

AMP-DCC Data Analysis Report

NUS

Phase 1

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

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1 Data

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

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

Table 1: Genotype array information

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

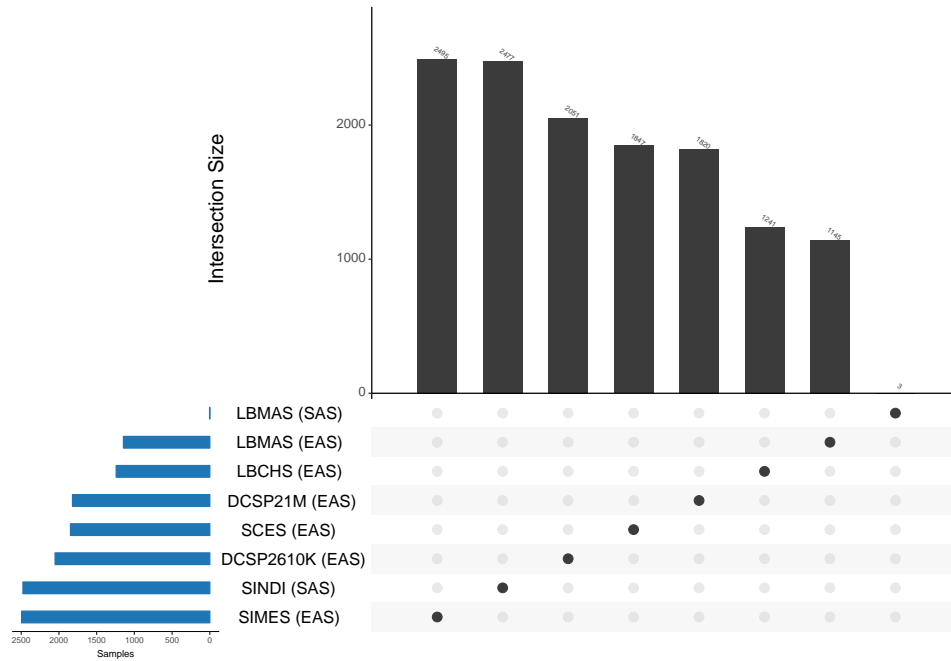


Figure 1: Samples remaining for analysis after quality control

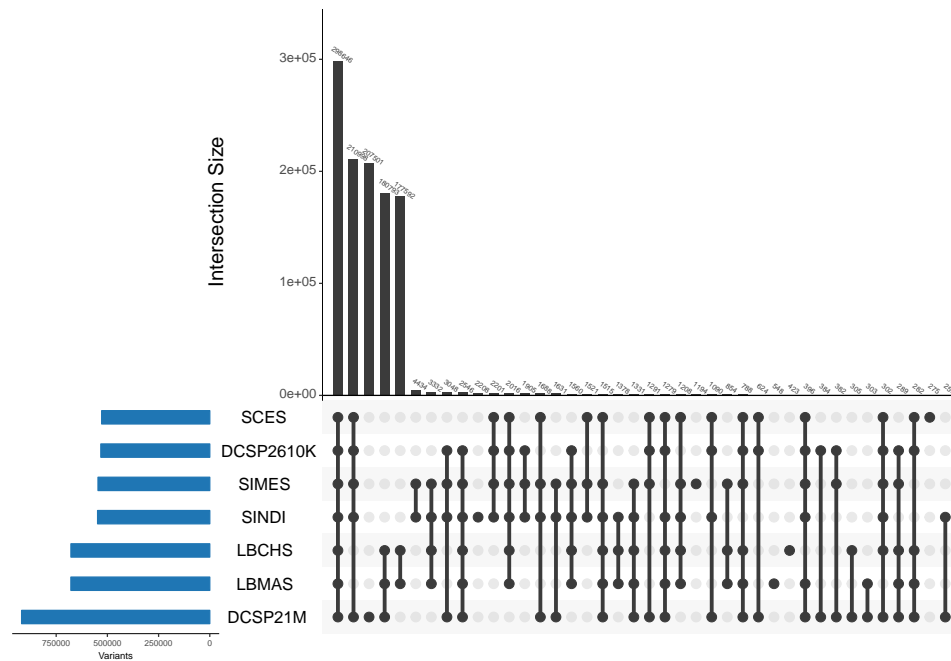


Figure 2: Variants remaining for analysis after quality control

2 Strategy

2.1 Sample structure and pipeline

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

2.1.1 Cohort-level analysis

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

Table 2: Cohort-level analysis

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

2.1.2 Meta-analysis

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

Table 3: Meta-analysis

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

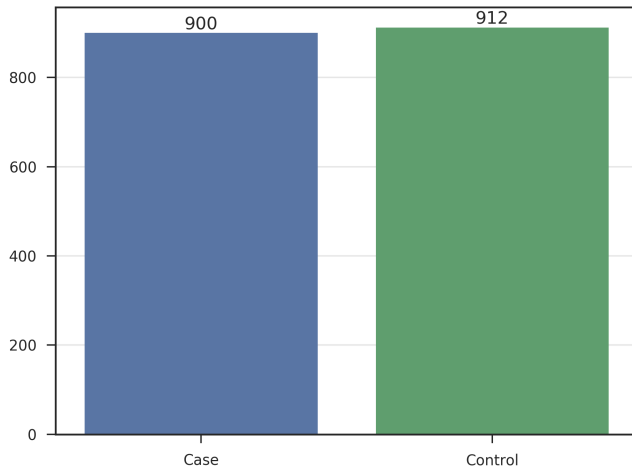
2.2 Ancestry Adjustment and Outlier Removal

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

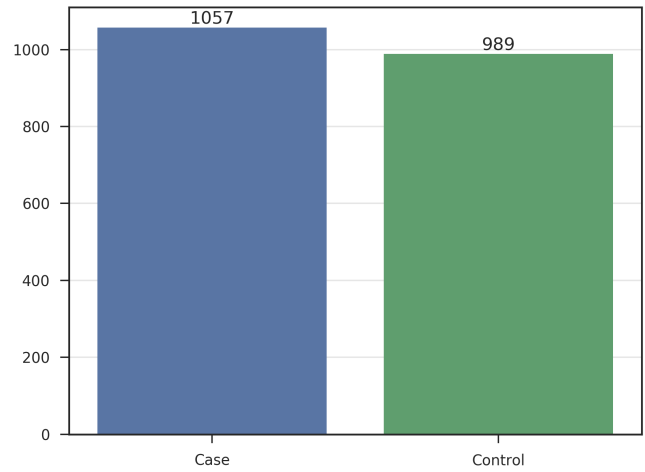
was repeated up to a maximum of ten times until no outliers were found, resulting in more homogeneous sample sets for each particular analysis. For this project, a hard minimum of 0 PC's to be included in analysis was set by the analyst.

3 Type 2 Diabetes (T2D)

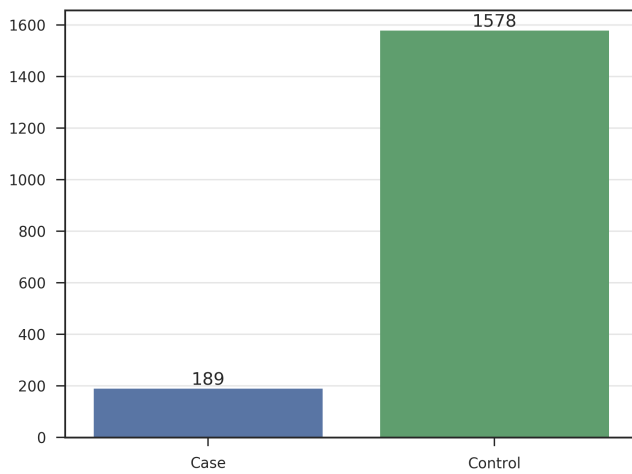
3.1 Summary



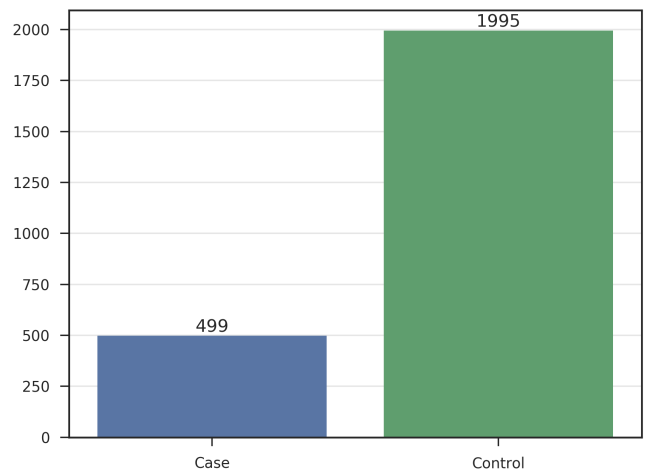
(a) DCSP21M_EAS



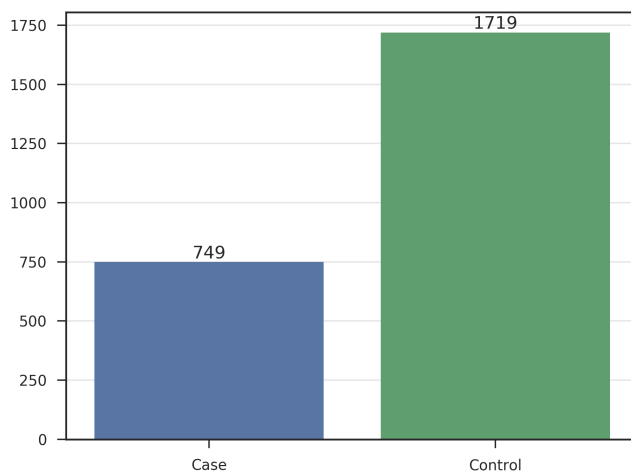
(b) DCSP2610K_EAS



(c) SCES_EAS



(d) SIMES_EAS



(e) SINDI_SAS

Figure 3: Distribution of T2D in META_NOLB by cohort

Table 4: Summary of samples removed from Type 2 Diabetes analysis by cohort and model

Cohort	Array	Ancestry	Trans	Covars	Total	-SampleQc	-KinshipCrossArray	-KinshipArray	-missObs	-PcOutlier
META_NOLB DCSP21M_EAS	DCSP21M	EAS	-	Age+SEX+BMI	1864	44	0	0	22	0
			-	Age+SEX	1864	44	0	0	9	0
META_NOLB DCSP2610K_EAS	DCSP2610K	EAS	-	Age+SEX	2087	36	0	0	6	10
			-	Age+SEX+BMI	2087	36	0	0	13	10
META_NOLB SCES_EAS	SCES	EAS	-	Age+SEX+BMI	1889	42	78	2	8	0
			-	Age+SEX	1889	42	78	2	2	5
META_NOLB SIMES_EAS	SIMES	EAS	-	Age+SEX+BMI	2542	47	1	131	19	0
			-	Age+SEX	2542	47	1	131	0	0
META_NOLB SINDI_SAS	SINDI	SAS	-	Age+SEX	2537	60	9	89	0	100
			-	Age+SEX+BMI	2537	60	9	89	7	111

Table 5: Summary of samples remaining for Type 2 Diabetes analysis by cohort and model

Cohort	Array	Ancestry	Trans	Covars	PCs	N	Male	Female	Case	Ctrl
META_NOLB DCSP21M_EAS	DCSP21M	EAS	-	Age+SEX+BMI	0	1798	1155	643	889	909
			-	Age+SEX	0	1811	1159	652	900	911
META_NOLB DCSP2610K_EAS	DCSP2610K	EAS	-	Age+SEX	0	2035	597	1438	1052	983
			-	Age+SEX+BMI	0	2028	595	1433	1045	983
META_NOLB SCES_EAS	SCES	EAS	-	Age+SEX+BMI	0	1759	903	856	188	1571
			-	Age+SEX	0	1760	902	858	189	1571
META_NOLB SIMES_EAS	SIMES	EAS	-	Age+SEX+BMI	1	2344	1168	1176	481	1863
			-	Age+SEX	1	2363	1178	1185	490	1873
META_NOLB SINDI_SAS	SINDI	SAS	-	Age+SEX	2	2279	1160	1119	708	1571
			-	Age+SEX+BMI	2	2261	1151	1110	702	1559

3.2 Calibration

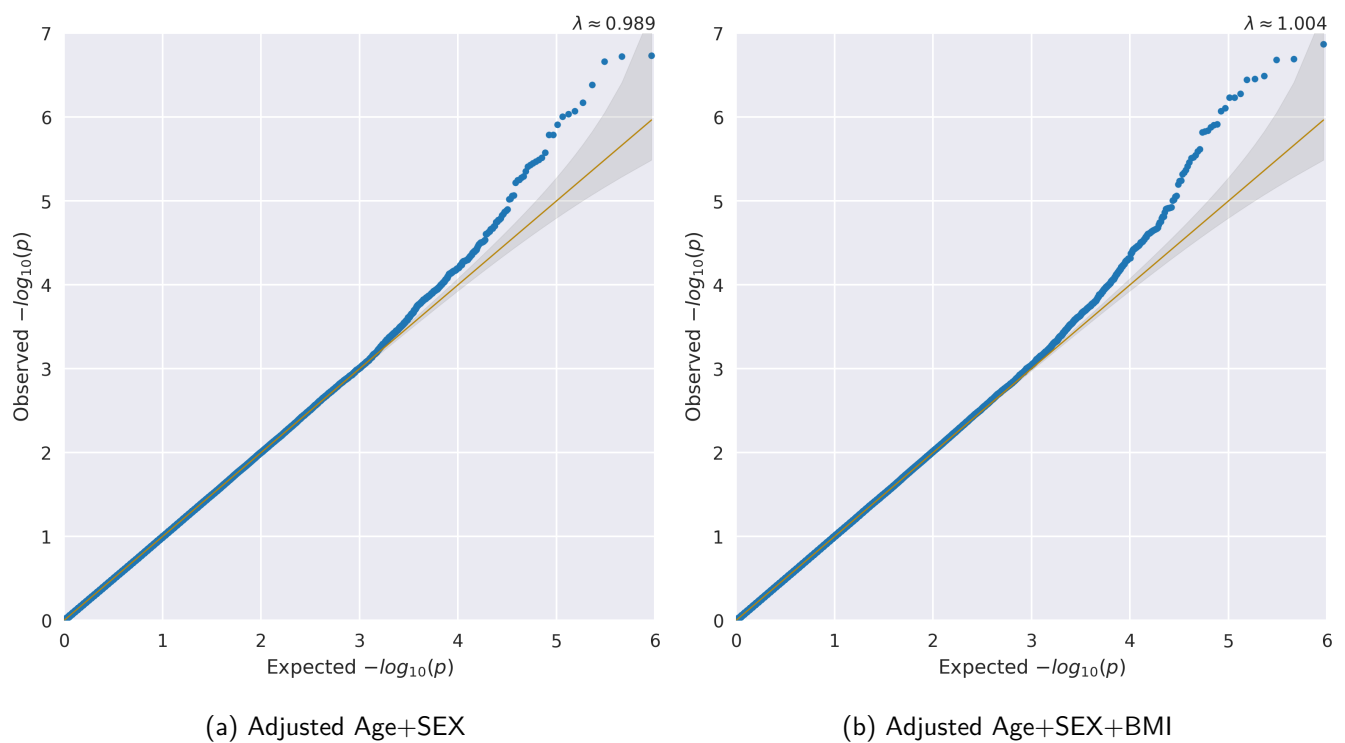
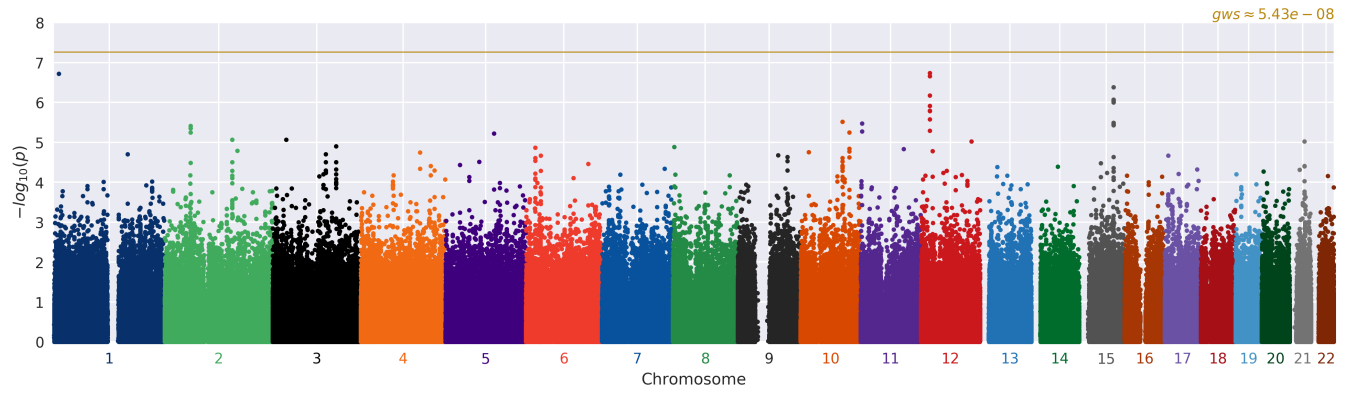
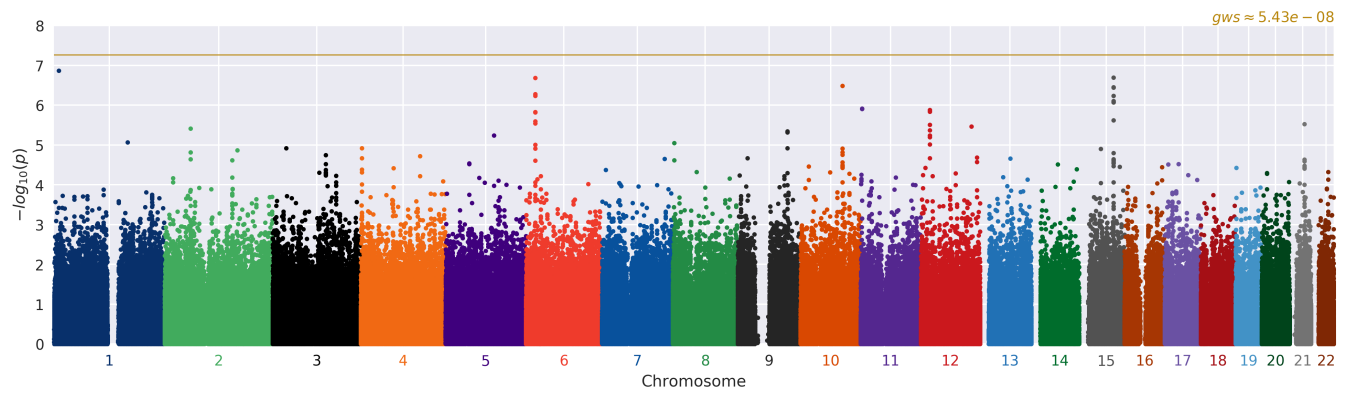


Figure 4: QQ plots for T2D in the META_NOLB analysis



(a) Adjusted Age+SEX



(b) Adjusted Age+SEX+BMI

Figure 5: Manhattan plots for T2D in the META_NOLB analysis

3.3 Top associations

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

CHR	POS	ID	EA	OA	GENE _{CLOSEST}	DIR	N	MALE	FEMALE	CASE	CTRL	FREQ _{AVG}	FREQ _{MIN}	FREQ _{MAX}	EFFECT	STDERR	OR	ZSCORE	P
12	20563134	rs978349	A	G	PDE3A	+++++	10,245	4,993	5,252	3,339	6,906	0.858	0.721	0.924	0.264	5.05 · 10 ⁻²	1.302	-5.215	1.84 · 10 ⁻⁷
1	10998509	rs744921	A	G	C1orf127	xxx++	4,642	2,338	2,304	1,198	3,444	1.49 · 10 ⁻²	2.33 · 10 ⁻³	2.79 · 10 ⁻²	0.933	0.179	2.542	5.21	1.89 · 10 ⁻⁷
15	77400388	rs3743478	C	T	PEAK1	+++++	10,248	4,996	5,252	3,339	6,909	0.384	0.339	0.456	0.188	3.71 · 10 ⁻²	1.207	5.063	4.13 · 10 ⁻⁷
15	77777632	rs7119	T	C	HMG20A	+++++	10,248	4,996	5,252	3,339	6,909	0.183	0.153	0.279	0.225	4.57 · 10 ⁻²	1.252	4.909	9.18 · 10 ⁻⁷
10	94347830	rs6583826	G	A	KIF11	+++++	10,247	4,995	5,252	3,339	6,908	0.745	0.722	0.77	0.192	4.11 · 10 ⁻²	1.212	-4.667	3.06 · 10 ⁻⁶
11	2858295	rs2299620	C	T	KCNQ1	+++++	10,200	4,968	5,232	3,329	6,871	0.268	2.22 · 10 ⁻²	0.359	0.211	4.53 · 10 ⁻²	1.234	-4.646	3.38 · 10 ⁻⁶
2	58068741	rs1106090	G	A	VRK2	+++++	10,248	4,996	5,252	3,339	6,909	0.471	0.416	0.561	0.169	3.66 · 10 ⁻²	1.184	-4.617	3.9 · 10 ⁻⁶
10	109871472	rs7912486	A	C	SORCS1	+xxxx	1,811	1,159	652	900	911	0.167	0.167	0.167	0.535	0.118	1.708	-4.541	5.6 · 10 ⁻⁶
5	108639741	rs6594369	A	G	PJA2	+++++	10,243	4,995	5,248	3,337	6,906	0.304	0.146	0.383	0.187	4.13 · 10 ⁻²	1.206	-4.525	6.05 · 10 ⁻⁶
2	152195934	rs4664356	G	A	TNFAIP6	+++++	10,245	4,994	5,251	3,339	6,906	0.451	0.384	0.489	0.162	3.64 · 10 ⁻²	1.176	4.451	8.54 · 10 ⁻⁶
3	30488348	rs4325953	C	T	TGFBR2	+++++	10,247	4,996	5,251	3,338	6,909	0.184	0.123	0.341	0.203	4.56 · 10 ⁻²	1.225	4.448	8.65 · 10 ⁻⁶
12	114120139	rs6489914	T	C	RBM19	xxx++	4,641	2,337	2,304	1,198	3,443	2.77 · 10 ⁻²	5.72 · 10 ⁻³	5.05 · 10 ⁻²	0.61	0.138	1.841	4.43	9.42 · 10 ⁻⁶
21	33385186	rs2833610	A	G	HUNK	+++++	10,245	4,994	5,251	3,338	6,907	0.433	0.39	0.479	0.164	3.71 · 10 ⁻²	1.179	-4.428	9.53 · 10 ⁻⁶
3	142541687	rs9841007	C	T	PCOLCE2	+++++	10,247	4,996	5,251	3,339	6,908	0.279	0.159	0.342	0.181	4.14 · 10 ⁻²	1.198	4.367	1.26 · 10 ⁻⁵
8	3853878	rs2554675	A	G	CSMD1	+++++	10,248	4,996	5,252	3,339	6,909	0.69	0.634	0.709	0.173	3.97 · 10 ⁻²	1.189	-4.36	1.3 · 10 ⁻⁵
6	20659459	rs6906327	A	G	CDKAL1	+++++	10,246	4,994	5,252	3,339	6,907	0.355	0.284	0.392	0.164	3.77 · 10 ⁻²	1.178	4.352	1.35 · 10 ⁻⁵
11	96870233	rs7124287	A	G	JRKL	+xxxx	1,811	1,159	652	900	911	0.141	0.141	0.141	0.545	0.126	1.725	4.331	1.48 · 10 ⁻⁵
2	163154363	rs13023380	G	A	IFIH1	+++++	10,241	4,992	5,249	3,338	6,903	8.62 · 10 ⁻²	4.42 · 10 ⁻³	0.305	0.283	6.56 · 10 ⁻²	1.327	-4.312	1.62 · 10 ⁻⁵
12	26989775	rs11048716	G	A	ITPR2	+++++	10,247	4,996	5,251	3,339	6,908	0.179	0.108	0.233	0.207	4.82 · 10 ⁻²	1.23	4.306	1.66 · 10 ⁻⁵
10	18408949	rs11012743	A	G	CACNB2	+++++	10,245	4,996	5,249	3,339	6,906	0.385	0.284	0.426	0.165	3.84 · 10 ⁻²	1.179	-4.293	1.76 · 10 ⁻⁵

