

AMP-DCC Data Analysis Report

METSIM

Phase 2

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Prepared by: Ryan Koesterer and Maria Costanzo on behalf of Broad Institute

Contact: AMP-DCC Analysis Team (amp-dcc-dat@broadinstitute.org)

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

Contents

1 Data	3
2 Strategy	5
2.1 Sample structure and pipeline	5
2.1.1 Cohort-level analysis	5
2.1.2 Merged results	5
2.2 Ancestry Adjustment and Outlier Removal	5
3 Serum Creatinine (SERUM_CREATININE)	7
3.1 Summary	7
3.2 Calibration	8
3.3 Top associations	9
3.4 Previously identified risk loci	9
4 Systolic Blood Pressure (SBP15)	10
4.1 Summary	10
4.2 Calibration	11
4.3 Top associations	12
4.4 Previously identified risk loci	12

5 HDL Cholesterol (HDL)	14
5.1 Summary	14
5.2 Calibration	15
5.3 Top associations	16
5.4 Previously identified risk loci	17
6 Estimated Glomerular Filtration Rate (eGFR)	19
6.1 Summary	19
6.2 Calibration	20
6.3 Top associations	21
6.4 Previously identified risk loci	21
7 Diastolic Blood Pressure (DBP10)	23
7.1 Summary	23
7.2 Calibration	24
7.3 Top associations	25
7.4 Previously identified risk loci	25
8 LDL Cholesterol (LDL_DIRECT)	27
8.1 Summary	27
8.2 Calibration	28
8.3 Top associations	29
8.4 Previously identified risk loci	31
9 Body Mass Index (BMI)	33
9.1 Summary	33
9.2 Calibration	34
9.3 Top associations	35
9.4 Previously identified risk loci	35
10 Acknowledgements	37
11 References	38

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, and OMNI. 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	metsim_exomechip_portal	bfile	N/A
OMNI	metsim_omniexpress_portal	bfile	N/A

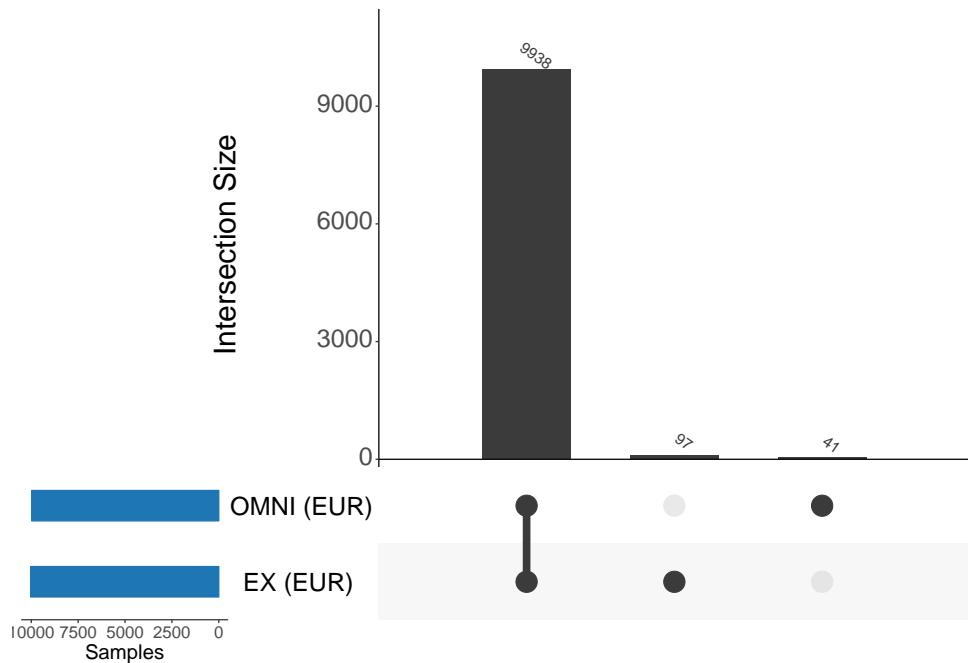


Figure 1: Samples remaining for analysis after quality control

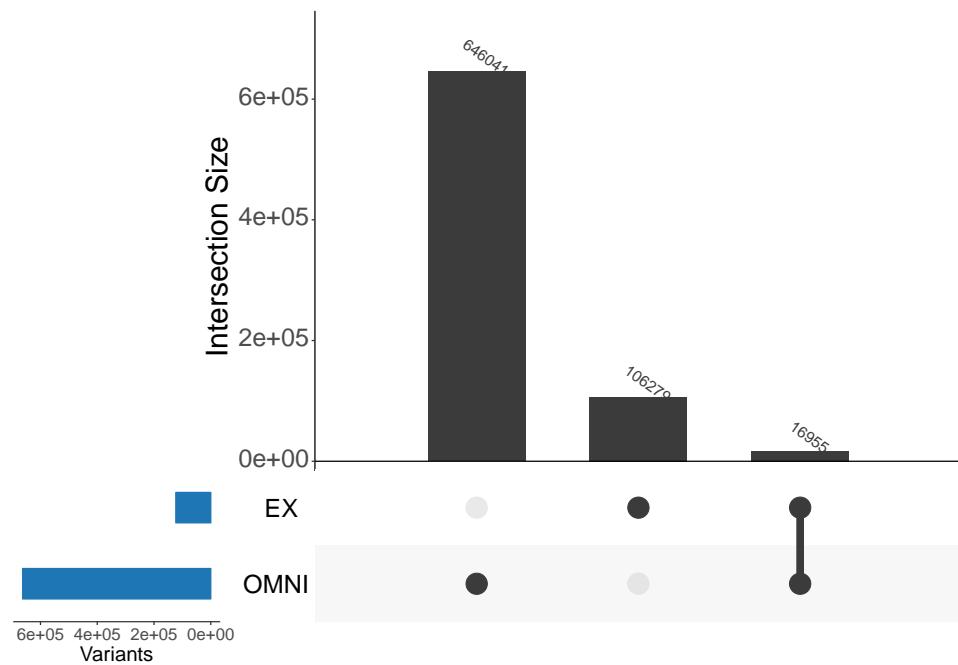


Figure 2: Variants remaining for analysis after quality control

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
OMNI_EUR	OMNI	EUR	NO

2.1.2 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 3 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 3: Merged results

ID	Cohorts/Metas	Report
MERGE	EX_EUR>OMNI_EUR	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

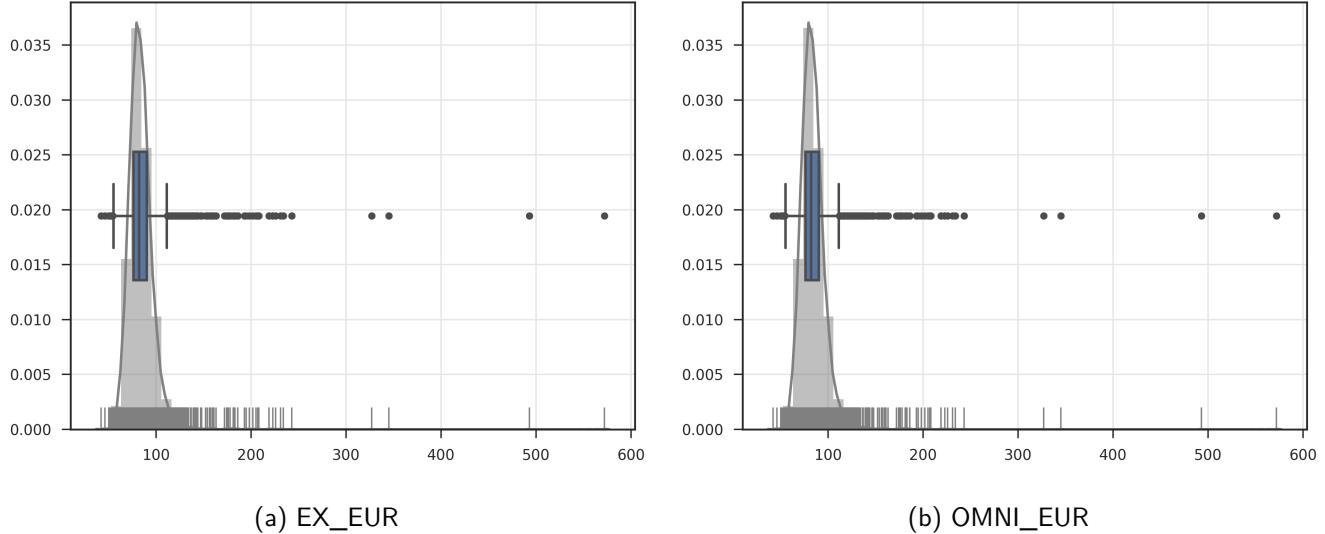


Figure 3: Distribution of SERUM_CREATININE in cohort-level analyses

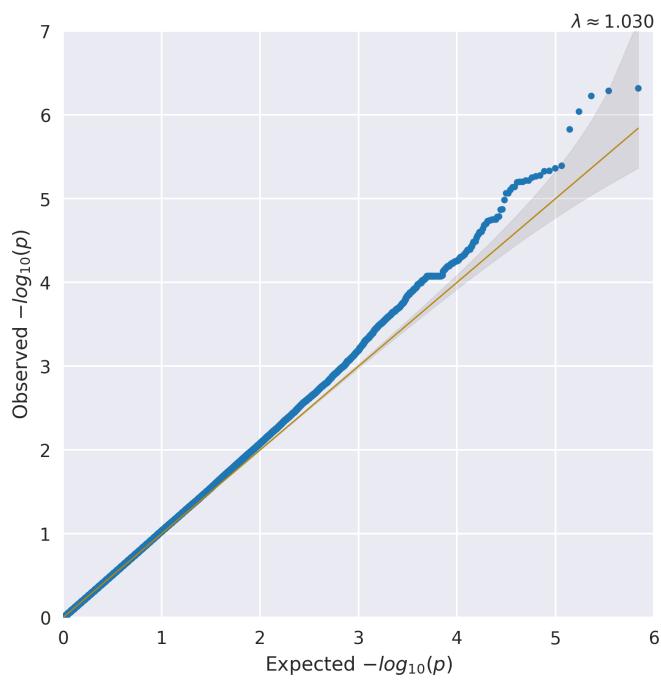
Table 4: Summary of samples removed from Serum Creatinine analysis by cohort and model

Cohort	Array	Ancestry	Trans	Covars	Total	-SampleQc	-missObs	-Kinship	-PcOutlier
EX_EUR	EX	EUR	invn	Age	10071	36	0	1518	1
OMNI_EUR	OMNI	EUR	invn	Age	10048	69	0	1497	1

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

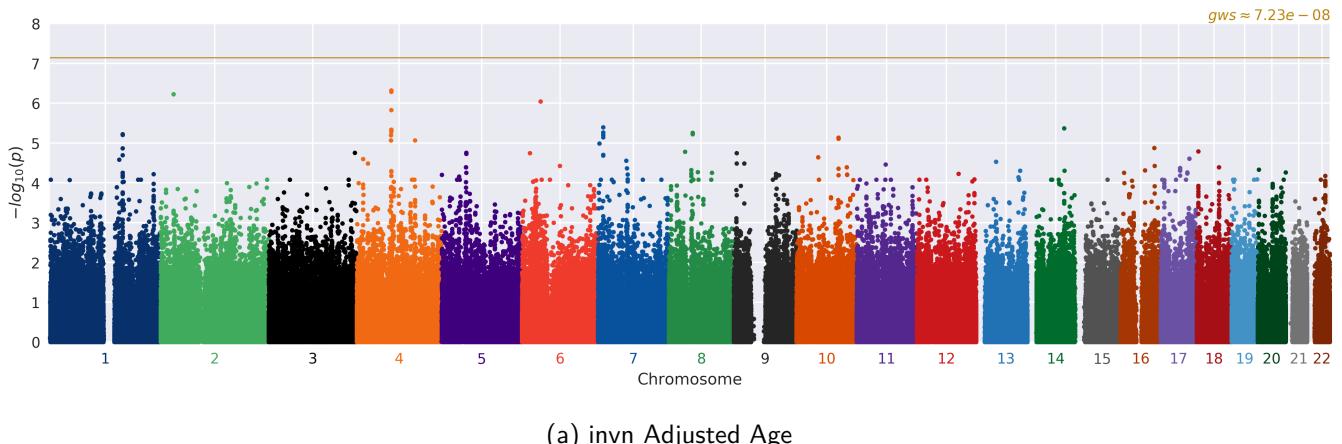
Cohort	Array	Ancestry	Trans	Covars	PCs	N	Male	Female	Max	Min	μ	\tilde{x}	σ
EX_EUR	EX	EUR	invn	Age	2	8516	8516	0	572.0	42.0	83.902	82.0	15.138
OMNI_EUR	OMNI	EUR	invn	Age	10	8481	8481	0	572.0	42.0	83.921	83.0	14.728

3.2 Calibration



(a) invn Adjusted Age

Figure 4: QQ plots for SERUM_CREATININE in the MERGE analysis



(a) invn Adjusted Age

Figure 5: Manhattan plots for SERUM_CREATININE in the MERGE analysis

3.3 Top associations

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

CHR	POS	ID	EA	OA	GENE _{CLOSEST}	COHORT	N	MALE	FEMALE	MAC	FREQ	EFFECT	STDERR	P
4	77398015	rs10032549	G	A	SHROOM3	OMNI_EUR	8,471	8,471	0	8,037	0.474	$7.74 \cdot 10^{-2}$	$1.54 \cdot 10^{-2}$	$4.8 \cdot 10^{-7}$
2	29268375	rs2276551	A	C	FAM179A	OMNI_EUR	8,479	8,479	0	1,596	$9.41 \cdot 10^{-2}$	0.13	$2.61 \cdot 10^{-2}$	$5.92 \cdot 10^{-7}$
6	42084146	rs10456507	A	C	C6orf132	OMNI_EUR	8,480	8,480	0	1,098	$6.47 \cdot 10^{-2}$	0.154	$3.14 \cdot 10^{-2}$	$9.07 \cdot 10^{-7}$
7	11581003	rs2072139	G	A	THSD7A	OMNI_EUR	8,478	8,478	0	2,566	0.151	$9.87 \cdot 10^{-2}$	$2.14 \cdot 10^{-2}$	$4.01 \cdot 10^{-6}$
14	82510077	rs2217448	T	C	SEL1L	OMNI_EUR	8,478	8,478	0	2,037	0.12	0.108	$2.36 \cdot 10^{-2}$	$4.31 \cdot 10^{-6}$
8	53355822	rs17228239	A	G	ST18	OMNI_EUR	8,480	8,480	0	8,376	0.506	$6.96 \cdot 10^{-2}$	$1.53 \cdot 10^{-2}$	$5.55 \cdot 10^{-6}$
1	163744838	rs10799961	G	A	NUF2	OMNI_EUR	8,480	8,480	0	6,725	0.603	$7.06 \cdot 10^{-2}$	$1.56 \cdot 10^{-2}$	$6.03 \cdot 10^{-6}$
4	77269262	rs10002448	A	G	CCDC158	OMNI_EUR	8,437	8,437	0	6,709	0.602	$7.11 \cdot 10^{-2}$	$1.57 \cdot 10^{-2}$	$6.32 \cdot 10^{-6}$
10	94517064	rs11187167	C	T	HHEX	OMNI_EUR	8,467	8,467	0	2,985	0.176	$9.03 \cdot 10^{-2}$	$2.01 \cdot 10^{-2}$	$7.28 \cdot 10^{-6}$
10	94538960	rs2497338	T	C	EXOC6	OMNI_EUR	8,481	8,481	0	3,664	0.784	$8.32 \cdot 10^{-2}$	$1.86 \cdot 10^{-2}$	$7.85 \cdot 10^{-6}$
4	130824678	rs3111741	G	A	C4orf33	OMNI_EUR	8,481	8,481	0	4,295	0.747	$7.8 \cdot 10^{-2}$	$1.75 \cdot 10^{-2}$	$8.53 \cdot 10^{-6}$
4	77228724	rs3796491	C	A	STBD1	OMNI_EUR	8,395	8,395	0	6,673	0.603	$6.99 \cdot 10^{-2}$	$1.57 \cdot 10^{-2}$	$8.58 \cdot 10^{-6}$
7	3060397	rs10950998	A	G	CARD11	OMNI_EUR	8,481	8,481	0	8,047	0.526	$6.79 \cdot 10^{-2}$	$1.54 \cdot 10^{-2}$	$1.03 \cdot 10^{-5}$
16	76021509	rs8055817	A	G	AC025287	OMNI_EUR	8,373	8,373	0	5,227	0.688	$7.19 \cdot 10^{-2}$	$1.65 \cdot 10^{-2}$	$1.33 \cdot 10^{-5}$
18	3655393	rs1675240	G	A	DLGAP1	OMNI_EUR	8,479	8,479	0	6,693	0.395	$6.81 \cdot 10^{-2}$	$1.58 \cdot 10^{-2}$	$1.63 \cdot 10^{-5}$
8	36995874	rs543946	T	C	KCNU1	OMNI_EUR	8,476	8,476	0	543	0.968	0.187	$4.34 \cdot 10^{-2}$	$1.65 \cdot 10^{-5}$
3	193811162	rs10933711	C	T	HES1	OMNI_EUR	8,480	8,480	0	6,161	0.363	$6.86 \cdot 10^{-2}$	$1.6 \cdot 10^{-2}$	$1.76 \cdot 10^{-5}$
5	55509576	rs16885032	C	T	ANKRD55	OMNI_EUR	8,481	8,481	0	561	$3.31 \cdot 10^{-2}$	0.184	$4.28 \cdot 10^{-2}$	$1.76 \cdot 10^{-5}$
6	18143854	rs17839843	G	A	TPMT	OMNI_EUR	8,478	8,478	0	22	$1.3 \cdot 10^{-3}$	0.914	0.213	$1.78 \cdot 10^{-5}$
9	6533092	rs138640017	G	C	GLDC	EX_EUR	8,516	8,516	0	153	$8.98 \cdot 10^{-3}$	0.349	$8.13 \cdot 10^{-2}$	$1.8 \cdot 10^{-5}$

3.4 Previously identified risk loci

Table 7 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 9 variants that show at least nominal significance ($p < 0.05$) in this study. Out of the 10 variants in both studies, 10 exhibit the same direction of effect with the known result (binomial test $p = 0.000977$).

