

AMP-DCC Data Analysis Report

BioMe

Phase 2

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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; EX, ILL, and AFFY. 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
EX	BioMe_EXOMECHIP	bfile	N/A
ILL	BioMe_ILLUMINA	bfile	N/A
AFFY	BioMe_AFFY	bfile	N/A

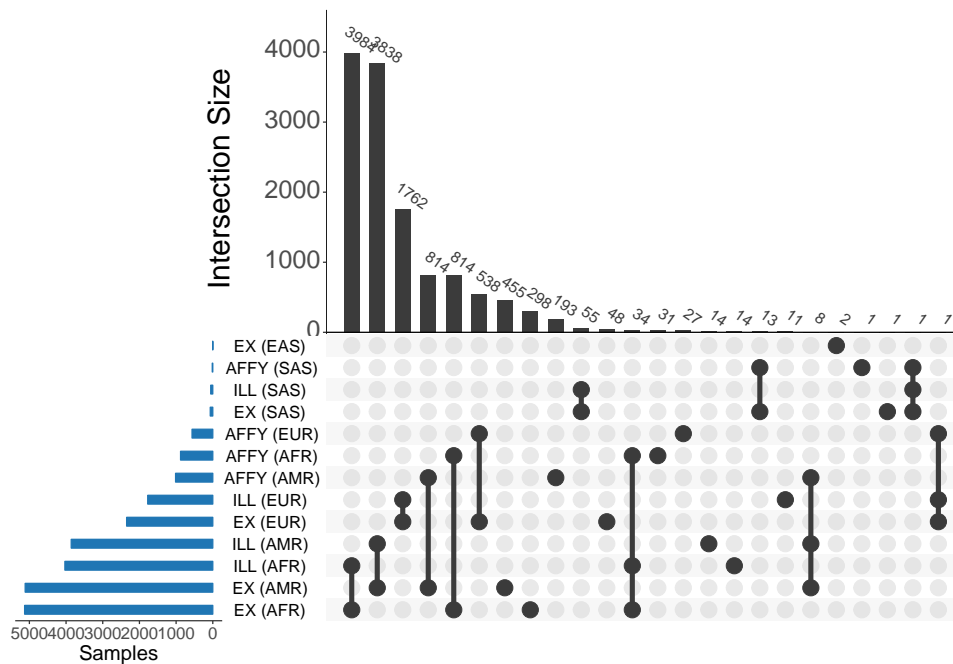


Figure 1: Samples remaining for analysis after quality control

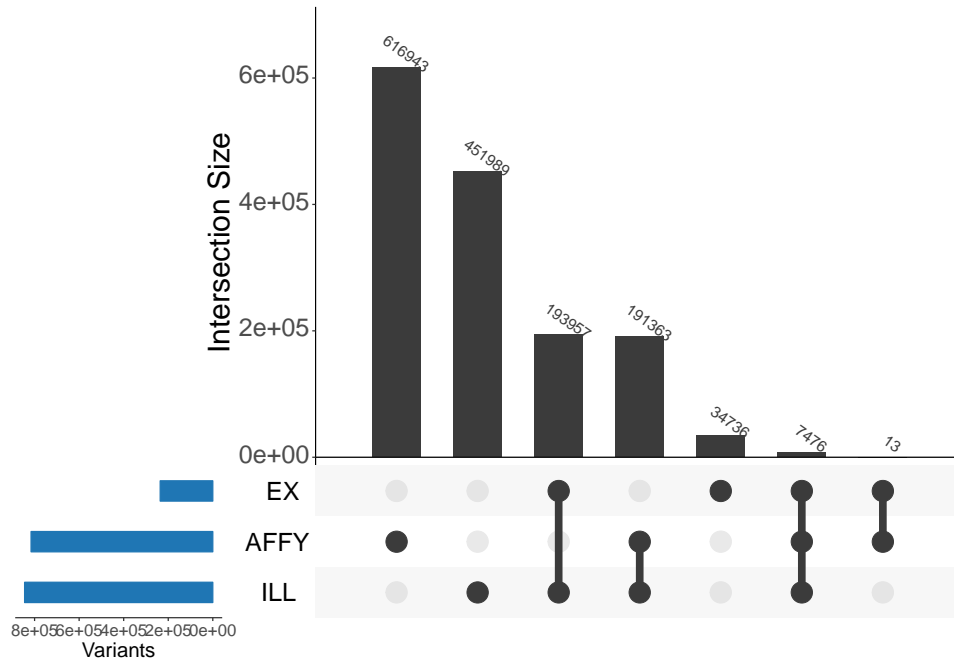


Figure 2: Variants remaining for analysis after quality control

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
EX_EUR	EX	EUR	NO
EX_AFR	EX	AFR	NO
EX_AMR	EX	AMR	NO
ILL_EUR	ILL	EUR	NO
ILL_AFR	ILL	AFR	NO
ILL_AMR	ILL	AMR	NO
AFFY_EUR	AFFY	EUR	NO
AFFY_AFR	AFFY	AFR	NO
AFFY_AMR	AFFY	AMR	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_EX			NO
	EX_EUR	0	
	EX_AFR	0	
	EX_AMR	57	
META_GWAS			NO
	ILL_EUR	0	
	ILL_AFR	0	
	ILL_AMR	0	
	AFFY_EUR	8	
	AFFY_AFR	154	
	AFFY_AMR	177	

2.1.3 Merged results

In order to present results in a comprehensive way, we identified a single reference set of results as the default and merged in results from other arrays where either the variant failed to provide a p -value or did not exist in the reference set. Table 4 describes the merges performed. The '>' symbol in the 'Cohorts/Metas' column implies the strategy used to combine the results. The left-most results set was kept as reference, while variants from the following set were merged in where applicable. This merge was repeated (ie. additively) for all sets listed from left to right.

Table 4: Merged results

ID	Cohorts/Metas	Report
MERGE	META_EX>META_GWAS	YES

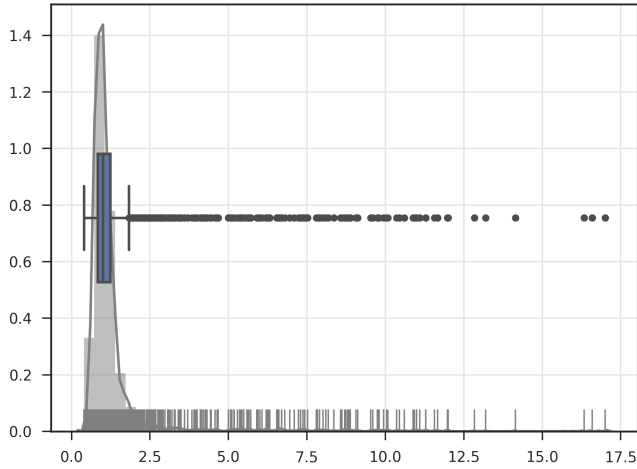
2.2 Ancestry Adjustment and Outlier Removal

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

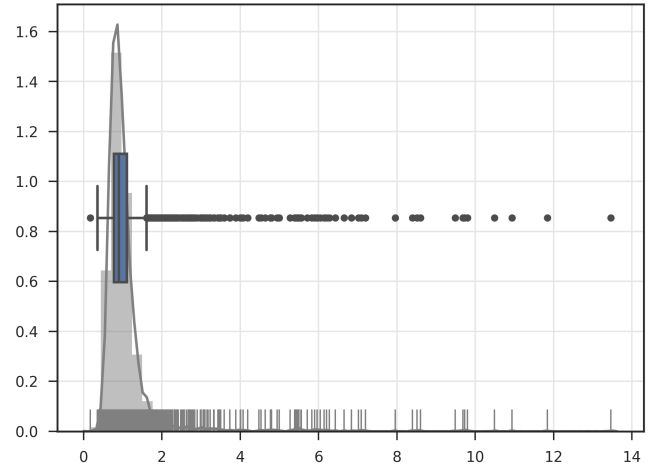
and all of the PC's. If the N th PC exhibited a statistically significant p -value ($p \leq 0.05$), we selected PC's $1 - N$ to be included in association testing. Once determined, any sample lying outside 6 standard deviations from the mean on any of the N PC's was marked as an outlier and removed from 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)

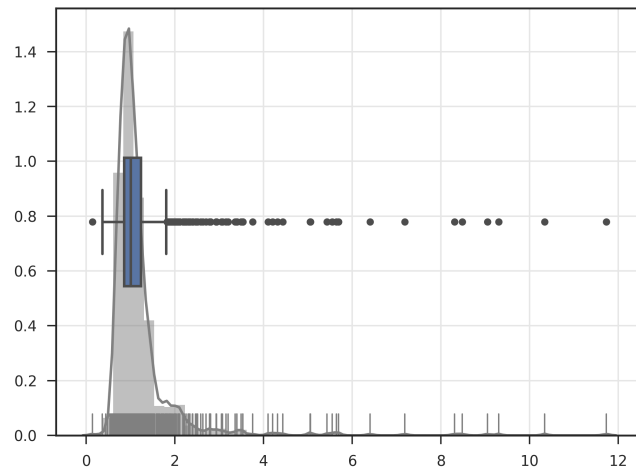
3.1 Summary



(a) EX_AFR

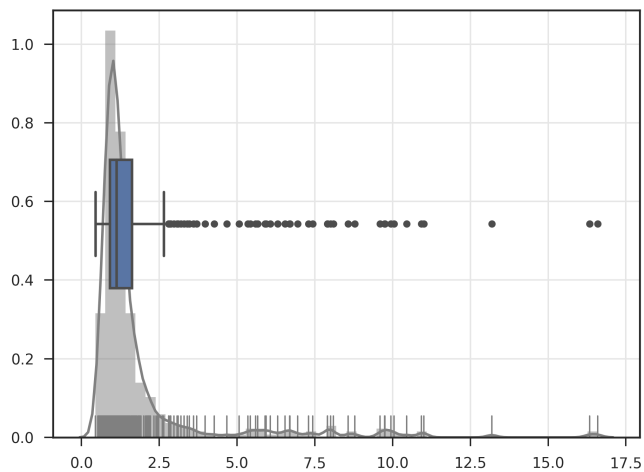


(b) EX_AMR

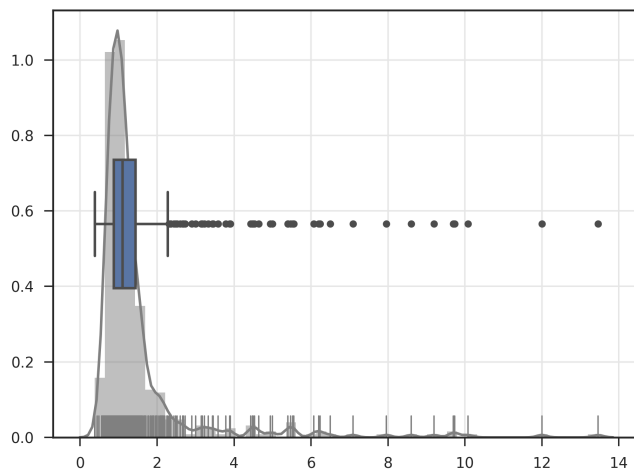


(c) EX_EUR

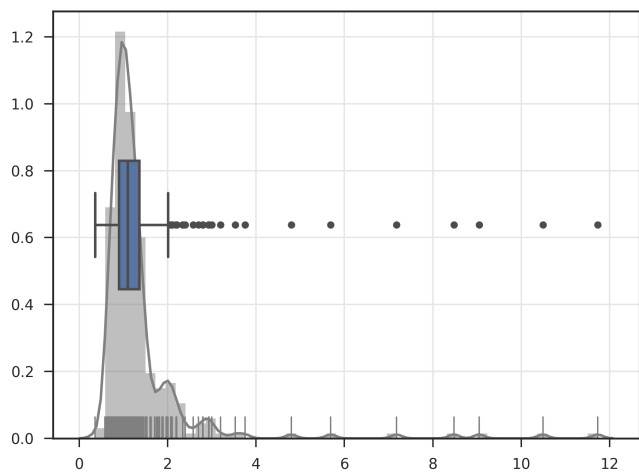
Figure 3: Distribution of SERUM_CREATININE in META_EX by cohort



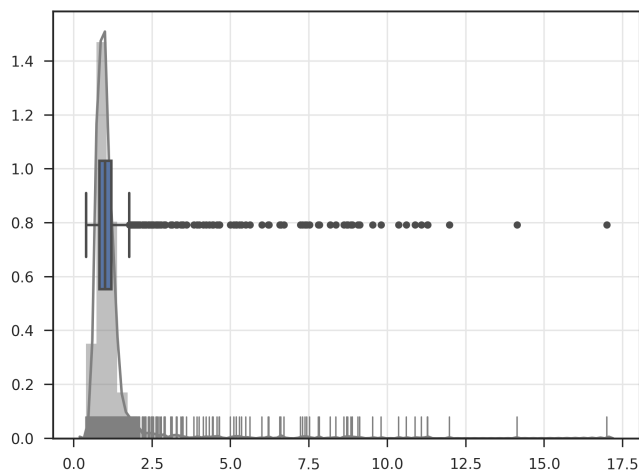
(a) AFFY_AFR



(b) AFFY_AMR



(c) AFFY_EUR



(d) ILL_AFR

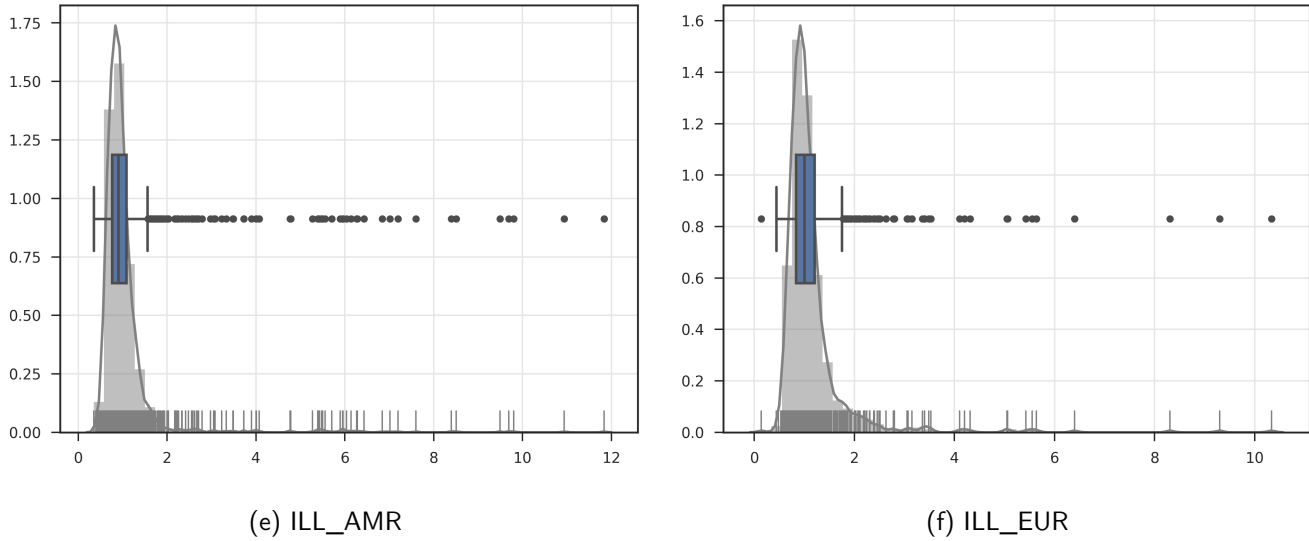


Figure 4: Distribution of SERUM_CREATININE in META_GWAS by cohort

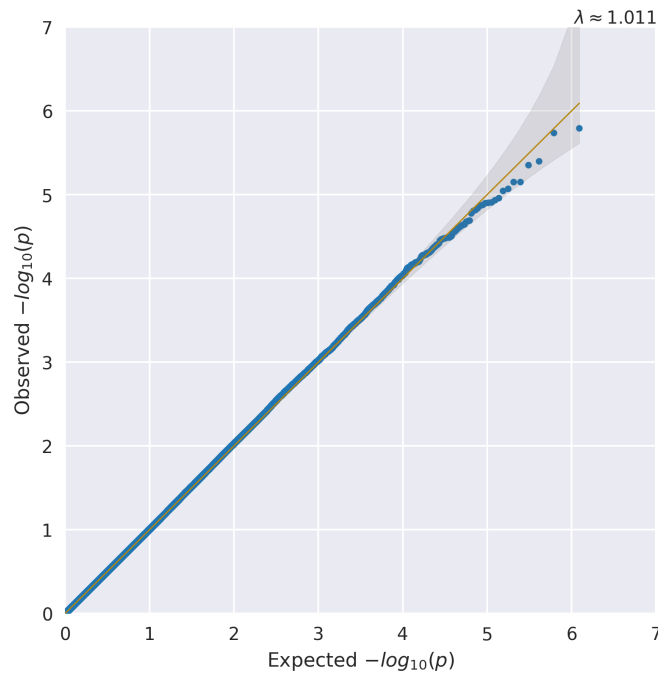
Table 5: Summary of samples removed from Serum Creatinine analysis by cohort and model

Cohort	Array	Ancestry	Trans	Covars	Total	-SampleQc	-missObs	-Kinship	-PcOutlier
META_EX EX_AFR	EX	AFR	invn	AGE_SERUM_CREATININE+SEX	5172	44	2385	173	51
META_EX EX_AMR	EX	AMR	invn	AGE_SERUM_CREATININE+SEX	5144	32	2545	260	0
META_EX EX_EUR	EX	EUR	invn	AGE_SERUM_CREATININE+SEX	2379	30	1273	3	0
META_GWAS AFFY_AFR	AFFY	AFR	invn	AGE_SERUM_CREATININE+SEX	897	18	353	97	0
META_GWAS AFFY_AMR	AFFY	AMR	invn	AGE_SERUM_CREATININE+SEX	1035	20	439	122	0
META_GWAS AFFY_EUR	AFFY	EUR	invn	AGE_SERUM_CREATININE+SEX	578	12	288	5	0
META_GWAS ILL_AFR	ILL	AFR	invn	AGE_SERUM_CREATININE+SEX	4077	46	1921	0	37
META_GWAS ILL_AMR	ILL	AMR	invn	AGE_SERUM_CREATININE+SEX	3884	26	1956	0	0
META_GWAS ILL_EUR	ILL	EUR	invn	AGE_SERUM_CREATININE+SEX	1797	23	983	0	0

Table 6: Summary of samples remaining for Serum Creatinine analysis by cohort and model

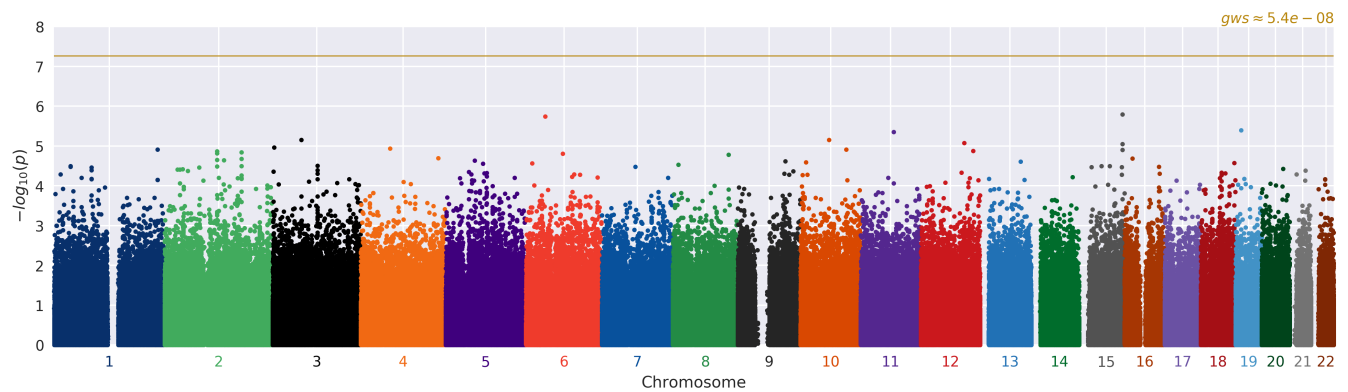
Cohort	Array	Ancestry	Trans	Covars	PCs	N	Male	Female	Max	Min	μ	\bar{x}	σ
META_EX EX_AFR	EX	AFR	invn	AGE_SERUM_CREATININE+SEX	8	2545	972	1573	17.0	0.39	1.331	1.0	1.447
META_EX EX_AMR	EX	AMR	invn	AGE_SERUM_CREATININE+SEX	1	2322	940	1382	13.46	0.35	1.103	0.91	0.925
META_EX EX_EUR	EX	EUR	invn	AGE_SERUM_CREATININE+SEX	1	1086	747	339	11.73	0.14	1.205	1.0	0.887
META_GWAS AFFY_AFR	AFFY	AFR	invn	AGE_SERUM_CREATININE+SEX	0	434	197	237	16.59	0.44	1.82	1.125	2.137
META_GWAS AFFY_AMR	AFFY	AMR	invn	AGE_SERUM_CREATININE+SEX	0	460	205	255	13.46	0.38	1.463	1.09	1.368
META_GWAS AFFY_EUR	AFFY	EUR	invn	AGE_SERUM_CREATININE+SEX	0	280	238	42	11.73	0.36	1.36	1.1	1.131
META_GWAS ILL_AFR	ILL	AFR	invn	AGE_SERUM_CREATININE+SEX	9	2091	777	1314	17.0	0.39	1.209	0.98	1.169
META_GWAS ILL_AMR	ILL	AMR	invn	AGE_SERUM_CREATININE+SEX	1	1914	757	1157	11.84	0.35	1.035	0.9	0.812
META_GWAS ILL_EUR	ILL	EUR	invn	AGE_SERUM_CREATININE+SEX	1	801	507	294	10.34	0.14	1.151	0.99	0.779

3.2 Calibration



(a) invn Adjusted AGE_SERUM_CREATININE+SEX

Figure 5: QQ plots for SERUM_CREATININE in the MERGE analysis



(a) invn Adjusted AGE_SERUM_CREATININE+SEX

Figure 6: Manhattan plots for SERUM_CREATININE in the MERGE analysis

3.3 Top associations

Table 7: Top variants in the MERGE invn Adjusted AGE_SERUM_CREATININE+SEX model (**bold** variants indicate previously identified associations)

CHR	POS	ID	EA	OA	GENE _{CLOSEST}	COHORT	DIR	N	MALE	FEMALE	FREQ _{AVG}	FREQ _{MIN}	FREQ _{MAX}	EFFECT	STDERR	OR	ZSCORE	P
15	97587651	rs234538	T	G	SPATA8	META_GWAS	+++xxx	4,804	2,041	2,763	0.427	0.341	0.512	$9.89 \cdot 10^{-2}$	$2.06 \cdot 10^{-2}$	1.104	4.798	$1.61 \cdot 10^{-6}$
6	43303503	rs2651202	A	G	ZNF318	META_GWAS	+++xxx	4,806	2,041	2,765	$1.53 \cdot 10^{-2}$	$4.3 \cdot 10^{-3}$	$3.93 \cdot 10^{-2}$	0.398	$8.34 \cdot 10^{-2}$	1.489	4.772	$1.82 \cdot 10^{-6}$
19	13035722	rs35087277	T	C	FARSA	META_EX	+++	5,953	2,659	3,294	$8.32 \cdot 10^{-3}$	$5.7 \cdot 10^{-3}$	$1.75 \cdot 10^{-2}$	0.456	$9.89 \cdot 10^{-2}$	1.578	-4.612	$3.99 \cdot 10^{-6}$
11	74170978	rs3867279	C	A	KCNE3	META_GWAS	+++xxx	4,806	2,041	2,765	0.169	0.128	0.202	0.126	$2.74 \cdot 10^{-2}$	1.134	-4.591	$4.42 \cdot 10^{-6}$
3	64206296	rs696231	A	G	PRICKLE2	META_GWAS	+++xxx	4,806	2,041	2,765	$9.95 \cdot 10^{-2}$	$7.68 \cdot 10^{-2}$	0.123	0.152	$3.39 \cdot 10^{-2}$	1.164	4.493	$7.03 \cdot 10^{-6}$
10	64128954	rs7096931	C	A	ZNF365	META_GWAS	+++xxx	4,805	2,041	2,764	0.218	0.205	0.235	0.111	$2.47 \cdot 10^{-2}$	1.117	-4.492	$7.06 \cdot 10^{-6}$
12	97606943	rs12322545	A	G	NEDD1	META_GWAS	+++xxx	4,805	2,041	2,764	0.273	0.166	0.394	0.104	$2.34 \cdot 10^{-2}$	1.11	4.454	$8.45 \cdot 10^{-6}$
3	3079127	rs3749363	T	G	CNTN4	META_GWAS	+++xxx	4,805	2,040	2,765	$9 \cdot 10^{-2}$	$6.6 \cdot 10^{-2}$	0.12	0.158	$3.6 \cdot 10^{-2}$	1.171	-4.399	$1.09 \cdot 10^{-5}$
4	66294649	rs7672488	G	A	EPHA5	META_GWAS	+++xxx	4,801	2,037	2,764	0.718	0.645	0.8	$1 \cdot 10^{-1}$	$2.28 \cdot 10^{-2}$	1.105	-4.384	$1.16 \cdot 10^{-5}$
1	233256280	rs717588	G	A	PCNX2	META_GWAS	+++xxx	4,806	2,041	2,765	0.784	0.617	0.876	0.111	$2.53 \cdot 10^{-2}$	1.117	4.372	$1.23 \cdot 10^{-5}$
10	103067687	rs590945	T	C	BTRC	META_GWAS	+++++	5,980	2,681	3,299	0.658	0.522	0.809	$8.73 \cdot 10^{-2}$	$2 \cdot 10^{-2}$	1.091	-4.37	$1.24 \cdot 10^{-5}$
12	118135896	rs605265	A	G	KSR2	META_GWAS	+++++	5,978	2,680	3,298	0.507	0.374	0.698	$8.23 \cdot 10^{-2}$	$1.89 \cdot 10^{-2}$	1.086	4.356	$1.33 \cdot 10^{-5}$
2	117724192	rs7608004	G	A	DDX18	META_GWAS	+++++	4,804	2,040	2,764	0.495	0.387	0.565	$8.82 \cdot 10^{-2}$	$2.03 \cdot 10^{-2}$	1.092	-4.352	$1.35 \cdot 10^{-5}$
2	172663394	rs6754817	T	C	SLC25A12	META_GWAS	xxx+++	1,174	640	534	0.293	0.26	0.327	0.196	$4.51 \cdot 10^{-2}$	1.216	4.337	$1.44 \cdot 10^{-5}$
6	82783397	rs16893850	T	C	IBTK	META_GWAS	xxx+++	1,169	639	530	$4.32 \cdot 10^{-2}$	$1.27 \cdot 10^{-2}$	$7.99 \cdot 10^{-2}$	0.434	0.1	1.543	4.32	$1.56 \cdot 10^{-5}$
8	125640964	rs4870915	G	A	MTSS1	META_GWAS	xxx+++	1,169	639	530	0.235	0.141	0.356	0.212	$4.93 \cdot 10^{-2}$	1.236	-4.305	$1.67 \cdot 10^{-5}$
4	174046753	rs10022850	C	A	GALNT7	META_GWAS	xxx+++	1,174	640	534	$2.73 \cdot 10^{-2}$	$1.79 \cdot 10^{-3}$	$5.65 \cdot 10^{-2}$	0.533	0.125	1.704	4.263	$2.02 \cdot 10^{-5}$
16	17530588	rs1559448	C	G	XYLT1	META_GWAS	xxx+++	1,173	639	534	$2.56 \cdot 10^{-3}$	$1.15 \cdot 10^{-3}$	$4.35 \cdot 10^{-3}$	1.734	0.407	5.663	4.259	$2.06 \cdot 10^{-5}$
2	172558172	rs2138348	T	G	DYNCl12	META_GWAS	xxx+++	1,174	640	534	0.292	0.258	0.325	0.193	$4.53 \cdot 10^{-2}$	1.213	4.254	$2.1 \cdot 10^{-5}$
2	132917161	rs6707621	G	A	ANKRD30BL	META_GWAS	xxx+++	1,173	640	533	0.13	$1.61 \cdot 10^{-2}$	0.258	0.273	$6.45 \cdot 10^{-2}$	1.314	4.235	$2.28 \cdot 10^{-5}$

3.4 Previously identified risk loci

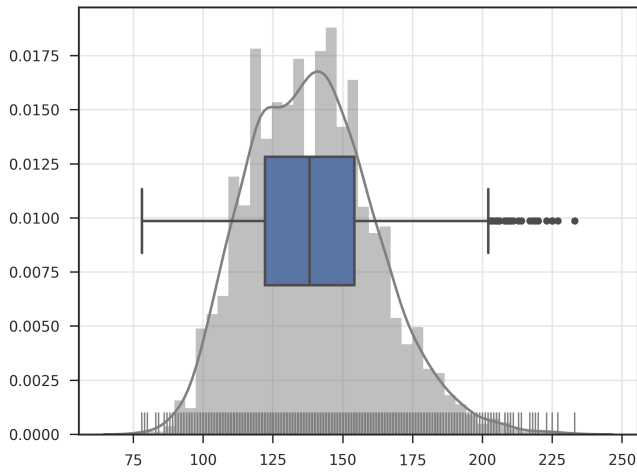
Table 8 shows statistics from the MERGE cohort for 10 loci that were shown to be significantly associated with Serum Creatinine in the 2016 Nature Communications paper by Kettunen et al [8]. Where a previously reported variant was not genotyped in the study (indicated by $\bar{R}^2 < 1$), if available, 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 1 variants that show at least nominal significance ($p < 0.05$) in this study. Out of the 10 variants in both studies, 9 exhibit the same direction of effect with the known result (binomial test $p = 0.0107$).