Table 7: Top variants in the META_NOLB Adjusted Age+SEX+BMI model (**bold** variants indicate previously identified associations)

CHR	POS	ID	EA	OA	GENE _{CLOSEST}	DIR	N	MALE	FEMALE	CASE	CTRL	FREQ _{AVG}	FREQ _{MIN}	FREQ _{MAX}	EFFECT	STDERR	OR	ZSCORE	P
1	10998509	rs744921	A	G	C1orf127	xxx++	4,605	2,319	2,286	1,183	3,422	1.47 · 10 ⁻²	2.35 · 10 ⁻³	2.74 · 10 ⁻²	0.959	0.182	2.609	5.272	1.35 · 10 ⁻⁷
15	77777632	rs7119	T	C	HMG20A	+++++	10,190	4,972	5,218	3,305	6,885	0.183	0.153	0.28	0.245	4.71 · 10 ⁻²	1.277	5.197	2.03 · 10 ⁻⁷
6	20659459	rs6906327	A	G	CDKAL1	+++++	10,188	4,970	5,218	3,305	6,883	0.355	0.284	0.393	0.203	3.91 · 10 ⁻²	1.225	5.193	2.07 · 10 ⁻⁷
10	94347830	rs6583826	G	A	KIF11	+++++	10,189	4,971	5,218	3,305	6,884	0.745	0.722	0.77	0.217	4.25 · 10 ⁻²	1.242	-5.109	3.23 · 10 ⁻⁷
15	77410878	rs12904384	G	T	PEAK1	+++++	10,189	4,971	5,218	3,305	6,884	0.163	0.128	0.275	0.252	4.94 · 10 ⁻²	1.286	5.093	3.52 · 10 ⁻⁷
11	2858440	rs2237896	G	A	KCNQ1	+++++	10,184	4,967	5,217	3,304	6,880	0.273	2.19 · 10 ⁻²	0.361	0.228	4.69 · 10 ⁻²	1.256	-4.853	1.22 · 10 ⁻⁶
12	20563134	rs978349	A	G	PDE3A	+++++	10,187	4,969	5,218	3,305	6,882	0.858	0.722	0.924	0.251	5.19 · 10 ⁻²	1.285	-4.836	1.32 · 10 ⁻⁶
21	33385186	rs2833610	A	G	HUNK	+++++	10,187	4,970	5,217	3,304	6,883	0.433	0.39	0.478	0.179	3.83 · 10 ⁻²	1.196	-4.671	3 · 10 ⁻⁶
12	114120139	rs6489914	T	C	RBM19	xxx++	4,604	2,318	2,286	1,183	3,421	2.74 · 10 ⁻²	5.76 · 10 ⁻³	4.98 · 10 ⁻²	0.646	0.139	1.908	4.642	3.45 · 10 ⁻⁶
2	58068741	rs1106090	G	A	VRK2	+++++	10,190	4,972	5,218	3,305	6,885	0.471	0.416	0.561	0.175	3.78 · 10 ⁻²	1.191	-4.619	3.85 · 10 ⁻⁶
9	111693132	rs838818	C	T	IKBKAP	+++++	10,184	4,967	5,217	3,305	6,879	0.317	0.256	0.428	0.183	3.99 · 10 ⁻²	1.201	4.584	4.57 · 10 ⁻⁶
5	108639741	rs6594369	A	G	PJA2	+++++	10,185	4,971	5,214	3,303	6,882	0.304	0.146	0.382	0.195	4.3 · 10 ⁻²	1.216	-4.536	5.72 · 10 ⁻⁶
1	165811684	rs4657478	A	G	UCK2	+++++	10,190	4,972	5,218	3,305	6,885	1.39 · 10 ⁻²	6.19 · 10 ⁻³	3.49 · 10 ⁻²	0.725	0.163	2.065	-4.448	8.65 · 10 ⁻⁶
8	3853878	rs2554675	A	G	CSMD1	+++++	10,190	4,972	5,218	3,305	6,885	0.691	0.635	0.71	0.182	4.09 · 10 ⁻²	1.199	-4.443	8.89 · 10 ⁻⁶
4	2616727	rs7657265	A	G	FAM193A	+xxxx	1,798	1,155	643	889	909	0.233	0.233	0.233	0.494	0.113	1.64	4.379	1.2 · 10 ⁻⁵
9	111728577	rs874863	G	A	CTNNA1	+++++	10,188	4,970	5,218	3,305	6,883	0.2	0.15	0.296	0.2	4.58 · 10 ⁻²	1.222	4.377	1.2 · 10 ⁻⁵
3	30488348	rs4325953	C	T	TGFBR2	+++++	10,189	4,972	5,217	3,304	6,885	0.183	0.122	0.341	0.205	4.68 · 10 ⁻²	1.227	4.376	1.21 · 10 ⁻⁵
15	48576238	rs3784617	T	A	SLC12A1	xxx+x	2,342	1,167	1,175	479	1,863	8.97 · 10 ⁻²	8.97 · 10 ⁻²	8.97 · 10 ⁻²	0.531	0.122	1.701	4.369	1.25 · 10 ⁻⁵
2	163154363	rs13023380	G	A	IFIH1	+++++	10,183	4,968	5,215	3,304	6,879	8.62 · 10 ⁻²	4.44 · 10 ⁻³	0.307	0.289	6.63 · 10 ⁻²	1.334	-4.349	1.37 · 10 ⁻⁵
10	94465559	rs5015480	C	T	HHEX	+++++	10,189	4,972	5,217	3,304	6,885	0.749	0.614	0.818	0.184	4.25 · 10 ⁻²	1.202	-4.324	1.53 · 10 ⁻⁵

3.4 Previously identified risk loci

Table 8 shows statistics from the META_NOLB cohort for 50 loci that were shown to be significantly associated with Type 2 Diabetes in the 2012 Nature Genetics paper by Morris et al [7]. 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 16 variants that show at least nominal significance ($p < 0.05$) in this study. Out of the 47 variants in both

studies, 31 exhibit the same direction of effect with the known result (binomial test $p = 0.02$).

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

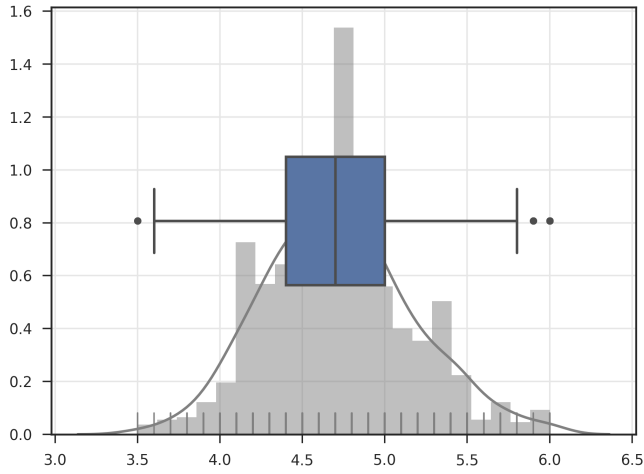
CHR	POS	ID	EA	OA	N	CASE	CTRL	FREQ _{AVG}	FREQ _{MIN}	FREQ _{MAX}	OR	P	DIR	GENE _{CLOSEST}	R ²	ID _{KNOWN}	N _{KNOWN}	CASE _{KNOWN}	CTRL _{KNOWN}	OR _{KNOWN}	P _{KNOWN}
10	114758349	rs7903146	T	C	10,248	3,339	6,909	8.5 · 10 ⁻²	2.19 · 10 ⁻²	0.285	1.22	1.44 · 10 ⁻³	++++	TCF7L2	1	rs7903146	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.389	1.2 · 10 ⁻¹³⁹
6	20679709	rs7756992	G	A	10,244	3,339	6,905	0.419	0.254	0.482	1.156	1.24 · 10 ⁻⁴	++++	CDKAL1	1	rs7756992	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.167	6.95 · 10 ⁻³⁵
9	22132076	rs2383208	A	G	10,243	3,338	6,905	0.335	0.158	0.399	1.164	1.54 · 10 ⁻⁴	++++	CDKN2B	1	rs2383208	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.178	6.73 · 10 ⁻²⁶
3	185511687	rs4402960	T	G	10,247	3,339	6,908	0.306	0.232	0.465	1.103	1.32 · 10 ⁻²	++++	IGFBP2	1	rs4402960	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.131	2.39 · 10 ⁻²³
16	53818460	rs3751812	T	G	10,246	3,339	6,907	0.212	0.12	0.331	1.186	1.05 · 10 ⁻⁴	++++	FTO	1	rs3751812	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.128	3.47 · 10 ⁻²³
8	118185025	rs3802177	G	A	1,809	898	911	0.452	0.452	0.452	1.156	9.99 · 10 ⁻²	+xxxx	SLC30A8	1	rs3802177	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.136	1.26 · 10 ⁻²¹
10	94462882	rs1111875	C	T	10,247	3,339	6,908	0.679	0.618	0.703	1.147	3.88 · 10 ⁻⁴	++++	HHEX	1	rs1111875	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.11	1.98 · 10 ⁻¹⁹
7	28196413	rs849135	A	G	1,811	900	911	7.45 · 10 ⁻³	7.45 · 10 ⁻³	7.45 · 10 ⁻³	1.31	0.596	+xxxx	JAZF1	1	rs849135	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	0.904	3.06 · 10 ⁻¹⁷
4	6303022	rs1801214	T	C	1,810	899	911	0.925	0.925	0.925	1.354	6.94 · 10 ⁻²	+xxxx	WFS1	1	rs1801214	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.102	3.3 · 10 ⁻¹⁵
10	94232247	rs2149632	T	C	10,246	3,338	6,908	0.634	0.533	0.677	1.155	1.38 · 10 ⁻⁴	++++	IDE	1	rs2149632	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.099	2.22 · 10 ⁻¹⁴
2	227093585	rs2943640	A	C	1,811	900	911	0.933	0.933	0.933	1.187	0.333	+xxxx	IRS1	1	rs2943640	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	0.912	2.69 · 10 ⁻¹⁴
10	94354204	rs3824735	T	G	10,203	3,330	6,873	0.63	0.507	0.668	1.165	5.4 · 10 ⁻⁵	++++	KIF11	1	rs3824735	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.007	7.43 · 10 ⁻¹³
3	123095312	rs6798189	G	A	6,451	2,098	4,353	7.82 · 10 ⁻²	5.52 · 10 ⁻⁴	0.189	1.022	0.151	-xxx+	ADCY5	1	rs6798189	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.108	9.08 · 10 ⁻¹³
3	12393125	rs1801282	G	C	1,811	900	911	3.51 · 10 ⁻²	3.51 · 10 ⁻²	3.51 · 10 ⁻²	1.122	0.994	+xxxx	PPARG	1	rs1801282	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	0.885	1.05 · 10 ⁻¹²
2	43690030	rs10203174	T	C	1,811	900	911	3.59 · 10 ⁻³	3.59 · 10 ⁻³	3.59 · 10 ⁻³	1.481	0.563	+xxxx	THADA	1	rs10203174	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	0.874	9.5 · 10 ⁻¹²
11	2847069	rs163184	G	T	10,238	3,336	6,902	0.45	0.391	0.509	1.138	3.5 · 10 ⁻⁴	++++	KCNQ1	1	rs163184	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.086	1.18 · 10 ⁻¹¹
11	92673828	rs1387153	G	C	10,245	3,337	6,908	0.436	0.373	0.475	1.017	0.64	++++	MTNR1B	1	rs1387153	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.093	1.59 · 10 ⁻¹¹
4	6315954	rs10804976	G	T	10,241	3,335	6,906	0.865	0.753	0.928	1.063	0.237	++++	PPP2R2C	1	rs10804976	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	0.922	3.77 · 10 ⁻¹¹
7	14898282	rs17168486	C	C	10,243	3,338	6,905	0.457	0.388	0.508	1.03	0.424	++++	DGKB	1	rs17168486	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.105	5.94 · 10 ⁻¹¹
3	64705365	rs6795735	T	C	10,238	3,335	6,903	0.738	0.713	0.774	1.022	0.597	+++	ADAMTS9	1	rs6795735	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	0.926	7.39 · 10 ⁻¹¹
10	80942631	rs12571751	A	G	1,811	900	911	0.409	0.409	0.409	1.049	0.6	+xxxx	ZMIZ1	1	rs12571751	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.078	1.02 · 10 ⁻¹⁰
5	76425867	rs7708285	G	A	10,164	3,313	6,851	0.908	0.842	0.943	1.05	0.422	++++	ZBED3	1	rs7708285	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.095	1.45 · 10 ⁻¹⁰
11	72433098	rs1552224	A	C	10,246	3,339	6,907	9.55 · 10 ⁻²	6.12 · 10 ⁻²	0.188	1.105	0.101	++++	ARAP1	1	rs1552224	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.107	1.79 · 10 ⁻¹⁰
17	36101156	rs7501939	T	C	10,247	3,339	6,908	0.739	0.712	0.751	1.049	0.243	++++	HNF1B	1	rs7501939	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.089	2.39 · 10 ⁻¹⁰
8	41519248	rs516946	T	C	1,808	898	910	0.867	0.867	0.867	1.015	0.908	+xxxx	ANK1	1	rs516946	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	0.916	2.49 · 10 ⁻¹⁰
2	227020653	rs7578326	G	A	10,247	3,339	6,908	0.145	9.9 · 10 ⁻²	0.176	1.017	0.739	+++	NYAP2	1	rs7578326	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	0.924	3.81 · 10 ⁻¹⁰
11	17408630	rs5215	C	T	10,232	3,332	6,900	0.633	0.601	0.651	1.131	1 · 10 ⁻³	++++	KCNJ11	1	rs5215	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.075	8.5 · 10 ⁻¹⁰
12	66212318	rs2261181	T	C	10,247	3,339	6,908	0.115	7.53 · 10 ⁻²	0.183	1.131	2.73 · 10 ⁻²	++++	HMG2A	1	rs2261181	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.126	1.16 · 10 ⁻⁹
3	23454790	rs1496653	A	G	10,245	3,338	6,907	0.209	0.184	0.246	1.03	0.509	++++	UBE2E2	1	rs1496653	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.085	3.56 · 10 ⁻⁹
15	77832762	rs7177055	A	G	10,247	3,338	6,909	0.378	0.325	0.463	1.163	4.95 · 10 ⁻⁵	++++	HMG20A	1	rs7177055	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.077	4.6 · 10 ⁻⁹
11	17418477	rs757110	C	A	10,240	3,336	6,904	0.614	0.571	0.631	1.105	7.14 · 10 ⁻³	++++	ABCC8	1	rs757110	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.074	5 · 10 ⁻⁹
9	84308948	rs2796441	G	A	1,811	900	911	0.609	0.609	0.609	1.239	1.63 · 10 ⁻²	+xxxx	TLE1	1	rs2796441	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.074	5.39 · 10 ⁻⁹
15	91544076	rs12899811	G	A	10,245	3,338	6,907	0.905	0.709	0.975	1.013	0.837	++++	VPS33B	1	rs12899811	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.076	6.34 · 10 ⁻⁹
12	71439589	rs7138300	T	C	1,811	900	911	0.34	0.34	0.34	1.015	0.282	+xxxx	CTD-2021H9.3	1	rs7138300	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	0.935	6.47 · 10 ⁻⁹
19	19407718	rs10401969	T	C	1,810	899	911	0.101	0.101	0.101	1.039	0.794	+xxxx	SUGP1	1	rs10401969	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	0.881	7.04 · 10 ⁻⁹
1	214154719	rs2075423	G	T	10,247	3,338	6,909	0.181	0.149	0.224	1.068	0.163	++++	PROX1	1	rs2075423	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.073	8.1 · 10 ⁻⁹
11	72629946	rs17244499	A	G	1,811	900	911	5.77 · 10 ⁻²	5.77 · 10 ⁻²	5.77 · 10 ⁻²	1.233	0.287	+xxxx	FCHSD2	1	rs17244499	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.086	1.07 · 10 ⁻⁸
18	57884750	rs12970134	G	C	10,239	3,335	6,904	0.195	0.13	0.331	1.069	0.146	++++	MC4R	1	rs12970134	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.078	1.19 · 10 ⁻⁸
2	165528624	rs1128249	T	G	1,811	900	911	9.36 · 10 ⁻²	9.36 · 10 ⁻²	9.36 · 10 ⁻²	1.147	0.359	+xxxx	COBLL1	1	rs1128249	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	0.933	1.7 · 10 ⁻⁸
13	80707429	rs1215468	A	G	1,811	900	911	0.283	0.283	0.283	1.222	3.78 · 10 ⁻²	+xxxx	SPRY2	1	rs1215468	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.075	2.09 · 10 ⁻⁸
2	60573870	rs243083	G	A	10,248	3,339	6,909	0.598	0.503	0.668	1.064	9.29 · 10 ⁻²	++++	BCL11A	1	rs243083	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.069	2.17 · 10 ⁻⁸
2	165501849	rs3923113	C	A	10,239	3,335	6,904	0.152	0.136	0.195	1.013	0.801	++++	GRB14	1	rs3923113	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	0.932	3.28 · 10 ⁻⁸
16	75247245	rs7202877	G	T	10,239	3,337	6,902	0.173	8.74 · 10 ⁻²	0.225	1.109	3.77 · 10 ⁻²	++++	CTRB1	1	rs7202877	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	0.895	3.5 · 10 ⁻⁸
2	43848664	rs11904361	C	T	1,810	900	910	2.76 · 10 ⁻³	2.76 · 10 ⁻³	2.76 · 10 ⁻³	1.849	0.444	+xxxx								

Table 9: Top known loci in META_NOLB model Adjusted Age+SEX+BMI (**bold** variants indicate matching direction of effect)

