0	1136	256	880	9.6	1.06	3.147	3.1	0.813
META LBCHS_EAS	LBCHS	EAS	invn	Age+Age2+SEX+BMI	0	1027	506	521	6.33	0.82	3.116	3.08	0.798
META LBMAS_EAS	LBMAS	EAS	invn	Age+Age2+SEX+BMI	0	853	430	423	7.28	0.81	3.495	3.45	0.914
META SCES_EAS	SCES	EAS	invn	Age+Age2+SEX+BMI	0	1331	675	656	7.85	0.52	3.472	3.42	0.872
META SIMES_EAS	SIMES	EAS	invn	Age+Age2+SEX+BMI	0	1905	963	942	9.23	0.68	3.629	3.56	0.985
META SINDI_SAS	SINDI	SAS	invn	Age+Age2+SEX+BMI	0	1547	776	771	8.93	1.08	3.552	3.5	0.902

9.2 Calibration



(a) invn Adjusted Age+Age2+SEX+BMI

Figure 26: QQ plots for LDL_MERGED in the META analysis



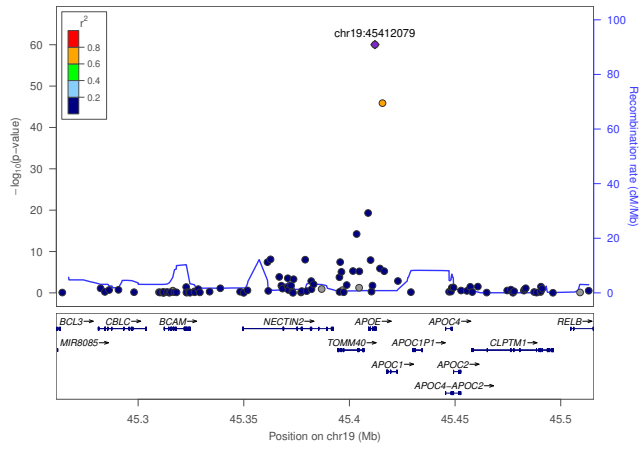
(a) invn Adjusted Age+Age2+SEX+BMI

Figure 27: Manhattan plots for LDL_MERGED in the META analysis

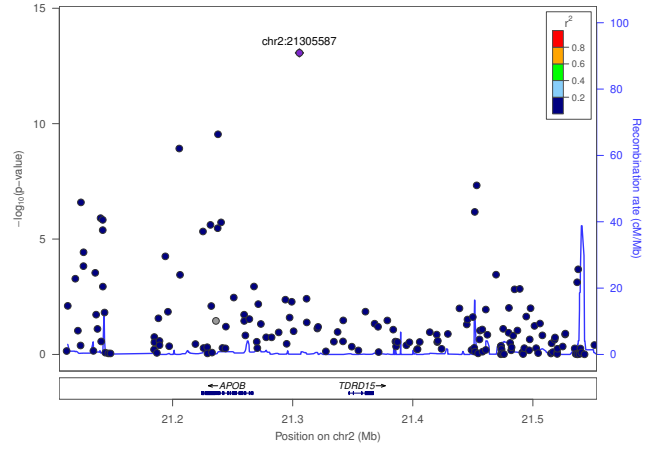
9.3 Top associations

Table 30: Top variants in the META invn Adjusted Age+Age2+SEX+BMI model (**bold** variants indicate previously identified associations)