Table 8: Top known loci in MERGE model invn Adjusted AGE_SERUM_CREATININE+SEX (**bold** variants indicate matching direction of effect)

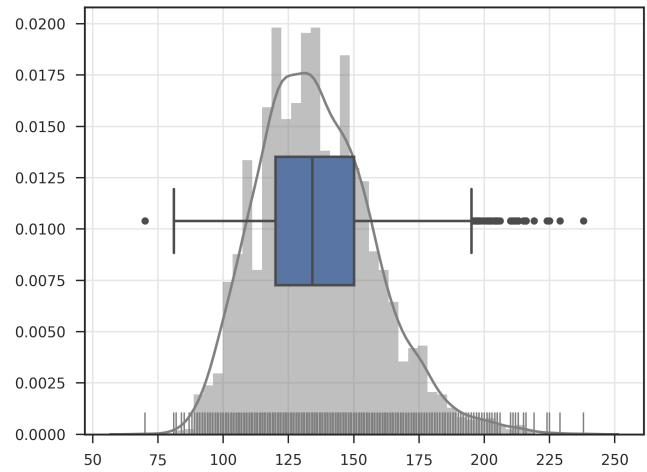
CHR	POS	ID	EA	OA	N	FREQ _{AVG}	FREQ _{MIN}	FREQ _{MAX}	EFFECT	STDERR	P	DIR	COHORT	GENE _{CLOSEST}	R ²	ID _{KNOWN}	N _{KNOWN}	EFFECT _{KNOWN}	STDERR _{KNOWN}	P _{KNOWN}
15	45636584	rs1153860	T	C	1,174	0.661	0.4	0.876	$1.42 \cdot 10^{-2}$	$4.66 \cdot 10^{-2}$	0.76	xxx+++	META_GWAS	GATM	1	rs1153860	24,925	$7.34 \cdot 10^{-2}$	$9.4 \cdot 10^{-3}$	$6.99 \cdot 10^{-15}$
15	45683795	rs1145077	T	G	1,172	0.662	0.394	0.88	$8.56 \cdot 10^{-3}$	$4.69 \cdot 10^{-2}$	0.855	xxx+++	META_GWAS	SPATA5L1	1	rs1145077	24,925	$7.35 \cdot 10^{-2}$	$9.44 \cdot 10^{-3}$	$8.05 \cdot 10^{-15}$
17	59465697	rs2079742	C	T	1,174	0.202	0.151	0.266	$3.07 \cdot 10^{-2}$	$5.1 \cdot 10^{-2}$	0.547	xxx+++	META_GWAS	BCAS3	1	rs2079742	24,925	$9.59 \cdot 10^{-2}$	$1.28 \cdot 10^{-2}$	$8.61 \cdot 10^{-14}$
15	45609773	rs1719250	A	G	1,174	0.611	0.541	0.667	$3.06 \cdot 10^{-2}$	$4.08 \cdot 10^{-2}$	0.453	xxx+++	META_GWAS	SLC28A2	1	rs1719250	24,925	$-6.51 \cdot 10^{-2}$	$9.52 \cdot 10^{-3}$	$8.52 \cdot 10^{-12}$
15	45729123	rs1974981	G	A	5,977	0.31	0.264	0.385	$2.69 \cdot 10^{-2}$	$1.98 \cdot 10^{-2}$	0.174	++++	META_GWAS	CL5orf48	1	rs1974981	24,925	$7.03 \cdot 10^{-2}$	$1.03 \cdot 10^{-2}$	$9.04 \cdot 10^{-12}$
7	151415041	rs10224002	G	A	5,955	0.35	0.285	0.407	$2.18 \cdot 10^{-2}$	$1.94 \cdot 10^{-2}$	0.263	+++	META_EX	PRKAC2	1	rs10224002	24,925	$7.07 \cdot 10^{-2}$	$1.11 \cdot 10^{-2}$	$1.89 \cdot 10^{-10}$
4	77420784	rs1986734	T	C	4,806	0.343	0.237	0.483	$2.32 \cdot 10^{-2}$	$2.2 \cdot 10^{-2}$	0.291	++xxx	META_GWAS	SHROOM3	1	rs1986734	24,925	$6.19 \cdot 10^{-2}$	$9.8 \cdot 10^{-3}$	$3.04 \cdot 10^{-10}$
6	160693107	rs3119311	C	T	4,806	0.145	0.101	0.196	$4.8 \cdot 10^{-2}$	$2.89 \cdot 10^{-2}$	$9.73 \cdot 10^{-2}$	+++xxx	META_GWAS	SLC22A2	1	rs3119311	24,925	$9.08 \cdot 10^{-2}$	$1.55 \cdot 10^{-2}$	$5.29 \cdot 10^{-9}$
17	59483766	rs8068318	C	T	5,954	0.434	0.271	0.699	$3.79 \cdot 10^{-2}$	$1.97 \cdot 10^{-2}$	$5.42 \cdot 10^{-2}$	+++	META_EX	TBX2	1	rs8068318	24,925	$6.21 \cdot 10^{-2}$	$1.08 \cdot 10^{-2}$	$8.69 \cdot 10^{-9}$
15	45801035	rs950027	C	T	5,979	0.745	0.48	0.916	$5.81 \cdot 10^{-2}$	$2.23 \cdot 10^{-2}$	$9.26 \cdot 10^{-3}$	+++++	META_GWAS	SLC30A4	1	rs950027	24,925	$5.28 \cdot 10^{-2}$	$9.32 \cdot 10^{-3}$	$1.59 \cdot 10^{-8}$

4 Systolic Blood Pressure (SBP15)

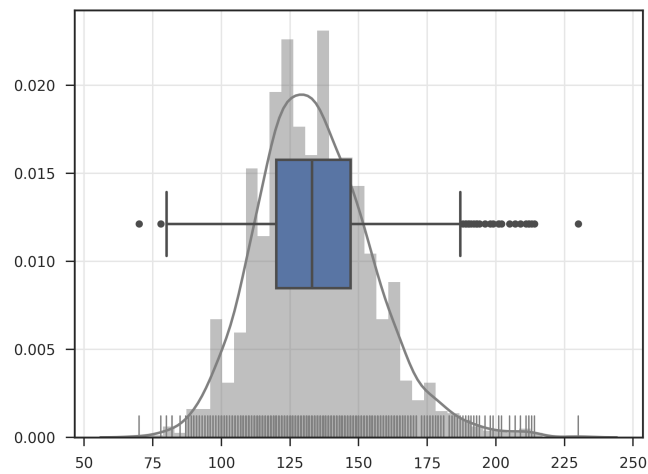
4.1 Summary



(a) EX_AFR

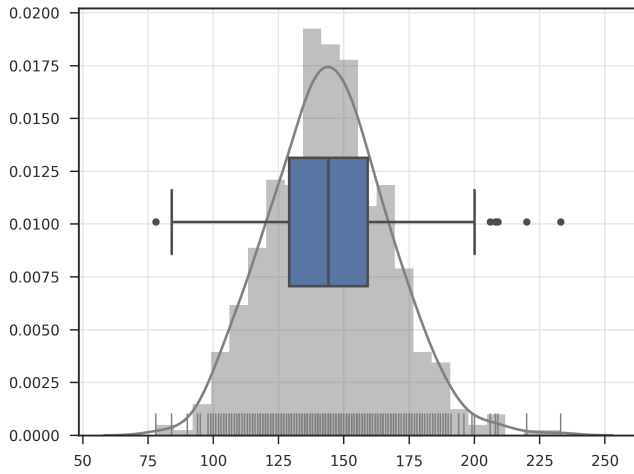


(b) EX_AMR

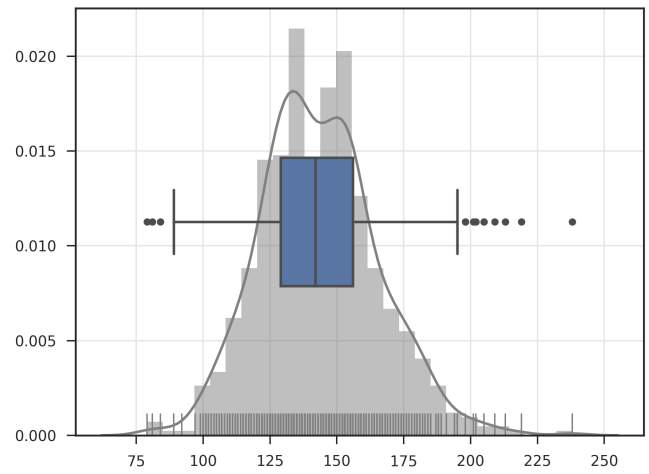


(c) EX_EUR

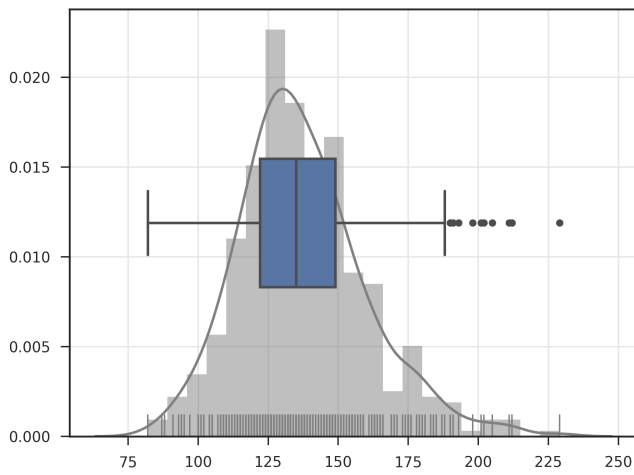
Figure 7: Distribution of SBP15 in META_EX by cohort



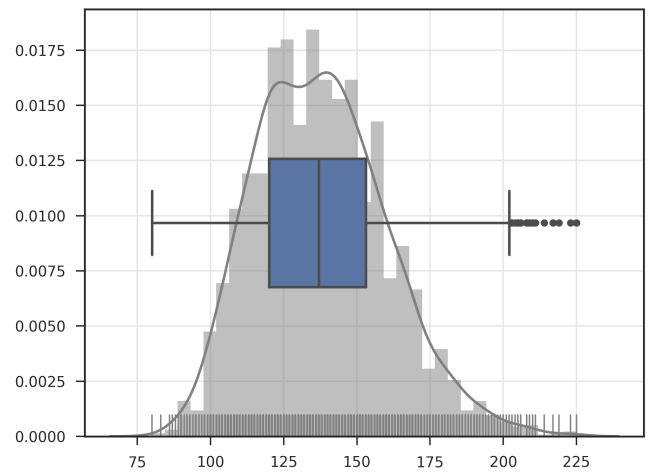
(a) AFFY_AFR



(b) AFFY_AMR



(c) AFFY_EUR



(d) ILL_AFR

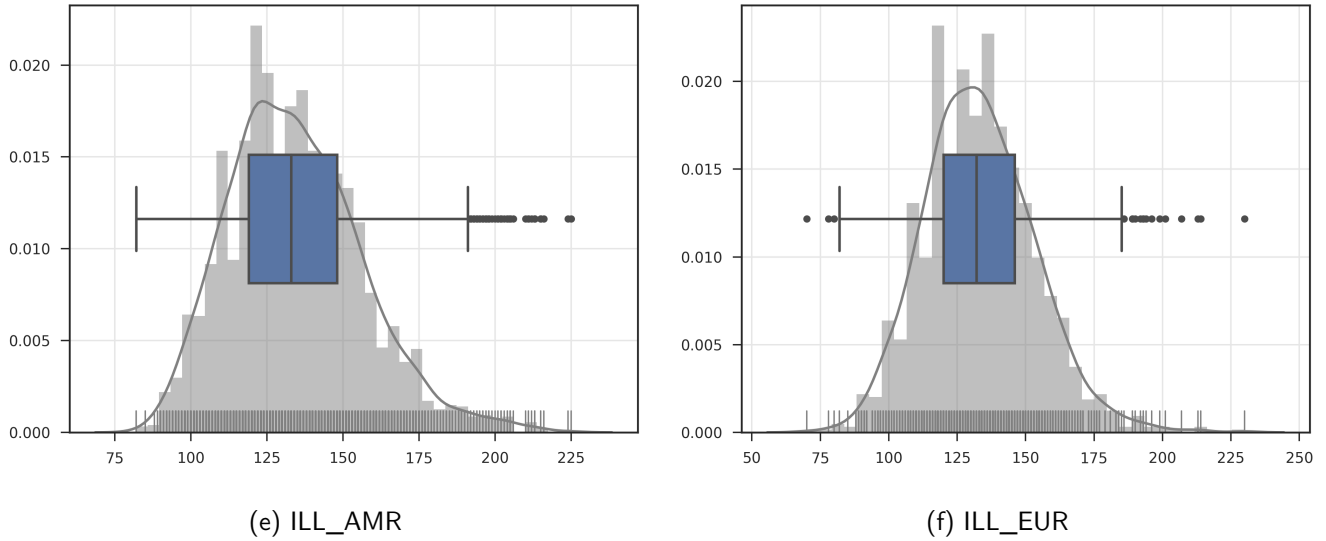


Figure 8: Distribution of SBP15 in META_GWAS by cohort

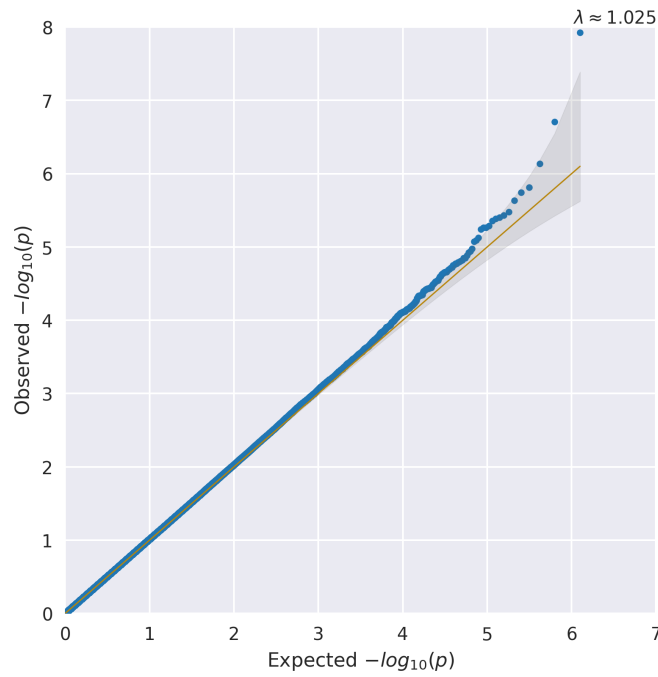
Table 9: Summary of samples removed from Systolic Blood Pressure analysis by cohort and model

Cohort	Array	Ancestry	Trans	Covars	Total	-SampleQc	-missObs	-Kinship	-PcOutlier
META_EX EX_AFR	EX	AFR	invn	AGE_BP+AGE_BP2+SEX+BMI	5172	44	1132	285	5
META_EX EX_AMR	EX	AMR	invn	AGE_BP+AGE_BP2+SEX+BMI	5144	32	1144	424	0
META_EX EX_EUR	EX	EUR	invn	AGE_BP+AGE_BP2+SEX+BMI	2379	30	626	6	1
META_GWAS AFFY_AFR	AFFY	AFR	invn	AGE_BP+AGE_BP2+SEX+BMI	897	18	208	127	0
META_GWAS AFFY_AMR	AFFY	AMR	invn	AGE_BP+AGE_BP2+SEX+BMI	1035	20	227	164	0
META_GWAS AFFY_EUR	AFFY	EUR	invn	AGE_BP+AGE_BP2+SEX+BMI	578	12	173	8	0
META_GWAS ILL_AFR	ILL	AFR	invn	AGE_BP+AGE_BP2+SEX+BMI	4077	46	893	4	0
META_GWAS ILL_AMR	ILL	AMR	invn	AGE_BP+AGE_BP2+SEX+BMI	3884	26	870	2	0
META_GWAS ILL_EUR	ILL	EUR	invn	AGE_BP+AGE_BP2+SEX+BMI	1797	23	456	1	0

Table 10: Summary of samples remaining for Systolic Blood Pressure analysis by cohort and model

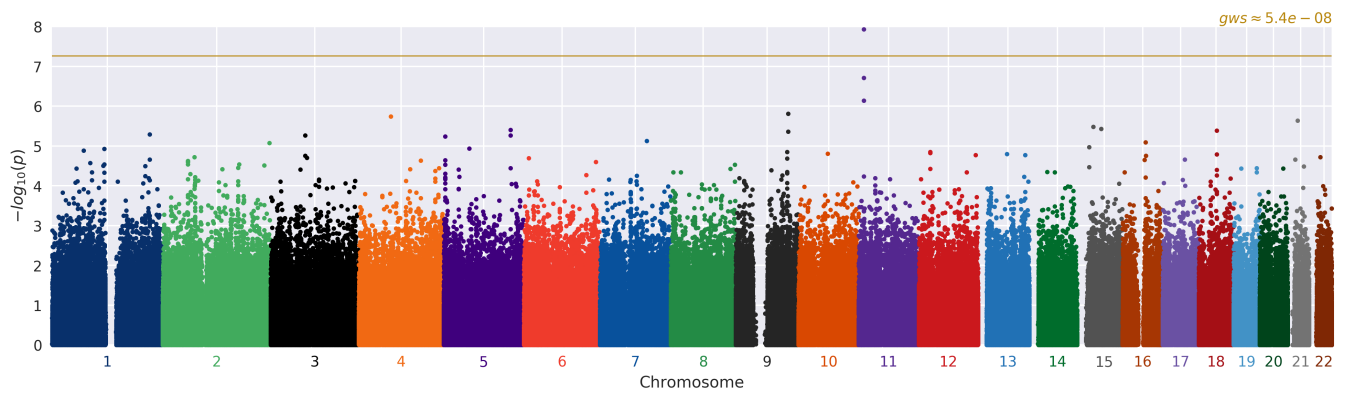
Cohort	Array	Ancestry	Trans	Covars	PCs	N	Male	Female	Max	Min	μ	\bar{x}	σ
META_EX EX_AFR	EX	AFR	invn	AGE_BP+AGE_BP2+SEX+BMI	0	3719	1311	2408	233.0	79.0	139.229	139.0	22.635
META_EX EX_AMR	EX	AMR	invn	AGE_BP+AGE_BP2+SEX+BMI	1	3553	1392	2161	238.0	81.0	135.615	134.0	22.326
META_EX EX_EUR	EX	EUR	invn	AGE_BP+AGE_BP2+SEX+BMI	8	1723	1150	573	230.0	70.0	134.22	133.0	20.786
META_GWAS AFFY_AFR	AFFY	AFR	invn	AGE_BP+AGE_BP2+SEX+BMI	0	550	240	310	233.0	79.0	144.856	145.0	22.874
META_GWAS AFFY_AMR	AFFY	AMR	invn	AGE_BP+AGE_BP2+SEX+BMI	0	627	273	354	238.0	81.0	143.046	141.0	21.842
META_GWAS AFFY_EUR	AFFY	EUR	invn	AGE_BP+AGE_BP2+SEX+BMI	0	391	319	72	212.0	82.0	137.235	135.0	22.431
META_GWAS ILL_AFR	ILL	AFR	invn	AGE_BP+AGE_BP2+SEX+BMI	0	3146	1080	2066	225.0	80.0	138.076	137.0	22.313
META_GWAS ILL_AMR	ILL	AMR	invn	AGE_BP+AGE_BP2+SEX+BMI	3	2994	1143	1851	225.0	82.0	134.365	133.0	22.02
META_GWAS ILL_EUR	ILL	EUR	invn	AGE_BP+AGE_BP2+SEX+BMI	0	1324	828	496	230.0	70.0	133.292	132.0	20.038

4.2 Calibration



(a) invn Adjusted AGE_BP+AGE_BP2+SEX+BMI

Figure 9: QQ plots for SBP15 in the MERGE analysis



(a) invn Adjusted AGE_BP+AGE_BP2+SEX+BMI

Figure 10: Manhattan plots for SBP15 in the MERGE analysis

4.3 Top associations

Table 11: Top variants in the MERGE invn Adjusted AGE_BP+AGE_BP2+SEX+BMI model (**bold** variants indicate previously identified associations)

CHR	POS	ID	EA	OA	GENE _{CLOSEST}	COHORT	DIR	N	MALE	FEMALE	FREQ _{AVG}	FREQ _{MIN}	FREQ _{MAX}	EFFECT	STDERR	OR	ZSCORE	P
11	11386594	rs1843784	T	A	GALNT18	META_GWAS	xxx+++	1,568	832	736	0.217	0.131	0.289	0.251	4.41 · 10 ⁻²	1.286	-5.703	1.18 · 10 ⁻⁸
9	117502242	rs2185935	C	T	TNFSF15	META_GWAS	+++++	9,032	3,883	5,149	0.183	8.74 · 10 ⁻²	0.353	9.43 · 10 ⁻²	1.96 · 10 ⁻²	1.099	-4.805	1.54 · 10 ⁻⁶
4	71984094	rs1985134	G	A	SLC4A4	META_GWAS	xxx+++	1,567	832	735	0.18	0.123	0.248	0.221	4.63 · 10 ⁻²	1.247	4.774	1.81 · 10 ⁻⁶
21	22624941	rs2826754	A	G	NCAM2	META_GWAS	++ +xxx	7,460	3,050	4,410	0.311	0.25	0.378	8.34 · 10 ⁻²	1.77 · 10 ⁻²	1.087	-4.724	2.32 · 10 ⁻⁶
15	36780723	rs7168196	C	T	CI5orf41	META_GWAS	+++++	9,030	3,881	5,149	0.335	0.281	0.416	7.38 · 10 ⁻²	1.59 · 10 ⁻²	1.077	4.65	3.32 · 10 ⁻⁶
15	54201160	rs2255116	G	T	UNC13C	META_GWAS	xxx+++	1,562	831	731	8.26 · 10 ⁻²	1.28 · 10 ⁻³	0.182	0.307	6.64 · 10 ⁻²	1.36	4.628	3.69 · 10 ⁻⁶
5	150282784	rs2290989	T	C	ZNF300	META_GWAS	xxx+++	1,568	832	736	3.44 · 10 ⁻²	2.09 · 10 ⁻²	4.99 · 10 ⁻²	0.447	9.7 · 10 ⁻²	1.564	-4.613	3.96 · 10 ⁻⁶
18	40453910	rs41444547	C	A	RIT2	META_GWAS	xxx+++	1,562	829	733	8.99 · 10 ⁻²	3.19 · 10 ⁻²	0.146	0.297	6.45 · 10 ⁻²	1.346	-4.607	4.08 · 10 ⁻⁶
9	117483943	rs7026324	G	A	RP11-402G3	META_GWAS	+++xxx	7,464	3,051	4,413	0.219	0.1	0.42	9.39 · 10 ⁻²	2.04 · 10 ⁻²	1.098	-4.592	4.39 · 10 ⁻⁶
1	220228658	rs10863529	A	G	BPNT1	META_GWAS	+++xxx	7,459	3,050	4,409	0.503	0.365	0.69	7.59 · 10 ⁻²	1.67 · 10 ⁻²	1.079	4.56	5.12 · 10 ⁻⁶
3	77419441	rs4234495	T	C	ROBO2	META_GWAS	xxx+++	1,568	832	736	0.805	0.767	0.827	0.204	4.48 · 10 ⁻²	1.226	-4.548	5.42 · 10 ⁻⁶
5	150199238	rs12659091	T	C	AC010441	META_GWAS	xxx+++	1,568	832	736	3.41 · 10 ⁻²	1.91 · 10 ⁻²	4.99 · 10 ⁻²	0.443	9.74 · 10 ⁻²	1.557	-4.547	5.44 · 10 ⁻⁶
5	3470914	rs2914204	T	C	IRX1	META_GWAS	xxx+++	1,564	829	735	0.765	0.56	0.926	0.204	4.5 · 10 ⁻²	1.226	-4.535	5.75 · 10 ⁻⁶
7	105554522	rs17152281	C	A	ATXN7L1	META_GWAS	xxx+++	1,556	826	730	0.141	0.129	0.161	0.234	5.22 · 10 ⁻²	1.263	-4.481	7.43 · 10 ⁻⁶
16	51656556	rs9674344	T	A	SALL1	META_GWAS	xxx+++	1,568	832	736	6.7 · 10 ⁻²	1.28 · 10 ⁻³	0.122	0.317	7.1 · 10 ⁻²	1.373	4.463	8.07 · 10 ⁻⁶
2	239600686	rs7594129	A	C	TWIST2	META_GWAS	+++++	9,032	3,883	5,149	0.588	0.459	0.727	6.87 · 10 ⁻²	1.54 · 10 ⁻²	1.071	4.453	8.46 · 10 ⁻⁶
15	27183589	rs1864793	T	C	GABRB3	META_GWAS	xxx+++	1,567	832	735	0.445	0.384	0.488	0.158	3.6 · 10 ⁻²	1.172	4.405	1.06 · 10 ⁻⁵
5	57939227	rs4997647	T	G	RAB3C	META_GWAS	+++xxx	7,462	3,049	4,413	9.29 · 10 ⁻²	7.02 · 10 ⁻²	0.103	0.124	2.84 · 10 ⁻²	1.132	4.387	1.15 · 10 ⁻⁵
1	118017634	rs10923312	A	T	MAN1A2	META_GWAS	xxx+++	1,568	832	736	0.125	0.112	0.141	0.235	5.37 · 10 ⁻²	1.265	-4.38	1.19 · 10 ⁻⁵
1	71024268	rs4612577	G	T	CTH	META_GWAS	xxx+++	1,568	832	736	0.471	0.403	0.5	0.157	3.61 · 10 ⁻²	1.17	4.36	1.3 · 10 ⁻⁵

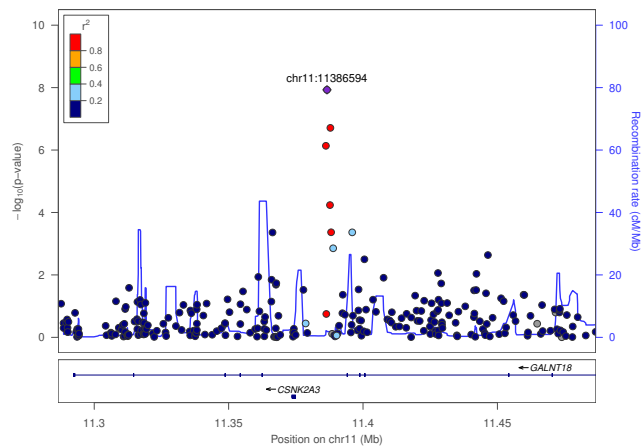


Figure 11: Regional plot for cohort MERGE model invn Adjusted AGE_BP+AGE_BP2+SEX+BMI: rs1843784 ±100kb

4.4 Previously identified risk loci

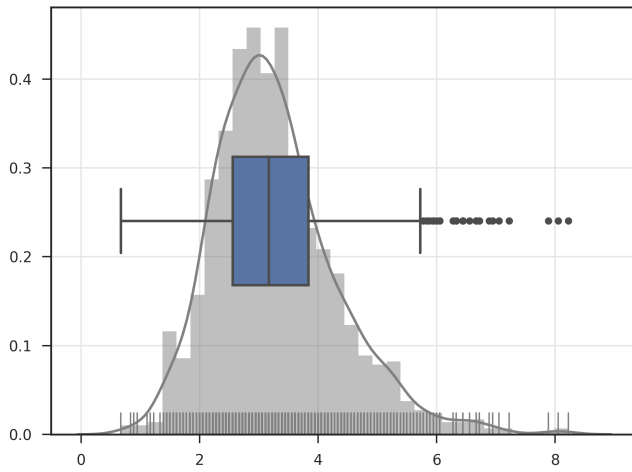
Table 12 shows statistics from the MERGE cohort for 22 loci that were shown to be significantly associated with Systolic Blood Pressure in the 2011 Nature paper by Ehret et al [17]. Where a previously reported variant was not genotyped in the study (indicated by $\bar{R}^2 < 1$), if available, a tagging 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 2 variants that show at least nominal significance ($p < 0.05$) in this study. Out of the 20 variants in both studies, 8 exhibit the same direction of effect with the known result (binomial test $p = 0.868$).

Table 12: Top known loci in MERGE model invn Adjusted AGE_BP+AGE_BP2+SEX+BMI (**bold** variants indicate matching direction of effect)

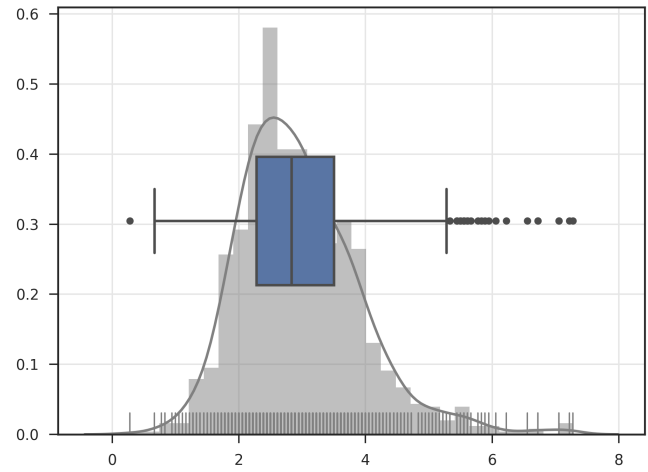
CHR	POS	ID	EA	OA	N	FREQ _{AVG}	FREQ _{MIN}	FREQ _{MAX}	EFFECT	STDERR	P	DIR	COHORT	GENE _{CLOSEST}	R ²	ID _{KNOWN}	N _{KNOWN}	EFFECT _{KNOWN}	STDERR _{KNOWN}	P _{KNOWN}
12	90060586	rs17249754	G	A	8,994	0.136	0.12	0.194	7.26 · 10 ⁻²	2.16 · 10 ⁻²	7.98 · 10 ⁻⁴	+++	META_EX	ATP2B1	1	rs17249754	2 · 10 ⁵	0.955	0.134	9.73 · 10 ⁻¹³
1	11862778	rs17367504	A	G	8,997	0.109	0.105	0.122	1.91 · 10 ⁻²	2.38 · 10 ⁻²	0.423	++	META_EX	MTHFR	1	rs17367504	2 · 10 ⁵	-0.861	0.136	2.11 · 10 ⁻¹⁰
1	11883731	rs12567136	C	T	9,032	0.112	0.107	0.137	5.29 · 10 ⁻³	2.32 · 10 ⁻²	0.82	++++	META_GWAS	CLCN6	1	rs12567136	2 · 10 ⁵	-0.847	0.135	3.41 · 10 ⁻¹⁰
15	75077367	rs1378942	C	A	1,568	0.356	0.106	0.619	6.17 · 10 ⁻²	4.19 · 10 ⁻²	0.141	xxx+++	META_GWAS	CSK	1	rs1378942	2 · 10 ⁵	0.632	0.101	3.43 · 10 ⁻¹⁰
10	104846178	rs11191548	T	C	8,997	7.62 · 10 ⁻²	4.55 · 10 ⁻²	0.103	3.49 · 10 ⁻²	2.81 · 10 ⁻²	0.215	+++	META_EX	CNNM2	1	rs11191548	2 · 10 ⁵	1.083	0.174	5.03 · 10 ⁻¹⁰
10	104594507	rs1004467	G	A	8,995	0.162	0.102	0.199	3.04 · 10 ⁻⁴	2.04 · 10 ⁻²	0.988	++	META_EX	CYP17A1	1	rs1004467	2 · 10 ⁵	1.01	0.164	6.61 · 10 ⁻¹⁰
10	104906211	rs11191580	C	T	8,994	6.39 · 10 ⁻²	2.11 · 10 ⁻²	9.67 · 10 ⁻²	2.62 · 10 ⁻²	3.07 · 10 ⁻²	0.394	+++	META_EX	NT5C2	1	rs11191580	2 · 10 ⁵	1.058	0.173	9.16 · 10 ⁻¹⁰
12	112007756	rs653178	C	T	8,997	0.744	0.439	0.926	7.24 · 10 ⁻³	1.86 · 10 ⁻²	0.697	++	META_EX	ATXN2	1	rs653178	2 · 10 ⁵	-0.605	9.88 · 10 ⁻²	9.3 · 10 ⁻¹⁰
12	89942390	rs11105328	A	G	9,030	0.135	0.108	0.194	7.53 · 10 ⁻²	2.18 · 10 ⁻²	5.4 · 10 ⁻⁴	++++	META_GWAS	POC1B-GALNT4	1	rs11105328	2 · 10 ⁵	-0.838	0.137	1.08 · 10 ⁻⁹
10	104660004	rs11191454	A	G	8,997	6.27 · 10 ⁻²	2.08 · 10 ⁻²	9.47 · 10 ⁻²	3.89 · 10 ⁻²	3.1 · 10 ⁻²	0.209	+++	META_EX	BORCS7-ASMT	1	rs11191454	2 · 10 ⁵	-1.043	0.171	1.12 · 10 ⁻⁹
10	11184608	rs3184504	T	C	8,997	0.744	0.44	0.926	8.1 · 10 ⁻³	1.86 · 10 ⁻²	0.664	++	META_EX	SH2B3	1	rs3184504	2 · 10 ⁵	0.598	9.93 · 10 ⁻²	1.69 · 10 ⁻⁹
4	81164723	rs1458038	T	C	7,463	0.173	8.3 · 10 ⁻²	0.26	3.53 · 10 ⁻²	2.21 · 10 ⁻²	0.11	+++xxx	META_GWAS	FGF5	1	rs1458038	2 · 10 ⁵	0.662	0.111	2.12 · 10 ⁻⁹
11	16902268	rs381815	C	T	7,463	0.229	0.191	0.279	3.65 · 10 ⁻²	1.95 · 10 ⁻²	6.08 · 10 ⁻²	+++xxx	META_GWAS	PLEKHA7	1	rs381815	2 · 10 ⁵	-0.655	0.11	2.45 · 10 ⁻⁹
10	104638480	rs3740390	C	T	1,566	8.3 · 10 ⁻²	5.74 · 10 ⁻²	0.104	2.92 · 10 ⁻²	6.53 · 10 ⁻²	0.655	xxx++	META_GWAS	AS3MT	1	rs3740390	2 · 10 ⁵	-1.005	0.172	4.61 · 10 ⁻⁹
10	104546284	rs486955	C	T	7,464	0.792	0.726	0.9	1.98 · 10 ⁻²	2.05 · 10 ⁻²	0.335	+++xxx	META_GWAS	WBP1L	1	rs486955	2 · 10 ⁵	-0.895	0.156	9.47 · 10 ⁻⁹
15	75107880	rs1716022	A	C	1,568	0.614	0.585	0.701	5.92 · 10 ⁻²	3.76 · 10 ⁻²	0.116	xxx+++	META_GWAS	LMAN1L	1	rs1716022	2 · 10 ⁵	-0.602	0.107	2.11 · 10 ⁻⁸
12	112072424	rs11065987	G	A	8,996	0.237	6.57 · 10 ⁻²	0.526	6.86 · 10 ⁻³	1.91 · 10 ⁻²	0.719	++	META_EX	BRAP	1	rs11065987	2 · 10 ⁵	0.57	0.102	2.12 · 10 ⁻⁸
15	75057203	rs4886406	G	T	7,464	0.677	0.617	0.721	3.84 · 10 ⁻⁴	1.77 · 10 ⁻²	0.983	+++xxx	META_GWAS	CYP1A2	1	rs4886406	2 · 10 ⁵	-0.599	0.108	3.06 · 10 ⁻⁸
12	112486818	rs17696736	A	G	8,996	0.24	6.65 · 10 ⁻²	0.54	1.23 · 10 ⁻³	1.9 · 10 ⁻²	0.949	++	META_EX	NAA25	1	rs17696736	2 · 10 ⁵	-0.549	9.96 · 10 ⁻²	3.43 · 10 ⁻⁸
12	112906415	rs11066320	A	G	7,464	0.767	0.46	0.933	4.89 · 10 ⁻³	2.1 · 10 ⁻²	0.816	+++xxx	META_GWAS	PTPN11	1	rs11066320	2 · 10 ⁵	-0.544	9.96 · 10 ⁻²	4.56 · 10 ⁻⁸
12	112486818	rs17696736	A	G	8,996	0.24	6.65 · 10 ⁻²	0.54	1.23 · 10 ⁻³	1.9 · 10 ⁻²	0.949	++	META_EX	TRAFD1	0.922	rs17630235	2 · 10 ⁵	-0.569	0.1	1.45 · 10 ⁻⁸
12	112486818	rs17696736	A	G	8,996	0.24	6.65 · 10 ⁻²	0.54	1.23 · 10 ⁻³	1.9 · 10 ⁻²	0.949	++	META_EX	HECTD4	0.913	rs11066188	2 · 10 ⁵	-0.567	0.101	1.72 · 10 ⁻⁸