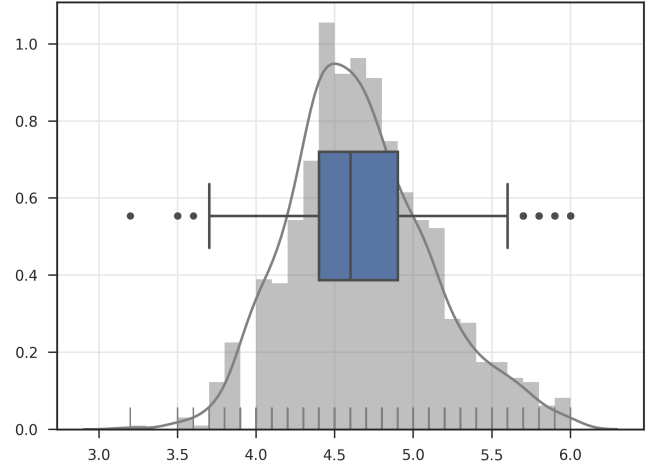
CHR	POS	ID	EA	OA	N	CASE	CTRL	FREQ _{AVG}	FREQ _{MIN}	FREQ _{MAX}	OR	P	DIR	GENE _{CLOSEST}	R ²	ID _{KNOWN}	N _{KNOWN}	CASE _{KNOWN}	CTRL _{KNOWN}	OR _{KNOWN}	P _{KNOWN}
10	114758349	rs7903146	T	C	10,190	3,305	6,885	8.5 · 10 ⁻²	2.19 · 10 ⁻²	0.285	1.236	8.23 · 10 ⁻⁴	++++	TCF7L2	1	rs7903146	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.389	1.2 · 10 ⁻¹³⁹
6	20679709	rs7756992	G	A	10,186	3,305	6,881	0.419	0.254	0.482	1.201	2.52 · 10 ⁻⁶	++++	CDKAL1	1	rs7756992	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.167	6.95 · 10 ⁻³⁵
9	22132076	rs2383208	A	G	10,185	3,304	6,881	0.336	0.157	0.4	1.194	2.12 · 10 ⁻⁵	++++	CDKN2B	1	rs2383208	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.178	6.73 · 10 ⁻²⁶
3	185511687	rs4402960	T	G	10,189	3,305	6,884	0.306	0.232	0.465	1.125	3.79 · 10 ⁻³	++++	IGF2BP2	1	rs4402960	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.131	2.39 · 10 ⁻²³
16	53818460	rs3751812	T	G	10,188	3,305	6,883	0.211	0.121	0.329	1.14	3.6 · 10 ⁻³	++++	FTO	1	rs3751812	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.128	3.47 · 10 ⁻²³
8	118185025	rs3802177	G	A	1,796	887	909	0.452	0.452	0.452	1.315	4.45 · 10 ⁻³	+xxxx	SLC30A8	1	rs3802177	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.136	1.26 · 10 ⁻²¹
10	94462882	rs1111875	C	T	10,189	3,305	6,884	0.679	0.619	0.703	1.17	8.65 · 10 ⁻⁵	++++	HHEX	1	rs1111875	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.11	1.98 · 10 ⁻¹⁹
7	28196413	rs849135	A	G	1,798	889	909	7.23 · 10 ⁻³	7.23 · 10 ⁻³	7.23 · 10 ⁻³	1.931	0.271	+xxxx	JAZF1	1	rs849135	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	0.904	3.06 · 10 ⁻¹⁷
4	6303022	rs1801214	T	C	1,797	888	909	0.924	0.924	0.924	1.657	4.89 · 10 ⁻³	+xxxx	WFS1	1	rs1801214	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.102	3.3 · 10 ⁻¹⁵
10	94232247	rs2149632	A	C	10,188	3,304	6,884	0.634	0.534	0.67	1.176	3.41 · 10 ⁻⁵	++++	IDE	1	rs2149632	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.099	2.22 · 10 ⁻¹⁴
2	227093985	rs2943640	T	C	1,798	889	909	0.932	0.932	0.932	1.187	0.37	+xxxx	IRS1	1	rs2943640	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	0.912	2.69 · 10 ⁻¹⁴
10	94354204	rs3824735	T	G	10,147	3,297	6,850	0.631	0.508	0.669	1.186	1.22 · 10 ⁻⁵	++++	KIF11	1	rs3824735	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.097	7.43 · 10 ⁻¹³
3	123095312	rs6798189	G	A	4,603	1,183	3,420	0.108	3.12 · 10 ⁻²	0.188	1.121	0.16	xxxx+	ADCY5	1	rs6798189	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.108	9.08 · 10 ⁻¹³
3	12393125	rs1801282	G	C	1,798	889	909	3.5 · 10 ⁻²	3.5 · 10 ⁻²	3.5 · 10 ⁻²	1.012	0.963	+xxxx	PPARG	1	rs1801282	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	0.885	1.05 · 10 ⁻¹²
2	43690030	rs10203174	T	C	1,798	889	909	3.34 · 10 ⁻³	3.34 · 10 ⁻³	3.34 · 10 ⁻³	1.57	0.565	+xxxx	THADA	1	rs10203174	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	0.874	9.5 · 10 ⁻¹²
11	2847069	rs163184	G	T	10,180	3,302	6,878	0.45	0.391	0.51	1.146	2.74 · 10 ⁻⁴	++++	KCNQ1	1	rs163184	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.086	1.18 · 10 ⁻¹¹
11	92673828	rs1387153	T	C	10,187	3,303	6,884	0.436	0.372	0.475	1.014	0.711	++++	MTNR1B	1	rs1387153	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.093	1.59 · 10 ⁻¹¹
4	6315954	rs10804976	G	T	10,183	3,301	6,882	0.865	0.753	0.928	1.04	0.452	++++	PPP2R2C	1	rs10804976	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	0.922	3.77 · 10 ⁻¹¹
7	14898282	rs17168486	T	C	10,185	3,304	6,881	0.457	0.339	0.507	1.022	0.561	++++	DGKB	1	rs17168486	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.105	5.94 · 10 ⁻¹¹
3	64705365	rs6795735	C	T	10,180	3,301	6,879	0.737	0.713	0.774	1.013	0.76	+++	ADAMTS9	1	rs6795735	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.105	7.39 · 10 ⁻¹¹
10	80942631	rs12571751	G	A	1,798	889	909	0.409	0.409	0.409	1.015	0.88	+xxxx	ZMIZ1	1	rs12571751	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	0.928	1.02 · 10 ⁻¹⁰
5	76425867	rs7708285	G	A	10,107	3,279	6,828	0.908	0.842	0.942	1.062	0.329	++++	ZBED3	1	rs7708285	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.095	1.45 · 10 ⁻¹⁰
11	72433098	rs1552224	A	C	10,188	3,305	6,883	9.54 · 10 ⁻²	6.14 · 10 ⁻²	0.188	1.113	8.82 · 10 ⁻²	++++	ARAF1	1	rs1552224	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.107	1.79 · 10 ⁻¹⁰
17	36101156	rs7501939	T	C	10,189	3,305	6,884	0.74	0.712	0.751	1.035	0.41	+++	HNF1B	1	rs7501939	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.089	2.39 · 10 ⁻¹⁰
8	41519248	rs516946	C	T	1,795	887	908	0.866	0.866	0.866	1.004	0.979	+xxxx	ANK1	1	rs516946	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.091	2.49 · 10 ⁻¹⁰
2	227020653	rs7578326	G	A	10,189	3,305	6,884	0.145	9.88 · 10 ⁻²	0.175	1.013	0.812	++++	NYAP2	1	rs7578326	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	0.924	3.81 · 10 ⁻¹⁰
11	17408630	rs5215	C	T	10,174	3,298	6,876	0.633	0.601	0.651	1.117	4.05 · 10 ⁻³	++++	KCNJ11	1	rs5215	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.075	8.5 · 10 ⁻¹⁰
12	66212318	rs2261181	T	C	10,189	3,305	6,884	0.115	7.49 · 10 ⁻²	0.183	1.152	1.39 · 10 ⁻²	++++	HMG2A	1	rs2261181	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.126	1.16 · 10 ⁻⁹
3	23454790	rs1496653	A	G	10,187	3,304	6,883	0.209	0.184	0.246	1.036	0.447	++++	UBE2E2	1	rs1496653	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.085	3.56 · 10 ⁻⁹
15	77832762	rs7177055	A	G	10,189	3,304	6,885	0.378	0.326	0.463	1.175	2.6 · 10 ⁻⁵	++++	HMG20A	1	rs7177055	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.077	4.6 · 10 ⁻⁹
11	17418477	rs757110	C	A	10,182	3,302	6,880	0.614	0.571	0.632	1.093	2.05 · 10 ⁻²	++++	ABCC8	1	rs757110	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.074	5 · 10 ⁻⁹
9	84308948	rs2796441	G	A	1,798	889	909	0.608	0.608	0.608	1.365	1.43 · 10 ⁻³	+xxxx	TLE1	1	rs2796441	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.074	5.39 · 10 ⁻⁹
15	91544076	rs12899811	A	C	10,187	3,304	6,883	0.905	0.709	0.975	1.02	0.753	++++	VPS33B	1	rs12899811	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.076	6.34 · 10 ⁻⁹
12	71439589	rs7138300	T	C	1,798	889	909	0.34	0.34	0.34	1.094	0.376	+xxxx	CTD-2021H9.3	1	rs7138300	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	0.935	6.47 · 10 ⁻⁹
19	19407718	rs10401969	G	C	1,797	888	909	0.101	0.101	0.101	1.076	0.64	+xxxx	SUGP1	1	rs10401969	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	0.881	7.04 · 10 ⁻⁹
1	214154719	rs2075423	T	T	10,189	3,304	6,885	0.181	0.149	0.224	1.086	8.83 · 10 ⁻²	++++	PROX1	1	rs2075423	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.073	8.1 · 10 ⁻⁹
11	72629946	rs17244499	A	G	1,798	889	909	5.78 · 10 ⁻²	5.78 · 10 ⁻²	5.78 · 10 ⁻²	1.321	0.209	+xxxx	FCHSD2	1	rs17244499	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.086	1.07 · 10 ⁻⁸
18	57884750	rs12970134	A	G	10,181	3,301	6,880	0.194	0.131	0.331	1.051	0.294	++++	MC4R	1	rs12970134	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.078	1.19 · 10 ⁻⁸
2	165528624	rs1128249	T	G	1,798	889	909	9.32 · 10 ⁻²	9.32 · 10 ⁻²	9.32 · 10 ⁻²	1.019	0.905	+xxxx	COBLL1	1	rs1128249	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	0.933	1.7 · 10 ⁻⁸
13	80707429	rs1215468	A	G	1,798	889	909	0.283	0.283	0.283	1.269	2.37 · 10 ⁻²	+xxxx	SPRY2	1	rs1215468	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.075	2.09 · 10 ⁻⁸
2	60573870	rs243083	G	A	10,190	3,305	6,885	0.598	0.503	0.668	1.086	3.24 · 10 ⁻²	++++	BCL11A	1	rs243083	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	1.069	2.17 · 10 ⁻⁸
2	165501849	rs3923113	G	A	10,181	3,301	6,880	0.152	0.136	0.194	1.002	0.975	++++	GRB1A	1	rs3923113	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	0.932	3.28 · 10 ⁻⁸
16	75247245	rs17202877	C	T	10,181	3,303	6,878	0.172	8.69 · 10 ⁻²	0.225	1.094	8.22 · 10 ⁻²	++++	CTRB1	1	rs17202877	1.5 · 10 ⁵	34,840	1.15 · 10 ⁵	0.895	3.5 · 10 ⁻⁸
2	43848664	rs11904361	C	T	1,797	889	908	2.78 · 10 ⁻³	2.78 · 10 ⁻³	2.78 · 10 ⁻³	2.262	0.354	+xxxx	PLEKHH2	1	rs11904361	1.5				

4 Fasting Glucose (GLU_FAST)

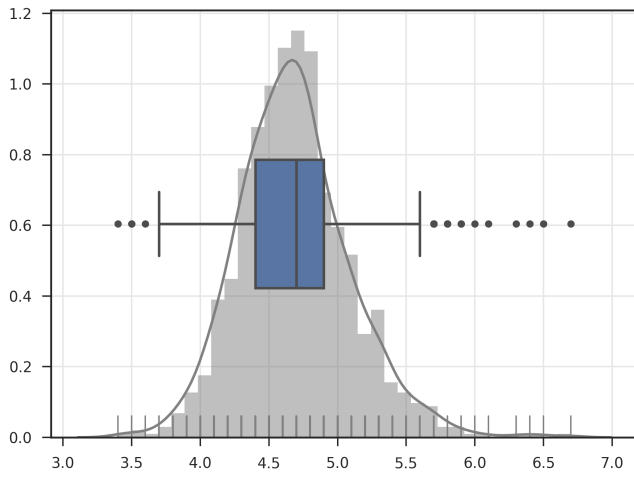
4.1 Summary



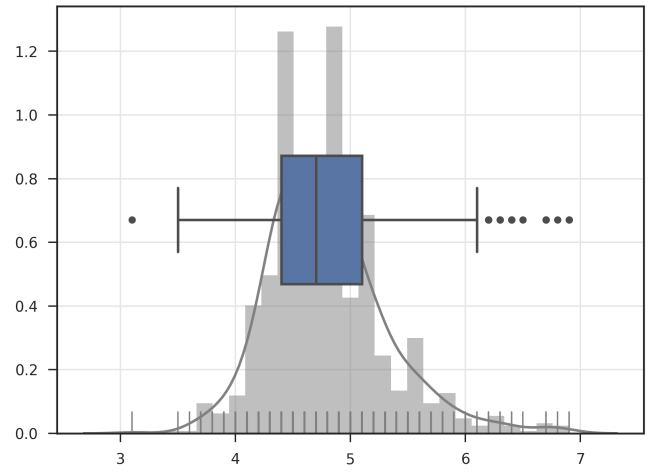
(a) DCSP21M_EAS



(b) DCSP2610K_EAS



(c) LBCHS_EAS



(d) LBMAS_EAS

Figure 6: Distribution of GLU_FAST in META_NOSEED by cohort

Table 10: Summary of samples removed from Fasting Glucose analysis by cohort and model

Cohort	Array	Ancestry	Trans	Covars	Total	-SampleQc	-KinshipCrossArray	-KinshipArray	-missObs	-PcOutlier
META_NOSEED DCSP21M_EAS	DCSP21M	EAS	invn	Age+SEX+BMI	1864	44	0	0	922	4
				Age+SEX	1864	44	0	0	920	5
META_NOSEED DCSP2610K_EAS	DCSP2610K	EAS	invn	Age+SEX+BMI	2087	36	0	0	1075	0
				Age+SEX	2087	36	0	0	1075	0
META_NOSEED LBCHS_EAS	LBCHS	EAS	invn	Age+SEX+BMI	1263	22	52	122	120	0
				Age+SEX	1263	22	52	122	120	0
META_NOSEED LBMAS_EAS	LBMAS	EAS	invn	Age+SEX+BMI	1185	40	5	240	197	6
				Age+SEX	1185	40	5	240	197	6

Table 11: Summary of samples remaining for Fasting Glucose analysis by cohort and model

Cohort	Array	Ancestry	Trans	Covars	PCs	N	Male	Female	Max	Min	μ	\bar{x}	σ
META_NOSEED DCSP21M_EAS	DCSP21M	EAS	invn	Age+SEX+BMI	6	894	569	325	6.0	3.5	4.717	4.7	0.451
				Age+SEX	6	895	570	325	6.0	3.5	4.717	4.7	0.451
META_NOSEED DCSP2610K_EAS	DCSP2610K	EAS	invn	Age+SEX+BMI	0	976	211	765	6.0	3.2	4.655	4.6	0.447
				Age+SEX	0	976	211	765	6.0	3.2	4.655	4.6	0.447
META_NOSEED LBCHS_EAS	LBCHS	EAS	invn	Age+SEX+BMI	0	947	473	474	6.7	3.5	4.682	4.7	0.415
				Age+SEX	0	947	473	474	6.7	3.5	4.682	4.7	0.415
META_NOSEED LBMAS_EAS	LBMAS	EAS	invn	Age+SEX+BMI	1	697	343	354	6.9	3.1	4.79	4.7	0.519
				Age+SEX	1	697	343	354	6.9	3.1	4.79	4.7	0.519

4.2 Calibration

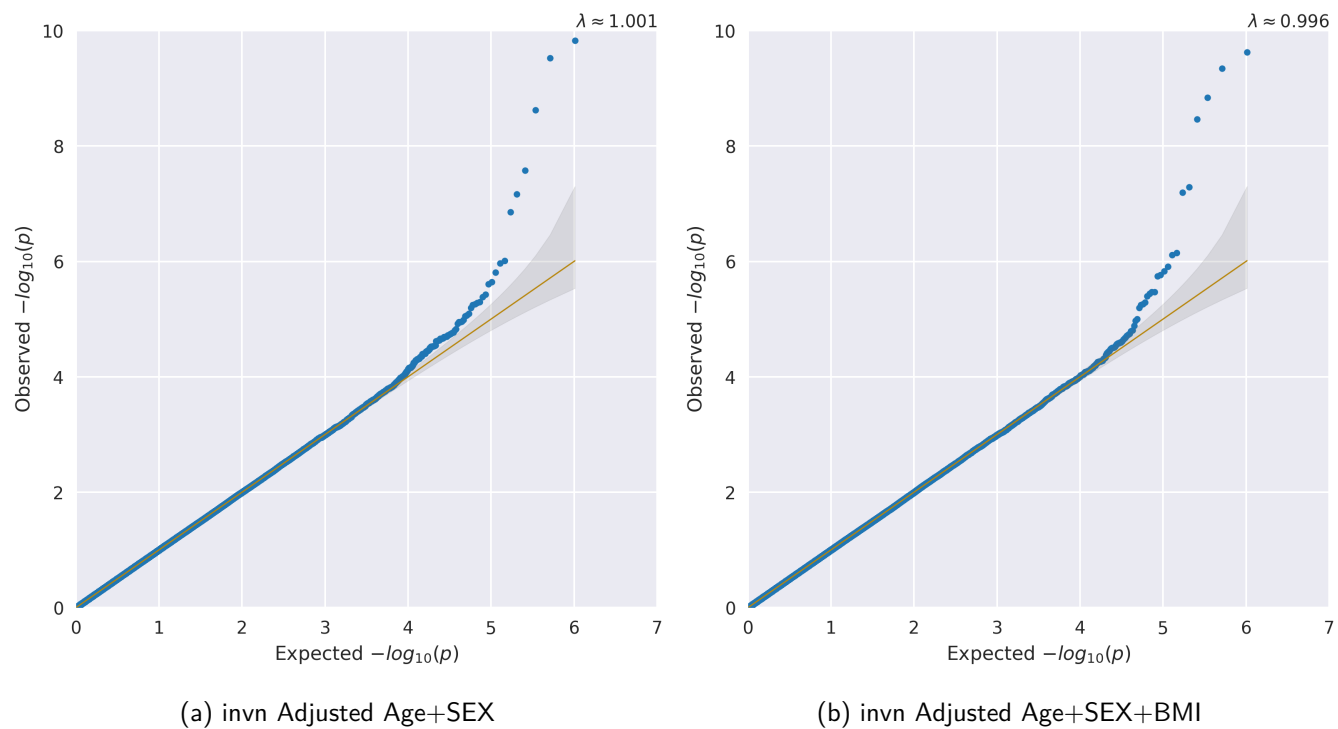
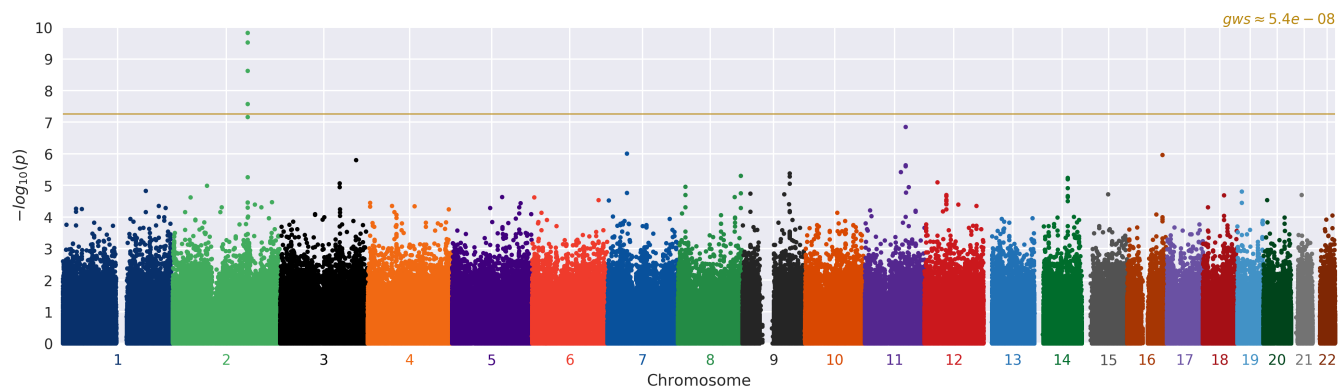
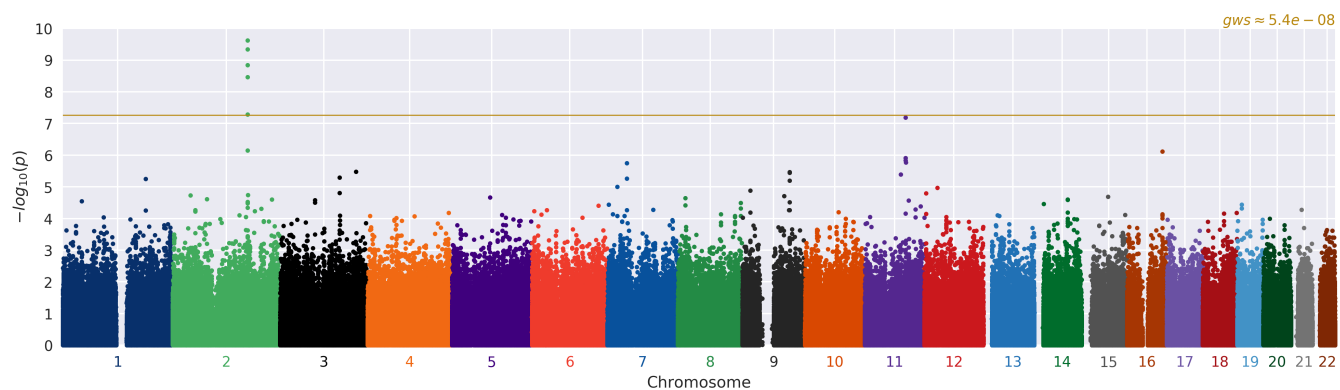


Figure 7: QQ plots for GLU_FAST in the META_NOSEED analysis



(a) invn Adjusted Age+SEX



(b) invn Adjusted Age+SEX+BMI

Figure 8: Manhattan plots for GLU_FAST in the META_NOSEED analysis

4.3 Top associations

Table 12: Top variants in the META_NOSEED invn Adjusted Age+SEX model (**bold** variants indicate previously identified associations)

CHR	POS	ID	EA	OA	GENECLOSEST	DIR	N	MALE	FEMALE	FREQ _{AVG}	FREQ _{MIN}	FREQ _{MAX}	EFFECT	STDERR	OR	ZSCORE	P
2	169766446	rs3732033	T	C	G6PC2	+++	2,539	1,386	1,153	0.127	0.108	0.164	0.267	$4.16 \cdot 10^{-2}$	1.306	-6.408	$1.47 \cdot 10^{-10}$
2	169751113	rs1522018	G	A	SPC25	+++	3,514	1,596	1,918	0.138	0.108	0.217	0.208	$3.49 \cdot 10^{-2}$	1.231	-5.97	$2.37 \cdot 10^{-9}$
11	92694757	rs10830961	G	A	MTNR1B	+++	2,535	1,383	1,152	0.469	0.449	0.478	0.148	$2.81 \cdot 10^{-2}$	1.159	5.267	$1.39 \cdot 10^{-7}$
7	44223721	rs730497	A	G	GCK	++x	1,870	781	1,089	0.201	0.199	0.203	0.199	$4.06 \cdot 10^{-2}$	1.22	4.898	$9.69 \cdot 10^{-7}$
16	80055968	rs11640960	T	C	MAF	++x	1,871	781	1,090	0.463	0.451	0.474	0.156	$3.19 \cdot 10^{-2}$	1.168	-4.878	$1.07 \cdot 10^{-6}$
3	171362785	rs2287579	T	C	PLD1	+++	2,534	1,383	1,151	$2.41 \cdot 10^{-2}$	$1.15 \cdot 10^{-2}$	$2.91 \cdot 10^{-2}$	0.438	$9.11 \cdot 10^{-2}$	1.549	4.803	$1.56 \cdot 10^{-6}$
11	81563834	rs12362287	C	T	FAM181B	xx+	1,643	815	828	$1.89 \cdot 10^{-2}$	$1.16 \cdot 10^{-2}$	$2.87 \cdot 10^{-2}$	0.596	0.129	1.815	4.626	$3.72 \cdot 10^{-6}$
9	106694482	rs10820566	A	G	SMC2	+++	3,500	1,587	1,913	0.507	0.491	0.523	0.111	$2.42 \cdot 10^{-2}$	1.118	4.604	$4.14 \cdot 10^{-6}$
8	142229891	rs2304279	A	G	SLC45A4	+++	895	570	325	0.807	0.807	0.807	0.273	$5.99 \cdot 10^{-2}$	1.314	-4.564	$5.02 \cdot 10^{-6}$
2	169782574	rs483234	T	C	ABCB11	+++	3,515	1,597	1,918	0.509	0.495	0.528	0.108	$2.38 \cdot 10^{-2}$	1.114	-4.546	$5.47 \cdot 10^{-6}$
14	75126566	rs12895862	C	T	AREL1	+++	3,515	1,597	1,918	0.16	0.141	0.178	0.146	$3.22 \cdot 10^{-2}$	1.158	4.538	$5.69 \cdot 10^{-6}$
14	75159007	rs2270424	A	G	AC007956	+++	3,515	1,597	1,918	0.162	0.143	0.18	0.145	$3.21 \cdot 10^{-2}$	1.156	4.515	$6.33 \cdot 10^{-6}$
12	29667680	rs299437	A	G	TMTC1	++x	1,869	780	1,089	0.325	0.312	0.337	0.158	$3.54 \cdot 10^{-2}$	1.171	-4.465	$8.01 \cdot 10^{-6}$
3	134825988	rs7374961	G	A	EPHB1	+++	3,514	1,597	1,917	0.734	0.605	0.769	0.12	$2.69 \cdot 10^{-2}$	1.127	4.449	$8.62 \cdot 10^{-6}$
2	77178484	rs17405711	G	A	LRRTM4	++x	2,539	1,386	1,153	$9.39 \cdot 10^{-2}$	$4.88 \cdot 10^{-2}$	0.113	0.212	$4.8 \cdot 10^{-2}$	1.236	4.412	$1.03 \cdot 10^{-5}$
8	17354086	rs2720546	T	C	SLC7A2	++x	1,871	781	1,090	0.899	0.898	0.9	0.241	$5.48 \cdot 10^{-2}$	1.273	4.395	$1.11 \cdot 10^{-5}$
11	99492475	rs11220671	A	G	CNTN5	xx+	1,644	816	828	0.193	0.19	0.197	0.192	$4.37 \cdot 10^{-2}$	1.211	-4.391	$1.13 \cdot 10^{-5}$
1	188455409	rs10912414	C	T	PLA2G4A	+++	3,514	1,596	1,918	0.608	0.436	0.657	0.109	$2.51 \cdot 10^{-2}$	1.115	4.332	$1.48 \cdot 10^{-5}$
19	10370542	rs11115	C	T	MRPL4	+++	3,515	1,597	1,918	0.314	0.304	0.321	0.111	$2.56 \cdot 10^{-2}$	1.117	-4.321	$1.56 \cdot 10^{-5}$
11	93313072	rs7114097	G	A	SMCO4	+++	2,539	1,386	1,153	0.221	0.212	0.232	0.142	$3.3 \cdot 10^{-2}$	1.153	4.301	$1.7 \cdot 10^{-5}$

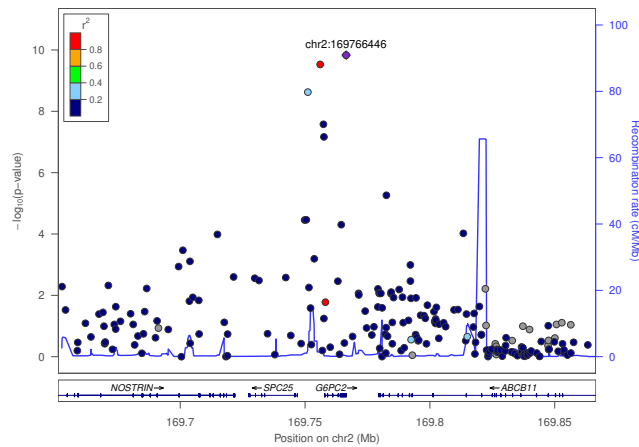


Figure 9: Regional plot for cohort META_NOSEED model invn Adjusted Age+SEX: rs3732033 ±100kb