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

CHR	POS	ID	EA	OA	N	FREQ	EFFECT	STDERR	P	COHORT	GENE _{CLOSEST}	R ²	ID _{KNOWN}	N _{KNOWN}	EFFECT _{KNOWN}	STDERR _{KNOWN}	P _{KNOWN}
15	45641225	rs2453533	A	C	8,515	0.583	$4.33 \cdot 10^{-2}$	$1.54 \cdot 10^{-2}$	$4.93 \cdot 10^{-3}$	EX_EUR	GATM	1	rs2453533	24,925	$7.37 \cdot 10^{-2}$	$9.39 \cdot 10^{-3}$	$5.03 \cdot 10^{-15}$
15	45695695	rs1153849	A	G	8,481	0.69	$4.3 \cdot 10^{-2}$	$1.65 \cdot 10^{-2}$	$9.2 \cdot 10^{-3}$	OMNI_EUR	SPATA5L1	1	rs1153849	24,925	$8.02 \cdot 10^{-2}$	$1.03 \cdot 10^{-2}$	$9.14 \cdot 10^{-15}$
17	59456589	rs9895661	C	T	8,517	0.196	$7.73 \cdot 10^{-2}$	$1.94 \cdot 10^{-2}$	$6.75 \cdot 10^{-5}$	EX_EUR	BCAS3	1	rs9895661	24,925	$8.79 \cdot 10^{-2}$	$1.23 \cdot 10^{-2}$	$8.25 \cdot 10^{-13}$
15	45729123	rs1974981	G	A	8,479	0.679	$3.48 \cdot 10^{-2}$	$1.64 \cdot 10^{-2}$	$3.42 \cdot 10^{-2}$	OMNI_EUR	C15orf48	1	rs1974981	24,925	$7.03 \cdot 10^{-2}$	$1.03 \cdot 10^{-2}$	$9.04 \cdot 10^{-12}$
7	151415041	rs10224002	G	A	8,515	0.775	$6.66 \cdot 10^{-2}$	$1.84 \cdot 10^{-2}$	$2.86 \cdot 10^{-4}$	EX_EUR	PRKAG2	1	rs10224002	24,925	$7.07 \cdot 10^{-2}$	$1.11 \cdot 10^{-2}$	$1.89 \cdot 10^{-10}$
15	45577783	rs1719236	C	A	8,480	0.403	$2.42 \cdot 10^{-2}$	$1.56 \cdot 10^{-2}$	0.12	OMNI_EUR	SLC28A2	1	rs1719236	24,925	$5.86 \cdot 10^{-2}$	$9.54 \cdot 10^{-3}$	$8.74 \cdot 10^{-10}$
4	77368847	rs17319721	A	G	8,517	0.599	$7.07 \cdot 10^{-2}$	$1.56 \cdot 10^{-2}$	$6.17 \cdot 10^{-6}$	EX_EUR	SHROOM3	1	rs17319721	24,925	$5.71 \cdot 10^{-2}$	$9.31 \cdot 10^{-3}$	$9.1 \cdot 10^{-10}$
6	160693107	rs3119311	C	T	8,479	0.893	$5.14 \cdot 10^{-2}$	$2.48 \cdot 10^{-2}$	$3.81 \cdot 10^{-2}$	OMNI_EUR	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	8,517	0.274	$4.59 \cdot 10^{-2}$	$1.72 \cdot 10^{-2}$	$7.52 \cdot 10^{-3}$	EX_EUR	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	8,475	0.521	$3.24 \cdot 10^{-2}$	$1.54 \cdot 10^{-2}$	$3.49 \cdot 10^{-2}$	OMNI_EUR	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

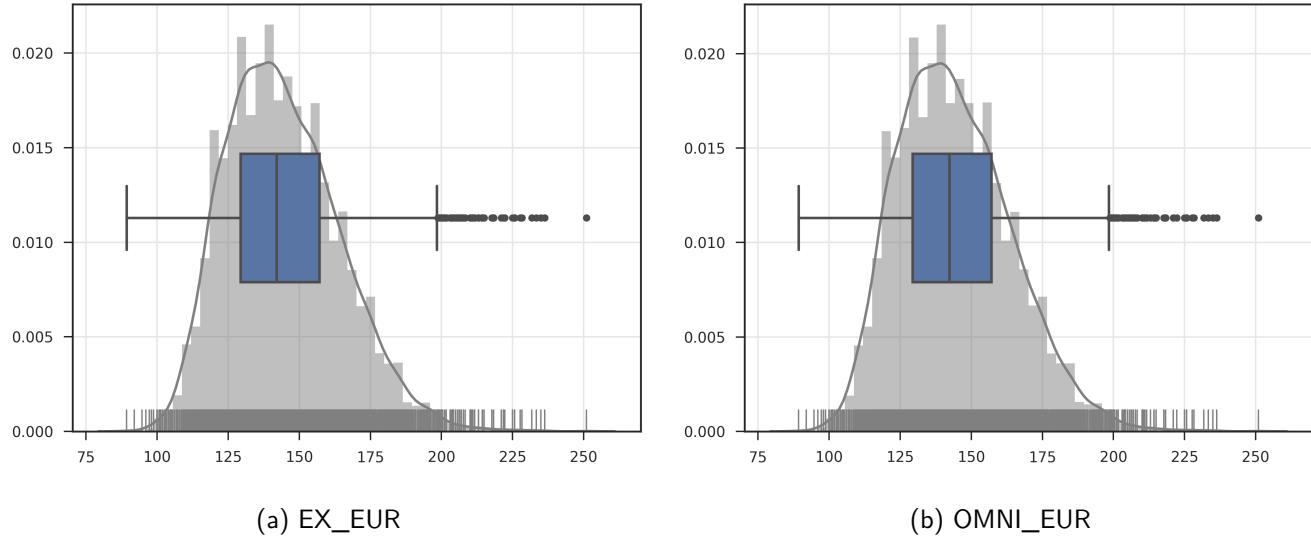


Figure 6: Distribution of SBP15 in cohort-level analyses

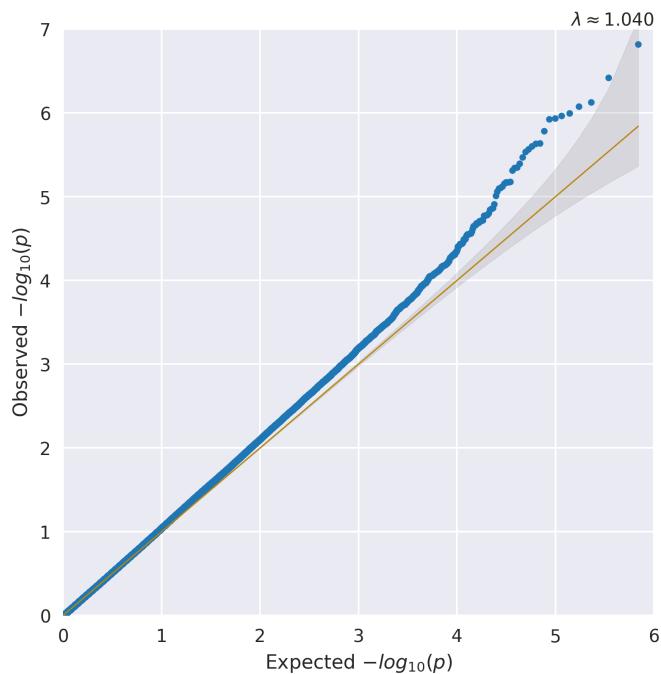
Table 8: Summary of samples removed from Systolic Blood Pressure analysis by cohort and model

Cohort	Array	Ancestry	Trans	Covars	Total	-SampleQc	-missObs	-Kinship	-PcOutlier
EX_EUR	EX	EUR	invn	Age+Age2+BMI	10071	36	5	1514	2
OMNI_EUR	OMNI	EUR	invn	Age+Age2+BMI	10048	69	5	1494	1

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

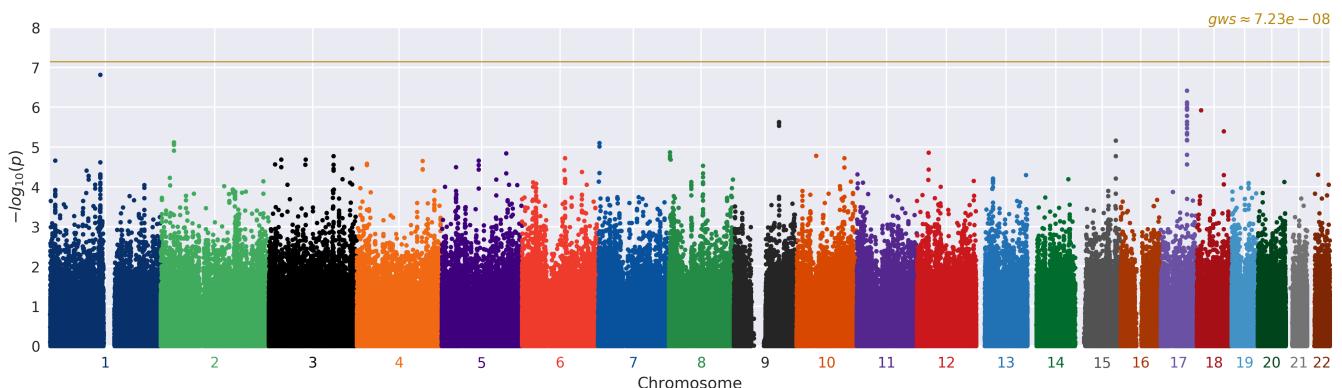
Cohort	Array	Ancestry	Trans	Covars	PCs	N	Male	Female	Max	Min	μ	\bar{x}	σ
EX_EUR	EX	EUR	invn	Age+Age2+BMI	10	8514	8514	0	251.0	89.3	144.242	142.3	19.909
OMNI_EUR	OMNI	EUR	invn	Age+Age2+BMI	8	8479	8479	0	251.0	89.3	144.263	142.3	19.903

4.2 Calibration



(a) invn Adjusted Age+Age2+BMI

Figure 7: QQ plots for SBP15 in the MERGE analysis



(a) invn Adjusted Age+Age2+BMI

Figure 8: Manhattan plots for SBP15 in the MERGE analysis

4.3 Top associations

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

CHR	POS	ID	EA	OA	GENE _{CLOSEST}	COHORT	N	MALE	FEMALE	MAC	FREQ	EFFECT	STDERR	P
1	113161350	rs11102516	A	G	ST7L	OMNI_EUR	8,479	8,479	0	3,480	0.205	$9.93 \cdot 10^{-2}$	$1.89 \cdot 10^{-2}$	$1.52 \cdot 10^{-7}$
17	59255231	rs917571	A	G	BCAS3	OMNI_EUR	8,478	8,478	0	3,255	0.808	$9.86 \cdot 10^{-2}$	$1.94 \cdot 10^{-2}$	$3.81 \cdot 10^{-7}$
18	9958623	rs29092	C	A	VAPA	OMNI_EUR	8,478	8,478	0	43	$2.54 \cdot 10^{-3}$	0.742	0.153	$1.19 \cdot 10^{-6}$
9	101619403	rs7864581	G	A	GALNT12	OMNI_EUR	8,478	8,478	0	4,745	0.72	$8 \cdot 10^{-2}$	$1.69 \cdot 10^{-2}$	$2.33 \cdot 10^{-6}$
18	60661358	rs7238945	G	T	PHLPP1	OMNI_EUR	8,374	8,374	0	1,862	0.111	0.114	$2.47 \cdot 10^{-2}$	$4.03 \cdot 10^{-6}$
15	91404788	rs4932371	C	T	FURIN	OMNI_EUR	8,393	8,393	0	4,748	0.283	$7.79 \cdot 10^{-2}$	$1.73 \cdot 10^{-2}$	$6.95 \cdot 10^{-6}$
2	29575197	rs6716914	T	G	ALK	OMNI_EUR	8,475	8,475	0	1,824	0.892	0.113	$2.51 \cdot 10^{-2}$	$7.59 \cdot 10^{-6}$
7	2920067	rs17132769	C	T	CARD11	OMNI_EUR	8,479	8,479	0	2,032	0.12	0.105	$2.35 \cdot 10^{-2}$	$7.96 \cdot 10^{-6}$
8	2304723	rs13259957	G	A	MYOM2	OMNI_EUR	8,479	8,479	0	688	$4.06 \cdot 10^{-2}$	0.17	$3.91 \cdot 10^{-2}$	$1.36 \cdot 10^{-5}$
12	26344726	rs1480036	C	T	SSPN	OMNI_EUR	8,477	8,477	0	4,723	0.721	$7.44 \cdot 10^{-2}$	$1.71 \cdot 10^{-2}$	$1.4 \cdot 10^{-5}$
5	144939151	rs17103387	C	T	PRELID2	OMNI_EUR	8,470	8,470	0	1,528	$9.02 \cdot 10^{-2}$	0.117	$2.69 \cdot 10^{-2}$	$1.43 \cdot 10^{-5}$
10	43747330	rs12244413	T	G	RASGEF1A	OMNI_EUR	8,476	8,476	0	1,144	$6.75 \cdot 10^{-2}$	0.132	$3.06 \cdot 10^{-2}$	$1.65 \cdot 10^{-5}$
3	145477425	rs16857193	C	T	AC107021	OMNI_EUR	8,477	8,477	0	1,200	$7.08 \cdot 10^{-2}$	0.129	$3 \cdot 10^{-2}$	$1.68 \cdot 10^{-5}$
6	96999725	rs1127175	T	C	UFL1	OMNI_EUR	8,476	8,476	0	5,616	0.331	$7 \cdot 10^{-2}$	$1.64 \cdot 10^{-2}$	$1.91 \cdot 10^{-5}$
10	107526521	rs4437963	T	C	SORCS3	OMNI_EUR	8,477	8,477	0	2,252	0.867	$9.67 \cdot 10^{-2}$	$2.26 \cdot 10^{-2}$	$1.92 \cdot 10^{-5}$
3	82701950	rs936035	C	A	GBE1	OMNI_EUR	8,467	8,467	0	3,764	0.778	$7.81 \cdot 10^{-2}$	$1.83 \cdot 10^{-2}$	$2.05 \cdot 10^{-5}$
8	3896853	rs12677236	T	C	CSMD1	OMNI_EUR	8,475	8,475	0	3,560	0.21	$7.96 \cdot 10^{-2}$	$1.87 \cdot 10^{-2}$	$2.07 \cdot 10^{-5}$
3	27652096	rs11710219	T	C	EOMES	OMNI_EUR	8,479	8,479	0	5,783	0.659	$6.93 \cdot 10^{-2}$	$1.63 \cdot 10^{-2}$	$2.08 \cdot 10^{-5}$
5	83329010	rs1428925	C	T	EDIL3	OMNI_EUR	8,476	8,476	0	573	$3.38 \cdot 10^{-2}$	0.182	$4.28 \cdot 10^{-2}$	$2.18 \cdot 10^{-5}$
1	12194451	rs1148472	C	T	TNFRSF8	OMNI_EUR	8,475	8,475	0	5,770	0.66	$6.92 \cdot 10^{-2}$	$1.63 \cdot 10^{-2}$	$2.21 \cdot 10^{-5}$

4.4 Previously identified risk loci

Table 11 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 10 variants that show at least nominal significance ($p < 0.05$) in this study. Out of the 20 variants in both studies, 11 exhibit the same direction of effect with the known result (binomial test $p = 0.412$).

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

CHR	POS	ID	EA	OA	N	FREQ	EFFECT	STDERR	P	COHORT	GENE_CLOSEST	R ²	ID_KNOWN	N_KNOWN	EFFECT_KNOWN	STDERR_KNOWN	P_KNOWN
12	90060586	rs17249754	G	A	8,512	0.923	6.46 · 10 ⁻²	2.9 · 10 ⁻²	2.61 · 10 ⁻²	EX_EUR	ATP2B1	1	rs17249754	2 · 10 ⁵	0.955	0.134	9.73 · 10 ⁻¹³
1	11862778	rs17367504	A	G	8,512	0.832	7.31 · 10 ⁻²	2.04 · 10 ⁻²	3.46 · 10 ⁻⁴	EX_EUR	MTHFR	1	rs17367504	2 · 10 ⁵	-0.861	0.136	2.11 · 10 ⁻¹⁰
1	11883731	rs12567136	C	T	8,479	0.832	7.65 · 10 ⁻²	2.05 · 10 ⁻²	1.92 · 10 ⁻⁴	OMNI_EUR	CLCN6	1	rs12567136	2 · 10 ⁵	-0.847	0.135	3.41 · 10 ⁻¹⁰
15	75077367	rs1378942	C	A	8,512	0.447	5.15 · 10 ⁻²	1.55 · 10 ⁻²	8.89 · 10 ⁻⁴	EX_EUR	CSK	1	rs1378942	2 · 10 ⁵	0.632	0.101	3.43 · 10 ⁻¹⁰
10	104846178	rs11191548	T	C	8,506	0.925	5.36 · 10 ⁻²	2.93 · 10 ⁻²	6.73 · 10 ⁻²	EX_EUR	CNNM2	1	rs11191548	2 · 10 ⁵	1.083	0.174	5.03 · 10 ⁻¹⁰
10	104594507	rs1004467	A	G	8,512	0.91	1.6 · 10 ⁻²	2.71 · 10 ⁻²	0.555	EX_EUR	CYP17A1	1	rs1004467	2 · 10 ⁵	-1.01	0.164	6.61 · 10 ⁻¹⁰
10	104906211	rs11191580	T	C	8,512	0.924	5.14 · 10 ⁻²	2.93 · 10 ⁻²	7.91 · 10 ⁻²	EX_EUR	NTSC2	1	rs11191580	2 · 10 ⁵	1.058	0.173	9.16 · 10 ⁻¹⁰
12	112007756	rs653178	C	T	8,512	0.398	3.9 · 10 ⁻²	1.55 · 10 ⁻²	1.19 · 10 ⁻²	EX_EUR	ATXN2	1	rs653178	2 · 10 ⁵	-0.605	9.88 · 10 ⁻²	9.3 · 10 ⁻¹⁰
12	89942390	rs11105328	A	G	8,479	0.927	5.94 · 10 ⁻²	2.94 · 10 ⁻²	4.33 · 10 ⁻²	OMNI_EUR	POC1B-GALNT4	1	rs11105328	2 · 10 ⁵	-0.838	0.137	1.08 · 10 ⁻⁹
10	104660004	rs11191454	A	G	8,512	0.923	3.77 · 10 ⁻²	2.9 · 10 ⁻²	0.194	EX_EUR	BORCS7-ASMT	1	rs11191454	2 · 10 ⁵	-1.043	0.171	1.12 · 10 ⁻⁹
12	111884608	rs3184504	T	C	8,511	0.388	3.92 · 10 ⁻²	1.56 · 10 ⁻²	1.18 · 10 ⁻²	EX_EUR	SH2B3	1	rs3184504	2 · 10 ⁵	0.598	9.93 · 10 ⁻²	1.69 · 10 ⁻⁹
4	81164723	rs1458038	T	C	8,478	0.692	7.54 · 10 ⁻³	1.65 · 10 ⁻²	0.647	OMNI_EUR	FGF5	1	rs1458038	2 · 10 ⁵	0.662	0.111	2.12 · 10 ⁻⁹
11	16902266	rs381815	T	C	8,439	0.767	2.67 · 10 ⁻²	1.82 · 10 ⁻²	0.142	OMNI_EUR	PLEKHA7	1	rs381815	2 · 10 ⁵	0.655	0.11	2.45 · 10 ⁻⁹
10	104546284	rs486955	T	C	8,479	0.111	4.82 · 10 ⁻³	2.47 · 10 ⁻²	0.845	OMNI_EUR	WBP1L	1	rs486955	2 · 10 ⁵	0.895	0.156	9.47 · 10 ⁻⁹
12	112072424	rs11065987	G	A	8,512	0.624	3.87 · 10 ⁻²	1.56 · 10 ⁻²	1.34 · 10 ⁻²	EX_EUR	BRAP	1	rs11065987	2 · 10 ⁵	0.57	0.102	2.12 · 10 ⁻⁸
15	75115895	rs7162232	G	A	8,478	0.332	4.48 · 10 ⁻²	1.63 · 10 ⁻²	6.07 · 10 ⁻³	OMNI_EUR	LMAN1L	1	rs7162232	2 · 10 ⁵	0.606	0.109	2.33 · 10 ⁻⁸
15	75057203	rs4886406	G	T	8,477	0.283	4.63 · 10 ⁻²	1.7 · 10 ⁻²	6.43 · 10 ⁻³	OMNI_EUR	CYP1A2	1	rs4886406	2 · 10 ⁵	-0.599	0.108	3.06 · 10 ⁻⁸
12	112486818	rs17696736	G	A	8,512	0.6	2.95 · 10 ⁻²	1.54 · 10 ⁻²	5.54 · 10 ⁻²	EX_EUR	NAA25	1	rs17696736	2 · 10 ⁵	0.549	9.96 · 10 ⁻²	3.43 · 10 ⁻⁸
12	112906415	rs11066320	A	G	8,477	0.399	2.36 · 10 ⁻²	1.55 · 10 ⁻²	0.127	OMNI_EUR	PTPN11	1	rs11066320	2 · 10 ⁵	-0.544	9.96 · 10 ⁻²	4.56 · 10 ⁻⁸
10	104652323	rs11191447	C	T	8,512	0.923	3.75 · 10 ⁻²	2.9 · 10 ⁻²	0.197	EX_EUR	AS3MT	1	rs3740390	2 · 10 ⁵	-1.005	0.172	4.61 · 10 ⁻⁹
12	112486818	rs17696736	G	A	8,512	0.6	2.95 · 10 ⁻²	1.54 · 10 ⁻²	5.54 · 10 ⁻²	EX_EUR	TRAFD1	0.922	rs17630235	2 · 10 ⁵	0.569	0.1	1.45 · 10 ⁻⁸
12	112486818	rs17696736	G	A	8,512	0.6	2.95 · 10 ⁻²	1.54 · 10 ⁻²	5.54 · 10 ⁻²	EX_EUR	HECTD4	0.913	rs11066188	2 · 10 ⁵	0.567	0.101	1.72 · 10 ⁻⁸