5 HDL Cholesterol (HDL)

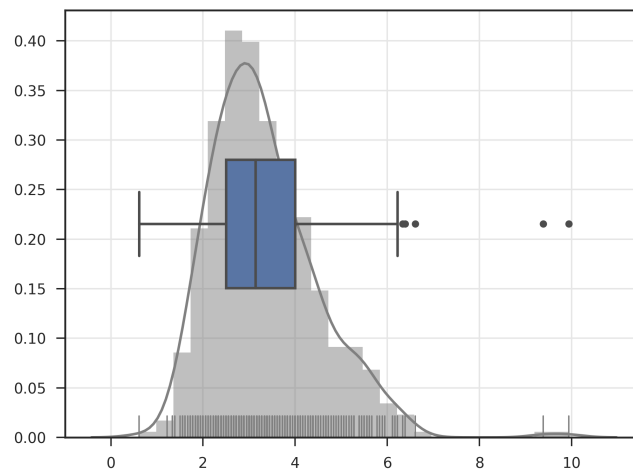
5.1 Summary



(a) EX_AFR

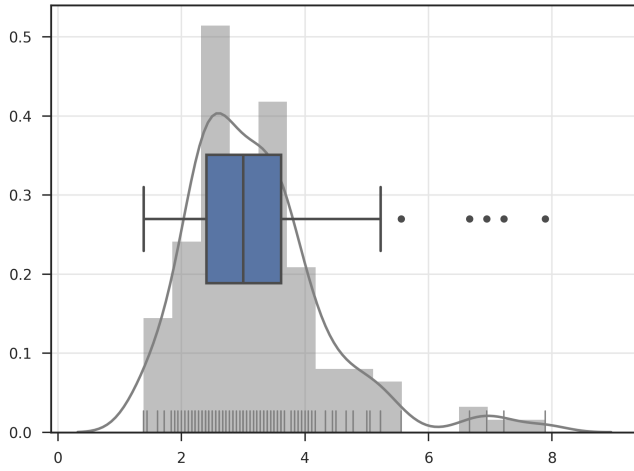


(b) EX_AMR

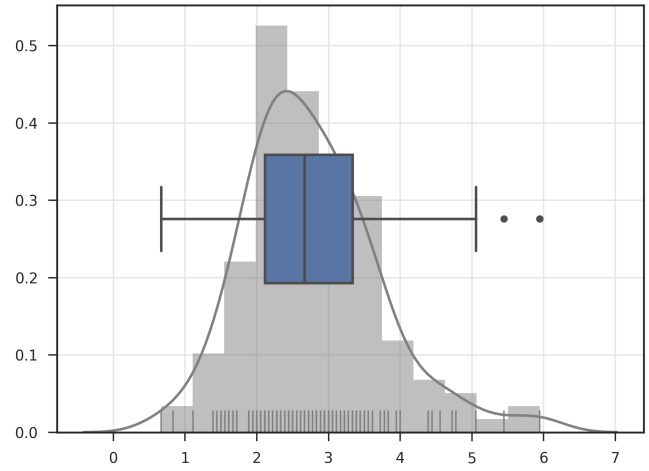


(c) EX_EUR

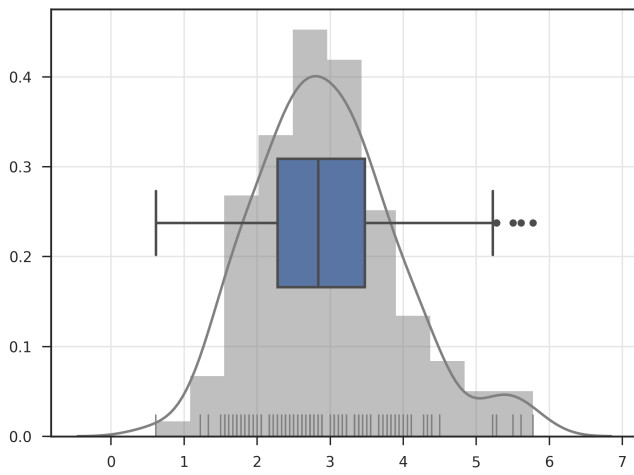
Figure 12: Distribution of HDL in META_EX by cohort



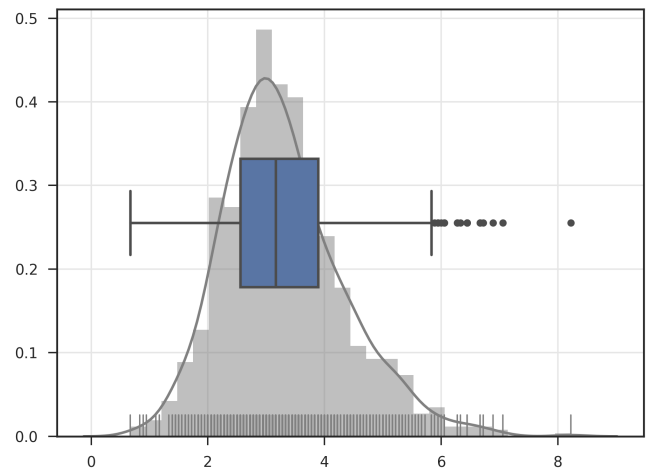
(a) AFFY_AFR



(b) AFFY_AMR



(c) AFFY_EUR



(d) ILL_AFR

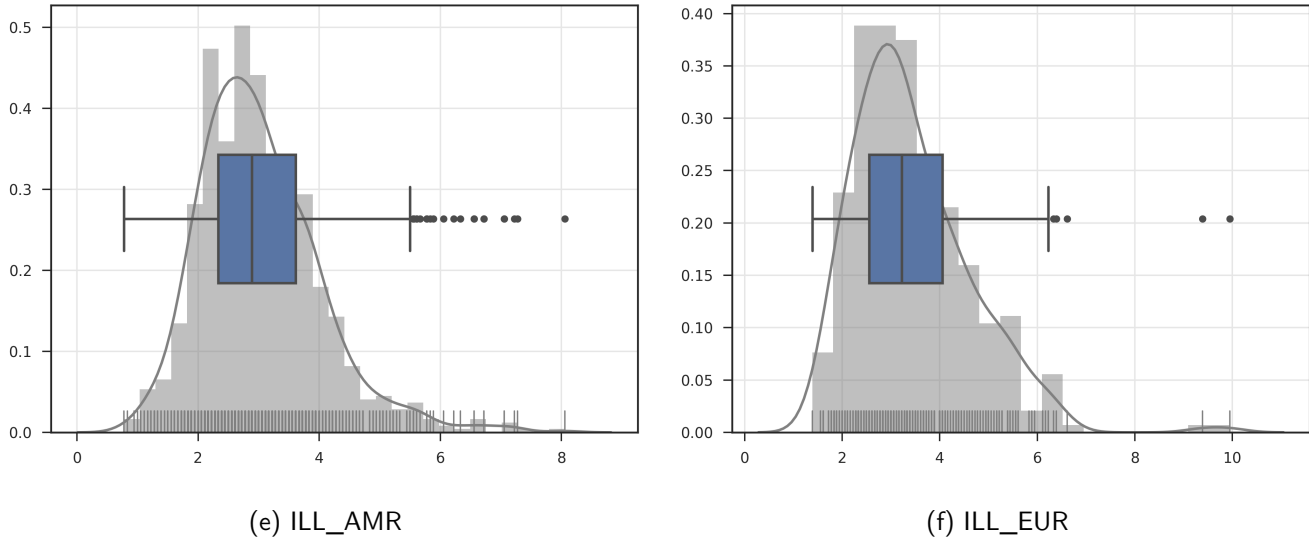


Figure 13: Distribution of HDL in META_GWAS by cohort

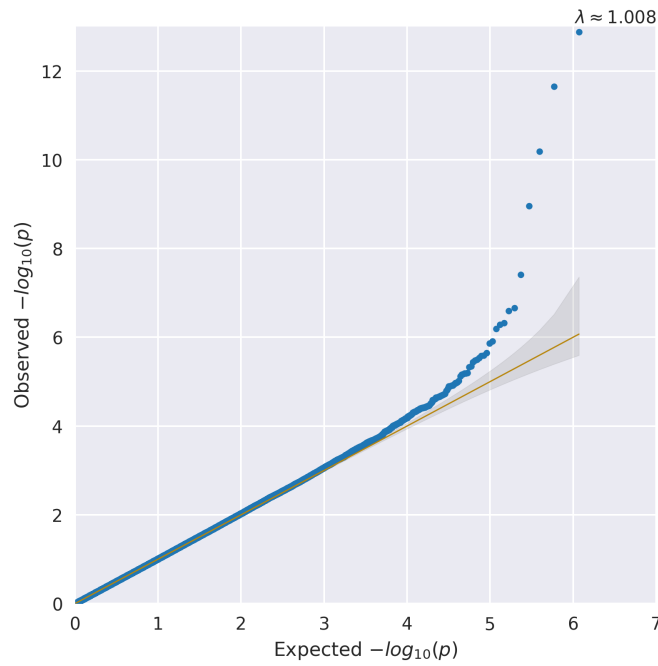
Table 13: Summary of samples removed from HDL Cholesterol analysis by cohort and model

Cohort	Array	Ancestry	Trans	Covars	Total	-SampleQc	-missObs	-Kinship	-PcOutlier
META_EX EX_AFR	EX	AFR	invn	AGE_LIPIDS+AGE_LIPIDS2+SEX+BMI	5172	44	4004	82	0
META_EX EX_AMR	EX	AMR	invn	AGE_LIPIDS+AGE_LIPIDS2+SEX+BMI	5144	32	4095	111	0
META_EX EX_EUR	EX	EUR	invn	AGE_LIPIDS+AGE_LIPIDS2+SEX+BMI	2379	30	1945	1	0
META_GWAS AFFY_AFR	AFFY	AFR	invn	AGE_LIPIDS+AGE_LIPIDS2+SEX+BMI	897	18	734	27	0
META_GWAS AFFY_AMR	AFFY	AMR	invn	AGE_LIPIDS+AGE_LIPIDS2+SEX+BMI	1035	20	897	27	6
META_GWAS AFFY_EUR	AFFY	EUR	invn	AGE_LIPIDS+AGE_LIPIDS2+SEX+BMI	578	12	467	1	0
META_GWAS ILL_AFR	ILL	AFR	invn	AGE_LIPIDS+AGE_LIPIDS2+SEX+BMI	4077	46	3121	1	14
META_GWAS ILL_AMR	ILL	AMR	invn	AGE_LIPIDS+AGE_LIPIDS2+SEX+BMI	3884	26	3039	0	1
META_GWAS ILL_EUR	ILL	EUR	invn	AGE_LIPIDS+AGE_LIPIDS2+SEX+BMI	1797	23	1475	0	4

Table 14: Summary of samples remaining for HDL Cholesterol analysis by cohort and model

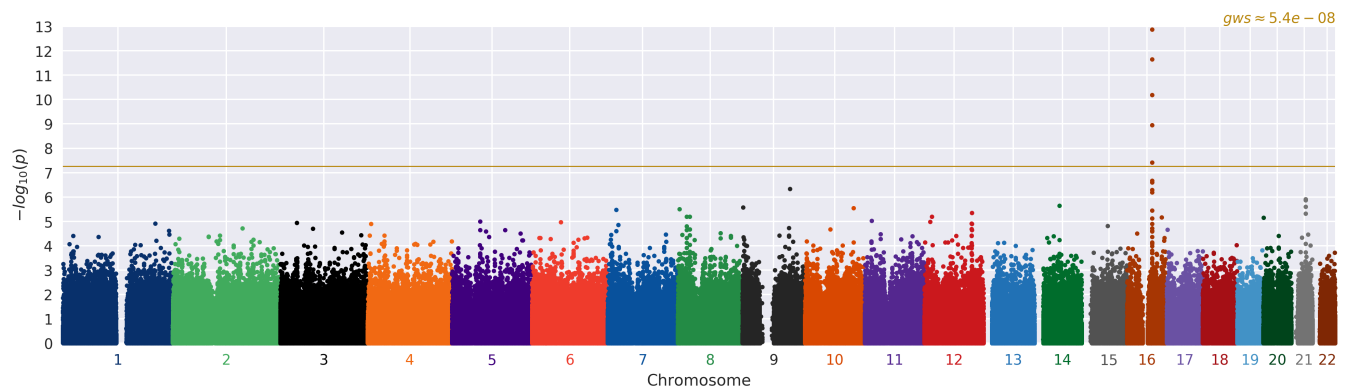
Cohort	Array	Ancestry	Trans	Covars	PCs	N	Male	Female	Max	Min	μ	\bar{x}	σ
META_EX EX_AFR	EX	AFR	invn	AGE_LIPIDS+AGE_LIPIDS2+SEX+BMI	0	1078	387	691	8.222	0.667	3.281	3.111	1.049
META_EX EX_AMR	EX	AMR	invn	AGE_LIPIDS+AGE_LIPIDS2+SEX+BMI	2	931	383	548	7.222	0.667	2.963	2.833	0.943
META_EX EX_EUR	EX	EUR	invn	AGE_LIPIDS+AGE_LIPIDS2+SEX+BMI	0	425	273	152	9.944	0.611	3.349	3.167	1.179
META_GWAS AFFY_AFR	AFFY	AFR	invn	AGE_LIPIDS+AGE_LIPIDS2+SEX+BMI	0	134	64	70	7.889	1.389	3.147	3.0	1.124
META_GWAS AFFY_AMR	AFFY	AMR	invn	AGE_LIPIDS+AGE_LIPIDS2+SEX+BMI	0	104	46	58	5.944	0.667	2.658	2.583	0.851
META_GWAS AFFY_EUR	AFFY	EUR	invn	AGE_LIPIDS+AGE_LIPIDS2+SEX+BMI	0	107	85	22	5.778	0.611	3.002	2.889	0.983
META_GWAS ILL_AFR	ILL	AFR	invn	AGE_LIPIDS+AGE_LIPIDS2+SEX+BMI	3	929	318	611	8.222	0.667	3.307	3.167	1.037
META_GWAS ILL_AMR	ILL	AMR	invn	AGE_LIPIDS+AGE_LIPIDS2+SEX+BMI	0	839	341	498	7.278	0.833	2.999	2.833	0.977
META_GWAS ILL_EUR	ILL	EUR	invn	AGE_LIPIDS+AGE_LIPIDS2+SEX+BMI	10	314	186	128	9.944	1.389	3.46	3.222	1.22

5.2 Calibration



(a) invn Adjusted AGE_LIPIDS+AGE_LIPIDS2+SEX+BMI

Figure 14: QQ plots for HDL in the MERGE analysis



(a) invn Adjusted AGE_LIPIDS+AGE_LIPIDS2+SEX+BMI

Figure 15: Manhattan plots for HDL in the MERGE analysis

5.3 Top associations

Table 15: Top variants in the MERGE invn Adjusted AGE_LIPIDS+AGE_LIPIDS2+SEX+BMI model (**bold** variants indicate previously identified associations)

CHR	POS	ID	EA	OA	GENE_CLOSEST	COHORT	DIR	N	MALE	FEMALE	FREQ_AVG	FREQ_MIN	FREQ_MAX	EFFECT	STDERR	OR	ZSCORE	P
16	56989590	rs247616	T	C	CETP	META_EX	+++	2,433	1,042	1,391	0.272	0.258	0.294	0.235	3.18 · 10 ⁻²	1.265	7.403	1.33 · 10 ⁻¹³
9	107180109	rs10991262	A	G	OR13F1	META_GWAS	+++xxx	2,082	845	1,237	0.336	0.313	0.428	0.166	3.29 · 10 ⁻²	1.18	5.038	4.7 · 10 ⁻⁷
21	32659136	rs2251255	G	A	TIAM1	META_GWAS	xxx+++	345	195	150	0.106	3.36 · 10 ⁻²	0.192	0.64	0.132	1.897	-4.852	1.22 · 10 ⁻⁶
14	56960032	rs1189273	T	C	TMEM260	META_GWAS	+++xxx	2,080	845	1,235	0.628	0.57	0.713	0.151	3.19 · 10 ⁻²	1.163	4.73	2.25 · 10 ⁻⁶
9	1472056	rs7853203	C	A	DMRT2	META_GWAS	xxx+++	345	195	150	4.78 · 10 ⁻²	1.87 · 10 ⁻²	7.48 · 10 ⁻²	0.813	0.173	2.256	-4.698	2.63 · 10 ⁻⁶
10	109888333	rs2151875	C	T	SORCS1	META_GWAS	+++xxx	2,081	845	1,236	0.129	9.55 · 10 ⁻²	0.169	0.216	4.61 · 10 ⁻²	1.241	-4.679	2.88 · 10 ⁻⁶
8	3720473	rs2975366	A	G	CSMD1	META_GWAS	xxx+++	345	195	150	0.332	0.266	0.403	0.359	7.7 · 10 ⁻²	1.432	-4.661	3.14 · 10 ⁻⁶
7	19461203	rs10486347	C	A	TWISTNB	META_GWAS	xxx+++	343	194	149	0.35	0.235	0.43	0.38	8.18 · 10 ⁻²	1.463	-4.651	3.3 · 10 ⁻⁶
12	107159405	rs10778508	T	C	RFX4	META_GWAS	xxx+++	345	195	150	0.441	0.409	0.489	0.329	7.17 · 10 ⁻²	1.39	4.589	4.46 · 10 ⁻⁶
8	19824492	rs13702	C	T	LPL	META_EX	++	2,434	1,043	1,391	0.429	0.335	0.532	0.131	2.91 · 10 ⁻²	1.14	4.513	6.38 · 10 ⁻⁶
8	26848328	rs17056484	A	G	ADRA1A	META_GWAS	xxx+++	344	195	149	0.112	6.54 · 10 ⁻²	0.175	0.546	0.121	1.726	4.51	6.47 · 10 ⁻⁶
12	16747034	rs10846380	T	C	LMO3	META_GWAS	+++++	2,424	1,038	1,386	0.285	0.222	0.392	0.142	3.16 · 10 ⁻²	1.153	4.51	6.49 · 10 ⁻⁶
16	78209069	rs11643308	T	G	WVVOX	META_GWAS	+++++	2,427	1,040	1,387	0.365	0.295	0.411	0.132	2.94 · 10 ⁻²	1.142	-4.5	6.8 · 10 ⁻⁶
20	283877	rs4815112	T	C	ZCCHC3	META_GWAS	+++++	2,426	1,040	1,386	0.533	0.365	0.725	0.135	3.01 · 10 ⁻²	1.145	-4.495	6.95 · 10 ⁻⁶
11	15443681	rs10766251	G	A	INSC	META_GWAS	xxx+++	345	195	150	0.629	0.467	0.728	0.353	7.98 · 10 ⁻²	1.424	-4.428	9.53 · 10 ⁻⁶
5	63098636	rs10075397	C	T	HTR1A	META_GWAS	xxx+++	345	195	150	0.635	0.5	0.769	0.335	7.58 · 10 ⁻²	1.397	-4.413	1.02 · 10 ⁻⁵
12	12812881	rs759747	A	G	GPR19	META_GWAS	xxx+++	344	194	150	0.967	0.952	0.981	0.89	0.202	2.436	-4.406	1.05 · 10 ⁻⁵
6	65657069	rs12200181	A	G	EYS	META_GWAS	xxx+++	345	195	150	0.175	9.33 · 10 ⁻²	0.266	0.437	9.93 · 10 ⁻²	1.548	-4.402	1.07 · 10 ⁻⁵
3	37487580	rs9844749	T	G	ITGA9	META_GWAS	+++++	2,426	1,040	1,386	0.144	2.34 · 10 ⁻²	0.242	0.186	4.23 · 10 ⁻²	1.204	-4.39	1.13 · 10 ⁻⁵
1	209800230	rs2076349	C	T	LAMB3	META_EX	+++	2,432	1,042	1,390	0.199	2.47 · 10 ⁻²	0.269	0.162	3.71 · 10 ⁻²	1.176	-4.375	1.21 · 10 ⁻⁵

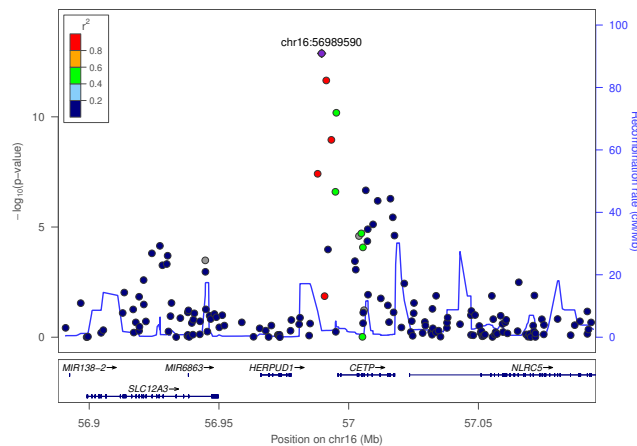


Figure 16: Regional plot for cohort MERGE model invn Adjusted AGE_LIPIDS+AGE_LIPIDS2+SEX+BMI: rs247616 ±100kb

5.4 Previously identified risk loci

Table 16 shows statistics from the MERGE cohort for 50 loci that were shown to be significantly associated with HDL Cholesterol in the 2013 Nature Genetics paper by Willer 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 6 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 16: Top known loci in MERGE model invn Adjusted AGE_LIPIDS+AGE_LIPIDS2+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	COHORT	GENE _{CLOSEST}	R ²	ID _{KNOWN}	N _{KNOWN}	EFFECT _{KNOWN}	STDERR _{KNOWN}	P _{KNOWN}
16	57005479	rs1532624	A	C	2,433	0.26	0.151	0.399	0.133	3.37 · 10 ⁻²	8.22 · 10 ⁻⁵	+++	META_EX	CETP	1	rs1532624	94,595	0.204	3.5 · 10 ⁻³	0
16	56985139	rs9989419	G	A	2,433	0.511	0.4	0.619	3.32 · 10 ⁻²	2.89 · 10 ⁻²	0.25	+++	META_EX	HERPUD1	1	rs9989419	94,595	0.147	3.6 · 10 ⁻³	0
15	58678512	rs10468017	T	C	2,433	0.212	0.157	0.294	4.22 · 10 ⁻²	3.57 · 10 ⁻²	0.238	+++	META_EX	LIPC	1	rs10468017	94,595	0.118	3.8 · 10 ⁻³	1.21 · 10 ⁻¹⁸⁸
8	19824492	rs13702	C	T	2,433	0.429	0.334	0.532	0.129	2.91 · 10 ⁻²	8.76 · 10 ⁻⁶	+++	META_EX	LPL	1	rs13702	94,595	0.106	3.8 · 10 ⁻³	1.28 · 10 ⁻¹⁶⁰
8	19928582	rs9644568	A	G	345	9.13 · 10 ⁻²	5.6 · 10 ⁻²	0.136	0.176	0.133	0.186	xxx++	META_GWAS	SLC18A1	1	rs9644568	94,595	0.127	5.4 · 10 ⁻³	4.07 · 10 ⁻¹¹⁰
18	47167214	rs4939883	C	T	2,432	0.689	0.537	0.866	4.67 · 10 ⁻²	3.24 · 10 ⁻²	0.15	+++	META_EX	LIPG	1	rs4939883	94,595	7.99 · 10 ⁻²	4.5 · 10 ⁻³	1.8 · 10 ⁻⁶⁶
9	107664301	rs1883025	C	T	2,433	0.298	0.253	0.319	8.51 · 10 ⁻²	3.11 · 10 ⁻²	6.15 · 10 ⁻³	+++	META_EX	ABCA1	1	rs1883025	94,595	6.98 · 10 ⁻²	4.1 · 10 ⁻³	1.5 · 10 ⁻⁶⁵
16	96866196	rs2241770	C	T	2,082	8.72 · 10 ⁻²	6.21 · 10 ⁻²	9.63 · 10 ⁻²	5.16 · 10 ⁻²	5.45 · 10 ⁻²	0.345	+++xxxx	META_GWAS	NUP93	1	rs2241770	94,595	-9.89 · 10 ⁻²	5.7 · 10 ⁻³	6.78 · 10 ⁻⁶⁰
2	21231524	rs676210	G	A	2,433	0.183	0.15	0.233	2.05 · 10 ⁻²	3.69 · 10 ⁻²	0.578	++	META_EX	APOB	1	rs676210	94,595	-6.6 · 10 ⁻²	4 · 10 ⁻³	2.35 · 10 ⁻⁵⁴
16	67928042	rs16942887	A	G	2,433	0.176	0.111	0.211	2.77 · 10 ⁻²	3.7 · 10 ⁻²	0.454	++	META_EX	PSKHL	1	rs16942887	94,595	8.31 · 10 ⁻²	5.1 · 10 ⁻³	8.28 · 10 ⁻⁵⁴
16	67897487	rs1124324	T	C	2,427	0.177	9.35 · 10 ⁻²	0.228	5.14 · 10 ⁻²	3.7 · 10 ⁻²	0.165	+++++	META_GWAS	NUTF2	1	rs1124324	94,595	8.28 · 10 ⁻²	5.1 · 10 ⁻³	1.82 · 10 ⁻⁵³
16	67879400	rs3809630	A	G	2,082	0.177	0.118	0.207	4.98 · 10 ⁻²	3.97 · 10 ⁻²	0.21	+++xxxx	META_GWAS	CENPT	1	rs3809630	94,595	8.28 · 10 ⁻²	5.1 · 10 ⁻³	2.05 · 10 ⁻⁵³
16	67758778	rs4474673	T	C	2,082	0.174	9.39 · 10 ⁻²	0.212	7.08 · 10 ⁻²	4.01 · 10 ⁻²	7.76 · 10 ⁻²	+++xxxx	META_GWAS	RANBP10	1	rs4474673	94,595	8.46 · 10 ⁻²	5.3 · 10 ⁻³	9.34 · 10 ⁻⁵²
16	67997920	rs3785100	C	T	2,433	0.185	0.138	0.212	2.99 · 10 ⁻²	3.61 · 10 ⁻²	0.408	++	META_EX	SLC12A4	1	rs3785100	94,595	7.97 · 10 ⁻²	5 · 10 ⁻³	2.22 · 10 ⁻⁵¹
16	67861134	rs2292316	G	C	345	0.18	9.81 · 10 ⁻²	0.235	5.41 · 10 ⁻²	0.101	0.591	xxx++	META_GWAS	TSNAXIP1	1	rs2292316	94,595	-7.88 · 10 ⁻²	5.1 · 10 ⁻³	3.2 · 10 ⁻⁴⁸
11	116648917	rs964184	C	G	2,430	0.8	0.788	0.854	6.2 · 10 ⁻²	3.65 · 10 ⁻²	8.9 · 10 ⁻²	+++	META_EX	ZPR1	1	rs964184	94,595	-0.107	7.1 · 10 ⁻³	6.09 · 10 ⁻⁴⁸
16	68039850	rs16957696	T	C	2,082	0.116	7.75 · 10 ⁻²	0.154	3.11 · 10 ⁻²	4.87 · 10 ⁻²	0.995	+++xxxx	META_GWAS	DPEP2	1	rs16957696	94,595	7.45 · 10 ⁻²	4.9 · 10 ⁻³	1.31 · 10 ⁻⁴⁶
16	56933519	rs11643718	A	G	2,432	6.95 · 10 ⁻²	2.55 · 10 ⁻²	0.105	3.28 · 10 ⁻²	5.85 · 10 ⁻²	0.996	--	META_EX	SLC12A3	1	rs11643718	94,595	8.22 · 10 ⁻²	5.4 · 10 ⁻³	2.98 · 10 ⁻⁴⁶
16	68099821	rs7201742	G	T	2,082	0.228	0.162	0.277	2.34 · 10 ⁻²	3.7 · 10 ⁻²	0.526	+++xxxx	META_GWAS	DUS2	1	rs7201742	94,595	7.36 · 10 ⁻²	4.6 · 10 ⁻³	5.13 · 10 ⁻⁴⁶
11	116603724	rs12272004	C	A	2,433	0.125	6.94 · 10 ⁻²	0.147	6.24 · 10 ⁻²	4.31 · 10 ⁻²	0.148	+++	META_EX	BUD13	1	rs12272004	94,595	0.102	7 · 10 ⁻³	1.16 · 10 ⁻⁴⁵
8	9183596	rs4841132	G	A	2,433	0.874	0.856	0.934	0.143	4.33 · 10 ⁻²	9.9 · 10 ⁻¹	+++	META_EX	PPP1R3B	1	rs4841132	94,595	8.16 · 10 ⁻²	5.8 · 10 ⁻³	4.83 · 10 ⁻⁴⁵
16	68150527	rs12447640	A	G	2,079	0.101	5.02 · 10 ⁻²	0.158	3.41 · 10 ⁻²	5.2 · 10 ⁻²	0.948	+++xxxx	META_GWAS	NFATC3	1	rs12447640	94,595	-7.3 · 10 ⁻²	4.9 · 10 ⁻³	5.07 · 10 ⁻⁴⁵
2	21123352	rs6711016	C	A	345	0.148	4.85 · 10 ⁻²	0.229	0.148	0.117	0.205	xxx+++	META_GWAS	LDAH	1	rs6711016	94,595	-5.69 · 10 ⁻²	4 · 10 ⁻³	9.32 · 10 ⁻⁴³
1	230295691	rs4846914	A	G	2,433	0.341	0.128	0.587	6.12 · 10 ⁻²	3.35 · 10 ⁻²	6.74 · 10 ⁻²	+++	META_EX	GALNT2	1	rs4846914	94,595	4.79 · 10 ⁻²	3.4 · 10 ⁻³	3.51 · 10 ⁻⁴¹
8	19746876	rs17482310	T	G	2,427	8.59 · 10 ⁻²	4.52 · 10 ⁻²	0.196	9.43 · 10 ⁻²	5.13 · 10 ⁻²	6.63 · 10 ⁻²	+++++	META_GWAS	INTS10	1	rs17482310	94,595	6.36 · 10 ⁻²	4.6 · 10 ⁻³	1.01 · 10 ⁻⁴⁰
15	58579956	rs2899624	G	A	2,082	0.134	0.133	0.134	9.49 · 10 ⁻²	4.5 · 10 ⁻²	0.833	+++xxxx	META_GWAS	ALDH1A2	1	rs2899624	94,595	-7.14 · 10 ⁻²	4.9 · 10 ⁻³	1.39 · 10 ⁻⁴⁰
16	68280317	rs3826164	G	A	345	0.104	5.97 · 10 ⁻²	0.144	6.93 · 10 ⁻²	0.122	0.571	xxx++	META_GWAS	PLA2G15	1	rs3826164	94,595	-7.34 · 10 ⁻²	5.2 · 10 ⁻³	2.56 · 10 ⁻⁴⁰
16	67922342	rs10468274	A	G	345	0.399	0.154	0.631	1.75 · 10 ⁻²	8.01 · 10 ⁻²	0.827	xxx+-	META_GWAS	NRN1L	1	rs10468274	94,595	6.39 · 10 ⁻²	4.6 · 10 ⁻³	2.39 · 10 ⁻³⁹
11	47294626	rs10501321	C	T	345	0.468	0.29	0.634	0.161	7.59 · 10 ⁻²	3.38 · 10 ⁻²	xxx+++	META_GWAS	MADD	1	rs10501321	94,595	4.83 · 10 ⁻²	3.6 · 10 ⁻³	3.54 · 10 ⁻³⁸
45	64575502	rs7679	C	T	2,427	9.37 · 10 ⁻²	3.96 · 10 ⁻²	0.161	1.36 · 10 ⁻²	4.96 · 10 ⁻²	0.784	--	META_EX	PCIF1	1	rs7679	94,595	-5.87 · 10 ⁻²	4.4 · 10 ⁻³	6.73 · 10 ⁻³⁸
11	47354787	rs1052373	T	C	2,432	0.41	0.282	0.506	2.11 · 10 ⁻²	2.96 · 10 ⁻²	0.476	+++	META_EX	MYBPC3	1	rs1052373	94,595	4.78 · 10 ⁻²	3.7 · 10 ⁻³	1.55 · 10 ⁻³⁶
20	44547068	rs17447545	A	G	2,081	0.184	0.175	0.195	3.31 · 10 ⁻²	4.03 · 10 ⁻²	0.412	+++xxxx	META_GWAS	PLTP	1	rs17447545	94,595	5.62 · 10 ⁻²	4.4 · 10 ⁻³	3.98 · 10 ⁻³⁶
11	47260272	rs2013867	C	T	345	0.433	0.271	0.567	0.108	7.51 · 10 ⁻²	0.149	xxx+++	META_GWAS	DBB2	1	rs2013867	94,595	4.8 · 10 ⁻²	3.7 · 10 ⁻³	4.88 · 10 ⁻³⁶
11	116660686	rs2266788	A	G	2,433	0.948	0.917	0.983	1.53 · 10 ⁻²	6.69 · 10 ⁻²	0.82	++	META_EX	APOA5	1	rs2266788	94,595	9.22 · 10 ⁻²	6.8 · 10 ⁻³	1.19 · 10 ⁻³⁵
18	47243912	rs6507945	C	A	2,427	0.665	0.556	0.773	2.81 · 10 ⁻²	3.13 · 10 ⁻²	0.369	+++++	META_GWAS	ACAA2	1	rs6507945	94,595	4.41 · 10 ⁻²	3.4 · 10 ⁻³	1.33 · 10 ⁻³⁴
20	43042364	rs1800961	C	T	2,433	2.4 · 10 ⁻²	6.49 · 10 ⁻³	4.09 · 10 ⁻²	0.178	9.56 · 10 ⁻²	6.31 · 10 ⁻²	+++	META_EX	HNF4A	1	rs1800961	94,595	0.127	9.9 · 10 ⁻³	1.64 · 10 ⁻³⁴
11	47275064	rs10838681	A	G	2,427	0.369	0.225	0.493	1.98 · 10 ⁻²	2.96 · 10 ⁻²	0.504	+++++	META_GWAS	NR1H3	1	rs10838681	94,595	4.8 · 10 ⁻²	3.8 · 10 ⁻³	1.72 · 10 ⁻³³
12	125261441	rs838879	A	G	345	0.549	0.369	0.873	1.01 · 10 ⁻²	7.96 · 10 ⁻²	0.899	xxx++	META_GWAS	SCARB1	1	rs838879	94,595	-4.93 · 10 ⁻²	4 · 10 ⁻³	9.37 · 10 ⁻³³
15	54797848	rs103294	T	C	2,081	0.124	8.89 · 10 ⁻²	0.157	3.65 · 10 ⁻²	4.64 · 10 ⁻²	0.432	+++xxxx	META_GWAS	LILRB2	1	rs103294	94,595	5.23 · 10 ⁻²	4.4 · 10 ⁻³	4 · 10 ⁻³⁰
8	126495818	rs10808546	C	T	2,082	0.344	0.331	0.382	2.95 · 10 ⁻²	3.33 · 10 ⁻²	0.374	+++xxxx	META_GWAS	TRIB1	1	rs10808546	94,595	-4.09 · 10 ⁻²	3.4 · 10 ⁻³	4.11 · 10 ⁻³⁰
16	68335392	rs11350	C	T	2,426	0.148	0.116	0.194	4.83 · 10 ⁻²	4.01 · 10 ⁻²	0.229	+++++	META_GWAS	SLC7A6	1	rs11350	94,595	6.19 · 10 ⁻²	5.1 · 10 ⁻³	1.05 · 10 ⁻²⁹
11	47270255	rs2167079	T	C	2,433	0.441	0.265	0.564	1.81 · 10 ⁻²	2.93 · 10 ⁻²	0.538	+++	META_EX	ACP2	1	rs2167079	94,595	5.77 · 10 ⁻²	4.8 · 10 ⁻³	1.19 · 10 ⁻²⁸
16	67671804	rs6499137	T	G	2,082	0.214	7.17 · 10 ⁻²	0.326	3.61 · 10 ⁻²	3.92 · 10 ⁻²	0.357	+++xxxx	META_GWAS	CTCF	1	rs6499137	94,595	-7.22 · 10 ⁻²	6.2 · 10 ⁻³	5.9 · 10 ⁻²⁸
11	61557803	rs102275	T	C	2,433	0.567	0.344	0.667	4.25 · 10 ⁻²	3.02 · 10 ⁻²	0.159	++	META_EX	TMEM258	1	rs102275	94,595	3.91 · 10 ⁻²	3.5 · 10 ⁻³	