Table 13: Top variants in the META_NOSEED invn Adjusted Age+SEX+BMI model (**bold** variants indicate previously identified associations)

CHR	POS	ID	EA	OA	GENE _{CLOSEST}	DIR	N	MALE	FEMALE	FREQ _{AVG}	FREQ _{MIN}	FREQ _{MAX}	EFFECT	STDERR	OR	ZSCORE	P
2	169756058	rs12623237	G	A	G6PC2	++++	3,511	1,594	1,917	0.127	0.106	0.164	0.224	$3.54 \cdot 10^{-2}$	1.252	-6.335	$2.37 \cdot 10^{-10}$
2	169751113	rs1522018	G	A	SPC25	++++	3,513	1,595	1,918	0.138	0.108	0.217	0.206	$3.49 \cdot 10^{-2}$	1.229	-5.909	$3.43 \cdot 10^{-9}$
11	92694757	rs10830961	G	A	MTNR1B	+xxx	2,534	1,382	1,152	0.469	0.449	0.478	0.152	$2.81 \cdot 10^{-2}$	1.164	5.407	$6.42 \cdot 10^{-8}$
2	169782574	rs483234	T	C	ABCB11	++++	3,514	1,596	1,918	0.509	0.495	0.528	0.118	$2.38 \cdot 10^{-2}$	1.125	-4.96	$7.06 \cdot 10^{-7}$
16	80055968	rs11640960	T	C	MAF	+xxx	1,870	780	1,090	0.463	0.451	0.474	0.158	$3.19 \cdot 10^{-2}$	1.171	-4.943	$7.68 \cdot 10^{-7}$
11	93313072	rs1114097	G	A	SMC04	+xxx	2,538	1,385	1,153	0.221	0.212	0.232	0.158	$3.3 \cdot 10^{-2}$	1.171	4.784	$1.72 \cdot 10^{-6}$
7	44223721	rs730497	A	G	GCK	+xxx	1,869	780	1,089	0.201	0.199	0.204	0.194	$4.06 \cdot 10^{-2}$	1.214	4.776	$1.79 \cdot 10^{-6}$
3	171362785	rs2287579	T	C	PLD1	+xxx	2,533	1,382	1,151	$2.41 \cdot 10^{-2}$	$1.15 \cdot 10^{-2}$	$2.91 \cdot 10^{-2}$	0.424	$9.12 \cdot 10^{-2}$	1.528	4.647	$3.37 \cdot 10^{-6}$
9	106707757	rs2197295	C	A	SMC2	++++	3,514	1,596	1,918	0.479	0.46	0.498	0.113	$2.43 \cdot 10^{-2}$	1.12	-4.646	$3.38 \cdot 10^{-6}$
11	81563834	rs12362287	C	T	FAM181B	xx++	1,643	815	828	$1.89 \cdot 10^{-2}$	$1.16 \cdot 10^{-2}$	$2.87 \cdot 10^{-2}$	0.595	0.129	1.812	4.61	$4.02 \cdot 10^{-6}$
3	134820091	rs7373984	C	T	EPHB1	+xxx	2,533	1,384	1,149	0.746	0.636	0.788	0.146	$3.21 \cdot 10^{-2}$	1.157	4.559	$5.13 \cdot 10^{-6}$
7	44235668	rs4607517	A	G	YKT6	++++	3,513	1,596	1,917	0.189	0.132	0.205	0.139	$3.05 \cdot 10^{-2}$	1.149	4.546	$5.47 \cdot 10^{-6}$
1	18845409	rs10912414	C	T	PLA2G4A	++++	3,513	1,595	1,918	0.609	0.436	0.657	0.114	$2.51 \cdot 10^{-2}$	1.121	4.539	$5.64 \cdot 10^{-6}$
7	21935986	rs1139225	T	C	DNAH11	++++	3,514	1,596	1,918	$2.43 \cdot 10^{-2}$	$1.69 \cdot 10^{-2}$	$4.09 \cdot 10^{-2}$	0.344	$7.8 \cdot 10^{-2}$	1.411	-4.418	$9.98 \cdot 10^{-6}$
12	29667680	rs299437	A	G	TMTC1	+xxx	1,868	779	1,089	0.325	0.312	0.337	0.156	$3.54 \cdot 10^{-2}$	1.169	-4.402	$1.07 \cdot 10^{-5}$
9	18009671	rs10810882	G	T	SH3GL2	++++	3,506	1,592	1,914	0.137	0.111	0.212	0.153	$3.51 \cdot 10^{-2}$	1.165	-4.359	$1.31 \cdot 10^{-5}$
12	3968331	rs10437816	A	G	PARP11	+xxx	894	569	325	0.418	0.418	0.418	0.213	$4.93 \cdot 10^{-2}$	1.237	-4.313	$1.61 \cdot 10^{-5}$
2	40321189	rs917977	C	T	SLC8A1	++++	3,510	1,595	1,915	0.852	0.842	0.858	0.143	$3.34 \cdot 10^{-2}$	1.154	4.282	$1.85 \cdot 10^{-5}$
9	94497680	rs4237215	A	C	ROR2	++++	3,512	1,596	1,916	0.503	0.474	0.59	0.104	$2.43 \cdot 10^{-2}$	1.109	-4.271	$1.94 \cdot 10^{-5}$
15	59690196	rs1717667	A	G	MYO1E	xx++	1,644	816	828	0.602	0.596	0.607	0.149	$3.5 \cdot 10^{-2}$	1.161	-4.258	$2.07 \cdot 10^{-5}$

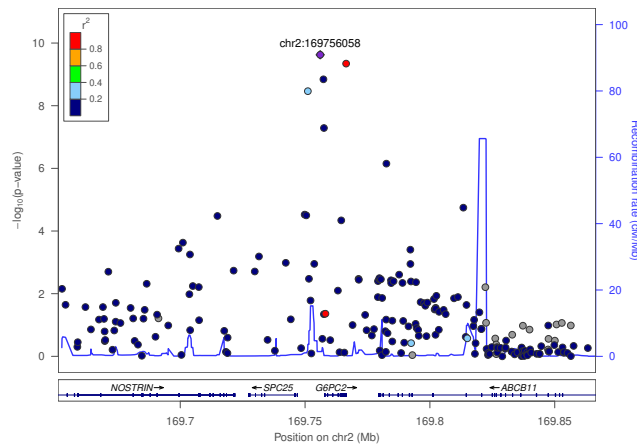


Figure 10: Regional plot for cohort META_NOSEED model invn Adjusted Age+SEX+BMI: rs12623237 $\pm 100kb$

4.4 Previously identified risk loci

Table 14 shows statistics from the META_NOSEED cohort for 50 loci that were shown to be significantly associated with Fasting Glucose in the 2012 Nature Genetics paper by Scott et al [9]. 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, 40 exhibit the same direction of effect with the known result (binomial test $p = 1.19e - 05$).

Table 14: Top known loci in META_NOSEED model invn Adjusted Age+SEX (**bold** variants indicate matching direction of effect)

CHR	POS	ID	EA	OA	N	FREQ _{AVG}	FREQ _{MIN}	FREQ _{MAX}	EFFECT	STDERR	P	DIR	GENECLOSEST	R ²	ID _{KNOWN}	N _{KNOWN}	EFFECT _{KNOWN}	STDERR _{KNOWN}	P _{KNOWN}
2	169763148	rs560887	C	T	3,515	0.964	0.959	0.973	0.188	6.42 · 10 ⁻²	3.46 · 10 ⁻³	++++	G6PC2	1	rs560887	1.33 · 10 ⁵	7.1 · 10 ⁻²	2.5 · 10 ⁻³	1.4 · 10 ⁻¹⁷⁸
2	169802252	rs853787	T	G	2,538	0.958	0.968	0.122	7 · 10 ⁻²	8.23 · 10 ⁻²	+xxx	ABCB11	1	rs853787	1.33 · 10 ⁵	6.1 · 10 ⁻²	2.2 · 10 ⁻³	5.51 · 10 ⁻¹⁶⁶	
11	92673828	rs1387153	T	C	3,515	0.456	0.412	0.486	0.113	2.41 · 10 ⁻²	2.46 · 10 ⁻⁶	++++	MTNR1B	1	rs1387153	1.33 · 10 ⁵	6.1 · 10 ⁻²	2.4 · 10 ⁻³	3.91 · 10 ⁻¹⁴³
7	44223721	rs1730497	A	G	1,870	0.201	0.199	0.203	0.199	4.06 · 10 ⁻²	9.69 · 10 ⁻⁷	+xxx	GCK	1	rs730497	1.33 · 10 ⁵	5.7 · 10 ⁻²	2.9 · 10 ⁻³	3.7 · 10 ⁻⁸⁷
2	169750483	rs477224	T	C	3,514	0.779	0.721	0.8	0.119	2.88 · 10 ⁻²	3.44 · 10 ⁻⁵	++++	SPC25	1	rs477224	1.33 · 10 ⁵	-3.6 · 10 ⁻²	2.3 · 10 ⁻³	6.02 · 10 ⁻⁵⁷
7	15065003	rs4719433	C	T	895	0.675	0.675	0.675	1.2 · 10 ⁻²	5.05 · 10 ⁻²	0.812	+xxx	DGKB	1	rs4719433	1.33 · 10 ⁵	2.9 · 10 ⁻²	2.1 · 10 ⁻³	1.59 · 10 ⁻⁴²
2	27730940	rs1260326	C	T	3,514	0.532	0.506	0.575	8.29 · 10 ⁻²	2.39 · 10 ⁻²	5.23 · 10 ⁻⁴	++++	GCKR	1	rs1260326	1.33 · 10 ⁵	2.9 · 10 ⁻²	2.1 · 10 ⁻³	2.17 · 10 ⁻⁴¹
8	118185733	rs11558471	A	G	2,539	0.459	0.435	0.475	5.48 · 10 ⁻²	2.83 · 10 ⁻²	5.3 · 10 ⁻²	+xxx	SLC30A8	1	rs11558471	1.33 · 10 ⁵	2.9 · 10 ⁻²	2.3 · 10 ⁻³	7.8 · 10 ⁻³⁷
2	169703974	rs11676084	G	A	1,871	8.82 · 10 ⁻³	7.17 · 10 ⁻³	1.06 · 10 ⁻²	0.159	0.176	0.365	+xxx	NOSTRIN	1	rs11676084	1.33 · 10 ⁵	2.8 · 10 ⁻²	2.4 · 10 ⁻³	3.65 · 10 ⁻³²
15	62383155	rs4502156	T	C	2,539	0.463	0.417	0.481	3.99 · 10 ⁻²	2.85 · 10 ⁻²	0.162	-x+	C2CD4A	1	rs4502156	1.33 · 10 ⁵	2.2 · 10 ⁻²	2.1 · 10 ⁻³	1.38 · 10 ⁻²⁵
11	45839709	rs11607883	G	A	1,871	0.246	0.245	0.247	1.12 · 10 ⁻²	3.84 · 10 ⁻²	0.771	+xx	SLC35C1	1	rs11607883	1.33 · 10 ⁵	2.1 · 10 ⁻²	2.1 · 10 ⁻³	6.32 · 10 ⁻²⁴
11	45855998	rs6485644	C	T	895	0.265	0.265	0.265	2.98 · 10 ⁻²	5.48 · 10 ⁻²	0.587	+xxx	CRCY2	1	rs6485644	1.33 · 10 ⁵	2.1 · 10 ⁻²	2.1 · 10 ⁻³	1.31 · 10 ⁻²³
10	114758349	rs7903146	C	T	3,515	2.45 · 10 ⁻²	1.8 · 10 ⁻²	4.09 · 10 ⁻²	3.11 · 10 ⁻²	7.71 · 10 ⁻²	0.687	-++	TCF7L2	1	rs7903146	1.33 · 10 ⁵	-2.2 · 10 ⁻²	2.4 · 10 ⁻³	2.71 · 10 ⁻²⁰
2	27685388	rs780110	A	G	895	0.161	0.161	0.161	2.76 · 10 ⁻²	6.6 · 10 ⁻²	0.675	+xxx	IFT172	1	rs780110	1.33 · 10 ⁵	1.9 · 10 ⁻²	2.1 · 10 ⁻³	3.82 · 10 ⁻²⁰
2	27839539	rs2068834	T	C	1,871	0.473	0.464	0.482	5.98 · 10 ⁻²	3.29 · 10 ⁻²	6.94 · 10 ⁻²	+xxx	ZNF512	1	rs2068834	1.33 · 10 ⁵	2.1 · 10 ⁻²	2.3 · 10 ⁻³	9.68 · 10 ⁻²⁰
11	61603510	rs174576	C	A	3,511	0.647	0.606	0.767	5.52 · 10 ⁻²	2.52 · 10 ⁻²	2.82 · 10 ⁻²	+++	FADS2	1	rs174576	1.33 · 10 ⁵	2 · 10 ⁻²	2.2 · 10 ⁻³	1.18 · 10 ⁻¹⁸
3	123065778	rs11708067	A	G	1,638	2.11 · 10 ⁻²	2.65 · 10 ⁻³	4.6 · 10 ⁻²	0.115	0.124	0.354	xx++	ADCY5	1	rs11708067	1.33 · 10 ⁵	2.3 · 10 ⁻²	2.6 · 10 ⁻³	1.3 · 10 ⁻¹⁸
11	61580635	rs174556	T	C	1,871	0.611	0.608	0.613	1.58 · 10 ⁻²	3.34 · 10 ⁻²	0.636	+xxx	FADS1	1	rs174556	1.33 · 10 ⁵	2 · 10 ⁻²	2.3 · 10 ⁻³	7.86 · 10 ⁻¹⁸
3	170713290	rs1280	C	T	895	5.59 · 10 ⁻³	5.59 · 10 ⁻³	5.59 · 10 ⁻³	0.288	0.318	0.365	+xxx	SLC2A2	1	rs1280	1.33 · 10 ⁵	-2.6 · 10 ⁻²	3.1 · 10 ⁻³	8.56 · 10 ⁻¹⁸
9	22132076	rs2383208	A	G	1,871	0.393	0.387	0.399	7.6 · 10 ⁻²	3.31 · 10 ⁻²	2.16 · 10 ⁻²	+xxx	CDKN2B	1	rs2383208	1.33 · 10 ⁵	2.3 · 10 ⁻²	2.7 · 10 ⁻³	2.16 · 10 ⁻¹⁷
11	61552680	rs174537	G	T	1,871	0.622	0.621	0.623	2.06 · 10 ⁻²	3.35 · 10 ⁻²	0.54	+xx	MYRF	1	rs174537	1.33 · 10 ⁵	1.9 · 10 ⁻²	2.2 · 10 ⁻³	2.35 · 10 ⁻¹⁷
11	61557803	rs102275	T	C	3,514	0.648	0.606	0.773	5.39 · 10 ⁻²	2.52 · 10 ⁻²	3.24 · 10 ⁻²	+++	TMEM258	1	rs102275	1.33 · 10 ⁵	1.9 · 10 ⁻²	2.2 · 10 ⁻³	4.97 · 10 ⁻¹⁷
11	113042093	rs10885122	G	T	1,642	0.932	0.924	0.939	0.133	6.99 · 10 ⁻²	5.75 · 10 ⁻²	xx++	ADRA2A	1	rs10885122	1.33 · 10 ⁵	2.7 · 10 ⁻²	3.3 · 10 ⁻³	6.32 · 10 ⁻¹⁷
5	95539448	rs4869272	T	C	3,515	0.643	0.634	0.654	2.42 · 10 ⁻²	2.48 · 10 ⁻²	0.33	+++	PCSK1	1	rs4869272	1.33 · 10 ⁵	1.8 · 10 ⁻²	2.2 · 10 ⁻³	1.02 · 10 ⁻¹⁷
13	28487599	rs11619319	G	A	2,534	0.466	0.45	0.475	5.41 · 10 ⁻²	2.79 · 10 ⁻²	5.28 · 10 ⁻²	+xxx	PDX1	1	rs11619319	1.33 · 10 ⁵	2 · 10 ⁻²	2.4 · 10 ⁻³	1.33 · 10 ⁻¹⁵
11	47318157	rs749067	T	C	3,509	2.84 · 10 ⁻²	2.1 · 10 ⁻²	4.32 · 10 ⁻²	6.79 · 10 ⁻²	7.28 · 10 ⁻²	0.351	+++	MADD	1	rs749067	1.33 · 10 ⁵	1.7 · 10 ⁻²	2.2 · 10 ⁻³	6.12 · 10 ⁻¹⁵
8	9177732	rs983309	T	G	3,515	0.984	0.965	0.991	1.38 · 10 ⁻²	9.52 · 10 ⁻²	0.885	-++	RP11-10A14.4	1	rs983309	1.33 · 10 ⁵	2.6 · 10 ⁻²	3.3 · 10 ⁻³	6.29 · 10 ⁻¹⁵
2	28003174	rs13030345	G	T	1,871	0.327	0.322	0.331	3.36 · 10 ⁻²	3.52 · 10 ⁻²	0.34	+xx	MRPL33	1	rs13030345	1.33 · 10 ⁵	2.1 · 10 ⁻²	2.8 · 10 ⁻³	3.84 · 10 ⁻¹⁴
11	47659135	rs7118178	G	A	3,512	0.31	0.291	0.322	1.1 · 10 ⁻²	2.59 · 10 ⁻²	0.671	+x+	MTCH2	1	rs7118178	1.33 · 10 ⁵	1.8 · 10 ⁻²	2.4 · 10 ⁻³	3.84 · 10 ⁻¹⁴
11	47600438	rs2280231	C	T	3,515	0.31	0.293	0.321	1.02 · 10 ⁻²	2.58 · 10 ⁻²	0.691	+x+	KBTBD4	1	rs2280231	1.33 · 10 ⁵	1.8 · 10 ⁻²	2.4 · 10 ⁻³	1.67 · 10 ⁻¹³
9	4293150	rs10814916	C	A	1,869	0.476	0.469	0.483	2.75 · 10 ⁻²	3.23 · 10 ⁻²	0.393	+xx	GLIS3	1	rs10814916	1.33 · 10 ⁵	1.6 · 10 ⁻²	2.2 · 10 ⁻³	2.26 · 10 ⁻¹³
2	169605967	rs2390732	G	A	3,514	0.451	0.438	0.466	6.34 · 10 ⁻²	2.4 · 10 ⁻²	8.26 · 10 ⁻³	++++	CERS6	1	rs2390732	1.33 · 10 ⁵	-1.5 · 10 ⁻²	2.1 · 10 ⁻³	7.1 · 10 ⁻¹³
7	50791579	rs6943153	T	C	3,513	0.764	0.741	0.818	4.98 · 10 ⁻²	2.81 · 10 ⁻²	7.68 · 10 ⁻²	++++	GRB10	1	rs6943153	1.33 · 10 ⁵	1.5 · 10 ⁻²	2.2 · 10 ⁻³	1.63 · 10 ⁻¹²
2	27860258	rs2141371	G	A	895	0.383	0.383	0.383	9.61 · 10 ⁻²	4.78 · 10 ⁻²	4.41 · 10 ⁻²	+xxx	GPN1	1	rs2141371	1.33 · 10 ⁵	1.7 · 10 ⁻²	2.5 · 10 ⁻³	6.59 · 10 ⁻¹²
11	72432985	rs11603334	G	A	2,539	7.5 · 10 ⁻²	6.86 · 10 ⁻²	9.11 · 10 ⁻²	5.52 · 10 ⁻²	5.39 · 10 ⁻²	0.306	+xxx	ARAP1	1	rs11603334	1.33 · 10 ⁵	1.9 · 10 ⁻²	2.8 · 10 ⁻³	1.12 · 10 ⁻¹¹
2	27951658	rs867282	T	C	3,515	0.429	0.422	0.44	2.93 · 10 ⁻²	2.42 · 10 ⁻²	0.226	++++	AC074091.13	1	rs867282	1.33 · 10 ⁵	1.7 · 10 ⁻²	2.5 · 10 ⁻³	1.76 · 10 ⁻¹¹
7	44162355	rs2979422	C	T	2,539	0.177	0.128	0.202	8.13 · 10 ⁻³	3.75 · 10 ⁻²	0.828	+x+	POLD2	1	rs2979422	1.33 · 10 ⁵	2 · 10 ⁻²	3 · 10 ⁻³	1.78 · 10 ⁻¹¹
1	214145706	rs340883	T	C	3,515	0.414	0.397	0.458	1.98 · 10 ⁻²	2.44 · 10 ⁻²	0.419	-++	PROX1	1	rs340883	1.33 · 10 ⁵	1.4 · 10 ⁻²	2.1 · 10 ⁻³	4.08 · 10 ⁻¹¹
2	27152874	rs1371614	C	T	3,515	0.144	0.138	0.152	4.68 · 10 ⁻²	3.43 · 10 ⁻²	0.173	++++	DPYSL5	1	rs1371614	1.33 · 10 ⁵	-1.6 · 10 ⁻²	2.4 · 10 ⁻³	7.09 · 10 ⁻¹¹
11	47275064	rs10838681	A	G	1,642	0.655	0.56	0.725	1.99 · 10 ⁻²	3.72 · 10 ⁻²	0.593	xx+	NR1H3	1	rs10838681	1.33 · 10 ⁵	1.5 · 10 ⁻²	2.4 · 10 ⁻³	8.84 · 10 ⁻¹¹
15	62424649	rs4775471	C	T	3,514	5.69 · 10 ⁻²	5.33 · 10 ⁻²	6.74 · 10 ⁻²	7.33 · 10 ⁻²	5.15 · 10 ⁻²	0.155	++++	C2CD4B	1	rs4775471	1.33 · 10 ⁵	1.6 · 10 ⁻²	2.5 · 10 ⁻³	9.73 · 10 ⁻¹¹
2	28113911	rs2305929	A	G	1,871	0.137	0.132	0.142	7.64 · 10 ⁻²	4.72 · 10 ⁻²	0.105	+xxx	RBKS	1	rs2305929	1.33 · 10 ⁵	1.8 · 10 ⁻²	2.7 · 10 ⁻³	1 · 10 ⁻¹⁰
9	139256766	rs3829109	A	G	2,537	4.04 · 10 ⁻²	3.58 · 10 ⁻²	4.75 · 10 ⁻²	6.03 · 10 ⁻²	7.21 · 10 ⁻²	0.403	+x+	DNLZ	1	rs3829109	1.33 · 10 ⁵	-1.7 · 10 ⁻²	2.7 · 10 ⁻³	1.13 · 10 ⁻¹⁰
11	72851463	rs1783598	T	C	1,870	0.575	0.568	0.581	4.18 · 10 ⁻²	3.38 · 10 ⁻²	0.217	+xx	FCHSD2	1	rs1783598	1.33 · 10 ⁵	1.7 · 10 ⁻²	2.6 · 10 ⁻³	1.19 · 10 ⁻¹⁰
11	47929846	rs6485795	G	A	2,539	0.379	0.327	0.471	4.84 · 10 ⁻²	2.9 · 10 ⁻²	9.52 · 10 ⁻²	+x+	NUP160	1	rs6485795	1.33 · 10 ⁵	1.5 · 10 ⁻²	2.3 · 10 ⁻³	1.81 · 10 ⁻¹⁰
11	47065072	rs10838651	A	G	1,644	9.12 · 10 ⁻⁴	5.28 · 10 ⁻⁴	1.43 · 10 ⁻³	0.207	0.576	0.72	xx++	C11orf49	1	rs10838651	1.33 · 10 ⁵	-2.1 · 10 ⁻²	3.3 · 10 ⁻³	1.9 · 10 ⁻¹⁰
14	100830818	rs12888855	C	A	895	0.141	0.141	0.141	0.101	6.97 · 10 ⁻²	0.148	+xxx	WARS	1	rs12888855	1.33 · 10 ⁵	1.6 · 10 ⁻²	2.5 · 10 ⁻³	5.04 · 10 ⁻¹⁰
20	22515495	rs6048171	C	T	892	6.28 · 10 ⁻²	6.28 · 10 ⁻²	6.28 · 10 ⁻²	6.05 · 10 ⁻²	9.76 · 10 ⁻²	0.535	+xxx							

