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Supplementary methods

Data sources

UK Biobank data UKB is a large prospective cohort study involving approximately 500,000 UK individuals aged 40-69 years at baseline, recruited from England, Wales, and Scotland between 2006 and 2010 ¹. All participants provided written informed consent, and ethical approval was received from the National Health Service North West Multi-Centre Research Ethics Committee. We only considered 472,050 participants of white descent. We defined a diagnosis of T2DM as the International Classification of Diseases, Tenth Revision (ICD-10) code E11, and a diagnosis of CAD as ICD-9 codes 410-414 and ICD-10 codes I20-I25.

For the analysis of association between T2DM and incident CAD, we excluded participants with a diagnosis of other diabetes (ICD-9 codes 250, 6480; ICD-10 codes E10, E12-E14, and O24) or with a history of CAD at baseline. Participants were also excluded if they had a diagnosis of CAD before T2DM during follow-up. In total, 448,363 participants were included.

For the analysis of association between CAD and incident T2DM, we excluded participants with a stroke diagnosis (ICD-9 codes 430, 431, 433, 434, and 436; ICD-10 codes I60, I61, I63, and I64) or with a history of T2DM at baseline. Participants were also excluded if they had a diagnosis of T2DM before CAD during follow-up. In total, 449,603 participants were included.

We also adjusted for important confounders/mediators in our two-sample MR. Details regarding the data sources of confounders/mediators are shown below.

BMI GWAS The largest GWAS of body mass index (BMI) was conducted meta-analyzing data across the Genetic Investigation of Anthropometric Traits consortium and UKB, totaling 806,834 individuals of European ancestry ². A total of 1,834 independent BMI-associated SNPs were identified and used as IVs. We extracted the effect size and relevant information of these IVs, as well as downloaded full set GWAS summary statistics for multivariable Mendelian randomization and mediation analyses.

SBP GWAS The largest GWAS of systolic blood pressure (SBP) was conducted meta-analyzing data across the International Consortium of Blood Pressure Genome Wide Association Studies and UKB, totaling 757,601 individuals of European ancestry ³. A total of 237 independent SBP-associated SNPs were identified and used as IVs. We extracted the effect size and relevant information of these IVs, as well as downloaded full set GWAS summary statistics for multivariable Mendelian randomization and mediation analyses.

C10AA GWAS The largest GWAS of taking HMG CoA reductase inhibitors (C10AA) was conducted in UKB, totaling 73,475 cases and 216,910 controls of European ancestry ⁴. A total of 97 independent C10AA-associated SNPs were identified and used as IVs. We extracted the effect size and relevant information of these IVs, as well as downloaded full set GWAS summary statistics for multivariable Mendelian randomization and mediation analyses.

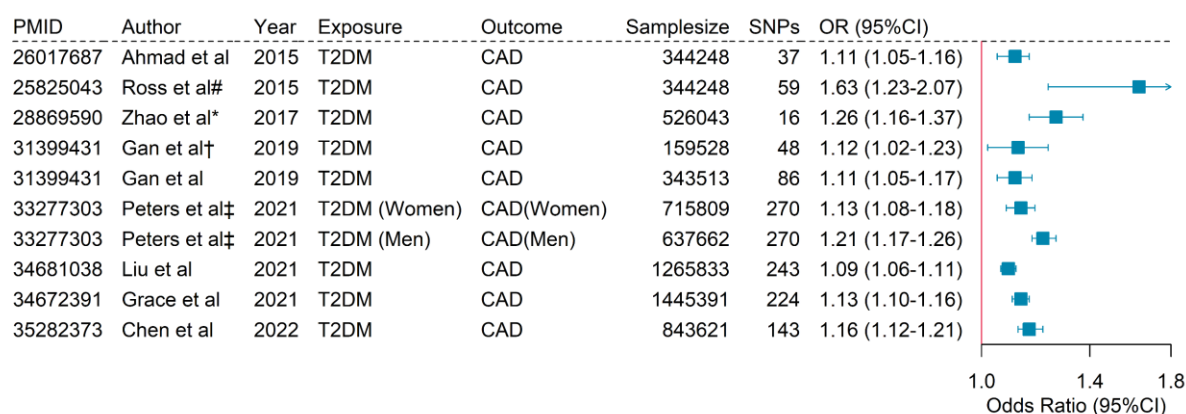
Code availability

Our methods used are as follows:

LDSC ⁵: <https://github.com/bulik/ldsc>; ρ -HESS ⁶: https://huwenboshi.github.io/hess/local_rho/ ; CPASSOC ⁷: <http://hal.case.edu/~xxz10/zhu-web/>; PLINK ⁸: <https://www.cog-genomics.org/plink/1.9/>; NHGRI-EBI GWAS Catalog ⁹: <https://www.ebi.ac.uk/gwas/>; PhenoScanner ^{10,11}: <http://www.phenoscanter.medschl.cam.ac.uk/>; VEP ¹²: <https://grch37.ensembl.org/info/docs/tools/vep/index.html>; FUMA ¹³: <https://fuma.ctglab.nl/>; TwoSampleMR ¹⁴: <https://mrcieu.github.io/TwoSampleMR/> ; LHC-MR ¹⁵: <https://github.com/LizaDarrous/lhcMR>.

Supplementary References

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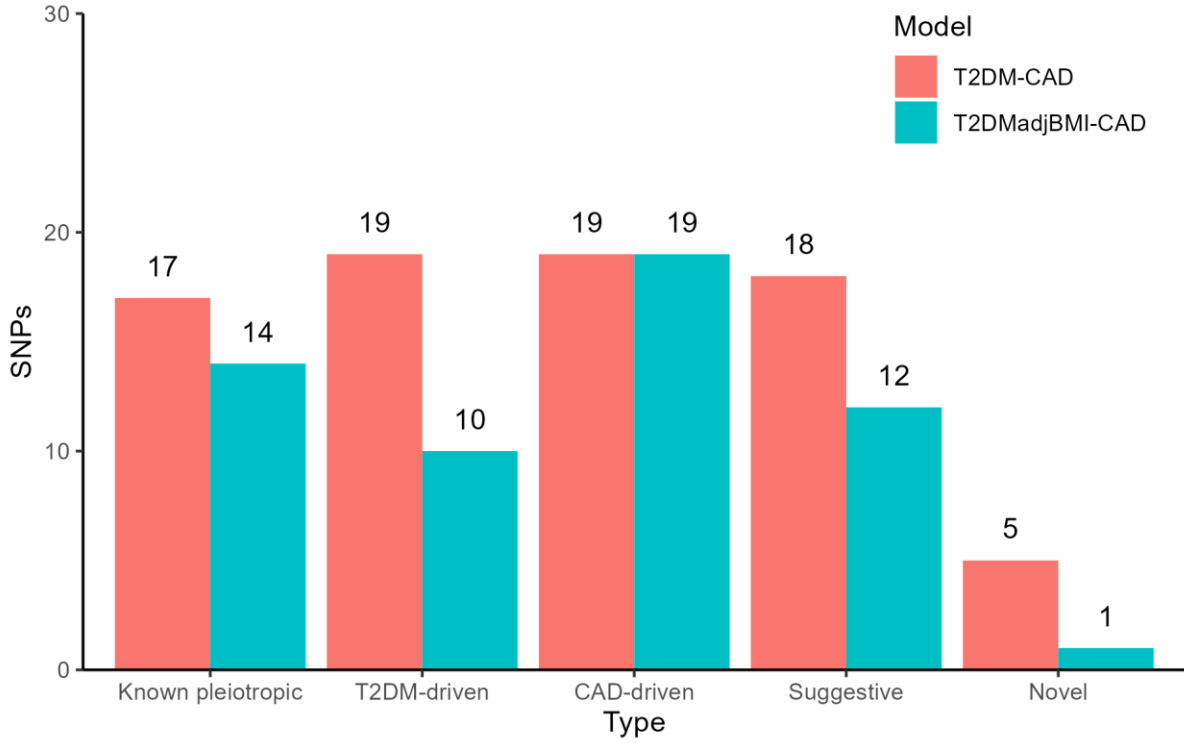


Supplementary Figure 1. Summary on the results of previous Mendelian randomization studies conducted for type 2 diabetes mellitus and coronary artery disease (only significant results are shown).

The boxes denote point estimate of the causal effects, and the error bars denote 95% confidence intervals.

[#]Effect sizes adjusted for the potential pleiotropic effects of low-density lipoprotein, high-density lipoprotein, total cholesterol, triglyceride, and body mass index. ^{*}SNPs that were associated with anthropometric traits (BMI, waist–hip ratio, waist circumference, waist–hip ratio adjusted for BMI, waist circumference adjusted for BMI, and hip), glucose/insulin or MAGIC traits (fasting glucose, 2-h glucose, fasting insulin, and proinsulin levels), blood lipids (HDL-C, LDL-C, and triglycerides), and blood pressure (systolic and diastolic) were excluded. [†]One-sample MR with effect sizes adjusted for age, sex, study area. [‡]Effect sizes adjusted for age, genotype array, and principal components of ancestry.

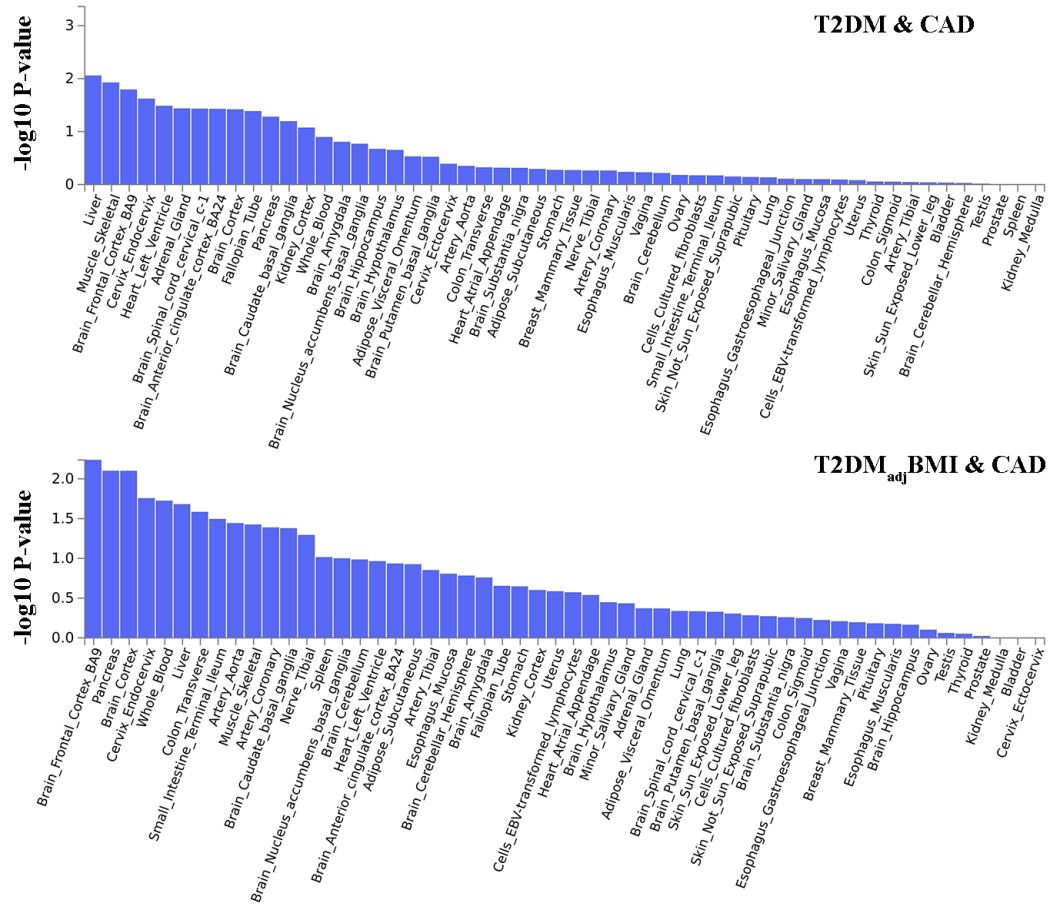
T2DM, type 2 diabetes mellitus; CAD, coronary artery disease; MR, Mendelian randomization; OR, odds ratio; CI, confidence interval. **Search strategy:** Database: PubMed; Query: (type 2 diabetes mellitus [MeSH Terms]) AND (coronary heart disease [MeSH Terms]); Date: 2023-04-30; N: 4822.



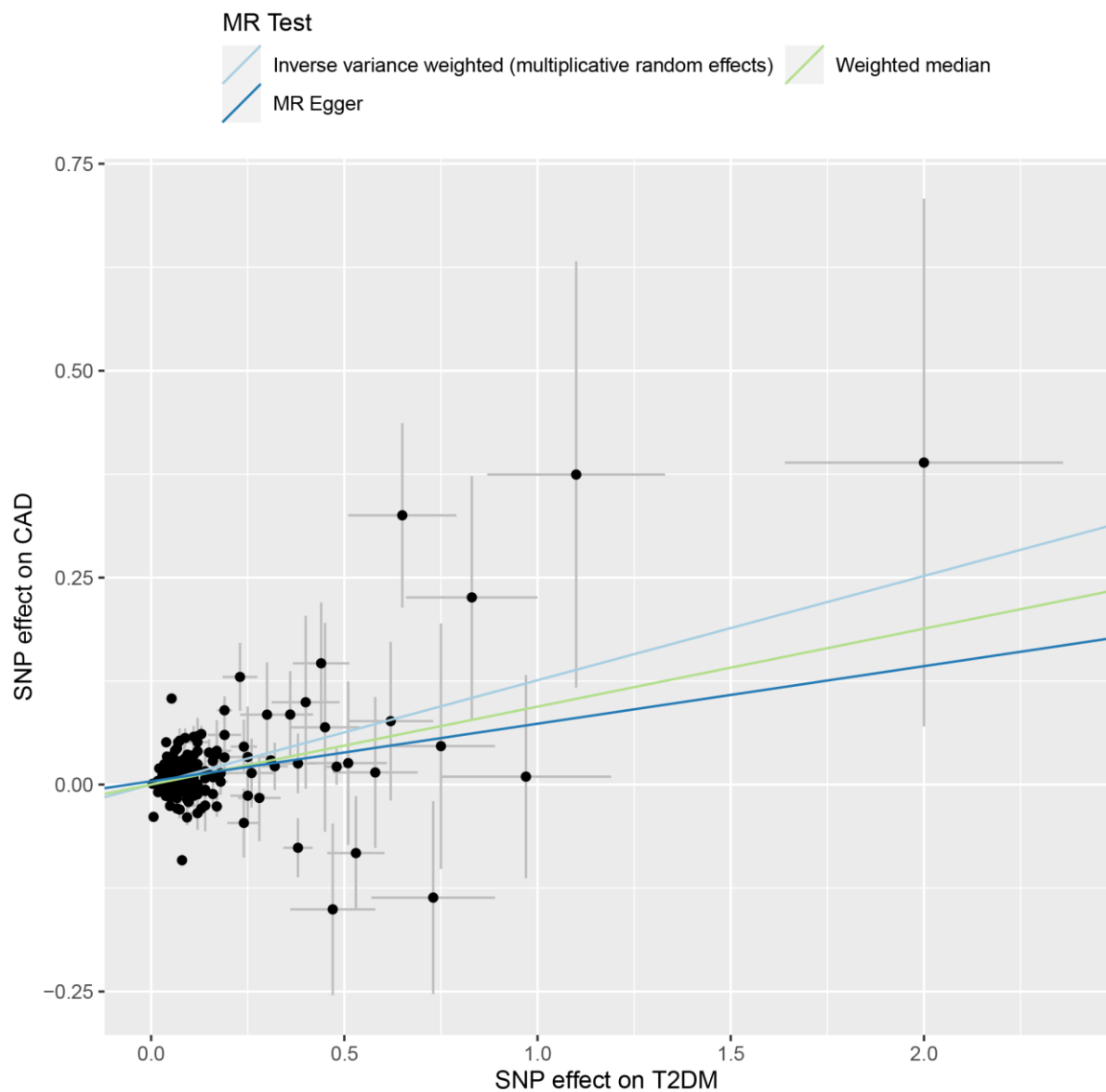
Supplementary Figure 2. Number of SNPs identified by the cross-trait meta-analysis combining data of type 2 diabetes mellitus and coronary artery disease (only SNPs with P -CPASSOC $< 5 \times 10^{-8}$ and single trait P -value $< 1 \times 10^{-5}$ are counted).

Known pleiotropic: a known pleiotropic SNP with P -value $< 5 \times 10^{-8}$ in both single traits. These SNPs are naturally pleiotropic SNPs even without CPASSOC testing; **T2DM-driven:** a pleiotropic SNP (P -CPASSOC $< 5 \times 10^{-8}$) with main effect driven by T2DM (P -value of T2DM $< 5 \times 10^{-8}$ but P -value of CAD $\geq 5 \times 10^{-8}$); **CAD-driven:** a pleiotropic SNP (P -CPASSOC $< 5 \times 10^{-8}$) with main effect driven by CAD (P -value of CAD $< 5 \times 10^{-8}$ but P -value of T2DM $\geq 5 \times 10^{-8}$); **Suggestive:** a suggestive SNP that with P -CPASSOC $< 5 \times 10^{-8}$ and P -value $\geq 5 \times 10^{-8}$ in both of the single trait GWAS, but are in LD with previously-identified single-trait associated SNPs (LD $r^2 \geq 0.05$); **Novel:** a novel SNP that would not have been identified through single trait GWAS, with P -CPASSOC $< 5 \times 10^{-8}$ and P -value $\geq 5 \times 10^{-8}$ in both of the single trait GWAS, and were not in LD with previously identified single-trait associated SNPs (LD $r^2 < 0.05$).

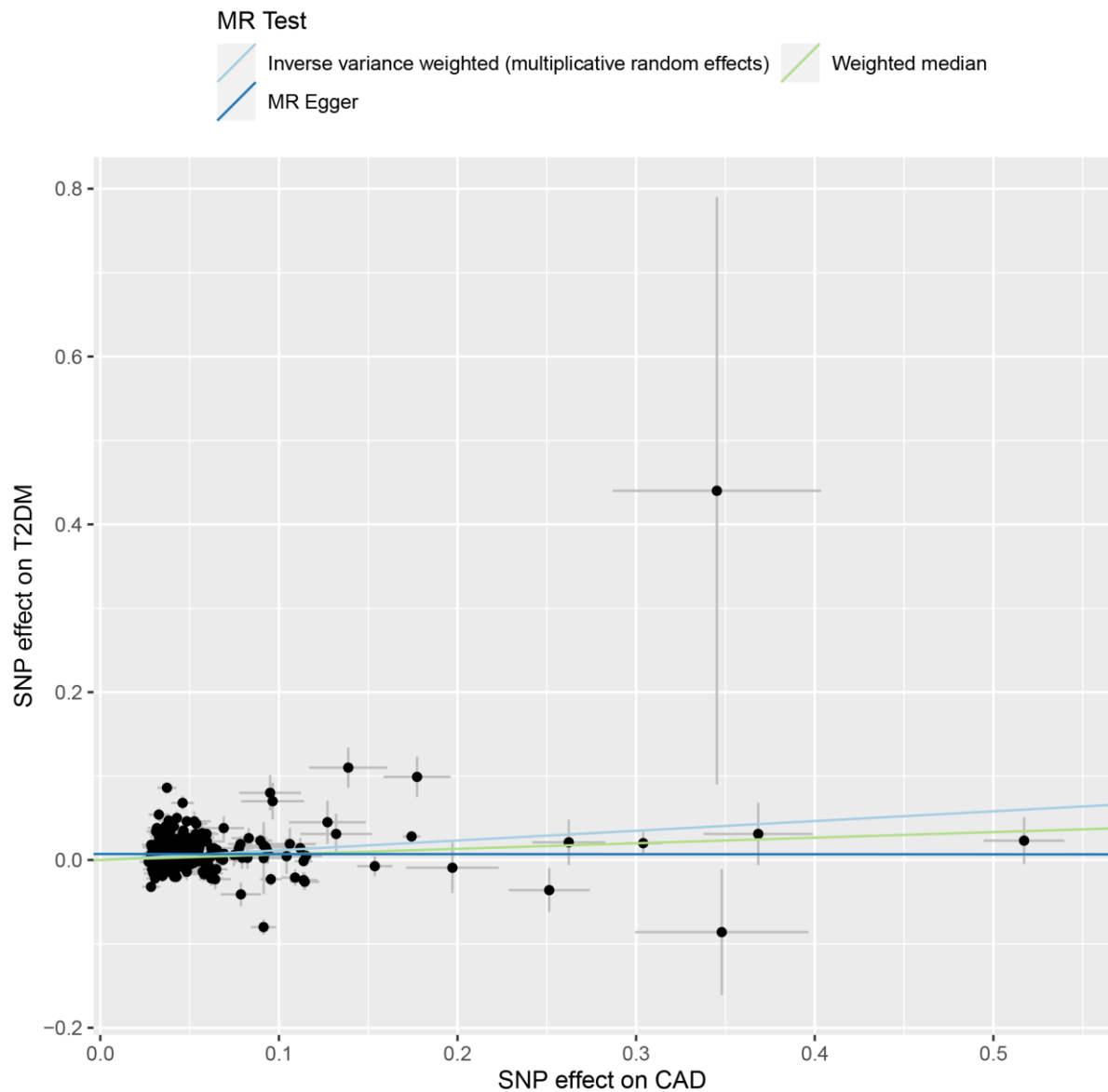
T2DM, type 2 diabetes mellitus; CAD, coronary artery disease; T2DM_{adj}BMI, type 2 diabetes mellitus adjusted for body mass index; LD, linkage disequilibrium.



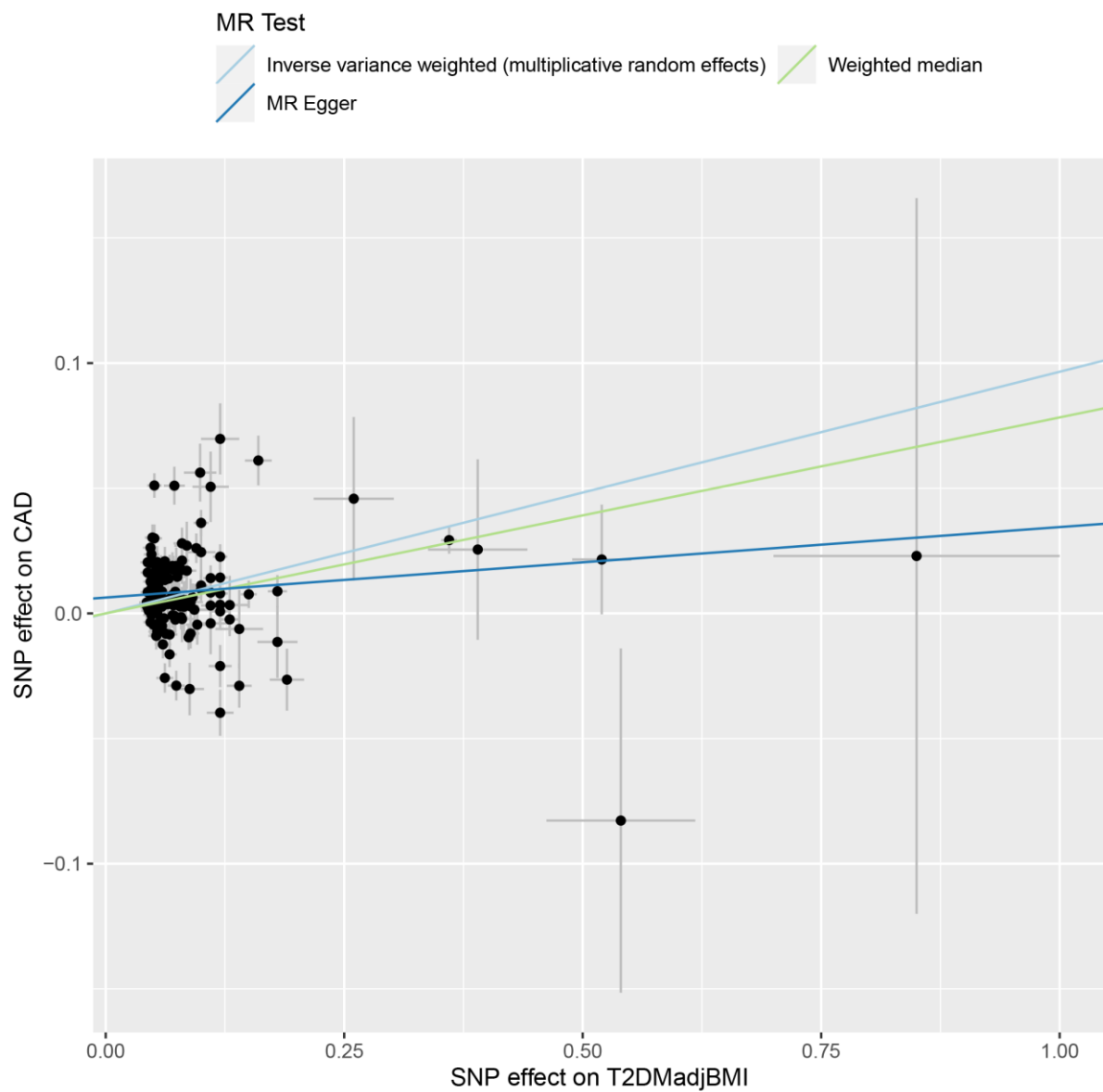
Supplementary Figure 3. GTEx tissue enrichment analysis for expression of cross-phenotype associated genes of type 2 diabetes mellitus and coronary artery disease. Red bar represents significant tissue enrichment after Bonferroni correction ($P < 9.26 \times 10^{-4}$). T2DM, type 2 diabetes mellitus; CAD, coronary artery disease; T2DM_{adj}BMI, type 2 diabetes mellitus adjusted for body mass index.