5 HDL Cholesterol (HDL)

5.1 Summary

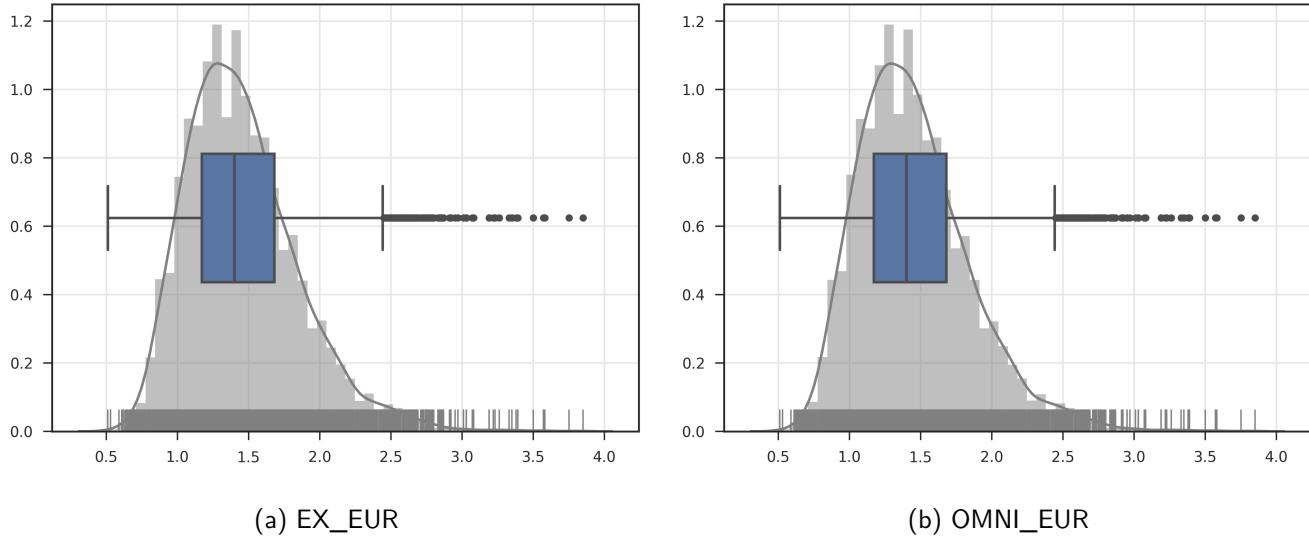


Figure 9: Distribution of HDL in cohort-level analyses

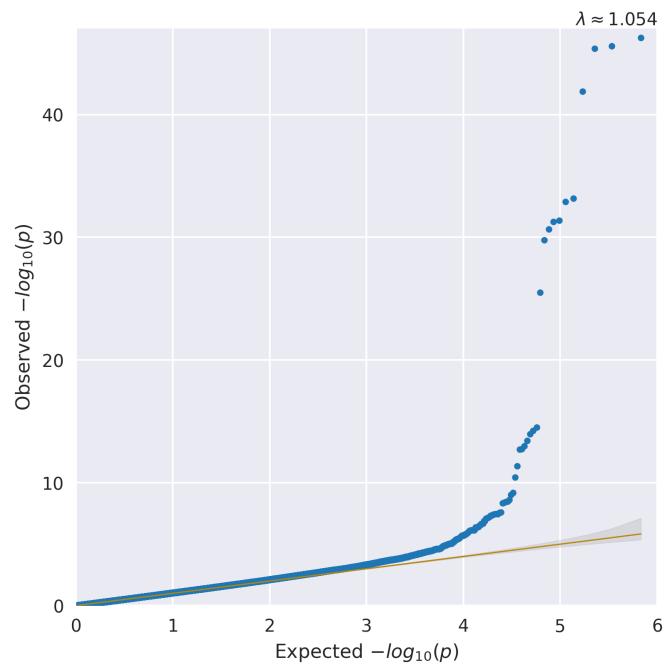
Table 12: Summary of samples removed from HDL Cholesterol analysis by cohort and model

Cohort	Array	Ancestry	Trans	Covars	Total	-SampleQc	-missObs	-Kinship	-PcOutlier
EX_EUR	EX	EUR	invn	Age+Age2+BMI	10071	36	2847	1104	2
OMNI_EUR	OMNI	EUR	invn	Age+Age2+BMI	10048	69	2840	1077	0

Table 13: Summary of samples remaining for HDL Cholesterol analysis by cohort and model

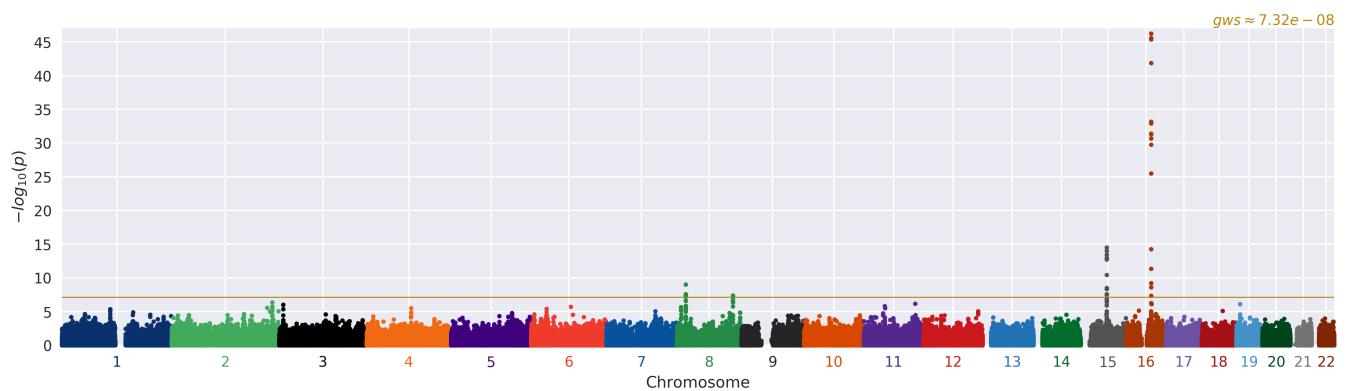
Cohort	Array	Ancestry	Trans	Covars	PCs	N	Male	Female	Max	Min	μ	\tilde{x}	σ
EX_EUR	EX	EUR	invn	Age+Age2+BMI	1	6091	6091	0	3.85	0.51	1.452	1.4	0.396
OMNI_EUR	OMNI	EUR	invn	Age+Age2+BMI	3	6078	6078	0	3.85	0.51	1.453	1.4	0.398

5.2 Calibration



(a) invn Adjusted Age+Age2+BMI

Figure 10: QQ plots for HDL in the MERGE analysis



(a) invn Adjusted Age+Age2+BMI

Figure 11: Manhattan plots for HDL in the MERGE analysis

5.3 Top associations

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

CHR	POS	ID	EA	OA	GENE_CLOSEST	COHORT	N	MALE	FEMALE	MAC	FREQ	EFFECT	STDERR	P
16	56988044	rs173539	T	C	CETP	EX_EUR	6,091	6,091	0	3,311	0.272	0.29	$1.99 \cdot 10^{-2}$	$5.67 \cdot 10^{-47}$
15	58678512	rs10468017	T	C	LIPC	EX_EUR	6,091	6,091	0	4,050	0.332	0.15	$1.9 \cdot 10^{-2}$	$3.03 \cdot 10^{-15}$
16	56985139	rs9989419	G	A	HERPUD1	EX_EUR	6,088	6,088	0	4,548	0.626	0.145	$1.85 \cdot 10^{-2}$	$5.77 \cdot 10^{-15}$
8	19816934	rs301	C	T	LPL	EX_EUR	6,090	6,090	0	2,603	0.214	0.135	$2.2 \cdot 10^{-2}$	$9.42 \cdot 10^{-10}$
8	126507389	rs2954038	A	C	TRIB1	EX_EUR	6,090	6,090	0	3,130	0.743	0.113	$2.06 \cdot 10^{-2}$	$4.08 \cdot 10^{-8}$
2	227020653	rs7578326	G	A	NYAP2	EX_EUR	6,091	6,091	0	4,376	0.359	$9.6 \cdot 10^{-2}$	$1.89 \cdot 10^{-2}$	$4.13 \cdot 10^{-7}$
16	57275033	rs16968135	A	G	RSPRY1	OMNI_EUR	6,078	6,078	0	504	$4.15 \cdot 10^{-2}$	0.225	$4.54 \cdot 10^{-2}$	$7.1 \cdot 10^{-7}$
11	116648917	rs964184	C	G	ZPR1	EX_EUR	6,091	6,091	0	1,558	0.872	0.134	$2.7 \cdot 10^{-2}$	$7.27 \cdot 10^{-7}$
16	57181134	rs2291406	C	T	CPNE2	OMNI_EUR	6,077	6,077	0	504	$4.15 \cdot 10^{-2}$	0.225	$4.54 \cdot 10^{-2}$	$7.38 \cdot 10^{-7}$
19	8429323	rs116843064	A	G	ANGPTL4	EX_EUR	6,091	6,091	0	289	$2.37 \cdot 10^{-2}$	0.292	$5.91 \cdot 10^{-2}$	$7.76 \cdot 10^{-7}$
3	9381122	rs2648549	G	A	THUMPD3	OMNI_EUR	6,076	6,076	0	6,034	0.503	$8.83 \cdot 10^{-2}$	$1.8 \cdot 10^{-2}$	$9.33 \cdot 10^{-7}$
11	47357479	rs35078470	C	T	MYBPC3	EX_EUR	6,091	6,091	0	344	$2.82 \cdot 10^{-2}$	0.263	$5.47 \cdot 10^{-2}$	$1.47 \cdot 10^{-6}$
2	227068080	exm-rs2943634	A	C	IRS1	EX_EUR	6,091	6,091	0	4,332	0.644	$9.08 \cdot 10^{-2}$	$1.9 \cdot 10^{-2}$	$1.84 \cdot 10^{-6}$
6	89967489	rs61739705	C	T	GABRR2	EX_EUR	6,091	6,091	0	10	$8.21 \cdot 10^{-4}$	1.503	0.316	$1.98 \cdot 10^{-6}$
8	9183596	rs4841132	G	A	PPP1R3B	EX_EUR	6,091	6,091	0	2,127	0.825	0.113	$2.39 \cdot 10^{-2}$	$2.2 \cdot 10^{-6}$
2	215661710	rs10498023	T	C	BARD1	OMNI_EUR	6,070	6,070	0	12	$9.88 \cdot 10^{-4}$	1.354	0.288	$2.7 \cdot 10^{-6}$
4	100301048	rs1826906	T	C	ADH1C	OMNI_EUR	6,077	6,077	0	4,010	0.33	$8.99 \cdot 10^{-2}$	$1.93 \cdot 10^{-2}$	$3.12 \cdot 10^{-6}$
11	48149491	rs61739179	G	A	PTPRJ	EX_EUR	6,091	6,091	0	346	$2.84 \cdot 10^{-2}$	0.255	$5.47 \cdot 10^{-2}$	$3.31 \cdot 10^{-6}$
6	35033854	rs820077	G	A	ANKS1A	OMNI_EUR	6,077	6,077	0	926	0.924	0.158	$3.42 \cdot 10^{-2}$	$3.83 \cdot 10^{-6}$
1	109817590	rs12740374	T	G	CELSR2	EX_EUR	6,091	6,091	0	2,778	0.228	$9.97 \cdot 10^{-2}$	$2.17 \cdot 10^{-2}$	$4.39 \cdot 10^{-6}$

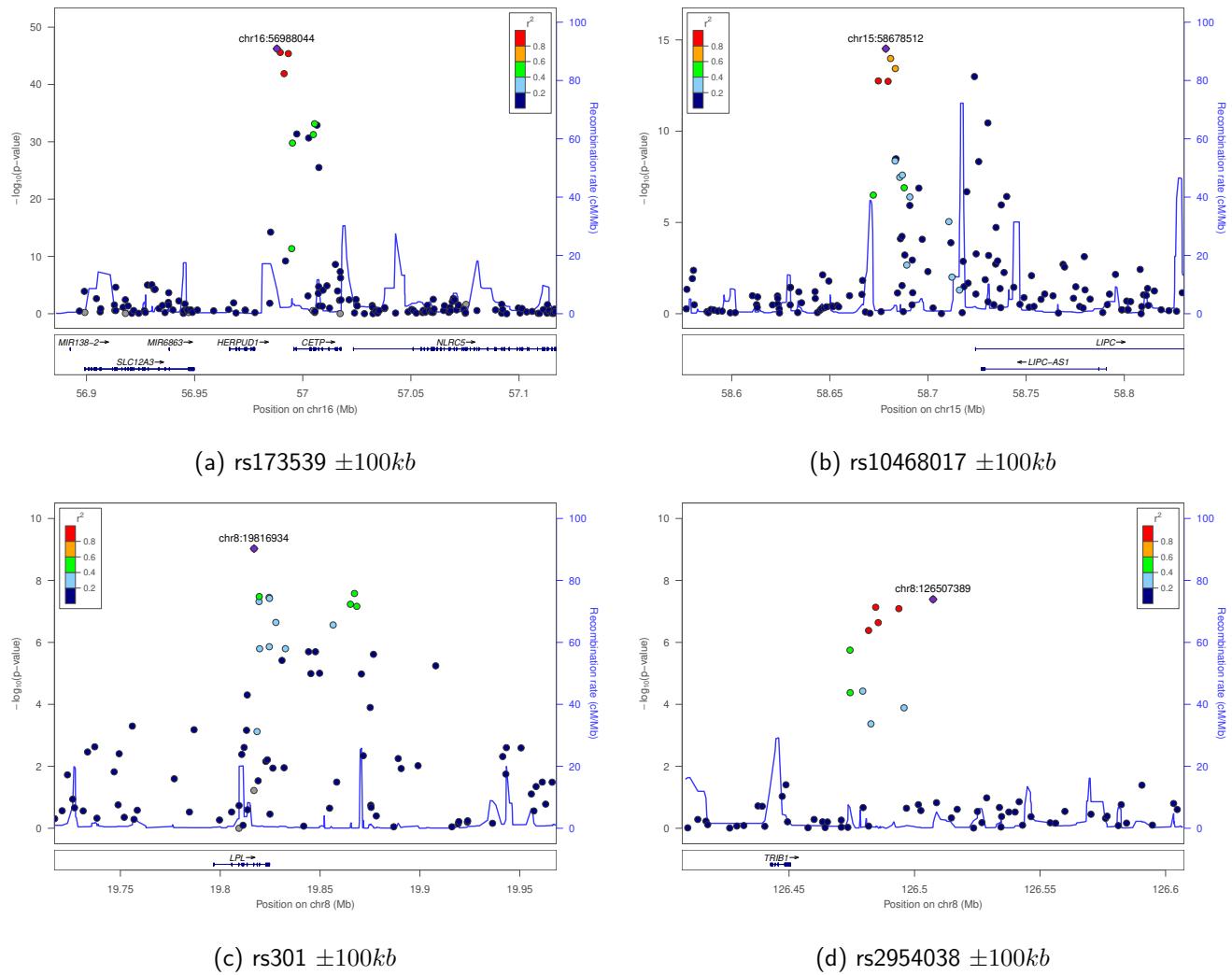


Figure 12: Regional plots for cohort MERGE model invn Adjusted Age+Age2+BMI

5.4 Previously identified risk loci

Table 15 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 [11]. Where a previously reported variant was not genotyped in the study (indicated by $\bar{R}^2 < 1$), if available, a tagging variant in LD with the reported variant ($\bar{R}^2 \geq 0.7$ and within 250kb) was provided. Tags were identified using 1000 Genomes data. There are 44 variants that show at least nominal significance ($p < 0.05$) in this study. Out of the 50 variants in both studies, 49 exhibit the same direction of effect with the known result (binomial test $p = 4.53e - 14$).