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

CHR	POS	ID	EA	OA	N	FREQ _{AVG}	FREQ _{MIN}	FREQ _{MAX}	EFFECT	STDERR	P	DIR	GENECLOSEST	R ²	ID _{KNOWN}	N _{KNOWN}	EFFECT _{KNOWN}	STDERR _{KNOWN}	P _{KNOWN}
2	169763148	rs560887	C	T	3,514	0.964	0.959	0.973	0.171	6.43 · 10 ⁻²	7.97 · 10 ⁻³	++++	G6PC2	1	rs560887	1.33 · 10 ⁵	7.1 · 10 ⁻²	2.5 · 10 ⁻³	1.4 · 10 ⁻¹⁷⁸
2	169802252	rs853787	T	G	2,537	0.958	0.951	0.968	8.87 · 10 ⁻²	7.01 · 10 ⁻²	0.205	+xxx	ABCB11	1	rs853787	1.33 · 10 ⁵	6.1 · 10 ⁻²	2.2 · 10 ⁻³	5.51 · 10 ⁻¹⁶⁶
11	92673828	rs1387153	T	C	3,514	0.456	0.412	0.486	0.116	2.41 · 10 ⁻²	1.48 · 10 ⁻⁶	++++	MTNR1B	1	rs1387153	1.33 · 10 ⁵	6.1 · 10 ⁻²	2.4 · 10 ⁻³	3.91 · 10 ⁻¹⁴³
7	44223721	rs730497	A	G	1,869	0.201	0.199	0.204	0.194	4.06 · 10 ⁻²	1.79 · 10 ⁻⁶	++++	GCK	1	rs730497	1.33 · 10 ⁵	5.7 · 10 ⁻²	2.9 · 10 ⁻³	3.7 · 10 ⁻⁸⁷
2	169750483	rs477224	T	C	3,513	0.779	0.721	0.8	0.12	2.88 · 10 ⁻²	3.16 · 10 ⁻⁵	++++	SPC25	1	rs477224	1.33 · 10 ⁵	-3.6 · 10 ⁻²	2.3 · 10 ⁻³	6.02 · 10 ⁻⁵⁷
7	15065003	rs4719433	C	T	894	0.674	0.674	0.674	2.52 · 10 ⁻²	5.05 · 10 ⁻²	0.619	+xxx	DGKB	1	rs4719433	1.33 · 10 ⁵	2.9 · 10 ⁻²	2.1 · 10 ⁻³	1.59 · 10 ⁻⁴²
2	27730940	rs1260326	C	T	3,513	0.532	0.507	0.575	7.24 · 10 ⁻²	2.39 · 10 ⁻²	2.48 · 10 ⁻³	++++	GCKR	1	rs1260326	1.33 · 10 ⁵	2.9 · 10 ⁻²	2.1 · 10 ⁻³	2.17 · 10 ⁻⁴¹
8	118185733	rs11558471	A	G	2,538	0.459	0.435	0.475	5.6 · 10 ⁻²	2.84 · 10 ⁻²	4.85 · 10 ⁻²	+xxx	SLC30A8	1	rs11558471	1.33 · 10 ⁵	2.9 · 10 ⁻²	2.3 · 10 ⁻³	7.8 · 10 ⁻³⁷
2	169703974	rs11676084	G	A	1,870	8.82 · 10 ⁻³	7.17 · 10 ⁻³	1.06 · 10 ⁻²	0.256	0.176	0.146	+xxx	NOSTRIN	1	rs11676084	1.33 · 10 ⁵	2.9 · 10 ⁻²	2.1 · 10 ⁻³	3.65 · 10 ⁻³²
15	62383155	rs4502156	T	C	2,538	0.463	0.417	0.481	2.73 · 10 ⁻²	2.86 · 10 ⁻²	0.34	-x+	C2CD4A	1	rs4502156	1.33 · 10 ⁵	2.2 · 10 ⁻²	2.1 · 10 ⁻³	1.38 · 10 ⁻²⁵
11	45839709	rs11607883	G	A	1,870	0.246	0.245	0.246	1.54 · 10 ⁻²	3.84 · 10 ⁻²	0.688	+xx	SLC35C1	1	rs11607883	1.33 · 10 ⁵	2.1 · 10 ⁻²	2.1 · 10 ⁻³	6.32 · 10 ⁻²⁴
11	45855998	rs6485644	C	T	894	0.264	0.264	0.264	4.53 · 10 ⁻²	5.49 · 10 ⁻²	0.409	+xxx	CRY2	1	rs6485644	1.33 · 10 ⁵	2.1 · 10 ⁻²	2.1 · 10 ⁻³	1.31 · 10 ⁻²³
10	114758349	rs7903146	C	T	3,514	2.45 · 10 ⁻²	1.8 · 10 ⁻²	4.09 · 10 ⁻²	1.3 · 10 ⁻²	7.72 · 10 ⁻²	0.866	-++	TCF7L2	1	rs7903146	1.33 · 10 ⁵	-2.2 · 10 ⁻²	2.4 · 10 ⁻³	2.71 · 10 ⁻²⁰
2	27685388	rs780110	A	G	894	0.162	0.162	0.162	2.97 · 10 ⁻²	6.6 · 10 ⁻²	0.653	+xxx	IFT172	1	rs780110	1.33 · 10 ⁵	1.9 · 10 ⁻²	2.1 · 10 ⁻³	3.82 · 10 ⁻²⁰
2	27839539	rs2068834	T	C	1,870	0.472	0.464	0.48	5.62 · 10 ⁻²	3.3 · 10 ⁻²	8.82 · 10 ⁻²	+xxx	ZNF512	1	rs2068834	1.33 · 10 ⁵	2.1 · 10 ⁻²	2.3 · 10 ⁻³	9.68 · 10 ⁻²⁰
11	61603510	rs174576	C	A	3,510	0.647	0.606	0.767	5.41 · 10 ⁻²	2.52 · 10 ⁻²	3.16 · 10 ⁻²	+xx	FADS2	1	rs174576	1.33 · 10 ⁵	2 · 10 ⁻²	2.2 · 10 ⁻³	1.18 · 10 ⁻¹⁸
3	123065778	rs11708067	A	G	1,638	2.11 · 10 ⁻²	2.65 · 10 ⁻³	4.6 · 10 ⁻²	0.14	0.124	0.26	xxx+	ADCY5	1	rs11708067	1.33 · 10 ⁵	2.3 · 10 ⁻²	2.6 · 10 ⁻³	1.3 · 10 ⁻¹⁸
11	61580635	rs174556	C	T	1,870	0.61	0.608	0.613	1.84 · 10 ⁻²	3.34 · 10 ⁻²	0.582	+xxx	FADS1	1	rs174556	1.33 · 10 ⁵	2 · 10 ⁻²	2.3 · 10 ⁻³	8.56 · 10 ⁻¹⁸
3	170713290	rs1280	C	T	894	5.59 · 10 ⁻³	5.59 · 10 ⁻³	5.59 · 10 ⁻³	0.313	0.318	0.325	+xxx	SLC2A2	1	rs1280	1.33 · 10 ⁵	-2.6 · 10 ⁻²	3.1 · 10 ⁻³	7.82 · 10 ⁻¹⁸
9	22132076	rs2383208	A	G	1,870	0.393	0.387	0.4	7.38 · 10 ⁻²	3.31 · 10 ⁻²	2.59 · 10 ⁻²	+xxx	CDKN2B	1	rs2383208	1.33 · 10 ⁵	2.3 · 10 ⁻²	2.7 · 10 ⁻³	2.16 · 10 ⁻¹⁷
11	61552680	rs174537	G	T	1,870	0.622	0.621	0.622	2.12 · 10 ⁻²	3.36 · 10 ⁻²	0.528	-xxx	MYRF	1	rs174537	1.33 · 10 ⁵	2.3 · 10 ⁻²	2.2 · 10 ⁻³	2.35 · 10 ⁻¹⁷
11	61557803	rs102275	T	C	3,513	0.647	0.606	0.773	5.24 · 10 ⁻²	2.52 · 10 ⁻²	3.78 · 10 ⁻²	+++	TMEM258	1	rs102275	1.33 · 10 ⁵	1.9 · 10 ⁻²	2.2 · 10 ⁻³	4.97 · 10 ⁻¹⁷
10	113042093	rs10885122	G	T	1,642	0.932	0.924	0.939	0.119	7 · 10 ⁻²	8.83 · 10 ⁻²	xxx+	ADRA2A	1	rs10885122	1.33 · 10 ⁵	2.7 · 10 ⁻²	3.3 · 10 ⁻³	6.32 · 10 ⁻¹⁷
5	95539448	rs4869272	T	C	3,514	0.643	0.634	0.654	4.44 · 10 ⁻²	2.49 · 10 ⁻²	7.42 · 10 ⁻²	++++	PCSK1	1	rs4869272	1.33 · 10 ⁵	1.8 · 10 ⁻²	2.2 · 10 ⁻³	1.02 · 10 ⁻¹⁷
13	28487599	rs11619319	G	A	2,533	0.466	0.45	0.475	6.59 · 10 ⁻²	2.8 · 10 ⁻²	1.86 · 10 ⁻²	+xxx	PDX1	1	rs11619319	1.33 · 10 ⁵	2 · 10 ⁻²	2.4 · 10 ⁻³	1.33 · 10 ⁻¹⁵
11	47318157	rs749067	T	C	3,508	2.84 · 10 ⁻²	2.1 · 10 ⁻²	4.32 · 10 ⁻²	8.75 · 10 ⁻²	7.29 · 10 ⁻²	0.23	+++	MADD	1	rs749067	1.33 · 10 ⁵	1.7 · 10 ⁻²	2.2 · 10 ⁻³	6.12 · 10 ⁻¹⁵
8	9177732	rs983309	G	T	3,514	0.984	0.965	0.991	1.83 · 10 ⁻³	9.53 · 10 ⁻²	0.985	++-	RP11-10A14.4	1	rs983309	1.33 · 10 ⁵	-2.6 · 10 ⁻²	3.3 · 10 ⁻³	6.29 · 10 ⁻¹⁵
2	28003174	rs13030345	G	T	1,870	0.326	0.322	0.33	3.07 · 10 ⁻²	3.53 · 10 ⁻²	0.385	-xx	MRPL33	1	rs13030345	1.33 · 10 ⁵	2.1 · 10 ⁻²	2.8 · 10 ⁻³	3.84 · 10 ⁻¹⁴
11	47659135	rs7118178	G	A	3,511	0.31	0.291	0.322	8.76 · 10 ⁻³	2.59 · 10 ⁻²	0.735	+++	MTCH2	1	rs7118178	1.33 · 10 ⁵	1.8 · 10 ⁻²	2.4 · 10 ⁻³	3.84 · 10 ⁻¹⁴
11	47600438	rs2280231	C	T	3,514	0.31	0.293	0.321	8.47 · 10 ⁻³	2.58 · 10 ⁻²	0.743	+++	KBTBD4	1	rs2280231	1.33 · 10 ⁵	1.8 · 10 ⁻²	2.4 · 10 ⁻³	1.67 · 10 ⁻¹³
9	4293150	rs10814916	C	A	1,868	0.476	0.469	0.483	4.91 · 10 ⁻²	3.23 · 10 ⁻²	0.128	-xxx	GLIS3	1	rs10814916	1.33 · 10 ⁵	1.6 · 10 ⁻²	2.2 · 10 ⁻³	2.26 · 10 ⁻¹³
2	169605967	rs2390732	G	A	3,513	0.452	0.44	0.466	5.2 · 10 ⁻²	2.4 · 10 ⁻²	3.06 · 10 ⁻²	++++	CERS6	1	rs2390732	1.33 · 10 ⁵	-1.5 · 10 ⁻²	2.1 · 10 ⁻³	7.1 · 10 ⁻¹³
7	50791579	rs6943153	T	C	3,512	0.764	0.741	0.818	4.51 · 10 ⁻²	2.82 · 10 ⁻²	0.11	+++	GRB10	1	rs6943153	1.33 · 10 ⁵	1.5 · 10 ⁻²	2.2 · 10 ⁻³	1.63 · 10 ⁻¹²
2	27860258	rs2141371	G	A	894	0.383	0.383	0.383	9.42 · 10 ⁻²	4.79 · 10 ⁻²	4.93 · 10 ⁻²	+xxx	GPN1	1	rs2141371	1.33 · 10 ⁵	1.7 · 10 ⁻²	2.5 · 10 ⁻³	6.59 · 10 ⁻¹²
11	72432985	rs11603334	G	A	2,538	7.53 · 10 ⁻²	6.86 · 10 ⁻²	9.11 · 10 ⁻²	7.27 · 10 ⁻²	5.39 · 10 ⁻²	0.178	+xxx	ARAP1	1	rs11603334	1.33 · 10 ⁵	1.9 · 10 ⁻²	2.8 · 10 ⁻³	1.12 · 10 ⁻¹¹
2	27951658	rs867282	T	C	3,514	0.429	0.422	0.44	2.25 · 10 ⁻²	2.43 · 10 ⁻²	0.354	+++	AC074091.13	1	rs867282	1.33 · 10 ⁵	1.7 · 10 ⁻²	2.5 · 10 ⁻³	1.76 · 10 ⁻¹¹
7	44162355	rs2979422	C	T	2,538	0.177	0.128	0.202	3.03 · 10 ⁻²	3.76 · 10 ⁻²	0.42	+x+	POLD2	1	rs2979422	1.33 · 10 ⁵	2 · 10 ⁻²	3 · 10 ⁻³	1.78 · 10 ⁻¹¹
1	214145706	rs340883	T	C	3,514	0.414	0.397	0.458	1.67 · 10 ⁻²	2.45 · 10 ⁻²	0.495	-+++	PROX1	1	rs340883	1.33 · 10 ⁵	1.4 · 10 ⁻²	2.1 · 10 ⁻³	4.08 · 10 ⁻¹¹
2	27152874	rs1371614	C	T	3,514	0.144	0.138	0.152	3.31 · 10 ⁻²	3.43 · 10 ⁻²	0.335	-+++	DPYSL5	1	rs1371614	1.33 · 10 ⁵	-1.6 · 10 ⁻²	2.4 · 10 ⁻³	7.09 · 10 ⁻¹¹
11	47275064	rs10838681	A	G	1,642	0.655	0.56	0.725	1.35 · 10 ⁻²	3.73 · 10 ⁻²	0.718	xxx+	RNIH3	1	rs10838681	1.33 · 10 ⁵	1.5 · 10 ⁻²	2.4 · 10 ⁻³	8.84 · 10 ⁻¹¹
15	62424649	rs4775471	C	T	3,513	5.69 · 10 ⁻²	5.33 · 10 ⁻²	6.74 · 10 ⁻²	7.29 · 10 ⁻²	5.16 · 10 ⁻²	0.157	++++	C2CD4B	1	rs4775471	1.33 · 10 ⁵	1.6 · 10 ⁻²	2.5 · 10 ⁻³	9.73 · 10 ⁻¹¹
2	28113911	rs2305929	A	G	1,870	0.137	0.133	0.142	8.2 · 10 ⁻²	4.72 · 10 ⁻²	8.21 · 10 ⁻²	+xxx	RBKS	1	rs2305929	1.33 · 10 ⁵	1.8 · 10 ⁻²	2.7 · 10 ⁻³	1 · 10 ⁻¹⁰
9	139256766	rs3829109	A	G	2,536	4.04 · 10 ⁻²	3.58 · 10 ⁻²	4.75 · 10 ⁻²	7.87 · 10 ⁻²	7.21 · 10 ⁻²	0.275	+xxx	DNLZ	1	rs3829109	1.33 · 10 ⁵	-1.7 · 10 ⁻²	2.7 · 10 ⁻³	1.13 · 10 ⁻¹⁰
11	72851463	rs1783598	T	C	1,869	0.575	0.568	0.581	3.53 · 10 ⁻²	3.39 · 10 ⁻²	0.298	-xxx	FCHSD2	1	rs1783598	1.33 · 10			

5 Fasting Insulin (INS_FAST)

5.1 Summary

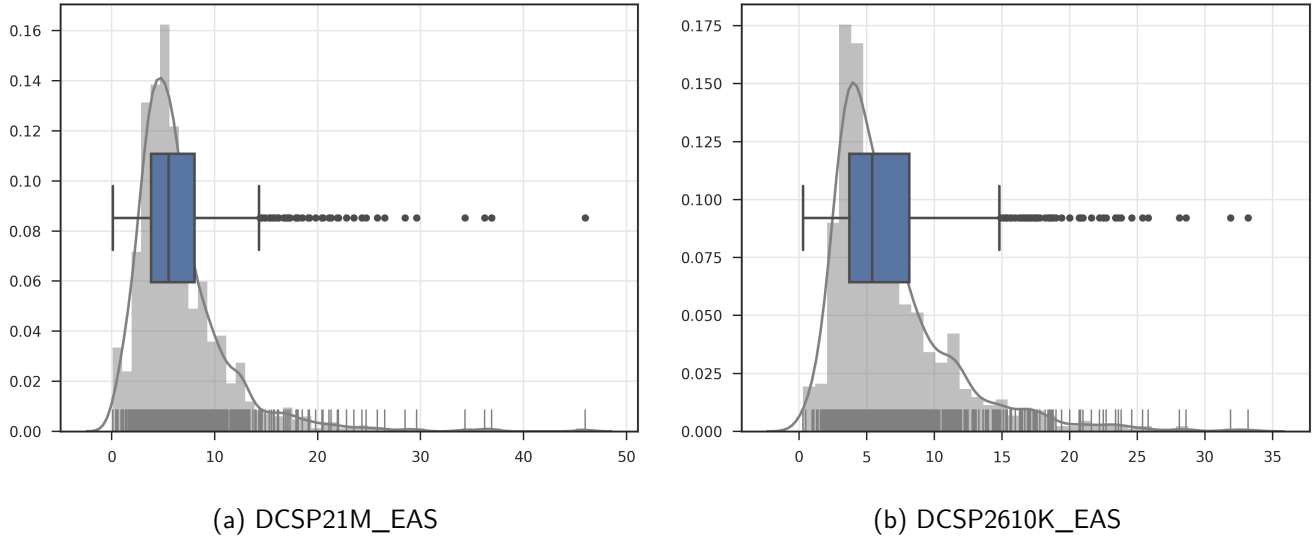


Figure 11: Distribution of INS_FAST in META_DCSP2 by cohort

Table 16: Summary of samples removed from Fasting Insulin analysis by cohort and model

Cohort	Array	Ancestry	Trans	Covars	Total	-SampleQc	-KinshipCrossArray	-KinshipArray	-missObs	-PcOutlier
META_DCSP2 DCSP21M_EAS	DCSP21M	EAS	invn	Age+SEX	1864	44	0	0	909	5
			invn	Age+SEX+BMI	1864	44	0	0	911	0
META_DCSP2 DCSP2610K_EAS	DCSP2610K	EAS	invn	Age+SEX	2087	36	0	0	1064	7
			invn	Age+SEX+BMI	2087	36	0	0	1064	0

Table 17: Summary of samples remaining for Fasting Insulin analysis by cohort and model

Cohort	Array	Ancestry	Trans	Covars	PCs	N	Male	Female	Max	Min	μ	\bar{x}	σ
META_DCSP2 DCSP21M_EAS	DCSP21M	EAS	invn	Age+SEX	0	906	577	329	46.0	0.1	6.57	5.5	4.502
			invn	Age+SEX+BMI	0	909	577	332	46.0	0.1	6.587	5.5	4.52
META_DCSP2 DCSP2610K_EAS	DCSP2610K	EAS	invn	Age+SEX	1	980	212	768	33.2	0.3	6.678	5.4	4.396
			invn	Age+SEX+BMI	0	987	213	774	33.2	0.3	6.688	5.4	4.407

5.2 Calibration

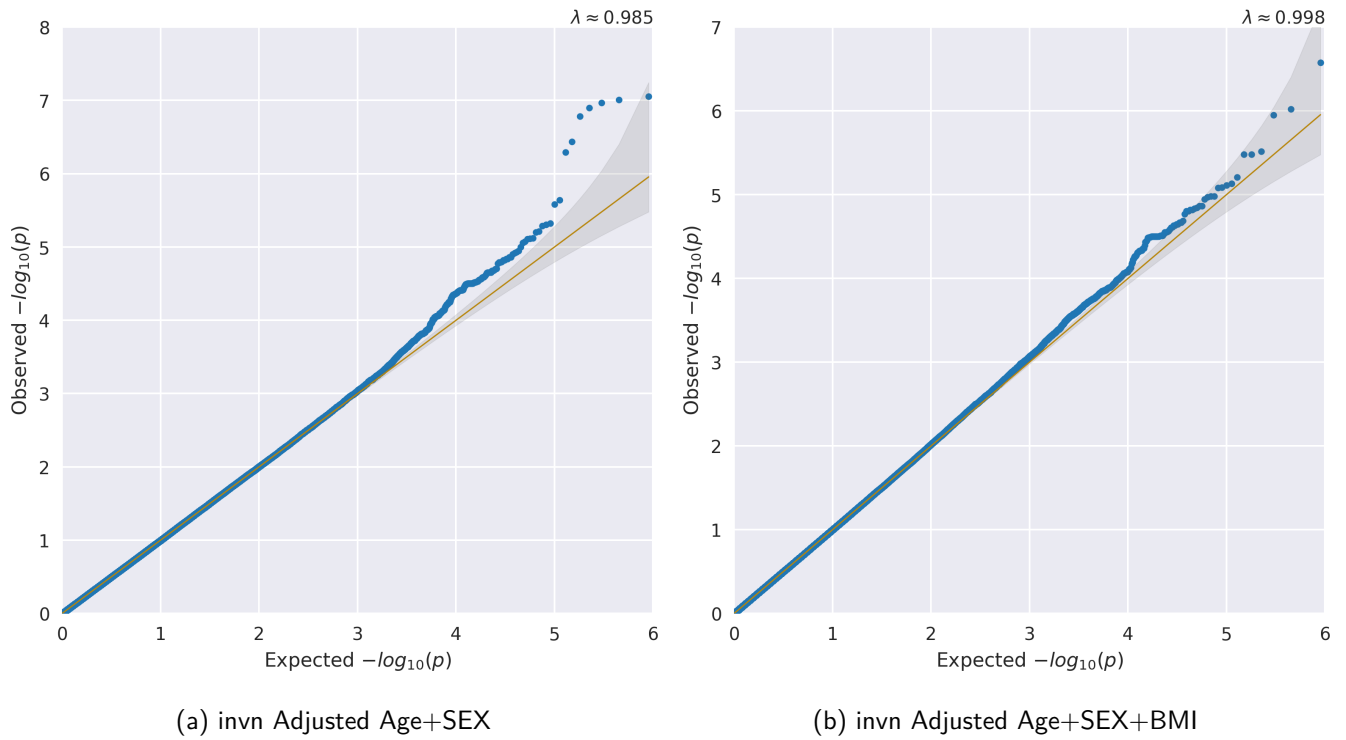
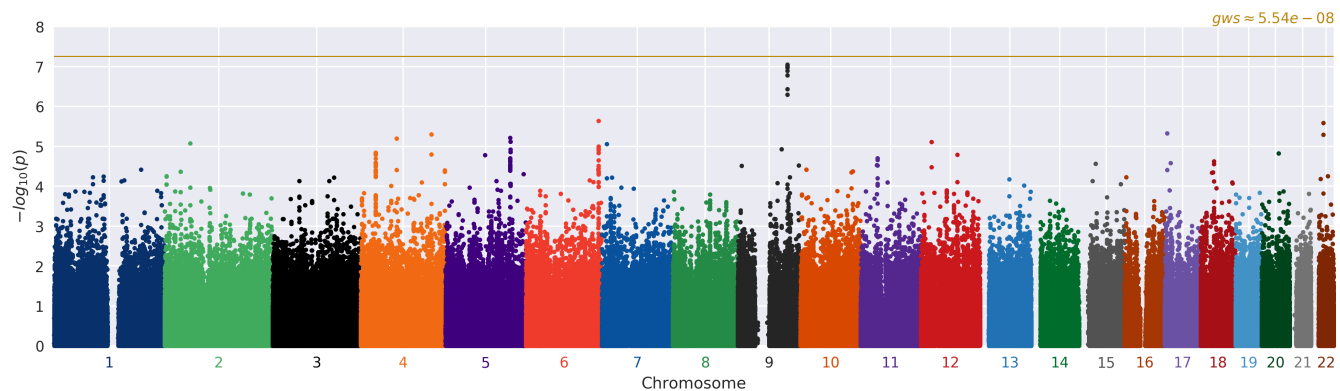
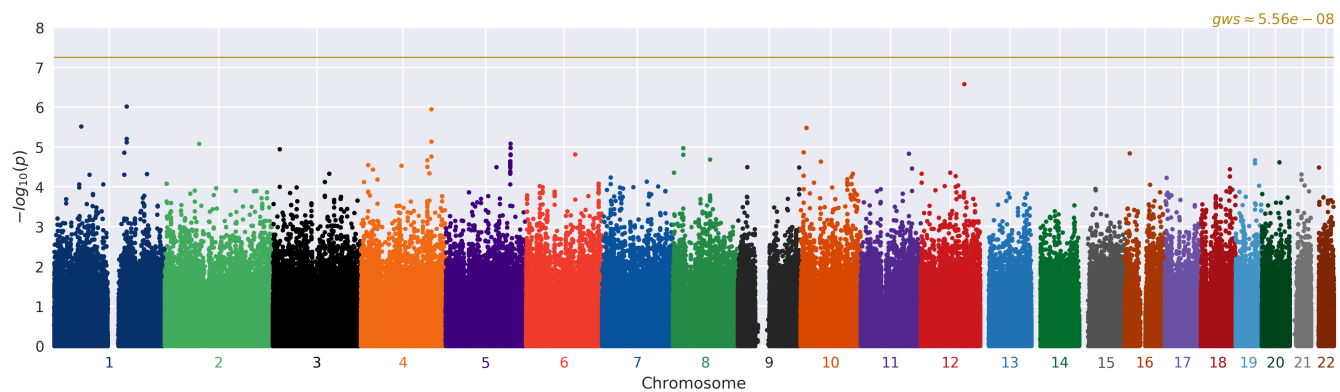