6 Estimated Glomerular Filtration Rate (eGFR)

6.1 Summary

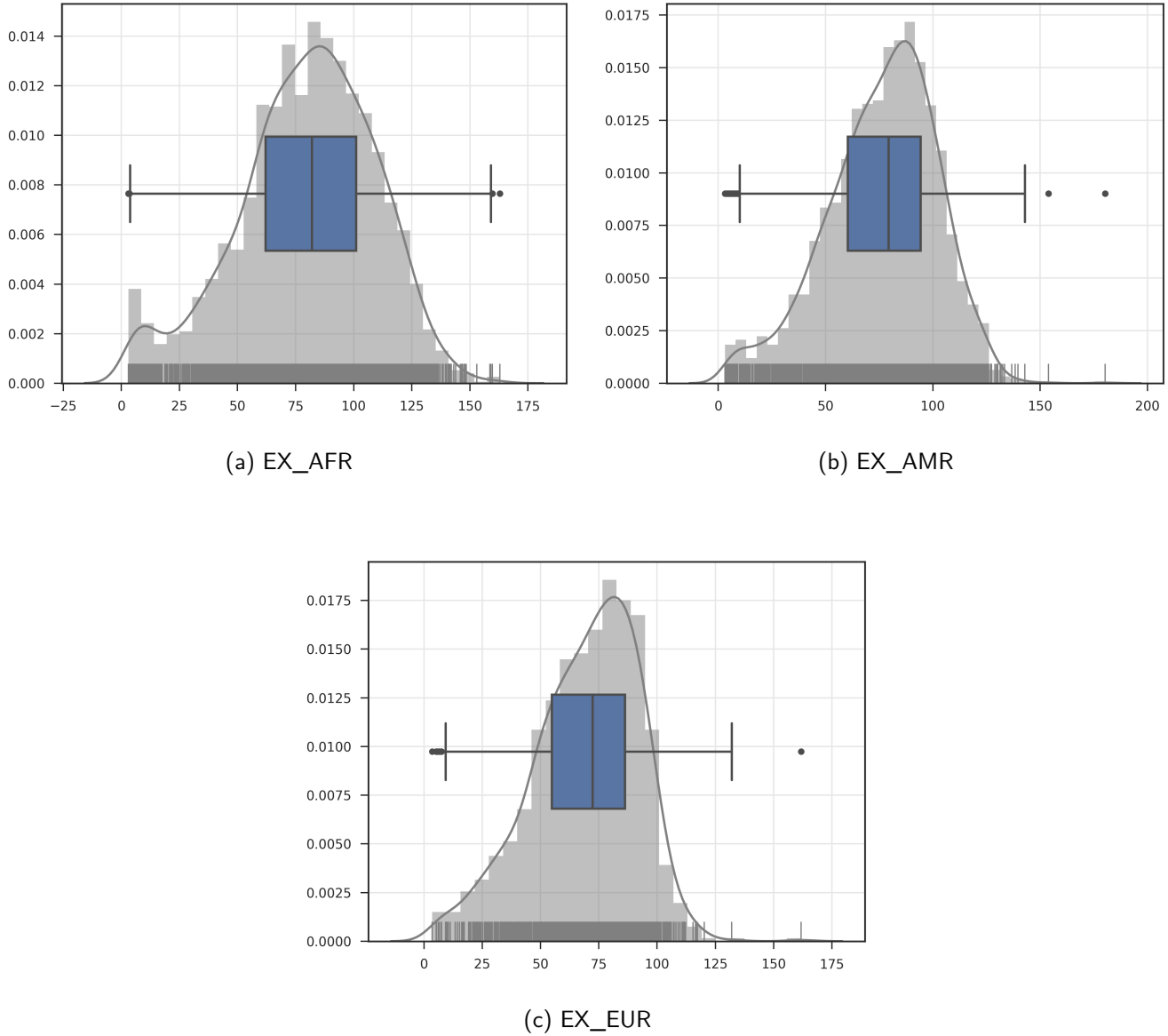
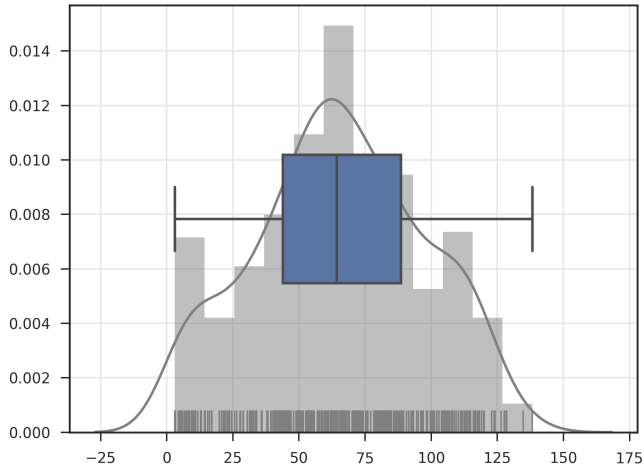
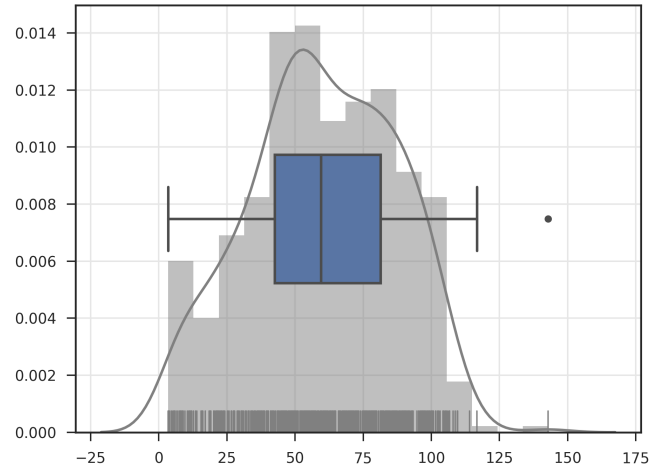


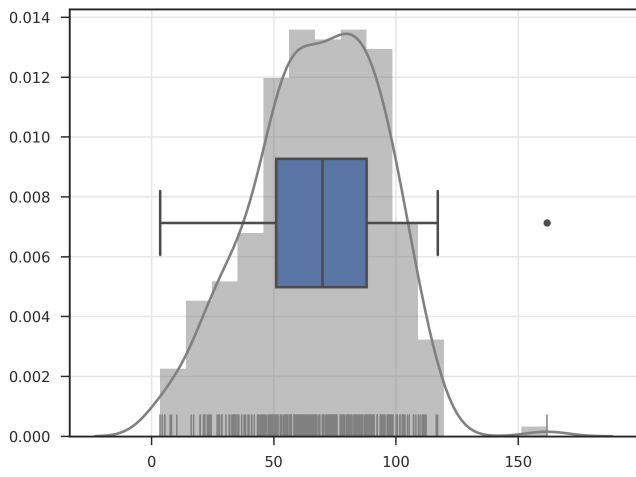
Figure 17: Distribution of eGFR in META_EX by cohort



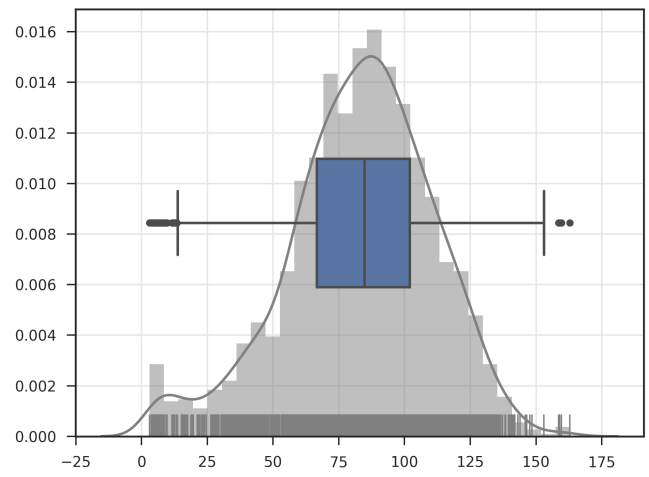
(a) AFFY_AFR



(b) AFFY_AMR



(c) AFFY_EUR



(d) ILL_AFR

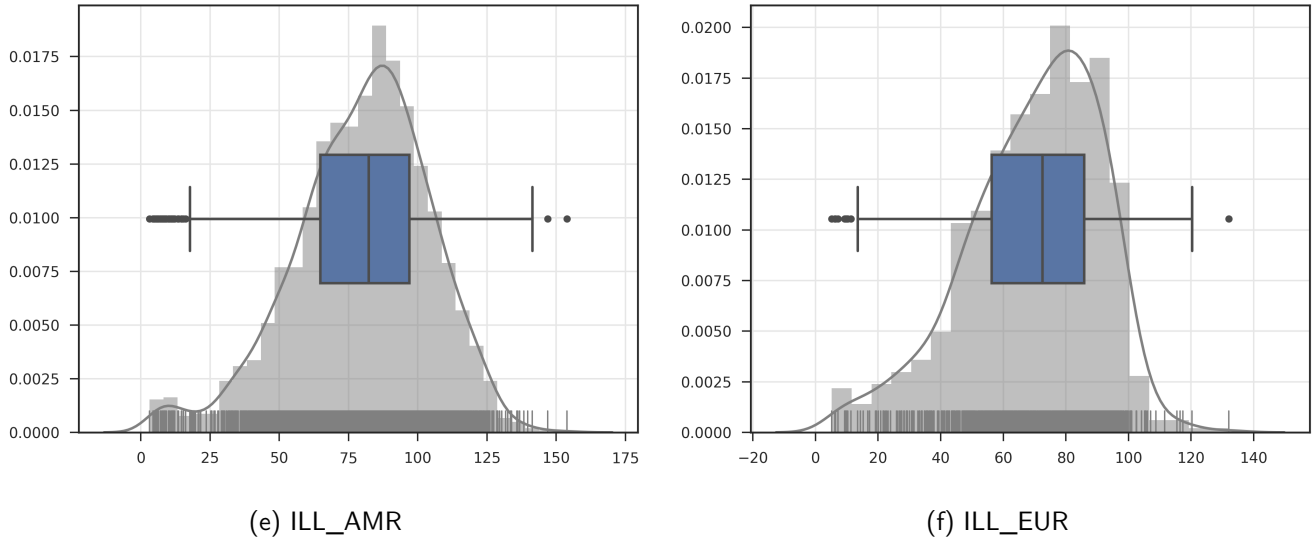


Figure 18: Distribution of eGFR in META_GWAS by cohort

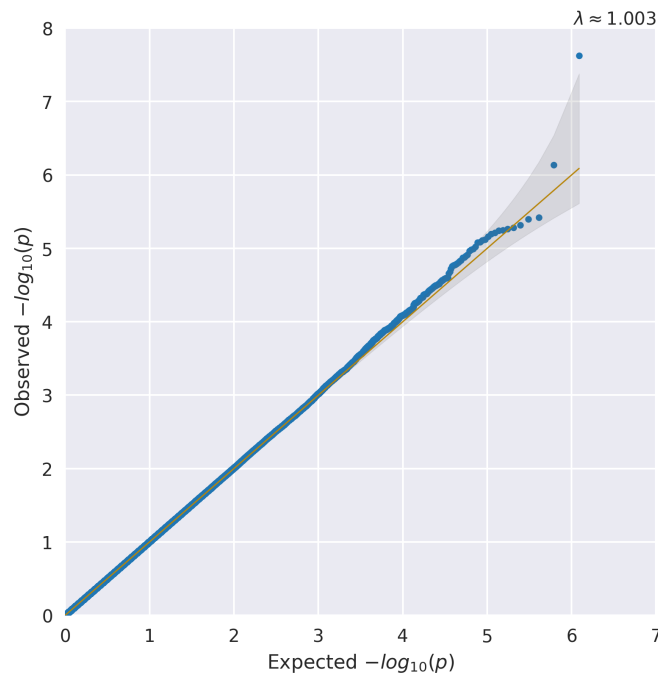
Table 17: Summary of samples removed from Estimated Glomerular Filtration Rate analysis by cohort and model

Cohort	Array	Ancestry	Trans	Covars	Total	-SampleQc	-missObs	-Kinship	-PcOutlier
META_EX EX_AFR	EX	AFR	invn		5172	44	2385	172	51
META_EX EX_AMR	EX	AMR	invn		5144	32	2545	259	0
META_EX EX_EUR	EX	EUR	invn		2379	30	1273	3	0
META_GWAS AFFY_AFR	AFFY	AFR	invn		897	18	353	97	0
META_GWAS AFFY_AMR	AFFY	AMR	invn		1035	20	439	122	0
META_GWAS AFFY_EUR	AFFY	EUR	invn		578	12	288	5	13
META_GWAS ILL_AFR	ILL	AFR	invn		4077	46	1921	0	4
META_GWAS ILL_AMR	ILL	AMR	invn		3884	26	1956	0	0
META_GWAS ILL_EUR	ILL	EUR	invn		1797	23	983	0	5

Table 18: Summary of samples remaining for Estimated Glomerular Filtration Rate analysis by cohort and model

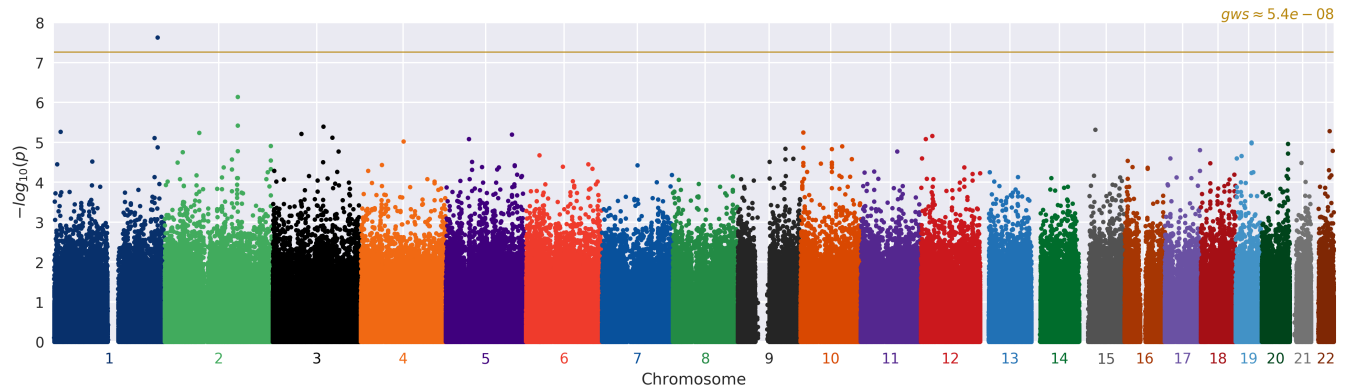
Cohort	Array	Ancestry	Trans	Covars	PCs	N	Male	Female	Max	Min	μ	\bar{x}	σ
META_EX EX_AFR	EX	AFR	invn		8	2546	974	1572	162.894	3.003	79.565	81.835	29.591
META_EX EX_AMR	EX	AMR	invn		3	2323	941	1382	153.861	3.157	76.127	79.22	25.365
META_EX EX_EUR	EX	EUR	invn		1	1086	747	339	161.756	3.514	69.307	72.276	22.572
META_GWAS AFFY_AFR	AFFY	AFR	invn		0	434	197	237	138.222	3.003	65.339	64.228	31.573
META_GWAS AFFY_AMR	AFFY	AMR	invn		0	460	205	255	142.856	3.692	60.091	59.134	26.455
META_GWAS AFFY_EUR	AFFY	EUR	invn		3	270	233	37	161.756	3.514	67.786	70.28	25.585
META_GWAS ILL_AFR	ILL	AFR	invn		1	2122	788	1334	162.894	3.003	83.187	84.708	27.861
META_GWAS ILL_AMR	ILL	AMR	invn		3	1914	757	1157	153.861	3.157	79.623	82.018	23.949
META_GWAS ILL_EUR	ILL	EUR	invn		4	796	505	291	131.997	5.202	69.718	72.562	21.273

6.2 Calibration



(a) invn Unadjusted

Figure 19: QQ plots for eGFR in the MERGE analysis



(a) invn Unadjusted

Figure 20: Manhattan plots for eGFR in the MERGE analysis

6.3 Top associations

Table 19: Top variants in the MERGE invn Unadjusted model (**bold** variants indicate previously identified associations)

CHR	POS	ID	EA	OA	GENE _{CLOSEST}	COHORT	DIR	N	MALE	FEMALE	FREQ _{AVG}	FREQ _{MIN}	FREQ _{MAX}	EFFECT	STDERR	OR	ZSCORE	P
1	233256280	rs717588	A	G	PCNX2	META_GWAS	+++xxx	4,832	2,050	2,782	0.785	0.618	0.876	0.141	$2.52 \cdot 10^{-2}$	1.151	-5.584	$2.36 \cdot 10^{-8}$
2	164332357	rs2704367	C	T	FIGN	META_GWAS	xxx+++	1,159	633	526	0.444	0.411	0.48	0.209	$4.22 \cdot 10^{-2}$	1.233	-4.954	$7.28 \cdot 10^{-7}$
3	113815580	rs12494543	C	A	QTRT2	META_GWAS	xxx+++	1,164	635	529	0.216	0.181	0.271	0.227	$4.93 \cdot 10^{-2}$	1.255	-4.61	$4.02 \cdot 10^{-6}$
15	36116795	rs11073126	A	G	DPH6	META_GWAS	+++xxx	4,831	2,050	2,781	0.108	$4.69 \cdot 10^{-2}$	0.185	0.151	$3.3 \cdot 10^{-2}$	1.163	4.574	$4.79 \cdot 10^{-6}$
22	41661154	rs2235852	T	G	RANGAP1	META_GWAS	+++++	5,993	2,683	3,310	0.317	0.214	0.404	$9.09 \cdot 10^{-2}$	$1.99 \cdot 10^{-2}$	1.095	4.556	$5.22 \cdot 10^{-6}$
1	14831919	rs10754859	T	C	KAZN	META_GWAS	xxx+++	1,164	635	529	0.791	0.772	0.809	0.23	$5.05 \cdot 10^{-2}$	1.258	-4.547	$5.44 \cdot 10^{-6}$
10	6210312	rs642104	T	C	PFKFB3	META_GWAS	xxx+++	1,162	633	529	0.172	$9.7 \cdot 10^{-2}$	0.269	0.242	$5.34 \cdot 10^{-2}$	1.274	4.54	$5.64 \cdot 10^{-6}$
2	77225981	rs17013535	C	T	LRRTM4	META_GWAS	xxx+++	1,164	635	529	$7.95 \cdot 10^{-2}$	$1.3 \cdot 10^{-2}$	0.128	0.345	$7.6 \cdot 10^{-2}$	1.412	-4.536	$5.74 \cdot 10^{-6}$
3	64527128	rs17070965	A	C	ADAMTS9	META_GWAS	+++xxx	4,832	2,050	2,782	$1.27 \cdot 10^{-2}$	$2.12 \cdot 10^{-3}$	$2.87 \cdot 10^{-2}$	0.419	$9.27 \cdot 10^{-2}$	1.521	-4.523	$6.09 \cdot 10^{-6}$
5	148659664	rs1438692	A	G	AFAP1L1	META_GWAS	+++xxx	4,828	2,049	2,779	0.33	0.269	0.394	$9.78 \cdot 10^{-2}$	$2.17 \cdot 10^{-2}$	1.103	4.515	$6.33 \cdot 10^{-6}$
12	25993356	rs41518252	G	A	RASSF8	META_GWAS	xxx+++	1,163	634	529	$6.88 \cdot 10^{-2}$	$5.54 \cdot 10^{-2}$	$7.72 \cdot 10^{-2}$	0.378	$8.41 \cdot 10^{-2}$	1.459	4.496	$6.91 \cdot 10^{-6}$
3	134079064	rs2241558	T	C	AMOTL2	META_GWAS	xxx+++	1,159	631	528	$4.31 \cdot 10^{-3}$	$3.75 \cdot 10^{-3}$	$4.62 \cdot 10^{-3}$	1.405	0.314	4.074	4.478	$7.54 \cdot 10^{-6}$
1	226055595	rs2292564	G	A	TMEM63A	META_GWAS	+++xxx	4,831	2,050	2,781	0.361	0.262	0.456	$9.59 \cdot 10^{-2}$	$2.15 \cdot 10^{-2}$	1.101	-4.47	$7.81 \cdot 10^{-6}$
12	11586582	rs2416674	C	A	PRB1	META_GWAS	xxx+++	1,164	635	529	0.626	0.465	0.773	0.19	$4.27 \cdot 10^{-2}$	1.21	-4.459	$8.23 \cdot 10^{-6}$
5	51912216	rs830890	T	G	ITGA1	META_GWAS	+++xxx	4,831	2,050	2,781	0.141	0.104	0.161	0.128	$2.88 \cdot 10^{-2}$	1.137	-4.457	$8.33 \cdot 10^{-6}$
4	96025302	rs7665167	T	G	BMPR1B	META_GWAS	xxx+++	1,161	634	527	0.827	0.806	0.856	0.24	$5.42 \cdot 10^{-2}$	1.272	-4.429	$9.47 \cdot 10^{-6}$
19	36392355	rs7254113	G	A	NFKBID	META_GWAS	+++xxx	4,830	2,049	2,781	0.13	$2.7 \cdot 10^{-2}$	0.218	0.137	$3.11 \cdot 10^{-2}$	1.147	-4.415	$1.01 \cdot 10^{-5}$
20	58698287	rs2145554	C	G	CDH26	META_GWAS	xxx+++	1,164	635	529	$7.13 \cdot 10^{-2}$	$5.11 \cdot 10^{-2}$	$8.76 \cdot 10^{-2}$	0.356	$8.1 \cdot 10^{-2}$	1.428	4.399	$1.09 \cdot 10^{-5}$
2	238143803	rs4490127	T	G	COL6A3	META_GWAS	+++xxx	4,832	2,050	2,782	0.728	0.541	0.883	0.105	$2.41 \cdot 10^{-2}$	1.111	4.373	$1.22 \cdot 10^{-5}$
10	93810872	rs1776209	G	A	CPEB3	META_GWAS	+++++	5,994	2,685	3,309	0.176	$6.55 \cdot 10^{-2}$	0.307	0.108	$2.48 \cdot 10^{-2}$	1.114	4.366	$1.26 \cdot 10^{-5}$

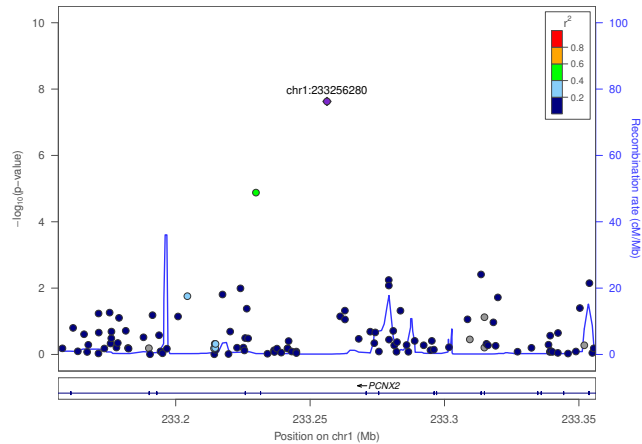


Figure 21: Regional plot for cohort MERGE model invn Unadjusted: rs717588 $\pm 100kb$

6.4 Previously identified risk loci

Table 20 shows statistics from the MERGE 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 [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 7 variants that show at least nominal significance ($p < 0.05$) in this study. Out of the 50 variants in both studies, 36 exhibit the same direction of effect with the known result (binomial test $p = 0.0013$).