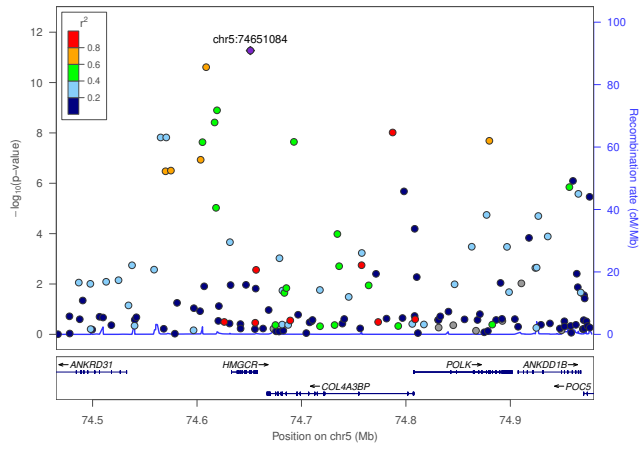
CHR	POS	ID	EA	OA	GENE _{CLOSEST}	DIR	N	MALE	FEMALE	FREQ _{AVG}	FREQ _{MIN}	FREQ _{MAX}	EFFECT	STDERR	OR	ZSCORE	P
19	45412079	rs7412	C	T	APOE	+x+xxxx	2,919	1,613	1,306	$8.6 \cdot 10^{-2}$	$8.47 \cdot 10^{-2}$	$8.74 \cdot 10^{-2}$	0.726	$4.42 \cdot 10^{-2}$	2.067	-16.443	$9.42 \cdot 10^{-61}$
19	45415640	rs445925	G	A	APOC1	+x+xxxx	2,925	1,615	1,310	0.1	$9.2 \cdot 10^{-2}$	0.117	0.6	$4.19 \cdot 10^{-2}$	1.823	-14.335	$1.32 \cdot 10^{-46}$
19	45403412	rs1160985	C	T	TOMM40	xx+xxxx	1,880	936	944	0.371	0.329	0.421	0.261	$3.34 \cdot 10^{-2}$	1.298	-7.807	$5.85 \cdot 10^{-15}$
2	21305587	rs11886946	A	C	APOB	+++++++	8,821	4,274	4,547	0.122	$7.11 \cdot 10^{-3}$	0.18	0.174	$2.33 \cdot 10^{-2}$	1.19	-7.461	$8.59 \cdot 10^{-14}$
5	74651084	rs3846662	G	A	HMGCR	+++++++	8,840	4,281	4,559	0.534	0.517	0.566	0.103	$1.5 \cdot 10^{-2}$	1.109	6.896	$5.37 \cdot 10^{-12}$
1	109815252	rs611917	A	G	CELSR2	++x+++	6,964	3,349	3,615	0.12	$6.51 \cdot 10^{-2}$	0.294	0.164	$2.7 \cdot 10^{-2}$	1.178	-6.076	$1.23 \cdot 10^{-9}$
19	19407718	rs10401969	T	C	SUGP1	+x+xxxx	2,924	1,614	1,310	0.105	$9.65 \cdot 10^{-2}$	0.115	0.259	$4.29 \cdot 10^{-2}$	1.296	-6.047	$1.48 \cdot 10^{-9}$
19	45362667	rs377702	G	A	NECTIN2	++x+++	6,963	3,349	3,614	0.113	$9.62 \cdot 10^{-2}$	0.142	0.155	$2.68 \cdot 10^{-2}$	1.167	-5.774	$7.73 \cdot 10^{-9}$
5	74787310	rs6896136	C	T	COL4A3BP	++x+++	6,963	3,348	3,615	0.535	0.521	0.56	$9.68 \cdot 10^{-2}$	$1.69 \cdot 10^{-2}$	1.102	5.738	$9.61 \cdot 10^{-9}$
5	74565153	rs10062361	T	C	ANKRD31	+++++	8,844	4,285	4,559	0.293	0.234	0.361	$9.35 \cdot 10^{-2}$	$1.65 \cdot 10^{-2}$	1.098	5.66	$1.51 \cdot 10^{-8}$
5	74879890	rs5744680	A	G	POLK	++x+++	6,959	3,347	3,612	0.532	0.513	0.559	$9.45 \cdot 10^{-2}$	$1.69 \cdot 10^{-2}$	1.099	5.607	$2.06 \cdot 10^{-8}$
2	21453211	rs10198972	G	A	TDRD15	+++++++	8,835	4,280	4,555	0.15	0.116	0.184	0.115	$2.11 \cdot 10^{-2}$	1.122	-5.462	$4.71 \cdot 10^{-8}$
19	19374061	rs8105094	C	T	HAPLN4	+x+xxxx	2,917	1,611	1,306	0.308	0.299	0.312	0.15	$2.82 \cdot 10^{-2}$	1.162	-5.31	$1.1 \cdot 10^{-7}$
19	19381715	rs2074301	G	A	TM6SF2	+x+xxxx	2,924	1,614	1,310	0.307	0.301	0.311	0.149	$2.82 \cdot 10^{-2}$	1.161	-5.28	$1.29 \cdot 10^{-7}$
17	75370468	rs93075	G	T	SEPT9	+++++++	8,841	4,285	4,556	0.693	0.653	0.713	$8.38 \cdot 10^{-2}$	$1.62 \cdot 10^{-2}$	1.087	5.179	$2.24 \cdot 10^{-7}$
6	91492352	rs12526569	G	A	MAP3K7	++x+++	6,964	3,349	3,615	0.246	0.153	0.296	$9.92 \cdot 10^{-2}$	$1.95 \cdot 10^{-2}$	1.104	-5.092	$3.55 \cdot 10^{-7}$
5	74959970	rs34355	G	A	ANKDD1B	+++++++	8,841	4,284	4,557	0.809	0.784	0.837	$9.44 \cdot 10^{-2}$	$1.91 \cdot 10^{-2}$	1.099	-4.934	$8.04 \cdot 10^{-7}$
19	19467937	rs2285627	C	T	MAU2	+x+xxxx	2,924	1,614	1,310	0.692	0.68	0.697	0.138	$2.83 \cdot 10^{-2}$	1.148	4.864	$1.15 \cdot 10^{-6}$
7	18340210	rs708127	G	A	HDAC9	+xxxxxx	1,044	679	365	0.261	0.261	0.261	0.243	$5.03 \cdot 10^{-2}$	1.275	4.827	$1.39 \cdot 10^{-6}$
5	132927454	rs171742	A	G	FSTL4	+x+xxxx	2,924	1,614	1,310	0.603	0.567	0.623	0.126	$2.69 \cdot 10^{-2}$	1.134	4.669	$3.03 \cdot 10^{-6}$