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

CHR	POS	ID	EA	OA	N	FREQ	EFFECT	STDERR	P	COHORT	GENE_CLOSEST	R ²	ID_KNOWN	N_KNOWN	EFFECT_KNOWN	STDERR_KNOWN	P_KNOWN
16	57005479	rs1532624	A	C	6,093	0.411	0.218	1.79 · 10 ⁻²	9.22 · 10 ⁻³⁴	EX_EUR	CETP	1	rs1532624	94,595	0.204	3.5 · 10 ⁻³	0
16	56985139	rs9989419	G	A	6,090	0.627	0.143	1.85 · 10 ⁻²	1.16 · 10 ⁻¹⁴	EX_EUR	HERPUD1	1	rs9989419	94,595	0.147	3.6 · 10 ⁻³	0
15	58678512	rs10468017	T	C	6,093	0.333	0.15	1.9 · 10 ⁻²	2.77 · 10 ⁻¹⁵	EX_EUR	LIPC	1	rs10468017	94,595	0.118	3.8 · 10 ⁻³	1.21 · 10 ⁻¹⁸⁸
8	19824492	rs13702	C	T	6,093	0.253	0.116	2.07 · 10 ⁻²	2.28 · 10 ⁻⁸	EX_EUR	LPL	1	rs13702	94,595	0.106	3.8 · 10 ⁻³	1.28 · 10 ⁻¹⁶⁰
18	47167214	rs4939883	C	T	6,093	0.837	1.89 · 10 ⁻²	2.45 · 10 ⁻²	0.439	EX_EUR	LIPG	1	rs4939883	94,595	7.99 · 10 ⁻²	4.5 · 10 ⁻³	1.8 · 10 ⁻⁶⁶
9	107664301	rs1883025	C	T	6,093	0.175	5.56 · 10 ⁻²	2.41 · 10 ⁻²	2.12 · 10 ⁻²	EX_EUR	ABCA1	1	rs1883025	94,595	6.98 · 10 ⁻²	4.1 · 10 ⁻³	1.5 · 10 ⁻⁵⁵
16	56866196	rs2241770	T	C	6,081	0.115	0.112	2.82 · 10 ⁻²	7.1 · 10 ⁻⁵	OMNI_EUR	NUP93	1	rs2241770	94,595	9.89 · 10 ⁻²	5.7 · 10 ⁻³	6.78 · 10 ⁻⁶⁰
2	21231524	rs676210	A	G	6,093	0.266	6.79 · 10 ⁻²	2.04 · 10 ⁻²	9.07 · 10 ⁻⁴	EX_EUR	APOB	1	rs676210	94,595	6.6 · 10 ⁻²	4 · 10 ⁻³	2.35 · 10 ⁻⁵⁴
16	67928042	rs16942887	A	G	6,093	0.166	9.03 · 10 ⁻²	2.45 · 10 ⁻²	2.26 · 10 ⁻⁴	EX_EUR	PSKH1	1	rs16942887	94,595	8.31 · 10 ⁻²	5.1 · 10 ⁻³	8.28 · 10 ⁻⁵⁴
16	67897487	rs1124324	T	C	6,080	0.169	8.94 · 10 ⁻²	2.43 · 10 ⁻²	2.34 · 10 ⁻⁴	OMNI_EUR	NUTF2	1	rs1124324	94,595	8.28 · 10 ⁻²	5.1 · 10 ⁻³	1.82 · 10 ⁻⁵³
16	67879400	rs3809630	A	G	6,081	0.169	9.06 · 10 ⁻²	2.43 · 10 ⁻²	1.93 · 10 ⁻⁴	OMNI_EUR	CENPT	1	rs3809630	94,595	8.28 · 10 ⁻²	5.1 · 10 ⁻³	2.05 · 10 ⁻⁵³
16	67758778	rs4474673	T	C	6,080	0.162	0.107	2.47 · 10 ⁻²	1.56 · 10 ⁻⁵	OMNI_EUR	RANBP10	1	rs4474673	94,595	8.46 · 10 ⁻²	5.3 · 10 ⁻³	9.34 · 10 ⁻⁵²
11	116648917	rs964184	C	G	6,093	0.872	0.132	2.69 · 10 ⁻²	8.88 · 10 ⁻⁷	EX_EUR	ZPR1	1	rs964184	94,595	-0.107	7.1 · 10 ⁻³	6.09 · 10 ⁻⁴⁸
16	68039850	rs16957696	T	C	6,081	0.176	8.25 · 10 ⁻²	2.4 · 10 ⁻²	5.91 · 10 ⁻⁴	OMNI_EUR	DPEP2	1	rs16957696	94,595	7.45 · 10 ⁻²	4.9 · 10 ⁻³	1.31 · 10 ⁻⁴⁶
16	56933519	rs11643718	A	G	6,093	0.133	4.35 · 10 ⁻²	2.65 · 10 ⁻²	0.1	EX_EUR	SLC12A3	1	rs11643718	94,595	8.22 · 10 ⁻²	5.4 · 10 ⁻³	2.98 · 10 ⁻⁴⁶
16	68099821	rs7201742	G	T	6,079	0.178	8.02 · 10 ⁻²	2.39 · 10 ⁻²	7.96 · 10 ⁻⁴	OMNI_EUR	DUS2	1	rs7201742	94,595	7.36 · 10 ⁻²	4.8 · 10 ⁻³	5.13 · 10 ⁻⁴⁶
11	116603724	rs12272004	C	A	6,093	5.34 · 10 ⁻²	0.119	4 · 10 ⁻²	3.02 · 10 ⁻³	EX_EUR	BUD13	1	rs12272004	94,595	0.102	7 · 10 ⁻³	1.16 · 10 ⁻⁴⁵
8	9183596	rs4841132	G	A	6,093	0.825	0.111	2.39 · 10 ⁻²	3.55 · 10 ⁻⁶	EX_EUR	PP1R3B	1	rs4841132	94,595	8.16 · 10 ⁻²	5.8 · 10 ⁻³	4.83 · 10 ⁻⁴⁵
16	68150527	rs12447640	G	A	6,075	0.176	8.29 · 10 ⁻²	2.4 · 10 ⁻²	5.56 · 10 ⁻⁴	OMNI_EUR	NFATC3	1	rs12447640	94,595	7.3 · 10 ⁻²	4.9 · 10 ⁻³	5.07 · 10 ⁻⁴⁵
16	67977382	rs1109166	C	T	6,081	0.198	7.64 · 10 ⁻²	2.28 · 10 ⁻²	8.31 · 10 ⁻⁴	OMNI_EUR	SLC12A4	1	rs1109166	94,595	6.5 · 10 ⁻²	4.5 · 10 ⁻³	1.15 · 10 ⁻⁴²
16	67967878	rs7187289	C	A	6,081	0.198	7.64 · 10 ⁻²	2.28 · 10 ⁻²	8.31 · 10 ⁻⁴	OMNI_EUR	PSMB10	1	rs7187289	94,595	6.42 · 10 ⁻²	4.4 · 10 ⁻³	6.51 · 10 ⁻⁴²
1	230295691	rs4846914	A	G	6,093	0.536	6.1 · 10 ⁻²	1.82 · 10 ⁻²	8.09 · 10 ⁻⁴	EX_EUR	GALNT2	1	rs4846914	94,595	4.79 · 10 ⁻²	3.4 · 10 ⁻³	3.51 · 10 ⁻⁴¹
8	19746876	rs17482310	T	G	6,079	0.105	7.01 · 10 ⁻²	2.96 · 10 ⁻²	1.79 · 10 ⁻²	OMNI_EUR	INTS10	1	rs17482310	94,595	6.36 · 10 ⁻²	4.6 · 10 ⁻³	1.01 · 10 ⁻⁴⁰
16	67911517	rs8060686	C	T	6,093	0.193	6.78 · 10 ⁻²	2.31 · 10 ⁻²	3.29 · 10 ⁻³	EX_EUR	EDC4	1	rs8060686	94,595	6.3 · 10 ⁻²	4.4 · 10 ⁻³	1.32 · 10 ⁻⁴⁰
15	58579956	rs2899624	A	G	6,078	9.89 · 10 ⁻²	7.71 · 10 ⁻²	3.03 · 10 ⁻²	1.09 · 10 ⁻²	OMNI_EUR	ALDH1A2	1	rs2899624	94,595	7.14 · 10 ⁻²	4.9 · 10 ⁻³	1.39 · 10 ⁻⁴⁰
8	19943027	rs13265868	A	G	6,065	0.432	4.33 · 10 ⁻²	1.82 · 10 ⁻²	1.72 · 10 ⁻²	OMNI_EUR	SLC18A1	1	rs13265868	94,595	4.78 · 10 ⁻²	3.5 · 10 ⁻³	6.1 · 10 ⁻⁴⁰
16	67922342	rs10468274	A	G	6,080	0.186	6.87 · 10 ⁻²	2.34 · 10 ⁻²	3.31 · 10 ⁻³	OMNI_EUR	NRN1L	1	rs10468274	94,595	6.39 · 10 ⁻²	4.6 · 10 ⁻³	2.39 · 10 ⁻³⁹
16	68282077	rs12444188	A	G	6,081	0.152	6.24 · 10 ⁻²	2.53 · 10 ⁻²	1.38 · 10 ⁻²	OMNI_EUR	PLA2G15	1	rs12444188	94,595	7.21 · 10 ⁻²	5.2 · 10 ⁻³	3.06 · 10 ⁻³⁹
20	44576502	rs7679	T	C	6,093	0.149	8.4 · 10 ⁻²	2.52 · 10 ⁻²	8.87 · 10 ⁻⁴	EX_EUR	PCIF1	1	rs7679	94,595	5.87 · 10 ⁻²	4.4 · 10 ⁻³	6.73 · 10 ⁻³⁸
16	67708897	rs12449157	G	A	6,093	0.185	7.93 · 10 ⁻²	2.34 · 10 ⁻²	7.22 · 10 ⁻⁴	EX_EUR	GFOD2	1	rs12449157	94,595	6.19 · 10 ⁻²	4.6 · 10 ⁻³	7.85 · 10 ⁻³⁷
11	47354787	rs1052373	T	C	6,092	0.441	5.56 · 10 ⁻²	1.83 · 10 ⁻²	2.34 · 10 ⁻³	EX_EUR	MYBPC3	1	rs1052373	94,595	4.78 · 10 ⁻²	3.7 · 10 ⁻³	1.55 · 10 ⁻³⁶
16	67699948	rs7187476	C	T	6,059	0.178	8.63 · 10 ⁻²	2.39 · 10 ⁻²	3.02 · 10 ⁻⁴	OMNI_EUR	ENKD1	1	rs7187476	94,595	6.46 · 10 ⁻²	4.8 · 10 ⁻³	2.17 · 10 ⁻³⁶
11	47298360	rs326214	G	A	6,093	0.559	5.56 · 10 ⁻²	1.83 · 10 ⁻²	2.35 · 10 ⁻³	EX_EUR	MADD	1	rs326214	94,595	6.09 · 10 ⁻²	4.5 · 10 ⁻³	2.17 · 10 ⁻³⁶
20	44547068	rs17447545	A	G	6,081	0.142	5.95 · 10 ⁻²	2.59 · 10 ⁻²	2.18 · 10 ⁻²	OMNI_EUR	PLTP	1	rs17447545	94,595	5.62 · 10 ⁻²	4.4 · 10 ⁻³	3.98 · 10 ⁻³⁶
11	116660686	rs2266788	A	G	6,092	0.921	0.116	3.34 · 10 ⁻²	4.96 · 10 ⁻⁴	EX_EUR	APOA5	1	rs2266788	94,595	9.22 · 10 ⁻²	6.8 · 10 ⁻³	1.19 · 10 ⁻³⁵
18	47243912	rs6507945	C	A	6,079	0.494	2.7 · 10 ⁻²	1.81 · 10 ⁻²	0.136	OMNI_EUR	ACAA2	1	rs6507945	94,595	4.41 · 10 ⁻²	3.4 · 10 ⁻³	1.33 · 10 ⁻³⁴
20	43042364	rs1800961	C	T	6,093	3.68 · 10 ⁻²	0.119	4.76 · 10 ⁻²	1.26 · 10 ⁻²	EX_EUR	HNF4A	1	rs1800961	94,595	0.127	9.9 · 10 ⁻³	1.64 · 10 ⁻³⁴
16	68013471	rs255049	C	T	6,050	0.217	5.7 · 10 ⁻²	2.22 · 10 ⁻²	1.03 · 10 ⁻²	EX_EUR	DPEP3	1	rs255049	94,595	5.64 · 10 ⁻²	4.4 · 10 ⁻³	2.26 · 10 ⁻³⁴
11	47275064	rs10838681	A	G	6,080	0.389	4.28 · 10 ⁻²	1.87 · 10 ⁻²	2.21 · 10 ⁻²	OMNI_EUR	NR1H3	1	rs10838681	94,595	4.8 · 10 ⁻²	3.8 · 10 ⁻³	1.72 · 10 ⁻³³
11	47260319	rs901746	G	A	6,081	0.44	4.13 · 10 ⁻²	1.83 · 10 ⁻²	2.4 · 10 ⁻²	OMNI_EUR	DDB2	1	rs901746	94,595	4.61 · 10 ⁻²	3.7 · 10 ⁻³	4.13 · 10 ⁻³³
12	125261593	rs838880	C	T	6,093	0.589	5.29 · 10 ⁻²	1.85 · 10 ⁻²	4.25 · 10 ⁻³	EX_EUR	SCARB1	1	rs838880	94,595	4.84 · 10 ⁻²	3.9 · 10 ⁻³	6.38 · 10 ⁻³²
19	54797848	rs103294	T	C	6,081	0.304	6.36 · 10 ⁻²	1.97 · 10 ⁻²	1.24 · 10 ⁻³	OMNI_EUR	LILRB2	1	rs103294	94,595	5.23 · 10 ⁻²	4.4 · 10 ⁻³	4 · 10 ⁻³⁰
8	126495818	rs10808546	T	C	6,038	0.439	6.96 · 10 ⁻²	1.82 · 10 ⁻²	1.33 · 10 ⁻⁴	OMNI_EUR	TRIB1	1	rs10808546	94,595	4.09 · 10 ⁻²	3.4 · 10 ⁻³	4.11 · 10 ⁻³⁰
16	68335392	rs11350	C	T	6,081	0.174	4.77 · 10 ⁻²	2.39 · 10 ⁻²	4.62 · 10 ⁻²	OMNI_EUR	SLC7A6	1	rs11350	94,595	6.19 · 10 ⁻²	5.1 · 10 ⁻³	1.05 · 10 ⁻²⁹
11	46743247	rs3136441	C	T	6,093	0.257	4.8 · 10 ⁻²	2.09 · 10 ⁻²	2.18 · 10 ⁻²	EX_EUR	F2	1	rs3136441	94,595	5.45 · 10 ⁻²	4.7 · 10 ⁻³	6.76 · 10 ⁻²⁹
11	47270255	rs2167079	T	C	6,093	0.44	5.79 · 10 ⁻²	1.83 · 10 ⁻²	1.53 · 10 ⁻³	EX_EUR	ACP2	1	rs2167079	94,595	5.77 · 10 ⁻²	4.8 · 10 ⁻³	1.19 · 10 ⁻²⁸
16	67671804	rs6499137	G	T	6,081	0.123	7.32 · 10 ⁻²	2.76 · 10 ⁻²	7.98 · 10 ⁻³	OMNI_EUR	CTCF	1	rs6499137	94,595	7.22 · 10 ⁻²	6.2 · 10 ⁻³	5.9 · 10 ⁻²⁸
11	61557803	rs102275	T	C	6,093	0.431	2.3 · 10 ⁻²	1.84 ·									

6 Estimated Glomerular Filtration Rate (eGFR)

6.1 Summary

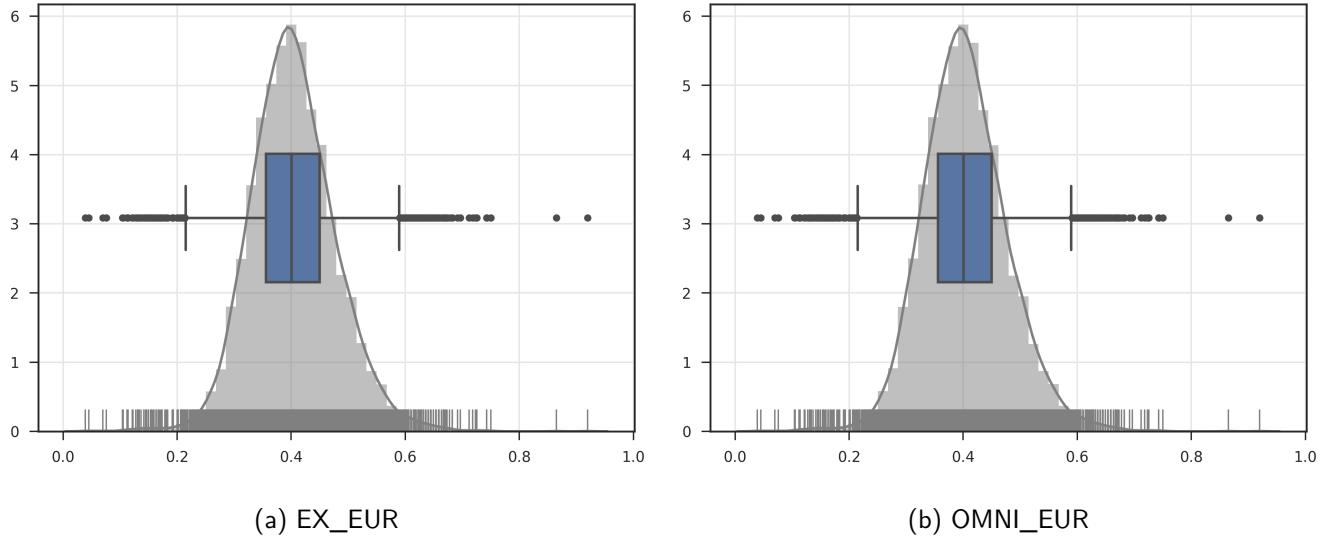


Figure 13: Distribution of eGFR in cohort-level analyses

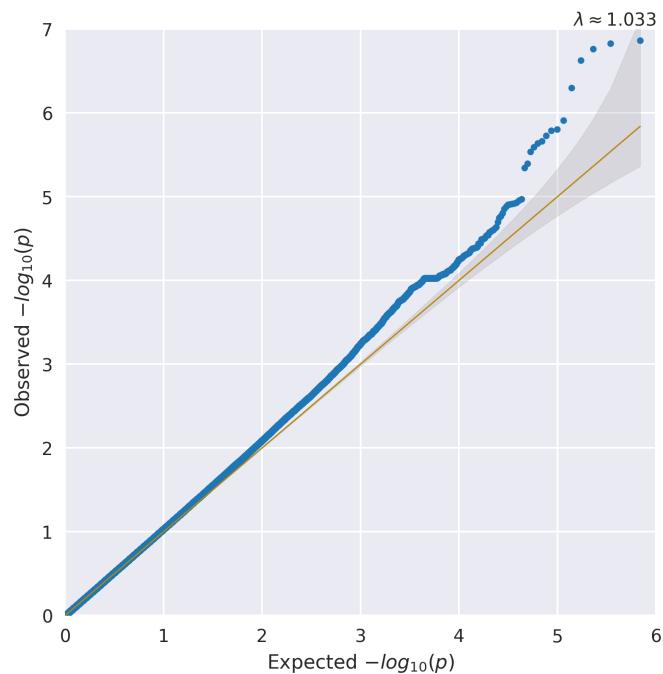
Table 16: Summary of samples removed from Estimated Glomerular Filtration Rate analysis by cohort and model

Cohort	Array	Ancestry	Trans	Covars	Total	-SampleQc	-missObs	-Kinship	-PcOutlier
EX_EUR	EX	EUR	invn		10071	36	0	1515	2
OMNI_EUR	OMNI	EUR	invn		10048	69	0	1497	1

Table 17: Summary of samples remaining for Estimated Glomerular Filtration Rate analysis by cohort and model

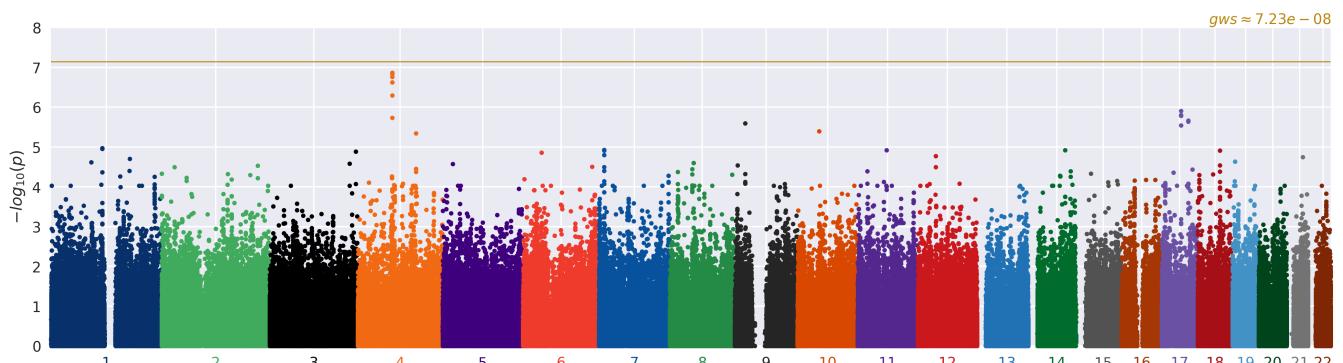
Cohort	Array	Ancestry	Trans	Covars	PCs	N	Male	Female	Max	Min	μ	\tilde{x}	σ
EX_EUR	EX	EUR	invn		1	8518	8518	0	0.92	0.039	0.404	0.4	0.074
OMNI_EUR	OMNI	EUR	invn		8	8481	8481	0	0.92	0.039	0.403	0.399	0.074