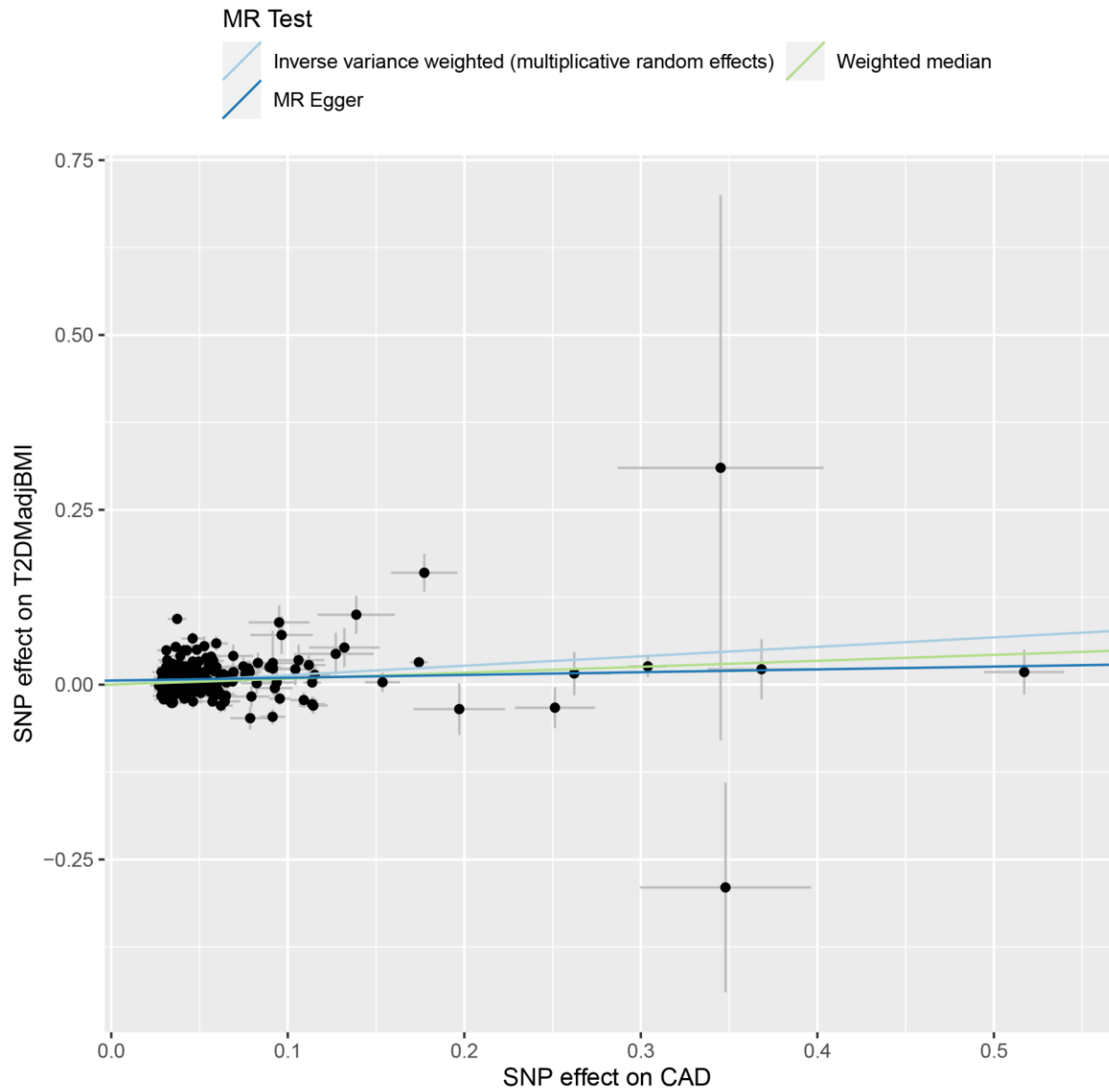
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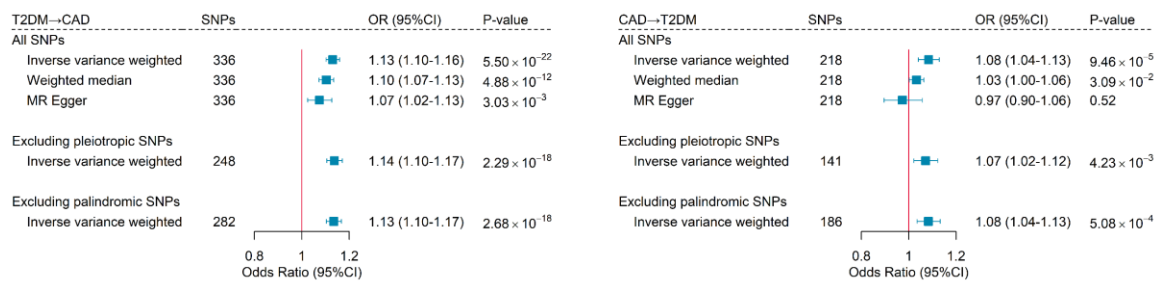
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Supplementary Figure 6. Scatter plot of SNP-coronary artery disease (CAD) size associations against SNP-type 2 diabetes mellitus adjusted for body mass index (T2DM_{adj}BMI) associations with estimates from different Mendelian randomization methods indicated by corresponding colored lines.



Supplementary Figure 7. Scatter plot of SNP-type 2 diabetes mellitus adjusted for body mass index (T2DM_{adjBMI}) size associations against SNP-coronary artery disease (CAD) associations with estimates from different Mendelian randomization methods indicated by corresponding colored lines.



Supplementary Figure 8. Bidirectional mendelian randomization analysis between type 2 diabetes mellitus and coronary artery disease in multi-ancestry individuals. The boxes denote point estimate of the causal effects, and the error bars denote 95% confidence intervals. Inverse-variance weighted approach was used as primary analysis, with MR-Egger and weighted median approaches used as sensitivity analysis. T2DM, type 2 diabetes mellitus; CAD, coronary artery disease.

Supplementary Table 1. Characteristics of genetic instruments of type 2 diabetes mellitus and their effect sizes with coronary artery disease.

SNP	CHR	BP	A1	A2	EAF	Exposure			Outcome			Pleiotropic traits
						Beta	SE	P-value	Beta	SE	P-value	
rs1005752	15	77818128	A	C	0.720	0.079	0.007	5.70E-29	0.017	0.005	1.43E-03	Metabolic traits, High density lipoprotein cholesterol levels, Triglyceride levels
rs10096633	8	19830921	T	C	0.120	-	0.010	8.70E-13	-0.051	0.008	1.50E-11	
rs10097617	8	95961626	T	C	0.480	0.051	0.006	1.10E-15	0.014	0.005	3.67E-03	
rs10193538	2	58981064	T	G	0.610	0.037	0.007	1.70E-08	0.003	0.005	6.15E-01	
rs10195252	2	165513091	T	C	0.590	0.060	0.006	1.60E-20	0.021	0.005	3.07E-05	Waist-to-hip ratio adjusted for body mass index, Waist-hip ratio, Waist circumference adjusted for BMI, Pulse pressure, Hip circumference adjusted for BMI, Triglycerides, Fasting blood insulin
rs10228066	7	15063569	T	C	0.540	0.066	0.006	1.90E-25	0.007	0.005	1.56E-01	Height
rs10305745	1	150786038	A	G	0.015	0.250	0.053	3.90E-06	0.033	0.061	5.85E-01	
rs10406327	19	33890838	C	G	0.520	0.035	0.006	4.60E-08	0.008	0.005	8.45E-02	
rs10406431	19	46157019	A	G	0.560	0.059	0.007	2.50E-19	0.018	0.005	2.90E-04	
rs1042725	12	66358347	T	C	0.490	0.054	0.006	1.60E-17	0.011	0.005	2.58E-02	Height, White blood cell count, Head circumference (infant), Birth weight
rs1043246	17	3828086	C	G	0.840	-	0.010	6.00E-10	-0.007	0.008	3.87E-01	
rs10469140	18	60668270	A	G	0.520	-	0.006	6.00E-06	-0.005	0.005	2.91E-01	
rs1061810	11	43877934	A	C	0.290	0.050	0.007	8.50E-13	0.018	0.005	7.07E-04	
rs10750397	11	128234144	A	G	0.280	0.045	0.007	2.00E-10	-0.011	0.005	4.90E-02	Fasting plasma glucose, Corrected insulin response, Insulin disposition index, Obesity-related traits, Incremental insulin, Homeostasis model assessment of beta-cell function, Acute insulin response, Glucose homeostasis traits, Birth weight, Insulin levels, Pulse pressure, Glycated hemoglobin levels, Metabolite levels, Corrected insulin response adjusted for insulin sensitivity index, Insulin secretion rate, Hemoglobin A1c levels, Offspring birth weight, Insulin levels adjusted for BMI, Peak insulin response, Glycemic traits (multi-trait analysis)
rs10757283	9	22134172	T	C	0.430	0.021	0.006	9.40E-04	0.020	0.005	7.85E-05	
rs10811660	9	22134068	A	G	0.170	-	0.009	6.60E-79	-0.009	0.006	1.73E-01	
rs10830963	11	92708710	C	G	0.720	-	0.007	1.50E-43	-0.010	0.006	7.96E-02	
rs10842994	12	27965150	T	C	0.190	-	0.008	2.50E-20	-0.004	0.006	4.79E-01	Body mass index, Self-reported math ability
rs10848958	12	4031104	T	C	0.200	-	0.008	4.90E-07	0.004	0.007	5.86E-01	
rs10882101	10	94462427	T	C	0.590	0.110	0.006	1.60E-62	0.023	0.005	4.98E-06	
rs10893829	11	128042575	T	C	0.850	0.057	0.009	2.70E-10	0.001	0.007	8.78E-01	
rs10908278	17	36099952	A	T	0.520	-	0.006	3.10E-30	0.010	0.005	5.64E-02	Body mass index, Self-reported math ability
rs10937721	4	6306763	C	G	0.590	0.087	0.007	1.60E-40	0.003	0.005	5.80E-01	
rs10938398	4	45186139	A	G	0.430	0.044	0.006	4.90E-12	0.025	0.005	3.73E-07	
rs10954772	8	30863938	T	C	0.310	0.041	0.007	2.30E-09	0.012	0.005	2.26E-02	
rs10962	17	36046451	C	G	0.230	0.043	0.008	4.30E-08	-0.010	0.006	1.03E-01	

rs10974438	9	4291928	A	C	0.640	- 0.051	0.007	1.60E-14	0.005	0.005	3.29E-01	Osteoarthritis, Height
rs11042596	11	2118860	T	G	0.340	- 0.036	0.007	2.70E-07	0.001	0.005	8.86E-01	Length of menstrual cycle
rs11063028	12	4300172	T	C	0.820	- 0.047	0.008	1.30E-08	0.001	0.006	9.31E-01	
rs11065299	12	121297815	A	G	0.075	0.080	0.012	2.80E-11	0.025	0.010	1.40E-02	
rs11070332	15	41809205	A	G	0.360	0.049	0.007	1.30E-13	0.016	0.005	2.31E-03	Medication use (drugs used in diabetes)
rs1112718	10	94479107	A	G	0.600	0.110	0.007	2.90E-59	0.020	0.005	7.80E-05	Medication use (drugs used in diabetes)
rs11137820	9	81359113	C	G	0.580	0.035	0.006	3.60E-08	0.003	0.005	4.93E-01	
rs111827885	4	616608	T	C	0.980	- 0.170	0.037	9.70E-06	-0.041	0.037	2.72E-01	
rs112498319	6	7035734	A	C	0.590	- 0.041	0.006	1.40E-10	-0.004	0.005	3.99E-01	
rs11257655	10	12307894	T	C	0.220	0.090	0.008	3.70E-32	0.026	0.006	9.97E-06	Body mass index, Medication use (drugs used in diabetes)
rs112595469	11	128583975	T	C	0.028	0.093	0.020	4.40E-06	-0.018	0.017	2.90E-01	
rs1127215	1	117532790	T	C	0.420	- 0.047	0.006	2.30E-13	-0.005	0.005	2.71E-01	
rs112915006	22	50604696	A	G	0.950	- 0.092	0.015	7.50E-10	-0.009	0.011	4.02E-01	
rs114447556	4	53207093	T	C	0.084	0.060	0.012	7.70E-07	0.020	0.010	4.64E-02	
rs114526150	1	214175531	T	G	0.980	- 0.073	0.022	9.10E-04	-0.005	0.019	7.90E-01	
rs11496066	7	102486254	T	C	0.820	0.047	0.008	1.20E-08	-0.015	0.007	2.59E-02	
rs115505614	5	102422968	T	C	0.050	0.170	0.015	1.70E-29	-0.026	0.012	3.23E-02	Male-pattern baldness
rs11642430	16	30045789	C	G	0.600	- 0.042	0.007	1.20E-10	-0.003	0.005	5.58E-01	
rs11657492	17	65648427	T	G	0.900	- 0.058	0.011	7.10E-08	0.002	0.008	8.08E-01	
rs11680058	2	16574669	A	G	0.860	0.058	0.010	1.30E-08	0.008	0.008	3.27E-01	
rs11688682	2	121347612	C	G	0.270	- 0.058	0.008	1.40E-14	-0.005	0.006	3.79E-01	Systolic blood pressure, Cardiovascular disease
rs11688931	2	121318166	C	G	0.850	0.061	0.009	1.10E-11	0.003	0.007	6.83E-01	
rs116913033	7	44365549	T	C	0.170	- 0.045	0.009	3.30E-07	-0.003	0.007	7.05E-01	
rs116953931	19	5224998	A	G	0.037	0.071	0.017	2.90E-05	0.009	0.014	5.13E-01	
rs11696357	20	43233649	A	G	0.930	0.053	0.014	1.40E-04	0.021	0.012	7.40E-02	
rs11699802	20	48832135	T	C	0.460	- 0.043	0.006	2.50E-11	-0.006	0.005	2.31E-01	
rs117001013	22	32348841	T	C	0.088	- 0.065	0.011	1.50E-08	0.002	0.009	8.09E-01	
rs11708067	3	123065778	A	G	0.770	0.089	0.008	1.30E-31	0.008	0.006	1.62E-01	Homeostasis model assessment of beta-cell function, Fasting blood glucose, Glycated hemoglobin levels
rs11709077	3	12336507	A	G	0.120	- 0.110	0.010	1.60E-27	-0.001	0.008	9.13E-01	Body mass index
rs11717959	3	185541213	T	G	0.380	0.039	0.007	1.70E-09	-0.003	0.005	5.34E-01	
rs117483894	15	57456802	A	G	0.960	- 0.093	0.017	3.90E-08	-0.013	0.013	3.26E-01	

rs11759026	6	126792095	A	G	0.770	- 0.067	0.008	1.30E-18	0.029	0.006	1.07E-06	Neuroticism, Lung function (FVC), Medication use (drugs used in diabetes), Intracranial volume, Educational attainment (years of education), Neuroticism
rs11786992	8	95685147	A	C	0.640	0.040	0.007	1.70E-09	-0.006	0.005	2.83E-01	
rs11793035	9	139507212	T	C	0.670	- 0.033	0.007	1.10E-05	-0.009	0.006	1.23E-01	
rs11820019	11	69448758	T	C	0.970	0.140	0.021	1.00E-11	-0.006	0.016	6.90E-01	
rs11842871	13	31042452	T	G	0.270	- 0.042	0.007	1.50E-08	-0.010	0.006	9.57E-02	
rs11926707	3	46925539	T	C	0.370	- 0.038	0.007	1.50E-08	-0.008	0.005	1.21E-01	Triglyceride levels x alcohol consumption (drinkers vs non-drinkers) interaction (2df), HDL cholesterol levels x alcohol consumption (regular vs non-regular drinkers) interaction (2df), Triglyceride levels x alcohol consumption (regular vs non-regular drinkers) interaction (2df), High light scatter reticulocyte count, Triglyceride levels, HDL cholesterol levels, HDL cholesterol levels x alcohol consumption (drinkers vs non-drinkers) interaction (2df), Triglycerides x physical activity interaction (2df test)
rs11967262	6	43760327	C	G	0.510	- 0.041	0.006	1.40E-10	-0.034	0.005	1.20E-11	
rs12001437	9	34074476	T	C	0.630	- 0.041	0.007	3.70E-10	-0.003	0.005	5.57E-01	
rs12048743	1	205114873	C	G	0.560	- 0.038	0.006	4.40E-09	-0.020	0.005	3.98E-05	
rs12140153	1	62579891	T	G	0.095	- 0.064	0.011	1.20E-08	-0.021	0.009	2.16E-02	
rs12236906	9	97497494	T	C	0.990	0.140	0.030	3.90E-06	0.016	0.020	4.19E-01	Sleep traits (multi-trait analysis), Body mass index, Body fat percentage, Morningness, Chronotype, Excessive daytime sleepiness, Morning vs. evening chronotype
rs12454712	18	60845884	T	C	0.610	0.049	0.007	5.10E-13	0.019	0.005	4.98E-04	
rs12578639	12	118489636	A	T	0.830	0.040	0.009	3.90E-06	-0.005	0.007	4.47E-01	
rs1260326	2	27730940	T	C	0.390	- 0.067	0.007	1.30E-24	0.016	0.005	1.27E-03	Lymphocyte counts, Serum total protein level, Neutrophil count, Branched-chain amino acid levels (Valine), Lipid metabolism phenotypes, C-reactive protein levels, Triglyceride levels, Urinary sodium to creatinine ratio, Total cholesterol levels, Gout, Alcohol consumption in current drinkers, Hypertriglyceridemia, White blood cell count, Hematocrit, Myeloid white cell count, Glomerular filtration rate, Glycemic traits (pregnancy), Serum uric acid levels, Platelet count, Blood metabolite ratios, Alcohol use disorder (consumption score), C-reactive protein levels or triglyceride levels (pleiotropy), Branched-chain amino acid levels (Leucine), Waist circumference and related phenotypes, Metabolite levels, Blood sugar levels, Coffee consumption (cups per day), Sum basophil neutrophil counts, Factor VII activity, Fasting blood glucose adjusted for BMI, Medication use (HMG CoA reductase inhibitors), Height, Protein C levels, Resting heart rate, Low density lipoprotein cholesterol levels, Fat-free mass, Chronic

kidney disease, Blood metabolite levels, Serum albumin level, Glomerular filtration rate in non diabetics (creatinine), Alcohol consumption, Plasma lactate levels, Fasting blood glucose, Lipid traits, Triglycerides x physical activity interaction (2df test), Two-hour glucose challenge, Metabolic traits, High light scatter reticulocyte percentage of red cells, Gallstone disease, Nonalcoholic fatty liver disease, Renal overload gout, Hematological and biochemical traits, Urate levels in overweight individuals, Liver enzyme levels (gamma-glutamyl transferase), Percent glycated albumin, Alcohol consumption (drinks per week) (MTAG), Crohn's disease, Estimated glomerular filtration rate, Chronic inflammatory diseases (ankylosing spondylitis, Crohn's disease, psoriasis, primary sclerosing cholangitis, ulcerative colitis) (pleiotropy), Red cell distribution width, Granulocyte count, Caffeine metabolism (plasma 1,7-dimethylxanthine (paraxanthine) to 1,3,7-trimethylxanthine (caffeine) ratio), Body mass index, Alcohol consumption (drinks per week), Inflammatory bowel disease, Branched-chain amino acid levels (Isoleucine), Serum alpha-1-antitrypsin levels, C-reactive protein levels or total cholesterol levels (pleiotropy), Lipoprotein-associated phospholipase A2 activity and mass, Sum neutrophil eosinophil counts, Non-albumin protein levels, Alcohol use disorder, Fasting blood insulin adjusted for BMI, Metabolite levels (small molecules and protein measures), Urolithiasis, Factor VII activity or levels, Cardiovascular disease risk factors, Gamma glutamyl transferase levels, Plateletcrit, Alcohol use disorder (total score)

rs12640250	4	17792869	A	C	0.290	- 0.039	0.007	4.50E-08	-0.017	0.006	2.07E-03
rs12642790	4	83578271	A	G	0.340	0.042	0.007	5.70E-10	0.001	0.005	8.26E-01
rs12680028	8	110123183	C	G	0.530	0.035	0.006	3.10E-08	0.000	0.005	9.74E-01
rs12719778	8	145879883	T	C	0.540	0.039	0.006	2.10E-09	-0.003	0.005	5.42E-01
rs12802972	11	1704596	A	G	0.430	0.030	0.007	3.60E-06	-0.002	0.005	7.17E-01
rs12811407	12	133069698	A	G	0.330	0.049	0.007	2.40E-12	0.001	0.005	7.97E-01
rs12910825	15	91511260	A	G	0.640	- 0.053	0.007	2.40E-15	-0.009	0.005	9.31E-02
rs12920022	16	89564055	A	T	0.160	0.053	0.009	2.90E-09	0.027	0.007	1.40E-04
rs1296328	4	137083193	A	C	0.450	0.035	0.006	4.30E-08	0.003	0.005	6.13E-01
rs13024606	2	165573194	T	C	0.047	0.055	0.015	3.80E-04	0.013	0.013	3.07E-01
rs13041756	20	21466795	T	C	0.890	- 0.058	0.010	1.30E-08	0.005	0.008	5.65E-01
rs13065698	3	152086533	A	G	0.600	0.039	0.007	3.60E-09	0.006	0.005	2.14E-01
rs13085136	3	72865183	T	C	0.072	- 0.074	0.013	1.40E-08	0.030	0.010	3.99E-03
rs1316776	5	78430607	A	C	0.350	- 0.046	0.007	3.50E-12	0.001	0.005	8.49E-01
rs1317617	10	81096589	A	G	0.200	- 0.035	0.008	1.10E-05	-0.003	0.006	6.76E-01
rs13262861	8	41508577	A	C	0.170	- 0.094	0.009	1.80E-27	-0.003	0.007	6.48E-01

Body mass index

rs1333052	9	22157908	A	C	0.660	0.018	0.007	9.10E-03	-0.009	0.005	7.57E-02	Medication use (drugs used in diabetes)
rs13426680	2	158339550	A	G	0.940	0.082	0.013	6.40E-10	0.001	0.010	8.87E-01	
rs1359790	13	80717156	A	G	0.280	-	0.007	5.70E-31	-0.006	0.006	2.46E-01	
rs13737	15	75932129	T	G	0.240	-	0.008	7.30E-10	-0.005	0.006	3.94E-01	
rs1377807	17	4045440	C	G	0.310	0.057	0.007	5.70E-17	0.013	0.005	1.97E-02	
rs138337556	5	101232944	A	G	NA	-	0.074	8.90E-13	0.083	0.069	2.29E-01	Childhood body mass index, Fat-free mass, Medication use (HMG CoA reductase inhibitors), Obesity, Chronotype, Body fat percentage, Pulse pressure, Dietary macronutrient intake, Body mass index, Morningness, Alcohol use disorder, Obesity (early onset extreme), Morning person, Hand grip strength
rs140242150	10	114702962	A	G	0.005	0.280	0.055	4.30E-07	-0.016	0.052	7.57E-01	
rs1412234	9	28410683	T	C	0.680	-	0.007	2.50E-10	-0.019	0.005	3.69E-04	
rs1412830	9	22043612	T	C	0.370	-	0.007	1.20E-15	-0.104	0.005	3.18E-88	
rs141521721	11	14763828	A	C	0.024	0.120	0.021	2.80E-08	0.000	0.018	9.82E-01	
rs1421085	16	53800954	T	C	0.580	-	0.006	2.40E-78	-0.017	0.005	5.09E-04	Body fat percentage, Extraversion, Worry, Alcohol consumption (drinks per week) (MTAG)
rs1426371	12	108629780	A	G	0.260	-	0.007	1.10E-11	-0.002	0.006	7.19E-01	
rs145678014	11	32927778	T	G	0.043	-	0.016	1.10E-11	-0.058	0.013	1.13E-05	
rs145904381	1	151017991	T	C	0.990	0.170	0.031	2.20E-08	0.036	0.024	1.31E-01	
rs146886108	5	14751305	T	C	0.006	-	0.047	8.70E-16	-0.026	0.036	4.79E-01	
rs148766658	8	41552046	T	C	0.960	-	0.017	7.90E-11	0.014	0.014	3.24E-01	Hair color
rs149364428	8	97737741	A	G	0.010	0.110	0.034	1.90E-12	0.046	0.033	1.60E-01	
rs1493694	1	120526982	T	C	0.110	0.084	0.010	2.10E-16	-0.005	0.008	5.72E-01	
rs150111048	3	185514421	A	G	0.760	-	0.021	9.10E-08	-0.013	0.011	2.20E-01	
rs1516728	3	185829891	A	T	0.760	0.110	0.007	1.60E-05	0.000	0.006	9.50E-01	
rs1531583	4	744972	T	G	0.046	0.032	0.015	1.20E-12	0.003	0.012	7.74E-01	Pancreatic cancer
rs1561927	8	129568078	T	C	0.730	-	0.007	1.90E-09	-0.012	0.006	3.39E-02	
rs1562396	7	130457914	A	G	0.680	-	0.007	7.60E-17	-0.018	0.005	7.49E-04	
rs1575972	9	22301092	A	T	0.033	0.058	0.018	2.00E-05	-0.017	0.014	2.10E-01	
rs1580278	4	104140848	A	C	0.530	-	0.006	2.90E-10	0.004	0.005	4.19E-01	
rs17013314	3	23510044	A	G	0.970	0.041	0.019	1.00E-10	0.012	0.014	4.04E-01	
rs1708302	7	28198677	T	C	0.490	-	0.006	4.20E-48	-0.011	0.005	2.53E-02	
rs17122772	14	23288935	C	G	0.770	0.092	0.008	2.00E-08	-0.020	0.006	9.27E-04	