Table 20: Top known loci in MERGE 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	COHORT	GENE _{CLOSEST}	R ²	ID _{KNOWN}	N _{KNOWN}	EFFECT _{KNOWN}	STDERR _{KNOWN}	P _{KNOWN}
15	45683795	rs1145077	G	T	1,162	0.664	0.392	0.88	8.32 · 10 ⁻³	4.72 · 10 ⁻²	0.86	xxx++	META_GWAS	SPATA5L1	1	rs1145077	1.33 · 10 ⁵	1.2 · 10 ⁻²	9.2 · 10 ⁻⁴	3.5 · 10 ⁻⁴²
16	20367690	rs12917707	T	G	5,954	0.111	4.78 · 10 ⁻²	0.164	7.3 · 10 ⁻²	2.96 · 10 ⁻²	1.37 · 10 ⁻²	+++	META_EX	UMOD	1	rs12917707	1.33 · 10 ⁵	1.6 · 10 ⁻²	1.2 · 10 ⁻³	1.2 · 10 ⁻⁴¹
15	45636584	rs1153860	C	T	1,164	0.663	0.398	0.876	1.12 · 10 ⁻²	4.69 · 10 ⁻²	0.812	xxx++	META_GWAS	GATM	1	rs1153860	1.33 · 10 ⁵	1.2 · 10 ⁻²	9.2 · 10 ⁻⁴	4.5 · 10 ⁻⁴¹
4	77368847	rs17319721	G	A	5,954	0.293	0.211	0.403	8.26 · 10 ⁻³	2.05 · 10 ⁻²	0.687	++	META_EX	SHROOM3	1	rs17319721	1.33 · 10 ⁵	1.1 · 10 ⁻²	9.2 · 10 ⁻⁴	1.3 · 10 ⁻³⁷
15	45723983	rs1547487	A	G	4,832	0.695	0.443	0.865	6.9 · 10 ⁻²	2.37 · 10 ⁻²	3.56 · 10 ⁻³	+++xxx	META_GWAS	C15orf48	1	rs1547487	1.33 · 10 ⁵	1.1 · 10 ⁻²	9.2 · 10 ⁻⁴	2 · 10 ⁻³²
16	20400839	rs11864909	T	C	4,831	0.189	9.97 · 10 ⁻²	0.263	3.49 · 10 ⁻²	2.65 · 10 ⁻²	0.187	+++xxx	META_GWAS	PDILT	1	rs11864909	1.33 · 10 ⁵	1.2 · 10 ⁻²	1 · 10 ⁻³	1 · 10 ⁻³⁰
7	151407801	rs7805747	G	A	5,953	0.295	0.251	0.342	3.11 · 10 ⁻²	2.01 · 10 ⁻²	0.122	+++	META_EX	PRKAG2	1	rs7805747	1.33 · 10 ⁵	1.3 · 10 ⁻²	1.1 · 10 ⁻³	8 · 10 ⁻²⁹
15	45609773	rs1719250	G	A	1,164	0.612	0.541	0.667	3.72 · 10 ⁻²	4.09 · 10 ⁻²	0.363	xxx++	META_GWAS	SLC28A2	1	rs1719250	1.33 · 10 ⁵	-1 · 10 ⁻²	9.2 · 10 ⁻⁴	4.5 · 10 ⁻²⁷
15	45801035	rs950027	T	C	5,995	0.746	0.48	0.916	5.52 · 10 ⁻²	2.25 · 10 ⁻²	1.4 · 10 ⁻²	++++	META_GWAS	SLC30A4	1	rs950027	1.33 · 10 ⁵	8.8 · 10 ⁻³	9.2 · 10 ⁻⁴	8.1 · 10 ⁻²³
5	176817636	rs6420094	A	G	5,954	0.269	0.21	0.36	6.36 · 10 ⁻³	3.08 · 10 ⁻²	0.759	++	META_EX	SLC34A1	1	rs6420094	1.33 · 10 ⁵	9.6 · 10 ⁻³	1 · 10 ⁻³	4.9 · 10 ⁻²²
5	176801131	rs10866705	C	A	5,985	0.773	0.728	0.811	5.6 · 10 ⁻³	2.16 · 10 ⁻²	0.795	++++	META_GWAS	RGS14	1	rs10866705	1.33 · 10 ⁵	-9.9 · 10 ⁻³	1 · 10 ⁻³	1.2 · 10 ⁻²¹
17	59456589	rs9895661	T	C	5,954	0.61	0.537	0.776	9.8 · 10 ⁻³	1.92 · 10 ⁻²	0.609	++	META_EX	BCAS3	1	rs9895661	1.33 · 10 ⁵	1.1 · 10 ⁻²	1.2 · 10 ⁻³	2.8 · 10 ⁻²¹
5	39397132	rs11959928	A	T	4,829	0.375	0.311	0.446	2.03 · 10 ⁻²	2.13 · 10 ⁻²	0.342	+++xxx	META_GWAS	DAB2	1	rs11959928	1.33 · 10 ⁵	8.3 · 10 ⁻³	9.2 · 10 ⁻⁴	1.7 · 10 ⁻²⁰
2	73679280	rs6546838	A	G	5,952	0.534	0.224	0.761	4.35 · 10 ⁻³	2.07 · 10 ⁻²	0.834	++	META_EX	ALMS1	1	rs6546838	1.33 · 10 ⁵	-9.3 · 10 ⁻³	1 · 10 ⁻³	7.7 · 10 ⁻²⁰
5	39362039	rs700229	C	T	1,164	0.352	0.267	0.42	1.42 · 10 ⁻²	4.38 · 10 ⁻²	0.745	xxx++	META_GWAS	C9	1	rs700229	1.33 · 10 ⁵	8.1 · 10 ⁻³	9.2 · 10 ⁻⁴	9.8 · 10 ⁻²⁰
4	77254804	rs907446	T	C	1,164	0.239	7.83 · 10 ⁻²	0.415	5.27 · 10 ⁻²	5.11 · 10 ⁻²	0.302	xxxx++	META_GWAS	CCDC158	1	rs907446	1.33 · 10 ⁵	-8 · 10 ⁻³	9.2 · 10 ⁻⁴	1 · 10 ⁻¹⁹
4	77220837	rs12506745	T	G	5,993	0.246	0.107	0.426	2.1 · 10 ⁻³	2.21 · 10 ⁻²	0.924	++++	META_GWAS	FAM47E-STBD1	1	rs12506745	1.33 · 10 ⁵	8.1 · 10 ⁻³	9.2 · 10 ⁻⁴	3.7 · 10 ⁻¹⁹
6	160675764	rs316009	T	C	4,832	0.908	0.888	0.92	6.14 · 10 ⁻²	3.53 · 10 ⁻²	8.16 · 10 ⁻²	+++xxx	META_GWAS	SLC22A2	1	rs316009	1.33 · 10 ⁵	1.3 · 10 ⁻²	1.4 · 10 ⁻³	4.4 · 10 ⁻¹⁹
11	30760335	rs3925584	C	T	5,954	0.278	0.117	0.479	4.85 · 10 ⁻³	2.18 · 10 ⁻²	0.824	++	META_EX	DCDC1	1	rs3925584	1.33 · 10 ⁵	7.6 · 10 ⁻³	9.2 · 10 ⁻⁴	7.6 · 10 ⁻¹⁸
8	23728721	rs6999484	G	A	4,826	0.335	0.325	0.38	7.3 · 10 ⁻³	2.15 · 10 ⁻²	0.735	+++xxx	META_GWAS	STC1	1	rs6999484	1.33 · 10 ⁵	7.1 · 10 ⁻³	9.2 · 10 ⁻⁴	1.9 · 10 ⁻¹⁵
15	53946593	rs491567	C	A	5,952	0.415	0.567	1 · 10 ⁻²	1.96 · 10 ⁻²	0.611	0.602	++	META_EX	WDR72	1	rs491567	1.33 · 10 ⁵	8.4 · 10 ⁻³	1 · 10 ⁻³	2.9 · 10 ⁻¹⁵
6	43806609	rs81858	A	G	5,954	0.527	0.371	0.693	2.25 · 10 ⁻³	1.92 · 10 ⁻²	0.907	++	META_EX	VEGFA	1	rs81858	1.33 · 10 ⁵	-8.1 · 10 ⁻³	1 · 10 ⁻³	7.5 · 10 ⁻¹⁵
9	71433212	rs1556751	A	G	4,832	0.636	0.574	0.705	4.39 · 10 ⁻²	2.15 · 10 ⁻²	4.1 · 10 ⁻²	+++xxx	META_GWAS	PIPSK1B	1	rs1556751	1.33 · 10 ⁵	7 · 10 ⁻³	9.2 · 10 ⁻⁴	9.9 · 10 ⁻¹⁵
17	37516722	rs8076494	T	C	1,164	0.365	0.23	0.469	7.94 · 10 ⁻²	4.32 · 10 ⁻²	6.58 · 10 ⁻²	xxx++	META_GWAS	FBXL20	1	rs8076494	1.33 · 10 ⁵	-7.6 · 10 ⁻³	1 · 10 ⁻³	2.3 · 10 ⁻¹⁴
17	37665554	rs12936996	A	G	1,164	0.543	0.341	0.769	3.59 · 10 ⁻²	4.34 · 10 ⁻²	0.408	xxx++	META_GWAS	CDK12	1	rs12936996	1.33 · 10 ⁵	-7.6 · 10 ⁻³	1 · 10 ⁻³	2.4 · 10 ⁻¹⁴
2	27730940	rs1260326	C	T	5,953	0.735	0.524	0.864	2.22 · 10 ⁻²	2.16 · 10 ⁻²	0.304	--	META_EX	GCKR	1	rs1260326	1.33 · 10 ⁵	-6.8 · 10 ⁻³	9.2 · 10 ⁻⁴	3.4 · 10 ⁻¹⁴
17	37591422	rs10445306	A	G	4,830	0.507	0.343	0.72	1.29 · 10 ⁻²	2.13 · 10 ⁻²	0.544	+++xxx	META_GWAS	MED1	1	rs10445306	1.33 · 10 ⁵	7.5 · 10 ⁻³	1 · 10 ⁻³	4.1 · 10 ⁻¹⁴
9	71397747	rs2017	C	T	4,830	0.602	0.527	0.678	1.65 · 10 ⁻²	2.11 · 10 ⁻²	0.435	+++xxx	META_GWAS	FAM122A	1	rs2017	1.33 · 10 ⁵	6.8 · 10 ⁻³	9.2 · 10 ⁻⁴	4.7 · 10 ⁻¹⁴
2	73878352	rs6759452	T	C	5,990	0.116	5.2 · 10 ⁻²	0.16	5.91 · 10 ⁻²	2.83 · 10 ⁻²	3.67 · 10 ⁻²	+++++	META_GWAS	NAT8	1	rs6759452	1.33 · 10 ⁵	9 · 10 ⁻³	1.2 · 10 ⁻³	4.7 · 10 ⁻¹⁴
15	76158983	rs1394125	G	A	5,952	0.342	0.308	0.404	1.46 · 10 ⁻²	1.93 · 10 ⁻²	0.45	++	META_EX	UBE2Q2	1	rs1394125	1.33 · 10 ⁵	7.3 · 10 ⁻³	1 · 10 ⁻³	5.5 · 10 ⁻¹⁴
3	141724644	rs2861422	C	T	1,162	0.308	0.25	0.372	3.05 · 10 ⁻²	4.46 · 10 ⁻²	0.494	xxx++	META_GWAS	TFDP2	1	rs2861422	1.33 · 10 ⁵	-7.4 · 10 ⁻³	1 · 10 ⁻³	9.1 · 10 ⁻¹³
19	33356891	rs12460876	C	T	5,954	0.351	0.269	0.47	2.34 · 10 ⁻³	1.94 · 10 ⁻²	0.904	--	META_EX	SLC7A9	1	rs12460876	1.33 · 10 ⁵	6.6 · 10 ⁻³	9.2 · 10 ⁻⁴	1.9 · 10 ⁻¹³
15	76304503	rs10851885	A	G	5,985	0.158	0.102	0.238	1.31 · 10 ⁻²	2.52 · 10 ⁻²	0.602	+++++	META_GWAS	NRG4	1	rs10851885	1.33 · 10 ⁵	7.5 · 10 ⁻³	1 · 10 ⁻³	2.5 · 10 ⁻¹³
17	59483766	rs8068318	T	C	5,953	0.434	0.271	0.699	6.16 · 10 ⁻²	1.98 · 10 ⁻²	1.86 · 10 ⁻³	+++	META_EX	TBX2	1	rs8068318	1.33 · 10 ⁵	7.6 · 10 ⁻³	1 · 10 ⁻³	3 · 10 ⁻¹³
1	150951477	rs267734	C	T	5,954	9.29 · 10 ⁻²	3.05 · 10 ⁻²	0.186	3.82 · 10 ⁻²	3.23 · 10 ⁻²	0.238	++	META_EX	ANXA9	1	rs267734	1.33 · 10 ⁵	7.9 · 10 ⁻³	1.1 · 10 ⁻³	4 · 10 ⁻¹³
4	77198986	rs6812193	T	C	5,952	0.383	0.34	0.436	6.54 · 10 ⁻³	1.9 · 10 ⁻²	0.731	+	META_EX	FAM47E	1	rs6812193	1.33 · 10 ⁵	6.6 · 10 ⁻³	9.2 · 10 ⁻⁴	4.1 · 10 ⁻¹³
20	52732362	rs17216707	T	C	1,164	0.167	6.34 · 10 ⁻²	0.235	2.75 · 10 ⁻³	5.66 · 10 ⁻²	0.961	xxx++	META_GWAS	CYP24A1	1	rs17216707	1.33 · 10 ⁵	-8.4 · 10 ⁻³	1.1 · 10 ⁻³	6 · 10 ⁻¹³
19	33364628	rs8101881	C	T	5,953	0.469	0.406	0.515	1.25 · 10 ⁻²	1.87 · 10 ⁻²	0.504	--	META_EX	CEP99	1	rs8101881	1.33 · 10 ⁵	6.4 · 10 ⁻³	9.2 · 10 ⁻⁴	8.1 · 10 ⁻¹³
5	176755841	rs6860069	C	T	4,831	0.38	0.343	0.426	1.35 · 10 ⁻²	2.1 · 10 ⁻²	0.519	+++xxx	META_GWAS	LMAN2	1	rs6860069	1.33 · 10 ⁵	6.8 · 10 ⁻³	9.2 · 10 ⁻⁴	8.2 · 10 ⁻¹³
7	77462459	rs17807736	C	A	5,996	0.185	0.15	0.246	8.61 · 10 ⁻³	2.37 · 10 ⁻²	0.717	++++	META_GWAS	PHF72	1	rs17807736	1.33 · 10 ⁵	7 · 10 ⁻³	1 · 10 ⁻³	9.5 · 10 ⁻¹³
7	77423152	rs1045463	C	T	4,830	0.162	0.11	0.238	2.79 · 10 ⁻³	2.81 · 10 ⁻²	0.921	+-xxx	META_GWAS	TMEM60	1	rs1045463	1.33 · 10 ⁵	7 · 10 ⁻³	1 · 10 ⁻³	1.1 · 10 ⁻¹²
1	150940625	rs267738	G	T	5,953	9.43 · 10 ⁻²	3.07 · 10 ⁻²	0.188	4.37 · 10 ⁻²	3.22 · 10 ⁻²	0.174	++	META_EX	CERS2	1	rs267738	1.33 · 10 ⁵	7.7 · 10 ⁻³	1.1 · 10 ⁻³	1.3 · 10 ⁻¹²
17	37726423	rs903507	C	T	1,164	0.252	0.165	0.313	1.61 · 10 ⁻²	4.87 · 10 ⁻²	0.74	xxx++	META_GWAS	NEUROD2	1	rs9035				

7 Diastolic Blood Pressure (DBP10)

7.1 Summary

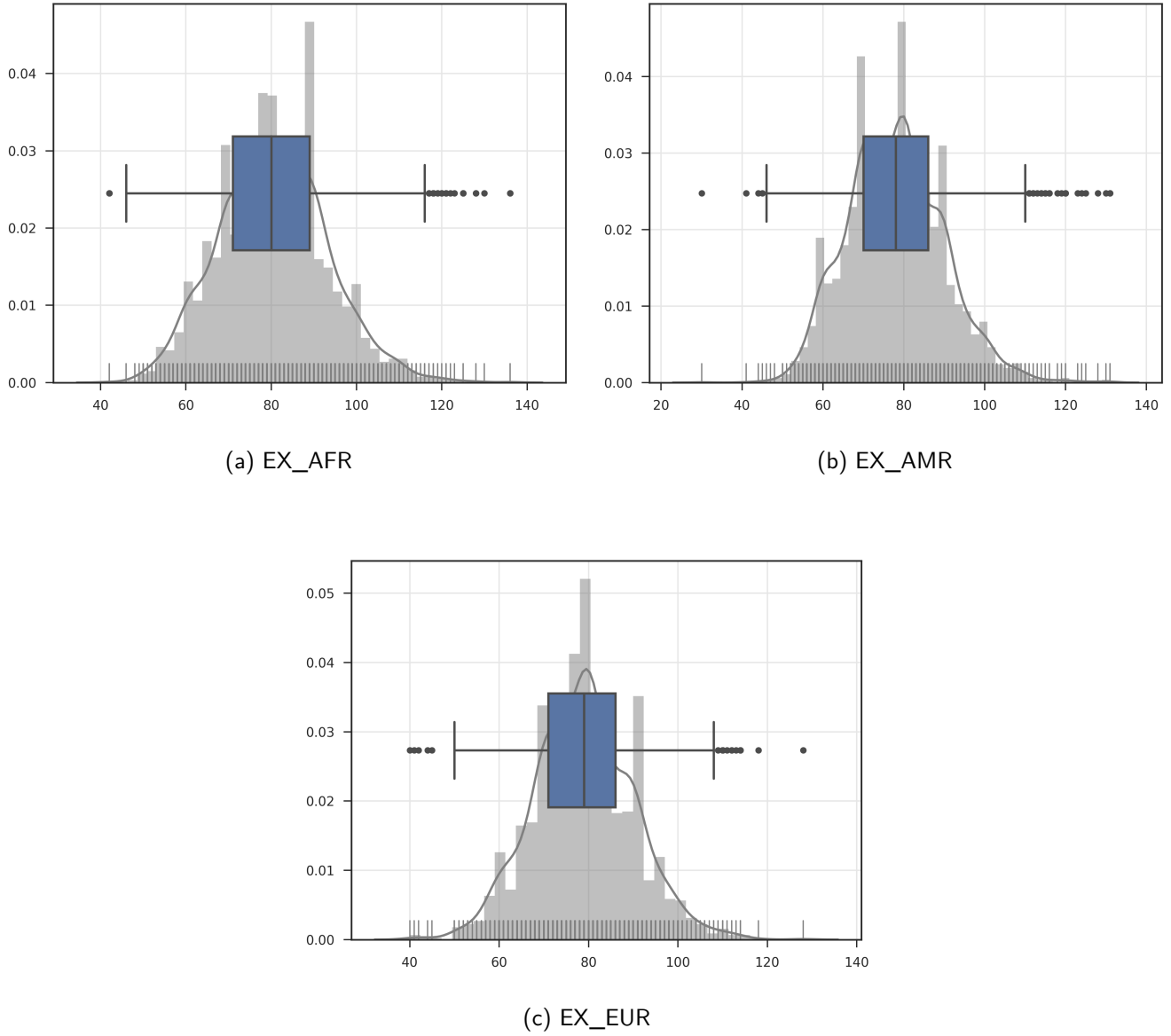
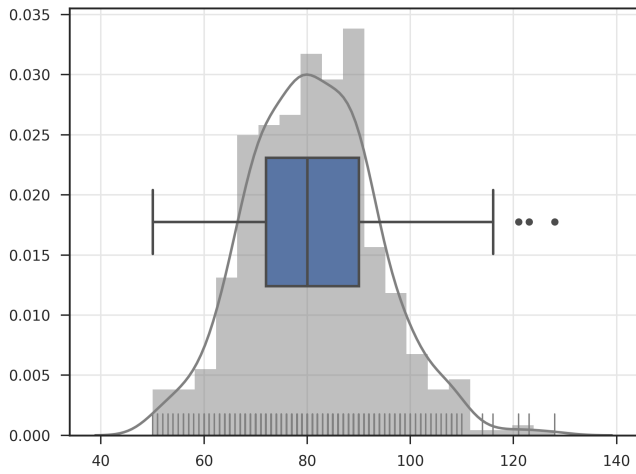
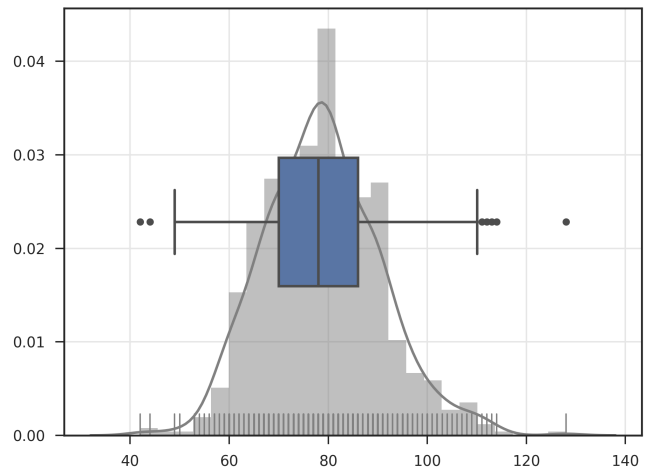


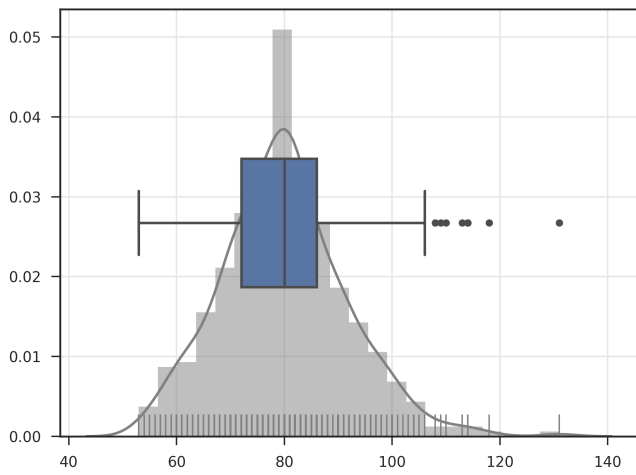
Figure 22: Distribution of DBP10 in META_EX by cohort



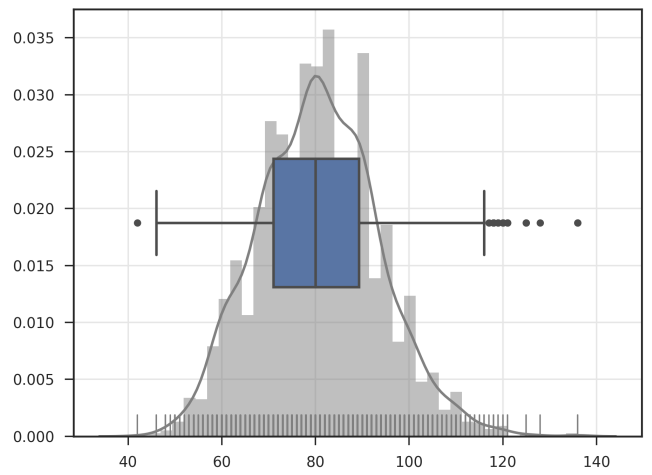
(a) AFFY_AFR



(b) AFFY_AMR



(c) AFFY_EUR



(d) ILL_AFR

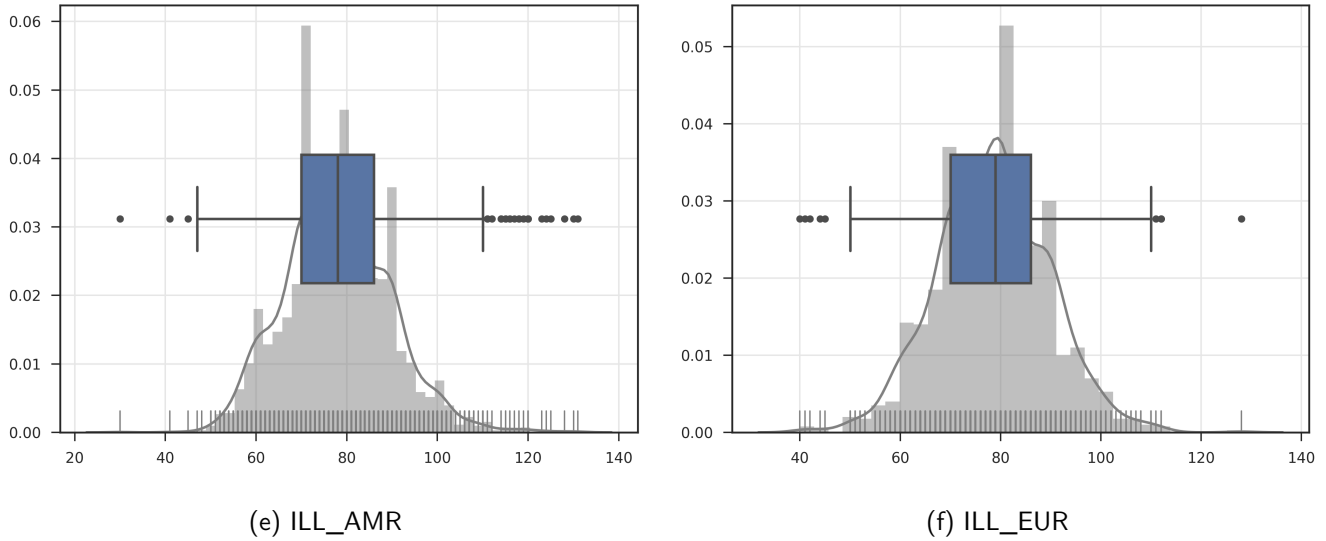


Figure 23: Distribution of DBP10 in META_GWAS by cohort

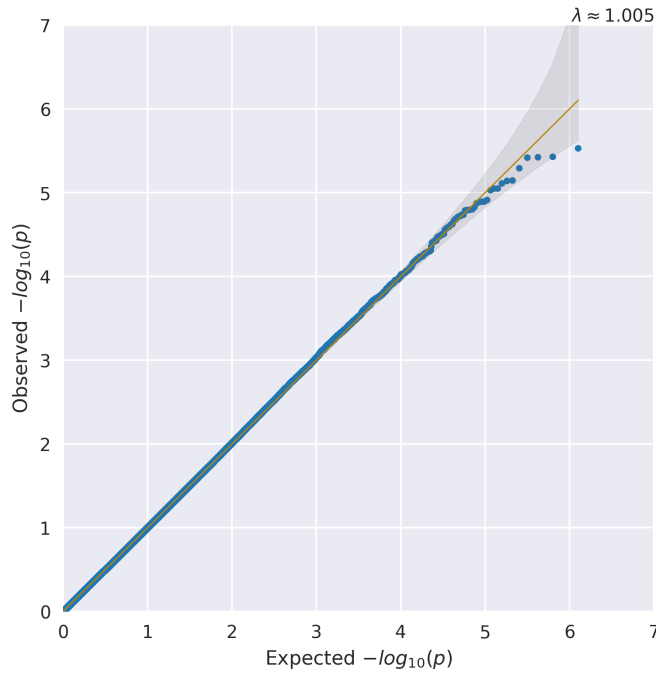
Table 21: Summary of samples removed from Diastolic Blood Pressure analysis by cohort and model

Cohort	Array	Ancestry	Trans	Covars	Total	-SampleQc	-missObs	-Kinship	-PcOutlier
META_EX EX_AFR	EX	AFR	invn	AGE_BP+AGE_BP2+SEX+BMI	5172	44	1132	285	5
META_EX EX_AMR	EX	AMR	invn	AGE_BP+AGE_BP2+SEX+BMI	5144	32	1144	424	0
META_EX EX_EUR	EX	EUR	invn	AGE_BP+AGE_BP2+SEX+BMI	2379	30	626	6	1
META_GWAS AFFY_AFR	AFFY	AFR	invn	AGE_BP+AGE_BP2+SEX+BMI	897	18	208	127	14
META_GWAS AFFY_AMR	AFFY	AMR	invn	AGE_BP+AGE_BP2+SEX+BMI	1035	20	227	166	0
META_GWAS AFFY_EUR	AFFY	EUR	invn	AGE_BP+AGE_BP2+SEX+BMI	578	12	173	8	0
META_GWAS ILL_AFR	ILL	AFR	invn	AGE_BP+AGE_BP2+SEX+BMI	4077	46	893	4	6
META_GWAS ILL_AMR	ILL	AMR	invn	AGE_BP+AGE_BP2+SEX+BMI	3884	26	870	2	0
META_GWAS ILL_EUR	ILL	EUR	invn	AGE_BP+AGE_BP2+SEX+BMI	1797	23	456	1	0

Table 22: Summary of samples remaining for Diastolic Blood Pressure analysis by cohort and model

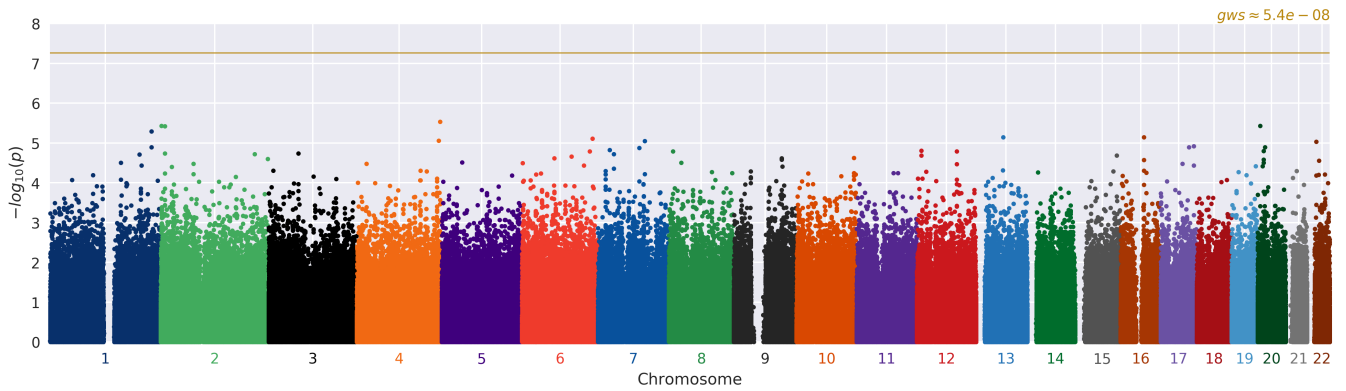
Cohort	Array	Ancestry	Trans	Covars	PCs	N	Male	Female	Max	Min	μ	\tilde{x}	σ
META_EX EX_AFR	EX	AFR	invn	AGE_BP+AGE_BP2+SEX+BMI	0	3719	1311	2408	136.0	42.0	80.732	80.0	12.782
META_EX EX_AMR	EX	AMR	invn	AGE_BP+AGE_BP2+SEX+BMI	3	3553	1392	2161	131.0	41.0	78.019	78.0	11.712
META_EX EX_EUR	EX	EUR	invn	AGE_BP+AGE_BP2+SEX+BMI	8	1723	1150	573	128.0	40.0	78.906	79.0	11.186
META_GWAS AFFY_AFR	AFFY	AFR	invn	AGE_BP+AGE_BP2+SEX+BMI	0	539	234	305	128.0	42.0	81.557	81.0	12.502
META_GWAS AFFY_AMR	AFFY	AMR	invn	AGE_BP+AGE_BP2+SEX+BMI	3	625	273	352	113.0	44.0	78.541	78.0	11.406
META_GWAS AFFY_EUR	AFFY	EUR	invn	AGE_BP+AGE_BP2+SEX+BMI	0	391	319	72	118.0	53.0	80.003	80.0	11.466
META_GWAS ILL_AFR	ILL	AFR	invn	AGE_BP+AGE_BP2+SEX+BMI	0	3140	1076	2064	136.0	42.0	80.619	80.0	12.756
META_GWAS ILL_AMR	ILL	AMR	invn	AGE_BP+AGE_BP2+SEX+BMI	1	2994	1143	1851	131.0	41.0	77.822	78.0	11.713
META_GWAS ILL_EUR	ILL	EUR	invn	AGE_BP+AGE_BP2+SEX+BMI	0	1324	828	496	128.0	40.0	78.491	79.0	11.057