Figure 12: QQ plots for INS_FAST in the META_DCSP2 analysis



(a) invn Adjusted Age+SEX



(b) invn Adjusted Age+SEX+BMI

Figure 13: Manhattan plots for INS_FAST in the META_DCSP2 analysis

5.3 Top associations

Table 18: Top variants in the META_DCSP2 invn Adjusted Age+SEX model (**bold** variants indicate previously identified associations)

CHR	POS	ID	EA	OA	GENE _{CLOSEST}	DIR	N	MALE	FEMALE	FREQ _{AVG}	FREQ _{MIN}	FREQ _{MAX}	EFFECT	STDERR	OR	ZSCORE	P
9	111695607	rs3763643	T	C	IKBKAP	+x	906	577	329	0.322	0.322	0.322	0.263	$4.92 \cdot 10^{-2}$	1.301	-5.349	$8.86 \cdot 10^{-8}$
9	111697054	rs1759842	A	G	FAM206A	+x	906	577	329	0.567	0.567	0.567	0.25	$4.7 \cdot 10^{-2}$	1.285	5.331	$9.78 \cdot 10^{-8}$
9	111746267	rs2282206	A	G	CTNNA1	+x	905	577	328	0.444	0.444	0.444	0.238	$4.69 \cdot 10^{-2}$	1.269	-5.085	$3.67 \cdot 10^{-7}$
6	163219891	rs1041632	C	T	PACRG	++	1,886	789	1,097	0.532	0.525	0.54	0.155	$3.29 \cdot 10^{-2}$	1.168	4.727	$2.28 \cdot 10^{-6}$
22	27785119	rs738504	G	A	MN1	++	1,886	789	1,097	$9.54 \cdot 10^{-2}$	$8.83 \cdot 10^{-2}$	0.102	0.258	$5.49 \cdot 10^{-2}$	1.294	-4.7	$2.6 \cdot 10^{-6}$
17	5591389	rs2716878	T	C	NLRP1	++	1,885	788	1,097	0.516	0.515	0.517	0.15	$3.28 \cdot 10^{-2}$	1.162	-4.576	$4.75 \cdot 10^{-6}$
4	158813228	rs1481231	C	T	FAM198B	+x	906	577	329	0.879	0.879	0.879	0.324	$7.09 \cdot 10^{-2}$	1.382	-4.566	$4.98 \cdot 10^{-6}$
5	145460855	rs17796870	C	T	SH3RF2	+x	906	577	329	0.248	0.248	0.248	0.243	$5.36 \cdot 10^{-2}$	1.274	-4.523	$6.09 \cdot 10^{-6}$
4	81103562	rs3755912	G	A	PRDM8	++	1,886	789	1,097	0.161	0.159	0.162	0.196	$4.34 \cdot 10^{-2}$	1.217	-4.515	$6.32 \cdot 10^{-6}$
5	145693202	rs17096590	C	T	RP11-449H3	+x	906	577	329	0.206	0.206	0.206	0.253	$5.66 \cdot 10^{-2}$	1.288	-4.476	$7.6 \cdot 10^{-6}$
5	145665917	rs10515567	T	C	RBM27	+x	906	577	329	0.212	0.212	0.212	0.252	$5.64 \cdot 10^{-2}$	1.287	-4.474	$7.69 \cdot 10^{-6}$
12	24451971	rs2661789	C	T	SOX5	++	1,885	789	1,096	0.168	0.162	0.175	0.193	$4.33 \cdot 10^{-2}$	1.214	4.472	$7.75 \cdot 10^{-6}$
2	57850836	rs820795	A	G	VRK2	+x	906	577	329	0.435	0.435	0.435	0.201	$4.51 \cdot 10^{-2}$	1.222	4.455	$8.4 \cdot 10^{-6}$
7	10744798	rs12537191	A	C	NDUFA4	+x	906	577	329	0.151	0.151	0.151	0.291	$6.54 \cdot 10^{-2}$	1.338	-4.445	$8.81 \cdot 10^{-6}$
6	162976039	rs9356044	C	T	PARK2	++	1,885	788	1,097	0.505	0.496	0.513	0.146	$3.31 \cdot 10^{-2}$	1.157	-4.417	$1 \cdot 10^{-5}$
9	98475674	rs1977620	C	T	ERCC6L2	+x	906	577	329	$4.75 \cdot 10^{-2}$	$4.75 \cdot 10^{-2}$	$4.75 \cdot 10^{-2}$	0.486	0.111	1.625	-4.382	$1.17 \cdot 10^{-5}$
4	33863879	rs10010176	T	C	ARAP2	+x	903	574	329	0.303	0.303	0.303	0.22	$5.08 \cdot 10^{-2}$	1.247	4.336	$1.45 \cdot 10^{-5}$
20	38240273	rs2208464	G	A	DHX35	++	1,886	789	1,097	0.248	0.247	0.249	0.165	$3.82 \cdot 10^{-2}$	1.18	-4.328	$1.5 \cdot 10^{-5}$
12	82479348	rs10778860	G	A	CCDC59	+x	903	576	327	0.657	0.657	0.657	0.218	$5.06 \cdot 10^{-2}$	1.244	4.312	$1.62 \cdot 10^{-5}$
5	88893232	rs4131497	C	T	MEF2C	++	1,886	789	1,097	0.905	0.904	0.906	0.233	$5.42 \cdot 10^{-2}$	1.263	-4.305	$1.67 \cdot 10^{-5}$

Table 19: Top variants in the META_DCSP2 invn Adjusted Age+SEX+BMI model (**bold** variants indicate previously identified associations)

CHR	POS	ID	EA	OA	GENE _{CLOSEST}	DIR	N	MALE	FEMALE	FREQ _{AVG}	FREQ _{MIN}	FREQ _{MAX}	EFFECT	STDERR	OR	ZSCORE	P
12	97526156	rs7953820	A	T	NEDD1	+x	907	577	330	0.287	0.287	0.287	0.265	$5.16 \cdot 10^{-2}$	1.304	5.148	$2.64 \cdot 10^{-7}$
1	163525477	rs10917799	G	A	NUF2	++	1,896	790	1,106	0.324	0.322	0.326	0.168	$3.44 \cdot 10^{-2}$	1.183	-4.901	$9.53 \cdot 10^{-7}$
4	158813228	rs1481231	C	T	FAM198B	+x	909	577	332	0.878	0.878	0.878	0.344	$7.06 \cdot 10^{-2}$	1.41	-4.869	$1.12 \cdot 10^{-6}$
1	61329593	rs581503	C	T	NFIA	++	1,896	790	1,106	$6.14 \cdot 10^{-2}$	$5.67 \cdot 10^{-2}$	$6.59 \cdot 10^{-2}$	0.314	$6.73 \cdot 10^{-2}$	1.369	4.667	$3.06 \cdot 10^{-6}$
10	13500616	rs12252553	C	T	BEND7	+x	909	577	332	$1.49 \cdot 10^{-2}$	$1.49 \cdot 10^{-2}$	$1.49 \cdot 10^{-2}$	0.898	0.193	2.455	4.651	$3.31 \cdot 10^{-6}$
2	77938924	rs17014417	C	T	LRRTM4	+x	906	577	329	0.402	0.402	0.402	0.216	$4.85 \cdot 10^{-2}$	1.241	-4.46	$8.21 \cdot 10^{-6}$
5	145665917	rs10515567	T	C	RBM27	+x	909	577	332	0.213	0.213	0.213	0.251	$5.64 \cdot 10^{-2}$	1.286	-4.459	$8.25 \cdot 10^{-6}$
8	23552773	rs10106897	A	G	NKX2-6	+x	909	577	332	0.707	0.707	0.707	0.226	$5.13 \cdot 10^{-2}$	1.253	-4.402	$1.07 \cdot 10^{-5}$
3	15462358	rs9853193	C	T	METTL6	+x	909	577	332	0.963	0.963	0.963	0.548	0.125	1.73	4.391	$1.13 \cdot 10^{-5}$
10	7250148	rs7920088	C	T	SFMBT2	++	1,896	790	1,106	0.103	0.101	0.105	0.229	$5.26 \cdot 10^{-2}$	1.257	-4.349	$1.37 \cdot 10^{-5}$
1	158025454	rs912640	G	A	KIRREL	+x	909	577	332	0.84	0.84	0.84	0.269	$6.19 \cdot 10^{-2}$	1.309	-4.348	$1.37 \cdot 10^{-5}$
16	11506308	rs8063141	G	A	CTD-3088G3	++	1,857	783	1,074	0.32	0.309	0.331	0.149	$3.43 \cdot 10^{-2}$	1.161	-4.339	$1.43 \cdot 10^{-5}$
11	108365182	rs893279	T	C	KDELC2	+x	909	577	332	0.432	0.432	0.432	0.204	$4.71 \cdot 10^{-2}$	1.226	4.333	$1.47 \cdot 10^{-5}$
6	110334236	rs9487281	C	T	GPR6	+x	909	577	332	$2.48 \cdot 10^{-2}$	$2.48 \cdot 10^{-2}$	$2.48 \cdot 10^{-2}$	0.655	0.151	1.925	4.325	$1.52 \cdot 10^{-5}$
5	145693202	rs17096590	C	T	RP11-449H3	+x	909	577	332	0.207	0.207	0.207	0.244	$5.66 \cdot 10^{-2}$	1.277	-4.317	$1.58 \cdot 10^{-5}$
8	83920104	rs959284	C	T	SNX16	++	1,896	790	1,106	0.848	0.843	0.852	0.19	$4.45 \cdot 10^{-2}$	1.209	4.258	$2.06 \cdot 10^{-5}$
19	43935170	rs2599469	G	T	TEX101	++	1,896	790	1,106	0.575	0.566	0.584	0.137	$3.24 \cdot 10^{-2}$	1.147	-4.249	$2.14 \cdot 10^{-5}$
4	149512511	rs12650275	A	C	NR3C2	+x	905	575	330	0.776	0.776	0.776	0.23	$5.41 \cdot 10^{-2}$	1.258	4.248	$2.16 \cdot 10^{-5}$
5	145531921	rs2963915	A	G	LARS	+x	909	577	332	0.789	0.789	0.789	0.239	$5.63 \cdot 10^{-2}$	1.269	4.238	$2.26 \cdot 10^{-5}$
10	45596024	rs9663396	T	G	ZNF22	++	1,896	790	1,106	$9.15 \cdot 10^{-2}$	$9.12 \cdot 10^{-2}$	$9.19 \cdot 10^{-2}$	0.235	$5.55 \cdot 10^{-2}$	1.265	4.231	$2.33 \cdot 10^{-5}$

5.4 Previously identified risk loci

Table 20 shows statistics from the META_DCSP2 cohort for 18 loci that were shown to be significantly associated with Fasting Insulin in the 2012 Nature Genetics paper by Scott 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 3 variants that show at least nominal significance ($p < 0.05$) in this study. Out of the 16 variants in both studies, 10 exhibit the same direction of effect with the known result (binomial test $p = 0.227$).

Table 20: Top known loci in META_DCSP2 model invn Adjusted Age+SEX (**bold** variants indicate matching direction of effect)

CHR	POS	ID	EA	OA	N	FREQ _{AVG}	FREQ _{MIN}	FREQ _{MAX}	EFFECT	STDERR	P	DIR	GENE _{CLOSEST}	R ²	ID _{KNOWN}	N _{KNOWN}	EFFECT _{KNOWN}	STDERR _{KNOWN}	P _{KNOWN}
2	27730940	rs1260326	C	T	1,885	0.52	0.509	0.531	1.89 · 10 ⁻²	3.26 · 10 ⁻²	0.562	++	GCKR	1	rs1260326	1.33 · 10 ⁵	2.1 · 10 ⁻²	2.1 · 10 ⁻³	2.74 · 10 ⁻²²
2	227099180	rs2943645	T	C	1,886	0.929	0.926	0.932	0.148	6.29 · 10 ⁻²	1.9 · 10 ⁻²	++	IRS1	1	rs2943645	1.33 · 10 ⁵	1.9 · 10 ⁻²	2.1 · 10 ⁻³	2.26 · 10 ⁻¹⁹
2	165513091	rs10195252	T	C	1,886	8.78 · 10 ⁻²	8.72 · 10 ⁻²	8.83 · 10 ⁻²	8.24 · 10 ⁻²	5.72 · 10 ⁻²	0.15	++	COBLL1	1	rs10195252	1.33 · 10 ⁵	1.7 · 10 ⁻²	2.1 · 10 ⁻³	1.26 · 10 ⁻¹⁶
2	227020653	rs7578326	A	G	1,886	0.145	0.142	0.148	1.5 · 10 ⁻²	4.53 · 10 ⁻²	0.741	+	NYAP2	1	rs7578326	1.33 · 10 ⁵	1.8 · 10 ⁻²	2.2 · 10 ⁻³	2.25 · 10 ⁻¹⁶
8	9185146	rs2126259	T	C	1,885	0.991	0.99	0.992	0.163	0.166	0.324	++	RP11-10A14.4	1	rs2126259	1.33 · 10 ⁵	2.4 · 10 ⁻²	3.3 · 10 ⁻³	3.3 · 10 ⁻¹³
5	53272664	rs4865796	G	A	905	0.875	0.875	0.875	0.132	7.28 · 10 ⁻²	6.9 · 10 ⁻²	+x	ARL15	1	rs4865796	1.33 · 10 ⁵	-1.5 · 10 ⁻²	2.2 · 10 ⁻³	2.16 · 10 ⁻¹²
3	12390484	rs17036328	T	C	906	3.42 · 10 ⁻²	3.42 · 10 ⁻²	3.42 · 10 ⁻²	0.277	0.129	3.2 · 10 ⁻²	+x	PPARG	1	rs17036328	1.33 · 10 ⁵	2.1 · 10 ⁻²	3 · 10 ⁻³	3.59 · 10 ⁻¹²
19	33899065	rs731839	A	G	906	0.451	0.451	0.451	0.105	4.74 · 10 ⁻²	2.73 · 10 ⁻²	+x	PEPD	1	rs731839	1.33 · 10 ⁵	-1.5 · 10 ⁻²	2.1 · 10 ⁻³	5.13 · 10 ⁻¹²
3	12116620	rs308971	G	A	1,884	0.804	0.804	0.804	2.66 · 10 ⁻²	4.16 · 10 ⁻²	0.523	++	TIMP4	1	rs308971	1.33 · 10 ⁵	2.1 · 10 ⁻²	3.1 · 10 ⁻³	2.97 · 10 ⁻¹¹
4	106071064	rs974801	A	G	1,886	0.589	0.586	0.592	4.12 · 10 ⁻²	3.32 · 10 ⁻²	0.214	++	TET2	1	rs974801	1.33 · 10 ⁵	-1.4 · 10 ⁻²	2.1 · 10 ⁻³	3.27 · 10 ⁻¹¹
4	157683685	rs1425486	C	T	905	0.296	0.296	0.296	4.68 · 10 ⁻²	5.1 · 10 ⁻²	0.359	+x	PDGFC	1	rs1425486	1.33 · 10 ⁵	1.4 · 10 ⁻²	2.2 · 10 ⁻³	2.84 · 10 ⁻¹⁰
2	27839539	rs2068834	C	T	1,886	0.471	0.464	0.478	6.93 · 10 ⁻³	3.27 · 10 ⁻²	0.832	-	ZNF512	1	rs2068834	1.33 · 10 ⁵	-1.4 · 10 ⁻²	2.3 · 10 ⁻³	1.24 · 10 ⁻⁹
1	219722104	rs4846565	G	A	1,886	0.221	0.218	0.225	2.78 · 10 ⁻²	3.88 · 10 ⁻²	0.475	++	LYPLAL1	1	rs4846565	1.33 · 10 ⁵	1.3 · 10 ⁻²	2.2 · 10 ⁻³	1.76 · 10 ⁻⁹
1	219750717	rs4846567	T	G	906	0.216	0.216	0.216	4.45 · 10 ⁻³	5.52 · 10 ⁻²	0.936	+x	SLC30A10	1	rs4846567	1.33 · 10 ⁵	-1.3 · 10 ⁻²	2.3 · 10 ⁻³	9.61 · 10 ⁻⁹
6	34764922	rs6912327	C	T	897	0.431	0.431	0.431	6.8 · 10 ⁻²	4.45 · 10 ⁻²	0.126	+x	UHRF1BP1	1	rs6912327	1.33 · 10 ⁵	-1.6 · 10 ⁻²	2.9 · 10 ⁻³	2.26 · 10 ⁻⁸
4	157616767	rs1464454	G	A	906	0.46	0.46	0.46	2.19 · 10 ⁻²	4.72 · 10 ⁻²	0.643	+x	RP11-171N4.2	1	rs1464454	1.33 · 10 ⁵	1.2 · 10 ⁻²	2.2 · 10 ⁻³	5.11 · 10 ⁻⁸
12	102910810	rs855211	G	A	1,886	0.65	0.634	0.666	6.01 · 10 ⁻²	3.37 · 10 ⁻²	7.45 · 10 ⁻²	++	IGF1	0.993	rs860598	1.33 · 10 ⁵	-1.5 · 10 ⁻²	2.7 · 10 ⁻³	1.46 · 10 ⁻⁸
4	89733882	rs6814344	G	A	1,886	0.72	0.718	0.721	3.88 · 10 ⁻³	3.62 · 10 ⁻²	0.915	-	FAM13A	0.984	rs3775380	1.33 · 10 ⁵	1.1 · 10 ⁻²	2 · 10 ⁻³	2.92 · 10 ⁻⁸

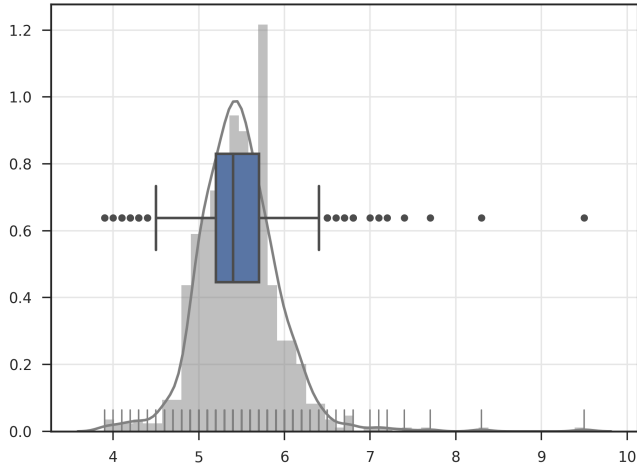
Table 21 shows statistics from the META_DCSP2 cohort for 18 loci that were shown to be significantly associated with Fasting Insulin in the 2012 Nature Genetics paper by Scott et al [15]. Where a previously reported variant was not genotyped in the study (indicated by $\bar{R}^2 < 1$), if available, 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 2 variants that show at least nominal significance ($p < 0.05$) in this study. Out of the 16 variants in both studies, 8 exhibit the same direction of effect with the known result (binomial test $p = 0.598$).