rs17168486	7	14898282	T	C	0.180	0.069	0.008	6.90E-17	0.009	0.006	1.60E-01	Blood sugar levels
rs17250977	5	14753745	A	G	0.960	-	0.018	3.70E-12	-0.025	0.015	1.00E-01	
rs17261179	5	51791225	T	C	0.520	0.034	0.006	8.20E-08	0.016	0.005	1.42E-03	
rs17522122	14	33302882	T	G	0.470	0.038	0.006	4.00E-09	0.014	0.005	3.91E-03	Body mass index, Cognitive function
rs17684074	18	54675384	C	G	0.260	-	0.007	3.50E-08	-0.007	0.006	2.42E-01	
rs17689007	8	9974824	A	G	0.470	-	0.006	1.70E-13	-0.009	0.005	7.35E-02	
rs177045	10	71321279	A	G	0.680	-	0.007	1.00E-12	-0.001	0.005	7.84E-01	
rs17772814	8	128711742	A	G	0.085	-	0.013	5.00E-10	-0.003	0.010	7.94E-01	
rs17791513	9	81905590	A	G	0.930	0.100	0.013	2.90E-14	0.024	0.010	1.18E-02	
rs17802463	2	25643221	T	G	0.270	-	0.007	3.50E-08	0.006	0.006	2.55E-01	
rs17819328	3	12489342	T	G	0.580	-	0.006	1.10E-06	-0.021	0.005	4.44E-05	Hip circumference adjusted for BMI, Gut microbiota (functional units), Waist-to-hip ratio adjusted for BMI, Waist-to-hip ratio adjusted for BMI x sex x age interaction (4df test), Waist-hip ratio
rs1783541	11	65294799	T	C	0.200	0.061	0.008	1.40E-14	-0.007	0.006	2.49E-01	
rs17836088	14	79932041	C	G	0.220	0.058	0.008	9.70E-14	0.011	0.006	8.35E-02	
rs1796330	12	71522953	C	G	0.430	-	0.006	3.20E-14	-0.008	0.005	9.30E-02	
rs1800574	12	121416864	T	C	0.030	0.160	0.019	8.90E-17	0.028	0.016	7.41E-02	
rs1800961	20	43042364	T	C	0.035	0.160	0.017	3.20E-20	-0.011	0.014	4.27E-01	Fibrinogen levels, HDL cholesterol levels x alcohol consumption (regular vs non-regular drinkers) interaction (2df), C-reactive protein levels or LDL-cholesterol levels (pleiotropy), Total cholesterol levels, LDL cholesterol levels x alcohol consumption (drinkers vs non-drinkers) interaction (2df), White blood cell count, HDL cholesterol levels x alcohol consumption (drinkers vs non-drinkers) interaction (2df), Sum neutrophil eosinophil counts, LDL cholesterol levels in current drinkers, C-reactive protein levels, Granulocyte count, High density lipoprotein cholesterol levels, Neutrophil count, Medication use (drugs used in diabetes), LDL cholesterol levels x alcohol consumption (regular vs non-regular drinkers) interaction (2df), Red blood cell count, Factor VII activity, C-reactive protein levels or total cholesterol levels (pleiotropy), Neutrophil percentage of white cells, HDL cholesterol x physical activity interaction (2df test), C-reactive protein levels or HDL-cholesterol levels (pleiotropy), Cholesterol, total, Sum basophil neutrophil counts, Gallstone disease, Myeloid white cell count, C-reactive protein, Hematocrit
rs1801212	4	6302519	A	G	0.710	0.091	0.007	3.60E-38	0.004	0.006	4.56E-01	
rs1801645	22	50356850	T	C	0.720	-	0.007	1.50E-10	-0.011	0.006	5.80E-02	
rs180988137	10	114751173	A	G	0.990	-	0.034	1.50E-21	-0.022	0.029	4.39E-01	
rs184509201	10	114740337	C	G	0.980	0.320	0.026	2.80E-12	0.014	0.022	5.30E-01	

rs187936726	8	96092422	A	G	0.980	-	0.022	2.30E-08	-0.058	0.019	2.60E-03
rs188247550	19	19396616	T	C	0.019	0.120	0.031	1.20E-05	-0.025	0.031	4.15E-01
rs1903002	4	89740894	C	G	0.500	-	0.006	3.00E-08	-0.011	0.005	2.33E-02
rs191830490	20	43023355	A	G	0.006	0.036	0.045	2.40E-07	-0.130	0.041	1.52E-03
rs199795270	16	30419384	C	G	0.007	0.230	0.045	4.90E-08	-0.013	0.037	7.17E-01
rs2028150	2	65655012	C	G	0.600	0.250	0.007	3.10E-15	0.000	0.005	9.56E-01
rs2052261	2	65355270	A	G	0.700	0.052	0.007	3.80E-06	0.001	0.005	8.70E-01
rs2066827	12	12871099	T	G	0.770	0.032	0.008	3.50E-08	-0.005	0.006	4.09E-01
rs2102278	4	52818664	A	G	0.680	-	0.007	4.50E-08	-0.007	0.005	1.80E-01
rs2189301	17	36063685	A	G	0.130	0.044	0.010	6.50E-10	0.001	0.008	9.03E-01
rs2197973	12	95928560	T	C	0.540	0.060	0.006	4.40E-08	0.020	0.005	6.68E-05
rs2237895	11	2857194	A	C	0.570	0.035	0.007	3.60E-44	-0.014	0.005	5.69E-03
rs2237897	11	2858546	T	C	0.046	-	0.017	1.80E-31	-0.033	0.012	8.03E-03
rs2238689	19	46178661	T	C	0.580	0.093	0.007	1.30E-14	0.015	0.005	2.60E-03
rs2249105	2	65287896	A	G	0.630	0.190	0.007	1.20E-15	0.010	0.005	4.05E-02
rs2258238	12	66221060	A	T	0.900	-	0.011	2.00E-25	-0.003	0.008	6.59E-01
rs2268078	20	32596704	A	G	0.660	0.110	0.007	2.90E-10	0.009	0.005	9.06E-02
rs2268382	7	130027037	A	C	0.670	0.043	0.007	4.30E-05	0.000	0.005	9.83E-01
rs2272163	3	77671721	A	C	0.380	-	0.007	1.20E-08	-0.006	0.005	2.13E-01
rs2280141	10	124193181	T	G	0.520	0.028	0.006	2.00E-13	0.008	0.005	1.28E-01
rs2283164	11	2579163	A	G	0.950	0.037	0.015	1.40E-05	0.020	0.012	9.27E-02
rs2283220	11	2755548	A	G	0.690	0.047	0.007	2.70E-09	0.004	0.005	4.26E-01
rs2307111	5	75003678	T	C	0.610	0.066	0.007	3.30E-16	0.010	0.005	4.14E-02
rs231349	11	2672821	T	C	0.100	0.043	0.011	1.40E-08	0.013	0.005	1.11E-01
rs231361	11	2691500	A	G	0.260	0.053	0.007	6.00E-18	-0.006	0.008	2.91E-01
rs234853	11	2850828	A	G	0.750	0.060	0.008	1.30E-04	0.008	0.006	1.66E-01
rs243024	2	60583665	A	G	0.460	0.029	0.006	4.40E-20	0.015	0.005	2.53E-03
rs2431115	5	55848669	A	G	0.400	0.058	0.007	6.60E-05	-0.004	0.005	4.41E-01
rs244665	5	133414622	A	G	0.700	0.026	0.007	2.30E-05	0.001	0.005	9.22E-01
rs2456530	15	53091553	T	C	0.130	0.030	0.010	4.70E-09	0.005	0.007	4.83E-01
rs2465043	6	51180765	A	G	0.360	0.056	0.007	2.00E-06	0.000	0.005	9.31E-01
rs2581787	3	53127677	T	G	0.560	0.032	0.006	3.00E-08	0.010	0.005	3.99E-02
rs2642588	10	71466578	T	G	0.300	0.036	0.007	6.30E-14	0.005	0.005	4.06E-01
rs2727301	17	61965043	T	C	0.750	0.052	0.007	1.90E-06	0.015	0.006	1.07E-02

Prostate cancer

Body mass index, Glucose homeostasis traits

Prostate cancer, Lipid traits (pleiotropy) (HIPO component 1)

Medication use (drugs used in diabetes)

Lung function (FEV1/FVC), Waist-hip ratio

Height

Body mass index, Diastolic blood pressure, Pulse pressure, Obesity, HDL cholesterol, Snoring

Medication use (drugs used in diabetes)

rs2767036	11	34982148	A	C	0.710	- 0.039	0.007	2.50E-08	-0.003	0.005	5.51E-01
rs2796441	9	84308948	A	G	0.410	- 0.066	0.007	8.50E-24	-0.006	0.005	2.66E-01
rs279744	5	53412620	A	C	0.310	- 0.037	0.007	1.30E-07	-0.023	0.005	1.48E-05
rs2800733	6	127416930	A	G	0.720	0.051	0.007	3.70E-13	-0.008	0.006	1.42E-01
rs2820446	1	219748818	C	G	0.710	0.057	0.007	3.70E-16	0.013	0.005	1.30E-02
rs28505901	9	139241030	A	G	0.250	- 0.076	0.008	2.60E-21	-0.028	0.006	7.28E-06
rs28525376	2	43207872	T	G	0.580	- 0.027	0.006	2.10E-05	-0.001	0.005	8.25E-01
rs28638142	12	121501461	A	C	0.044	0.093	0.016	7.20E-09	-0.009	0.013	4.55E-01
rs286925	11	34642668	A	G	0.180	0.039	0.008	2.70E-06	0.009	0.006	1.62E-01
rs28719468	18	53452144	T	C	0.840	- 0.034	0.009	7.40E-05	-0.023	0.007	5.59E-04
rs2872246	3	183738460	A	C	0.450	0.036	0.006	1.80E-08	0.000	0.005	9.93E-01
rs28819812	4	157652753	A	C	0.320	- 0.040	0.007	2.70E-08	-0.012	0.005	2.55E-02
rs2908334	7	15206239	T	C	0.630	0.019	0.007	3.50E-03	0.003	0.005	5.42E-01
rs291367	1	235690800	A	G	0.370	- 0.044	0.007	6.10E-10	-0.001	0.005	8.18E-01
rs2925979	16	81534790	T	C	0.300	0.053	0.007	2.10E-14	0.024	0.005	1.17E-05
rs2972144	2	227101411	A	G	0.360	- 0.094	0.007	7.90E-46	-0.036	0.005	2.81E-12
rs3111316	19	13038415	A	G	0.590	0.046	0.007	1.60E-12	0.006	0.005	2.17E-01
rs3115960	16	75516534	C	G	0.630	- 0.006	0.007	3.40E-01	0.039	0.005	4.99E-14
rs3217792	12	4384696	T	C	0.087	- 0.120	0.012	2.50E-22	0.004	0.009	6.67E-01
rs3217860	12	4399050	A	G	0.740	- 0.057	0.007	2.00E-14	-0.004	0.006	4.86E-01
rs329122	5	133864599	A	G	0.430	0.037	0.006	9.20E-09	0.012	0.005	1.71E-02
rs340874	1	214159256	T	C	0.440	- 0.068	0.006	5.60E-26	-0.003	0.005	5.12E-01
rs34298980	6	40409243	T	C	0.500	0.040	0.007	1.20E-09	0.004	0.005	4.92E-01
rs34454109	20	51223594	A	T	0.770	0.044	0.008	8.80E-09	0.012	0.006	3.53E-02
rs34584161	13	26776999	A	G	0.760	0.048	0.008	2.90E-10	0.003	0.006	5.71E-01

Schizophrenia

High density lipoprotein cholesterol levels, Waist-to-hip ratio adjusted for body mass index, Triglycerides, HDL cholesterol levels x alcohol consumption (drinkers vs non-drinkers) interaction (2df), HDL cholesterol levels x alcohol consumption (regular vs non-regular drinkers) interaction (2df), HDL cholesterol x physical activity interaction (2df test), Triglyceride levels x alcohol consumption (regular vs non-regular drinkers) interaction (2df), Triglyceride levels x alcohol consumption (drinkers vs non-drinkers) interaction (2df), Adiponectin levels, Waist-hip ratio, Waist-to-hip ratio adjusted for BMI x sex x age interaction (4df test), Waist-to-hip ratio adjusted for BMI x sex interaction

Estimated glomerular filtration rate

Medication use (drugs used in diabetes)

Body mass index

Homeostasis model assessment of beta-cell function, Fasting blood glucose

rs34715063	15	38873115	T	C	0.880	- 0.076	0.010	3.30E-14	-0.005	0.008	5.07E-01	
rs348330	1	229672955	A	G	0.640	- 0.051	0.007	3.90E-14	-0.009	0.005	7.89E-02	
rs34855406	17	40731411	C	G	0.280	0.050	0.007	3.20E-12	0.028	0.005	3.31E-07	
rs34855922	10	114871594	A	G	0.720	0.034	0.007	2.50E-06	0.007	0.006	2.04E-01	
rs34965774	12	118412373	A	G	0.140	0.054	0.009	3.50E-09	0.007	0.007	2.93E-01	
rs35352848	3	23455582	T	C	0.790	0.071	0.008	9.50E-20	-0.008	0.006	1.79E-01	
rs35497231	3	152433628	T	C	0.680	- 0.034	0.007	5.80E-07	-0.010	0.005	5.26E-02	
rs35654957	4	1010077	T	C	0.630	- 0.030	0.007	7.50E-06	-0.013	0.005	1.80E-02	Femoral neck bone mineral density
rs35895680	17	47060322	A	C	0.320	- 0.055	0.007	3.80E-15	-0.035	0.005	2.37E-10	Systolic blood pressure, Myocardial infarction
rs35913461	2	653575	T	C	0.170	- 0.056	0.009	5.90E-11	-0.024	0.007	1.97E-04	
rs35999103	2	147861633	T	C	0.150	0.052	0.009	8.30E-09	0.005	0.007	5.00E-01	
rs362307	4	3241845	T	C	0.077	0.074	0.012	1.10E-09	0.021	0.010	2.98E-02	Automobile speeding propensity, Worry/vulnerability (special factor of neuroticism), Worry too long after an embarrassing experience, General cognitive ability, Educational attainment (years of education)
rs3751837	16	3583173	T	C	0.220	0.044	0.008	1.70E-08	0.016	0.006	8.40E-03	Lung function (FVC), Body mass index, FEV1
rs3768321	1	40035928	T	G	0.200	0.085	0.008	1.30E-26	0.015	0.006	2.31E-02	Red cell distribution width, HDL cholesterol, Mean corpuscular hemoglobin, HDL cholesterol x physical activity interaction (2df test)
rs3772071	2	161135544	T	C	0.710	0.048	0.007	1.60E-11	0.018	0.005	1.03E-03	
rs3774723	3	63962339	A	G	0.160	- 0.065	0.009	2.00E-13	-0.014	0.007	3.86E-02	
rs3798519	6	50788778	A	C	0.820	- 0.058	0.008	1.10E-12	-0.029	0.006	2.54E-06	Urolithiasis, Blood urea nitrogen levels
rs3802177	8	118185025	A	G	0.310	- 0.110	0.007	6.30E-55	-0.008	0.005	1.36E-01	Medication use (drugs used in diabetes), Fasting plasma glucose, Body mass index
rs3810291	19	47569003	A	G	0.670	0.046	0.007	1.20E-11	0.019	0.005	2.74E-04	Body mass index, Fat-free mass, Menarche (age at onset), Hip circumference, Waist circumference, Smoking initiation (ever regular vs never regular) (MTAG)
rs3811978	5	52100489	A	G	0.830	- 0.053	0.009	4.20E-10	0.004	0.006	4.96E-01	
rs3826482	17	3860356	A	T	0.580	0.036	0.007	4.80E-08	0.006	0.005	2.12E-01	
rs3845281	5	14610134	A	G	0.096	- 0.048	0.011	1.40E-05	-0.007	0.009	4.48E-01	
rs3887925	3	186665645	T	C	0.550	0.055	0.006	1.40E-17	-0.002	0.005	6.92E-01	
rs39328	7	103444978	T	C	0.430	0.036	0.006	3.00E-08	0.002	0.005	6.15E-01	
rs41277236	10	71332301	T	C	0.043	0.096	0.017	6.40E-09	0.017	0.013	1.96E-01	
rs4148856	12	123450765	C	G	0.780	0.049	0.008	2.20E-10	0.000	0.006	9.92E-01	
rs4238013	12	4376089	T	C	0.790	- 0.058	0.008	3.30E-13	-0.003	0.006	6.78E-01	
rs4279506	7	23512896	C	G	0.390	- 0.039	0.007	5.70E-09	-0.003	0.005	5.46E-01	

rs4281707	16	53501946	A	G	0.460	- 0.035	0.006	3.60E-08	-0.008	0.005	1.01E-01	Low density lipoprotein cholesterol levels, Cerebrospinal fluid AB1-42 levels, Waist-hip ratio, Parental longevity (mother's attained age), Cognitive decline (age-related), Alzheimer's disease biomarkers, Platelet count, Cerebrospinal fluid p-tau levels in mild cognitive impairment, Alzheimer's disease, C-reactive protein levels, Blood protein levels, Alzheimer's disease progression score, Vigorous physical activity, Cerebral amyloid deposition (PET imaging), Total cholesterol levels, Parental longevity (father's attained age), Cerebrospinal fluid t-tau levels in mild cognitive impairment, Triglycerides, Parental lifespan, High density lipoprotein cholesterol levels, Mortality, Red cell distribution width, Insomnia, Parkinson's disease (age of onset), Hippocampal volume, Logical memory (immediate recall), Neurofibrillary tangles or cerebral amyloid angiopathy (pleiotropy), Lewy body disease, Parental longevity (both parents in top 10%), Cerebrospinal fluid p-tau levels, Cerebrospinal AB1-42 levels in Alzheimer's disease dementia, Cerebral amyloid deposition positivity (PET imaging), Brain imaging, Parental longevity (combined parental age at death), Advanced age-related macular degeneration, Dementia with Lewy bodies, Logical memory (delayed recall), Neuritic plaques or neurofibrillary tangles (pleiotropy), Cerebrospinal AB1-42 levels in normal cognition, Cerebrospinal AB1-42 levels in mild cognitive impairment, Cerebrospinal fluid t-tau levels, Moderate to vigorous physical activity levels, Cortical amyloid beta load, Parental longevity (father's age at death), Parental longevity (mother's age at death), Neuritic plaques or cerebral amyloid angiopathy (pleiotropy), Parental longevity (combined parental attained age, Martingale residuals)
rs429358	19	45411941	T	C	0.850	0.080	0.009	1.80E-18	-0.091	0.007	3.73E-38	
rs445084	11	2908754	A	G	0.640	- 0.032	0.007	2.20E-06	-0.001	0.005	9.03E-01	
rs4457053	5	76424949	A	G	0.700	- 0.059	0.007	1.40E-17	-0.006	0.006	2.40E-01	
rs465002	5	55808475	T	C	0.740	0.073	0.007	3.80E-23	0.017	0.006	1.71E-03	HDL cholesterol levels x alcohol consumption (regular vs non-regular drinkers) interaction (2df), HDL cholesterol levels x alcohol consumption (drinkers vs non-drinkers) interaction (2df), Triglyceride levels, HDL cholesterol levels, Triglyceride levels x alcohol consumption (drinkers vs non-drinkers) interaction (2df), Triglyceride levels x alcohol consumption (regular vs non-regular drinkers) interaction (2df)
rs4686471	3	187740899	T	C	0.390	- 0.060	0.007	3.10E-20	0.001	0.005	8.85E-01	
rs4688760	3	49980596	T	C	0.680	0.043	0.007	4.50E-10	0.019	0.005	2.79E-04	Insomnia symptoms (never/rarely vs. sometimes/usually), Insomnia symptoms (never/rarely vs. usually)
rs4709746	6	164133001	T	C	0.130	- 0.056	0.010	5.00E-09	-0.019	0.007	9.70E-03	Heel bone mineral density, Diastolic blood pressure, Height
rs4736819	8	41509915	T	C	0.550	0.064	0.006	2.10E-23	0.000	0.005	9.84E-01	

rs474513	6	160770312	A	G	0.520	0.039	0.006	1.00E-09	0.051	0.005	1.57E-25	
rs4771648	13	110431626	A	G	0.330	-	0.007	8.90E-08	-0.002	0.005	6.49E-01	
rs4776970	15	68080886	A	T	0.640	0.039	0.007	6.20E-09	0.015	0.005	4.18E-03	Body mass index, Waist circumference, Weight
rs4804833	19	7970635	A	G	0.390	0.047	0.007	1.10E-12	0.004	0.005	4.44E-01	
rs4810426	20	43001721	T	C	0.110	0.082	0.011	6.90E-15	-0.004	0.008	6.14E-01	
rs4925109	17	17661802	A	G	0.320	0.048	0.007	3.90E-12	0.026	0.005	6.55E-07	Educational attainment (years of education)
rs4929965	11	2197286	A	G	0.380	0.070	0.007	4.80E-25	0.007	0.005	1.66E-01	
rs4930091	11	2372356	T	C	0.240	-	0.008	1.10E-04	-0.010	0.006	9.06E-02	
rs4932265	15	90423293	T	C	0.270	0.065	0.007	7.20E-20	0.007	0.006	2.25E-01	
rs4946812	6	107431688	A	G	0.330	-	0.007	1.00E-08	0.004	0.006	5.20E-01	
rs4977213	8	145507304	T	C	0.630	-	0.007	4.40E-14	-0.016	0.005	2.12E-03	
rs505922	9	136149229	T	C	0.670	-	0.007	5.40E-12	-0.026	0.005	7.82E-07	
rs510807	9	3965689	A	C	0.490	0.028	0.006	1.70E-05	0.001	0.005	8.14E-01	
rs5213	11	17408404	T	C	0.640	-	0.007	1.90E-26	-0.004	0.005	4.47E-01	Medication use (drugs used in diabetes)
rs523288	18	57848369	A	T	0.760	-	0.007	7.50E-14	-0.029	0.006	1.95E-07	
rs528122639	11	33091735	A	G	0.001	0.750	0.140	1.20E-07	0.046	0.148	7.54E-01	
rs528350911	15	53747228	C	G	0.990	-	0.043	2.10E-08	0.046	0.042	2.67E-01	
rs536643418	10	114699835	C	G	0.990	-	0.073	1.90E-09	-0.147	0.074	4.63E-02	
rs539515	1	177889025	A	C	0.800	-	0.008	1.20E-10	-0.008	0.006	2.06E-01	Hand grip strength, Body mass index
rs549498088	10	71347311	T	C	0.006	0.450	0.089	4.70E-07	0.069	0.126	5.84E-01	
rs553014999	1	219584164	T	C	NA	-	0.140	5.60E-06	-0.325	0.111	3.52E-03	
rs555759341	11	2151761	C	G	0.005	0.360	0.059	1.60E-09	0.085	0.052	1.06E-01	
rs55653563	9	97001682	A	C	0.730	0.043	0.007	3.20E-09	0.005	0.006	4.15E-01	
rs557027608	12	97779248	A	G	0.001	0.830	0.170	4.80E-07	0.226	0.146	1.23E-01	
rs558308082	17	65820153	C	G	0.001	0.730	0.160	3.20E-06	-0.137	0.116	2.41E-01	
rs559138871	3	129470067	T	C	0.002	0.400	0.088	6.30E-06	0.099	0.104	3.41E-01	
rs560716466	20	45317678	A	G	0.003	0.300	0.070	1.90E-05	0.084	0.063	1.81E-01	
rs56337234	4	1784403	T	C	0.500	-	0.007	1.40E-17	0.002	0.005	6.40E-01	
rs56348580	12	121432117	C	G	0.310	-	0.007	3.80E-19	-0.030	0.006	5.45E-08	
rs56376556	7	102038318	T	C	0.053	0.079	0.015	2.20E-07	0.000	0.013	9.69E-01	
rs569511541	17	52140805	A	G	NA	-	0.360	1.50E-08	-0.389	0.319	2.23E-01	
rs571342427	11	2182519	T	C	NA	-	0.110	4.60E-08	-0.015	0.091	8.72E-01	
rs57235767	11	93013531	T	C	0.290	-	0.007	6.60E-11	0.000	0.005	9.72E-01	

rs57327348	8	10808687	A	T	0.780	0.053	0.008	2.10E-11	0.001	0.006	8.89E-01	Fasting blood glucose
rs5758223	22	41489920	A	G	0.720	0.038	0.007	4.60E-08	0.010	0.006	8.61E-02	
rs576406049	4	89857291	T	C	0.001	0.510	0.100	1.50E-06	0.026	0.099	7.93E-01	
rs576674	13	33554302	A	G	0.830	-	0.009	6.80E-10	-0.001	0.006	8.72E-01	
						0.053						
rs58432198	1	51256091	T	C	0.120	-	0.010	1.80E-10	-0.009	0.008	2.66E-01	HDL cholesterol
rs58730668	4	185717759	T	C	0.860	0.065	0.009	1.00E-13	-0.001	0.007	8.95E-01	
rs601945	6	32573415	A	G	0.820	-	0.009	2.70E-21	-0.017	0.007	1.94E-02	
rs60276348	17	62203304	T	C	0.140	0.080	0.010	2.90E-08	0.014	0.008	7.46E-02	
rs6063048	20	45598564	A	G	0.280	-	0.007	5.80E-11	-0.009	0.006	1.26E-01	
						0.047						HDL cholesterol
rs6070625	20	57394628	C	G	0.480	-	0.006	3.20E-12	-0.003	0.005	4.89E-01	
rs61676547	17	65892507	C	G	0.190	0.044	0.008	1.00E-11	0.025	0.006	9.00E-05	
rs61850200	10	71321658	C	G	0.280	0.055	0.007	2.00E-02	0.004	0.006	4.56E-01	
rs61881115	11	68997225	A	G	0.160	-	0.009	6.80E-07	-0.001	0.007	9.35E-01	
						0.043						Lung function (FEV1/FVC), Smoking status, Hip circumference, Body fat distribution (arm fat ratio), Hand grip strength, Body fat distribution (leg fat ratio), Weight, Obese vs. thin
rs62007683	14	103894071	T	G	0.350	-	0.007	3.80E-08	-0.014	0.005	5.39E-03	
rs62080313	18	36278709	T	C	0.880	0.037	0.010	9.10E-09	0.011	0.008	1.71E-01	
						0.056						
rs62107261	2	422144	T	C	0.950	-	0.016	1.80E-11	0.035	0.014	8.79E-03	
rs62271373	3	150066540	A	T	0.055	0.110	0.014	1.00E-09	0.056	0.012	1.14E-06	Heel bone mineral density, Waist-hip ratio, Red blood cell count
rs62357230	5	52315682	A	G	0.034	0.074	0.018	6.70E-05	0.053	0.015	3.47E-04	
rs62368490	5	44534364	T	C	0.031	0.078	0.020	1.20E-04	0.002	0.017	9.08E-01	
rs62370480	5	52774510	A	G	0.220	0.039	0.008	3.70E-07	0.003	0.006	5.96E-01	
rs62482405	7	102987583	T	G	0.920	-	0.012	1.60E-06	-0.003	0.009	7.77E-01	
						0.056						Body fat percentage, Waist circumference
rs62492368	7	150537635	A	G	0.310	0.044	0.007	1.50E-10	0.002	0.005	7.10E-01	
rs6458354	6	43814190	T	C	0.710	-	0.007	3.70E-13	0.009	0.005	9.99E-02	
						0.051						
rs6459733	7	156930550	C	G	0.330	-	0.007	3.90E-17	-0.016	0.005	2.29E-03	
						0.058						Body fat percentage, Waist circumference
rs649961	3	124926637	T	C	0.470	0.038	0.006	1.30E-09	0.006	0.005	1.96E-01	
rs6518681	22	30609554	A	G	0.086	-	0.012	9.60E-13	-0.027	0.010	4.49E-03	
						0.083						
rs6545714	2	59307725	A	G	0.610	-	0.007	1.70E-08	-0.010	0.005	5.67E-02	
						0.037						Body fat percentage, Waist circumference
rs6600191	16	295795	T	C	0.820	0.061	0.009	7.00E-13	0.004	0.006	5.63E-01	
rs66477705	2	121378852	T	C	0.970	0.080	0.018	1.50E-05	0.007	0.014	5.94E-01	
rs6708643	2	43430440	A	G	0.500	0.038	0.006	3.30E-09	-0.014	0.005	5.91E-03	
rs67232546	11	128398938	T	C	0.210	0.056	0.008	1.40E-12	-0.006	0.006	3.44E-01	
rs67254669	11	17470143	A	G	NA	-	0.110	2.90E-08	-0.077	0.096	4.24E-01	Lung function (FVC), Peak expiratory flow, FEV1, Waist-hip ratio
						0.620						
rs6780171	3	185503456	A	T	0.310	0.110	0.007	2.50E-58	0.014	0.005	6.25E-03	Lung function (FVC), Peak expiratory flow, FEV1, Waist-hip ratio