6.2 Calibration



(a) invn Unadjusted

Figure 14: QQ plots for eGFR in the MERGE analysis



(a) invn Unadjusted

Figure 15: Manhattan plots for eGFR in the MERGE analysis

6.3 Top associations

Table 18: Top variants in the MERGE invn Unadjusted model (**bold** variants indicate previously identified associations)

CHR	POS	ID	EA	OA	GENE _{CLOSEST}	COHORT	N	MALE	FEMALE	MAC	FREQ	EFFECT	STDERR	P
4	77398015	rs10032549	A	G	SHROOM3	OMNI_EUR	8,471	8,471	0	8,035	0.526	$8.1 \cdot 10^{-2}$	$1.54 \cdot 10^{-2}$	$1.37 \cdot 10^{-5}$
17	43483774	rs1230101	G	A	ARHGAP27	OMNI_EUR	8,477	8,477	0	5,852	0.655	$7.82 \cdot 10^{-2}$	$1.61 \cdot 10^{-2}$	$1.24 \cdot 10^{-6}$
17	59456589	rs9895661	T	C	BCAS3	EX_EUR	8,518	8,518	0	3,338	0.196	$9.2 \cdot 10^{-2}$	$1.94 \cdot 10^{-2}$	$2.19 \cdot 10^{-6}$
9	23656678	rs1329035	T	C	ELAVL2	OMNI_EUR	8,475	8,475	0	3,779	0.223	$8.69 \cdot 10^{-2}$	$1.85 \cdot 10^{-2}$	$2.55 \cdot 10^{-6}$
10	48438147	rs1902724	T	G	GDF10	OMNI_EUR	8,480	8,480	0	4,168	0.246	$8.21 \cdot 10^{-2}$	$1.78 \cdot 10^{-2}$	$4.02 \cdot 10^{-6}$
4	130824678	rs3111741	A	G	C4orf33	OMNI_EUR	8,481	8,481	0	4,293	0.253	$8.03 \cdot 10^{-2}$	$1.75 \cdot 10^{-2}$	$4.55 \cdot 10^{-6}$
1	115738343	rs1076754	T	C	NGF	OMNI_EUR	8,480	8,480	0	4,740	0.721	$7.44 \cdot 10^{-2}$	$1.69 \cdot 10^{-2}$	$1.07 \cdot 10^{-5}$
7	11604426	rs7805116	A	G	THSD7A	OMNI_EUR	8,481	8,481	0	2,612	0.846	$9.32 \cdot 10^{-2}$	$2.13 \cdot 10^{-2}$	$1.18 \cdot 10^{-5}$
11	65338363	rs143562975	A	C	SSSCA1	EX_EUR	8,518	8,518	0	4	1	2.183	0.499	$1.21 \cdot 10^{-5}$
14	82510077	rs2217448	C	T	SEL1L	OMNI_EUR	8,479	8,479	0	2,040	0.88	0.103	$2.36 \cdot 10^{-2}$	$1.21 \cdot 10^{-5}$
18	49570773	rs4318302	A	C	DCC	OMNI_EUR	8,478	8,478	0	4,327	0.255	$7.73 \cdot 10^{-2}$	$1.77 \cdot 10^{-2}$	$1.24 \cdot 10^{-5}$
3	193811162	rs10933711	T	C	HES1	OMNI_EUR	8,480	8,480	0	6,158	0.637	$6.97 \cdot 10^{-2}$	$1.6 \cdot 10^{-2}$	$1.31 \cdot 10^{-5}$
6	42084146	rs10456507	C	A	C6orf132	OMNI_EUR	8,480	8,480	0	1,098	0.935	0.137	$3.14 \cdot 10^{-2}$	$1.4 \cdot 10^{-5}$
12	40273222	rs4277185	T	G	SLC2A13	OMNI_EUR	8,442	8,442	0	3,846	0.772	$7.85 \cdot 10^{-2}$	$1.82 \cdot 10^{-2}$	$1.69 \cdot 10^{-5}$
21	36172283	rs2073354	T	G	RUNX1	OMNI_EUR	8,463	8,463	0	932	0.945	0.145	$3.38 \cdot 10^{-2}$	$1.78 \cdot 10^{-5}$
1	177179432	rs17380506	G	A	BRINP2	OMNI_EUR	8,480	8,480	0	1,377	0.919	0.12	$2.8 \cdot 10^{-2}$	$2 \cdot 10^{-5}$
19	5711930	rs11085147	T	C	LONP1	EX_EUR	8,518	8,518	0	1,476	0.913	0.115	$2.71 \cdot 10^{-2}$	$2.31 \cdot 10^{-5}$
1	90601121	rs6428572	C	T	ZNF326	OMNI_EUR	8,478	8,478	0	1,149	0.932	0.129	$3.06 \cdot 10^{-2}$	$2.4 \cdot 10^{-5}$
8	53355822	rs17228239	G	A	ST18	OMNI_EUR	8,480	8,480	0	8,376	0.494	$6.46 \cdot 10^{-2}$	$1.53 \cdot 10^{-2}$	$2.51 \cdot 10^{-5}$
3	179529649	rs141827659	C	A	PEX5L	EX_EUR	8,518	8,518	0	2	1	2.965	0.705	$2.62 \cdot 10^{-5}$

6.4 Previously identified risk loci

Table 19 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 [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 32 variants that show at least nominal significance ($p < 0.05$) in this study. Out of the 50 variants in both studies, 46 exhibit the same direction of effect with the known result (binomial test $p = 2.23e - 10$).

Table 19: Top known loci in MERGE model invn Unadjusted (**bold** variants indicate matching direction of effect)

CHR	POS	ID	EA	OA	N	FREQ	EFFECT	STDERR	P	COHORT	GENE_CLOSEST	R ²	ID_KNOWN	N_KNOWN	EFFECT_KNOWN	STDERR_KNOWN	P_KNOWN
15	45641225	rs2453533	C	A	8,516	0.417	3.67 · 10 ⁻²	1.54 · 10 ⁻²	1.7 · 10 ⁻²	EX_EUR	GATM	1	rs2453533	1.33 · 10 ⁵	1.2 · 10 ⁻²	9.2 · 10 ⁻⁴	4.3 · 10 ⁻⁴²
16	20367690	rs12917707	T	G	8,518	0.228	5.56 · 10 ⁻²	1.82 · 10 ⁻²	2.28 · 10 ⁻³	EX_EUR	UMOD	1	rs12917707	1.33 · 10 ⁵	1.6 · 10 ⁻²	1.2 · 10 ⁻³	1.2 · 10 ⁻⁴¹
4	77368847	rs17319721	G	A	8,518	0.401	7.9 · 10 ⁻²	1.56 · 10 ⁻²	4.35 · 10 ⁻⁷	EX_EUR	SHROOM3	1	rs17319721	1.33 · 10 ⁵	1.1 · 10 ⁻²	9.2 · 10 ⁻⁴	1.3 · 10 ⁻³⁷
15	45695695	rs1153849	G	A	8,481	0.31	3.27 · 10 ⁻²	1.65 · 10 ⁻²	4.75 · 10 ⁻²	OMNI_EUR	SPATA5L1	1	rs1153849	1.33 · 10 ⁵	1.2 · 10 ⁻²	1 · 10 ⁻³	1.2 · 10 ⁻³³
15	45723983	rs1547487	A	G	8,468	0.392	3.9 · 10 ⁻²	1.56 · 10 ⁻²	1.26 · 10 ⁻²	OMNI_EUR	C15orf48	1	rs1547487	1.33 · 10 ⁵	1.1 · 10 ⁻²	9.2 · 10 ⁻⁴	2 · 10 ⁻³²
16	20400839	rs11864909	T	C	8,475	0.29	4.33 · 10 ⁻²	1.7 · 10 ⁻²	1.1 · 10 ⁻²	OMNI_EUR	PDILT	1	rs11864909	1.33 · 10 ⁵	1.2 · 10 ⁻²	1 · 10 ⁻³	1 · 10 ⁻³⁰
7	151407801	rs7805747	G	A	8,518	0.175	5.19 · 10 ⁻²	2.02 · 10 ⁻²	1.01 · 10 ⁻²	EX_EUR	PRKG2	1	rs7805747	1.33 · 10 ⁵	1.3 · 10 ⁻²	1.1 · 10 ⁻³	8 · 10 ⁻²⁹
15	45801035	rs950027	T	C	8,475	0.479	3.66 · 10 ⁻²	1.54 · 10 ⁻²	1.73 · 10 ⁻²	OMNI_EUR	SLC30A4	1	rs950027	1.33 · 10 ⁵	8.8 · 10 ⁻³	9.2 · 10 ⁻⁴	8.1 · 10 ⁻²³
5	176817636	rs6420094	A	G	8,517	0.43	3.44 · 10 ⁻²	1.55 · 10 ⁻²	2.65 · 10 ⁻²	EX_EUR	SLC34A1	1	rs6420094	1.33 · 10 ⁵	9.6 · 10 ⁻³	1 · 10 ⁻³	4.9 · 10 ⁻²²
15	45567529	rs12440356	T	C	8,478	0.403	2.1 · 10 ⁻²	1.56 · 10 ⁻²	0.177	OMNI_EUR	SLC28A2	1	rs12440356	1.33 · 10 ⁵	8.9 · 10 ⁻³	9.2 · 10 ⁻⁴	8.9 · 10 ⁻²²
5	176801131	rs10866705	A	C	8,479	0.648	4.67 · 10 ⁻²	1.62 · 10 ⁻²	3.94 · 10 ⁻³	OMNI_EUR	RGS14	1	rs10866705	1.33 · 10 ⁵	9.9 · 10 ⁻³	1 · 10 ⁻³	1.2 · 10 ⁻²¹
17	59456589	rs9895661	T	C	8,518	0.804	9.16 · 10 ⁻²	1.94 · 10 ⁻²	2.33 · 10 ⁻⁶	EX_EUR	BCAS3	1	rs9895661	1.33 · 10 ⁵	1.1 · 10 ⁻²	1.2 · 10 ⁻³	2.8 · 10 ⁻²¹
2	73679280	rs6546838	A	G	8,518	0.236	1.04 · 10 ⁻²	1.8 · 10 ⁻²	0.564	EX_EUR	ALMS1	1	rs6546838	1.33 · 10 ⁵	-9.3 · 10 ⁻³	1 · 10 ⁻³	7.7 · 10 ⁻²⁰
4	77330682	rs4272041	A	G	8,477	0.424	5.39 · 10 ⁻²	1.56 · 10 ⁻²	5.48 · 10 ⁻⁴	OMNI_EUR	CCDC158	1	rs4272041	1.33 · 10 ⁵	8 · 10 ⁻³	9.2 · 10 ⁻⁴	1.3 · 10 ⁻¹⁹
5	39359323	rs835218	A	C	8,473	0.385	5.33 · 10 ⁻²	1.59 · 10 ⁻²	8.05 · 10 ⁻⁴	OMNI_EUR	C9	1	rs835218	1.33 · 10 ⁵	8 · 10 ⁻³	9.2 · 10 ⁻⁴	1.7 · 10 ⁻¹⁹
4	77220837	rs12506745	T	G	8,478	0.42	5.11 · 10 ⁻²	1.56 · 10 ⁻²	1.06 · 10 ⁻³	OMNI_EUR	FAM47E-STBD1	1	rs12506745	1.33 · 10 ⁵	8 · 10 ⁻³	9.2 · 10 ⁻⁴	3.7 · 10 ⁻¹⁹
6	160675764	rs316009	T	C	8,475	0.947	5.39 · 10 ⁻²	3.41 · 10 ⁻²	0.114	OMNI_EUR	SLC22A2	1	rs316009	1.33 · 10 ⁵	1.3 · 10 ⁻²	1.4 · 10 ⁻³	4.4 · 10 ⁻¹⁹
11	30760335	rs3925584	C	T	8,518	0.484	4.91 · 10 ⁻²	1.51 · 10 ⁻²	1.14 · 10 ⁻³	EX_EUR	DCCD1	1	rs3925584	1.33 · 10 ⁵	7.6 · 10 ⁻³	9.2 · 10 ⁻⁴	7.6 · 10 ⁻¹⁸
5	39423907	rs10512696	C	T	8,481	0.387	5.44 · 10 ⁻²	1.59 · 10 ⁻²	6.15 · 10 ⁻⁴	OMNI_EUR	DAB2	1	rs10512696	1.33 · 10 ⁵	7.6 · 10 ⁻³	9.2 · 10 ⁻⁴	3.8 · 10 ⁻¹⁶
4	77228724	rs3796491	A	C	8,395	0.603	6.29 · 10 ⁻²	1.57 · 10 ⁻²	6.4 · 10 ⁻⁵	OMNI_EUR	STBD1	1	rs3796491	1.33 · 10 ⁵	7.2 · 10 ⁻³	9.2 · 10 ⁻⁴	1.9 · 10 ⁻¹⁵
8	23728271	rs6999484	G	A	8,480	0.463	3.54 · 10 ⁻²	1.55 · 10 ⁻²	2.22 · 10 ⁻²	OMNI_EUR	STC1	1	rs6999484	1.33 · 10 ⁵	7.1 · 10 ⁻³	9.2 · 10 ⁻⁴	1.9 · 10 ⁻¹⁵
15	53946593	rs491567	C	A	8,518	0.294	2.06 · 10 ⁻³	1.67 · 10 ⁻²	0.902	EX_EUR	WDR72	1	rs491567	1.33 · 10 ⁵	8.4 · 10 ⁻³	1 · 10 ⁻³	2.9 · 10 ⁻¹⁵
6	43806609	rs881858	G	A	8,518	0.689	4.62 · 10 ⁻²	1.65 · 10 ⁻²	5.21 · 10 ⁻³	EX_EUR	VEGFA	1	rs881858	1.33 · 10 ⁵	8.1 · 10 ⁻³	1 · 10 ⁻³	7.5 · 10 ⁻¹⁵
9	71433212	rs1556751	A	G	8,478	0.688	2.33 · 10 ⁻²	1.65 · 10 ⁻²	0.159	OMNI_EUR	PIP5K1B	1	rs1556751	1.33 · 10 ⁵	7 · 10 ⁻³	9.2 · 10 ⁻⁴	9.9 · 10 ⁻¹⁵
17	37543328	rs7221875	A	G	8,481	0.164	2.19 · 10 ⁻²	2.08 · 10 ⁻²	0.292	OMNI_EUR	FBXL20	1	rs7221875	1.33 · 10 ⁵	7.6 · 10 ⁻³	1 · 10 ⁻³	2.9 · 10 ⁻¹⁴
2	27730940	rs1260326	T	C	8,516	0.632	2.23 · 10 ⁻²	1.57 · 10 ⁻²	0.157	EX_EUR	GCKR	1	rs1260326	1.33 · 10 ⁵	6.8 · 10 ⁻³	9.2 · 10 ⁻⁴	3.4 · 10 ⁻¹⁴
17	37591422	rs10445306	A	G	8,481	0.836	2.16 · 10 ⁻²	2.08 · 10 ⁻²	0.299	OMNI_EUR	MED1	1	rs10445306	1.33 · 10 ⁵	7.5 · 10 ⁻³	1 · 10 ⁻³	4.1 · 10 ⁻¹⁴
9	71397747	rs2017	C	T	8,471	0.683	2 · 10 ⁻²	1.64 · 10 ⁻²	0.225	OMNI_EUR	FAM122A	1	rs2017	1.33 · 10 ⁵	6.8 · 10 ⁻³	9.2 · 10 ⁻⁴	4.7 · 10 ⁻¹⁴
2	73878352	rs6759452	T	C	8,479	9.86 · 10 ⁻²	3.57 · 10 ⁻³	2.58 · 10 ⁻²	0.89	OMNI_EUR	NAT8	1	rs6759452	1.33 · 10 ⁵	9 · 10 ⁻³	1.2 · 10 ⁻³	4.7 · 10 ⁻¹⁴
15	76158983	rs1394125	G	A	8,518	0.26	4.42 · 10 ⁻²	1.76 · 10 ⁻²	1.2 · 10 ⁻²	EX_EUR	UBE2Q2	1	rs1394125	1.33 · 10 ⁵	7.3 · 10 ⁻³	1 · 10 ⁻³	5.5 · 10 ⁻¹⁴
3	141743951	rs7644383	C	T	8,355	0.756	4.08 · 10 ⁻²	1.81 · 10 ⁻²	2.39 · 10 ⁻²	OMNI_EUR	TFDP2	1	rs7644383	1.33 · 10 ⁵	7.3 · 10 ⁻³	1 · 10 ⁻³	1.5 · 10 ⁻¹³
19	33356891	rs12460876	C	T	8,518	0.319	3.45 · 10 ⁻²	1.64 · 10 ⁻²	3.49 · 10 ⁻²	EX_EUR	SLC7A9	1	rs12460876	1.33 · 10 ⁵	6.6 · 10 ⁻³	9.2 · 10 ⁻⁴	1.9 · 10 ⁻¹³
15	76304503	rs10851885	A	G	8,477	0.136	5.27 · 10 ⁻²	2.26 · 10 ⁻²	1.96 · 10 ⁻²	OMNI_EUR	NRG4	1	rs10851885	1.33 · 10 ⁵	7.5 · 10 ⁻³	1 · 10 ⁻³	2.5 · 10 ⁻¹³
17	59483766	rs8068318	T	C	8,518	0.726	5.57 · 10 ⁻²	1.72 · 10 ⁻²	1.2 · 10 ⁻³	EX_EUR	TBX2	1	rs8068318	1.33 · 10 ⁵	7.6 · 10 ⁻³	1 · 10 ⁻³	3 · 10 ⁻¹³
1	150951477	rs267734	C	T	8,518	0.192	7.09 · 10 ⁻²	1.95 · 10 ⁻²	2.8 · 10 ⁻⁴	EX_EUR	ANXA9	1	rs267734	1.33 · 10 ⁵	7.9 · 10 ⁻³	1.1 · 10 ⁻³	4 · 10 ⁻¹³
4	77198986	rs6812193	T	C	8,518	0.362	4.11 · 10 ⁻²	1.6 · 10 ⁻²	1.01 · 10 ⁻²	EX_EUR	FAM47E	1	rs6812193	1.33 · 10 ⁵	6.6 · 10 ⁻³	9.2 · 10 ⁻⁴	4.1 · 10 ⁻¹³
19	33364628	rs8101881	C	T	8,518	0.678	3.48 · 10 ⁻²	1.63 · 10 ⁻²	3.3 · 10 ⁻²	EX_EUR	CEP89	1	rs8101881	1.33 · 10 ⁵	6.4 · 10 ⁻³	9.2 · 10 ⁻⁴	8.1 · 10 ⁻¹³
5	176755841	rs6860069	C	T	8,481	0.298	1.27 · 10 ⁻²	1.68 · 10 ⁻²	0.449	OMNI_EUR	LMAN2	1	rs6860069	1.33 · 10 ⁵	6.8 · 10 ⁻³	9.2 · 10 ⁻⁴	8.2 · 10 ⁻¹³
7	77467459	rs17807736	A	C	8,480	0.225	4.05 · 10 ⁻²	1.86 · 10 ⁻²	2.9 · 10 ⁻²	OMNI_EUR	PHTF2	1	rs17807736	1.33 · 10 ⁵	7 · 10 ⁻³	1 · 10 ⁻³	9.5 · 10 ⁻¹³
7	77423152	rs1045463	C	T	8,476	0.225	4.21 · 10 ⁻²	1.86 · 10 ⁻²	2.33 · 10 ⁻²	OMNI_EUR	TMEM60	1	rs1045463	1.33 · 10 ⁵	7 · 10 ⁻³	1 · 10 ⁻³	1.1 · 10 ⁻¹²
1	150940625	rs267738	G	T	8,518	0.186	7.42 · 10 ⁻²	1.97 · 10 ⁻²	1.72 · 10 ⁻⁴	EX_EUR	CERS2	1	rs267738	1.33 · 10 ⁵	7.7 · 10 ⁻³	1.1 · 10 ⁻³	1.3 · 10 ⁻¹²
17	37393395	rs12950186	C	A	8,466	0.92	2.93 · 10 ⁻³	2.86 · 10 ⁻²	0.918	OMNI_EUR	STAC2	1	rs12950186	1.33 · 10 ⁵	-8.5 · 10 ⁻³	1.2 · 10 ⁻³	1.7 · 10 ⁻¹²
17	37699376	rs11657058	G	T	8,481	0.92	5.28 · 10 ⁻³	2.85 · 10 ⁻²	0.853	OMNI_EUR	CDK12	1	rs11657058	1.33 · 10 ⁵	-8.3 · 10 ⁻³	1.2 · 10 ⁻³	3.6 · 10 ⁻¹²
12	349298	rs10774021	C	T	8,515	0.692	9.25 · 10 ⁻³	1.66 · 10 ⁻²	0.576	EX_EUR	SLC6A13	1	rs10774021	1.33 · 10 ⁵	6.3 · 10 ⁻³	9.2 · 10 ⁻⁴	4.8 · 10 ⁻¹²
7	77416439	rs6465825	T	C	8,518	0.331	3.88 · 10 ⁻²	1.63 · 10 ⁻²	1.73 · 10 ⁻²	EX_EUR	RSBNIL	1	rs6465825	1.33 · 10 ⁵	6.2 · 10 ⁻³	9.2 · 10 ⁻⁴	4.9 · 10 ⁻¹²
2	211547400	rs13386028	C	A	8,472	0.441	5.08 · 10 ⁻³	1.54 · 10 ⁻²	0.742	OMNI_EUR	CPS1	1	rs13386028	1.33 · 10 ⁵	-6.3 · 10 ⁻³	9.2 · 10 ⁻⁴	6.8 · 10 ⁻¹²
15	45902779	rs12909221															