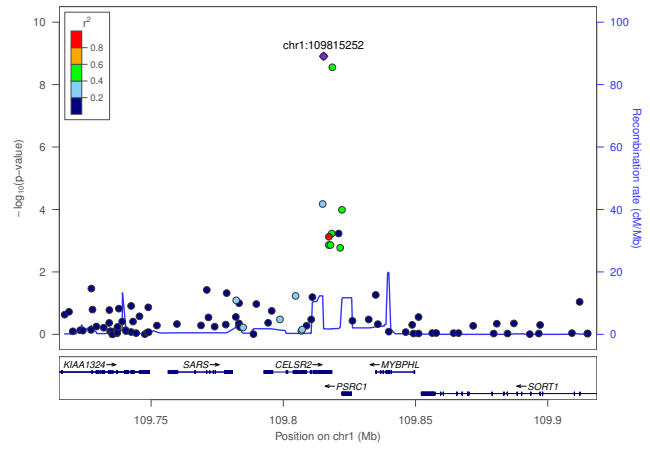
(a) rs7412 ±100kb



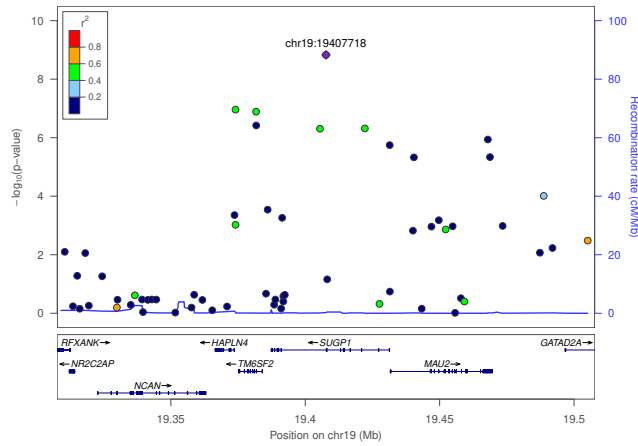
(b) rs11886946 ±100kb



(c) rs3846662 ±100kb



(d) rs611917 ±100kb



(e) rs10401969 ±100kb

Figure 28: Regional plots for cohort META model invn Adjusted Age+Age2+SEX+BMI

9.4 Previously identified risk loci

Table 31 shows statistics from the META cohort for 50 loci that were shown to be significantly associated with LDL Cholesterol in the 2013 Nature Genetics paper by Willer et al [14]. Where a previously reported variant was not genotyped in the study (indicated by $\bar{R}^2 < 1$), if available, a tagging variant in LD with the reported variant ($\bar{R}^2 \geq 0.7$ and within 250kb) was provided. Tags were identified using 1000 Genomes data. There are 23 variants that show at least nominal significance ($p < 0.05$) in this study. Out of the 50 variants in both studies, 43 exhibit the same direction of effect with the known result (binomial test $p = 1.05e - 07$).