rs6821438	4	95091911	A	G	0.530	0.042	0.006	5.40E-11	-0.002	0.005	7.32E-01	
rs6884702	5	44682589	A	G	0.610	-	0.007	5.80E-09	0.001	0.005	8.00E-01	
rs6885132	5	14768092	C	G	0.900	0.078	0.011	9.50E-13	0.011	0.008	1.89E-01	
rs6976111	7	117495667	A	C	0.310	0.042	0.007	1.50E-08	0.016	0.005	1.99E-03	General factor of neuroticism
rs7022807	9	19067833	A	G	0.600	-	0.006	3.60E-10	-0.020	0.005	6.02E-05	
rs702634	5	53271420	A	G	0.690	0.051	0.007	2.10E-13	0.016	0.005	3.39E-03	Urinary albumin excretion, Reticulocyte fraction of red cells, High light scatter reticulocyte count
rs703972	10	80952826	C	G	0.470	-	0.006	2.50E-28	0.001	0.005	7.63E-01	
rs7078559	10	93924663	T	C	0.580	0.049	0.006	1.70E-14	0.014	0.005	4.31E-03	
rs7115753	11	45912013	A	G	0.450	0.038	0.006	4.80E-09	-0.004	0.005	4.69E-01	
rs7124681	11	47529947	A	C	0.410	0.037	0.006	6.40E-09	-0.004	0.005	4.45E-01	Body mass index
rs71372253	17	29413019	T	C	0.940	-	0.013	4.30E-08	-0.021	0.011	5.50E-02	
rs7178762	15	63871292	T	C	0.540	-	0.006	7.00E-10	-0.016	0.005	9.88E-04	
rs718314	12	26453283	A	G	0.750	-	0.007	1.10E-10	0.012	0.006	2.67E-02	Waist circumference adjusted for body mass index, Waist-to-hip ratio adjusted for body mass index, Triglycerides, Renal cell carcinoma, Waist-hip ratio
rs7222481	17	9785187	C	G	0.320	0.039	0.007	1.70E-08	0.010	0.005	7.48E-02	
rs7240767	18	7070642	T	C	0.620	-	0.007	2.00E-08	0.001	0.005	7.76E-01	
rs7249758	19	4948862	A	G	0.200	0.045	0.008	1.20E-08	0.028	0.006	4.61E-06	
rs72802342	16	75234872	A	C	0.077	-	0.012	1.30E-27	-0.061	0.010	7.82E-10	Blood protein levels, Advanced age-related macular degeneration
rs72926932	18	53050646	A	C	0.920	-	0.011	3.60E-13	-0.005	0.009	6.26E-01	
rs73224262	12	121882395	T	C	0.007	0.190	0.043	9.70E-06	0.060	0.042	1.55E-01	
rs73226260	12	121380541	A	G	0.033	-	0.019	7.00E-11	-0.040	0.016	1.11E-02	
rs738408	22	44324730	T	C	0.230	0.049	0.008	1.80E-10	-0.026	0.006	1.04E-05	Aspartate aminotransferase levels, Plateletcrit, Hemoglobin concentration, Alanine aminotransferase (ALT) levels after remission induction therapy in acute lymphoblastic leukemia (ALL), Total cholesterol levels, Red cell distribution width, Hematocrit
rs74368513	3	64460694	A	G	0.004	-	0.059	1.10E-05	-0.014	0.042	7.36E-01	
rs74452128	18	58056566	A	C	0.024	-	0.022	7.40E-11	-0.039	0.016	1.51E-02	
rs745903616	19	44938870	A	G	0.001	0.470	0.110	8.40E-06	-0.151	0.104	1.46E-01	
rs74653713	3	152417881	A	C	0.043	-	0.016	5.70E-09	-0.004	0.013	7.46E-01	
rs75253922	19	7240848	T	C	0.810	-	0.008	2.20E-08	-0.021	0.006	1.38E-03	
rs75423501	3	47242923	A	G	0.900	-	0.011	4.10E-08	-0.041	0.009	8.10E-06	
rs759111467	12	97562756	A	G	0.000	1.100	0.230	2.10E-06	0.375	0.257	1.46E-01	

rs76011118	9	22133773	A	G	0.034	0.190	0.019	1.70E-22	0.090	0.017	1.14E-07	Body mass index, Pulse pressure, Medication use (HMG CoA reductase inhibitors), Heel bone mineral density, Medication use (drugs used in diabetes), Cardiovascular disease, Systolic blood pressure, Height
rs76197067	18	52604955	A	G	NA	-0.970	0.220	1.10E-05	-0.010	0.123	9.38E-01	
rs76251711	13	59184234	A	G	0.990	-0.120	0.031	1.20E-04	-0.051	0.029	7.85E-02	
rs76263492	3	54828827	T	G	0.045	0.091	0.016	6.30E-09	-0.004	0.012	7.47E-01	
rs7629630	3	168218841	A	T	0.860	0.051	0.009	2.20E-08	-0.002	0.007	8.28E-01	
rs7645517	3	186675277	A	G	0.058	0.046	0.014	9.50E-04	-0.010	0.010	3.46E-01	
rs76549217	5	14768766	T	C	0.029	0.100	0.020	4.60E-07	0.009	0.018	6.15E-01	
rs7669833	4	153513369	A	T	0.300	-0.054	0.007	1.80E-14	-0.003	0.005	6.16E-01	
rs76811102	20	42905415	T	C	0.042	0.069	0.017	3.30E-05	0.010	0.014	4.67E-01	
rs76895963	12	4384844	T	G	0.980	0.480	0.027	5.30E-70	0.022	0.022	3.26E-01	
rs7719891	5	86577352	A	G	0.740	-0.040	0.007	2.90E-08	-0.002	0.006	7.17E-01	Medication use (drugs used in diabetes)
rs77464186	11	72460398	A	C	0.840	0.110	0.009	2.30E-33	-0.002	0.007	7.20E-01	
rs7756992	6	20679709	A	G	0.730	-0.140	0.007	3.00E-87	-0.008	0.005	1.64E-01	Glycated hemoglobin levels, Insulin secretion rate
rs77864822	12	97848775	A	G	0.930	0.073	0.013	2.20E-08	0.019	0.010	6.36E-02	
rs78020297	16	53758720	A	G	0.052	0.034	0.014	2.00E-02	0.025	0.011	2.95E-02	Male-pattern baldness, Blood protein levels
rs78025551	10	114757956	C	G	0.850	0.150	0.009	8.40E-63	0.012	0.007	9.49E-02	
rs78403475	9	139235606	C	G	0.100	-0.035	0.011	1.50E-03	0.001	0.009	8.96E-01	Fasting blood glucose, Glycated hemoglobin levels, Body mass index, Waist circumference, Schizophrenia vs type 2 diabetes, Clinical laboratory measurements, Pulse pressure, Proinsulin levels, Metabolic syndrome, Medication use (HMG CoA reductase inhibitors), Peak insulin response, Hip circumference, Systolic blood pressure, Fasting blood insulin, Medication use (drugs used in diabetes)
rs78408340	5	102338739	C	G	0.990	-0.380	0.038	3.20E-23	0.076	0.036	3.24E-02	
rs7847880	9	20662703	T	C	0.160	-0.044	0.009	6.80E-07	-0.019	0.007	4.68E-03	
rs7867635	9	20241069	T	C	0.590	-0.036	0.007	4.10E-08	-0.008	0.005	1.12E-01	
rs78840640	7	23434606	C	G	0.980	-0.120	0.022	2.00E-07	0.035	0.020	8.72E-02	Red blood cell count
rs7903146	10	114758349	T	C	0.290	0.310	0.007	1.00E-200	0.029	0.005	6.40E-08	
rs79103584	9	4243045	A	T	0.014	-0.140	0.029	6.40E-07	0.008	0.021	7.15E-01	
rs7918400	10	114703136	T	C	0.480	-0.004	0.006	5.40E-01	-0.001	0.005	8.54E-01	
rs7943101	11	32460873	T	C	0.160	0.044	0.009	4.20E-07	0.024	0.007	2.48E-04	
rs79687284	1	214150821	C	G	0.035	0.180	0.018	9.20E-23	0.003	0.016	8.28E-01	Medication use (drugs used in diabetes), Fasting plasma glucose
rs7987740	13	109947213	T	C	0.610	0.036	0.007	4.10E-08	0.007	0.005	1.56E-01	

Medication use (drugs used in diabetes)

Male-pattern baldness, Blood protein levels

Fasting blood glucose, Glycated hemoglobin levels, Body mass index, Waist circumference, Schizophrenia vs type 2 diabetes, Clinical laboratory measurements, Pulse pressure, Proinsulin levels, Metabolic syndrome, Medication use (HMG CoA reductase inhibitors), Peak insulin response, Hip circumference, Systolic blood pressure, Fasting blood insulin, Medication use (drugs used in diabetes)

Red blood cell count

Medication use (drugs used in diabetes), Fasting plasma glucose

rs80102379	11	2634177	T	G	0.018	- 0.086	0.026	1.10E-03	-0.031	0.021	1.43E-01	
rs8010382	14	91963722	A	G	0.580	- 0.038	0.007	8.10E-09	0.001	0.005	8.40E-01	
rs80147536	2	43698028	A	T	0.900	0.130	0.011	2.70E-30	-0.029	0.009	9.53E-04	
rs8017808	14	38848419	T	G	0.260	- 0.041	0.007	2.60E-08	0.001	0.006	9.13E-01	Medication use (drugs used in diabetes)
rs80244329	8	118404672	A	G	0.022	- 0.110	0.024	7.70E-06	-0.024	0.020	2.41E-01	
rs8032939	15	38834033	T	C	0.750	- 0.043	0.007	8.40E-09	-0.026	0.006	3.65E-06	Rheumatoid arthritis
rs8037894	15	62394264	C	G	0.430	- 0.047	0.006	3.70E-13	0.004	0.005	4.78E-01	
rs8046545	16	28915217	A	G	0.640	- 0.037	0.007	2.30E-08	0.002	0.005	6.65E-01	
rs8107974	19	19388500	A	T	0.920	- 0.093	0.012	6.30E-15	0.040	0.009	1.59E-05	
rs862016	20	57551099	A	G	0.920	- 0.055	0.012	4.90E-06	0.003	0.010	7.64E-01	
rs862320	16	69651866	T	C	0.420	- 0.042	0.006	5.10E-11	-0.017	0.005	9.53E-04	Body mass index
rs878521	7	44255643	A	G	0.250	0.057	0.007	1.60E-14	0.021	0.006	3.00E-04	Metabolite levels (small molecules and protein measures), Fasting blood glucose
rs917195	7	30728452	T	C	0.230	- 0.051	0.008	5.60E-11	-0.007	0.006	2.22E-01	
rs9379084	6	7231843	A	G	0.110	- 0.097	0.011	2.30E-20	0.021	0.008	1.22E-02	Heel bone mineral density, Height, Medication use (drugs used in diabetes), Breast cancer
rs9430095	1	206593900	C	G	0.490	0.036	0.006	2.30E-08	-0.007	0.005	1.51E-01	
rs9494624	6	137300960	A	G	0.290	0.041	0.007	7.60E-09	-0.004	0.005	4.61E-01	
rs9505097	6	7255650	T	C	0.200	- 0.041	0.008	3.30E-07	-0.018	0.006	3.67E-03	
rs9537803	13	58366634	T	C	0.720	- 0.034	0.007	1.30E-06	-0.005	0.006	3.64E-01	
rs9563615	13	59077406	A	T	0.710	0.042	0.007	3.90E-09	0.006	0.005	2.96E-01	
rs9569864	13	58965435	T	C	0.180	- 0.048	0.008	8.50E-09	-0.012	0.006	6.35E-02	
rs963740	13	51096095	A	T	0.710	0.039	0.007	2.60E-08	0.005	0.005	3.46E-01	Blood urea nitrogen levels
rs96844	5	56196604	A	G	0.740	- 0.038	0.007	1.70E-07	-0.021	0.005	1.43E-04	
rs9687832	5	55861595	A	G	0.200	0.067	0.008	4.90E-17	0.044	0.006	2.01E-12	
rs9828772	3	129333182	C	G	0.900	0.059	0.011	4.20E-08	0.024	0.008	2.85E-03	
rs9860730	3	64701146	A	G	0.700	0.055	0.007	7.40E-15	-0.008	0.005	1.15E-01	Waist-hip ratio, Waist circumference adjusted for body mass index, Waist-to-hip ratio adjusted for BMI x sex interaction, Waist circumference adjusted for BMI (adjusted for smoking behaviour), Waist-to-hip ratio adjusted for BMI x sex x age interaction (4df test)
rs9873618	3	170733076	A	G	0.290	- 0.066	0.007	8.50E-21	-0.003	0.005	6.08E-01	Fasting plasma glucose

rs9957145	18	56876228	A	G	0.170	- 0.050	0.009	6.70E-09	0.002	0.006	7.30E-01
rs184660829	1	115144899	T	C	1.000	- 2.100	0.370	2.50E-08			
rs543786825	15	42201410	T	C	0.000	1.200	0.250	3.80E-06			
rs755734872	19	12938471	T	C	0.001	0.830	0.190	1.60E-05			
rs533172266	19	46351837	T	C	0.001	0.850	0.180	3.40E-06			
rs562386202	2	118071061	A	G	1.000	- 1.200	0.210	4.20E-08			
rs555402748	6	67387490	T	C	0.000	1.300	0.240	4.60E-08			
9:139737088:G:A	9	139737088	A	G	0.001	1.000	0.230	8.10E-06			

SNP, single nucleotide polymorphisms; CHR, chromosome; BP, physical position of SNP (base-pairs); A1, effect allele; A2, non-effect allele; EAF: effect allele frequency; Beta, effect allele beta coefficient.

Supplementary Table 2. Characteristics of genetic instruments of type 2 diabetes mellitus adjusted for BMI and their effect sizes with coronary artery disease.

SNP	CHR	BP	A1	A2	EAF	Exposure			Outcome			Pleiotropic traits
						Beta	SE	P-value	Beta	SE	P-value	
rs1005752	15	77818128	A	C	0.720	0.071	0.008	7.80E-18	0.017	0.005	1.43E-03	Metabolic traits, High density lipoprotein cholesterol levels, Triglyceride levels
rs10096633	8	19830921	T	C	0.120	-0.072	0.011	2.10E-10	-0.051	0.008	1.50E-11	
rs10097617	8	95961626	T	C	0.480	0.050	0.008	2.00E-11	0.014	0.005	3.67E-03	
rs10195252	2	165513091	T	C	0.590	0.080	0.008	5.70E-26	0.021	0.005	3.07E-05	Waist-to-hip ratio adjusted for body mass index, Waist-hip ratio, Waist circumference adjusted for BMI, Pulse pressure, Hip circumference adjusted for BMI, Triglycerides, Fasting blood insulin
rs10228066	7	15063569	T	C	0.540	0.071	0.008	2.20E-21	0.007	0.005	1.56E-01	Height
rs10406327	19	33890838	C	G	0.520	0.044	0.008	3.00E-09	0.008	0.005	8.45E-02	
rs10406431	19	46157019	A	G	0.560	0.058	0.008	1.80E-14	0.018	0.005	2.90E-04	
rs10811660	9	22134068	A	G	0.170	-0.180	0.010	5.90E-69	-0.009	0.006	1.73E-01	Fasting plasma glucose, Corrected insulin response, Insulin disposition index, Obesity-related traits, Incremental insulin, Homeostasis model assessment of beta-cell function, Acute insulin response, Glucose homeostasis traits, Birth weight, Insulin levels, Pulse pressure, Glycated hemoglobin levels, Metabolite levels, Corrected insulin response adjusted for insulin sensitivity index, Insulin secretion rate, Hemoglobin A1c levels, Offspring birth weight, Insulin levels adjusted for BMI, Peak insulin response, Glycemic traits (multi-trait analysis)
rs10830963	11	92708710	C	G	0.720	-0.100	0.008	2.80E-36	-0.010	0.006	7.96E-02	
rs10842994	12	27965150	T	C	0.200	-0.077	0.009	2.00E-16	-0.004	0.006	4.79E-01	
rs10882101	10	94462427	T	C	0.590	0.120	0.008	1.60E-57	0.023	0.005	4.98E-06	Osteoarthritis, Height
rs10908278	17	36099952	A	T	0.520	-0.087	0.008	2.60E-31	0.010	0.005	5.64E-02	
rs10937721	4	6306763	C	G	0.590	0.089	0.008	1.80E-31	0.003	0.005	5.80E-01	
rs10974438	9	4291928	A	C	0.640	-0.059	0.008	3.20E-14	0.005	0.005	3.29E-01	Medication use (drugs used in diabetes)
rs11070332	15	41809205	A	G	0.350	0.048	0.008	9.60E-10	0.016	0.005	2.31E-03	
rs11202627	10	89769340	T	C	0.150	0.057	0.010	4.70E-08	-0.003	0.007	6.60E-01	
rs11257655	10	12307894	T	C	0.210	0.095	0.009	7.70E-26	0.026	0.006	9.97E-06	Body mass index, Medication use (drugs used in diabetes)
rs1127215	1	117532790	T	C	0.410	-0.050	0.008	6.20E-11	-0.005	0.005	2.71E-01	
rs113414093	2	219859171	A	G	0.051	0.120	0.020	6.60E-09	0.070	0.014	8.73E-07	
rs115505614	5	102422968	T	C	0.050	0.190	0.018	3.80E-27	-0.026	0.012	3.23E-02	Male-pattern baldness
rs11688682	2	121347612	C	G	0.270	-0.065	0.009	1.60E-13	-0.005	0.006	3.79E-01	
rs11699802	20	48832135	T	C	0.470	-0.056	0.008	1.00E-13	-0.006	0.005	2.31E-01	
rs117001013	22	32348841	T	C	0.081	-0.080	0.014	8.00E-09	0.002	0.009	8.09E-01	Systolic blood pressure, Cardiovascular disease
rs11708067	3	123065778	A	G	0.770	0.110	0.009	3.10E-33	0.008	0.006	1.62E-01	
rs11709077	3	12336507	A	G	0.130	-0.120	0.011	5.00E-25	-0.001	0.008	9.13E-01	
rs11759026	6	126792095	A	G	0.770	-0.074	0.009	1.20E-16	0.029	0.006	1.07E-06	Homeostasis model assessment of beta-cell function, Fasting blood glucose, Glycated hemoglobin levels
rs11820019	11	69448758	T	C	0.970	0.140	0.025	1.40E-08	-0.006	0.016	6.90E-01	
rs11926707	3	46925539	T	C	0.380	-0.047	0.008	1.70E-09	-0.008	0.005	1.21E-01	
rs12454712	18	60845884	T	C	0.620	0.070	0.008	5.60E-19	0.019	0.005	4.98E-04	Body mass index
rs1260326	2	27730940	T	C	0.400	-0.067	0.008	7.40E-19	0.016	0.005	1.27E-03	

												levels, Gout, Alcohol consumption in current drinkers, Hypertriglyceridemia, White blood cell count, Hematocrit, Myeloid white cell count, Glomerular filtration rate, Glycemic traits (pregnancy), Serum uric acid levels, Platelet count, Blood metabolite ratios, Alcohol use disorder (consumption score), C-reactive protein levels or triglyceride levels (pleiotropy), Branched-chain amino acid levels (Leucine), Waist circumference and related phenotypes, Metabolite levels, Blood sugar levels, Coffee consumption (cups per day), Sum basophil neutrophil counts, Factor VII activity, Fasting blood glucose adjusted for BMI, Medication use (HMG CoA reductase inhibitors), Height, Protein C levels, Resting heart rate, Low density lipoprotein cholesterol levels, Fat-free mass, Chronic kidney disease, Blood metabolite levels, Serum albumin level, Glomerular filtration rate in non diabetics (creatinine), Alcohol consumption, Plasma lactate levels, Fasting blood glucose, Lipid traits, Triglycerides x physical activity interaction (2df test), Two-hour glucose challenge, Metabolic traits, High light scatter reticulocyte percentage of red cells, Gallstone disease, Nonalcoholic fatty liver disease, Renal overload gout, Hematological and biochemical traits, Urate levels in overweight individuals, Liver enzyme levels (gamma-glutamyl transferase), Percent glycated albumin, Alcohol consumption (drinks per week) (MTAG), Crohn's disease, Estimated glomerular filtration rate, Chronic inflammatory diseases (ankylosing spondylitis, Crohn's disease, psoriasis, primary sclerosing cholangitis, ulcerative colitis) (pleiotropy), Red cell distribution width, Granulocyte count, Caffeine metabolism (plasma 1,7-dimethylxanthine (paraxanthine) to 1,3,7-trimethylxanthine (caffeine) ratio), Body mass index, Alcohol consumption (drinks per week), Inflammatory bowel disease, Branched-chain amino acid levels (Isoleucine), Serum alpha1-antitrypsin levels, C-reactive protein levels or total cholesterol levels (pleiotropy), Lipoprotein-associated phospholipase A2 activity and mass, Sum neutrophil eosinophil counts, Non-albumin protein levels, Alcohol use disorder, Fasting blood insulin adjusted for BMI, Metabolite levels (small molecules and protein measures), Urolithiasis, Factor VII activity or levels, Cardiovascular disease risk factors, Gamma glutamyl transferase levels, Plateletcrit, Alcohol use disorder (total score)
rs12642790	4	83578271	A	G	0.340	0.045	0.008	1.00E-08	0.001	0.005	8.26E-01	
rs12910825	15	91511260	A	G	0.640	-0.059	0.008	2.20E-14	-0.009	0.005	9.31E-02	
rs13085136	3	72865183	T	C	0.073	-0.088	0.015	5.60E-09	0.030	0.010	3.99E-03	
rs13262861	8	41508577	A	C	0.170	-0.110	0.010	7.40E-27	-0.003	0.007	6.48E-01	
rs13426680	2	158339550	A	G	0.940	0.093	0.015	1.40E-09	0.001	0.010	8.87E-01	
rs1359790	13	80717156	A	G	0.280	-0.091	0.008	6.50E-28	-0.006	0.006	2.46E-01	Medication use (drugs used in diabetes)
rs13737	15	75932129	T	G	0.250	-0.050	0.009	1.10E-08	-0.005	0.006	3.94E-01	
rs1377807	17	4045440	C	G	0.310	0.053	0.008	2.70E-11	0.013	0.005	1.97E-02	
rs138337556	5	101232944	A	G	NA	-0.540	0.078	5.20E-12	0.083	0.069	2.29E-01	
rs1421085	16	53800954	T	C	0.590	-0.054	0.008	9.90E-13	-0.017	0.005	5.09E-04	Childhood body mass index, Fat-free mass, Medication use (HMG CoA reductase inhibitors), Obesity, Chronotype, Body fat percentage, Pulse pressure, Dietary macronutrient intake, Body mass index, Morningness, Alcohol use disorder, Obesity (early onset extreme), Morning person, Hand grip strength
rs1426371	12	108629780	A	G	0.260	-0.051	0.009	3.50E-09	-0.002	0.006	7.19E-01	Body fat percentage, Extraversion, Worry, Alcohol consumption (drinks per week) (MTAG)
rs146886108	5	14751305	T	C	0.007	-0.390	0.052	5.60E-14	-0.026	0.036	4.79E-01	
rs149364428	8	97737741	A	G	0.009	0.260	0.042	3.80E-10	0.046	0.033	1.60E-01	
rs1493694	1	120526982	T	C	0.110	0.096	0.012	1.70E-15	-0.005	0.008	5.72E-01	

rs1531583	4	744972	T	G	0.041	0.130	0.019	8.80E-12	0.003	0.012	7.74E-01
rs1562396	7	130457914	A	G	0.680	-0.067	0.008	1.10E-16	-0.018	0.005	7.49E-04
rs1641523	17	7549681	T	C	0.570	-0.044	0.008	8.30E-09	-0.002	0.005	6.44E-01
rs1708302	7	28198677	T	C	0.490	-0.100	0.008	8.70E-41	-0.011	0.005	2.53E-02
rs17122772	14	23288935	C	G	0.780	-0.052	0.009	8.00E-09	-0.020	0.006	9.27E-04
rs17772814	8	128711742	A	G	0.082	-0.082	0.015	4.00E-08	-0.003	0.010	7.94E-01
rs17791513	9	81905590	A	G	0.930	0.100	0.015	8.10E-12	0.024	0.010	1.18E-02
rs1783541	11	65294799	T	C	0.210	0.054	0.009	4.40E-09	-0.007	0.006	2.49E-01
rs1796330	12	71522953	C	G	0.430	-0.051	0.008	1.00E-11	-0.008	0.005	9.30E-02
rs1800961	20	43042364	T	C	0.033	0.180	0.021	9.20E-18	-0.011	0.014	4.27E-01
rs1801645	22	50356850	T	C	0.740	-0.055	0.009	1.90E-10	-0.011	0.006	5.80E-02
rs2066827	12	12871099	T	G	0.770	-0.051	0.009	4.40E-08	-0.005	0.006	4.09E-01
rs2237895	11	2857194	A	C	0.580	-0.110	0.008	9.90E-47	-0.014	0.005	5.69E-03
rs2249105	2	65287896	A	G	0.630	0.050	0.008	8.40E-11	0.010	0.005	4.05E-02
rs2258238	12	66221060	A	T	0.890	-0.120	0.012	1.90E-21	-0.003	0.008	6.59E-01
rs2280141	10	124193181	T	G	0.520	0.047	0.008	3.70E-10	0.008	0.005	1.28E-01
rs243024	2	60583665	A	G	0.460	0.059	0.008	4.50E-15	0.015	0.005	2.53E-03
rs2642588	10	71466578	T	G	0.300	-0.050	0.008	1.20E-09	0.005	0.005	4.06E-01
rs2796441	9	84308948	A	G	0.410	-0.080	0.008	1.30E-25	-0.006	0.005	2.66E-01
rs2800733	6	127416930	A	G	0.710	0.063	0.008	2.40E-14	-0.008	0.006	1.42E-01
rs2820446	1	219748818	C	G	0.710	0.062	0.008	5.80E-14	0.013	0.005	1.30E-02
rs28505901	9	139241030	A	G	0.250	-0.080	0.009	2.80E-19	-0.028	0.006	7.28E-06
rs2925979	16	81534790	T	C	0.300	0.048	0.008	2.50E-09	0.024	0.005	1.17E-05
rs2972144	2	227101411	A	G	0.360	-0.100	0.008	2.90E-40	-0.036	0.005	2.81E-12
rs2982521	6	139835329	A	T	0.380	0.044	0.008	8.80E-09	0.020	0.005	1.40E-04
rs3111316	19	13038415	A	G	0.590	0.051	0.008	1.60E-11	0.006	0.005	2.17E-01
rs329122	5	133864599	A	G	0.420	0.055	0.008	2.00E-13	0.012	0.005	1.71E-02