Table 21: Top known loci in META_DCSP2 model invn Adjusted Age+SEX+BMI (**bold** variants indicate matching direction of effect)

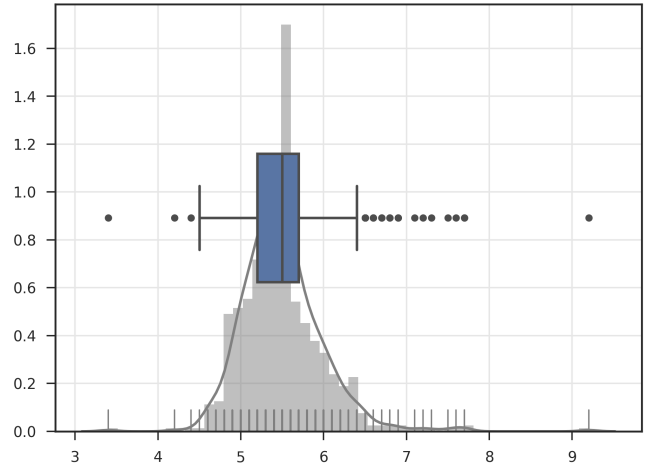
CHR	POS	ID	EA	OA	N	FREQ _{AVG}	FREQ _{MIN}	FREQ _{MAX}	EFFECT	STDERR	P	DIR	GENE _{CLOSEST}	R ²	ID _{KNOWN}	N _{KNOWN}	EFFECT _{KNOWN}	STDERR _{KNOWN}	P _{KNOWN}
2	27730940	rs1260326	T	C	1,895	0.521	0.51	0.531	9.35 · 10 ⁻³	3.26 · 10 ⁻²	0.775	++	GCKR	1	rs1260326	1.33 · 10 ⁵	-2.1 · 10 ⁻²	2.1 · 10 ⁻³	2.74 · 10 ⁻²²
2	227099180	rs2943645	T	C	1,896	0.93	0.926	0.933	0.136	6.3 · 10 ⁻²	3.12 · 10 ⁻²	++	IRS1	1	rs2943645	1.33 · 10 ⁵	1.9 · 10 ⁻²	2.1 · 10 ⁻³	2.26 · 10 ⁻¹⁹
2	165513091	rs10195252	T	C	1,896	8.73 · 10 ⁻²	8.66 · 10 ⁻²	8.8 · 10 ⁻²	9.43 · 10 ⁻²	5.72 · 10 ⁻²	9.94 · 10 ⁻²	++	COBLL1	1	rs10195252	1.33 · 10 ⁵	1.7 · 10 ⁻²	2.1 · 10 ⁻³	1.26 · 10 ⁻¹⁶
2	227020653	rs7578326	A	G	1,896	0.145	0.142	0.147	1.65 · 10 ⁻²	4.53 · 10 ⁻²	0.715	-	NYAP2	1	rs7578326	1.33 · 10 ⁵	1.8 · 10 ⁻²	2.2 · 10 ⁻³	2.25 · 10 ⁻¹⁶
8	9185146	rs2126259	T	C	1,895	0.99	0.988	0.992	0.234	0.158	0.137	++	RP11-10A14.4	1	rs2126259	1.33 · 10 ⁵	2.4 · 10 ⁻²	3.3 · 10 ⁻³	3.3 · 10 ⁻¹³
5	53272664	rs4865796	G	A	908	0.874	0.874	0.874	8.34 · 10 ⁻²	7.28 · 10 ⁻²	0.252	+x	ARL15	1	rs4865796	1.33 · 10 ⁵	-1.5 · 10 ⁻²	2.2 · 10 ⁻³	2.16 · 10 ⁻¹²
3	12390484	rs17036328	T	C	909	3.41 · 10 ⁻²	3.41 · 10 ⁻²	3.41 · 10 ⁻²	0.174	0.129	0.177	+x	PPARG	1	rs17036328	1.33 · 10 ⁵	2.1 · 10 ⁻²	3 · 10 ⁻³	3.59 · 10 ⁻¹²
19	33899065	rs731839	A	G	909	0.451	0.451	0.451	3.22 · 10 ⁻²	4.74 · 10 ⁻²	0.497	+x	PEPD	1	rs731839	1.33 · 10 ⁵	-1.5 · 10 ⁻²	2.1 · 10 ⁻³	5.13 · 10 ⁻¹²
3	12116620	rs308971	G	A	1,894	0.805	0.805	0.805	5.09 · 10 ⁻²	4.16 · 10 ⁻²	0.221	++	TIMP4	1	rs308971	1.33 · 10 ⁵	2.1 · 10 ⁻²	3.1 · 10 ⁻³	2.97 · 10 ⁻¹¹
4	106071064	rs974801	A	G	1,896	0.588	0.585	0.591	1.57 · 10 ⁻²	3.32 · 10 ⁻²	0.636	++	TET2	1	rs974801	1.33 · 10 ⁵	-1.4 · 10 ⁻²	2.1 · 10 ⁻³	3.27 · 10 ⁻¹¹
4	157683685	rs1425486	C	T	908	0.296	0.296	0.296	7.29 · 10 ⁻²	5.09 · 10 ⁻²	0.152	+x	PDGFC	1	rs1425486	1.33 · 10 ⁵	1.4 · 10 ⁻²	2.2 · 10 ⁻³	2.84 · 10 ⁻¹⁰
2	27839539	rs2068834	C	T	1,896	0.47	0.464	0.477	2.13 · 10 ⁻²	3.26 · 10 ⁻²	0.515	-	ZNF512	1	rs2068834	1.33 · 10 ⁵	-1.4 · 10 ⁻²	2.3 · 10 ⁻³	1.24 · 10 ⁻⁹
1	219722104	rs4846565	G	A	1,896	0.221	0.218	0.224	3.14 · 10 ⁻²	3.88 · 10 ⁻²	0.418	++	LYPLAL1	1	rs4846565	1.33 · 10 ⁵	-1.3 · 10 ⁻²	2.2 · 10 ⁻³	1.76 · 10 ⁻⁹
1	219750717	rs4846567	T	G	909	0.217	0.217	0.217	2.45 · 10 ⁻²	5.51 · 10 ⁻²	0.656	+x	SLC30A10	1	rs4846567	1.33 · 10 ⁵	-1.3 · 10 ⁻²	2.3 · 10 ⁻³	9.61 · 10 ⁻⁹
6	34764922	rs6912327	C	T	900	0.431	0.431	0.431	6.56 · 10 ⁻²	4.44 · 10 ⁻²	0.14	+x	UHRF1BP1	1	rs6912327	1.33 · 10 ⁵	-1.6 · 10 ⁻²	2.9 · 10 ⁻³	2.26 · 10 ⁻⁸
4	157616767	rs1464454	G	A	909	0.46	0.46	0.46	6.28 · 10 ⁻²	4.72 · 10 ⁻²	0.183	+x	RP11-171N4.2	1	rs1464454	1.33 · 10 ⁵	1.2 · 10 ⁻²	2.2 · 10 ⁻³	5.11 · 10 ⁻⁸
12	102910810	rs855211	G	A	1,896	0.651	0.634	0.666	0.101	3.36 · 10 ⁻²	2.51 · 10 ⁻³	++	IGF1	0.993	rs860598	1.33 · 10 ⁵	-1.5 · 10 ⁻²	2.7 · 10 ⁻³	1.46 · 10 ⁻⁸
4	89733882	rs6814344	G	A	1,896	0.72	0.719	0.721	7.03 · 10 ⁻³	3.6 · 10 ⁻²	5.1 · 10 ⁻²	++	FAM13A	0.984	rs3775380	1.33 · 10 ⁵	1.1 · 10 ⁻²	2 · 10 ⁻³	2.92 · 10 ⁻⁸

6 Hemoglobin A1c (HBA1C_PCT)

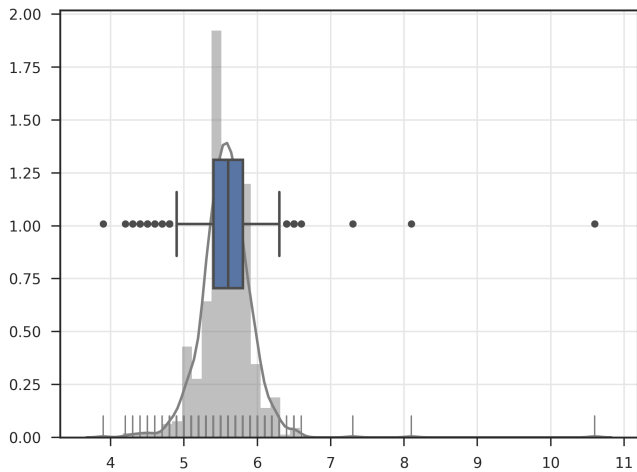
6.1 Summary



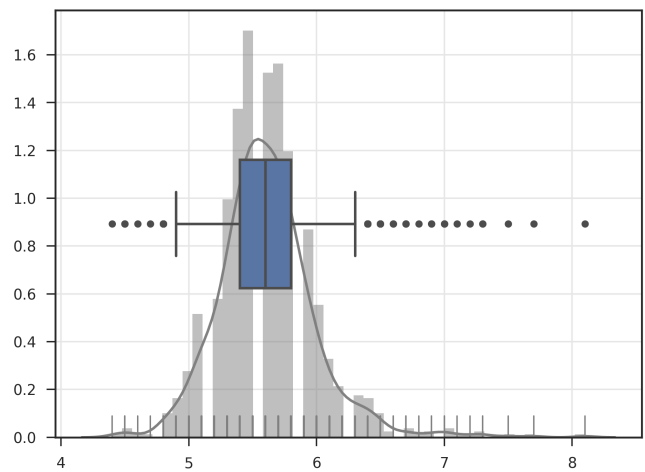
(a) DCSP21M_EAS



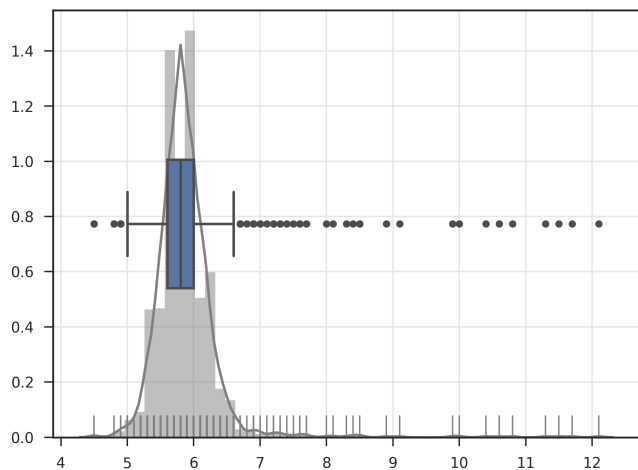
(b) DCSP2610K_EAS



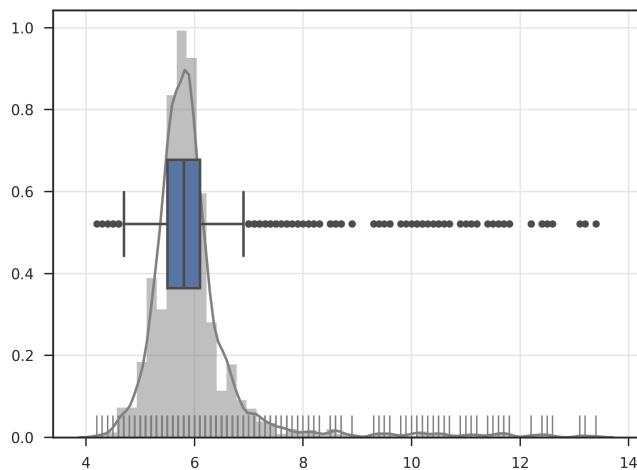
(c) LBCHS_EAS



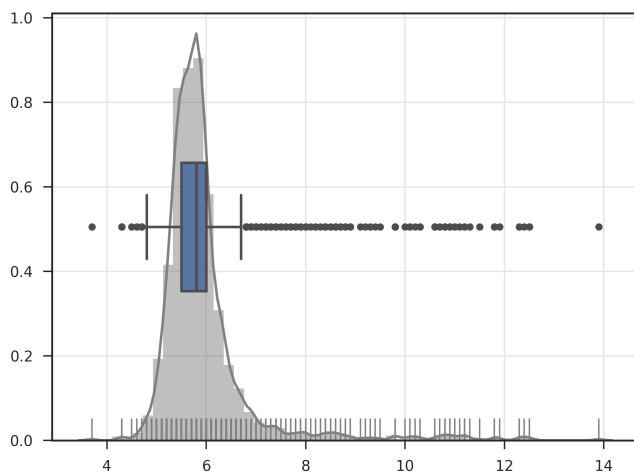
(d) LBMAS_EAS



(e) SCES_EAS



(f) SIMES_EAS



(g) SINDI_SAS

Figure 14: Distribution of HBA1C_PCT in META by cohort

Table 22: Summary of samples removed from Hemoglobin A1c analysis by cohort and model

Cohort	Array	Ancestry	Trans	Covars	Total	-SampleQc	-KinshipCrossArray	-KinshipArray	-missObs	-PcOutlier
META DCSP21M_EAS	DCSP21M	EAS	invn	Age+SEX+BMI	1864	44	0	0	1066	0
				Age+SEX	1864	44	0	0	1064	0
META DCSP2610K_EAS	DCSP2610K	EAS	invn	Age+SEX+BMI	2087	36	0	0	1366	0
				Age+SEX	2087	36	0	0	1366	1
META LBCHS_EAS	LBCHS	EAS	invn	Age+SEX	1263	22	52	122	5	11
				Age+SEX+BMI	1263	22	52	122	5	11
META LBMAS_EAS	LBMAS	EAS	invn	Age+SEX+BMI	1185	40	5	240	92	0
				Age+SEX	1185	40	5	240	92	0
META SCES_EAS	SCES	EAS	invn	Age+SEX	1889	42	93	2	191	0
				Age+SEX+BMI	1889	42	93	2	196	0
META SIMES_EAS	SIMES	EAS	invn	Age+SEX	2542	47	160	115	449	0
				Age+SEX+BMI	2542	47	160	115	458	22
META SINDI_SAS	SINDI	SAS	invn	Age+SEX+BMI	2537	60	15	91	758	0
				Age+SEX	2537	60	15	91	754	25

Table 23: Summary of samples remaining for Hemoglobin A1c analysis by cohort and model

Cohort	Array	Ancestry	Trans	Covars	PCs	N	Male	Female	Max	Min	μ	\bar{x}	σ
META DCSP21M_EAS	DCSP21M	EAS	invn	Age+SEX+BMI	0	754	474	280	9.5	3.9	5.472	5.4	0.482
				Age+SEX	0	756	476	280	9.5	3.9	5.472	5.4	0.482
META DCSP2610K_EAS	DCSP2610K	EAS	invn	Age+SEX+BMI	1	685	121	564	9.2	3.4	5.5	5.5	0.493
				Age+SEX	1	684	121	563	9.2	3.4	5.499	5.5	0.494
META LBCHS_EAS	LBCHS	EAS	invn	Age+SEX	0	1051	524	527	10.6	3.9	5.573	5.6	0.365
				Age+SEX+BMI	0	1051	524	527	10.6	3.9	5.573	5.6	0.365
META LBMAS_EAS	LBMAS	EAS	invn	Age+SEX+BMI	0	808	398	410	8.1	4.4	5.618	5.6	0.379
				Age+SEX	0	808	398	410	8.1	4.4	5.618	5.6	0.379
META SCES_EAS	SCES	EAS	invn	Age+SEX	0	1561	789	772	12.1	4.5	5.889	5.8	0.556
				Age+SEX+BMI	0	1556	787	769	12.1	4.5	5.889	5.8	0.556
META SIMES_EAS	SIMES	EAS	invn	Age+SEX	0	1771	911	860	13.4	4.2	5.987	5.8	0.981
				Age+SEX+BMI	0	1740	894	846	13.4	4.2	5.989	5.8	0.983
META SINDI_SAS	SINDI	SAS	invn	Age+SEX+BMI	0	1613	816	797	13.9	3.7	5.943	5.8	0.974
				Age+SEX	0	1592	808	784	13.9	3.7	5.946	5.8	0.979

6.2 Calibration

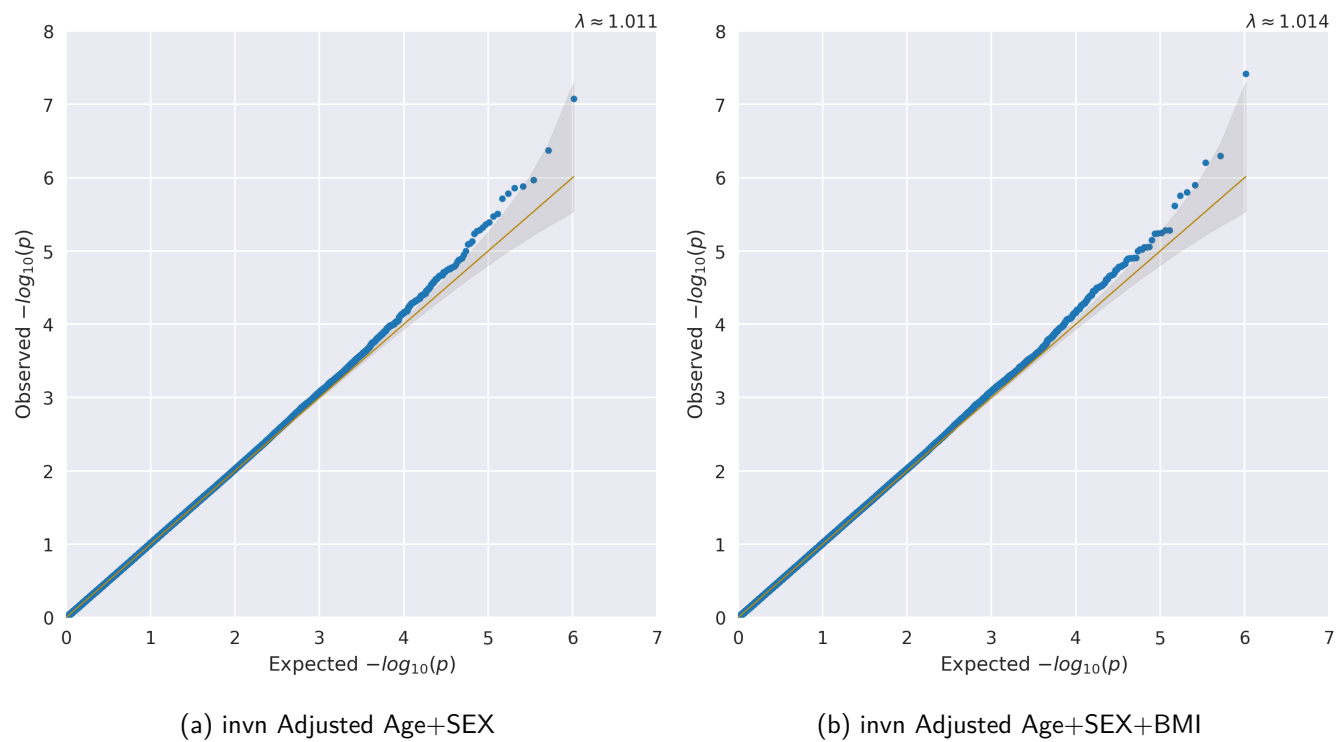
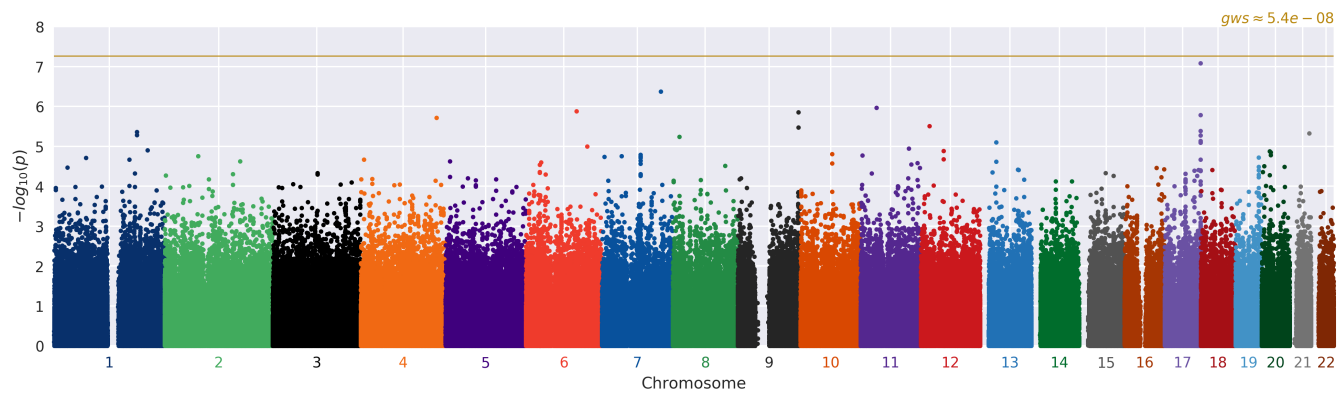
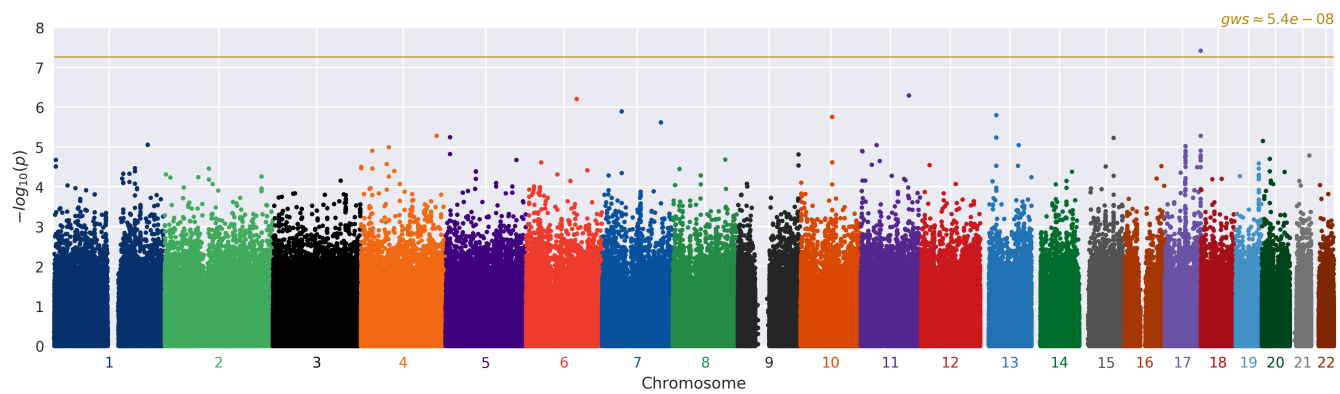


Figure 15: QQ plots for HBA1C_PCT in the META analysis



(a) invn Adjusted Age+SEX



(b) invn Adjusted Age+SEX+BMI

Figure 16: Manhattan plots for HBA1C_PCT in the META analysis

6.3 Top associations

Table 24: Top variants in the META invn Adjusted Age+SEX model (**bold** variants indicate previously identified associations)