Table 31: Top known loci in META model invn Adjusted Age+Age2+SEX+BMI (**bold** variants indicate matching direction of effect)

CHR	POS	ID	EA	OA	N	FREQ _{AVG}	FREQ _{MIN}	FREQ _{MAX}	EFFECT	STDERR	P	DIR	GENECLOSEST	R ²	ID _{KNOWN}	N _{KNOWN}	EFFECT _{KNOWN}	STDERR _{KNOWN}	P _{KNOWN}
19	45415640	rs445925	G	A	2.925	0.1	$9.2 \cdot 10^{-2}$	0.117	0.6	$4.19 \cdot 10^{-2}$	$1.32 \cdot 10^{-46}$	++++xxx	APOC1	1	rs445925	94,595	0.363	$8.1 \cdot 10^{-3}$	0
19	45412079	rs7412	C	T	2.919	$8.6 \cdot 10^{-2}$	$8.47 \cdot 10^{-2}$	$8.74 \cdot 10^{-2}$	0.726	$4.42 \cdot 10^{-2}$	$9.42 \cdot 10^{-61}$	++++xxx	APOE	1	rs7412	94,595	0.59	$1.01 \cdot 10^{-2}$	0
1	109818530	rs646776	T	C	8.829	0.893	0.716	0.934	0.147	$2.48 \cdot 10^{-2}$	$2.8 \cdot 10^{-9}$	+++++++	CELSR2	1	rs646776	94,595	0.16	$4.4 \cdot 10^{-3}$	$1.63 \cdot 10^{-272}$
1	109822166	rs599839	A	G	2.904	0.888	0.825	0.917	0.162	$4.18 \cdot 10^{-2}$	$1.02 \cdot 10^{-4}$	++++xxx	PSRC1	1	rs599839	94,595	0.16	$4.4 \cdot 10^{-3}$	$3.85 \cdot 10^{-268}$
19	11202306	rs6511720	G	T	8.840	$2.92 \cdot 10^{-2}$	$9.26 \cdot 10^{-3}$	$7.08 \cdot 10^{-2}$	0.204	$4.48 \cdot 10^{-2}$	$5.1 \cdot 10^{-6}$	+++++++	LDLR	1	rs6511720	94,595	0.221	$6.1 \cdot 10^{-3}$	$3.75 \cdot 10^{-292}$
19	45395619	rs2075650	G	A	8.843	$9.79 \cdot 10^{-2}$	$7.63 \cdot 10^{-2}$	0.121	0.138	$2.5 \cdot 10^{-2}$	$3.57 \cdot 10^{-8}$	+++++++	TOMM40	1	rs2075650	94,595	0.177	$5.5 \cdot 10^{-3}$	$1.72 \cdot 10^{-214}$
2	21263900	rs1367117	A	G	2.924	0.131	0.124	0.139	$8.49 \cdot 10^{-2}$	$3.9 \cdot 10^{-2}$	$2.93 \cdot 10^{-2}$	++++xxx	APOB	1	rs1367117	94,595	0.119	$4 \cdot 10^{-3}$	$9.48 \cdot 10^{-183}$
19	45242173	rs1531517	A	G	2.925	0.153	0.15	0.158	$3.07 \cdot 10^{-2}$	$3.65 \cdot 10^{-2}$	0.4	++++xxx	BCL3	1	rs1531517	94,595	-0.22	$8 \cdot 10^{-3}$	$9.51 \cdot 10^{-163}$
2	21368217	rs17399838	G	G	6.963	$3.16 \cdot 10^{-2}$	$1.44 \cdot 10^{-3}$	0.104	$9.75 \cdot 10^{-2}$	$4.89 \cdot 10^{-2}$	$4.64 \cdot 10^{-2}$	-xxxx+	TDRD15	1	rs17399838	94,595	0.129	$5.1 \cdot 10^{-3}$	$5.2 \cdot 10^{-134}$
19	45333834	rs4803760	T	C	8.832	0.672	0.627	0.737	$1.06 \cdot 10^{-2}$	$1.61 \cdot 10^{-2}$	0.511	-++++	BCAM	1	rs4803760	94,595	-0.119	$4.9 \cdot 10^{-3}$	$2.47 \cdot 10^{-123}$