7 Diastolic Blood Pressure (DBP10)

7.1 Summary

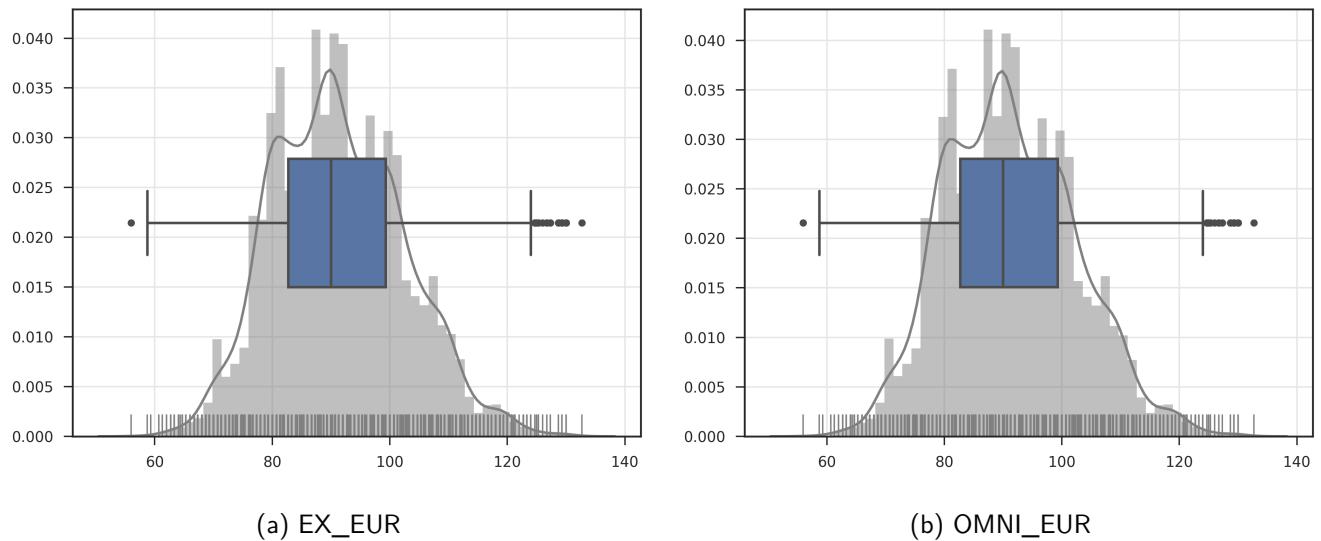


Figure 16: Distribution of DBP10 in cohort-level analyses

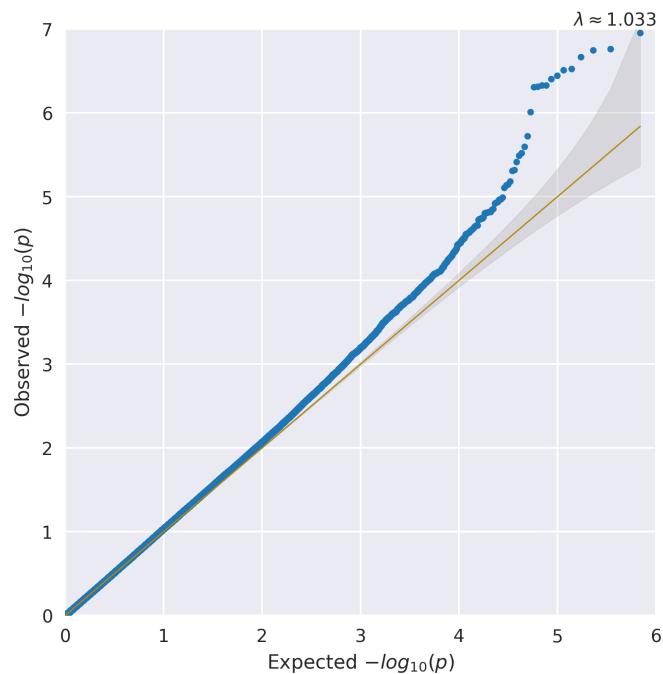
Table 20: Summary of samples removed from Diastolic Blood Pressure analysis by cohort and model

Cohort	Array	Ancestry	Trans	Covars	Total	-SampleQc	-missObs	-Kinship	-PcOutlier
EX_EUR	EX	EUR	invn	Age+Age2+BMI	10071	36	5	1517	1
OMNI_EUR	OMNI	EUR	invn	Age+Age2+BMI	10048	69	5	1494	0

Table 21: Summary of samples remaining for Diastolic Blood Pressure analysis by cohort and model

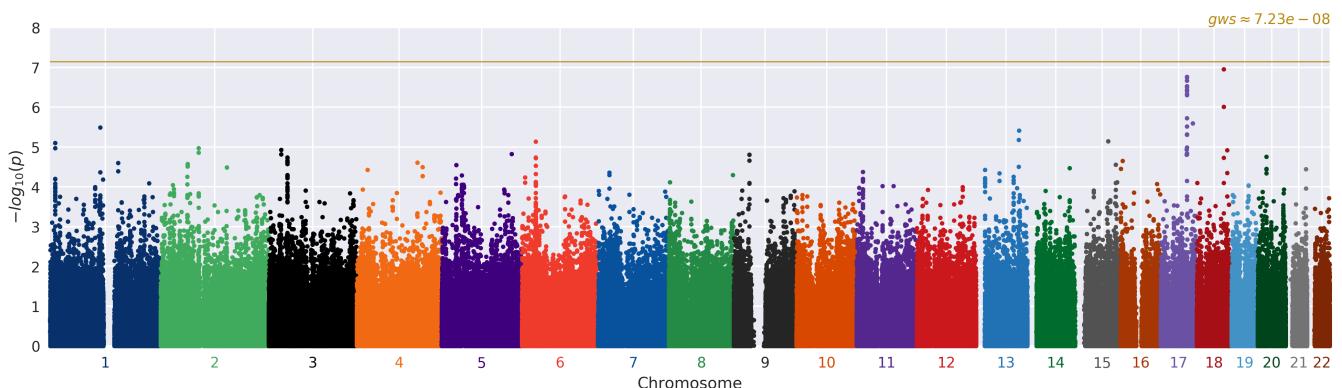
Cohort	Array	Ancestry	Trans	Covars	PCs	N	Male	Female	Max	Min	μ	\tilde{x}	σ
EX_EUR	EX	EUR	invn	Age+Age2+BMI	10	8512	8512	0	132.7	58.7	91.318	90.7	11.119
OMNI_EUR	OMNI	EUR	invn	Age+Age2+BMI	4	8480	8480	0	132.7	56.0	91.289	90.15	11.145

7.2 Calibration



(a) invn Adjusted Age+Age2+BMI

Figure 17: QQ plots for DBP10 in the MERGE analysis



(a) invn Adjusted Age+Age2+BMI

Figure 18: Manhattan plots for DBP10 in the MERGE analysis

7.3 Top associations

Table 22: Top variants in the MERGE invn Adjusted Age+Age2+BMI model (**bold** variants indicate previously identified associations)

CHR	POS	ID	EA	OA	GENE _{CLOSEST}	COHORT	N	MALE	FEMALE	MAC	FREQ	EFFECT	STDERR	P
18	60661358	rs7238945	G	T	PHLPP1	OMNI_EUR	8,375	8,375	0	1,860	0.111	0.131	$2.47 \cdot 10^{-2}$	$1.1 \cdot 10^{-7}$
17	59087808	rs9652858	A	G	BCAS3	OMNI_EUR	8,476	8,476	0	2,709	0.16	0.109	$2.08 \cdot 10^{-2}$	$1.73 \cdot 10^{-7}$
17	72126787	rs4789620	C	T	RPL38	OMNI_EUR	8,479	8,479	0	570	0.966	0.2	$4.26 \cdot 10^{-2}$	$2.54 \cdot 10^{-6}$
1	113161350	rs11102516	A	G	ST7L	OMNI_EUR	8,480	8,480	0	3,482	0.205	$8.82 \cdot 10^{-2}$	$1.89 \cdot 10^{-2}$	$3.24 \cdot 10^{-6}$
13	96013885	rs7992512	A	G	ABCC4	OMNI_EUR	8,473	8,473	0	2,586	0.153	$9.89 \cdot 10^{-2}$	$2.14 \cdot 10^{-2}$	$3.83 \cdot 10^{-6}$
15	74486444	rs974456	C	T	STRA6	OMNI_EUR	8,473	8,473	0	6,071	0.358	$7.2 \cdot 10^{-2}$	$1.6 \cdot 10^{-2}$	$7.15 \cdot 10^{-6}$
6	31177503	rs3132505	G	T	POU5F1	OMNI_EUR	8,480	8,480	0	2,670	0.157	$9.48 \cdot 10^{-2}$	$2.11 \cdot 10^{-2}$	$7.29 \cdot 10^{-6}$
1	11905974	rs5068	A	G	NPPA	OMNI_EUR	8,480	8,480	0	2,001	0.118	0.107	$2.4 \cdot 10^{-2}$	$7.86 \cdot 10^{-6}$
1	11876662	rs17376328	G	A	CLCN6	OMNI_EUR	8,477	8,477	0	2,003	0.118	0.106	$2.4 \cdot 10^{-2}$	$1.07 \cdot 10^{-5}$
2	85480715	rs17763853	G	A	TCF7L1	OMNI_EUR	8,479	8,479	0	4,442	0.262	$7.67 \cdot 10^{-2}$	$1.74 \cdot 10^{-2}$	$1.08 \cdot 10^{-5}$
17	58359510	rs11652788	G	A	USP32	OMNI_EUR	8,480	8,480	0	1,707	0.101	0.112	$2.55 \cdot 10^{-2}$	$1.15 \cdot 10^{-5}$
3	27651544	rs12715123	T	C	EOMES	OMNI_EUR	8,475	8,475	0	5,228	0.692	$7.33 \cdot 10^{-2}$	$1.67 \cdot 10^{-2}$	$1.18 \cdot 10^{-5}$
18	68050814	rs3943675	G	A	SOC56	OMNI_EUR	8,478	8,478	0	8,256	0.513	$6.71 \cdot 10^{-2}$	$1.53 \cdot 10^{-2}$	$1.21 \cdot 10^{-5}$
5	157523151	rs10045606	G	A	CLINT1	OMNI_EUR	8,480	8,480	0	4,064	0.24	$7.7 \cdot 10^{-2}$	$1.78 \cdot 10^{-2}$	$1.51 \cdot 10^{-5}$
9	35374982	rs2149368	G	A	UNC13B	OMNI_EUR	8,480	8,480	0	3,472	0.205	$8.22 \cdot 10^{-2}$	$1.9 \cdot 10^{-2}$	$1.55 \cdot 10^{-5}$
17	58504201	rs11655643	C	T	C17orf64	OMNI_EUR	8,479	8,479	0	1,708	0.101	0.11	$2.55 \cdot 10^{-2}$	$1.56 \cdot 10^{-5}$
20	19280659	rs6081560	A	G	SLC24A3	OMNI_EUR	8,479	8,479	0	5,351	0.316	$7.11 \cdot 10^{-2}$	$1.65 \cdot 10^{-2}$	$1.75 \cdot 10^{-5}$
6	31206979	rs2394895	T	C	HLA-C	EX_EUR	8,511	8,511	0	2,665	0.157	$9.12 \cdot 10^{-2}$	$2.13 \cdot 10^{-2}$	$1.81 \cdot 10^{-5}$
3	41853161	rs7632387	T	C	ULK4	OMNI_EUR	8,446	8,446	0	3,850	0.228	$7.83 \cdot 10^{-2}$	$1.83 \cdot 10^{-2}$	$1.82 \cdot 10^{-5}$
18	60878883	rs9955190	A	G	BCL2	OMNI_EUR	8,478	8,478	0	5,944	0.351	$6.85 \cdot 10^{-2}$	$1.6 \cdot 10^{-2}$	$1.85 \cdot 10^{-5}$

7.4 Previously identified risk loci

Table 23 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 11 variants that show at least nominal significance ($p < 0.05$) in this study. Out of the 23 variants in both studies, 8 exhibit the same direction of effect with the known result (binomial test $p = 0.953$).

Table 23: Top known loci in MERGE model invn Adjusted Age+Age2+BMI (**bold** variants indicate matching direction of effect)