Fibrinogen levels, HDL cholesterol levels x alcohol consumption (regular vs non-regular drinkers) interaction (2df), C-reactive protein levels or LDL-cholesterol levels (pleiotropy), Total cholesterol levels, LDL cholesterol levels x alcohol consumption (drinkers vs non-drinkers) interaction (2df), White blood cell count, HDL cholesterol levels x alcohol consumption (drinkers vs non-drinkers) interaction (2df), Sum neutrophil eosinophil counts, LDL cholesterol levels in current drinkers, C-reactive protein levels, Granulocyte count, High density lipoprotein cholesterol levels, Neutrophil count, Medication use (drugs used in diabetes), LDL cholesterol levels x alcohol consumption (regular vs non-regular drinkers) interaction (2df), Red blood cell count, Factor VII activity, C-reactive protein levels or total cholesterol levels (pleiotropy), Neutrophil percentage of white cells, HDL cholesterol x physical activity interaction (2df test), C-reactive protein levels or HDL-cholesterol levels (pleiotropy), Cholesterol, total, Sum basophil neutrophil counts, Gallstone disease, Myeloid white cell count, C-reactive protein, Hematocrit

Prostate cancer

Prostate cancer, Lipid traits (pleiotropy) (HIPO component 1)

Medication use (drugs used in diabetes)

Height

Schizophrenia

High density lipoprotein cholesterol levels, Waist-to-hip ratio adjusted for body mass index, Triglycerides, HDL cholesterol levels x alcohol consumption (drinkers vs non-drinkers) interaction (2df), HDL cholesterol levels x alcohol consumption (regular vs non-regular drinkers) interaction (2df), HDL cholesterol x physical activity interaction (2df test), Triglyceride levels x alcohol consumption (regular vs non-regular drinkers) interaction (2df), Triglyceride levels x alcohol consumption (drinkers vs non-drinkers) interaction (2df), Adiponectin levels, Waist-hip ratio, Waist-to-hip ratio adjusted for BMI x sex x age interaction (4df test), Waist-to-hip ratio adjusted for BMI x sex interaction

Medication use (HMG CoA reductase inhibitors)

Estimated glomerular filtration rate

Body mass index

rs340874	1	214159256	T	C	0.450	-0.071	0.008	4.80E-21	-0.003	0.005	5.12E-01	Homeostasis model assessment of beta-cell function, Fasting blood glucose
rs34584161	13	26776999	A	G	0.760	0.051	0.009	5.20E-09	0.003	0.006	5.71E-01	
rs34715063	15	38873115	T	C	0.880	-0.084	0.012	3.70E-13	-0.005	0.008	5.07E-01	
rs348330	1	229672955	A	G	0.640	-0.052	0.008	3.70E-11	-0.009	0.005	7.89E-02	
rs35352848	3	23455582	T	C	0.790	0.089	0.009	5.40E-22	-0.008	0.006	1.79E-01	
rs3768321	1	40035928	T	G	0.200	0.075	0.009	9.60E-16	0.015	0.006	2.31E-02	Red cell distribution width, HDL cholesterol, Mean corpuscular hemoglobin, HDL cholesterol x physical activity interaction (2df test)
rs3774723	3	63962339	A	G	0.160	-0.066	0.010	1.70E-10	-0.014	0.007	3.86E-02	
rs3802177	8	118185025	A	G	0.310	-0.120	0.008	3.80E-53	-0.008	0.005	1.36E-01	Medication use (drugs used in diabetes), Fasting plasma glucose, Body mass index
rs3811978	5	52100489	A	G	0.830	-0.057	0.010	9.10E-09	0.004	0.006	4.96E-01	
rs3887925	3	186665645	T	C	0.550	0.061	0.008	3.70E-16	-0.002	0.005	6.92E-01	
rs3934712	5	157928196	T	C	0.790	-0.051	0.009	3.20E-08	-0.016	0.006	5.84E-03	
rs4148856	12	123450765	C	G	0.790	0.054	0.009	2.40E-09	0.000	0.006	9.92E-01	
rs4279506	7	23512896	C	G	0.390	-0.043	0.008	2.80E-08	-0.003	0.005	5.46E-01	
rs4457053	5	76424949	A	G	0.690	-0.069	0.008	1.50E-17	-0.006	0.006	2.40E-01	
rs465002	5	55808475	T	C	0.740	0.080	0.009	7.60E-21	0.017	0.006	1.71E-03	HDL cholesterol levels x alcohol consumption (regular vs non-regular drinkers) interaction (2df), HDL cholesterol levels x alcohol consumption (drinkers vs non-drinkers) interaction (2df), Triglyceride levels, HDL cholesterol levels, Triglyceride levels x alcohol consumption (drinkers vs non-drinkers) interaction (2df), Triglyceride levels x alcohol consumption (regular vs non-regular drinkers) interaction (2df)
rs4686471	3	187740899	T	C	0.390	-0.070	0.008	1.10E-19	0.001	0.005	8.85E-01	Heel bone mineral density, Diastolic blood pressure, Height
rs4709746	6	164133001	T	C	0.130	-0.074	0.011	3.50E-11	-0.019	0.007	9.70E-03	
rs474513	6	160770312	A	G	0.520	0.051	0.008	1.30E-11	0.051	0.005	1.57E-25	
rs4804833	19	7970635	A	G	0.390	0.054	0.008	1.60E-12	0.004	0.005	4.44E-01	Educational attainment (years of education)
rs4923543	11	28534898	A	G	0.330	0.043	0.008	4.50E-08	0.004	0.005	3.98E-01	
rs4925109	17	17661802	A	G	0.310	0.047	0.008	5.30E-09	0.026	0.005	6.55E-07	
rs4929965	11	2197286	A	G	0.380	0.070	0.008	1.60E-19	0.007	0.005	1.66E-01	
rs4932265	15	90423293	T	C	0.260	0.077	0.009	7.70E-20	0.007	0.006	2.25E-01	Red cell distribution width
rs4976033	5	67714246	A	G	0.590	-0.047	0.008	1.00E-09	-0.013	0.005	1.33E-02	
rs4977213	8	145507304	T	C	0.620	-0.062	0.008	1.20E-15	-0.016	0.005	2.12E-03	Medication use (drugs used in diabetes)
rs5213	11	17408404	T	C	0.640	-0.080	0.008	6.50E-25	-0.004	0.005	4.47E-01	
rs56337234	4	1784403	T	C	0.500	-0.073	0.008	1.30E-21	0.002	0.005	6.40E-01	Heel bone mineral density, Waist-hip ratio, Red blood cell count
rs56348580	12	121432117	C	G	0.310	-0.051	0.008	2.00E-10	-0.030	0.006	5.45E-08	
rs58432198	1	51256091	T	C	0.120	-0.073	0.012	1.40E-09	-0.009	0.008	2.66E-01	
rs58730668	4	185717759	T	C	0.860	0.072	0.011	2.50E-11	-0.001	0.007	8.95E-01	
rs59944054	20	62693175	A	G	0.240	0.048	0.009	4.60E-08	0.010	0.006	9.52E-02	
rs601945	6	32573415	A	G	0.820	-0.085	0.010	1.50E-17	-0.017	0.007	1.94E-02	
rs6063048	20	45598564	A	G	0.270	-0.053	0.008	2.40E-10	-0.009	0.006	1.26E-01	
rs6070625	20	57394628	C	G	0.480	-0.051	0.008	1.40E-11	-0.003	0.005	4.89E-01	
rs62271373	3	150066540	A	T	0.057	0.099	0.017	2.50E-09	0.056	0.012	1.14E-06	
rs62492368	7	150537635	A	G	0.310	0.050	0.008	3.80E-10	0.002	0.005	7.10E-01	
rs6458354	6	43814190	T	C	0.710	-0.053	0.008	7.40E-11	0.009	0.005	9.99E-02	Lung function (FVC), Peak expiratory flow, FEV1, Waist-hip ratio
rs6459733	7	156930550	C	G	0.330	-0.062	0.008	1.00E-14	-0.016	0.005	2.29E-03	
rs6518681	22	30609554	A	G	0.087	-0.085	0.013	2.00E-10	-0.027	0.010	4.49E-03	
rs6600191	16	295795	T	C	0.820	0.065	0.010	3.80E-11	0.004	0.006	5.63E-01	
rs67232546	11	128398938	T	C	0.210	0.057	0.009	9.50E-10	-0.006	0.006	3.44E-01	
rs6780171	3	185503456	A	T	0.310	0.120	0.008	2.40E-51	0.014	0.005	6.25E-03	

rs7022807	9	19067833	A	G	0.610	-0.048	0.008	3.20E-10	-0.020	0.005	6.02E-05	Urinary albumin excretion, Reticulocyte fraction of red cells, High light scatter reticulocyte count
rs702634	5	53271420	A	G	0.690	0.060	0.008	9.70E-14	0.016	0.005	3.39E-03	
rs703972	10	80952826	C	G	0.460	-0.079	0.008	3.40E-26	0.001	0.005	7.63E-01	
rs7178762	15	63871292	T	C	0.540	-0.044	0.008	4.40E-09	-0.016	0.005	9.88E-04	Waist circumference adjusted for body mass index, Waist-to-hip ratio adjusted for body mass index, Triglycerides, Renal cell carcinoma, Waist-hip ratio
rs718314	12	26453283	A	G	0.750	-0.060	0.009	3.00E-12	0.012	0.006	2.67E-02	
rs72631105	10	122915345	A	G	0.190	0.058	0.010	3.70E-09	0.008	0.006	1.99E-01	
rs72802342	16	75234872	A	C	0.078	-0.160	0.014	2.70E-29	-0.061	0.010	7.82E-10	Blood protein levels, Advanced age-related macular degeneration Schizophrenia
rs72926932	18	53050646	A	C	0.920	-0.089	0.013	3.60E-11	-0.005	0.009	6.26E-01	
rs738408	22	44324730	T	C	0.220	0.062	0.009	3.00E-12	-0.026	0.006	1.04E-05	
rs75253922	19	7240848	T	C	0.810	-0.054	0.010	1.10E-08	-0.021	0.006	1.38E-03	Aspartate aminotransferase levels, Plateletcrit, Hemoglobin concentration, Alanine aminotransferase (ALT) levels after remission induction therapy in acute lymphoblastic leukemia (ALL), Total cholesterol levels, Red cell distribution width, Hematocrit
rs76263492	3	54828827	T	G	0.044	0.110	0.019	1.40E-08	-0.004	0.012	7.47E-01	
rs7669833	4	153513369	A	T	0.300	-0.059	0.008	4.40E-13	-0.003	0.005	6.16E-01	
rs76895963	12	4384844	T	G	0.980	0.520	0.031	1.30E-64	0.022	0.022	3.26E-01	Body mass index, Pulse pressure, Medication use (HMG CoA reductase inhibitors), Heel bone mineral density, Medication use (drugs used in diabetes), Cardiovascular disease, Systolic blood pressure, Height
rs77136196	6	34247047	T	C	0.042	0.110	0.019	1.60E-09	0.051	0.014	3.19E-04	
rs77464186	11	72460398	A	C	0.840	0.130	0.010	9.00E-37	-0.002	0.007	7.20E-01	
rs7756992	6	20679709	A	G	0.720	-0.150	0.008	1.40E-73	-0.008	0.005	1.64E-01	Medication use (drugs used in diabetes) Glycated hemoglobin levels, Insulin secretion rate
rs7903146	10	114758349	T	C	0.290	0.360	0.008	1.00E-200	0.029	0.005	6.40E-08	
rs79046683	2	96913918	T	G	0.005	0.850	0.150	3.00E-08	0.023	0.143	8.73E-01	
rs7978610	12	124468572	C	G	0.330	-0.049	0.008	7.70E-10	-0.030	0.005	7.65E-09	Fasting blood glucose, Glycated hemoglobin levels, Body mass index, Waist circumference, Schizophrenia vs type 2 diabetes, Clinical laboratory measurements, Pulse pressure, Proinsulin levels, Metabolic syndrome, Medication use (HMG CoA reductase inhibitors), Peak insulin response, Hip circumference, Systolic blood pressure, Fasting blood insulin, Medication use (drugs used in diabetes)
rs80147536	2	43698028	A	T	0.900	0.140	0.013	2.30E-26	-0.029	0.009	9.53E-04	
rs8017808	14	38848419	T	G	0.250	-0.048	0.009	3.70E-08	0.001	0.006	9.13E-01	
rs8037894	15	62394264	C	G	0.430	-0.047	0.008	4.40E-10	0.004	0.005	4.78E-01	Medication use (drugs used in diabetes)
rs8107974	19	19388500	A	T	0.920	-0.120	0.014	8.00E-18	0.040	0.009	1.59E-05	
rs878521	7	44255643	A	G	0.250	0.062	0.009	8.70E-13	0.021	0.006	3.00E-04	
rs9379084	6	7231843	A	G	0.110	-0.120	0.012	3.8E-23	0.021	0.008	1.22E-02	Metabolite levels (small molecules and protein measures), Fasting blood glucose Heel bone mineral density, Height, Medication use (drugs used in diabetes), Breast cancer
rs963740	13	51096095	A	T	0.710	0.046	0.008	1.4E-08	0.005	0.005	3.46E-01	
rs9860730	3	64701146	A	G	0.700	0.067	0.008	4.1E-16	-0.008	0.005	1.15E-01	
rs9873618	3	170733076	A	G	0.290	-0.078	0.008	2.7E-21	-0.003	0.005	6.08E-01	Waist-hip ratio, Waist circumference adjusted for body mass index, Waist-to-hip ratio adjusted for BMI x sex interaction, Waist circumference adjusted for BMI (adjusted for smoking behaviour), Waist-to-hip ratio adjusted for BMI x sex x age interaction (4df test) Fasting plasma glucose
rs562386202	2	118071061	A	G	1.000	-1.200	0.210	1.8E-08				
rs555402748	6	67387490	T	C	0.000	1.400	0.250	1.1E-08				

SNP, single nucleotide polymorphisms; CHR, chromosome; BP, physical position of SNP (base-pairs); A1, effect allele; A2, non-effect allele; EAF: effect allele frequency; Beta, effect allele beta coefficient.

Supplementary Table 3. Characteristics of genetic instruments of coronary artery disease and their effect sizes with type 2 diabetes mellitus.

SNP	CHR	BP	A1	A2	EAF	Exposure			Outcome			Pleiotropic traits
						Beta	SE	P-value	Beta	SE	P-value	
rs10131894	14	75446879	C	G	0.441	-0.036	0.005	7.59E-13	-0.008	0.007	2.00E-01	Mean corpuscular hemoglobin
rs10176176	2	85762048	A	T	0.519	-0.057	0.005	4.27E-31	0.014	0.006	2.80E-02	
rs1034246	6	43068370	T	G	0.263	-0.035	0.006	6.39E-10	-0.014	0.007	4.80E-02	
rs10410487	19	17829608	T	C	0.461	-0.040	0.005	3.34E-15	0.009	0.007	1.90E-01	
rs10422256	19	11216617	A	G	0.500	0.032	0.005	2.88E-10	0.005	0.006	4.70E-01	
rs10455872	6	161010118	A	G	0.932	-0.304	0.010	2.18E-186	-0.020	0.013	1.00E-01	Aortic-valve calcification, Parental longevity (mother's age at death), Total cholesterol levels, Lipoprotein phospholipase A2 activity in cardiovascular disease, Parental longevity (both parents in top 10%), Metabolite levels (lipoprotein measures), Response to statins (LDL cholesterol change), Low density lipoprotein cholesterol levels, Lp (a) levels, Response to statin therapy, Aortic valve stenosis, Lipoprotein-associated phospholipase A2 activity change in response to statin therapy, Parental longevity (father's age at death)
rs10477741	5	131795310	T	G	0.867	-0.048	0.007	3.49E-11	-0.027	0.010	3.80E-03	
rs10486389	7	20300416	A	G	0.719	-0.035	0.006	6.51E-10	0.005	0.007	5.00E-01	
rs10488763	11	110244360	A	T	0.865	-0.041	0.007	1.31E-08	-0.004	0.010	7.10E-01	
rs10493891	16	81510742	T	C	0.268	-0.032	0.006	2.05E-08	-0.018	0.007	1.40E-02	
rs1051338	10	91007360	T	G	0.689	-0.059	0.005	1.40E-28	0.011	0.007	1.20E-01	C-reactive protein levels Estimated glomerular filtration rate, Systemic lupus erythematosus, Retinal vascular caliber, Left ventricle diastolic internal dimension, Asthma (childhood onset), Glycated hemoglobin levels, Asthma (age of onset), Hypothyroidism
rs10774625	12	111910219	A	G	0.460	0.057	0.005	1.47E-28	0.023	0.007	8.00E-04	
rs10790800	11	126262638	A	G	0.675	0.030	0.005	9.12E-09	-0.004	0.007	5.30E-01	
rs10811183	9	19436055	A	G	0.171	0.037	0.007	1.60E-08	-0.002	0.009	8.10E-01	
rs10841443	12	20220033	C	G	0.328	-0.040	0.005	3.85E-14	0.010	0.007	1.70E-01	
rs10857147	4	81181072	A	T	0.707	-0.041	0.005	5.13E-14	-0.009	0.007	2.20E-01	Hypertension, Mean arterial pressure, Creatinine levels, Pulse pressure, Medication use (diuretics), Systolic blood pressure, Medication use (calcium channel blockers), Diastolic blood pressure, Red blood cell count, Serum uric acid levels
rs10928241	2	145831428	T	C	0.292	0.041	0.005	1.85E-14	-0.020	0.007	4.00E-03	
rs10930115	2	164930382	A	T	0.793	0.040	0.006	5.07E-11	-0.014	0.008	8.00E-02	
rs10951983	7	6446027	A	G	0.782	0.040	0.006	1.22E-10	0.020	0.008	9.60E-03	
rs10961206	9	13724051	A	T	0.904	0.052	0.008	8.10E-10	-0.004	0.011	7.30E-01	
rs11079536	17	62392403	T	G	0.540	0.035	0.005	1.01E-12	0.012	0.006	5.80E-02	C-reactive protein levels, Blood protein levels, Post bronchodilator FEV1/FVC ratio, Post bronchodilator FEV1, Autism spectrum disorder
rs11080107	17	27938424	T	C	0.512	-0.034	0.005	5.84E-12	-0.025	0.006	1.30E-04	
rs11107903	12	95507971	A	G	0.075	-0.083	0.010	5.29E-18	-0.026	0.012	3.40E-02	
rs11206803	1	56877509	T	C	0.471	0.037	0.005	7.01E-14	0.007	0.006	2.40E-01	
rs112238647	15	79051705	T	C	0.060	-0.069	0.011	1.07E-09	-0.038	0.014	6.10E-03	
rs112635299	14	94838142	T	G	0.017	-0.139	0.022	1.98E-10	-0.110	0.024	1.00E-05	Height
rs112949822	5	108085190	A	G	0.083	-0.055	0.009	1.14E-09	0.002	0.011	8.80E-01	
rs1132274	20	17596155	A	C	0.168	0.037	0.007	1.80E-08	-0.007	0.009	4.30E-01	
rs114192718	2	128785663	T	C	0.077	0.054	0.010	2.58E-08	0.004	0.012	7.40E-01	
rs11466359	19	41837615	A	G	0.162	-0.055	0.007	5.47E-16	-0.013	0.009	1.30E-01	
rs11523031	9	21843842	A	G	0.556	0.045	0.005	3.55E-19	0.000	0.006	9.50E-01	Red cell distribution width, Medication use (calcium channel blockers), Medication use (agents acting on the renin-angiotensin system), Systolic blood pressure, Menarche (age at onset), Platelet count, White blood cell count (basophil), Cardiovascular disease, Plateletcrit, Diastolic blood pressure, Height
rs11556924	7	129663496	T	C	0.355	-0.050	0.005	3.78E-21	-0.014	0.007	2.80E-02	

rs11585169	1	150572037	A	T	0.553	0.038	0.005	1.04E-14	0.022	0.006	5.10E-04	Pulse pressure
Low density lipoprotein cholesterol levels, LDL cholesterol levels x alcohol consumption (drinkers vs non-drinkers) interaction (2df), Total cholesterol levels, Response to statins (LDL cholesterol change), Metabolite levels (lipoprotein measures), Osteoarthritis of the knee (with total joint replacement), Plasma proprotein convertase subtilisin/kexin type 9 levels in stable coronary artery disease, Medication use (HMG CoA reductase inhibitors), LDL cholesterol levels x alcohol consumption (regular vs non-regular drinkers) interaction (2df), Cardiovascular disease, Cholesterol, total, LDL cholesterol x physical activity interaction (2df test)												
rs11591147	1	55505647	T	G	0.015	-0.251	0.023	1.32E-28	0.036	0.026	1.60E-01	
rs11601507	11	5701074	A	C	0.075	0.062	0.009	4.40E-11	0.014	0.013	2.60E-01	Low density lipoprotein cholesterol levels, Mean platelet volume
rs11617955	13	110818102	A	T	0.116	-0.078	0.008	1.19E-22	-0.014	0.010	1.60E-01	
rs11619113	13	110918660	C	G	0.875	-0.067	0.007	2.22E-19	-0.002	0.010	8.60E-01	
rs11655024	17	59232365	T	C	0.198	0.045	0.006	3.92E-12	0.022	0.008	6.90E-03	Glomerular filtration rate, Creatinine levels
rs11663411	18	56960510	T	C	0.712	-0.030	0.005	2.60E-08	-0.005	0.007	4.90E-01	
Triglyceride levels x alcohol consumption (regular vs non-regular drinkers) interaction (2df), Triglyceride levels, High density lipoprotein cholesterol levels, HDL cholesterol levels x alcohol consumption (drinkers vs non-drinkers) interaction (2df), Waist-to-hip ratio adjusted for BMI (additive genetic model), HDL cholesterol levels x alcohol consumption (regular vs non-regular drinkers) interaction (2df), Red cell distribution width, Total cholesterol levels in HDL, Triglyceride levels x alcohol consumption (drinkers vs non-drinkers) interaction (2df), Metabolite levels (lipoprotein measures), Phospholipid levels in large HDL												
rs116843064	19	8429323	A	G	0.022	-0.177	0.019	3.56E-21	-0.099	0.024	2.30E-05	
rs11752218	6	57145562	T	C	0.067	0.075	0.010	4.01E-14	0.006	0.013	6.40E-01	
rs1177562	11	118949331	T	C	0.398	0.033	0.005	7.60E-11	0.028	0.007	1.90E-05	
rs12112877	7	106941324	T	C	0.713	-0.035	0.006	3.72E-10	0.019	0.007	7.30E-03	
rs1230666	1	114173410	A	G	0.152	0.052	0.007	5.10E-13	0.021	0.009	1.90E-02	Gut microbiota (bacterial taxa), Breast cancer, Thyroid peroxidase antibody levels
rs12445401	16	72148419	A	G	0.800	-0.036	0.006	9.49E-09	-0.030	0.008	2.10E-04	
rs12446515	16	56987015	T	C	0.315	-0.037	0.005	9.75E-12	0.000	0.007	9.90E-01	Total cholesterol levels
rs12484557	22	24555861	A	G	0.938	0.060	0.010	4.01E-09	0.022	0.013	1.00E-01	
rs12500824	4	77416627	A	G	0.355	0.030	0.005	3.15E-09	-0.011	0.007	1.00E-01	Alanine transaminase levels
rs1250247	2	216299629	C	G	0.290	0.048	0.006	2.37E-18	0.011	0.007	1.20E-01	Pulse pressure, Systolic blood pressure
rs12691049	16	15909513	A	C	0.419	-0.030	0.005	2.54E-09	-0.003	0.007	6.60E-01	
Medication use (HMG CoA reductase inhibitors), Low density lipoprotein cholesterol levels, Total cholesterol levels, Lipoprotein phospholipase A2 activity in cardiovascular disease, Height, Lipoprotein-associated phospholipase A2 activity and mass, Blood protein levels, Medication use (antithrombotic agents), High density lipoprotein cholesterol levels, Cardiovascular disease												
rs12740374	1	109817590	T	G	0.216	-0.095	0.006	1.36E-57	0.023	0.008	2.50E-03	Low density lipoprotein cholesterol levels, Total cholesterol levels, Cardiovascular disease, Medication use (HMG CoA reductase inhibitors), LDL cholesterol x physical activity interaction (2df test)
rs12916	5	74656539	T	C	0.593	-0.028	0.005	1.31E-08	0.032	0.007	4.10E-06	
rs12965923	18	47213682	A	G	0.231	0.039	0.006	5.62E-11	-0.002	0.008	8.30E-01	
rs13120678	4	148273397	A	G	0.750	0.046	0.006	3.53E-15	0.009	0.008	2.70E-01	
rs13124853	4	146784774	A	G	0.531	0.029	0.005	3.14E-09	0.005	0.006	4.70E-01	
rs13169691	5	118448279	T	C	0.151	0.040	0.007	2.58E-08	-0.005	0.009	5.60E-01	
rs13222797	7	117100046	T	G	0.581	-0.031	0.005	5.51E-10	0.022	0.006	6.70E-04	
rs139012	22	43623972	A	G	0.271	-0.032	0.006	2.13E-08	-0.015	0.007	3.40E-02	
rs148812085	2	203877233	T	C	0.121	0.114	0.008	5.11E-50	-0.024	0.010	1.50E-02	
rs149487184	21	35605863	T	C	0.024	0.096	0.018	4.11E-08	0.070	0.022	2.00E-03	Systolic blood pressure
rs1510758	8	25061807	A	G	0.745	0.032	0.006	3.09E-08	0.006	0.008	4.00E-01	