19	45373565	rs395908	A	G	2.925	0.15	0.129	0.195	0.128	$3.67 \cdot 10^{-2}$	$4.93 \cdot 10^{-4}$	++++xxx	NECTIN2	1	rs395908	94,595	-0.157	$7.5 \cdot 10^{-3}$	$1.11 \cdot 10^{-94}$
2	44073881	rs6544713	T	C	6.961	0.948	0.798	0.999	0.116	$4.07 \cdot 10^{-2}$	$4.17 \cdot 10^{-3}$	-xxxx+	ABCG5	1	rs6544713	94,595	$8.06 \cdot 10^{-2}$	$4.1 \cdot 10^{-3}$	$4.84 \cdot 10^{-83}$
5	74656539	rs12916	C	T	2.925	0.525	0.513	0.543	$7.85 \cdot 10^{-2}$	$2.62 \cdot 10^{-2}$	$2.75 \cdot 10^{-3}$	++++xxx	HMGCR	1	rs12916	94,595	$7.33 \cdot 10^{-2}$	$3.8 \cdot 10^{-3}$	$7.79 \cdot 10^{-78}$
19	11161537	rs3786722	A	C	1.045	$8.95 \cdot 10^{-2}$	$8.95 \cdot 10^{-2}$	$8.95 \cdot 10^{-2}$	$3.26 \cdot 10^{-2}$	$7.55 \cdot 10^{-2}$	0.666	+xxxxxx	SMARCA4	1	rs3786722	94,595	$-7.54 \cdot 10^{-2}$	$4.3 \cdot 10^{-3}$	$5.52 \cdot 10^{-63}$
5	74689249	rs6878990	C	T	1.020	0.488	0.488	0.488	$4.8 \cdot 10^{-2}$	$4.45 \cdot 10^{-2}$	0.281	+xxxxxx	COL4A3BP	1	rs6878990	94,595	$6.45 \cdot 10^{-2}$	$3.7 \cdot 10^{-3}$	$5.83 \cdot 10^{-63}$
19	45176340	rs2965157	T	C	1.045	$1.58 \cdot 10^{-2}$	$1.58 \cdot 10^{-2}$	$1.58 \cdot 10^{-2}$	0.117	0.177	0.509	+xxxxxx	CEACAM19	1	rs2965157	94,595	0.189	$1.12 \cdot 10^{-2}$	$7.29 \cdot 10^{-62}$
5	74569856	rs4704200	T	G	8.833	0.556	0.539	0.59	$7.65 \cdot 10^{-2}$	$1.5 \cdot 10^{-2}$	$3.39 \cdot 10^{-7}$	+++++++	ANKRD31	1	rs4704200	94,595	$6.44 \cdot 10^{-2}$	$3.7 \cdot 10^{-3}$	$1.3 \cdot 10^{-61}$
5	74879890	rs5744680	A	G	6.958	0.531	0.513	0.559	$9.44 \cdot 10^{-2}$	$1.69 \cdot 10^{-2}$	$2.1 \cdot 10^{-8}$	++++xxx	POLK	1	rs5744680	94,595	$6.44 \cdot 10^{-2}$	$3.7 \cdot 10^{-3}$	$2.96 \cdot 10^{-61}$
19	10950125	rs11881156	C	T	2.925	0.131	$7.62 \cdot 10^{-2}$	0.154	$3.45 \cdot 10^{-2}$	$3.92 \cdot 10^{-2}$	0.379	++++xxx	C19orf38	1	rs11881156	94,595	$8.11 \cdot 10^{-2}$	$4.9 \cdot 10^{-3}$	$1.7 \cdot 10^{-55}$
19	19407718	rs10401969	T	C	2.924	0.105	$9.65 \cdot 10^{-2}$	0.115	0.259	$4.29 \cdot 10^{-2}$	$1.48 \cdot 10^{-9}$	++++xxx	SUGP1	1	rs10401969	94,595	0.118	$7.2 \cdot 10^{-3}$	$2.65 \cdot 10^{-54}$
1	55496039	rs11206510	T	C	8.843	$4.81 \cdot 10^{-2}$	$3.65 \cdot 10^{-2}$	$5.41 \cdot 10^{-2}$	$3.69 \cdot 10^{-2}$	$3.54 \cdot 10^{-2}$	0.296	+++++++	PCSK9	1	rs11206510	94,595	$8.31 \cdot 10^{-2}$	$5 \cdot 10^{-3}$	$2.38 \cdot 10^{-53}$