7.2 Calibration



(a) invn Adjusted AGE_BP+AGE_BP2+SEX+BMI

Figure 24: QQ plots for DBP10 in the MERGE analysis



(a) invn Adjusted AGE_BP+AGE_BP2+SEX+BMI

Figure 25: Manhattan plots for DBP10 in the MERGE analysis

7.3 Top associations

Table 23: Top variants in the MERGE invn Adjusted AGE_BP+AGE_BP2+SEX+BMI model (**bold** variants indicate previously identified associations)

CHR	POS	ID	EA	OA	GENE _{CLOSEST}	COHORT	DIR	N	MALE	FEMALE	FREQ _{AVG}	FREQ _{MIN}	FREQ _{MAX}	EFFECT	STDERR	OR	ZSCORE	P
4	187813575	rs736880	A	C	FAT1	META_GWAS	+++++	9,013	3,873	5,140	0.804	0.722	0.92	$8.88 \cdot 10^{-2}$	$1.9 \cdot 10^{-2}$	1.093	-4.675	$2.94 \cdot 10^{-6}$
2	1981503	rs6721182	C	A	MYT1L	META_GWAS	+++xxx	7,456	3,045	4,411	0.227	0.166	0.287	$9.18 \cdot 10^{-2}$	$1.98 \cdot 10^{-2}$	1.096	4.627	$3.72 \cdot 10^{-6}$
20	5644184	rs8119133	A	C	GPCPD1	META_GWAS	+++++	9,012	3,872	5,140	0.309	0.261	0.446	$7.5 \cdot 10^{-2}$	$1.62 \cdot 10^{-2}$	1.078	4.625	$3.75 \cdot 10^{-6}$
2	9389812	rs2666214	G	T	ASAP2	META_GWAS	xxx+++	1,553	826	727	0.533	0.438	0.676	0.168	$3.63 \cdot 10^{-2}$	1.183	-4.623	$3.79 \cdot 10^{-6}$
1	228633197	rs16848614	T	C	HIST3H2A	META_GWAS	+++xxx	7,449	3,042	4,407	$7.16 \cdot 10^{-2}$	$4.07 \cdot 10^{-2}$	$9.4 \cdot 10^{-2}$	0.146	$3.19 \cdot 10^{-2}$	1.157	-4.56	$5.1 \cdot 10^{-6}$
16	52172190	rs11645663	G	A	TOX3	META_GWAS	xxx+++	1,555	826	729	0.159	$8.53 \cdot 10^{-2}$	0.233	0.224	$4.99 \cdot 10^{-2}$	1.251	-4.489	$7.16 \cdot 10^{-6}$
13	60616431	rs9646034	T	C	DIAPH3	META_GWAS	+++++	9,009	3,873	5,136	$1.41 \cdot 10^{-2}$	$6.05 \cdot 10^{-3}$	$4.6 \cdot 10^{-2}$	0.283	$6.31 \cdot 10^{-2}$	1.328	4.487	$7.22 \cdot 10^{-6}$
6	158502528	exm590335	G	A	SYNJ2	META_EX	+++	8,995	3,853	5,142	$2.78 \cdot 10^{-4}$	$1.34 \cdot 10^{-4}$	$5.8 \cdot 10^{-4}$	1.994	0.446	7.347	-4.472	$7.74 \cdot 10^{-6}$
4	184572036	rs4547833	T	C	RWDD4	META_GWAS	+++xxx	7,456	3,047	4,409	0.226	0.214	0.237	$8.65 \cdot 10^{-2}$	$1.95 \cdot 10^{-2}$	1.09	4.444	$8.83 \cdot 10^{-6}$
7	105554522	rs17152281	C	A	ATXN7L1	META_GWAS	xxx+++	1,544	821	723	0.142	0.13	0.161	0.232	$5.21 \cdot 10^{-2}$	1.26	-4.442	$8.93 \cdot 10^{-6}$
22	21003610	rs4822389	T	C	PI4KA	META_GWAS	+++xxx	7,444	3,041	4,403	0.164	$7.43 \cdot 10^{-2}$	0.24	$9.93 \cdot 10^{-2}$	$2.24 \cdot 10^{-2}$	1.104	-4.434	$9.27 \cdot 10^{-6}$
17	74546939	rs752049	T	C	CYGB	META_GWAS	+++++	9,012	3,872	5,140	0.233	0.2	0.253	$7.72 \cdot 10^{-2}$	$1.76 \cdot 10^{-2}$	1.08	4.376	$1.21 \cdot 10^{-5}$
1	228579788	rs4653951	C	T	TRIM11	META_GWAS	+++++	9,005	3,870	5,135	$6.65 \cdot 10^{-2}$	$3.34 \cdot 10^{-2}$	$8.99 \cdot 10^{-2}$	0.129	$2.96 \cdot 10^{-2}$	1.138	-4.365	$1.27 \cdot 10^{-5}$
20	16783688	rs7267583	T	C	OTOR	META_GWAS	+++++	9,010	3,872	5,138	$9.02 \cdot 10^{-2}$	$1.89 \cdot 10^{-3}$	0.163	0.116	$2.65 \cdot 10^{-2}$	1.123	4.365	$1.27 \cdot 10^{-5}$
17	63371880	rs4790945	G	A	RGS9	META_GWAS	+++xxx	7,458	3,047	4,411	0.15	$9.82 \cdot 10^{-2}$	0.208	0.101	$2.32 \cdot 10^{-2}$	1.107	-4.362	$1.29 \cdot 10^{-5}$
7	93083708	rs17165475	T	C	CALCR	META_GWAS	+++++	9,005	3,872	5,133	0.116	$1.89 \cdot 10^{-3}$	0.223	0.106	$2.44 \cdot 10^{-2}$	1.112	4.355	$1.33 \cdot 10^{-5}$
7	25968712	rs7810017	A	G	NFE2L3	META_GWAS	xxx+++	1,555	826	729	0.397	0.356	0.415	0.157	$3.61 \cdot 10^{-2}$	1.169	-4.331	$1.49 \cdot 10^{-5}$
12	10437066	rs7297855	A	G	KLRD1	META_GWAS	+++xxx	7,457	3,046	4,411	$7.46 \cdot 10^{-2}$	$7.55 \cdot 10^{-4}$	0.135	0.138	$3.19 \cdot 10^{-2}$	1.148	4.319	$1.57 \cdot 10^{-5}$
20	13035593	rs1431431	C	T	SPTLC3	META_GWAS	+++++	9,011	3,872	5,139	0.297	0.237	0.352	$7.02 \cdot 10^{-2}$	$1.63 \cdot 10^{-2}$	1.073	-4.317	$1.58 \cdot 10^{-5}$
8	9877986	rs9329211	G	A	MSRA	META_GWAS	+++++	9,013	3,873	5,140	0.172	$7.67 \cdot 10^{-3}$	0.317	$8.99 \cdot 10^{-2}$	$2.09 \cdot 10^{-2}$	1.094	-4.313	$1.61 \cdot 10^{-5}$

7.4 Previously identified risk loci

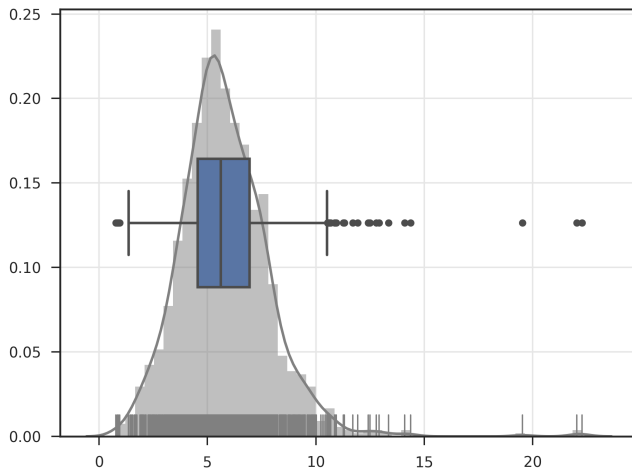
Table 24 shows statistics from the MERGE cohort for 26 loci that were shown to be significantly associated with Diastolic Blood Pressure in the 2011 Nature paper by Ehret et al [10]. Where a previously reported variant was not genotyped in the study (indicated by $\bar{R}^2 < 1$), if available, a tagging 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 2 variants that show at least nominal significance ($p < 0.05$) in this study. Out of the 24 variants in both studies, 8 exhibit the same direction of effect with the known result (binomial test $p = 0.968$).

Table 24: Top known loci in MERGE model invn Adjusted AGE_BP+AGE_BP2+SEX+BMI (**bold** variants indicate matching direction of effect)

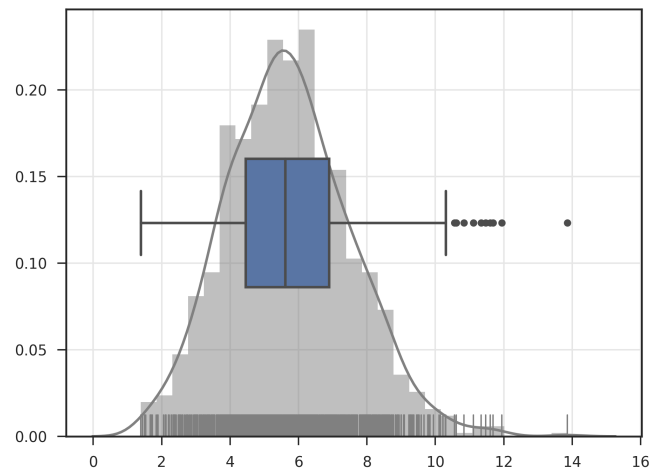
CHR	POS	ID	EA	OA	N	FREQ _{AVG}	FREQ _{MIN}	FREQ _{MAX}	EFFECT	STDERR	P	DIR	COHORT	GENE _{CLOSEST}	R ²	ID _{KNOWN}	N _{KNOWN}	EFFECT _{KNOWN}	STDERR _{KNOWN}	P _{KNOWN}
12	112007756	rs653178	C	T	8,998	0.744	0.439	0.927	2.54 · 10 ⁻²	1.9 · 10 ⁻²	0.181	+++	META_EX	ATXN2	1	rs653178	2 · 10 ⁵	-0.48	6.26 · 10 ⁻²	1.64 · 10 ⁻¹⁴
12	111884608	rs3184504	T	C	8,998	0.744	0.44	0.926	2.46 · 10 ⁻²	1.9 · 10 ⁻²	0.195	++	META_EX	SH2B3	1	rs3184504	2 · 10 ⁵	0.48	6.29 · 10 ⁻²	2.33 · 10 ⁻¹⁴
4	81164723	rs1458038	T	C	7,457	0.173	8.3 · 10 ⁻²	0.26	3.69 · 10 ⁻²	2.21 · 10 ⁻²	9.47 · 10 ⁻²	+++xxx	META_GWAS	FGF5	1	rs1458038	2 · 10 ⁵	0.503	7.02 · 10 ⁻²	7.91 · 10 ⁻¹³
12	112072424	rs11065987	G	A	8,997	0.237	6.56 · 10 ⁻²	0.526	2.67 · 10 ⁻²	1.94 · 10 ⁻²	0.168	+++	META_EX	BRAP	1	rs11065987	2 · 10 ⁵	0.449	6.46 · 10 ⁻²	3.43 · 10 ⁻¹²
15	75077367	rs1378942	C	A	1,556	0.357	0.106	0.619	6.47 · 10 ⁻³	4.29 · 10 ⁻²	0.88	xxx+++	META_GWAS	CSK	1	rs1378942	2 · 10 ⁵	0.445	6.4 · 10 ⁻²	3.47 · 10 ⁻¹²
12	112486818	rs17696736	G	A	8,997	0.24	6.64 · 10 ⁻²	0.54	2.33 · 10 ⁻²	1.93 · 10 ⁻²	0.229	+++	META_EX	NAA25	1	rs17696736	2 · 10 ⁵	0.422	6.34 · 10 ⁻²	2.8 · 10 ⁻¹¹
12	112906415	rs11066320	A	G	7,458	0.767	0.46	0.933	8.6 · 10 ⁻³	2.08 · 10 ⁻²	0.68	+++xxx	META_GWAS	PTPN11	1	rs11066320	2 · 10 ⁵	-0.413	6.32 · 10 ⁻²	6.32 · 10 ⁻¹¹
15	75057203	rs4886406	T	G	7,458	0.677	0.617	0.721	9.87 · 10 ⁻³	1.77 · 10 ⁻²	0.577	+++xxx	META_GWAS	CYP1A2	1	rs4886406	2 · 10 ⁵	0.426	6.85 · 10 ⁻²	4.83 · 10 ⁻¹⁰
15	75125645	rs6495122	C	A	8,997	0.395	0.272	0.504	3.19 · 10 ⁻³	1.57 · 10 ⁻²	0.839	++	META_EX	CPLX3	1	rs6495122	2 · 10 ⁵	0.383	6.23 · 10 ⁻²	8.41 · 10 ⁻¹⁰
15	75115895	rs7162232	A	G	7,458	0.619	0.586	0.705	1.42 · 10 ⁻²	1.7 · 10 ⁻²	0.402	+++xxx	META_GWAS	LMAN1L	1	rs7162232	2 · 10 ⁵	-0.416	6.89 · 10 ⁻²	1.58 · 10 ⁻⁹
7	2512545	rs2969070	A	G	1,555	0.759	0.584	0.917	7.83 · 10 ⁻²	4.37 · 10 ⁻²	7.3 · 10 ⁻²	xxx+++	META_GWAS	GRIFIN	1	rs2969070	2 · 10 ⁵	-0.386	6.47 · 10 ⁻²	2.57 · 10 ⁻⁹
12	90008959	rs2681472	A	G	8,993	0.125	9.68 · 10 ⁻²	0.195	1.76 · 10 ⁻²	2.25 · 10 ⁻²	0.435	++	META_EX	ATP2B1	1	rs2681472	2 · 10 ⁵	-0.492	8.36 · 10 ⁻²	3.9 · 10 ⁻⁹
15	75140854	rs3765066	G	A	7,457	0.385	0.164	0.62	2.34 · 10 ⁻²	1.83 · 10 ⁻²	0.199	+++xxx	META_GWAS	SCAMP2	1	rs3765066	2 · 10 ⁵	0.382	6.51 · 10 ⁻²	4.17 · 10 ⁻⁹
10	63524591	rs1530440	C	T	8,998	0.125	6.13 · 10 ⁻²	0.201	4.51 · 10 ⁻²	2.29 · 10 ⁻²	4.84 · 10 ⁻²	+++	META_EX	Clorf107	1	rs1530440	2 · 10 ⁵	-0.459	7.92 · 10 ⁻²	6.71 · 10 ⁻⁹
1	11883731	rs12567136	C	T	9,014	0.112	0.107	0.137	4.08 · 10 ⁻²	2.32 · 10 ⁻²	7.94 · 10 ⁻²	++++	META_GWAS	CLCN6	1	rs12567136	2 · 10 ⁵	-0.488	8.56 · 10 ⁻²	1.15 · 10 ⁻⁸
1	11862778	rs17367504	A	G	8,998	0.109	0.105	0.122	3.48 · 10 ⁻²	2.38 · 10 ⁻²	0.144	++	META_EX	MTHFR	1	rs17367504	2 · 10 ⁵	-0.49	8.61 · 10 ⁻²	1.29 · 10 ⁻⁸
12	89942390	rs11105328	A	G	9,013	0.135	0.107	0.194	3.28 · 10 ⁻²	2.18 · 10 ⁻²	0.132	++++	META_GWAS	POC1B-GALNT4	1	rs11105328	2 · 10 ⁵	-0.487	8.66 · 10 ⁻²	1.83 · 10 ⁻⁸
12	111818701	rs11065884	A	G	7,457	0.508	0.197	0.734	1.49 · 10 ⁻²	1.79 · 10 ⁻²	0.405	++xxx	META_GWAS	FAM109A	1	rs11065884	2 · 10 ⁵	-0.409	7.42 · 10 ⁻²	3.57 · 10 ⁻⁸
15	75234610	rs11072518	C	T	7,456	0.578	0.54	0.606	1.47 · 10 ⁻²	1.67 · 10 ⁻²	0.379	+++xxx	META_GWAS	COX5A	1	rs11072518	2 · 10 ⁵	-0.355	6.45 · 10 ⁻²	3.78 · 10 ⁻⁸
6	26107463	rs198846	A	G	8,996	0.87	0.846	0.882	2.82 · 10 ⁻²	2.22 · 10 ⁻²	0.202	+++	META_EX	HIST1H1T	1	rs198846	2 · 10 ⁵	-0.487	8.85 · 10 ⁻²	3.8 · 10 ⁻⁸
6	26091179	rs1799945	G	C	8,996	7.89 · 10 ⁻²	2.63 · 10 ⁻²	0.144	5.84 · 10 ⁻²	2.81 · 10 ⁻²	3.74 · 10 ⁻²	+++	META_EX	HFE	1	rs1799945	2 · 10 ⁵	-0.482	8.82 · 10 ⁻²	4.78 · 10 ⁻⁸
12	111780644	rs7306529	C	T	1,549	0.328	0.159	0.429	1.53 · 10 ⁻²	3.91 · 10 ⁻²	0.695	xxx+++	META_GWAS	CUX2	1	rs7306529	2 · 10 ⁵	-0.413	7.56 · 10 ⁻²	4.87 · 10 ⁻⁸
15	75185670	rs7495739	A	G	1,555	0.455	0.348	0.514	1.93 · 10 ⁻²	3.61 · 10 ⁻²	0.594	xxx+++	META_GWAS	MPI	1	rs7495739	2 · 10 ⁵	-0.335	6.15 · 10 ⁻²	5.02 · 10 ⁻⁸
6	26107463	rs198846	A	G	8,996	0.87	0.846	0.882	2.82 · 10 ⁻²	2.22 · 10 ⁻²	0.202	+++	META_EX	HIST1H2BC	1	rs198833	2 · 10 ⁵	-0.485	8.88 · 10 ⁻²	4.58 · 10 ⁻⁸
12	112486818	rs17696736	G	A	8,997	0.24	6.64 · 10 ⁻²	0.54	2.33 · 10 ⁻²	1.93 · 10 ⁻²	0.229	+++	META_EX	TRAFD1	0.922	rs17630235	2 · 10 ⁵	0.447	6.4 · 10 ⁻²	2.92 · 10 ⁻¹²
12	112486818	rs17696736	G	A	8,997	0.24	6.64 · 10 ⁻²	0.54	2.33 · 10 ⁻²	1.93 · 10 ⁻²	0.229	+++	META_EX	HECTD4	0.913	rs11066188	2 · 10 ⁵	0.447	6.41 · 10 ⁻²	3.06 · 10 ⁻¹²

8 LDL Cholesterol (LDL_DIRECT)

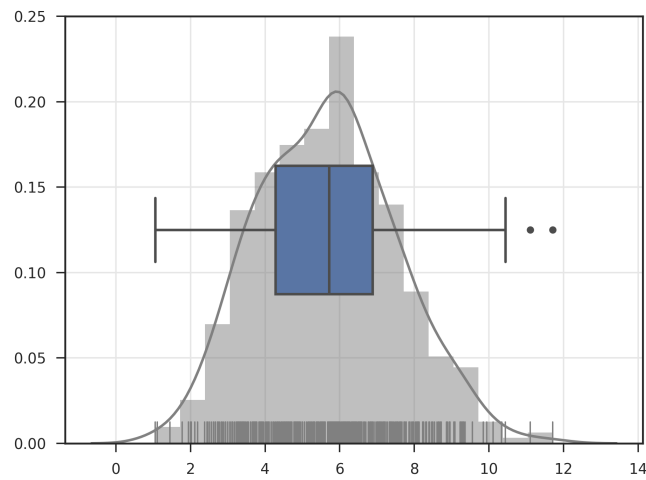
8.1 Summary



(a) EX_AFR

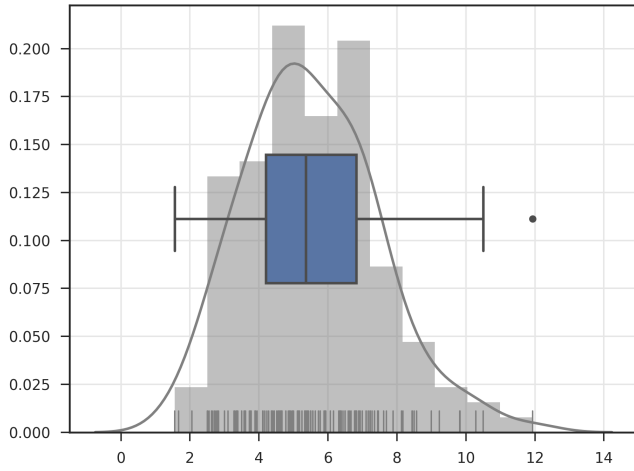


(b) EX_AMR

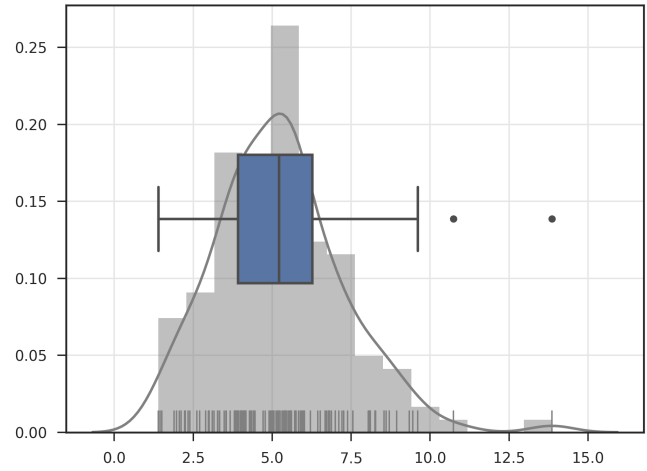


(c) EX_EUR

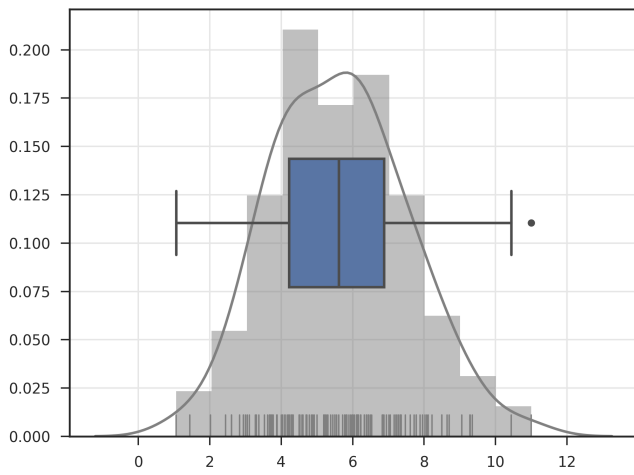
Figure 26: Distribution of LDL_DIRECT in META_EX by cohort



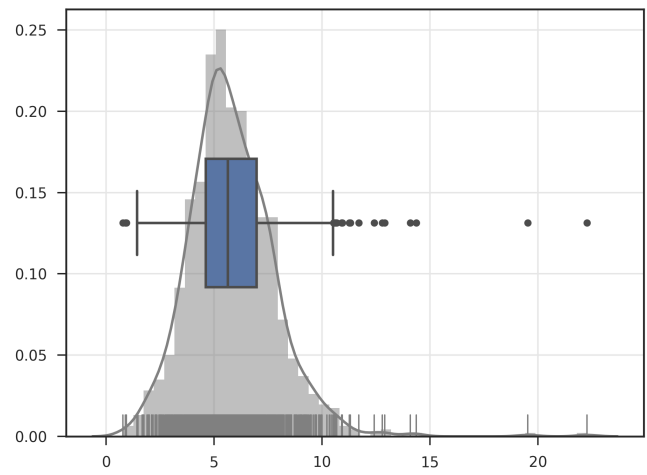
(a) AFFY_AFR



(b) AFFY_AMR



(c) AFFY_EUR



(d) ILL_AFR

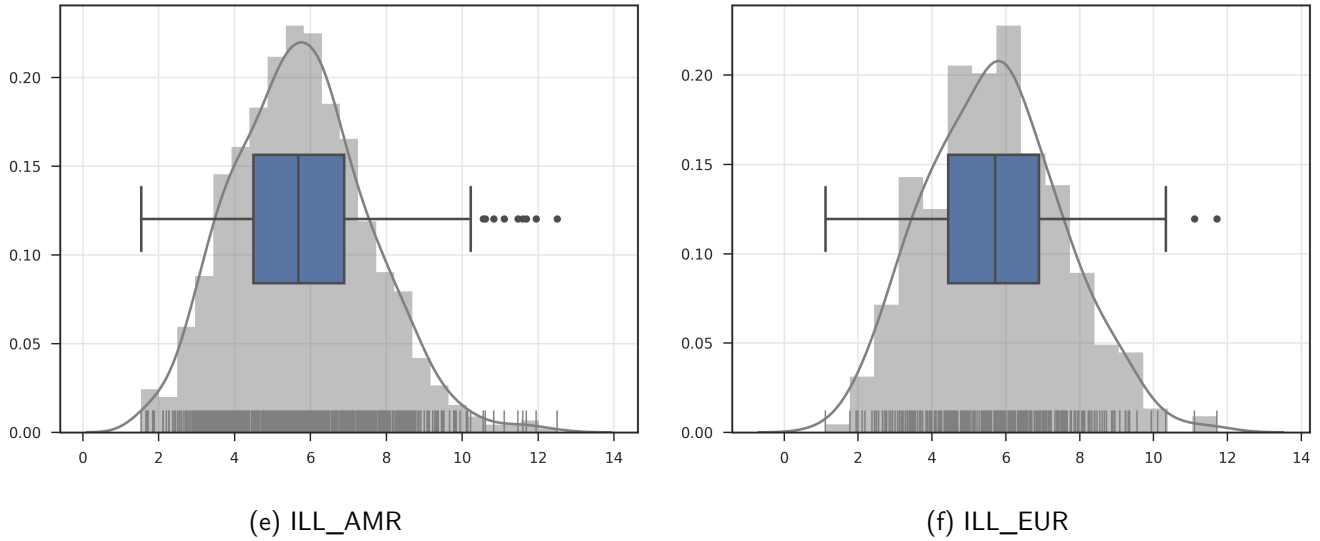


Figure 27: Distribution of LDL_DIRECT in META_GWAS by cohort

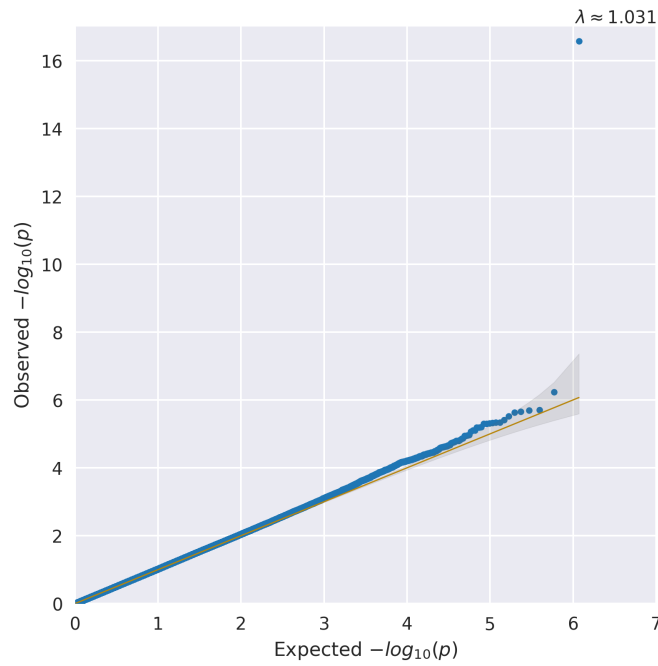
Table 25: Summary of samples removed from LDL Cholesterol analysis by cohort and model

Cohort	Array	Ancestry	Trans	Covars	Total	-SampleQc	-missObs	-Kinship	-PcOutlier
META_EX EX_AFR	EX	AFR	invn	AGE_LIPIDS+AGE_LIPIDS2+SEX+BMI	5172	44	4000	81	21
META_EX EX_AMR	EX	AMR	invn	AGE_LIPIDS+AGE_LIPIDS2+SEX+BMI	5144	32	4084	111	0
META_EX EX_EUR	EX	EUR	invn	AGE_LIPIDS+AGE_LIPIDS2+SEX+BMI	2379	30	1942	1	0
META_GWAS AFFY_AFR	AFFY	AFR	invn	AGE_LIPIDS+AGE_LIPIDS2+SEX+BMI	897	18	734	27	0
META_GWAS AFFY_AMR	AFFY	AMR	invn	AGE_LIPIDS+AGE_LIPIDS2+SEX+BMI	1035	20	895	27	11
META_GWAS AFFY_EUR	AFFY	EUR	invn	AGE_LIPIDS+AGE_LIPIDS2+SEX+BMI	578	12	465	1	0
META_GWAS ILL_AFR	ILL	AFR	invn	AGE_LIPIDS+AGE_LIPIDS2+SEX+BMI	4077	46	3117	1	0
META_GWAS ILL_AMR	ILL	AMR	invn	AGE_LIPIDS+AGE_LIPIDS2+SEX+BMI	3884	26	3031	0	0
META_GWAS ILL_EUR	ILL	EUR	invn	AGE_LIPIDS+AGE_LIPIDS2+SEX+BMI	1797	23	1474	0	1

Table 26: Summary of samples remaining for LDL Cholesterol analysis by cohort and model

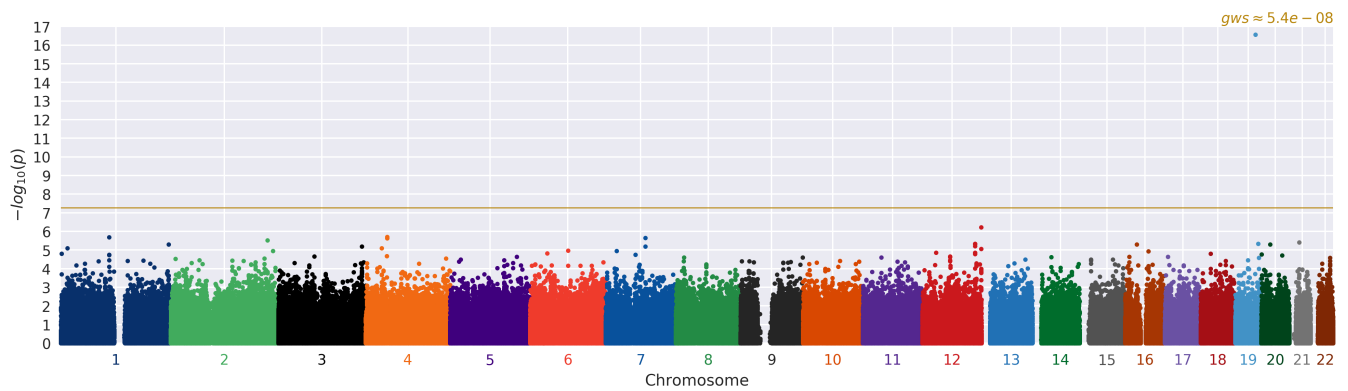
Cohort	Array	Ancestry	Trans	Covars	PCs	N	Male	Female	Max	Min	μ	\bar{x}	σ
META_EX EX_AFR	EX	AFR	invn	AGE_LIPIDS+AGE_LIPIDS2+SEX+BMI	7	1062	382	680	22.278	0.778	5.794	5.583	2.086
META_EX EX_AMR	EX	AMR	invn	AGE_LIPIDS+AGE_LIPIDS2+SEX+BMI	6	942	389	553	11.944	1.389	5.697	5.611	1.779
META_EX EX_EUR	EX	EUR	invn	AGE_LIPIDS+AGE_LIPIDS2+SEX+BMI	0	428	276	152	11.711	1.056	5.706	5.728	1.855
META_GWAS AFFY_AFR	AFFY	AFR	invn	AGE_LIPIDS+AGE_LIPIDS2+SEX+BMI	0	134	64	70	11.933	1.667	5.459	5.344	1.845
META_GWAS AFFY_AMR	AFFY	AMR	invn	AGE_LIPIDS+AGE_LIPIDS2+SEX+BMI	0	101	46	55	10.744	1.389	5.124	5.167	1.851
META_GWAS AFFY_EUR	AFFY	EUR	invn	AGE_LIPIDS+AGE_LIPIDS2+SEX+BMI	0	109	87	22	11.0	1.056	5.599	5.5	1.866
META_GWAS ILL_AFR	ILL	AFR	invn	AGE_LIPIDS+AGE_LIPIDS2+SEX+BMI	0	946	326	620	22.278	0.778	5.823	5.65	2.027
META_GWAS ILL_AMR	ILL	AMR	invn	AGE_LIPIDS+AGE_LIPIDS2+SEX+BMI	0	847	345	502	11.944	1.533	5.756	5.667	1.778
META_GWAS ILL_EUR	ILL	EUR	invn	AGE_LIPIDS+AGE_LIPIDS2+SEX+BMI	0	318	188	130	11.711	1.111	5.739	5.739	1.849