rs167479	19	11526765	T	G	0.471	-0.035	0.005	5.63E-11	0.000	0.007	1.00E+00	Systolic blood pressure, Diastolic blood pressure, Medication use (calcium channel blockers), Pulse pressure, Medication use (beta blocking agents), Hypertension, Medication use (agents acting on the renin-angiotensin system), Mean arterial pressure, Medication use (diuretics), Cardiovascular disease
rs16986953	2	19942473	A	G	0.084	0.082	0.009	7.11E-20	0.003	0.013	8.40E-01	Systolic blood pressure, Diastolic blood pressure
rs17080093	6	150997440	T	C	0.078	-0.051	0.009	2.39E-08	-0.001	0.012	9.50E-01	
rs17083333	4	54572066	T	G	0.312	-0.030	0.005	1.23E-08	-0.008	0.006	2.10E-01	
rs17086617	13	28962686	T	C	0.689	-0.040	0.005	1.02E-13	-0.011	0.007	1.00E-01	
rs17163363	1	222828704	T	C	0.695	0.069	0.006	4.87E-36	0.007	0.007	3.10E-01	
rs17263917	5	9552338	A	G	0.150	-0.056	0.007	1.45E-15	0.001	0.009	8.90E-01	
rs17406518	20	33799176	A	C	0.894	0.047	0.008	2.98E-09	-0.010	0.010	3.40E-01	
rs17566555	10	12275947	A	G	0.497	-0.032	0.005	4.33E-11	-0.032	0.006	4.10E-07	
rs17581137	15	96146414	A	C	0.752	0.033	0.006	8.32E-09	-0.004	0.007	6.30E-01	Systolic blood pressure, Mean arterial pressure, Blood pressure, QRS duration, Pulse pressure, Cardiovascular disease, Medication use (calcium channel blockers), Aortic root size, QRS complex (Cornell)
rs17608766	17	45013271	T	C	0.869	-0.044	0.007	1.69E-09	-0.011	0.009	2.50E-01	
rs17680741	10	82251514	T	C	0.705	0.034	0.005	2.27E-10	-0.012	0.007	7.90E-02	
rs17843797	3	124453022	T	G	0.877	-0.059	0.008	1.50E-14	0.015	0.010	1.10E-01	
rs1800469	19	41860296	A	G	0.311	0.042	0.005	4.19E-15	-0.008	0.007	2.60E-01	Colorectal cancer, Blood protein levels
rs1807214	15	89565257	A	C	0.898	0.064	0.009	2.35E-13	-0.023	0.012	4.90E-02	
rs184278183	6	161177756	T	C	0.008	0.368	0.031	2.47E-33	0.031	0.037	4.10E-01	Lipoprotein (a) levels
rs185244	3	138092889	T	C	0.162	0.060	0.007	3.22E-19	0.031	0.008	1.30E-04	
rs186696265	6	161111700	T	C	0.014	0.517	0.023	8.54E-116	0.023	0.028	4.10E-01	Lipoprotein phospholipase A2 activity in cardiovascular disease, Low density lipoprotein cholesterol levels, Lipoprotein(a) levels adjusted for apolipoprotein(a) isoforms, Total cholesterol levels, Lipoprotein (a) levels, Parental longevity (combined parental attained age, Martingale residuals)
rs1870634	10	44480811	T	G	0.345	-0.052	0.005	5.24E-24	-0.005	0.007	5.00E-01	Red cell distribution width
rs1892971	11	102795606	A	G	0.223	-0.039	0.006	5.14E-10	-0.001	0.008	9.30E-01	
rs192425087	6	161032250	T	C	0.990	-0.348	0.048	7.15E-13	0.086	0.075	2.50E-01	
rs1967604	9	110530324	A	G	0.282	0.045	0.006	4.64E-16	0.003	0.007	6.80E-01	
rs1998043	6	161097871	A	G	0.835	-0.062	0.007	1.46E-20	0.022	0.009	1.30E-02	
rs2001846	8	126478450	T	C	0.473	0.047	0.005	6.02E-22	-0.003	0.006	6.20E-01	
rs2008614	20	47433150	T	C	0.861	0.043	0.007	1.46E-09	0.012	0.009	2.00E-01	
rs2067831	10	105643223	C	G	0.271	0.042	0.005	2.61E-14	-0.014	0.007	5.00E-02	
rs2107595	7	19049388	A	G	0.176	0.065	0.006	3.61E-24	-0.011	0.009	1.90E-01	Stroke, Moyamoya disease, Systolic blood pressure, Ischemic stroke, Pulse pressure, Medication use (agents acting on the renin-angiotensin system), Large artery stroke
rs2107732	7	45077978	A	G	0.092	-0.049	0.009	1.53E-08	-0.026	0.011	1.70E-02	
rs2161967	2	218680529	T	G	0.439	0.033	0.005	6.89E-11	0.004	0.006	4.90E-01	
rs2207132	20	39142516	A	G	0.036	0.092	0.015	6.65E-10	0.017	0.018	3.40E-01	Total cholesterol levels, Medication use (HMG CoA reductase inhibitors), Low density lipoprotein cholesterol levels, Triglycerides
rs2215614	7	35277093	A	C	0.622	0.034	0.005	2.96E-11	-0.008	0.007	2.10E-01	
rs2244608	12	121416988	A	G	0.669	-0.048	0.005	2.35E-20	-0.046	0.007	2.00E-11	LDL cholesterol levels x alcohol consumption (regular vs non-regular drinkers) interaction (2df), HDL cholesterol levels x alcohol consumption (drinkers vs non-drinkers) interaction (2df), LDL cholesterol levels, HDL cholesterol levels, Total cholesterol levels, Urate levels, HDL cholesterol levels x alcohol consumption (regular vs non-regular drinkers) interaction (2df)
rs2306363	11	65405600	T	G	0.205	-0.041	0.006	1.46E-11	-0.040	0.008	3.80E-07	Diastolic blood pressure x alcohol consumption interaction (2df test), Pulse pressure, HDL cholesterol, Diastolic blood pressure x alcohol consumption (light vs heavy) interaction (2df test), Medication use (agents acting on the renin-angiotensin system),

Systolic blood pressure, Mean arterial pressure x alcohol consumption interaction (2df test), Systolic blood pressure x alcohol consumption (light vs heavy) interaction (2df test), Systolic blood pressure x alcohol consumption interaction (2df test), Diastolic blood pressure, Mean arterial pressure x alcohol consumption (light vs heavy) interaction (2df test)											
rs2327426	6	134202690	T	C	0.698	0.061	0.005	4.47E-30	-0.007	0.007	3.20E-01
rs2410859	17	73841285	T	C	0.670	0.031	0.005	4.32E-09	0.011	0.007	1.20E-01
rs243071	2	60619028	A	G	0.446	0.029	0.005	2.65E-08	0.018	0.006	4.50E-03
rs2457480	10	44740010	A	G	0.902	0.104	0.012	2.98E-17	0.004	0.021	8.30E-01
rs2492304	6	134378151	A	T	0.489	0.035	0.005	1.06E-12	-0.006	0.006	3.30E-01
rs2493298	1	3325912	A	C	0.140	0.048	0.007	2.10E-11	-0.014	0.010	1.40E-01
rs249760	5	141915692	T	C	0.244	0.032	0.006	4.05E-08	0.007	0.008	3.90E-01
rs2672592	10	124230750	T	G	0.363	-0.032	0.005	2.47E-10	0.001	0.007	9.00E-01
rs268	8	19813529	A	G	0.982	-0.132	0.020	4.10E-11	-0.031	0.024	2.00E-01
Medication use (agents acting on the renin-angiotensin system)											
Medication use (HMG CoA reductase inhibitors), Metabolic syndrome, Triglycerides, HDL cholesterol											
rs2681472	12	90008959	A	G	0.816	-0.055	0.006	2.46E-18	-0.008	0.009	3.50E-01
Diastolic blood pressure, Mean arterial pressure, Pulse pressure, Systolic blood pressure, Hypertension											
rs2683260	15	81385552	T	G	0.185	0.041	0.006	2.63E-10	-0.001	0.009	9.20E-01
rs283485	2	233645691	A	G	0.343	0.034	0.005	1.01E-10	0.021	0.007	2.30E-03
rs2839812	11	103673294	A	T	0.705	-0.065	0.005	1.90E-33	-0.012	0.007	8.90E-02
rs2843152	1	2245570	C	G	0.280	0.042	0.006	7.26E-13	0.011	0.008	1.70E-01
rs28451064	21	35593827	A	G	0.129	0.109	0.008	1.64E-46	-0.021	0.010	3.10E-02
Pulse pressure, Heel bone mineral density, Waist-hip ratio											
rs2891168	9	22098619	A	G	0.516	-0.174	0.005	1.00E-200	-0.028	0.006	8.70E-06
Medication use (beta blocking agents)											
rs2909217	17	66463985	T	C	0.790	0.036	0.006	3.83E-09	-0.009	0.008	2.90E-01
rs2983896	6	97029871	A	G	0.220	-0.036	0.006	1.44E-09	0.007	0.008	3.60E-01
rs34232196	1	55489542	T	C	0.240	-0.053	0.006	6.59E-20	-0.006	0.007	4.50E-01
rs34330586	3	135800409	A	T	0.771	0.047	0.006	3.50E-15	0.035	0.008	4.20E-06
rs34606058	12	115353368	T	C	0.626	-0.029	0.005	7.69E-09	-0.001	0.007	9.10E-01
rs34759087	3	49162284	T	C	0.113	-0.053	0.008	6.23E-11	-0.031	0.010	1.90E-03
Experiencing mood swings											
rs34917849	8	95278307	C	G	0.128	0.042	0.007	1.11E-08	0.022	0.010	2.10E-02
rs34991912	3	14926351	T	C	0.433	0.034	0.005	7.29E-12	0.022	0.006	6.70E-04
Systolic blood pressure											
rs35611688	2	148377860	T	C	0.660	-0.030	0.005	1.54E-08	0.016	0.007	1.90E-02
rs357494	3	153937753	A	G	0.869	0.057	0.008	4.91E-14	0.032	0.009	4.70E-04
rs360153	11	9762274	T	C	0.419	-0.038	0.005	2.98E-14	0.010	0.007	1.20E-01
Diastolic blood pressure											
rs36033161	14	100123487	T	C	0.828	0.068	0.007	1.34E-24	0.006	0.009	4.60E-01
rs3776307	5	142494165	A	G	0.549	-0.036	0.005	6.70E-12	-0.009	0.006	1.90E-01
rs3783113	13	110834746	T	C	0.358	0.040	0.005	6.53E-15	0.002	0.007	7.60E-01
rs3796587	4	156638073	C	G	0.813	0.064	0.006	6.04E-23	0.014	0.008	8.20E-02
Medication use (calcium channel blockers), Systolic blood pressure x alcohol consumption interaction (2df test), Systolic blood pressure, Diastolic blood pressure, Height, Cardiovascular disease, Medication use (beta blocking agents), Eczema, Medication use (HMG CoA reductase inhibitors), Diastolic blood pressure x alcohol consumption interaction (2df test), Medication use (agents acting on the renin-angiotensin system), Medication use (diuretics)											
rs3918226	7	150690176	T	C	0.081	0.112	0.009	4.60E-32	0.014	0.012	2.30E-01
Waist-to-hip ratio adjusted for BMI x sex x age interaction (4df test), Waist circumference adjusted for body mass index, Waist-to-hip ratio adjusted for body mass index											
rs3936510	5	55860866	T	G	0.187	0.046	0.006	2.60E-13	0.068	0.008	1.10E-16
Gamma glutamyl transferase levels, Heel bone mineral density, Liver enzyme levels (gamma-glutamyl transferase)											
rs4074793	5	52193125	A	G	0.923	-0.053	0.009	1.61E-08	-0.046	0.012	1.10E-04

rs4140748	2	230005505	A	G	0.602	0.031	0.005	1.25E-09	-0.007	0.007	3.00E-01	Gallstone disease, Low density lipoprotein cholesterol levels, Total cholesterol levels, Phytosterol levels
rs4245791	2	44074431	T	C	0.689	-0.049	0.005	1.01E-19	0.004	0.007	6.00E-01	
rs4266144	3	156852592	C	G	0.685	-0.031	0.005	5.60E-09	-0.001	0.007	9.00E-01	
rs429358	19	45411941	T	C	0.848	-0.091	0.007	3.73E-38	0.080	0.009	1.80E-18	Low density lipoprotein cholesterol levels, Cerebrospinal fluid AB1-42 levels, Waist-hip ratio, Parental longevity (mother's attained age), Cognitive decline (age-related), Alzheimer's disease biomarkers, Platelet count, Cerebrospinal fluid p-tau levels in mild cognitive impairment, Alzheimer's disease, C-reactive protein levels, Blood protein levels, Alzheimer's disease progression score, Vigorous physical activity, Cerebral amyloid deposition (PET imaging), Total cholesterol levels, Parental longevity (father's attained age), Cerebrospinal fluid t-tau levels in mild cognitive impairment, Triglycerides, Parental lifespan, High density lipoprotein cholesterol levels, Mortality, Red cell distribution width, Insomnia, Parkinson's disease (age of onset), Hippocampal volume, Logical memory (immediate recall), Neurofibrillary tangles or cerebral amyloid angiopathy (pleiotropy), Lewy body disease, Parental longevity (both parents in top 10%), Cerebrospinal fluid p-tau levels, Cerebrospinal AB1-42 levels in Alzheimer's disease dementia, Cerebral amyloid deposition positivity (PET imaging), Brain imaging, Parental longevity (combined parental age at death), Advanced age-related macular degeneration, Dementia with Lewy bodies, Logical memory (delayed recall), Neuritic plaques or neurofibrillary tangles (pleiotropy), Cerebrospinal AB1-42 levels in normal cognition, Cerebrospinal AB1-42 levels in mild cognitive impairment, Cerebrospinal fluid t-tau levels, Moderate to vigorous physical activity levels, Cortical amyloid beta load, Parental longevity (father's age at death), Parental longevity (mother's age at death), Neuritic plaques or cerebral amyloid angiopathy (pleiotropy), Parental longevity (combined parental attained age, Martingale residuals)
rs4345341	5	121278751	A	T	0.182	0.038	0.006	3.87E-09	0.007	0.008	4.20E-01	Insomnia
rs4537761	11	9323353	T	C	0.913	-0.055	0.009	1.75E-09	-0.016	0.012	2.00E-01	
rs4643373	17	47123423	T	C	0.720	0.038	0.006	4.49E-12	0.047	0.007	1.90E-11	
rs4646249	8	18260431	T	G	0.295	0.035	0.006	8.18E-10	0.020	0.007	4.90E-03	Obesity (early onset extreme)
rs4662330	2	144186475	T	C	0.839	0.046	0.007	7.30E-12	-0.008	0.009	3.70E-01	
rs472495	1	55521313	T	G	0.633	0.038	0.005	3.71E-13	-0.008	0.007	2.30E-01	
rs476828	18	57852587	T	C	0.745	-0.033	0.006	1.43E-08	-0.054	0.007	3.80E-13	Femoral neck bone mineral density, Intraocular pressure
rs4773141	13	110954353	C	G	0.638	-0.047	0.005	3.12E-18	-0.006	0.007	3.80E-01	
rs4790881	17	2068932	A	C	0.696	0.048	0.005	1.29E-19	-0.002	0.007	8.20E-01	
rs4907571	13	113618496	T	C	0.713	-0.036	0.006	2.79E-08	-0.005	0.007	5.30E-01	Low density lipoprotein cholesterol levels, Total cholesterol levels, Carotid intima media thickness
rs4938809	11	120363937	T	C	0.666	-0.029	0.005	4.59E-08	-0.005	0.007	4.80E-01	
rs494207	10	44741256	A	G	0.131	-0.076	0.007	9.94E-25	-0.007	0.010	5.20E-01	
rs515135	2	21286057	T	C	0.185	-0.058	0.006	3.58E-19	0.017	0.008	3.70E-02	Allergic disease (asthma, hay fever or eczema), Thyroid cancer, Asthma or allergic disease (pleiotropy), Asthma
rs55753709	10	96029170	T	C	0.664	-0.038	0.005	2.18E-13	0.000	0.007	9.90E-01	
rs55997232	19	11188117	T	C	0.107	-0.114	0.008	2.33E-44	0.026	0.010	1.10E-02	
rs56062135	15	67455630	T	C	0.225	-0.058	0.006	2.27E-22	-0.027	0.007	2.90E-04	
rs56170783	1	57016131	A	C	0.915	0.115	0.009	1.733E-38	0.005	0.011	6.70E-01	
rs56195640	6	160720747	A	G	0.117	0.091	0.014	2.584E-10	0.002	0.043	9.60E-01	
rs56408342	8	22048490	A	G	0.058	0.079	0.011	2.3E-12	-0.041	0.014	3.30E-03	
rs582384	2	45896437	A	C	0.534	0.028	0.005	1.552E-08	0.007	0.006	3.10E-01	
rs584961	11	75277628	A	G	0.115	-0.062	0.008	1.499E-14	-0.003	0.010	7.50E-01	

rs588136	15	58730498	T	C	0.781	-0.037	0.006	6.974E-10	0.004	0.008	5.80E-01	Lipid traits, Blood metabolite levels, Triglyceride levels Heel bone mineral density
rs6006426	22	30669883	A	G	0.556	0.034	0.005	9.895E-12	0.007	0.006	2.70E-01	
rs60154123	1	210468999	T	C	0.153	0.039	0.007	1.6E-08	0.013	0.009	1.30E-01	
rs6026739	20	57739469	A	T	0.874	-0.048	0.007	1.119E-10	-0.009	0.010	3.80E-01	Medication use (agents acting on the renin-angiotensin system), Systolic blood pressure
rs6088595	20	33358499	A	T	0.364	0.033	0.005	9.892E-11	0.021	0.007	1.10E-03	
rs6102343	20	39924279	A	G	0.235	0.034	0.006	5.179E-09	0.019	0.008	1.40E-02	Height, Colorectal cancer
rs61776719	1	38461319	A	C	0.540	0.036	0.005	5.739E-12	-0.005	0.007	4.30E-01	
rs61797068	1	115902514	C	G	0.158	-0.040	0.007	4.276E-09	0.006	0.009	5.30E-01	
rs61806987	1	169314833	A	G	0.576	0.035	0.005	6.845E-12	0.005	0.006	4.20E-01	
rs62362364	5	55441571	C	G	0.208	-0.038	0.006	2.943E-09	0.006	0.008	4.60E-01	Mean arterial pressure, Diastolic blood pressure, Pulse pressure, Systolic blood pressure, Medication use (calcium channel blockers), Mean arterial pressure x alcohol consumption (light vs heavy) interaction (2df test), Blood pressure, Hypertension, Systolic blood pressure x alcohol consumption interaction (2df test), Chronic obstructive pulmonary disease or high blood pressure (pleiotropy), Parental longevity (combined parental attained age, Martingale residuals)
rs633185	11	100593538	C	G	0.701	0.039	0.005	5.567E-13	0.012	0.007	1.00E-01	
rs6475608	9	22101702	T	C	0.397	-0.090	0.007	1.069E-41	-0.023	0.008	3.80E-03	
rs651007	9	136153875	T	C	0.206	0.054	0.006	1.282E-18	0.043	0.008	4.60E-08	Blood protein levels, Serum alkaline phosphatase levels, Total cholesterol levels, Fasting blood glucose, Blood metabolite levels, Iron status biomarkers (ferritin levels), Serum metabolite levels, Hematocrit, Metabolite levels, Low density lipoprotein cholesterol levels, E-selectin levels, End-stage coagulation
rs66778572	8	19916120	A	G	0.282	-0.039	0.006	1.331E-12	-0.033	0.007	2.10E-06	
rs6686750	1	154419843	A	G	0.425	0.039	0.005	1.87E-15	0.011	0.006	7.40E-02	Height
rs6740731	2	145270592	A	G	0.171	0.043	0.007	1.674E-10	0.025	0.009	4.80E-03	
rs67807996	1	149995265	A	G	0.380	0.040	0.006	1.135E-12	0.009	0.007	2.10E-01	
rs6841581	4	148401190	A	G	0.148	0.078	0.007	2.653E-30	0.019	0.009	4.50E-02	
rs6883598	5	127926190	A	C	0.735	-0.034	0.006	9.742E-10	0.005	0.007	4.90E-01	Waist-to-hip ratio adjusted for body mass index, Waist-hip ratio, Systolic blood pressure, Cardiovascular disease, HDL cholesterol levels, Triglyceride levels
rs6905288	6	43758873	A	G	0.571	0.037	0.005	5.022E-13	0.040	0.007	6.60E-10	
rs6909752	6	22612629	A	G	0.347	0.035	0.005	1.669E-11	0.003	0.007	6.20E-01	
rs6919211	6	133999868	C	G	0.816	-0.036	0.006	1.001E-08	-0.017	0.008	3.70E-02	
rs6932293	6	160535878	T	C	0.973	-0.262	0.020	1.727E-37	-0.021	0.027	4.30E-01	Central corneal thickness, Medication use (calcium channel blockers)
rs7118294	11	32380521	T	C	0.493	-0.033	0.005	1.799E-11	-0.012	0.006	6.70E-02	
rs71313931	22	19960184	C	G	0.705	-0.032	0.005	2.302E-09	-0.021	0.007	2.90E-03	
rs7133378	12	124409502	A	G	0.317	-0.031	0.005	3.961E-09	-0.034	0.007	8.50E-07	Body mass index, Body fat percentage, Waist-to-hip ratio adjusted for body mass index, Waist-hip ratio, Reticulocyte count
rs71646019	1	59433354	T	C	0.208	0.038	0.006	6.053E-10	-0.014	0.008	8.30E-02	
rs7173743	15	79141784	T	C	0.554	0.069	0.005	3.257E-44	0.000	0.006	9.80E-01	Insomnia, Medication use (beta blocking agents)
rs7183988	15	91428589	T	G	0.468	0.060	0.005	2.689E-33	0.004	0.007	5.80E-01	
rs7189462	16	81907867	T	G	0.403	0.029	0.005	7.762E-09	-0.011	0.007	8.10E-02	
rs7246865	19	17219105	A	G	0.274	0.033	0.006	1.915E-08	0.009	0.007	2.10E-01	Reticulocyte fraction of red cells, Systolic blood pressure, Medication use (agents acting on the renin-angiotensin system), Cardiovascular disease, Waist-hip ratio
rs72658867	19	11231203	A	G	0.016	-0.197	0.026	2.798E-14	0.009	0.030	7.60E-01	
rs72836800	6	1617327	T	C	0.873	0.051	0.008	3.111E-11	0.003	0.010	7.20E-01	Lipoprotein (a) levels
rs7296737	12	125336956	T	C	0.398	-0.036	0.005	6.535E-13	-0.009	0.007	1.90E-01	
rs7333991	13	111108436	T	C	0.784	-0.051	0.006	5.08E-17	0.005	0.008	5.10E-01	
rs733701	6	39171862	T	C	0.254	0.043	0.006	2.816E-13	-0.020	0.007	5.50E-03	
rs73596816	6	161017363	A	G	0.034	0.106	0.015	3.563E-13	0.019	0.019	3.20E-01	

rs7412	19	45412079	T	C	0.075	-0.154	0.010	1.039E-54	0.007	0.012	5.50E-01	Blood protein levels, Medication use (salicylic acid and derivatives), Lipoprotein (a) levels, Total cholesterol levels, Immature fraction of reticulocytes, Metabolite levels (lipoprotein measures), Medication use (agents acting on the renin-angiotensin system), Medication use (calcium channel blockers), High density lipoprotein cholesterol levels, Carotid intima media thickness, Red cell distribution width, Pulse pressure, Lipoprotein(a) levels adjusted for apolipoprotein(a) isoforms, Low density lipoprotein cholesterol levels, Alzheimer's disease, Lipid traits, Ideal cardiovascular health (clinical and behavioural), Alzheimer's disease or family history of Alzheimer's disease, High light scatter reticulocyte count, Systolic blood pressure, Family history of Alzheimer's disease, Mean corpuscular hemoglobin, Reticulocyte fraction of red cells, Reticulocyte count, Cardiovascular disease, Triglycerides, High light scatter reticulocyte percentage of red cells, Medication use (antithrombotic agents), Alzheimer's disease (late onset), Lipid metabolism phenotypes, Cardiovascular risk factors, Lipoprotein-associated phospholipase A2 activity change in response to darapladib treatment in cardiovascular disease, Response to statins (LDL cholesterol change), Medication use (HMG CoA reductase inhibitors), Lipoprotein phospholipase A2 activity in cardiovascular disease, Red blood cell count
rs7440763	4	156433520	T	G	0.874	-0.060	0.008	4.444E-15	0.006	0.010	5.60E-01	Low density lipoprotein cholesterol levels, High density lipoprotein cholesterol levels, Total cholesterol levels
rs7485656	12	125315647	A	G	0.835	-0.066	0.007	2.655E-22	-0.006	0.009	5.40E-01	
rs7500448	16	83045790	A	G	0.758	0.050	0.006	1.108E-17	0.000	0.007	9.60E-01	Diastolic blood pressure, Pulse pressure, Systolic blood pressure
rs75160195	12	54521594	T	C	0.053	0.094	0.011	5.311E-17	0.010	0.015	4.90E-01	
rs7678555	4	120909501	A	C	0.712	-0.045	0.005	3.077E-16	-0.008	0.007	2.40E-01	Low density lipoprotein cholesterol levels, Total cholesterol levels
rs76866386	2	44075483	T	C	0.938	0.079	0.010	1.576E-14	0.003	0.013	8.40E-01	
rs76959412	9	22011083	C	G	0.016	-0.127	0.021	2.867E-09	-0.045	0.026	8.60E-02	Red blood cell count
rs77347777	3	52848207	T	C	0.109	-0.051	0.008	1.51E-09	-0.025	0.011	1.60E-02	
rs77787671	10	104776205	T	C	0.094	-0.069	0.009	2.761E-15	-0.004	0.011	7.10E-01	High density lipoprotein cholesterol levels, Triglycerides, Low density lipoprotein cholesterol levels, Heel bone mineral density, Systolic blood pressure, Medication use (HMG CoA reductase inhibitors)
rs78030362	19	18575193	A	G	0.927	-0.093	0.010	1.048E-20	-0.015	0.013	2.30E-01	
rs781663	4	57781754	A	G	0.801	-0.043	0.006	1.074E-11	0.007	0.008	3.70E-01	Heel bone mineral density
rs79018195	6	161024291	T	C	0.991	-0.345	0.058	3.38E-09	-0.440	0.350	2.10E-01	
rs79598313	1	27284913	T	C	0.024	0.095	0.017	3.604E-08	0.080	0.021	1.40E-04	Eczema
rs7991314	13	33126074	T	C	0.641	0.029	0.005	1.788E-08	0.015	0.007	2.70E-02	
rs8000794	13	99434810	C	G	0.459	0.027	0.005	4.316E-08	-0.002	0.006	7.30E-01	Chronic obstructive pulmonary disease or coronary artery disease (pleiotropy)
rs8046696	16	75442143	T	G	0.422	-0.047	0.005	1.641E-20	0.003	0.006	6.20E-01	
rs8068844	17	40571284	T	C	0.656	-0.032	0.005	6.963E-10	-0.038	0.007	1.80E-08	Pulse pressure
rs8108474	19	46301479	T	C	0.350	0.035	0.005	1.124E-11	0.022	0.007	1.30E-03	
rs8124182	20	44608901	A	G	0.156	0.047	0.007	4.461E-12	0.019	0.009	2.80E-02	Pulse pressure
rs869396	4	169688000	A	C	0.480	-0.034	0.005	8.86E-12	0.000	0.006	9.60E-01	
rs884811	10	99923763	C	G	0.557	0.029	0.005	3.085E-09	0.008	0.006	2.10E-01	Pulse pressure
rs885150	9	124420173	T	C	0.731	-0.037	0.006	1.978E-11	0.000	0.007	1.00E+00	
rs894211	8	19865747	T	C	0.265	-0.046	0.006	1.38E-16	-0.032	0.007	6.60E-06	Systolic blood pressure, Pulse pressure, Migraine, Hypertension, Headache, Alcohol consumption (drinks per week), Cervical artery dissection, Migraine without aura, Medication use (antimigraine preparations), Migraine - clinic-based, Diastolic blood pressure, Coronary artery calcification
rs9266631	6	31346898	A	G	0.207	-0.043	0.007	5.917E-11	-0.050	0.008	4.80E-10	
rs9337951	10	30317073	A	G	0.332	0.054	0.005	1.385E-23	0.007	0.007	3.10E-01	
rs9349379	6	12903957	A	G	0.586	-0.114	0.005	4.02E-114	0.001	0.006	8.30E-01	