19	10090953	rs11881315	C	C	6.960	0.127	$7.77 \cdot 10^{-2}$	0.167	$2.36 \cdot 10^{-2}$	$2.55 \cdot 10^{-2}$	0.355	+xxxx+	DNM2	1	rs11881315	94,595	$7.42 \cdot 10^{-2}$	$4.8 \cdot 10^{-3}$	$7.75 \cdot 10^{-50}$
2	44065090	rs6756629	G	A	8.841	$2.01 \cdot 10^{-2}$	$1.46 \cdot 10^{-2}$	$3.46 \cdot 10^{-2}$	0.119	$5.39 \cdot 10^{-2}$	$2.67 \cdot 10^{-2}$	+++++++	ABCG5	1	rs6756629	94,595	0.131	$8.8 \cdot 10^{-3}$	$1.29 \cdot 10^{-49}$
8	126482621	rs2954022	C	A	1.880	0.527	0.509	0.543	$4.09 \cdot 10^{-2}$	$3.29 \cdot 10^{-2}$	0.214	xxx+xxx	TRIB1	1	rs2954022	94,595	$5.46 \cdot 10^{-2}$	$3.6 \cdot 10^{-3}$	$2.39 \cdot 10^{-47}$
1	109834938	rs17645031	C	T	8.841	$3.75 \cdot 10^{-2}$	$2.52 \cdot 10^{-2}$	$6.33 \cdot 10^{-2}$	$7.64 \cdot 10^{-2}$	$3.98 \cdot 10^{-2}$	$5.45 \cdot 10^{-2}$	+++++++	MYBPHL	1	rs17645031	94,595	0.1	$6.7 \cdot 10^{-3}$	$4.76 \cdot 10^{-47}$
19	45225345	rs2965109	C	T	2.924	0.439	0.392	0.52	$5.53 \cdot 10^{-2}$	$2.68 \cdot 10^{-2}$	$3.9 \cdot 10^{-2}$	-x+xxx	CEACAM16	1	rs2965109	94,595	$5.46 \cdot 10^{-2}$	$3.9 \cdot 10^{-3}$	$6.65 \cdot 10^{-45}$
9	136154168	rs579459	C	T	2.924	0.179	0.159	0.19	0.13	$3.42 \cdot 10^{-2}$	$1.53 \cdot 10^{-4}$	++++xxx	ABO	1	rs579459	94,595	$6.65 \cdot 10^{-2}$	$4.5 \cdot 10^{-3}$	$2.42 \cdot 10^{-44}$
19	19329924	rs2228603	C	T	6.962	$4.75 \cdot 10^{-2}$	$2.7 \cdot 10^{-2}$	$6.61 \cdot 10^{-2}$	$1.88 \cdot 10^{-2}$	$3.98 \cdot 10^{-2}$	0.637	-xxx+	NCAN	1	rs2228603	94,595	0.104	$7.2 \cdot 10^{-3}$	$4.43 \cdot 10^{-44}$
1	109782190	rs611060	C	T	8.843	0.145	$5.79 \cdot 10^{-2}$	0.433	$4.04 \cdot 10^{-2}$	$2.32 \cdot 10^{-2}$	$8.14 \cdot 10^{-2}$	+++++	SARS	1	rs611060	94,595	$5.34 \cdot 10^{-2}$	$3.7 \cdot 10^{-3}$	$4.27 \cdot 10^{-42}$
16	72108093	rs2000999	A	G	6.956	0.283	0.235	0.423	$6.76 \cdot 10^{-2}$	$1.86 \cdot 10^{-2}$	$2.89 \cdot 10^{-4}$	++++xxx	HPR	1	rs2000999	94,595	$6.5 \cdot 10^{-2}$	$4.6 \cdot 10^{-3}$	$4.22 \cdot 10^{-41}$
11	61609750	rs174583	C	T	1.880	0.677	0.607	0.761	$1.88 \cdot 10^{-2}$	$3.54 \cdot 10^{-2}$	0.595	xxx+xxx	FADS2	1	rs174583	94,595	$5.22 \cdot 10^{-2}$	$3.8 \cdot 10^{-3}$	$7 \cdot 10^{-41}$
5	74924890	rs1427924	G	A	1.037	0.304	0.304	0.304	$2.88 \cdot 10^{-2}$	$4.84 \cdot 10^{-2}$	0.552	+xxxxxx	ANKDD1B	1	rs1427924	94,595	$6.28 \cdot 10^{-2}$	$4.4 \cdot 10^{-3}$	$2.4 \cdot 10^{-40}$