8.2 Calibration



(a) invn Adjusted AGE_LIPIDS+AGE_LIPIDS2+SEX+BMI

Figure 28: QQ plots for LDL_DIRECT in the MERGE analysis



(a) invn Adjusted AGE_LIPIDS+AGE_LIPIDS2+SEX+BMI

Figure 29: Manhattan plots for LDL_DIRECT in the MERGE analysis

8.3 Top associations

Table 27: Top variants in the MERGE invn Adjusted AGE_LIPIDS+AGE_LIPIDS2+SEX+BMI model (**bold** variants indicate previously identified associations)

CHR	POS	ID	EA	OA	GENE _{CLOSEST}	COHORT	DIR	N	MALE	FEMALE	FREQ _{AVG}	FREQ _{MIN}	FREQ _{MAX}	EFFECT	STDERR	OR	ZSCORE	P
19	45412079	rs7412	C	T	APOE	META_EX	+++	2,432	1,047	1,385	$8.26 \cdot 10^{-2}$	$5.1 \cdot 10^{-2}$	0.116	0.439	$5.19 \cdot 10^{-2}$	1.551	-8.459	$2.7 \cdot 10^{-17}$
12	133021330	rs4883531	G	A	MUC8	META_GWAS	++++xxx	2,111	859	1,252	0.635	0.61	0.66	0.157	$3.14 \cdot 10^{-2}$	1.17	4.994	$5.92 \cdot 10^{-7}$
4	48222160	rs16851721	C	T	TEC	META_GWAS	xxx+++	344	197	147	0.657	0.596	0.703	0.381	$8.01 \cdot 10^{-2}$	1.464	4.755	$1.98 \cdot 10^{-6}$
1	109817192	rs7528419	A	G	CELSR2	META_GWAS	+++xxx	2,110	859	1,251	0.252	0.195	0.279	0.163	$3.44 \cdot 10^{-2}$	1.177	-4.749	$2.05 \cdot 10^{-6}$
7	90135511	rs10487118	C	A	CLDN12	META_GWAS	xxx+++	344	197	147	0.11	$4.1 \cdot 10^{-2}$	0.161	0.559	0.118	1.749	4.734	$2.2 \cdot 10^{-6}$
2	218680591	rs41383244	A	G	TNS1	META_GWAS	xxx+++	344	197	147	0.211	$7.09 \cdot 10^{-2}$	0.372	0.445	$9.52 \cdot 10^{-2}$	1.56	-4.671	$2.99 \cdot 10^{-6}$
21	22926491	rs7281895	A	G	NCAM2	META_GWAS	++++xxx	2,111	859	1,252	0.694	0.525	0.769	0.156	$3.39 \cdot 10^{-2}$	1.169	-4.618	$3.87 \cdot 10^{-6}$
12	119482036	rs11064646	G	A	SRRM4	META_GWAS	xxx+++	344	197	147	0.61	0.522	0.702	0.365	$7.96 \cdot 10^{-2}$	1.44	4.585	$4.54 \cdot 10^{-6}$
19	51572155	rs1001538	C	T	KLK13	META_GWAS	+++xxx	2,111	859	1,252	0.46	0.324	0.575	0.145	$3.16 \cdot 10^{-2}$	1.156	4.581	$4.62 \cdot 10^{-6}$
20	19806241	rs17371935	G	A	RIN2	META_GWAS	xxx+++	343	196	147	$2.92 \cdot 10^{-2}$	$1.12 \cdot 10^{-2}$	$5.05 \cdot 10^{-2}$	0.982	0.215	2.669	4.569	$4.91 \cdot 10^{-6}$
16	26328263	rs1424211	T	C	HS3ST4	META_GWAS	+++xxx	2,111	859	1,252	0.939	0.899	0.964	0.293	$6.41 \cdot 10^{-2}$	1.34	-4.566	$4.97 \cdot 10^{-6}$
1	244155946	rs7511723	T	C	ZBTB18	META_GWAS	++++xxx	2,106	857	1,249	0.236	0.12	0.301	0.168	$3.68 \cdot 10^{-2}$	1.183	-4.562	$5.06 \cdot 10^{-6}$
7	90140673	rs17867686	A	C	CDK14	META_GWAS	xxx+++	344	197	147	0.105	$3.73 \cdot 10^{-2}$	0.161	0.544	0.121	1.723	4.513	$6.4 \cdot 10^{-6}$
3	189017265	rs7647662	C	T	TPRG1	META_GWAS	xxx+++	344	197	147	0.499	0.33	0.694	0.336	$7.45 \cdot 10^{-2}$	1.399	-4.509	$6.5 \cdot 10^{-6}$
1	15589886	rs10927751	G	A	FHAD1	META_GWAS	xxx+++	344	197	147	0.128	$8.72 \cdot 10^{-2}$	0.179	0.535	0.12	1.707	-4.467	$7.94 \cdot 10^{-6}$
4	35807973	rs4832782	A	G	ARAP2	META_GWAS	xxx+++	344	197	147	0.14	0.124	0.158	0.462	0.104	1.588	-4.467	$7.94 \cdot 10^{-6}$
6	86059902	rs9450247	A	G	NTSE	META_GWAS	++++++	2,445	1,052	1,393	0.174	$8.91 \cdot 10^{-2}$	0.25	0.17	$3.87 \cdot 10^{-2}$	1.186	-4.403	$1.07 \cdot 10^{-5}$
2	231326201	rs11681514	G	C	SP100	META_GWAS	xxx+++	344	197	147	0.219	0.174	0.248	0.388	$8.83 \cdot 10^{-2}$	1.474	4.395	$1.11 \cdot 10^{-5}$
7	25276424	rs757202	C	T	NPVF	META_GWAS	++++++	2,455	1,056	1,399	0.665	0.541	0.757	0.135	$3.08 \cdot 10^{-2}$	1.145	4.391	$1.13 \cdot 10^{-5}$
16	52575907	rs4784223	A	G	TOX3	META_GWAS	xxx+++	342	197	145	0.332	0.22	0.399	0.354	$8.07 \cdot 10^{-2}$	1.425	-4.388	$1.15 \cdot 10^{-5}$

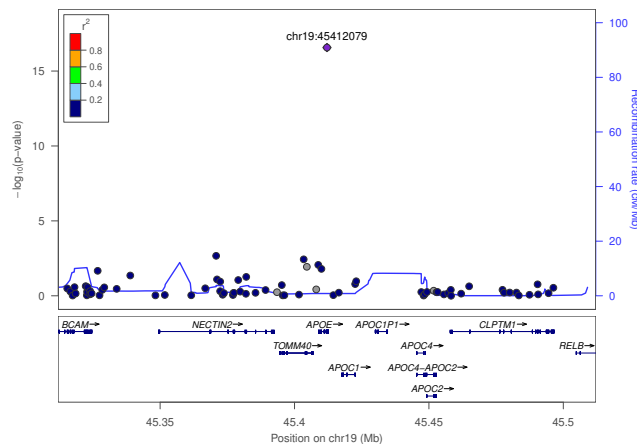


Figure 30: Regional plot for cohort MERGE model invn Adjusted AGE_LIPIDS+AGE_LIPIDS2+SEX+BMI: rs7412 ±100kb

8.4 Previously identified risk loci

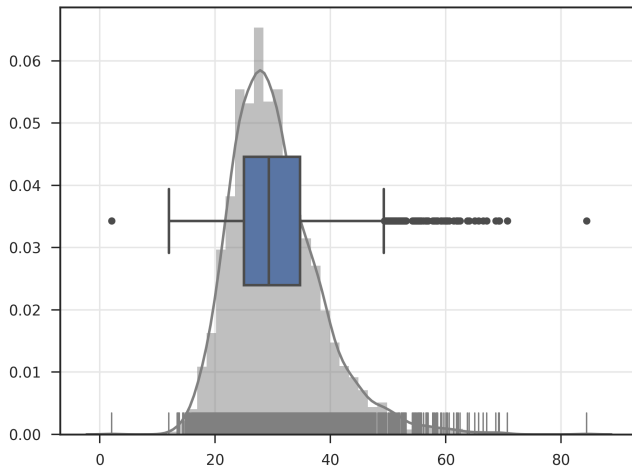
Table 28 shows statistics from the MERGE cohort for 50 loci that were shown to be significantly associated with LDL Cholesterol in the 2013 Nature Genetics paper by Willer et al [15]. Where a previously reported variant was not genotyped in the study (indicated by $\bar{R}^2 < 1$), if available, a tagging 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 7 variants that show at least nominal significance ($p < 0.05$) in this study. Out of the 50 variants in both studies, 35 exhibit the same direction of effect with the known result (binomial test $p = 0.0033$).

Table 28: Top known loci in MERGE model invn Adjusted AGE_LIPIDS+AGE_LIPIDS2+SEX+BMI (**bold** variants indicate matching direction of effect)

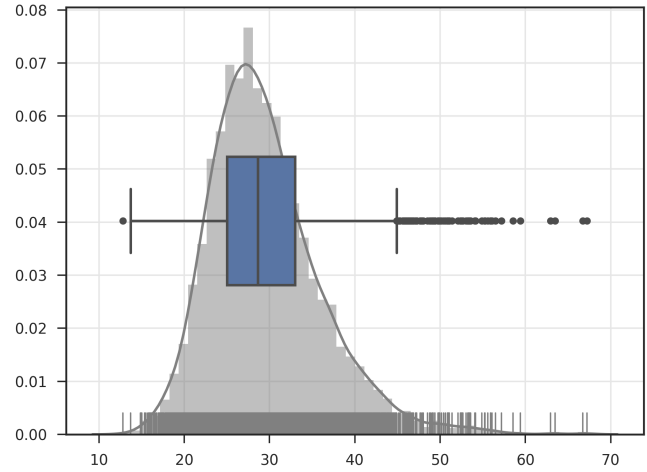
CHR	POS	ID	EA	OA	N	FREQ _{AVG}	FREQ _{MIN}	FREQ _{MAX}	EFFECT	STDERR	P	DIR	COHORT	GENE _{CLOSEST}	R ²	ID _{KNOWN}	N _{KNOWN}	EFFECT _{KNOWN}	STDERR _{KNOWN}	P _{KNOWN}
19	45412079	rs7412	C	T	2,429	8.28 · 10 ⁻²	5.11 · 10 ⁻²	0.116	0.44	5.19 · 10 ⁻²	2.2 · 10 ⁻¹⁷	+++	META_EX	APOE	1	rs7412	94,595	0.59	1.01 · 10 ⁻²	0
1	109818530	rs646776	T	C	2,111	0.705	0.651	0.802	0.137	3.3 · 10 ⁻²	3.48 · 10 ⁻⁵	+++xxx	META_GWAS	CELSR2	1	rs646776	94,595	0.16	4.4 · 10 ⁻³	1.63 · 10 ⁻²⁷²
1	109822166	rs599839	A	G	2,428	0.501	0.265	0.797	4.74 · 10 ⁻²	3.24 · 10 ⁻²	0.143	+++	META_EX	PSRC1	1	rs599839	94,595	0.16	4.4 · 10 ⁻³	2.75 · 10 ⁻²⁶⁸
19	11202306	rs6511720	G	T	2,428	0.125	0.107	0.137	0.139	4.39 · 10 ⁻²	1.55 · 10 ⁻³	+++	META_EX	LDLR	1	rs6511720	94,595	0.221	6.1 · 10 ⁻³	3.85 · 10 ⁻²⁶²
19	45395619	rs2075650	G	A	2,429	0.115	0.104	0.123	5.94 · 10 ⁻³	4.51 · 10 ⁻²	0.895	+++	META_EX	TOMM40	1	rs2075650	94,595	0.177	5.5 · 10 ⁻³	1.72 · 10 ⁻²¹⁴
2	21263900	rs1367117	A	G	2,429	0.202	0.106	0.292	3.16 · 10 ⁻²	3.66 · 10 ⁻²	0.388	+++	META_EX	APOB	1	rs1367117	94,595	0.119	4 · 10 ⁻³	9.48 · 10 ⁻¹⁸³
19	45422946	rs4420638	G	A	2,429	0.164	0.111	0.221	6.32 · 10 ⁻²	3.9 · 10 ⁻²	0.105	+++	META_EX	APOC1	1	rs4420638	94,595	0.225	7.7 · 10 ⁻³	1.51 · 10 ⁻¹⁷⁸
19	45242173	rs1531517	G	A	2,111	0.142	8.38 · 10 ⁻²	0.212	4.23 · 10 ⁻²	4.42 · 10 ⁻²	0.339	+++xxxx	META_GWAS	BCL3	1	rs1531517	94,595	0.22	8 · 10 ⁻³	9.51 · 10 ⁻¹⁶³
1	55505647	rs11591147	G	T	2,429	1.03 · 10 ⁻²	2.83 · 10 ⁻³	1.87 · 10 ⁻²	0.206	0.145	0.154	+++	META_EX	PCSK9	1	rs11591147	94,595	0.497	1.8 · 10 ⁻²	8.58 · 10 ⁻¹⁴³
2	215126316	rs2337383	G	A	2,110	0.211	0.13	0.286	5.07 · 10 ⁻²	3.77 · 10 ⁻²	0.178	+++xxxx	META_GWAS	TDRD15	1	rs2337383	94,595	9.85 · 10 ⁻²	3.9 · 10 ⁻³	1.08 · 10 ⁻¹³¹
19	45333834	rs4803760	C	T	2,111	0.911	0.819	0.951	5.3 · 10 ⁻²	5.6 · 10 ⁻²	0.345	+++xxxx	META_GWAS	BCAM	1	rs4803760	94,595	0.119	4.9 · 10 ⁻³	2.47 · 10 ⁻¹³³
19	45382034	rs6859	A	G	2,429	0.605	0.547	0.668	5.7 · 10 ⁻²	2.93 · 10 ⁻²	5.17 · 10 ⁻²	+++	META_EX	NECTIN2	1	rs6859	94,595	8.35 · 10 ⁻²	3.9 · 10 ⁻³	4.65 · 10 ⁻⁸⁸
2	44073881	rs6544713	T	C	2,429	0.784	0.703	0.852	8.34 · 10 ⁻²	3.58 · 10 ⁻²	1.97 · 10 ⁻²	+++	META_EX	ABCG8	1	rs6544713	94,595	8.06 · 10 ⁻²	4.1 · 10 ⁻³	4.84 · 10 ⁻⁸³
5	74656539	rs12916	C	T	2,111	0.296	0.239	0.396	5.95 · 10 ⁻²	3.39 · 10 ⁻²	7.94 · 10 ⁻²	+++xxxx	META_GWAS	HMGC8	1	rs12916	94,595	7.33 · 10 ⁻²	3.8 · 10 ⁻³	7.79 · 10 ⁻⁷⁸
19	45176340	rs2965157	C	T	344	0.267	2.75 · 10 ⁻²	0.545	8.4 · 10 ⁻²	0.103	0.413	xxxx+++	META_GWAS	CEACAM19	1	rs2965157	94,595	-0.189	1.12 · 10 ⁻²	7.29 · 10 ⁻⁶²
11	11159525	rs12052058	G	T	344	0.157	6.34 · 10 ⁻²	0.252	0.115	0.107	0.284	xxxx+++	META_GWAS	SMARCA4	1	rs12052058	94,595	7.5 · 10 ⁻²	4.3 · 10 ⁻³	9.66 · 10 ⁻⁶²
5	74569856	rs4704200	T	C	2,111	0.59	0.456	0.707	6.13 · 10 ⁻²	3.2 · 10 ⁻²	5.59 · 10 ⁻²	+++xxxx	META_GWAS	ANKRD31	1	rs4704200	94,595	6.44 · 10 ⁻²	3.7 · 10 ⁻³	1.3 · 10 ⁻⁶¹
5	74879890	rs5744680	A	G	344	0.594	0.395	0.84	5.75 · 10 ⁻²	8.46 · 10 ⁻²	0.497	xxxx+++	META_GWAS	POLK	1	rs5744680	94,595	6.44 · 10 ⁻²	3.7 · 10 ⁻³	2.96 · 10 ⁻⁶¹
19	45296806	rs3208856	C	T	2,429	3.87 · 10 ⁻²	2.8 · 10 ⁻²	4.85 · 10 ⁻²	7.3 · 10 ⁻³	7.5 · 10 ⁻²	0.922	+++	META_EX	CBL3	1	rs3208856	94,595	0.295	1.91 · 10 ⁻²	4.03 · 10 ⁻⁵⁶
19	10950125	rs11881156	T	C	2,110	0.127	0.108	0.204	1.81 · 10 ⁻²	4.67 · 10 ⁻²	0.699	+++xxxx	META_GWAS	C19orf38	1	rs11881156	94,595	-8.11 · 10 ⁻²	4.9 · 10 ⁻³	1.7 · 10 ⁻⁵⁵
19	19407718	rs10401969	T	C	2,429	0.125	6.07 · 10 ⁻²	0.166	0.119	4.42 · 10 ⁻²	7.24 · 10 ⁻³	+++	META_EX	SUGP1	1	rs10401969	94,595	0.118	7.2 · 10 ⁻³	2.65 · 10 ⁻⁵⁴
2	44065090	rs6756629	A	G	2,427	7.79 · 10 ⁻²	7.16 · 10 ⁻²	8.42 · 10 ⁻²	5.35 · 10 ⁻²	5.37 · 10 ⁻²	0.319	+++	META_EX	ABCG5	1	rs6756629	94,595	-0.131	8.8 · 10 ⁻³	1.29 · 10 ⁻⁴⁹
8	126481747	rs2980875	G	A	344	0.395	0.34	0.441	3.93 · 10 ⁻²	7.67 · 10 ⁻²	0.608	xxxx+++	META_GWAS	TRIB1	1	rs2980875	94,595	-5.47 · 10 ⁻²	3.6 · 10 ⁻³	2.3 · 10 ⁻⁴⁷
1	109833187	rs17584208	A	G	344	7.99 · 10 ⁻²	5.05 · 10 ⁻²	0.104	0.151	0.137	0.271	xxxx+++	META_GWAS	MYBPHL	1	rs17584208	94,595	-0.101	6.7 · 10 ⁻³	4.39 · 10 ⁻⁴⁷
19	19658472	rs16996148	G	T	2,429	0.114	6.31 · 10 ⁻²	0.15	5.06 · 10 ⁻²	4.5 · 10 ⁻²	0.26	+++	META_EX	CILP2	1	rs16996148	94,595	9.86 · 10 ⁻²	6.7 · 10 ⁻³	1.97 · 10 ⁻⁴⁵
19	45225345	rs2965109	T	C	2,455	0.459	0.406	0.481	1.65 · 10 ⁻³	2.85 · 10 ⁻²	0.954	++++	META_GWAS	CEACAM16	1	rs2965109	94,595	-5.46 · 10 ⁻²	3.9 · 10 ⁻³	6.65 · 10 ⁻⁴⁵
9	136154168	rs579459	C	T	2,429	0.171	0.137	0.234	4.84 · 10 ⁻²	3.78 · 10 ⁻²	0.201	+++	META_EX	ABO	1	rs579459	94,595	6.65 · 10 ⁻²	4.5 · 10 ⁻³	2.42 · 10 ⁻⁴⁴
19	19329924	rs2228603	C	T	2,429	2.68 · 10 ⁻²	1.41 · 10 ⁻²	5.61 · 10 ⁻²	0.122	9.09 · 10 ⁻²	0.18	+++	META_EX	NCAN	1	rs2228603	94,595	0.104	7.2 · 10 ⁻³	4.43 · 10 ⁻⁴⁴
1	109782190	rs611060	T	C	2,111	0.488	0.338	0.612	3.39 · 10 ⁻¹	3.06 · 10 ⁻²	0.991	---xxxx	META_GWAS	SARS	1	rs611060	94,595	-5.34 · 10 ⁻²	3.7 · 10 ⁻³	4.27 · 10 ⁻⁴²
16	72108093	rs2000999	A	G	2,426	0.133	7.68 · 10 ⁻²	0.195	2.99 · 10 ⁻²	4.25 · 10 ⁻²	0.482	+++	META_EX	HRP	1	rs2000999	94,595	6.5 · 10 ⁻²	4.6 · 10 ⁻³	4.22 · 10 ⁻⁴¹
11	61609750	rs174583	C	T	2,429	0.344	0.264	0.436	9.15 · 10 ⁻³	3.18 · 10 ⁻²	0.774	+++	META_EX	FADS2	1	rs174583	94,595	5.22 · 10 ⁻²	3.8 · 10 ⁻³	7 · 10 ⁻⁴¹
5	74579183	rs4704221	A	T	344	0.599	0.408	0.84	3.18 · 10 ⁻²	8.39 · 10 ⁻²	0.705	xxxx+++	META_GWAS	COL4A3BP	1	rs4704221	94,595	-6.3 · 10 ⁻²	4.5 · 10 ⁻³	2.03 · 10 ⁻⁴⁰
5	74924890	rs1427924	A	G	344	0.307	0.252	0.373	3.23 · 10 ⁻²	8.67 · 10 ⁻²	0.71	xxxx+++	META_GWAS	ANKDD1B	1	rs1427924	94,595	-6.28 · 10 ⁻²	4.4 · 10 ⁻³	2.4 · 10 ⁻⁴⁰
11	61571478	rs174550	T	C	2,429	0.231	6.79 · 10 ⁻²	0.376	7.82 · 10 ⁻²	3.79 · 10 ⁻²	3.92 · 10 ⁻²	+++	META_EX	FADS1	1	rs174550	94,595	5.14 · 10 ⁻²	3.8 · 10 ⁻³	7.03 · 10 ⁻⁴⁰
11	6157803	rs102275	T	C	2,429	0.566	0.342	0.666	3.86 · 10 ⁻²	3.05 · 10 ⁻²	0.207	+++	META_EX	TMEM258	1	rs102275	94,595	5.12 · 10 ⁻²	3.8 · 10 ⁻³	7.61 · 10 ⁻⁴⁰
19	19723215	rs10500212	C	T	2,110	0.116	6.45 · 10 ⁻²	0.15	8.79 · 10 ⁻²	4.79 · 10 ⁻²	6.63 · 10 ⁻²	+++xxxx	META_GWAS	PBX4	1	rs10500212	94,595	9.15 · 10 ⁻²	6.7 · 10 ⁻³	8.95 · 10 ⁻⁴⁰
1	55713628	rs4927207	A	G	2,111	0.145	0.128	0.16	7.34 · 10 ⁻²	4.42 · 10 ⁻²	9.71 · 10 ⁻²	+++xxxx	META_GWAS	USP24	1	rs4927207	94,595	-6.92 · 10 ⁻²	4.9 · 10 ⁻³	2.36 · 10 ⁻³⁹
11	61551356	rs174535	T	C	2,111	0.298	0.192	0.407	4.75 · 10 ⁻²	3.45 · 10 ⁻²	0.169	+++xxxx	META_GWAS	MYRF	1	rs174535	94,595	5.04 · 10 ⁻²	3.8 · 10 ⁻³	1.75 · 10 ⁻³⁸
19	19379549	rs58542926	C	T	2,429	4.63 · 10 ⁻²	3.2 · 10 ⁻²	5.84 · 10 ⁻²	0.148	6.84 · 10 ⁻²	3.03 · 10 ⁻²	+++	META_EX	TM6SF2	1	rs58542926	94,595	0.128	9.5 · 10 ⁻³	1.96 · 10 ⁻³⁸
16	56989590	rs247616	C	T	2,428	0.271	0.258	0.292	1.56 · 10 ⁻²	3.23 · 10 ⁻²	0.628	+++	META_EX	CETP	1	rs247616	94,595	5.47 · 10 ⁻²	4.1 · 10 ⁻³	2.57 · 10 ⁻³⁷
19	19746151	rs2304128	T	G	2,111	0.132	6.92 · 10 ⁻²	0.169	2.52 · 10 ⁻²	4.58 · 10 ⁻²	0.582	+++xxxx	META_GWAS	GMIP	1	rs2304128	94,595	-9.02 · 10 ⁻²	6.8 · 10 ⁻³	4.23 · 10 ⁻³⁷
19	19505087	rs10415849	C	T	344	0.129	0.11	0.149	0.121	0.117	0.3	xxxx+++	META_GWAS	GATAD2A	1	rs10415849	94,595	7.28 · 10 ⁻²	5.7 · 10 ⁻³	4.25 · 10 ⁻³⁶
2	21123352	rs6711016	A	C	344	0.148	4.85 · 10 ⁻²	0.229	2.42 · 10 ⁻²	0.118	0.838	xxxx+	META_GWAS	LDHA	1	rs6711016	94,595	-5.51 · 10 ⁻²	4.3 · 10 ⁻³	1.1 · 10 ⁻³⁵
11	61560081	rs174538	G	A	2,111	0.21	6.03 · 10 ⁻²	0.347	7.34 · 10 ⁻²	3.98 · 10 ⁻²	6.52 · 10 ⁻²	+++xxxx	META_GWAS	FEN1	1	rs174538	94,595	5 · 10 ⁻²	4 · 10 ⁻³	1.07 · 10 ⁻³⁴

9 Body Mass Index (BMI)

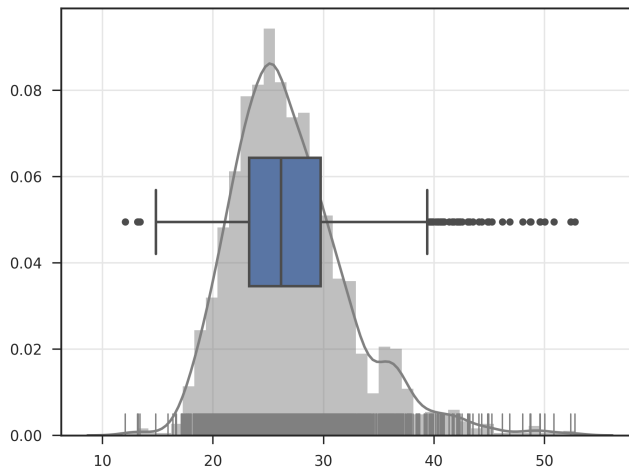
9.1 Summary



(a) EX_AFR

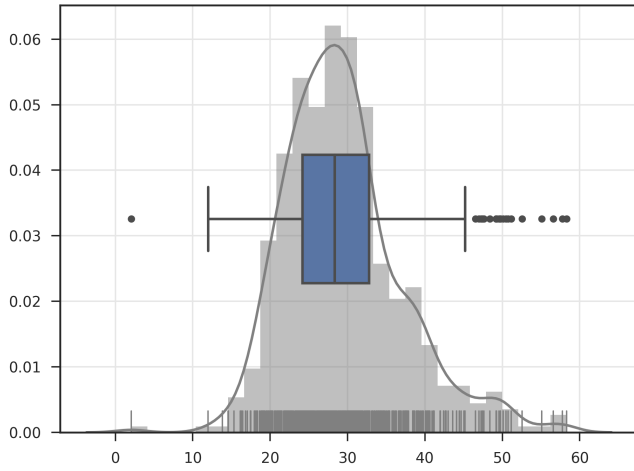


(b) EX_AMR

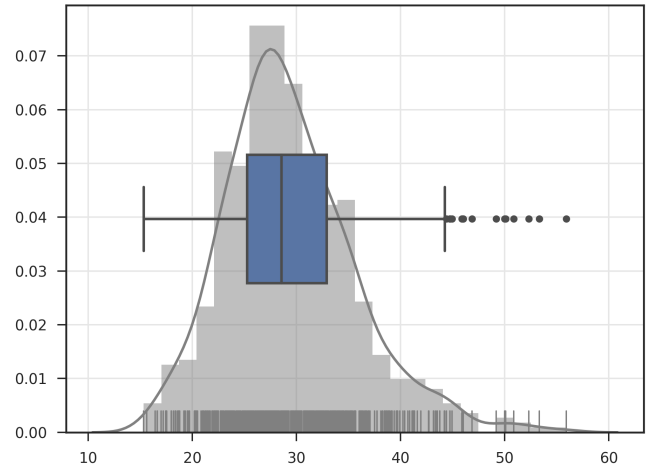


(c) EX_EUR

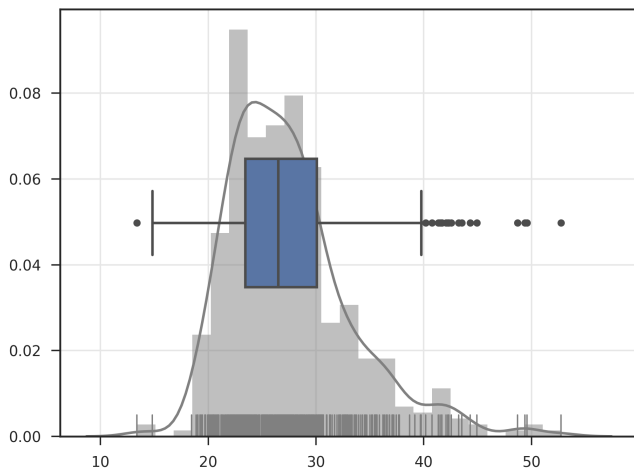
Figure 31: Distribution of BMI in META_EX by cohort