rs9361867	6	82595959	T	C	0.458	-0.035	0.005	5.107E-12	-0.002	0.006	7.10E-01	Medication use (thyroid preparations), Hand grip strength, Prostate cancer, Prostate cancer (advanced)
rs9469899	6	34793124	A	G	0.358	0.035	0.005	1.472E-11	-0.007	0.007	3.10E-01	
rs9515203	13	111049623	T	C	0.742	0.063	0.006	6.485E-28	-0.016	0.007	2.90E-02	
rs952227	2	227062080	A	G	0.344	-0.037	0.005	1.123E-12	-0.086	0.007	3.00E-37	
rs964184	11	116648917	C	G	0.848	-0.058	0.007	4.409E-17	-0.022	0.009	1.60E-02	Triglycerides, Mean corpuscular hemoglobin concentration, Mean platelet volume, Phospholipid levels (plasma), High light scatter reticulocyte count, Eosinophil counts, Medication use (agents acting on the renin-angiotensin system), Age-related diseases, mortality and associated endophenotypes, Red cell distribution width, Reticulocyte fraction of red cells, Medication use (salicylic acid and derivatives), High density lipoprotein cholesterol levels, Very long-chain saturated fatty acid levels (fatty acid 20:0), Blood protein levels, Platelet distribution width, Circulating phylloquinone levels, Reticulocyte count, High light scatter reticulocyte percentage of red cells, Postprandial triglyceride response to high fat diet meal, Lipoprotein-associated phospholipase A2 activity and mass, Metabolic syndrome, Total cholesterol levels, Cardiovascular disease, Medication use (antithrombotic agents), Cholesterol efflux capacity (ABCA-1 dependent assay), Hypertriglyceridemia, Response to Vitamin E supplementation, Age-related disease endophenotypes, Metabolite levels (lipoprotein measures), Low density lipoprotein cholesterol levels, Triglycerides x physical activity interaction (2df test), Very low density lipoprotein cholesterol levels, Metabolite levels, Medication use (HMG CoA reductase inhibitors), Vitamin E levels, Blood metabolite levels
rs9945890	18	46515916	T	G	0.642	0.035	0.005	2.53E-11	0.012	0.007	8.00E-02	
rs9951447	18	20009691	T	C	0.586	-0.032	0.005	3.501E-10	-0.007	0.007	2.80E-01	
rs7413494	1	2985885	C	G	0.612	-0.035	0.006	1.013E-09				
rs34229028	3	172117455	A	A	0.607	-0.034	0.006	3.112E-09				
rs36002015	4	82625720	G	C	0.321	-0.041	0.006	8.196E-13				
rs35510806	6	126678331	T	T	0.519	0.033	0.005	5.134E-10				
rs28867400	6	161104918	A	A	0.009	0.364	0.046	2.699E-15				
rs62435159	7	1911281	A	G	0.236	-0.038	0.007	2.461E-08				
rs756142636	7	139760540	T	T	0.217	-0.036	0.007	3.807E-08				
rs41312891	9	123726749	G	C	0.066	-0.062	0.011	5.873E-09				

rs11316597	11	13295751	A	AT	0.692	0.034	0.006	7.732E-09
				T				
rs72447384	12	7178440	T	AT	0.123	-0.056	0.008	2.452E-11
				TT				
				A				
rs7177201	15	79065380	T	C	0.290	0.075	0.006	3.418E-32
rs12936927	17	17726965	T	C	0.604	-0.035	0.006	2.917E-10
rs12952244	17	40270081	A	G	0.869	-0.053	0.008	1.839E-10
				G				
rs5820757	17	47417942	G	A	0.551	-0.047	0.006	7.301E-17
				G				
				TT				
				AT				
rs768453105	19	41790086	G	G	0.170	0.068	0.007	7.266E-21
				G				
				T				
				A				
rs183657985	19	45742498	T	C	0.253	0.040	0.006	2.077E-10
rs5760309	22	24677831	T	G	0.026	-0.103	0.017	3.486E-09

SNP, single nucleotide polymorphisms; CHR, chromosome; BP, physical position of SNP (base-pairs); A1, effect allele; A2, non-effect allele; EAF: effect allele frequency; Beta, effect allele beta coefficient.

Supplementary Table 4. Characteristics of genetic instruments of coronary artery disease and their effect sizes with type 2 diabetes mellitus adjusted for BMI.

SNP	CHR	BP	A1	A2	EAF	Exposure			Outcome			Pleiotropic traits
						Beta	SE	P-value	Beta	SE	P-value	
rs10131894	14	75446879	C	G	0.441	-0.036	0.005	7.59E-13	-0.013	0.008	9.50E-02	Mean corpuscular hemoglobin
rs10176176	2	85762048	A	T	0.519	-0.057	0.005	4.27E-31	0.024	0.008	1.30E-03	
rs1034246	6	43068370	T	G	0.263	-0.035	0.006	6.39E-10	-0.013	0.008	1.10E-01	
rs10410487	19	17829608	T	C	0.461	-0.040	0.005	3.34E-15	0.000	0.008	9.60E-01	
rs10422256	19	11216617	A	G	0.500	0.032	0.005	2.88E-10	0.000	0.008	9.80E-01	
rs10455872	6	161010118	A	G	0.932	-0.304	0.010	2.18E-186	-0.026	0.015	7.30E-02	Aortic-valve calcification, Parental longevity (mother's age at death), Total cholesterol levels, Lipoprotein phospholipase A2 activity in cardiovascular disease, Parental longevity (both parents in top 10%), Metabolite levels (lipoprotein measures), Response to statins (LDL cholesterol change), Low density lipoprotein cholesterol levels, Lp (a) levels, Response to statin therapy, Aortic valve stenosis, Lipoprotein-associated phospholipase A2 activity change in response to statin therapy, Parental longevity (father's age at death)
rs10477741	5	131795310	T	G	0.867	-0.048	0.007	3.49E-11	-0.023	0.011	4.30E-02	
rs10486389	7	20300416	A	G	0.719	-0.035	0.006	6.51E-10	-0.003	0.009	7.40E-01	
rs10488763	11	110244360	A	T	0.865	-0.041	0.007	1.31E-08	-0.011	0.011	3.30E-01	
rs10493891	16	81510742	T	C	0.268	-0.032	0.006	2.05E-08	-0.011	0.008	1.80E-01	
rs1051338	10	91007360	T	G	0.689	-0.059	0.005	1.40E-28	0.011	0.008	1.80E-01	C-reactive protein levels Estimated glomerular filtration rate, Systemic lupus erythematosus, Retinal vascular caliber, Left ventricle diastolic internal dimension, Asthma (childhood onset), Glycated hemoglobin levels, Asthma (age of onset), Hypothyroidism
rs10774625	12	111910219	A	G	0.460	0.057	0.005	1.47E-28	0.040	0.008	8.30E-08	
rs10790800	11	126262638	A	G	0.675	0.030	0.005	9.12E-09	-0.016	0.008	4.80E-02	
rs10811183	9	19436055	A	G	0.171	0.037	0.007	1.60E-08	0.010	0.010	3.20E-01	
rs10841443	12	20220033	C	G	0.328	-0.040	0.005	3.85E-14	0.013	0.008	1.00E-01	
rs10857147	4	81181072	A	T	0.707	-0.041	0.005	5.13E-14	-0.020	0.008	1.50E-02	Hypertension, Mean arterial pressure, Creatinine levels, Pulse pressure, Medication use (diuretics), Systolic blood pressure, Medication use (calcium channel blockers), Diastolic blood pressure, Red blood cell count, Serum uric acid levels
rs10928241	2	145831428	T	C	0.292	0.041	0.005	1.85E-14	-0.020	0.008	1.50E-02	
rs10930115	2	164930382	A	T	0.793	0.040	0.006	5.07E-11	-0.007	0.009	4.80E-01	
rs10951983	7	6446027	A	G	0.782	0.040	0.006	1.22E-10	0.025	0.009	5.10E-03	
rs10961206	9	13724051	A	T	0.904	0.052	0.008	8.10E-10	-0.007	0.012	6.00E-01	
rs11079536	17	62392403	T	G	0.540	0.035	0.005	1.01E-12	0.010	0.008	2.10E-01	C-reactive protein levels, Blood protein levels, Post bronchodilator FEV1/FVC ratio, Post bronchodilator FEV1, Autism spectrum disorder
rs11080107	17	27938424	T	C	0.512	-0.034	0.005	5.84E-12	-0.014	0.008	6.20E-02	
rs11107903	12	95507971	A	G	0.075	-0.083	0.010	5.29E-18	-0.031	0.015	3.00E-02	
rs11206803	1	56877509	T	C	0.471	0.037	0.005	7.01E-14	0.008	0.008	2.90E-01	
rs11223864	15	79051705	T	C	0.060	-0.069	0.011	1.07E-09	-0.041	0.016	1.10E-02	
rs11263529	14	94838142	T	G	0.017	-0.139	0.022	1.98E-10	-0.100	0.027	2.40E-04	Height
rs11294982	5	108085190	A	G	0.083	-0.055	0.009	1.14E-09	-0.005	0.013	7.40E-01	
rs1132274	20	17596155	A	C	0.168	0.037	0.007	1.80E-08	-0.001	0.010	9.20E-01	

rs114192718	2	128785663	T	C	0.077	0.054	0.010	2.58E-08	0.007	0.015	6.50E-01	Red cell distribution width, Medication use (calcium channel blockers), Medication use (agents acting on the renin-angiotensin system), Systolic blood pressure, Menarche (age at onset), Platelet count, White blood cell count (basophil), Cardiovascular disease, Plateletcrit, Diastolic blood pressure, Height
rs11466359	19	41837615	A	G	0.162	-0.055	0.007	5.47E-16	-0.029	0.010	4.30E-03	
rs11523031	9	21843842	A	G	0.556	0.045	0.005	3.55E-19	0.006	0.008	4.00E-01	
rs11556924	7	129663496	T	C	0.355	-0.050	0.005	3.78E-21	-0.018	0.008	1.70E-02	Pulse pressure Low density lipoprotein cholesterol levels, LDL cholesterol levels x alcohol consumption (drinkers vs non-drinkers) interaction (2df), Total cholesterol levels, Response to statins (LDL cholesterol change), Metabolite levels (lipoprotein measures), Osteoarthritis of the knee (with total joint replacement), Plasma proprotein convertase subtilisin/kexin type 9 levels in stable coronary artery disease, Medication use (HMG CoA reductase inhibitors), LDL cholesterol levels x alcohol consumption (regular vs non-regular drinkers) interaction (2df), Cardiovascular disease, Cholesterol, total, LDL cholesterol x physical activity interaction (2df test)
rs11585169	1	150572037	A	T	0.553	0.038	0.005	1.04E-14	0.014	0.008	6.70E-02	
rs11591147	1	55505647	T	G	0.015	-0.251	0.023	1.32E-28	0.033	0.029	2.50E-01	
rs11601507	11	5701074	A	C	0.075	0.062	0.009	4.40E-11	0.011	0.015	4.60E-01	Low density lipoprotein cholesterol levels, Mean platelet volume
rs11617955	13	110818102	A	T	0.116	-0.078	0.008	1.19E-22	-0.023	0.012	5.10E-02	
rs11619113	13	110918660	C	G	0.875	-0.067	0.007	2.22E-19	-0.013	0.011	2.60E-01	
rs11655024	17	59232365	T	C	0.198	0.045	0.006	3.92E-12	0.027	0.010	5.40E-03	Glomerular filtration rate, Creatinine levels
rs11663411	18	56960510	T	C	0.712	-0.030	0.005	2.60E-08	-0.004	0.008	6.70E-01	
rs116843064	19	8429323	A	G	0.022	-0.177	0.019	3.56E-21	-0.160	0.027	1.10E-08	Triglyceride levels x alcohol consumption (regular vs non-regular drinkers) interaction (2df), Triglyceride levels, High density lipoprotein cholesterol levels, HDL cholesterol levels x alcohol consumption (drinkers vs non-drinkers) interaction (2df), Waist-to-hip ratio adjusted for BMI (additive genetic model), HDL cholesterol levels x alcohol consumption (regular vs non-regular drinkers) interaction (2df), Red cell distribution width, Total cholesterol levels in HDL, Triglyceride levels x alcohol consumption (drinkers vs non-drinkers) interaction (2df), Metabolite levels (lipoprotein measures), Phospholipid levels in large HDL
rs11752218	6	57145562	T	C	0.067	0.075	0.010	4.01E-14	0.026	0.015	6.80E-02	
rs1177562	11	118949331	T	C	0.398	0.033	0.005	7.60E-11	0.022	0.008	4.50E-03	
rs12112877	7	106941324	T	C	0.713	-0.035	0.006	3.72E-10	0.026	0.008	1.40E-03	Gut microbiota (bacterial taxa), Breast cancer, Thyroid peroxidase antibody levels
rs1230666	1	114173410	A	G	0.152	0.052	0.007	5.10E-13	0.011	0.011	2.90E-01	
rs12445401	16	72148419	A	G	0.800	-0.036	0.006	9.49E-09	-0.015	0.009	1.10E-01	Total cholesterol levels
rs12446515	16	56987015	T	C	0.315	-0.037	0.005	9.75E-12	-0.005	0.008	5.20E-01	
rs12484557	22	24555861	A	G	0.938	0.060	0.010	4.01E-09	0.025	0.016	1.10E-01	Alanine transaminase levels
rs12500824	4	77416627	A	G	0.355	0.030	0.005	3.15E-09	-0.009	0.008	2.40E-01	
rs1250247	2	216299629	C	G	0.290	0.048	0.006	2.37E-18	0.014	0.008	8.60E-02	Pulse pressure, Systolic blood pressure
rs12691049	16	15909513	A	C	0.419	-0.030	0.005	2.54E-09	0.002	0.008	8.40E-01	
rs12740374	1	109817590	T	G	0.216	-0.095	0.006	1.36E-57	0.020	0.009	2.70E-02	Medication use (HMG CoA reductase inhibitors), Low density lipoprotein cholesterol levels, Total cholesterol levels, Lipoprotein phospholipase A2 activity in cardiovascular disease, Height, Lipoprotein-associated phospholipase A2 activity and mass, Blood protein levels, Medication use

												(antithrombotic agents), High density lipoprotein cholesterol levels, Cardiovascular disease
rs12916	5	74656539	T	C	0.593	-0.028	0.005	1.31E-08	0.016	0.008	3.40E-02	Low density lipoprotein cholesterol levels, Total cholesterol levels, Cardiovascular disease, Medication use (HMG CoA reductase inhibitors), LDL cholesterol x physical activity interaction (2df test)
rs12965923	18	47213682	A	G	0.231	0.039	0.006	5.62E-11	-0.009	0.009	3.30E-01	
rs13120678	4	148273397	A	G	0.750	0.046	0.006	3.53E-15	0.011	0.009	2.30E-01	
rs13124853	4	146784774	A	G	0.531	0.029	0.005	3.14E-09	0.011	0.008	1.50E-01	
rs13169691	5	118448279	T	C	0.151	0.040	0.007	2.58E-08	-0.003	0.011	7.50E-01	
rs13222797	7	117100046	T	G	0.581	-0.031	0.005	5.51E-10	0.021	0.008	6.50E-03	
rs139012	22	43623972	A	G	0.271	-0.032	0.006	2.13E-08	-0.019	0.008	2.10E-02	
rs14881208 5	2	203877233	T	C	0.121	0.114	0.008	5.11E-50	-0.028	0.011	1.30E-02	
rs14948718 4	21	35605863	T	C	0.024	0.096	0.018	4.11E-08	0.071	0.027	8.20E-03	Systolic blood pressure
rs1510758	8	25061807	A	G	0.745	0.032	0.006	3.09E-08	0.016	0.009	7.30E-02	
rs167479	19	11526765	T	G	0.471	-0.035	0.005	5.63E-11	0.007	0.008	4.00E-01	Systolic blood pressure, Diastolic blood pressure, Medication use (calcium channel blockers), Pulse pressure, Medication use (beta blocking agents), Hypertension, Medication use (agents acting on the renin-angiotensin system), Mean arterial pressure, Medication use (diuretics), Cardiovascular disease
rs16986953	2	19942473	A	G	0.084	0.082	0.009	7.11E-20	0.002	0.015	9.00E-01	
rs17080093	6	150997440	T	C	0.078	-0.051	0.009	2.39E-08	0.012	0.015	4.10E-01	Systolic blood pressure, Diastolic blood pressure
rs17083333	4	54572066	T	G	0.312	-0.030	0.005	1.23E-08	-0.003	0.008	6.80E-01	
rs17086617	13	28962686	T	C	0.689	-0.040	0.005	1.02E-13	-0.027	0.008	7.80E-04	
rs17163363	1	222828704	T	C	0.695	0.069	0.006	4.87E-36	0.018	0.008	3.50E-02	
rs17263917	5	9552338	A	G	0.150	-0.056	0.007	1.45E-15	0.010	0.010	3.10E-01	
rs17406518	20	33799176	A	C	0.894	0.047	0.008	2.98E-09	-0.010	0.012	4.00E-01	
rs17566555	10	12275947	A	G	0.497	-0.032	0.005	4.33E-11	-0.032	0.008	2.50E-05	
rs17581137	15	96146414	A	C	0.752	0.033	0.006	8.32E-09	0.000	0.009	9.80E-01	
rs17608766	17	45013271	T	C	0.869	-0.044	0.007	1.69E-09	-0.011	0.011	3.10E-01	Systolic blood pressure, Mean arterial pressure, Blood pressure, QRS duration, Pulse pressure, Cardiovascular disease, Medication use (calcium channel blockers), Aortic root size, QRS complex (Cornell)
rs17680741	10	82251514	T	C	0.705	0.034	0.005	2.27E-10	-0.026	0.008	1.50E-03	
rs17843797	3	124453022	T	G	0.877	-0.059	0.008	1.50E-14	0.008	0.011	4.60E-01	
rs1800469	19	41860296	A	G	0.311	0.042	0.005	4.19E-15	-0.015	0.008	7.50E-02	Colorectal cancer, Blood protein levels
rs1807214	15	89565257	A	C	0.898	0.064	0.009	2.35E-13	-0.024	0.014	7.40E-02	
rs18427818 3	6	161177756	T	C	0.008	0.368	0.031	2.47E-33	0.022	0.043	6.00E-01	Lipoprotein (a) levels
rs185244	3	138092889	T	C	0.162	0.060	0.007	3.22E-19	0.059	0.010	7.00E-09	
rs18669626 5	6	161111700	T	C	0.014	0.517	0.023	8.54E-116	0.018	0.032	5.70E-01	Lipoprotein phospholipase A2 activity in cardiovascular disease, Low density lipoprotein cholesterol levels, Lipoprotein(a) levels adjusted for apolipoprotein(a) isoforms, Total cholesterol levels, Lipoprotein (a) levels, Parental longevity (combined parental attained age, Martingale residuals)
rs1870634	10	44480811	T	G	0.345	-0.052	0.005	5.24E-24	-0.008	0.008	3.00E-01	
rs1892971	11	102795606	A	G	0.223	-0.039	0.006	5.14E-10	0.010	0.009	2.60E-01	
rs19242508 7	6	161032250	T	C	0.990	-0.348	0.048	7.15E-13	0.290	0.150	5.60E-02	
rs1967604	9	110530324	A	G	0.282	0.045	0.006	4.64E-16	0.002	0.008	7.80E-01	Red cell distribution width

rs1998043	6	161097871	A	G	0.835	-0.062	0.007	1.46E-20	0.030	0.010	3.50E-03	Low density lipoprotein cholesterol levels
rs2001846	8	126478450	T	C	0.473	0.047	0.005	6.02E-22	0.004	0.008	5.70E-01	
rs2008614	20	47433150	T	C	0.861	0.043	0.007	1.46E-09	0.015	0.011	1.70E-01	
rs2067831	10	105643223	C	G	0.271	0.042	0.005	2.61E-14	-0.007	0.008	4.10E-01	
rs2107595	7	19049388	A	G	0.176	0.065	0.006	3.61E-24	-0.016	0.010	1.20E-01	Stroke, Moyamoya disease, Systolic blood pressure, Ischemic stroke, Pulse pressure, Medication use (agents acting on the renin-angiotensin system), Large artery stroke
rs2107732	7	45077978	A	G	0.092	-0.049	0.009	1.53E-08	-0.033	0.013	1.20E-02	
rs2161967	2	218680529	T	G	0.439	0.033	0.005	6.89E-11	0.008	0.008	3.00E-01	
rs2207132	20	39142516	A	G	0.036	0.092	0.015	6.65E-10	0.023	0.021	2.80E-01	
rs2215614	7	35277093	A	C	0.622	0.034	0.005	2.96E-11	-0.006	0.008	4.10E-01	Total cholesterol levels, Medication use (HMG CoA reductase inhibitors), Low density lipoprotein cholesterol levels, Triglycerides
rs2244608	12	121416988	A	G	0.669	-0.048	0.005	2.35E-20	-0.050	0.008	3.50E-10	
rs2306363	11	65405600	T	G	0.205	-0.041	0.006	1.46E-11	-0.049	0.009	1.80E-07	
rs2327426	6	134202690	T	C	0.698	0.061	0.005	4.47E-30	-0.009	0.008	2.80E-01	
rs2410859	17	73841285	T	C	0.670	0.031	0.005	4.32E-09	0.025	0.008	2.20E-03	Medication use (agents acting on the renin-angiotensin system)
rs243071	2	60619028	A	G	0.446	0.029	0.005	2.65E-08	0.018	0.008	1.60E-02	
rs2457480	10	44740010	A	G	0.902	0.104	0.012	2.98E-17	0.022	0.023	3.30E-01	
rs2492304	6	134378151	A	T	0.489	0.035	0.005	1.06E-12	-0.006	0.008	4.00E-01	
rs2493298	1	3325912	A	C	0.140	0.048	0.007	2.10E-11	-0.007	0.011	5.30E-01	Medication use (HMG CoA reductase inhibitors), Metabolic syndrome, Triglycerides, HDL cholesterol
rs249760	5	141915692	T	C	0.244	0.032	0.006	4.05E-08	0.007	0.009	4.40E-01	
rs2672592	10	124230750	T	G	0.363	-0.032	0.005	2.47E-10	0.005	0.008	5.50E-01	
rs268	8	19813529	A	G	0.982	-0.132	0.020	4.10E-11	-0.053	0.028	5.80E-02	
rs2681472	12	90008959	A	G	0.816	-0.055	0.006	2.46E-18	-0.005	0.010	6.10E-01	Diastolic blood pressure, Mean arterial pressure, Pulse pressure, Systolic blood pressure, Hypertension
rs2683260	15	81385552	T	G	0.185	0.041	0.006	2.63E-10	-0.010	0.010	3.40E-01	
rs283485	2	233645691	A	G	0.343	0.034	0.005	1.01E-10	0.023	0.008	3.70E-03	
rs2839812	11	103673294	A	T	0.705	-0.065	0.005	1.90E-33	-0.003	0.008	7.10E-01	
rs2843152	1	2245570	C	G	0.280	0.042	0.006	7.26E-13	0.014	0.009	1.10E-01	Pulse pressure, Heel bone mineral density, Waist-hip ratio
rs28451064	21	35593827	A	G	0.129	0.109	0.008	1.64E-46	-0.022	0.011	5.60E-02	
rs2891168	9	22098619	A	G	0.516	-0.174	0.005	1.00E-200	-0.032	0.007	1.30E-05	
rs2909217	17	66463985	T	C	0.790	0.036	0.006	3.83E-09	-0.014	0.009	1.40E-01	
rs2983896	6	97029871	A	G	0.220	-0.036	0.006	1.44E-09	0.000	0.009	1.00E+00	Medication use (beta blocking agents)
rs34232196	1	55489542	T	C	0.240	-0.053	0.006	6.59E-20	-0.009	0.009	3.20E-01	