11	61571478	rs174550	T	C	1.879	0.674	0.605	0.758	$1.66 \cdot 10^{-2}$	$3.53 \cdot 10^{-2}$	0.637	xxx+xxx	FADS1	1	rs174550	94,595	$5.14 \cdot 10^{-2}$	$3.8 \cdot 10^{-3}$	$7.03 \cdot 10^{-40}$
11	61557803	rs102275	T	C	6.937	0.542	0.188	0.77	$1.12 \cdot 10^{-2}$	$1.85 \cdot 10^{-2}$	0.543	+xxx+	TMEM258	1	rs102275	94,595	$5.12 \cdot 10^{-2}$	$3.8 \cdot 10^{-3}$	$7.61 \cdot 10^{-40}$
19	19723215	rs10500212	C	T	2.924	0.124	$9.59 \cdot 10^{-2}$	0.192	0.135	$4 \cdot 10^{-2}$	$7.43 \cdot 10^{-4}$	++++xxx	PBX4	1	rs10500212	94,595	$9.15 \cdot 10^{-2}$	$6.7 \cdot 10^{-3}$	$8.95 \cdot 10^{-40}$
1	55713628	rs4927207	G	A	8.840	0.177	0.141	0.247	$3.51 \cdot 10^{-2}$	$1.99 \cdot 10^{-2}$	$7.68 \cdot 10^{-2}$	+++++++	USP24	1	rs4927207	94,595	$6.92 \cdot 10^{-2}$	$4.9 \cdot 10^{-3}$	$2.36 \cdot 10^{-39}$
11	61552680	rs174537	G	T	5.055	0.49	0.186	0.631	$1.69 \cdot 10^{-2}$	$2.16 \cdot 10^{-2}$	0.435	+xx+x	MYRF	1	rs174537	94,595	$5.09 \cdot 10^{-2}$	$3.8 \cdot 10^{-3}$	$3.94 \cdot 10^{-39}$
19	19746151	rs2304128	C	T	8.842	$8.17 \cdot 10^{-2}$	$5.63 \cdot 10^{-2}$	0.142	$7.48 \cdot 10^{-2}$	$2.77 \cdot 10^{-2}$	$6.92 \cdot 10^{-3}$	+++++++	GMIP	1	rs2304128	94,595	$9.02 \cdot 10^{-2}$	$6.8 \cdot 10^{-3}$	$4.23 \cdot 10^{-37}$
19	19505087	rs10415849	G	T	6.963	0.177	0.152	0.203	$6.42 \cdot 10^{-2}$	$2.18 \cdot 10^{-2}$	$3.3 \cdot 10^{-3}$	+xxxx+	GATAD2A	1	rs10415849	94,595	$7.28 \cdot 10^{-2}$	$5.7 \cdot 10^{-3}$	$4.25 \cdot 10^{-36}$
2	21123352	rs6711016	A	C	1.045	0.549	0.549	0.549	$3.72 \cdot 10^{-2}$	$4.5 \cdot 10^{-2}$	0.409	+xxxxxx	LDAH	1	rs6711016	94,595	$-5.51 \cdot 10^{-2}$	$4.3 \cdot 10^{-3}$	$1.1 \cdot 10^{-35}$
11	61560081	rs174538	G	A	2.925	0.651	0.601	0.75	$9.32 \cdot 10^{-3}$	$2.76 \cdot 10^{-2}$	0.736	+x+xxx	FEN1	1	rs174538	94,595	$5 \cdot 10^{-2}$	$4 \cdot 10^{-3}$	$1.07 \cdot 10^{-34}$
16	56993324	rs3764261	A	C	8.841	0.175	0.133	0.281	$1.2 \cdot 10^{-2}$	$1.97 \cdot 10^{-2}$	0.545	+++++	CETP	1	rs3764261	94,595	$-5.28 \cdot 10^{-2}$	$4.2 \cdot 10^{-3}$	$2.22 \cdot 10^{-34}$
1	63050598	rs3850634	T	G	1.045	0.212	0.212	0.212	$5.38 \cdot 10^{-2}$	$5.23 \cdot 10^{-2}$	0.304	+xxxxxx	DOCK7	1	rs3850634	94,595	$4.99 \cdot 10^{-2}$	$3.9 \cdot$	