CHR	POS	ID	EA	OA	GENE_CLOSEST	DIR	N	MALE	FEMALE	FREQ_AVG	FREQ_MIN	FREQ_MAX	EFFECT	STDERR	OR	ZSCORE	P
17	80685426	rs1046875	A	G	FN3KRP	+++++++	8,221	4,025	4,196	0.529	0.483	0.627	8.45 · 10 ⁻²	1.58 · 10 ⁻²	1.088	-5.36	8.33 · 10 ⁻⁸
7	132234790	rs1426499	T	C	PLXNA4	+++xxxx	6,364	3,105	3,259	0.442	0.311	0.519	9.06 · 10 ⁻²	1.79 · 10 ⁻²	1.095	5.058	4.23 · 10 ⁻⁷
11	35253272	rs13347	C	T	CD44	+++++++	8,214	4,024	4,190	0.293	0.164	0.347	8.42 · 10 ⁻²	1.73 · 10 ⁻²	1.088	-4.878	1.07 · 10 ⁻⁶
6	113547561	rs12191383	C	A	MARCKS	+xxxxxx	756	476	280	0.225	0.225	0.225	0.295	6.1 · 10 ⁻²	1.343	4.838	1.31 · 10 ⁻⁶
9	136123840	rs4363269	G	A	ABO	+++xxxx	6,364	3,105	3,259	0.153	9.55 · 10 ⁻²	0.19	0.12	2.49 · 10 ⁻²	1.128	4.827	1.39 · 10 ⁻⁶
17	80733549	rs11078011	G	A	TBCD	+++++++	8,219	4,025	4,194	0.382	0.329	0.416	7.75 · 10 ⁻²	1.62 · 10 ⁻²	1.081	-4.793	1.65 · 10 ⁻⁶
4	170901428	rs9312463	C	T	MFAP3L	+xxxxxx	756	476	280	0.897	0.897	0.897	0.407	8.54 · 10 ⁻²	1.502	-4.76	1.93 · 10 ⁻⁶
12	19927800	rs2731620	T	C	AEBP2	xx+xxxx	1,854	920	934	0.766	0.718	0.803	0.181	3.88 · 10 ⁻²	1.198	-4.662	3.13 · 10 ⁻⁶
17	80795783	rs7225515	A	G	ZNF750	+++xxxx	6,364	3,105	3,259	0.415	0.296	0.478	8.36 · 10 ⁻²	1.82 · 10 ⁻²	1.087	4.608	4.07 · 10 ⁻⁶
1	187039464	rs10911992	C	T	PLA2G4A	+xxxxxx	2,615	1,398	1,217	0.335	0.294	0.422	0.135	2.93 · 10 ⁻²	1.144	4.595	4.33 · 10 ⁻⁶
21	43805965	rs2839502	G	A	TMPRSS3	+++++++	8,219	4,026	4,193	0.277	0.177	0.352	8.1 · 10 ⁻²	1.77 · 10 ⁻²	1.084	-4.576	4.75 · 10 ⁻⁶
8	14879087	rs12550664	A	C	SGCZ	+++xxxx	6,363	3,104	3,259	0.472	0.414	0.544	8.01 · 10 ⁻²	1.77 · 10 ⁻²	1.083	4.533	5.8 · 10 ⁻⁶
13	36389317	rs9565575	G	A	DCLK1	+++xxxx	6,364	3,105	3,259	0.321	0.263	0.364	8.48 · 10 ⁻²	1.9 · 10 ⁻²	1.089	4.467	7.92 · 10 ⁻⁶
6	137731441	rs9321604	T	C	OLIG3	+++++++	8,222	4,027	4,195	0.622	0.53	0.711	7.13 · 10 ⁻²	1.61 · 10 ⁻²	1.074	4.417	1 · 10 ⁻⁵
11	108494855	rs990253	G	A	EXPH5	+++++++	8,218	4,023	4,195	0.268	0.212	0.393	7.81 · 10 ⁻²	1.78 · 10 ⁻²	1.081	-4.39	1.13 · 10 ⁻⁵
1	210699305	rs11583907	T	C	HHAT	+++xxxx	6,364	3,105	3,259	0.159	8.13 · 10 ⁻²	0.23	0.107	2.45 · 10 ⁻²	1.113	4.368	1.25 · 10 ⁻⁵
12	51510234	rs12826153	C	A	TFCP2	+xxxxxx	756	476	280	0.192	0.192	0.192	0.278	6.36 · 10 ⁻²	1.32	-4.361	1.29 · 10 ⁻⁵
20	17686769	rs4814637	T	G	BANF2	+xxxxxx	2,615	1,398	1,217	0.299	0.267	0.372	0.133	3.06 · 10 ⁻²	1.143	4.356	1.32 · 10 ⁻⁵
20	20054076	rs6035542	A	G	CFAP61	xx+xxxx	1,858	922	936	2.91 · 10 ⁻²	1.79 · 10 ⁻²	3.76 · 10 ⁻²	0.43	9.9 · 10 ⁻²	1.537	-4.343	1.4 · 10 ⁻⁵
10	71376535	rs2927384	A	C	C10orf35	+x+xxxx	2,615	1,398	1,217	0.767	0.748	0.783	0.139	3.22 · 10 ⁻²	1.15	4.322	1.55 · 10 ⁻⁵

Table 25: Top variants in the META invn Adjusted Age+SEX+BMI model (**bold** variants indicate previously identified associations)

CHR	POS	ID	EA	OA	GENE_CLOSEST	DIR	N	MALE	FEMALE	FREQ_AVG	FREQ_MIN	FREQ_MAX	EFFECT	STDERR	OR	ZSCORE	P
17	80685426	rs1046875	A	G	FN3KRP	+++++++	8,205	4,012	4,193	0.53	0.484	0.63	8.68 · 10 ⁻²	1.58 · 10 ⁻²	1.091	-5.499	3.81 · 10 ⁻⁸
11	108494855	rs990253	G	A	EXPH5	+++++++	8,202	4,010	4,192	0.269	0.212	0.393	8.93 · 10 ⁻²	1.78 · 10 ⁻²	1.093	-5.025	5.03 · 10 ⁻⁷
6	113547561	rs12191383	C	A	MARCKS	+xxxxxx	754	474	280	0.225	0.225	0.225	0.304	6.1 · 10 ⁻²	1.355	4.985	6.2 · 10 ⁻⁷
7	44235668	rs4607517	A	G	YKT6	+++++++	8,204	4,012	4,192	0.16	0.117	0.212	0.104	2.14 · 10 ⁻²	1.109	4.847	1.26 · 10 ⁻⁶
13	36389317	rs9565575	G	A	DCLK1	+++xxxx	6,348	3,092	3,256	0.321	0.263	0.366	9.12 · 10 ⁻²	1.9 · 10 ⁻²	1.096	4.801	1.58 · 10 ⁻⁶
10	71376535	rs2927384	A	C	C10orf35	+x+xxxx	2,613	1,396	1,217	0.768	0.748	0.783	0.154	3.22 · 10 ⁻²	1.167	4.78	1.75 · 10 ⁻⁶
7	132234790	rs1426499	T	C	PLXNA4	+++xxxx	6,348	3,092	3,256	0.442	0.312	0.52	8.45 · 10 ⁻²	1.79 · 10 ⁻²	1.088	4.715	2.41 · 10 ⁻⁶
17	80795783	rs7225515	A	G	ZNF750	+++xxxx	6,348	3,092	3,256	0.414	0.294	0.477	8.28 · 10 ⁻²	1.82 · 10 ⁻²	1.086	4.556	5.2 · 10 ⁻⁶
4	170901428	rs9312463	C	T	MFAP3L	+xxxxxx	754	474	280	0.898	0.898	0.898	0.39	8.57 · 10 ⁻²	1.478	-4.555	5.24 · 10 ⁻⁶
5	9793237	rs1008253	A	C	TAS2R1	+x+xxxx	2,613	1,396	1,217	0.427	0.417	0.447	0.126	2.77 · 10 ⁻²	1.134	-4.539	5.66 · 10 ⁻⁶
15	77400388	rs3743478	C	T	PEAK1	+++++++	8,207	4,014	4,193	0.371	0.334	0.439	7.31 · 10 ⁻²	1.61 · 10 ⁻²	1.076	4.532	5.84 · 10 ⁻⁶
20	2321665	rs214832	C	T	TGM3	+x+xxxx	2,612	1,395	1,217	0.875	0.819	0.904	0.189	4.21 · 10 ⁻²	1.208	4.492	7.07 · 10 ⁻⁶
1	210699305	rs11583907	T	C	HHAT	+++xxxx	6,348	3,092	3,256	0.159	8.06 · 10 ⁻²	0.229	0.109	2.46 · 10 ⁻²	1.115	4.447	8.72 · 10 ⁻⁶
13	86408521	rs10220124	G	A	SLITRK6	xx+xxxx	1,858	922	936	6.46 · 10 ⁻²	5.89 · 10 ⁻²	6.9 · 10 ⁻²	0.3	6.76 · 10 ⁻²	1.35	-4.442	8.92 · 10 ⁻⁶
11	35253272	rs13347	C	T	CD44	+++++++	8,198	4,011	4,187	0.293	0.166	0.346	7.68 · 10 ⁻²	1.73 · 10 ⁻²	1.08	-4.442	8.93 · 10 ⁻⁶
17	46296204	rs16953941	C	A	SKAP1	+xxxxxx	754	474	280	0.22	0.22	0.22	0.273	6.15 · 10 ⁻²	1.313	-4.43	9.43 · 10 ⁻⁶
4	63397548	rs6848319	T	G	ADGRL3	+++++++	8,203	4,012	4,191	0.904	0.886	0.914	0.118	2.66 · 10 ⁻²	1.125	4.417	1 · 10 ⁻⁵
17	80801745	rs7219521	A	G	TBCD	+++++++	8,205	4,013	4,192	0.496	0.342	0.571	6.93 · 10 ⁻²	1.59 · 10 ⁻²	1.072	4.371	1.24 · 10 ⁻⁵
4	25881877	rs7681279	T	C	SEL1L3	+++++++	8,203	4,011	4,192	0.307	0.283	0.338	7.36 · 10 ⁻²	1.68 · 10 ⁻²	1.076	4.37	1.24 · 10 ⁻⁵
11	2858295	rs2299620	C	T	KCNQ1	+++x+	6,311	3,070	3,241	0.265	2.39 · 10 ⁻²	0.367	9.2 · 10 ⁻²	2.11 · 10 ⁻²	1.096	-4.367	1.26 · 10 ⁻⁵

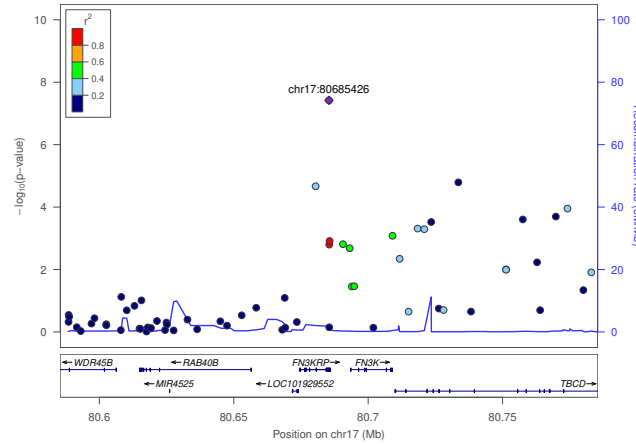


Figure 17: Regional plot for cohort META model invn Adjusted Age+SEX+BMI: rs1046875 ±100kb

6.4 Previously identified risk loci

Table 26 shows statistics from the META cohort for 19 loci that were shown to be significantly associated with Hemoglobin A1c in the 2010 Diabetes paper by Soranzo et al [16]. Where a previously reported variant was not genotyped in the study (indicated by $\bar{R}^2 < 1$), if available, a tagging variant in LD with the reported variant ($\bar{R}^2 \geq 0.7$ and within 250kb) was provided. Tags were identified using 1000 Genomes data. There are 8 variants that show at least nominal significance ($p < 0.05$) in this study. Out of the 19 variants in both studies, 16 exhibit the same direction of effect with the known result (binomial test $p = 0.00221$).

Table 26: Top known loci in META model invn Adjusted Age+SEX (**bold** variants indicate matching direction of effect)

CHR	POS	ID	EA	OA	N	FREQ _{AVG}	FREQ _{MIN}	FREQ _{MAX}	EFFECT	STDERR	P	DIR	GENECLOSEST	R ²	ID _{KNOWN}	N _{KNOWN}	EFFECT _{KNOWN}	STDERR _{KNOWN}	P _{KNOWN}
17	80685533	rs1046896	T	C	2,613	0.496	0.484	0.504	8.85 · 10 ⁻²	2.8 · 10 ⁻²	1.55 · 10 ⁻³	++x+xxx	FN3KRP	1	rs1046896	46,368	3.46 · 10 ⁻²	3.2 · 10 ⁻³	1.58 · 10 ⁻²⁶
10	71099888	rs10159477	G	A	8,221	2.72 · 10 ⁻²	7.31 · 10 ⁻⁴	0.113	4.48 · 10 ⁻³	4.93 · 10 ⁻²	0.928	---+	HK1	1	rs10159477	46,368	5.86 · 10 ⁻²	5.6 · 10 ⁻³	3.19 · 10 ⁻²⁵
17	80795783	rs7225515	A	G	6,364	0.415	0.296	0.478	8.42 · 10 ⁻²	1.82 · 10 ⁻²	3.52 · 10 ⁻⁵	+++x+++	ZNF750	1	rs7225515	46,368	3.56 · 10 ⁻²	3.9 · 10 ⁻³	2.31 · 10 ⁻²⁰
6	26093141	rs1800562	A	G	1,592	1.26 · 10 ⁻³	1.26 · 10 ⁻³	1.26 · 10 ⁻³	9.13 · 10 ⁻²	0.501	0.855	xxxxxxx	HFE	1	rs1800562	46,368	-6.36 · 10 ⁻²	6.9 · 10 ⁻³	2.59 · 10 ⁻²⁰
17	80800027	rs4075209	T	G	756	0.478	0.478	0.478	0.15	5.21 · 10 ⁻²	4.05 · 10 ⁻³	+xxxxxxx	TBCD	1	rs4075209	46,368	3.5 · 10 ⁻²	3.9 · 10 ⁻³	1.08 · 10 ⁻¹⁹
7	44223721	rs730497	A	G	6,363	0.156	0.117	0.212	9.17 · 10 ⁻²	2.45 · 10 ⁻²	1.85 · 10 ⁻⁴	+xxxx+++	GCK	1	rs730497	46,368	4.07 · 10 ⁻²	4.6 · 10 ⁻³	3.83 · 10 ⁻¹⁹
7	44235668	rs4607517	A	G	8,220	0.159	0.116	0.212	9.2 · 10 ⁻²	2.15 · 10 ⁻²	1.8 · 10 ⁻⁵	+++++++	YKT6	1	rs4607517	46,368	4.05 · 10 ⁻²	4.6 · 10 ⁻³	6.3 · 10 ⁻¹⁹
2	169791438	rs552976	G	A	8,222	0.95	0.831	0.988	4.25 · 10 ⁻²	3.71 · 10 ⁻²	0.252	+++---	ABCB11	1	rs552976	46,368	2.9 · 10 ⁻²	3.4 · 10 ⁻³	8.16 · 10 ⁻¹⁸
2	169763148	rs560887	C	T	8,221	0.956	0.904	0.974	3.07 · 10 ⁻²	3.84 · 10 ⁻²	0.423	+++++	G6PC2	1	rs560887	46,368	3.18 · 10 ⁻²	3.7 · 10 ⁻³	1.04 · 10 ⁻¹⁷
22	37462936	rs855791	A	G	8,221	0.457	0.433	0.5	4.61 · 10 ⁻²	1.56 · 10 ⁻²	3.11 · 10 ⁻³	+++++++	TMPRSS6	1	rs855791	46,368	2.71 · 10 ⁻²	3.6 · 10 ⁻³	2.74 · 10 ⁻¹⁴
6	25821770	rs17342717	C	T	6,363	4.95 · 10 ⁻³	7.31 · 10 ⁻⁴	1.41 · 10 ⁻²	5.76 · 10 ⁻²	0.125	0.646	++x+++	SLC17A1	1	rs17342717	46,368	4.49 · 10 ⁻²	6.3 · 10 ⁻³	1.26 · 10 ⁻¹²
8	41630405	rs4737009	A	G	2,615	0.491	0.398	0.544	4.78 · 10 ⁻²	2.79 · 10 ⁻²	8.61 · 10 ⁻²	++x+xxx	ANK1	1	rs4737009	46,368	2.69 · 10 ⁻²	3.9 · 10 ⁻³	6.12 · 10 ⁻¹²
17	80693899	rs3848403	T	C	756	0.581	0.581	0.581	9.96 · 10 ⁻²	5.25 · 10 ⁻²	5.79 · 10 ⁻²	+xxxxxxx	FN3K	1	rs3848403	46,368	3.84 · 10 ⁻²	5.7 · 10 ⁻³	1.88 · 10 ⁻¹¹
11	92673828	rs1387153	T	C	8,223	0.432	0.368	0.466	2.41 · 10 ⁻³	1.58 · 10 ⁻²	0.879	+++---	MTNR1B	1	rs1387153	46,368	2.58 · 10 ⁻²	3.9 · 10 ⁻³	3.96 · 10 ⁻¹¹
2	169750483	rs477224	T	C	8,221	0.776	0.71	0.834	6.36 · 10 ⁻²	1.87 · 10 ⁻²	6.88 · 10 ⁻⁴	+++---	SPC25	1	rs477224	46,368	-2.36 · 10 ⁻²	3.7 · 10 ⁻³	2.05 · 10 ⁻¹⁰
1	158618455	rs2246434	A	G	2,615	0.43	0.419	0.439	3.36 · 10 ⁻²	2.76 · 10 ⁻²	0.222	+x+xxx	SPTA1	1	rs2246434	46,368	2.27 · 10 ⁻²	3.9 · 10 ⁻³	6.04 · 10 ⁻⁹
13	113329598	rs12868291	C	T	5,652	7.96 · 10 ⁻²	6.28 · 10 ⁻²	9.63 · 10 ⁻²	0.102	3.49 · 10 ⁻²	3.44 · 10 ⁻³	+xxxx+++	ATP11A	1	rs12868291	46,368	3.15 · 10 ⁻²	5.5 · 10 ⁻³	8.53 · 10 ⁻⁹
6	25624395	rs7765813	T	G	2,614	1.76 · 10 ⁻²	1.18 · 10 ⁻²	2.38 · 10 ⁻²	6.15 · 10 ⁻³	0.104	0.953	+x+xxx	LRRIC16A	1	rs7765813	46,368	-3.43 · 10 ⁻²	6.1 · 10 ⁻³	1.66 · 10 ⁻⁸
17	80908501	rs12949939	C	T	2,615	0.207	0.173	0.266	4.84 · 10 ⁻²	3.46 · 10 ⁻²	0.161	-x+xxx	B3GNTL1	1	rs12949939	46,368	2.03 · 10 ⁻²	3.7 · 10 ⁻³	3.19 · 10 ⁻⁸

Table 27 shows statistics from the META cohort for 19 loci that were shown to be significantly associated with Hemoglobin A1c in the 2010 Diabetes paper by Soranzo et al [16]. 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 19 variants in both studies, 15 exhibit the same direction of effect with the known result (binomial test $p = 0.00961$).

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

CHR	POS	ID	EA	OA	N	FREQ _{AVG}	FREQ _{MIN}	FREQ _{MAX}	EFFECT	STDERR	P	DIR	GENE _{CLOSEST}	R ²	ID _{KNOWN}	N _{KNOWN}	EFFECT _{KNOWN}	STDERR _{KNOWN}	P _{KNOWN}
17	80685533	rs1046896	T	C	2,611	0.496	0.484	0.503	8.84 · 10 ⁻²	2.8 · 10 ⁻²	1.59 · 10 ⁻³	++x++xxx	FN3KRP	1	rs1046896	46,368	3.46 · 10 ⁻²	3.2 · 10 ⁻³	1.58 · 10 ⁻²⁶
10	71099888	rs10159477	G	A	8,206	2.71 · 10 ⁻²	7.3 · 10 ⁻⁴	0.112	1.29 · 10 ⁻²	4.94 · 10 ⁻²	0.794	--++++	HK1	1	rs10159477	46,368	5.86 · 10 ⁻²	5.6 · 10 ⁻³	3.19 · 10 ⁻²⁵
17	80795783	rs7225515	A	G	6,349	0.414	0.294	0.477	8.28 · 10 ⁻²	1.82 · 10 ⁻²	5.22 · 10 ⁻⁶	++xx++++	ZNF750	1	rs7225515	46,368	3.56 · 10 ⁻²	3.9 · 10 ⁻³	2.31 · 10 ⁻²⁰
6	26093141	rs1800562	A	G	1,613	1.24 · 10 ⁻³	1.24 · 10 ⁻³	1.24 · 10 ⁻³	0.189	0.501	0.705	xxxxxxxx+	HFE	1	rs1800562	46,368	-6.36 · 10 ⁻²	6.9 · 10 ⁻³	2.59 · 10 ⁻²⁰
17	80800027	rs4075209	T	G	754	0.477	0.477	0.477	0.149	5.22 · 10 ⁻²	4.36 · 10 ⁻³	+xxxxxxxx	TBCD	1	rs4075209	46,368	3.5 · 10 ⁻²	3.9 · 10 ⁻³	1.08 · 10 ⁻¹⁹
7	44223721	rs730497	A	G	6,348	0.157	0.117	0.213	0.1	2.45 · 10 ⁻²	4.38 · 10 ⁻³	++xx++++	GCK	1	rs730497	46,368	4.07 · 10 ⁻²	4.6 · 10 ⁻³	3.83 · 10 ⁻¹⁹
7	44235668	rs4607517	A	G	8,205	0.16	0.116	0.212	0.104	2.14 · 10 ⁻²	1.23 · 10 ⁻⁶	+++++++	YKT6	1	rs4607517	46,368	4.05 · 10 ⁻²	4.6 · 10 ⁻³	6.3 · 10 ⁻¹⁹
2	169791438	rs552976	G	A	8,207	0.95	0.831	0.988	2.87 · 10 ⁻²	3.71 · 10 ⁻²	0.438	+++++	ABCB11	1	rs552976	46,368	2.9 · 10 ⁻²	3.4 · 10 ⁻³	8.16 · 10 ⁻¹⁸
2	169763148	rs560887	C	T	8,206	0.956	0.904	0.974	2.66 · 10 ⁻²	3.83 · 10 ⁻²	0.488	+++++	G6PC2	1	rs560887	46,368	3.18 · 10 ⁻²	3.7 · 10 ⁻³	1.04 · 10 ⁻¹⁷
22	37462936	rs855791	A	G	8,205	0.457	0.432	0.5	4.7 · 10 ⁻²	1.56 · 10 ⁻²	2.64 · 10 ⁻³	+++++++	TMPRS56	1	rs855791	46,368	2.71 · 10 ⁻²	3.6 · 10 ⁻³	2.74 · 10 ⁻¹⁴
6	25821770	rs17342717	T	C	6,348	4.96 · 10 ⁻³	7.3 · 10 ⁻⁴	1.39 · 10 ⁻²	3.48 · 10 ⁻³	0.125	0.978	--x--+	SLC17A1	1	rs17342717	46,368	-4.49 · 10 ⁻²	6.3 · 10 ⁻³	1.26 · 10 ⁻¹²
8	41630405	rs4737009	A	G	2,613	0.49	0.398	0.543	5.13 · 10 ⁻²	2.79 · 10 ⁻²	6.55 · 10 ⁻²	++x++xxx	ANK1	1	rs4737009	46,368	2.69 · 10 ⁻²	3.9 · 10 ⁻³	6.12 · 10 ⁻¹²
17	80693899	rs3848403	T	C	754	0.58	0.58	0.58	0.111	5.26 · 10 ⁻²	3.51 · 10 ⁻²	+xxxxxxxx	FN3K	1	rs3848403	46,368	3.84 · 10 ⁻²	5.7 · 10 ⁻³	1.88 · 10 ⁻¹¹
11	92673828	rs1387153	T	C	8,208	0.432	0.369	0.466	8.51 · 10 ⁻³	1.58 · 10 ⁻²	0.591	+++++	MTNR1B	1	rs1387153	46,368	2.58 · 10 ⁻²	3.9 · 10 ⁻³	3.96 · 10 ⁻¹¹
2	169750483	rs477224	T	C	8,206	0.777	0.712	0.836	5.87 · 10 ⁻²	1.88 · 10 ⁻²	1.76 · 10 ⁻³	+++++	SPC25	1	rs477224	46,368	-2.36 · 10 ⁻²	3.7 · 10 ⁻³	2.05 · 10 ⁻¹⁰
1	158618455	rs2246434	A	G	2,613	0.43	0.42	0.439	2.66 · 10 ⁻²	2.76 · 10 ⁻²	0.335	+x+-xxx	SPTA1	1	rs2246434	46,368	2.27 · 10 ⁻²	3.9 · 10 ⁻³	6.04 · 10 ⁻⁹
13	113329598	rs12868291	C	T	5,636	8 · 10 ⁻²	6.3 · 10 ⁻²	9.56 · 10 ⁻²	0.107	3.49 · 10 ⁻²	2.17 · 10 ⁻³	+xxxx++	ATP11A	1	rs12868291	46,368	3.15 · 10 ⁻²	5.5 · 10 ⁻³	8.53 · 10 ⁻⁹
6	25624395	rs7765813	T	G	2,612	1.74 · 10 ⁻²	1.18 · 10 ⁻²	2.38 · 10 ⁻²	2.03 · 10 ⁻²	0.105	0.846	+x+-xxx	LRRC16A	1	rs7765813	46,368	-3.43 · 10 ⁻²	6.1 · 10 ⁻³	1.66 · 10 ⁻⁸
17	80908501	rs12949939	C	T	2,613	0.207	0.172	0.266	2.5 · 10 ⁻²	3.46 · 10 ⁻²	0.47	-x+-xxx	B3GNTL1	1	rs12949939	46,368	2.03 · 10 ⁻²	3.7 · 10 ⁻³	3.19 · 10 ⁻⁸

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