CHR	POS	ID	EA	OA	N	FREQ	EFFECT	STDEERR	P	COHORT	GENE_CLOSEST	R ²	ID_KNOWN	N_KNOWN	EFFECT_KNOWN	STDEERR_KNOWN	P_KNOWN
12	112007756	rs653178	C	T	8,512	0.398	$3.6 \cdot 10^{-2}$	$1.55 \cdot 10^{-2}$	$2.06 \cdot 10^{-2}$	EX_EUR	ATXN2	1	rs653178	$2 \cdot 10^5$	-0.48	$6.26 \cdot 10^{-2}$	$1.64 \cdot 10^{-14}$
12	11184608	rs3184504	T	C	8,511	0.388	$3.85 \cdot 10^{-2}$	$1.56 \cdot 10^{-2}$	$1.35 \cdot 10^{-2}$	EX_EUR	SH2B3	1	rs3184504	$2 \cdot 10^5$	0.48	$6.29 \cdot 10^{-2}$	$2.33 \cdot 10^{-14}$
4	81164723	rs1458038	T	C	8,479	0.692	$1.48 \cdot 10^{-2}$	$1.65 \cdot 10^{-2}$	0.37	OMNI_EUR	FGF5	1	rs1458038	$2 \cdot 10^5$	0.503	$7.02 \cdot 10^{-2}$	$7.91 \cdot 10^{-13}$
12	112072424	rs11065987	G	A	8,512	0.624	$3.38 \cdot 10^{-2}$	$1.57 \cdot 10^{-2}$	$3.1 \cdot 10^{-2}$	EX_EUR	BRAP	1	rs11065987	$2 \cdot 10^5$	0.449	$6.46 \cdot 10^{-2}$	$3.43 \cdot 10^{-12}$
15	75077367	rs1378942	C	A	8,512	0.447	$4.02 \cdot 10^{-2}$	$1.55 \cdot 10^{-2}$	$9.58 \cdot 10^{-3}$	EX_EUR	CSK	1	rs1378942	$2 \cdot 10^5$	0.445	$6.4 \cdot 10^{-2}$	$3.47 \cdot 10^{-12}$
12	112486818	rs17696736	G	A	8,512	0.6	$2.25 \cdot 10^{-2}$	$1.54 \cdot 10^{-2}$	0.146	EX_EUR	NAA25	1	rs17696736	$2 \cdot 10^5$	0.422	$6.34 \cdot 10^{-2}$	$2.8 \cdot 10^{-11}$
12	112906415	rs11066320	A	G	8,478	0.399	$1.62 \cdot 10^{-2}$	$1.55 \cdot 10^{-2}$	0.295	OMNI_EUR	PTPN11	1	rs11066320	$2 \cdot 10^5$	-0.413	$6.32 \cdot 10^{-2}$	$6.32 \cdot 10^{-11}$
15	75057203	rs4886406	G	T	8,478	0.283	$3.26 \cdot 10^{-2}$	$1.7 \cdot 10^{-2}$	$5.52 \cdot 10^{-2}$	OMNI_EUR	CYP1A2	1	rs4886406	$2 \cdot 10^5$	-0.426	$6.85 \cdot 10^{-2}$	$4.83 \cdot 10^{-10}$
15	75125645	rs6495122	A	C	8,512	0.53	$2.61 \cdot 10^{-2}$	$1.54 \cdot 10^{-2}$	$9.06 \cdot 10^{-2}$	EX_EUR	CPLX3	1	rs6495122	$2 \cdot 10^5$	-0.383	$6.23 \cdot 10^{-2}$	$8.41 \cdot 10^{-10}$
15	75115895	rs7162232	G	A	8,479	0.332	$3.47 \cdot 10^{-2}$	$1.63 \cdot 10^{-2}$	$3.39 \cdot 10^{-2}$	OMNI_EUR	LMAN1L	1	rs7162232	$2 \cdot 10^5$	0.416	$6.89 \cdot 10^{-2}$	$1.58 \cdot 10^{-9}$
12	90008959	rs2681472	A	G	8,510	0.924	$6.33 \cdot 10^{-2}$	$2.92 \cdot 10^{-2}$	$3 \cdot 10^{-2}$	EX_EUR	ATP2B1	1	rs2681472	$2 \cdot 10^5$	-0.492	$8.36 \cdot 10^{-2}$	$3.9 \cdot 10^{-9}$
15	75140854	rs3765066	G	A	8,480	0.432	$2.93 \cdot 10^{-2}$	$1.58 \cdot 10^{-2}$	$6.34 \cdot 10^{-2}$	OMNI_EUR	SCAMP2	1	rs3765066	$2 \cdot 10^5$	0.382	$6.51 \cdot 10^{-2}$	$4.17 \cdot 10^{-9}$
10	63524591	rs1530440	C	T	8,511	0.801	$1.49 \cdot 10^{-2}$	$1.93 \cdot 10^{-2}$	0.441	EX_EUR	C10orf107	1	rs1530440	$2 \cdot 10^5$	-0.459	$7.92 \cdot 10^{-2}$	$6.71 \cdot 10^{-9}$
1	11883731	rs12567136	C	T	8,480	0.832	$7.91 \cdot 10^{-2}$	$2.05 \cdot 10^{-2}$	$1.17 \cdot 10^{-4}$	OMNI_EUR	CLCN6	1	rs12567136	$2 \cdot 10^5$	-0.488	$8.56 \cdot 10^{-2}$	$1.15 \cdot 10^{-8}$
1	11862778	rs17367504	A	G	8,512	0.832	$6.67 \cdot 10^{-2}$	$2.05 \cdot 10^{-2}$	$1.12 \cdot 10^{-3}$	EX_EUR	MTHFR	1	rs17367504	$2 \cdot 10^5$	-0.49	$8.61 \cdot 10^{-2}$	$1.29 \cdot 10^{-8}$
12	89942390	rs11105328	A	G	8,480	0.927	$5.85 \cdot 10^{-2}$	$2.94 \cdot 10^{-2}$	$4.65 \cdot 10^{-2}$	OMNI_EUR	POC1B-GALNT4	1	rs11105328	$2 \cdot 10^5$	-0.487	$8.66 \cdot 10^{-2}$	$1.83 \cdot 10^{-8}$
12	111798553	rs3742004	A	G	8,479	0.79	$3.97 \cdot 10^{-2}$	$1.89 \cdot 10^{-2}$	$3.6 \cdot 10^{-2}$	OMNI_EUR	FAM109A	1	rs3742004	$2 \cdot 10^5$	-0.429	$7.66 \cdot 10^{-2}$	$2.15 \cdot 10^{-8}$
15	75234610	rs11072518	T	C	8,480	0.472	$2.74 \cdot 10^{-2}$	$1.55 \cdot 10^{-2}$	$7.8 \cdot 10^{-2}$	OMNI_EUR	COX5A	1	rs11072518	$2 \cdot 10^5$	0.355	$6.45 \cdot 10^{-2}$	$3.78 \cdot 10^{-8}$
6	26107463	rs198846	A	G	8,512	0.101	$1.9 \cdot 10^{-2}$	$2.55 \cdot 10^{-2}$	0.456	EX_EUR	HIST1H1T	1	rs198846	$2 \cdot 10^5$	-0.487	$8.85 \cdot 10^{-2}$	$3.8 \cdot 10^{-8}$
6	26091179	rs1799945	G	C	8,512	0.9	$1.83 \cdot 10^{-2}$	$2.56 \cdot 10^{-2}$	0.474	EX_EUR	HFE	1	rs1799945	$2 \cdot 10^5$	-0.482	$8.82 \cdot 10^{-2}$	$4.78 \cdot 10^{-8}$
12	111788402	rs10219736	C	T	8,476	0.791	$4.08 \cdot 10^{-2}$	$1.9 \cdot 10^{-2}$	$3.14 \cdot 10^{-2}$	OMNI_EUR	CUX2	1	rs10219736	$2 \cdot 10^5$	-0.414	$7.58 \cdot 10^{-2}$	$4.88 \cdot 10^{-8}$
6	26107463	rs198846	A	G	8,512	0.101	$1.9 \cdot 10^{-2}$	$2.55 \cdot 10^{-2}$	0.456	EX_EUR	HIST1H2BC	1	rs198833	$2 \cdot 10^5$	-0.485	$8.88 \cdot 10^{-2}$	$4.58 \cdot 10^{-8}$
15	75189930	rs1130741	A	G	8,512	0.572	$1.87 \cdot 10^{-2}$	$1.57 \cdot 10^{-2}$	0.234	EX_EUR	MPI	1	rs7495739	$2 \cdot 10^5$	-0.335	$6.15 \cdot 10^{-2}$	$5.02 \cdot 10^{-8}$
12	112486818	rs17696736	G	A	8,512	0.6	$2.25 \cdot 10^{-2}$	$1.54 \cdot 10^{-2}$	0.146	EX_EUR	TRAFD1	0.922	rs17630235	$2 \cdot 10^5$	0.447	$6.4 \cdot 10^{-2}$	$2.92 \cdot 10^{-12}$
12	112486818	rs17696736	G	A	8,512	0.6	$2.25 \cdot 10^{-2}$	$1.54 \cdot 10^{-2}$	0.146	EX_EUR	HECTD4	0.913	rs11066188	$2 \cdot 10^5$	0.447	$6.41 \cdot 10^{-2}$	$3.06 \cdot 10^{-12}$
7	2508072	rs2906166	T	C	8,479	0.261	$3.28 \cdot 10^{-2}$	$1.75 \cdot 10^{-2}$	$6.14 \cdot 10^{-2}$	OMNI_EUR	GRIFIN	0.819	rs2969070	$2 \cdot 10^5$	-0.386	$6.47 \cdot 10^{-2}$	$2.57 \cdot 10^{-9}$

8 LDL Cholesterol (LDL_DIRECT)

8.1 Summary

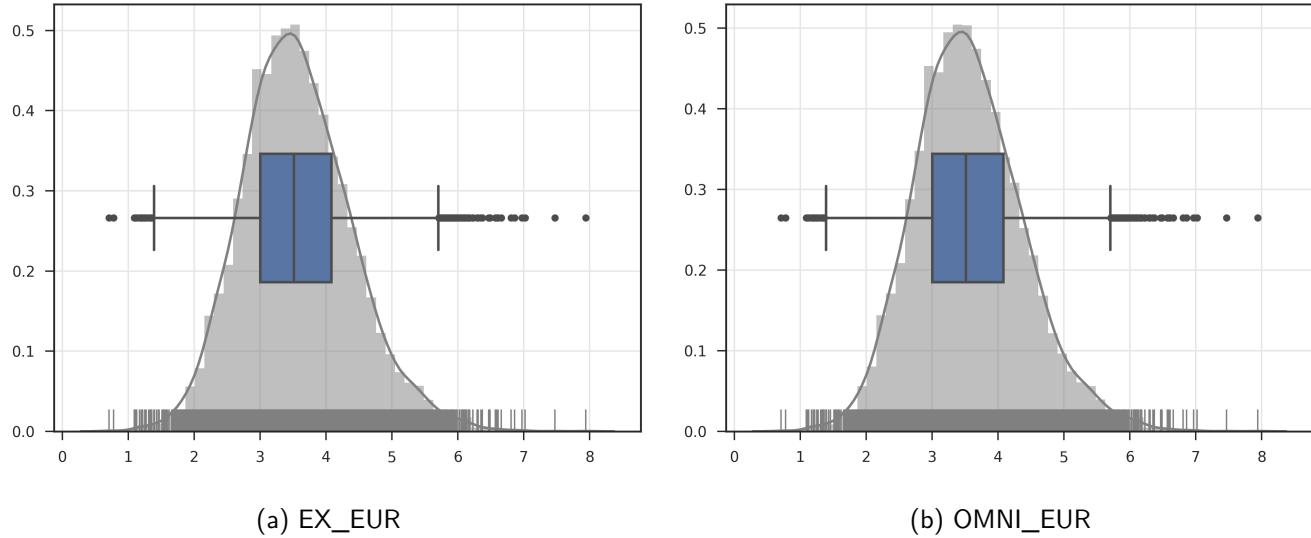


Figure 19: Distribution of LDL_DIRECT in cohort-level analyses

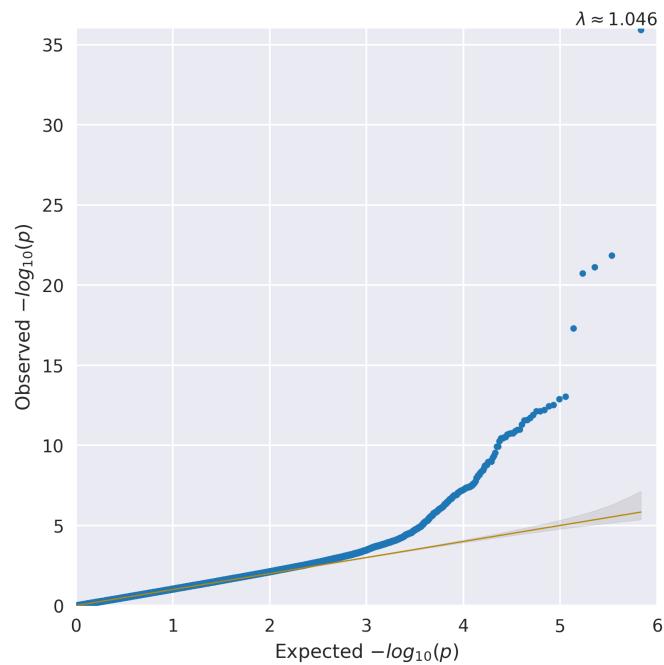
Table 24: Summary of samples removed from LDL Cholesterol analysis by cohort and model

Cohort	Array	Ancestry	Trans	Covars	Total	-SampleQc	-missObs	-Kinship	-PcOutlier
EX_EUR	EX	EUR	invn	Age+Age2+BMI	10071	36	2848	1104	2
OMNI_EUR	OMNI	EUR	invn	Age+Age2+BMI	10048	69	2841	1074	0

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

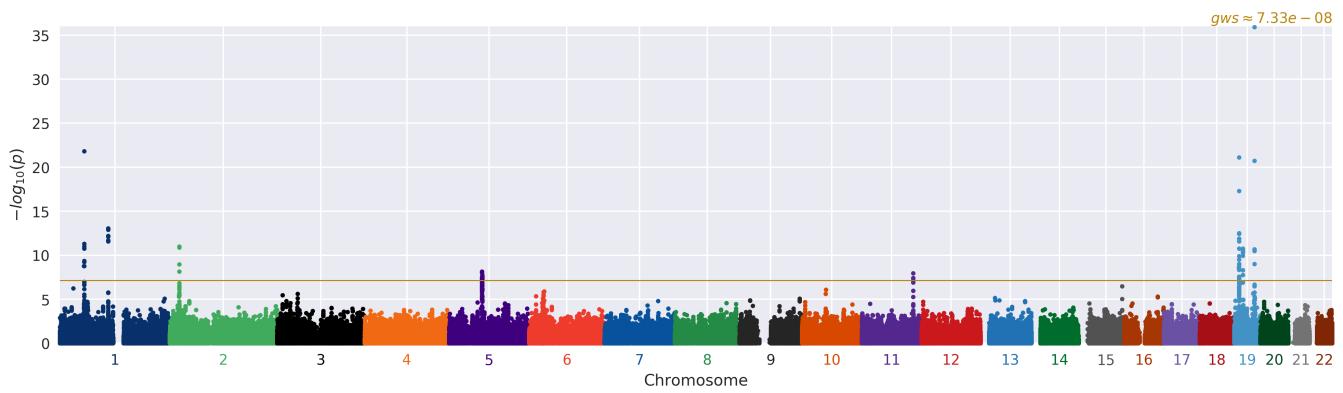
Cohort	Array	Ancestry	Trans	Covars	PCs	N	Male	Female	Max	Min	μ	\tilde{x}	σ
EX_EUR	EX	EUR	invn	Age+Age2+BMI	10	6090	6090	0	7.47	0.71	3.564	3.51	0.83
OMNI_EUR	OMNI	EUR	invn	Age+Age2+BMI	4	6080	6080	0	7.94	0.71	3.564	3.52	0.831

8.2 Calibration



(a) invn Adjusted Age+Age2+BMI

Figure 20: QQ plots for LDL_DIRECT in the MERGE analysis



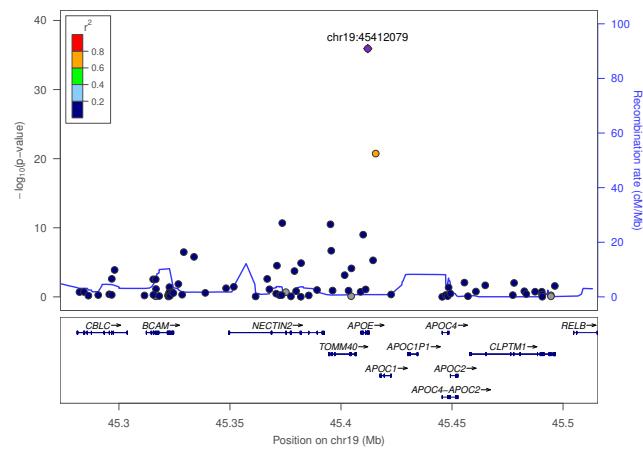
(a) invn Adjusted Age+Age2+BMI

Figure 21: Manhattan plots for LDL_DIRECT in the MERGE analysis

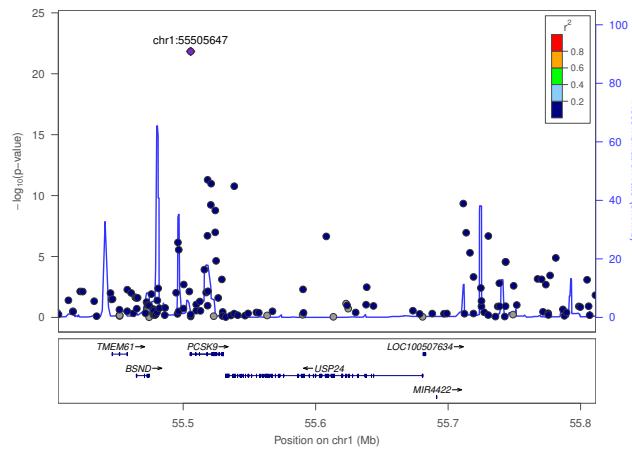
8.3 Top associations

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

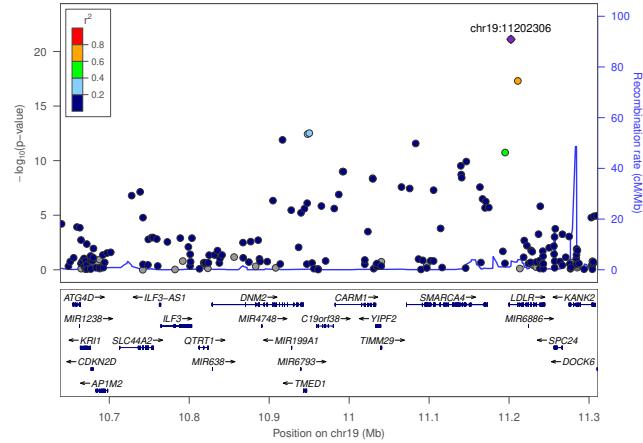
CHR	POS	ID	EA	OA	GENE _{CLOSEST}	COHORT	N	MALE	FEMALE	MAC	FREQ	EFFECT	STDERR	P
19	45412079	rs7412	C	T	APOE	EX_EUR	6,089	6,089	0	611	0.95	0.529	$4.15 \cdot 10^{-2}$	$1.2 \cdot 10^{-36}$
1	55505647	rs11591147	G	T	PCSK9	EX_EUR	6,090	6,090	0	576	0.953	0.414	$4.22 \cdot 10^{-2}$	$1.46 \cdot 10^{-22}$
19	11202306	rs6511720	G	T	LDLR	EX_EUR	6,090	6,090	0	1,570	0.871	0.261	$2.71 \cdot 10^{-2}$	$7.63 \cdot 10^{-22}$
19	45415640	rs445925	G	A	APOC1	EX_EUR	6,090	6,090	0	819	0.933	0.348	$3.64 \cdot 10^{-2}$	$1.82 \cdot 10^{-21}$
1	109817192	rs7528419	A	G	CELSR2	OMNI_EUR	6,076	6,076	0	2,739	0.775	0.162	$2.17 \cdot 10^{-2}$	$8.94 \cdot 10^{-14}$
19	10950125	rs11881156	C	T	C19orf38	OMNI_EUR	6,079	6,079	0	2,001	0.835	0.178	$2.44 \cdot 10^{-2}$	$3.01 \cdot 10^{-13}$
19	10916684	rs2287029	C	T	DNM2	OMNI_EUR	6,076	6,076	0	1,990	0.836	0.174	$2.45 \cdot 10^{-2}$	$1.25 \cdot 10^{-12}$
1	109821511	rs602633	G	T	PSRC1	EX_EUR	6,086	6,086	0	2,779	0.228	0.153	$2.17 \cdot 10^{-2}$	$1.95 \cdot 10^{-12}$
19	11083210	rs4804554	G	T	SMARCA4	OMNI_EUR	6,079	6,079	0	2,608	0.785	0.155	$2.21 \cdot 10^{-2}$	$2.66 \cdot 10^{-12}$
2	21277922	rs6548010	G	A	APOB	OMNI_EUR	6,080	6,080	0	3,433	0.718	0.138	$2.02 \cdot 10^{-2}$	$1.01 \cdot 10^{-11}$
1	55538552	rs10493176	T	G	USP24	OMNI_EUR	6,080	6,080	0	2,914	0.76	0.144	$2.14 \cdot 10^{-2}$	$1.7 \cdot 10^{-11}$
19	19379549	rs58542926	C	T	TM6SF2	EX_EUR	6,089	6,089	0	735	0.94	0.255	$3.79 \cdot 10^{-2}$	$1.7 \cdot 10^{-11}$
19	45373565	rs395908	G	A	NECTIN2	OMNI_EUR	6,078	6,078	0	766	0.937	0.251	$3.73 \cdot 10^{-2}$	$2.09 \cdot 10^{-11}$
19	19723215	rs10500212	C	T	PBX4	OMNI_EUR	6,080	6,080	0	742	0.939	0.25	$3.75 \cdot 10^{-2}$	$2.97 \cdot 10^{-11}$
19	45395266	rs157580	A	G	TOMM40	EX_EUR	6,090	6,090	0	3,321	0.273	0.135	$2.03 \cdot 10^{-2}$	$3.16 \cdot 10^{-11}$
19	19662220	rs17216525	C	T	CILP2	EX_EUR	6,090	6,090	0	755	0.938	0.248	$3.73 \cdot 10^{-2}$	$3.55 \cdot 10^{-11}$
19	19407718	rs10401969	T	C	SUGP1	EX_EUR	6,090	6,090	0	731	0.94	0.252	$3.79 \cdot 10^{-2}$	$3.56 \cdot 10^{-11}$
19	19329924	rs2228603	C	T	NCAN	EX_EUR	6,090	6,090	0	786	0.935	0.236	$3.66 \cdot 10^{-2}$	$1.16 \cdot 10^{-10}$
19	10991827	rs11880628	G	A	CARM1	OMNI_EUR	6,077	6,077	0	2,884	0.763	0.131	$2.14 \cdot 10^{-2}$	$9.98 \cdot 10^{-10}$
2	21320516	rs2337383	G	A	TDRD15	OMNI_EUR	6,080	6,080	0	3,067	0.748	0.128	$2.09 \cdot 10^{-2}$	$1.06 \cdot 10^{-9}$