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11 References

- [1] Plink1.9, <https://www.cog-genomics.org/plink2>.
- [2] Kent WJ, Sugnet CW, Furey TS, Roskin KM, Pringle TH, Zahler AM, Haussler D. The human genome browser at UCSC. *Genome Res.* 2002 Jun;12(6):996-1006. LiftOver http://hgdownload.soe.ucsc.edu/admin/exe/linux.x86_64/liftOver.
- [3] Conomos MP. GENetic ESTimation and Inference in Structured samples (GENESIS): Statistical methods for analyzing genetic data from samples with population structure and/or relatedness, <https://www.rdocumentation.org/packages/GENESIS/versions/2.2.2>.
- [4] <http://people.virginia.edu/~wc9c/KING/>.
- [5] 1000 Genomes Phase 3 v5, https://mathgen.stats.ox.ac.uk/impute/1000GP_Phase3.html.
- [6] Seed C, Bloemendal A, Bloom JM, Goldstein JI, King D, Poterba T, Neale BM. Hail: An Open-Source Framework for Scalable Genetic Data Analysis. In preparation. <https://github.com/hail-is/hail>.
- [7] Morris A, et al. Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. *Nat Genet.* 2012 Sep; 44(9): 981-990. Published online 2012 Aug 12. doi: 10.1038/ng.2383
- [8] Kettunen J, et al. Genome-wide study for circulating metabolites identifies 62 loci and reveals novel systemic effects of LPA. *Nature Communications.* 2016; 11122(2016). doi:10.1038/ncomms11122
- [9] Scott RA, et al. Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. *Nat Genet.* 2012 Sep;44(9):991-1005. doi: 10.1038/ng.2385. Epub 2012 Aug 12
- [10] Ehret G, et al. Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. *Nature.* 2011 Oct; 478: 103-109. doi:10.1038/nature10405
- [11] Willer C, et al. Discovery and Refinement of Loci Associated with Lipid Levels. *Nature Genetics.* 2013 Nov; 45(11): 1274-1283. doi:10.1038/ng.2797
- [12] Pattaro C, et al. Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. *Nat Comm.* 2016 Jan; 7:10023; Published online 2016 Jan 21. doi: 10.1038/ncomms10023
- [13] Locke A, et al. Genetic studies of body mass index yield new insights for obesity biology. *Nature.* 2015 Feb; 518(7538): 197-206. doi:10.1038/nature14177
- [14] Willer C, et al. Discovery and Refinement of Loci Associated with Lipid Levels. *Nature Genetics.* 2013 Nov; 45(11): 1274-1283. doi:10.1038/ng.2797

- [15] Scott RA, et al. Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. *Nat Genet.* 2012 Sep;44(9):991-1005. doi: 10.1038/ng.2385. Epub 2012 Aug 12
- [16] Soranzo N, et al. Common variants at 10 genomic loci influence hemoglobin A1(C) levels via glycemic and nonglycemic pathways. *Diabetes.* 2010 Dec;59(12):3229-39. doi: 10.2337/db10-0502. Epub 2010 Sep 21
- [17] Ehret G, et al. Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. *Nature.* 2011 Oct; 478: 103-109. doi:10.1038/nature10405
- [18] Gilbert C, Ruebenacker O, Koesterer R, Massung J, Flannick J. Loamstream. loamstream 1.4-SNAPSHOT (1.3-329-g0da8aac) branch: cg-h2-replacement commit: 0da8aac39f7f23cc5442b14a6ee77a767e1d9e35 built on: 2019-09-30T14:53:18.723Z. <https://github.com/broadinstitute/dig-loam-stream>.
- [19] Koesterer R, Gilbert C, Ruebenacker O, Massung J, Flannick J. AMP-DCC Data Analysis Pipeline. dig-loam-2.5.26. <https://github.com/broadinstitute/dig-loam>.