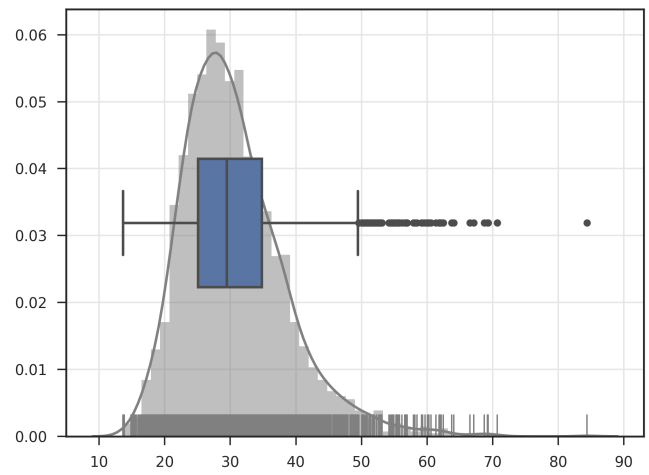
(a) AFFY_AFR



(b) AFFY_AMR



(c) AFFY_EUR



(d) ILL_AFR

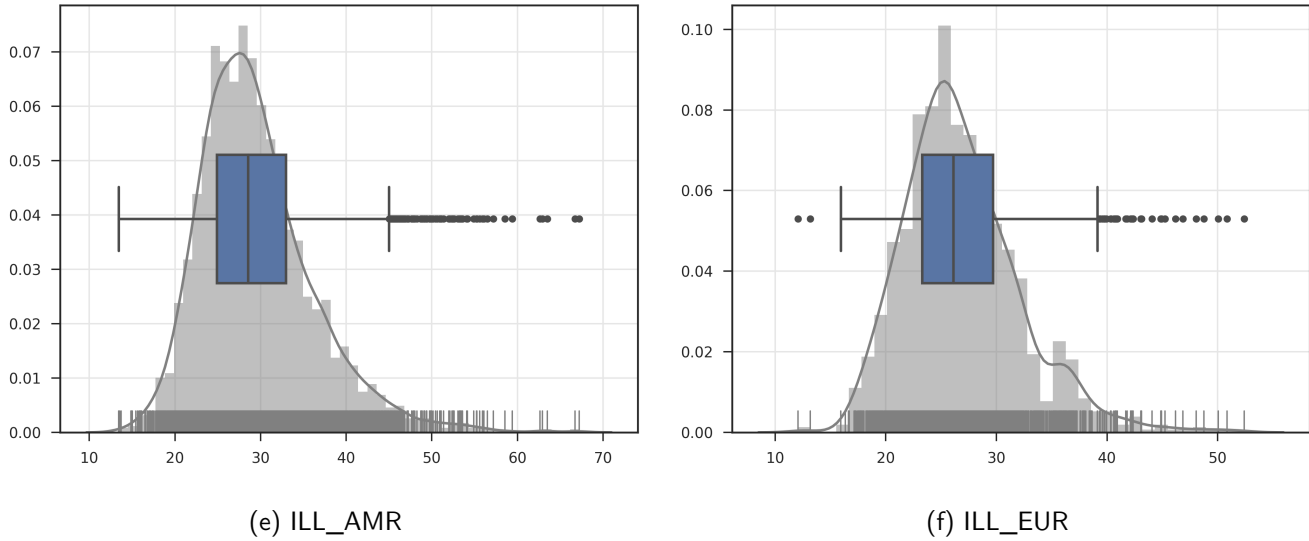


Figure 32: Distribution of BMI in META_GWAS by cohort

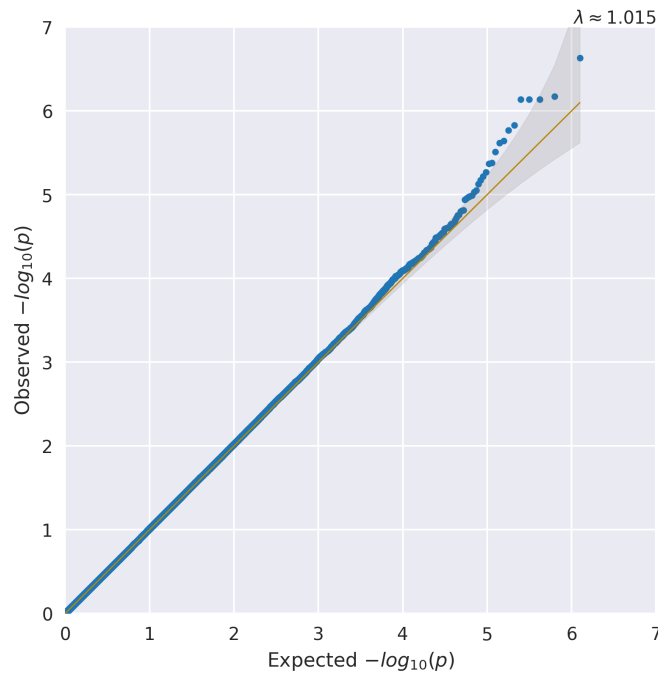
Table 29: Summary of samples removed from Body Mass Index analysis by cohort and model

Cohort	Array	Ancestry	Trans	Covars	Total	-SampleQc	-missObs	-Kinship	-PcOutlier
META_EX EX_AFR	EX	AFR	invn	AGE_ANTHRO+AGE_ANTHRO2+SEX	5172	44	1106	282	0
META_EX EX_AMR	EX	AMR	invn	AGE_ANTHRO+AGE_ANTHRO2+SEX	5144	32	1128	426	0
META_EX EX_EUR	EX	EUR	invn	AGE_ANTHRO+AGE_ANTHRO2+SEX	2379	30	586	6	0
META_GWAS AFFY_AFR	AFFY	AFR	invn	AGE_ANTHRO+AGE_ANTHRO2+SEX	897	18	200	129	15
META_GWAS AFFY_AMR	AFFY	AMR	invn	AGE_ANTHRO+AGE_ANTHRO2+SEX	1035	20	227	165	5
META_GWAS AFFY_EUR	AFFY	EUR	invn	AGE_ANTHRO+AGE_ANTHRO2+SEX	578	12	164	8	7
META_GWAS ILL_AFR	ILL	AFR	invn	AGE_ANTHRO+AGE_ANTHRO2+SEX	4077	46	872	4	0
META_GWAS ILL_AMR	ILL	AMR	invn	AGE_ANTHRO+AGE_ANTHRO2+SEX	3884	26	857	2	0
META_GWAS ILL_EUR	ILL	EUR	invn	AGE_ANTHRO+AGE_ANTHRO2+SEX	1797	23	425	1	0

Table 30: Summary of samples remaining for Body Mass Index analysis by cohort and model

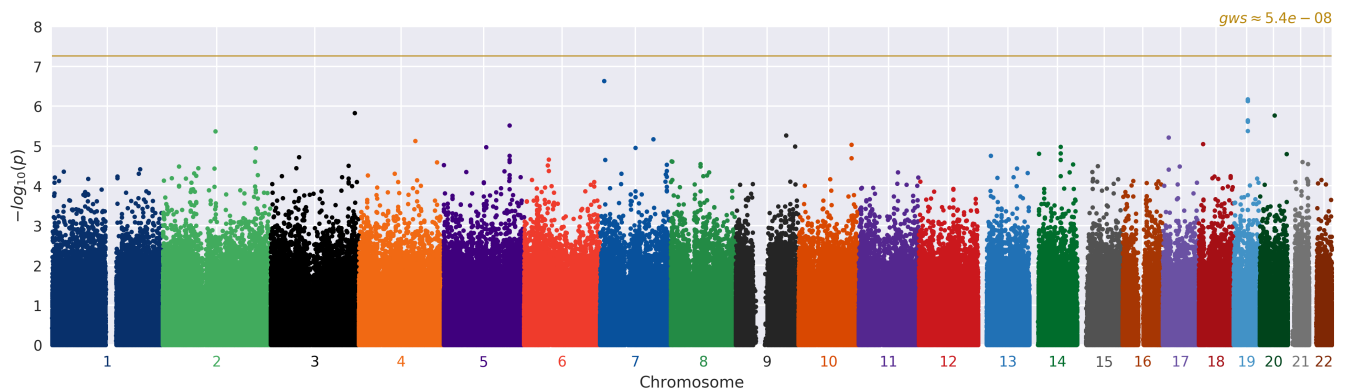
Cohort	Array	Ancestry	Trans	Covars	PCs	N	Male	Female	Max	Min	μ	\hat{x}	σ
META_EX EX_AFR	EX	AFR	invn	AGE_ANTHRO+AGE_ANTHRO2+SEX	0	3753	1323	2430	84.409	2.048	30.302	29.159	7.872
META_EX EX_AMR	EX	AMR	invn	AGE_ANTHRO+AGE_ANTHRO2+SEX	3	3567	1401	2166	67.228	13.714	29.438	28.498	6.568
META_EX EX_EUR	EX	EUR	invn	AGE_ANTHRO+AGE_ANTHRO2+SEX	0	1764	1177	587	52.743	12.053	26.953	26.128	5.398
META_GWAS AFFY_AFR	AFFY	AFR	invn	AGE_ANTHRO+AGE_ANTHRO2+SEX	0	544	237	307	58.331	2.048	29.425	28.342	7.714
META_GWAS AFFY_AMR	AFFY	AMR	invn	AGE_ANTHRO+AGE_ANTHRO2+SEX	6	622	273	349	55.913	15.333	29.358	28.529	6.212
META_GWAS AFFY_EUR	AFFY	EUR	invn	AGE_ANTHRO+AGE_ANTHRO2+SEX	0	395	324	71	52.743	13.383	27.308	26.306	5.716
META_GWAS ILL_AFR	ILL	AFR	invn	AGE_ANTHRO+AGE_ANTHRO2+SEX	0	3167	1085	2082	84.409	13.43	30.536	29.352	7.899
META_GWAS ILL_AMR	ILL	AMR	invn	AGE_ANTHRO+AGE_ANTHRO2+SEX	3	3007	1148	1859	67.228	13.714	29.555	28.509	6.688
META_GWAS ILL_EUR	ILL	EUR	invn	AGE_ANTHRO+AGE_ANTHRO2+SEX	0	1355	846	509	52.389	12.053	26.855	26.046	5.281

9.2 Calibration



(a) invn Adjusted AGE_ANTHRO+AGE_ANTHRO2+SEX

Figure 33: QQ plots for BMI in the MERGE analysis



(a) invn Adjusted AGE_ANTHRO+AGE_ANTHRO2+SEX

Figure 34: Manhattan plots for BMI in the MERGE analysis

9.3 Top associations

Table 31: Top variants in the MERGE invn Adjusted AGE_ANTHRO+AGE_ANTHRO2+SEX model (**bold** variants indicate previously identified associations)

CHR	POS	ID	EA	OA	GENE _{CLOSEST}	COHORT	DIR	N	MALE	FEMALE	FREQ _{AVG}	FREQ _{MIN}	FREQ _{MAX}	EFFECT	STDERR	OR	ZSCORE	P
7	9469697	rs12111963	C	T	NXPB1	META_GWAS	xxx+++	1,561	834	727	$5.22 \cdot 10^{-2}$	$1.27 \cdot 10^{-3}$	0.104	0.419	$8.11 \cdot 10^{-2}$	1.521	-5.171	$2.33 \cdot 10^{-7}$
19	32480688	rs12610055	G	A	ZNF507	META_GWAS	xxx+++	1,561	834	727	0.429	0.334	0.547	0.179	$3.6 \cdot 10^{-2}$	1.196	4.969	$6.73 \cdot 10^{-7}$
3	189016395	rs7644778	G	T	TPRG1	META_GWAS	+++++	9,090	3,913	5,177	$9.18 \cdot 10^{-2}$	$1.14 \cdot 10^{-2}$	0.179	0.125	$2.6 \cdot 10^{-2}$	1.133	-4.813	$1.49 \cdot 10^{-6}$
20	33501958	rs140958101	A	C	ACSS2	META_EX	+++	9,084	3,901	5,183	$4.95 \cdot 10^{-4}$	$2.83 \cdot 10^{-4}$	$6.66 \cdot 10^{-4}$	1.593	0.333	4.918	4.787	$1.7 \cdot 10^{-6}$
5	147880181	rs6881498	A	G	HTR4	META_GWAS	xxx+++	1,560	834	726	0.602	0.415	0.796	0.172	$3.69 \cdot 10^{-2}$	1.188	-4.666	$3.07 \cdot 10^{-6}$
2	118822403	rs11687724	C	T	INSIG2	META_GWAS	+++xxx	7,528	3,079	4,449	$5.32 \cdot 10^{-2}$	$4.67 \cdot 10^{-2}$	$5.81 \cdot 10^{-2}$	0.167	$3.63 \cdot 10^{-2}$	1.182	-4.598	$4.27 \cdot 10^{-6}$
9	113171262	rs16914997	G	A	SVEP1	META_GWAS	+++++	9,088	3,912	5,176	0.213	0.194	0.242	$8.19 \cdot 10^{-2}$	$1.8 \cdot 10^{-2}$	1.085	-4.549	$5.39 \cdot 10^{-6}$
17	13023456	rs2322788	T	C	ELAC2	META_GWAS	+++xxx	7,524	3,076	4,448	0.638	0.589	0.688	$7.73 \cdot 10^{-2}$	$1.71 \cdot 10^{-2}$	1.08	4.524	$6.07 \cdot 10^{-6}$
7	119915432	exm652814	T	C	KCND2	META_EX	+++	9,083	3,900	5,183	$2.75 \cdot 10^{-4}$	$1.33 \cdot 10^{-4}$	$8.51 \cdot 10^{-4}$	2.009	0.446	7.455	4.503	$6.7 \cdot 10^{-6}$
4	127336047	rs12647099	G	A	FAT4	META_GWAS	+++xxx	7,526	3,078	4,448	0.408	0.273	0.505	$7.66 \cdot 10^{-2}$	$1.71 \cdot 10^{-2}$	1.08	-4.481	$7.44 \cdot 10^{-6}$
18	9759714	rs12970907	A	C	RAB31	META_GWAS	+++xxx	7,527	3,077	4,450	0.174	0.15	0.203	$9.56 \cdot 10^{-2}$	$2.15 \cdot 10^{-2}$	1.1	-4.443	$8.89 \cdot 10^{-6}$
10	119233375	rs242967	A	G	EMX2	META_GWAS	+++xxx	7,529	3,079	4,450	0.705	0.625	0.792	$8.03 \cdot 10^{-2}$	$1.81 \cdot 10^{-2}$	1.084	-4.434	$9.27 \cdot 10^{-6}$
9	133552145	rs10751506	G	A	PRDM12	META_GWAS	+++++	9,089	3,912	5,177	0.854	0.691	0.961	$9.65 \cdot 10^{-2}$	$2.19 \cdot 10^{-2}$	1.101	4.413	$1.02 \cdot 10^{-5}$
14	70522684	rs10142899	A	C	SLC8A3	META_GWAS	xxx+++	1,561	834	727	0.449	0.418	0.492	0.159	$3.62 \cdot 10^{-2}$	1.173	-4.408	$1.04 \cdot 10^{-5}$
5	95849216	rs261965	G	A	PCSK1	META_GWAS	xxx+++	1,561	834	727	0.974	0.945	0.999	0.506	0.115	1.658	4.402	$1.07 \cdot 10^{-5}$
7	79678973	rs7778622	A	G	GNAI1	META_GWAS	xxx+++	1,561	834	727	0.445	0.33	0.582	0.159	$3.63 \cdot 10^{-2}$	1.173	4.394	$1.11 \cdot 10^{-5}$
2	209185355	rs10932260	T	C	PIKFYVE	META_GWAS	+++xxx	7,527	3,079	4,448	0.632	0.459	0.84	$7.83 \cdot 10^{-2}$	$1.78 \cdot 10^{-2}$	1.082	4.388	$1.15 \cdot 10^{-5}$
14	21802579	rs17103594	A	T	RPGRI1	META_GWAS	xxx+++	1,561	834	727	$4.04 \cdot 10^{-2}$	$8.86 \cdot 10^{-3}$	$8.18 \cdot 10^{-2}$	0.406	$9.4 \cdot 10^{-2}$	1.501	-4.322	$1.55 \cdot 10^{-5}$
20	60685349	rs6142952	T	G	LSM14B	META_GWAS	xxx+++	1,559	833	726	0.596	0.302	0.832	0.178	$4.12 \cdot 10^{-2}$	1.195	4.317	$1.58 \cdot 10^{-5}$
13	28566951	rs2504240	G	A	URAD	META_GWAS	+++xxx	7,529	3,079	4,450	0.303	0.198	0.416	$7.78 \cdot 10^{-2}$	$1.81 \cdot 10^{-2}$	1.081	-4.294	$1.75 \cdot 10^{-5}$

9.4 Previously identified risk loci

Table 32 shows statistics from the MERGE cohort for 50 loci that were shown to be significantly associated with Body Mass Index in the 2015 Nature paper by Locke 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 10 variants that show at least nominal significance ($p < 0.05$) in this study. Out of the 50 variants in both studies, 35 exhibit the same direction of effect with the known result (binomial test $p = 0.0033$).

Table 32: Top known loci in MERGE model invn Adjusted AGE_ANTHRO+AGE_ANTHRO2+SEX (**bold** variants indicate matching direction of effect)

CHR	POS	ID	EA	OA	N	FREQ _{AVG}	FREQ _{MIN}	FREQ _{MAX}	EFFECT	STDERR	P	DIR	COHORT	GENE _{CLOSEST}	R ²	ID _{KNOWN}	N _{KNOWN}	EFFECT _{KNOWN}	STDERR _{KNOWN}	P _{KNOWN}
16	53803574	rs1558902	A	T	9,027	0.233	9.52 · 10 ⁻²	0.455	7.05 · 10 ⁻²	1.89 · 10 ⁻²	1.96 · 10 ⁻⁴	+++	META_EX	FTO	1	rs1558902	3.22 · 10 ⁵	-8.18 · 10 ⁻²	3.1 · 10 ⁻³	7.51 · 10 ⁻¹⁵³
18	57829135	rs6567160	C	T	7,525	0.193	0.177	0.221	7.29 · 10 ⁻²	2.05 · 10 ⁻²	3.85 · 10 ⁻⁴	+++xxx	META_GWAS	MC4R	1	rs6567160	3.22 · 10 ⁵	5.56 · 10 ⁻²	3.6 · 10 ⁻³	3.93 · 10 ⁻⁵³
2	651105	rs2867110	G	C	1,561	0.21	0.187	0.251	8.58 · 10 ⁻²	4.42 · 10 ⁻²	5.22 · 10 ⁻²	xxxx+++	META_GWAS	TMEM18	1	rs2867110	3.22 · 10 ⁵	5.98 · 10 ⁻²	4 · 10 ⁻³	3.4 · 10 ⁻⁵⁰
18	57766512	rs1539952	G	A	9,079	0.22	0.196	0.247	4.46 · 10 ⁻²	1.79 · 10 ⁻²	1.26 · 10 ⁻²	+++++	META_GWAS	PMAIP1	1	rs1539952	3.22 · 10 ⁵	4.85 · 10 ⁻²	3.6 · 10 ⁻³	1.61 · 10 ⁻⁴²
4	45182527	rs10938397	A	G	9,077	0.334	0.253	0.441	9.54 · 10 ⁻³	1.57 · 10 ⁻²	0.544	---	META_EX	GNPDA2	1	rs10938397	3.22 · 10 ⁵	-4.02 · 10 ⁻²	3.1 · 10 ⁻³	3.21 · 10 ⁻³⁸
1	177889480	rs543874	G	A	9,077	0.218	0.152	0.262	4.23 · 10 ⁻²	1.8 · 10 ⁻²	1.89 · 10 ⁻²	+++	META_EX	SEC16B	1	rs543874	3.22 · 10 ⁵	4.82 · 10 ⁻²	3.9 · 10 ⁻³	2.62 · 10 ⁻³⁵
6	50865820	rs943005	T	C	7,529	0.153	9.03 · 10 ⁻²	0.212	6.1 · 10 ⁻²	2.31 · 10 ⁻²	8.3 · 10 ⁻³	+++xxx	META_GWAS	TFAP2B	1	rs943005	3.22 · 10 ⁵	4.43 · 10 ⁻²	4 · 10 ⁻³	1.39 · 10 ⁻²⁸
11	27684517	rs11030104	A	G	9,079	0.123	4.04 · 10 ⁻²	0.245	5.26 · 10 ⁻³	2.32 · 10 ⁻²	0.82	+++++	META_GWAS	BDNF	1	rs11030104	3.22 · 10 ⁵	4.14 · 10 ⁻²	3.8 · 10 ⁻³	5.56 · 10 ⁻²⁸
1	72751185	rs3101336	C	T	7,520	0.607	0.534	0.684	1.04 · 10 ⁻²	1.66 · 10 ⁻²	0.533	+++xxx	META_GWAS	NEGR1	1	rs3101336	3.22 · 10 ⁵	3.34 · 10 ⁻²	3.1 · 10 ⁻³	2.66 · 10 ⁻²⁶
12	50247468	rs7138803	G	A	9,077	0.246	0.167	0.397	4.07 · 10 ⁻³	1.78 · 10 ⁻²	0.816	+	META_EX	BCDIN3D	1	rs7138803	3.22 · 10 ⁵	-3.15 · 10 ⁻²	4.1 · 10 ⁻³	8.15 · 10 ⁻²⁴
2	25150296	rs10182181	A	G	1,559	0.62	0.468	0.845	1.8 · 10 ⁻²	4.06 · 10 ⁻²	0.659	xxx+	META_GWAS	ADCY3	1	rs10182181	3.22 · 10 ⁵	-3.07 · 10 ⁻²	3.1 · 10 ⁻³	8.78 · 10 ⁻²⁴
16	28667804	rs4788101	T	C	7,528	0.314	0.264	0.363	2.09 · 10 ⁻²	1.77 · 10 ⁻²	0.236	+++xxx	META_GWAS	SH2B1	1	rs4788101	3.22 · 10 ⁵	3.07 · 10 ⁻²	3.1 · 10 ⁻³	4.82 · 10 ⁻²³
16	28855727	rs4788099	T	C	7,528	0.315	0.266	0.363	2.09 · 10 ⁻²	1.77 · 10 ⁻²	0.238	+++xxx	META_GWAS	TUFM	1	rs4788099	3.22 · 10 ⁵	3.05 · 10 ⁻²	3.1 · 10 ⁻³	1.13 · 10 ⁻²²
16	28846668	rs12325113	C	T	7,523	0.205	6.91 · 10 ⁻²	0.321	2.95 · 10 ⁻²	2.14 · 10 ⁻²	0.168	+++xxx	META_GWAS	ATXN2L	1	rs12325113	3.22 · 10 ⁵	3.04 · 10 ⁻²	3.1 · 10 ⁻³	1.26 · 10 ⁻²²
3	185822353	rs10513801	T	G	7,523	7.14 · 10 ⁻²	2.7 · 10 ⁻²	0.132	1.77 · 10 ⁻²	3.23 · 10 ⁻²	0.583	+++xxx	META_GWAS	ETV5	1	rs10513801	3.22 · 10 ⁵	4.48 · 10 ⁻²	4.7 · 10 ⁻³	1.07 · 10 ⁻²¹
11	27578946	rs1013442	A	T	1,561	0.161	6.34 · 10 ⁻²	0.238	3.32 · 10 ⁻²	4.85 · 10 ⁻²	0.494	xxxx+++	META_GWAS	LINC7	1	rs1013442	3.22 · 10 ⁵	-3.32 · 10 ⁻²	3.6 · 10 ⁻³	3.36 · 10 ⁻²⁰
19	46202172	rs2287019	C	T	9,079	0.149	0.114	0.223	5.42 · 10 ⁻²	2.1 · 10 ⁻²	1 · 10 ⁻²	+++	META_EX	QPCTL	1	rs2287019	3.22 · 10 ⁵	3.6 · 10 ⁻²	4.2 · 10 ⁻³	4.59 · 10 ⁻¹⁸
16	19944363	rs11639988	G	A	1,562	0.183	0.143	0.248	2.16 · 10 ⁻²	4.62 · 10 ⁻²	0.641	xxx+++	META_GWAS	GPRC5B	1	rs11639988	3.22 · 10 ⁵	-3.97 · 10 ⁻²	4.6 · 10 ⁻³	5.36 · 10 ⁻¹⁸
19	46180184	rs11672660	C	T	7,528	0.152	0.111	0.239	5.46 · 10 ⁻²	2.31 · 10 ⁻²	1.8 · 10 ⁻²	+++---	META_GWAS	GIPR	1	rs11672660	3.22 · 10 ⁵	3.45 · 10 ⁻²	4 · 10 ⁻³	8.49 · 10 ⁻¹⁸
16	28490517	rs151181	C	T	9,077	0.262	0.158	0.336	1.23 · 10 ⁻²	1.74 · 10 ⁻²	0.478	+	META_EX	CLN3	1	rs151181	3.22 · 10 ⁵	2.69 · 10 ⁻²	3.1 · 10 ⁻³	8.51 · 10 ⁻¹⁸
16	28543381	rs12446550	A	G	9,077	0.311	0.236	0.372	2.88 · 10 ⁻²	1.78 · 10 ⁻²	0.106	+++xxx	META_GWAS	NUPR1	1	rs12446550	3.22 · 10 ⁵	2.6 · 10 ⁻²	3.1 · 10 ⁻³	1.46 · 10 ⁻¹⁷
15	68086638	rs2241423	G	A	9,078	0.342	0.277	0.374	1.86 · 10 ⁻²	1.58 · 10 ⁻²	0.237	+++	META_EX	MAP2K5	1	rs2241423	3.22 · 10 ⁵	3.1 · 10 ⁻²	3.7 · 10 ⁻³	2.37 · 10 ⁻¹⁷
12	50251910	rs4898539	T	G	1,562	0.734	0.63	0.784	2.75 · 10 ⁻²	4.04 · 10 ⁻²	0.496	xxxx+++	META_GWAS	FAIM2	1	rs4898539	3.22 · 10 ⁵	2.76 · 10 ⁻²	3.3 · 10 ⁻³	3.26 · 10 ⁻¹⁷
11	47650993	rs3817334	T	C	9,078	0.329	0.256	0.398	4.01 · 10 ⁻²	1.58 · 10 ⁻²	1.09 · 10 ⁻²	+++	META_EX	MTCH2	1	rs3817334	3.22 · 10 ⁵	2.62 · 10 ⁻²	3.1 · 10 ⁻³	5.15 · 10 ⁻¹⁷
5	75015242	rs2112347	T	G	9,075	0.437	0.379	0.509	2.48 · 10 ⁻²	1.51 · 10 ⁻²	0.101	+++	META_EX	POC5	1	rs2112347	3.22 · 10 ⁵	2.61 · 10 ⁻²	3.1 · 10 ⁻³	6.19 · 10 ⁻¹⁷
12	50223013	rs11169170	T	C	1,562	0.354	0.291	0.449	3.9 · 10 ⁻³	3.85 · 10 ⁻²	0.919	xxx+	META_GWAS	NCKAP5L	1	rs11169170	3.22 · 10 ⁵	2.54 · 10 ⁻²	3 · 10 ⁻³	6.35 · 10 ⁻¹⁷
16	28898793	rs6565259	C	T	7,529	0.437	0.301	0.515	4.64 · 10 ⁻³	1.67 · 10 ⁻²	0.781	+++xxx	META_GWAS	ATP2A1	1	rs6565259	3.22 · 10 ⁵	2.69 · 10 ⁻²	3.2 · 10 ⁻³	8.11 · 10 ⁻¹⁷
16	28631585	rs1968752	G	T	1,558	0.587	0.49	0.683	2.4 · 10 ⁻²	3.62 · 10 ⁻²	0.507	xxxx+	META_GWAS	SULT1A1	1	rs1968752	3.22 · 10 ⁵	-2.72 · 10 ⁻²	3.3 · 10 ⁻³	9.06 · 10 ⁻¹⁷
11	47529947	rs7124681	A	C	7,527	0.331	0.259	0.393	4.94 · 10 ⁻²	1.74 · 10 ⁻²	4.61 · 10 ⁻³	+++xxx	META_GWAS	CELF1	1	rs7124681	3.22 · 10 ⁵	2.59 · 10 ⁻²	3.1 · 10 ⁻³	1.16 · 10 ⁻¹⁶
15	68114974	rs4776982	A	G	9,091	0.323	0.254	0.345	1.31 · 10 ⁻²	1.59 · 10 ⁻²	0.408	+++++	META_GWAS	SKOR1	1	rs4776982	3.22 · 10 ⁵	3.11 · 10 ⁻²	3.8 · 10 ⁻³	2.61 · 10 ⁻¹⁶
16	28959700	rs17640009	G	A	7,528	0.287	0.235	0.329	3.29 · 10 ⁻²	1.81 · 10 ⁻²	6.91 · 10 ⁻²	+++xxx	META_GWAS	SFG29	1	rs17640009	3.22 · 10 ⁵	2.53 · 10 ⁻²	3.1 · 10 ⁻³	5.46 · 10 ⁻¹⁶
16	28922149	rs11646653	C	T	9,089	0.707	0.659	0.745	7.58 · 10 ⁻³	1.64 · 10 ⁻²	0.643	+++xx	META_GWAS	RABEP2	1	rs11646653	3.22 · 10 ⁵	2.68 · 10 ⁻²	3.3 · 10 ⁻³	5.57 · 10 ⁻¹⁶
2	25158008	rs713586	T	C	1,560	0.634	0.482	0.861	2.74 · 10 ⁻²	4.11 · 10 ⁻²	0.505	xxx++	META_GWAS	DNAJC27	1	rs713586	3.22 · 10 ⁵	-3.02 · 10 ⁻²	3.8 · 10 ⁻³	1.91 · 10 ⁻¹⁵
17	47569003	rs3810291	A	G	9,074	0.382	0.178	0.658	1.25 · 10 ⁻²	1.65 · 10 ⁻²	0.449	+++	META_EX	ZC3H4	1	rs3810291	3.22 · 10 ⁵	2.83 · 10 ⁻²	3.6 · 10 ⁻³	4.81 · 10 ⁻¹⁵
3	185847441	rs16860471	T	G	9,090	0.133	0.12	0.156	7.39 · 10 ⁻³	2.2 · 10 ⁻²	0.737	+++++	META_GWAS	DGKG	1	rs16860471	3.22 · 10 ⁵	-3.7 · 10 ⁻²	4.7 · 10 ⁻³	5.86 · 10 ⁻¹⁵
1	74995225	rs7551507	T	C	1,562	0.354	0.142	0.565	2.71 · 10 ⁻²	4.04 · 10 ⁻²	0.502	xxx++	META_GWAS	FPGT-TNNI3K	1	rs7551507	3.22 · 10 ⁵	-2.41 · 10 ⁻²	3.1 · 10 ⁻³	8.86 · 10 ⁻¹⁵
14	79899454	rs7141420	C	T	9,090	0.593	0.53	0.623	1.57 · 10 ⁻²	1.52 · 10 ⁻²	0.918	+++++	META_GWAS	NRXN3	1	rs7141420	3.22 · 10 ⁵	-2.35 · 10 ⁻²	3.1 · 10 ⁻³	1.23 · 10 ⁻¹⁴
3	85820181	rs13098327	A	G	1,558	0.139	5.52 · 10 ⁻²	0.246	4.18 · 10 ⁻²	5.21 · 10 ⁻²	0.422	xxx++	META_GWAS	CADM2	1	rs13098327	3.22 · 10 ⁵	2.95 · 10 ⁻²	3.9 · 10 ⁻³	2.53 · 10 ⁻¹⁴
5	74956517	rs253414	T	C	9,091	0.524	0.402	0.635	1.22 · 10 ⁻²	1.51 · 10 ⁻²	0.421	+++++	META_GWAS	ANKDD1B	1	rs253414	3.22 · 10 ⁵	2.68 · 10 ⁻²	3.5 · 10 ⁻³	2.86 · 10 ⁻¹⁴
11	47624714	rs12419692	A	C	1,560	0.227	8.73 · 10 ⁻²	0.343	2.05 · 10 ⁻²	4.23 · 10 ⁻²	0.628	xxx++	META_GWAS	C1QTNF4	1	rs12419692	3.22 · 10 ⁵	2.37 · 10 ⁻²	3.2 · 10 ⁻³	6.12 · 10 ⁻¹⁴
9	28414339	rs10968576	G	A	9,079	0.217	0.168	0.276	1.18 · 10 ⁻²	1.79 · 10 ⁻²	0.511	---	META_EX	LINGO2	1	rs10968576	3.22 · 10 ⁵	2.49 · 10 ⁻²	3.3 · 10 ⁻³	6.61 · 10 ⁻¹⁴
1	110154688	rs17024393	T	C	7,522	5.48 · 10 ⁻²	1.77 · 10 ⁻²	9.34 · 10 ⁻²	8.78 · 10 ⁻³	3.6 · 10 ⁻²	0.807	+++xxx	META_GWAS	GNAT2	1	rs17024393	3.22 · 10 ⁵	-6.58 · 10 ⁻²	8.8 · 10 ⁻³	7.03 · 10 ⁻¹⁴
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