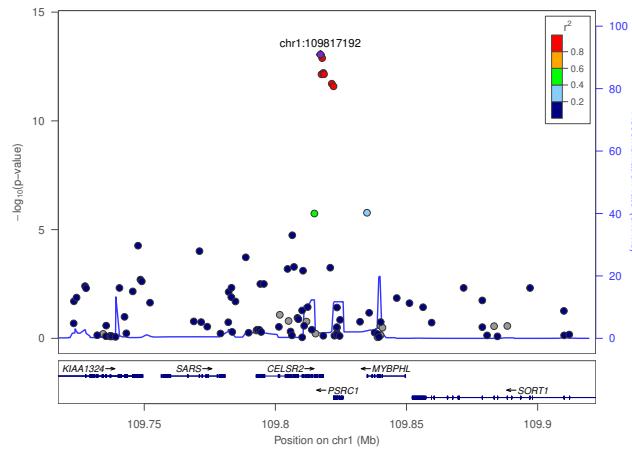
(a) rs7412 ±100kb



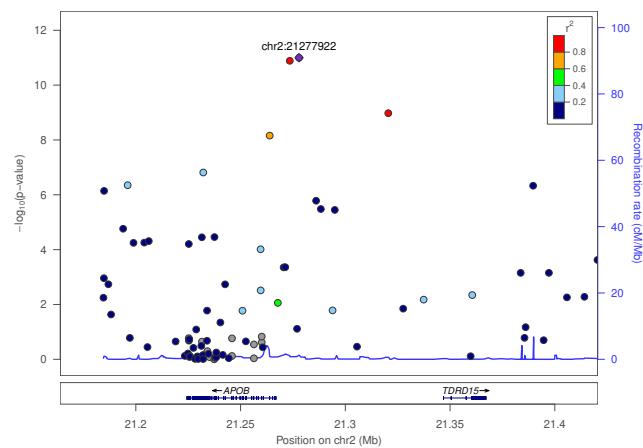
(b) rs11591147 ±100kb



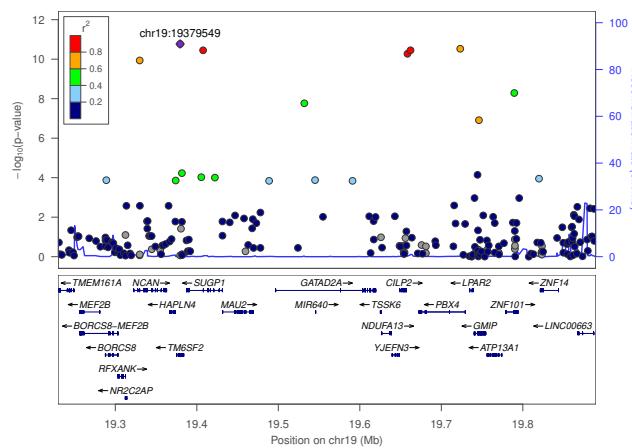
(c) rs6511720 ±100kb



(d) rs7528419 ±100kb



(e) rs6548010 ±100kb



(f) rs58542926 ±100kb

Figure 22: Regional plots for cohort MERGE model invn Adjusted Age+Age2+BMI (Continued on next page)

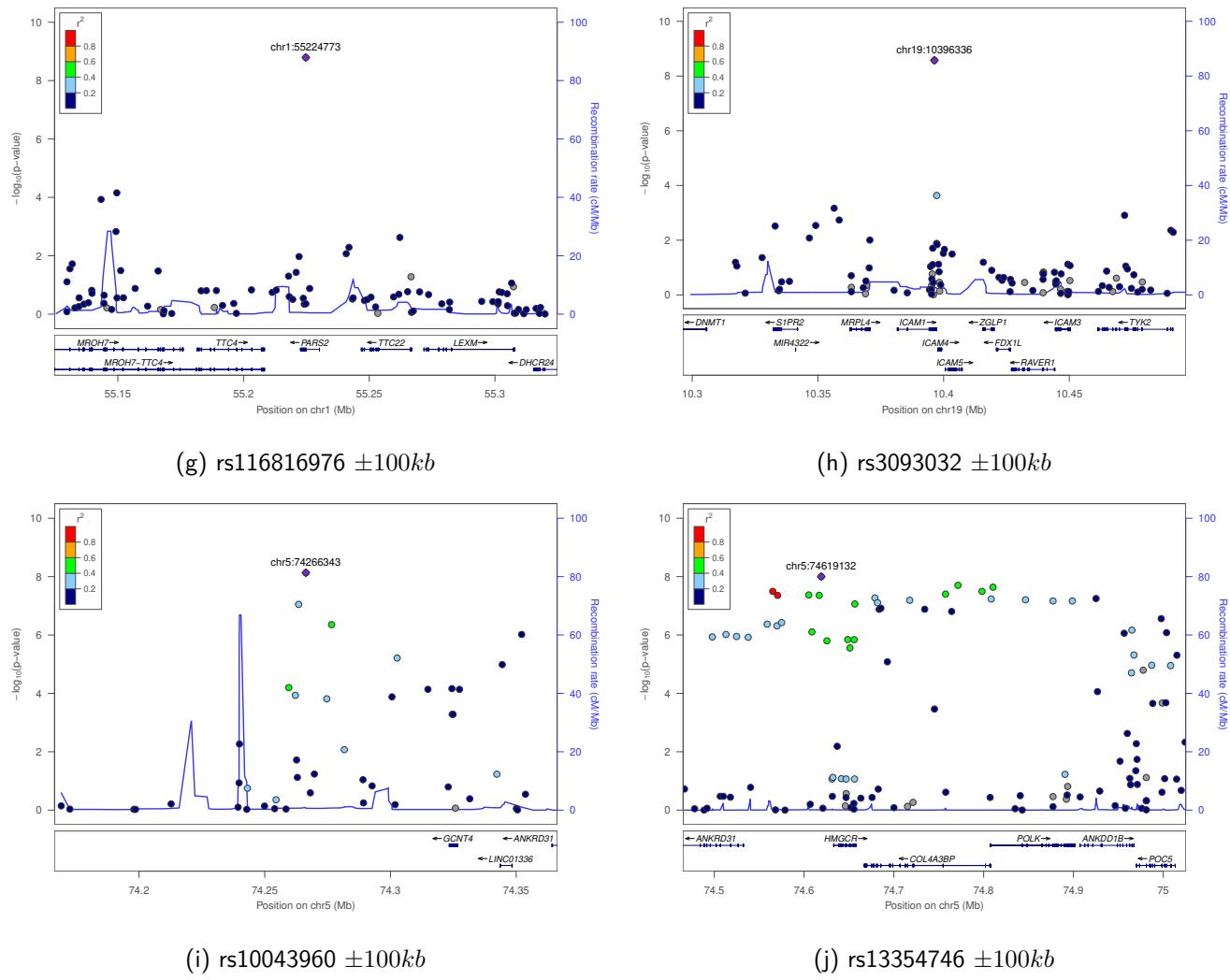


Figure 22: Regional plots for cohort MERGE model invn Adjusted Age+Age2+BMI (Continued)

8.4 Previously identified risk loci

Table 27 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 [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 49 variants that show at least nominal significance ($p < 0.05$) in this study. Out of the 50 variants in both studies, 50 exhibit the same direction of effect with the known result (binomial test $p = 8.88e - 16$).

9 Body Mass Index (BMI)

9.1 Summary

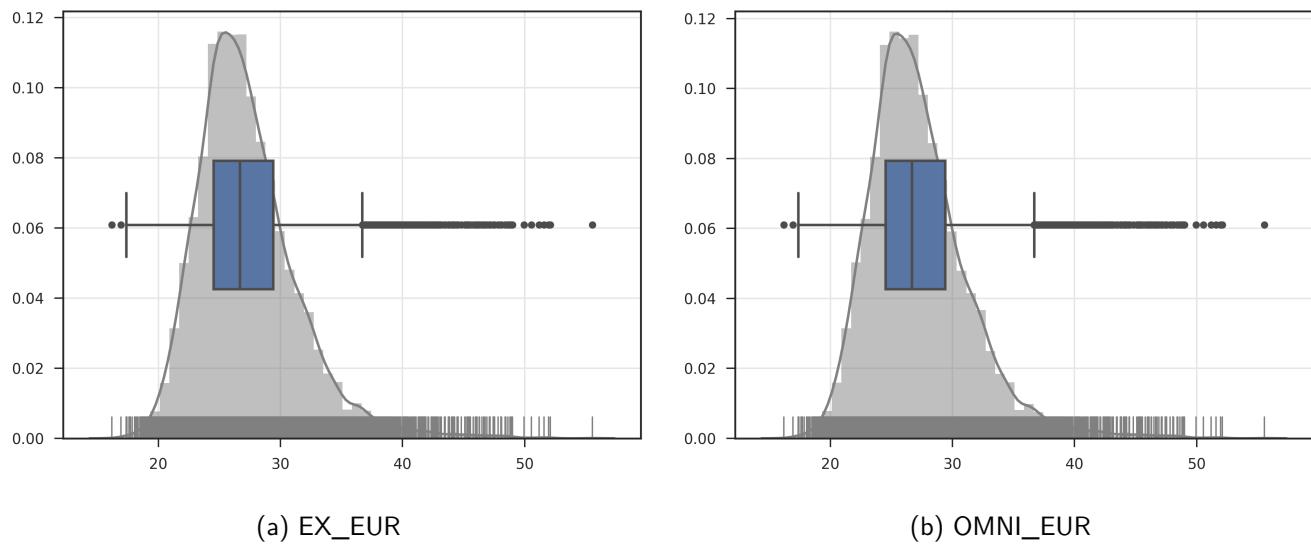


Figure 23: Distribution of BMI in cohort-level analyses

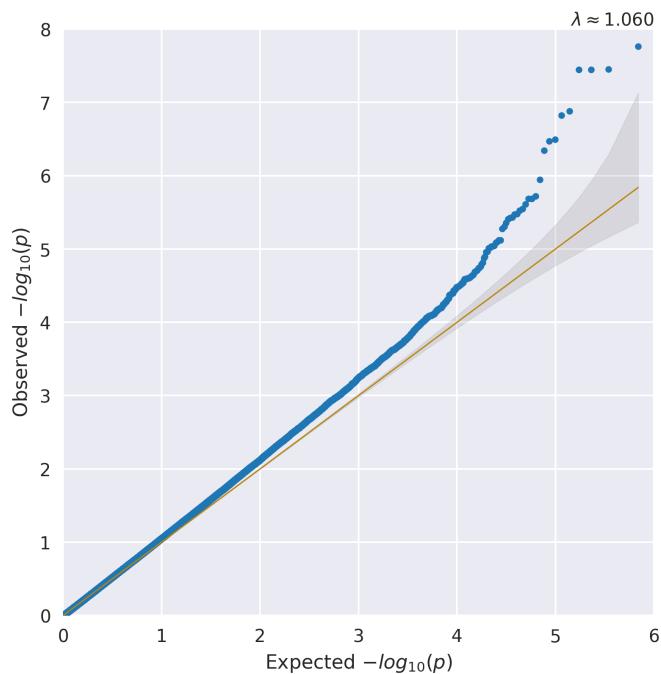
Table 28: Summary of samples removed from Body Mass Index analysis by cohort and model

Cohort	Array	Ancestry	Trans	Covars	Total	-SampleQc	-missObs	-Kinship	-PcOutlier
EX_EUR	EX	EUR	invn	Age+Age2	10071	36	4	1518	1
OMNI_EUR	OMNI	EUR	invn	Age+Age2	10048	69	4	1495	1

Table 29: Summary of samples remaining for Body Mass Index analysis by cohort and model

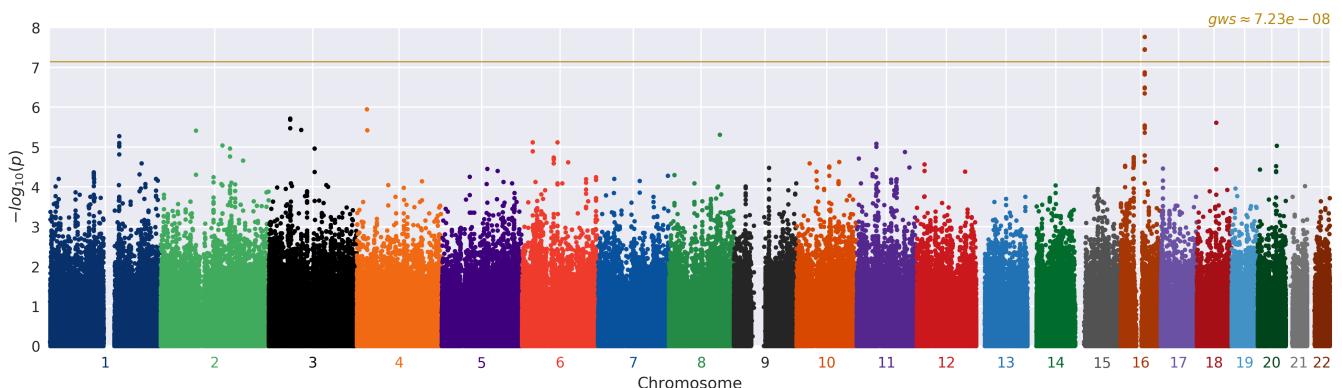
Cohort	Array	Ancestry	Trans	Covars	PCs	N	Male	Female	Max	Min	μ	\tilde{x}	σ
EX_EUR	EX	EUR	invn	Age+Age2	5	8512	8512	0	55.54	16.947	27.293	26.644	4.205
OMNI_EUR	OMNI	EUR	invn	Age+Age2	9	8479	8479	0	55.54	16.947	27.284	26.673	4.192

9.2 Calibration



(a) invn Adjusted Age+Age2

Figure 24: QQ plots for BMI in the MERGE analysis



(a) invn Adjusted Age+Age2

Figure 25: Manhattan plots for BMI in the MERGE analysis

9.3 Top associations

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

CHR	POS	ID	EA	OA	GENE _{CLOSEST}	COHORT	N	MALE	FEMALE	MAC	FREQ	EFFECT	STDERR	P
16	53825488	rs9941349	T	C	FTO	EX_EUR	8,510	8,510	0	6,978	0.59	$8.81 \cdot 10^{-2}$	$1.56 \cdot 10^{-2}$	$1.71 \cdot 10^{-8}$
4	23165631	rs11932311	C	T	GBA3	OMNI_EUR	8,470	8,470	0	5,274	0.689	$8 \cdot 10^{-2}$	$1.64 \cdot 10^{-2}$	$1.13 \cdot 10^{-6}$
3	48487338	rs9876781	G	A	ATRIP	EX_EUR	8,512	8,512	0	6,561	0.615	$7.38 \cdot 10^{-2}$	$1.55 \cdot 10^{-2}$	$1.91 \cdot 10^{-6}$
3	48419897	rs6442117	T	C	FBXW12	EX_EUR	8,512	8,512	0	6,548	0.385	$7.35 \cdot 10^{-2}$	$1.55 \cdot 10^{-2}$	$2.06 \cdot 10^{-6}$
18	43948285	rs6507697	C	T	RNF165	OMNI_EUR	8,479	8,479	0	5,130	0.303	$7.93 \cdot 10^{-2}$	$1.68 \cdot 10^{-2}$	$2.44 \cdot 10^{-6}$
3	72690645	rs4676890	T	C	SHQ1	OMNI_EUR	8,478	8,478	0	3,904	0.77	$8.42 \cdot 10^{-2}$	$1.82 \cdot 10^{-2}$	$3.68 \cdot 10^{-6}$
2	79039355	rs896530	A	G	REG3G	OMNI_EUR	8,479	8,479	0	4,781	0.282	$7.83 \cdot 10^{-2}$	$1.7 \cdot 10^{-2}$	$3.9 \cdot 10^{-6}$
8	115157455	rs11988087	T	C	CSMD3	OMNI_EUR	8,478	8,478	0	728	0.957	0.172	$3.76 \cdot 10^{-2}$	$4.96 \cdot 10^{-6}$
1	155508882	rs6696888	A	G	ASH1L	EX_EUR	8,511	8,511	0	7,063	0.415	$7.15 \cdot 10^{-2}$	$1.57 \cdot 10^{-2}$	$5.29 \cdot 10^{-6}$
6	23998157	rs554400	A	G	NRSN1	OMNI_EUR	8,472	8,472	0	1,802	0.894	0.112	$2.49 \cdot 10^{-2}$	$7.59 \cdot 10^{-6}$
6	79835010	rs6454096	A	G	PHIP	OMNI_EUR	8,443	8,443	0	6,825	0.596	$7.05 \cdot 10^{-2}$	$1.58 \cdot 10^{-2}$	$7.62 \cdot 10^{-6}$
1	155873314	rs2993207	C	T	RIT1	OMNI_EUR	8,458	8,458	0	6,295	0.372	$7.1 \cdot 10^{-2}$	$1.59 \cdot 10^{-2}$	$7.98 \cdot 10^{-6}$
11	44098000	rs178524	C	T	ACCS	OMNI_EUR	8,476	8,476	0	5,205	0.693	$7.4 \cdot 10^{-2}$	$1.66 \cdot 10^{-2}$	$8.2 \cdot 10^{-6}$
1	155860091	rs1749405	A	G	SYT11	OMNI_EUR	8,479	8,479	0	6,534	0.385	$7 \cdot 10^{-2}$	$1.58 \cdot 10^{-2}$	$9.04 \cdot 10^{-6}$
2	138716177	rs62168710	A	G	HNMT	EX_EUR	8,512	8,512	0	8,166	0.48	$6.84 \cdot 10^{-2}$	$1.54 \cdot 10^{-2}$	$9.1 \cdot 10^{-6}$
20	42720099	rs932415	A	C	JPH2	OMNI_EUR	8,476	8,476	0	3,744	0.779	$8.21 \cdot 10^{-2}$	$1.85 \cdot 10^{-2}$	$9.25 \cdot 10^{-6}$
1	155891045	rs625658	C	A	KIAA0907	OMNI_EUR	8,479	8,479	0	6,317	0.373	$7.03 \cdot 10^{-2}$	$1.59 \cdot 10^{-2}$	$9.66 \cdot 10^{-6}$
11	44142934	rs7935138	C	T	EXT2	OMNI_EUR	8,478	8,478	0	5,416	0.681	$7.27 \cdot 10^{-2}$	$1.64 \cdot 10^{-2}$	$9.81 \cdot 10^{-6}$
3	103057272	rs9862353	C	A	ZPLD1	OMNI_EUR	8,478	8,478	0	4,017	0.763	$7.88 \cdot 10^{-2}$	$1.79 \cdot 10^{-2}$	$1.09 \cdot 10^{-5}$
2	155423435	rs4461221	T	C	GALNT13	OMNI_EUR	8,479	8,479	0	6,209	0.366	$7.01 \cdot 10^{-2}$	$1.59 \cdot 10^{-2}$	$1.1 \cdot 10^{-5}$

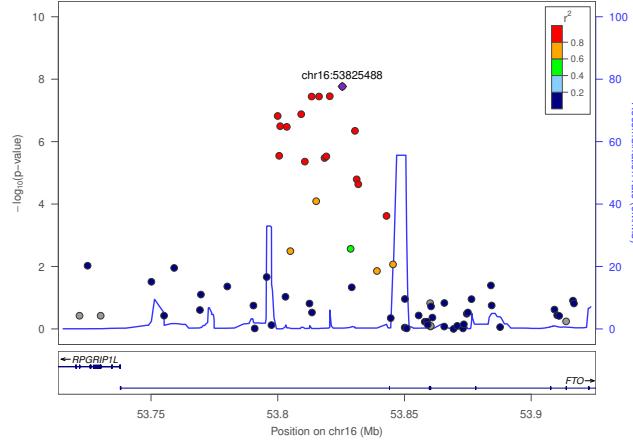


Figure 26: Regional plot for cohort MERGE model invn Adjusted Age+Age2: rs9941349 $\pm 100\text{kb}$

9.4 Previously identified risk loci

Table 31 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 [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

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