rs34330586	3	135800409	A	T	0.771	0.047	0.006	3.50E-15	0.019	0.009	3.00E-02	
rs34606058	12	115353368	T	C	0.626	-0.029	0.005	7.69E-09	0.005	0.008	5.10E-01	
rs34759087	3	49162284	T	C	0.113	-0.053	0.008	6.23E-11	-0.019	0.011	1.00E-01	Experiencing mood swings
rs34917849	8	95278307	C	G	0.128	0.042	0.007	1.11E-08	0.026	0.011	2.10E-02	
rs34991912	3	14926351	T	C	0.433	0.034	0.005	7.29E-12	0.024	0.008	1.70E-03	Systolic blood pressure
rs35611688	2	148377860	T	C	0.660	-0.030	0.005	1.54E-08	0.021	0.008	6.80E-03	
rs357494	3	153937753	A	G	0.869	0.057	0.008	4.91E-14	0.025	0.011	1.80E-02	
rs360153	11	9762274	T	C	0.419	-0.038	0.005	2.98E-14	0.013	0.008	1.00E-01	Diastolic blood pressure
rs36033161	14	100123487	T	C	0.828	0.068	0.007	1.34E-24	0.013	0.010	1.80E-01	
rs3776307	5	142494165	A	G	0.549	-0.036	0.005	6.70E-12	-0.012	0.008	1.10E-01	
rs3783113	13	110834746	T	C	0.358	0.040	0.005	6.53E-15	0.003	0.008	7.30E-01	
rs3796587	4	156638073	C	G	0.813	0.064	0.006	6.04E-23	0.015	0.010	1.10E-01	
rs3918226	7	150690176	T	C	0.081	0.112	0.009	4.60E-32	0.028	0.014	4.20E-02	Medication use (calcium channel blockers), Systolic blood pressure x alcohol consumption interaction (2df test), Systolic blood pressure, Diastolic blood pressure, Height, Cardiovascular disease, Medication use (beta blocking agents), Eczema, Medication use (HMG CoA reductase inhibitors), Diastolic blood pressure x alcohol consumption interaction (2df test), Medication use (agents acting on the renin-angiotensin system), Medication use (diuretics)
rs3936510	5	55860866	T	G	0.187	0.046	0.006	2.60E-13	0.066	0.010	4.00E-12	Waist-to-hip ratio adjusted for BMI x sex x age interaction (4df test), Waist circumference adjusted for body mass index, Waist-to-hip ratio adjusted for body mass index
rs4074793	5	52193125	A	G	0.923	-0.053	0.009	1.61E-08	-0.055	0.014	6.50E-05	Gamma glutamyl transferase levels, Heel bone mineral density, Liver enzyme levels (gamma-glutamyl transferase)
rs4140748	2	230005505	A	G	0.602	0.031	0.005	1.25E-09	-0.008	0.008	2.90E-01	
rs4245791	2	44074431	T	C	0.689	-0.049	0.005	1.01E-19	0.005	0.008	5.20E-01	Gallstone disease, Low density lipoprotein cholesterol levels, Total cholesterol levels, Phytosterol levels
rs4266144	3	156852592	C	G	0.685	-0.031	0.005	5.60E-09	-0.002	0.008	8.30E-01	
rs429358	19	45411941	T	C	0.848	-0.091	0.007	3.73E-38	0.046	0.011	1.40E-05	Low density lipoprotein cholesterol levels, Cerebrospinal fluid AB1-42 levels, Waist-hip ratio, Parental longevity (mother's attained age), Cognitive decline (age-related), Alzheimer's disease biomarkers, Platelet count, Cerebrospinal fluid p-tau levels in mild cognitive impairment, Alzheimer's disease, C-reactive protein levels, Blood protein levels, Alzheimer's disease progression score, Vigorous physical activity, Cerebral amyloid deposition (PET imaging), Total cholesterol levels, Parental longevity (father's attained age), Cerebrospinal fluid t-tau levels in mild cognitive impairment, Triglycerides, Parental lifespan, High density lipoprotein cholesterol levels, Mortality, Red cell distribution width, Insomnia, Parkinson's disease (age of onset), Hippocampal volume, Logical memory (immediate recall), Neurofibrillary tangles or cerebral amyloid angiopathy (pleiotropy), Lewy body disease, Parental longevity (both parents in top 10%), Cerebrospinal fluid p-tau levels, Cerebrospinal AB1-42 levels in Alzheimer's disease dementia, Cerebral amyloid deposition positivity (PET imaging), Brain imaging, Parental longevity (combined parental age at death), Advanced age-related macular degeneration, Dementia with Lewy bodies, Logical memory (delayed recall), Neuritic plaques or neurofibrillary tangles (pleiotropy), Cerebrospinal AB1-42 levels in normal cognition, Cerebrospinal AB1-42 levels in mild cognitive impairment, Cerebrospinal fluid t-tau levels,

rs4345341	5	121278751	A	T	0.182	0.038	0.006	3.87E-09	0.004	0.010	7.00E-01	Moderate to vigorous physical activity levels, Cortical amyloid beta load, Parental longevity (father's age at death), Parental longevity (mother's age at death), Neuritic plaques or cerebral amyloid angiopathy (pleiotropy), Parental longevity (combined parental attained age, Martingale residuals)
rs4537761	11	9323353	T	C	0.913	-0.055	0.009	1.75E-09	-0.002	0.014	9.20E-01	
rs4643373	17	47123423	T	C	0.720	0.038	0.006	4.49E-12	0.029	0.008	3.50E-04	Insomnia
rs4646249	8	18260431	T	G	0.295	0.035	0.006	8.18E-10	0.030	0.008	2.40E-04	
rs4662330	2	144186475	T	C	0.839	0.046	0.007	7.30E-12	-0.024	0.010	1.80E-02	
rs472495	1	55521313	T	G	0.633	0.038	0.005	3.71E-13	-0.009	0.008	2.40E-01	
rs476828	18	57852587	T	C	0.745	-0.033	0.006	1.43E-08	-0.016	0.009	7.30E-02	Obesity (early onset extreme)
rs4773141	13	110954353	C	G	0.638	-0.047	0.005	3.12E-18	-0.007	0.008	4.20E-01	
rs4790881	17	2068932	A	C	0.696	0.048	0.005	1.29E-19	-0.002	0.008	8.20E-01	Femoral neck bone mineral density, Intraocular pressure
rs4907571	13	113618496	T	C	0.713	-0.036	0.006	2.79E-08	-0.014	0.008	9.90E-02	
rs4938809	11	120363937	T	C	0.666	-0.029	0.005	4.59E-08	-0.002	0.008	8.40E-01	
rs494207	10	44741256	A	G	0.131	-0.076	0.007	9.94E-25	-0.015	0.012	1.90E-01	
rs515135	2	21286057	T	C	0.185	-0.058	0.006	3.58E-19	0.017	0.010	8.90E-02	Low density lipoprotein cholesterol levels, Total cholesterol levels, Carotid intima media thickness
rs55753709	10	96029170	T	C	0.664	-0.038	0.005	2.18E-13	0.006	0.008	4.30E-01	
rs55997232	19	11188117	T	C	0.107	-0.114	0.008	2.33E-44	0.030	0.012	1.10E-02	
rs56062135	15	67455630	T	C	0.225	-0.058	0.006	2.27E-22	-0.034	0.009	9.30E-05	Allergic disease (asthma, hay fever or eczema), Thyroid cancer, Asthma or allergic disease (pleiotropy), Asthma
rs56170783	1	57016131	A	C	0.915	0.115	0.009	1.73E-38	0.014	0.013	2.90E-01	
rs56195640	6	160720747	A	G	0.117	0.091	0.014	2.58E-10	0.031	0.046	5.00E-01	
rs56408342	8	22048490	A	G	0.058	0.079	0.011	2.30E-12	-0.048	0.016	3.50E-03	
rs582384	2	45896437	A	C	0.534	0.028	0.005	1.55E-08	0.004	0.008	6.40E-01	
rs584961	11	75277628	A	G	0.115	-0.062	0.008	1.50E-14	0.013	0.012	2.90E-01	
rs588136	15	58730498	T	C	0.781	-0.037	0.006	6.97E-10	0.001	0.009	9.60E-01	Lipid traits, Blood metabolite levels, Triglyceride levels
rs6006426	22	30669883	A	G	0.556	0.034	0.005	9.90E-12	0.002	0.008	7.70E-01	Heel bone mineral density
rs60154123	1	210468999	T	C	0.153	0.039	0.007	1.60E-08	0.015	0.010	1.60E-01	
rs6026739	20	57739469	A	T	0.874	-0.048	0.007	1.12E-10	-0.023	0.011	4.50E-02	Medication use (agents acting on the renin-angiotensin system), Systolic blood pressure
rs6088595	20	33358499	A	T	0.364	0.033	0.005	9.89E-11	0.018	0.008	2.30E-02	
rs6102343	20	39924279	A	G	0.235	0.034	0.006	5.18E-09	0.017	0.009	6.10E-02	
rs61776719	1	38461319	A	C	0.540	0.036	0.005	5.74E-12	-0.011	0.008	1.50E-01	Height, Colorectal cancer
rs61797068	1	115902514	C	G	0.158	-0.040	0.007	4.28E-09	0.007	0.010	5.20E-01	
rs61806987	1	169314833	A	G	0.576	0.035	0.005	6.85E-12	0.005	0.008	4.80E-01	
rs62362364	5	55441571	C	G	0.208	-0.038	0.006	2.94E-09	0.008	0.009	3.80E-01	
rs633185	11	100593538	C	G	0.701	0.039	0.005	5.57E-13	0.006	0.008	4.40E-01	Mean arterial pressure, Diastolic blood pressure, Pulse pressure, Systolic blood pressure, Medication use (calcium channel blockers), Mean arterial pressure x alcohol consumption (light vs heavy) interaction (2df test), Blood pressure, Hypertension, Systolic blood pressure x alcohol consumption interaction (2df test), Chronic obstructive pulmonary disease or high blood pressure (pleiotropy), Parental longevity (combined parental attained age, Martingale residuals)
rs6475608	9	22101702	T	C	0.397	-0.090	0.007	1.07E-41	-0.025	0.009	3.60E-03	
rs651007	9	136153875	T	C	0.206	0.054	0.006	1.28E-18	0.038	0.009	2.30E-05	Blood protein levels, Serum alkaline phosphatase levels, Total cholesterol levels, Fasting blood glucose, Blood metabolite levels, Iron status biomarkers (ferritin levels), Serum metabolite levels, Hematocrit,

												Metabolite levels, Low density lipoprotein cholesterol levels, E-selectin levels, End-stage coagulation
rs66778572	8	19916120	A	G	0.282	-0.039	0.006	1.33E-12	-0.041	0.008	6.90E-07	
rs6686750	1	154419843	A	G	0.425	0.039	0.005	1.87E-15	0.014	0.008	6.60E-02	
rs6740731	2	145270592	A	G	0.171	0.043	0.007	1.67E-10	0.020	0.010	5.70E-02	
rs67807996	1	149995265	A	G	0.380	0.040	0.006	1.14E-12	0.016	0.008	5.70E-02	Height
rs6841581	4	148401190	A	G	0.148	0.078	0.007	2.65E-30	0.018	0.011	9.00E-02	
rs6883598	5	127926190	A	C	0.735	-0.034	0.006	9.74E-10	0.004	0.009	6.40E-01	
rs6905288	6	43758873	A	G	0.571	0.037	0.005	5.02E-13	0.054	0.008	9.90E-13	Waist-to-hip ratio adjusted for body mass index, Waist-hip ratio, Systolic blood pressure, Cardiovascular disease, HDL cholesterol levels, Triglyceride levels
rs6909752	6	22612629	A	G	0.347	0.035	0.005	1.67E-11	-0.002	0.008	8.50E-01	
rs6919211	6	133999868	C	G	0.816	-0.036	0.006	1.00E-08	-0.023	0.010	1.90E-02	
rs6932293	6	160535878	T	C	0.973	-0.262	0.020	1.73E-37	-0.016	0.031	6.10E-01	
rs7118294	11	32380521	T	C	0.493	-0.033	0.005	1.80E-11	-0.004	0.008	5.80E-01	
rs71313931	22	19960184	C	G	0.705	-0.032	0.005	2.30E-09	-0.022	0.008	7.00E-03	Central corneal thickness, Medication use (calcium channel blockers)
rs7133378	12	124409502	A	G	0.317	-0.031	0.005	3.96E-09	-0.049	0.008	1.10E-09	Body mass index, Body fat percentage, Waist-to-hip ratio adjusted for body mass index, Waist-hip ratio, Reticulocyte count
rs71646019	1	59433354	T	C	0.208	0.038	0.006	6.05E-10	-0.009	0.009	3.60E-01	
rs7173743	15	79141784	T	C	0.554	0.069	0.005	3.26E-44	0.005	0.008	5.50E-01	
rs7183988	15	91428589	T	G	0.468	0.060	0.005	2.69E-33	0.004	0.008	5.80E-01	Insomnia, Medication use (beta blocking agents)
rs7189462	16	81907867	T	G	0.403	0.029	0.005	7.76E-09	-0.007	0.008	3.90E-01	
rs7246865	19	17219105	A	G	0.274	0.033	0.006	1.92E-08	0.016	0.009	6.60E-02	Reticulocyte fraction of red cells, Systolic blood pressure, Medication use (agents acting on the renin-angiotensin system), Cardiovascular disease, Waist-hip ratio
rs72658867	19	11231203	A	G	0.016	-0.197	0.026	2.80E-14	0.035	0.037	3.50E-01	
rs72836800	6	1617327	T	C	0.873	0.051	0.008	3.11E-11	-0.011	0.011	3.00E-01	
rs7296737	12	125336956	T	C	0.398	-0.036	0.005	6.54E-13	-0.013	0.008	8.50E-02	
rs7333991	13	111108436	T	C	0.784	-0.051	0.006	5.08E-17	0.004	0.009	6.90E-01	
rs733701	6	39171862	T	C	0.254	0.043	0.006	2.82E-13	-0.014	0.009	1.00E-01	
rs73596816	6	161017363	A	G	0.034	0.106	0.015	3.56E-13	0.035	0.022	1.00E-01	Lipoprotein (a) levels
												Blood protein levels, Medication use (salicylic acid and derivatives), Lipoprotein (a) levels, Total cholesterol levels, Immature fraction of reticulocytes, Metabolite levels (lipoprotein measures), Medication use (agents acting on the renin-angiotensin system), Medication use (calcium channel blockers), High density lipoprotein cholesterol levels, Carotid intima media thickness, Red cell distribution width, Pulse pressure, Lipoprotein(a) levels adjusted for apolipoprotein(a) isoforms, Low density lipoprotein cholesterol levels, Alzheimer's disease, Lipid traits, Ideal cardiovascular health (clinical and behavioural), Alzheimer's disease or family history of Alzheimer's disease, High light scatter reticulocyte count, Systolic blood pressure, Family history of Alzheimer's disease, Mean corpuscular hemoglobin, Reticulocyte fraction of red cells, Reticulocyte count, Cardiovascular disease, Triglycerides, High light scatter reticulocyte percentage of red cells, Medication use (antithrombotic agents), Alzheimer's disease (late onset), Lipid metabolism phenotypes, Cardiovascular risk factors, Lipoprotein-associated phospholipase A2 activity change in response to darapladib treatment in cardiovascular disease, Response to statins (LDL cholesterol change), Medication use
rs7412	19	45412079	T	C	0.075	-0.154	0.010	1.04E-54	-0.004	0.014	8.00E-01	

rs7440763	4	156433520	T	G	0.874	-0.060	0.008	4.44E-15	0.004	0.012	7.70E-01	(HMG CoA reductase inhibitors), Lipoprotein phospholipase A2 activity in cardiovascular disease, Red blood cell count
rs7485656	12	125315647	A	G	0.835	-0.066	0.007	2.66E-22	-0.011	0.011	3.20E-01	Low density lipoprotein cholesterol levels, High density lipoprotein cholesterol levels, Total cholesterol levels
rs7500448	16	83045790	A	G	0.758	0.050	0.006	1.11E-17	-0.004	0.009	6.30E-01	Diastolic blood pressure, Pulse pressure, Systolic blood pressure
rs75160195	12	54521594	T	C	0.053	0.094	0.011	5.31E-17	0.003	0.017	8.50E-01	
rs7678555	4	120909501	A	C	0.712	-0.045	0.005	3.08E-16	-0.018	0.008	3.10E-02	
rs76866386	2	44075483	T	C	0.938	0.079	0.010	1.58E-14	-0.017	0.015	2.60E-01	Low density lipoprotein cholesterol levels, Total cholesterol levels
rs76959412	9	22011083	C	G	0.016	-0.127	0.021	2.87E-09	-0.044	0.030	1.50E-01	
rs77347777	3	52848207	T	C	0.109	-0.051	0.008	1.51E-09	-0.012	0.012	3.20E-01	
rs77787671	10	104776205	T	C	0.094	-0.069	0.009	2.76E-15	-0.012	0.013	3.80E-01	
rs78030362	19	18575193	A	G	0.927	-0.093	0.010	1.05E-20	0.005	0.015	7.30E-01	Red blood cell count
rs781663	4	57781754	A	G	0.801	-0.043	0.006	1.07E-11	0.006	0.010	5.50E-01	
rs79018195	6	161024291	T	C	0.991	-0.345	0.058	3.38E-09	-0.310	0.390	4.20E-01	
rs79598313	1	27284913	T	C	0.024	0.095	0.017	3.60E-08	0.089	0.024	1.70E-04	High density lipoprotein cholesterol levels, Triglycerides, Low density lipoprotein cholesterol levels, Heel bone mineral density, Systolic blood pressure, Medication use (HMG CoA reductase inhibitors)
rs7991314	13	33126074	T	C	0.641	0.029	0.005	1.79E-08	0.008	0.008	2.90E-01	Heel bone mineral density
rs8000794	13	99434810	C	G	0.459	0.027	0.005	4.32E-08	-0.001	0.008	8.70E-01	
rs8046696	16	75442143	T	G	0.422	-0.047	0.005	1.64E-20	-0.012	0.008	1.00E-01	
rs8068844	17	40571284	T	C	0.656	-0.032	0.005	6.96E-10	-0.035	0.008	8.90E-06	Eczema
rs8108474	19	46301479	T	C	0.350	0.035	0.005	1.12E-11	0.025	0.008	1.50E-03	Chronic obstructive pulmonary disease or coronary artery disease (pleiotropy)
rs8124182	20	44608901	A	G	0.156	0.047	0.007	4.46E-12	0.018	0.010	7.60E-02	
rs869396	4	169688000	A	C	0.480	-0.034	0.005	8.86E-12	-0.002	0.008	8.20E-01	Pulse pressure
rs884811	10	99923763	C	G	0.557	0.029	0.005	3.09E-09	-0.009	0.008	2.10E-01	
rs885150	9	124420173	T	C	0.731	-0.037	0.006	1.98E-11	-0.004	0.009	6.50E-01	
rs894211	8	19865747	T	C	0.265	-0.046	0.006	1.38E-16	-0.033	0.008	1.00E-04	
rs9266631	6	31346898	A	G	0.207	-0.043	0.007	5.92E-11	-0.049	0.009	1.50E-07	
rs9337951	10	30317073	A	G	0.332	0.054	0.005	1.39E-23	0.004	0.008	5.90E-01	Pulse pressure
rs9349379	6	12903957	A	G	0.586	-0.114	0.005	4.02E-114	-0.003	0.008	6.90E-01	Systolic blood pressure, Pulse pressure, Migraine, Hypertension, Headache, Alcohol consumption (drinks per week), Cervical artery dissection, Migraine without aura, Medication use (antimigraine preparations), Migraine - clinic-based, Diastolic blood pressure, Coronary artery calcification
rs9361867	6	82595959	T	C	0.458	-0.035	0.005	5.11E-12	-0.009	0.008	2.10E-01	
rs9469899	6	34793124	A	G	0.358	0.035	0.005	1.47E-11	-0.025	0.008	1.50E-03	Medication use (thyroid preparations), Hand grip strength, Prostate cancer, Prostate cancer (advanced)
rs9515203	13	111049623	T	C	0.742	0.063	0.006	6.49E-28	-0.016	0.009	6.10E-02	
rs952227	2	227062080	A	G	0.344	-0.037	0.005	1.12E-12	-0.094	0.008	1.00E-32	
rs964184	11	116648917	C	G	0.848	-0.058	0.007	4.41E-17	-0.019	0.011	8.20E-02	Triglycerides, Mean corpuscular hemoglobin concentration, Mean platelet volume, Phospholipid levels (plasma), High light scatter reticulocyte count, Eosinophil counts, Medication use (agents acting on the renin-angiotensin system), Age-related diseases, mortality and associated endophenotypes, Red cell distribution width, Reticulocyte fraction of red cells, Medication use (salicylic acid and derivatives), High density lipoprotein cholesterol levels, Very long-chain saturated fatty acid levels (fatty acid 20:0), Blood protein levels, Platelet distribution width,

Circulating phylloquinone levels, Reticulocyte count, High light scatter reticulocyte percentage of red cells, Postprandial triglyceride response to high fat diet meal, Lipoprotein-associated phospholipase A2 activity and mass, Metabolic syndrome, Total cholesterol levels, Cardiovascular disease, Medication use (antithrombotic agents), Cholesterol efflux capacity (ABCA-1 dependent assay), Hypertriglyceridemia, Response to Vitamin E supplementation, Age-related disease endophenotypes, Metabolite levels (lipoprotein measures), Low density lipoprotein cholesterol levels, Triglycerides x physical activity interaction (2df test), Very low density lipoprotein cholesterol levels, Metabolite levels, Medication use (HMG CoA reductase inhibitors), Vitamin E levels, Blood metabolite levels

rs9945890	18	46515916	T	G	0.642	0.035	0.005	2.53E-11	0.020	0.008	9.30E-03
rs9951447	18	20009691	T	C	0.586	-0.032	0.005	3.50E-10	-0.009	0.008	2.50E-01
rs7413494	1	2985885	C	G	0.612	-0.035	0.006	1.01E-09			
rs34229028	3	172117455	A	A C	0.607	-0.034	0.006	3.11E-09			
rs36002015	4	82625720	G	G T	0.321	-0.041	0.006	8.20E-13			
rs35510806	6	126678331	T	TA	0.519	0.033	0.005	5.13E-10			
rs28867400	6	161104918	A	G	0.009	0.364	0.046	2.70E-15			
rs62435159	7	1911281	A	G	0.236	-0.038	0.007	2.46E-08			
rs75614263 6	7	139760540	T	TC C CT G CT CT C G C	0.217	-0.036	0.007	3.81E-08			
rs41312891	9	123726749	G	A A A	0.066	-0.062	0.011	5.87E-09			
rs11316597	11	13295751	A	AT TA	0.692	0.034	0.006	7.73E-09			
rs72447384	12	7178440	T	TT TA	0.123	-0.056	0.008	2.45E-11			
rs7177201	15	79065380	T	C	0.290	0.075	0.006	3.42E-32			
rs12936927	17	17726965	T	C	0.604	-0.035	0.006	2.92E-10			
rs12952244	17	40270081	A	G	0.869	-0.053	0.008	1.84E-10			
rs5820757	17	47417942	G	G A G TT	0.551	-0.047	0.006	7.30E-17			
rs76845310 5	19	41790086	G	AT G G TA	0.170	0.068	0.007	7.27E-21			

rs18365798	19	45742498	T	C	0.253	0.040	0.006	2.08E-10
5								
rs5760309	22	24677831	T	G	0.026	-0.103	0.017	3.49E-09

SNP, single nucleotide polymorphisms; CHR, chromosome; BP, physical position of SNP (base-pairs); A1, effect allele; A2, non-effect allele; EAF: effect allele frequency; Beta, effect allele beta coefficient.

Supplementary Table 5. Data sources, sample sizes, number of instruments and F-statistics.

Traits	IV	Sample size	R ² (%)	F statistics	Author	Ethnicity	Journal	Year	Websites for full summary statistics
T2DM	386	74,124 cases / 824,006 controls	2.47	57.27	Anubha Mahajan	European	Nature Genetics	2018	http://diagram-consortium.org/
T2DM _{adj} BMI	152	50,409 cases / 523,897 controls	2.06	85.65					
CAD	241	181,522 cases / 984,168 controls	1.44	76.02	Krishna G. Aragam	Predominantly (95%) European	Nature Genetics	2022	http://www.cardiogramplusc4d.org/

IV: instrumental variables. T2DM, type 2 diabetes mellitus; T2DM_{adj}BMI, type 2 diabetes mellitus adjusted for body mass index; CAD, coronary artery disease.

$R^2 = 2 \times \beta^2 \times \text{MAF} \times (1 - \text{MAF}) / (2 \times \beta^2 \times \text{MAF} \times (1 - \text{MAF}) + 2 \times \text{se}(\beta)^2 \times N \times \text{MAF} \times (1 - \text{MAF}))$, β denotes the SNP effect, MAF denotes minor allele frequency, N denotes the sample size.

$F = ((N - K - 1) / K) \times (R^2 / (1 - R^2))$, N denotes the sample size, K denotes the number of IVs.

Supplementary Table 6. Baseline Characteristics of UK Biobank participants by type 2 diabetes mellitus status at the baseline.

Characteristics	All	With T2DM	Without T2DM
Total (N)	448,363	5,653	442,710
Sex			
Female	249,698 (55.7%)	2,363 (41.8%)	247,335 (55.9%)
Male	198,665 (44.3%)	3,290 (58.2%)	195,375 (44.1%)
Age at recruitment (years), mean $\pm$ SD	56.5 $\pm$ 8.0	60.5 $\pm$ 6.7	56.4 $\pm$ 8.0
Assessment center			
England	396,035 (88.3%)	5,120 (90.6%)	390,915 (88.3%)
Scotland	33,099 (7.4%)	224 (4.0%)	32,875 (7.4%)
Wales	19,229 (4.3%)	309 (5.5%)	18,920 (4.3%)
Average total household income before tax			
<£18,000	82,071 (21.4%)	1,937 (41.7%)	80,134 (21.1%)
£18,000 to £30,999	97,216 (25.3%)	1,366 (29.4%)	95,850 (25.3%)
£31,000 to £51,999	102,274 (26.6%)	875 (18.8%)	101,399 (26.7%)
£52,000 to £100,000	80,872 (21.1%)	410 (8.8%)	80,462 (21.2%)
>£100,000	21,537 (5.6%)	62 (1.3%)	21,475 (5.7%)
Townsend deprivation index at recruitment			
<-2.00 (least deprived)	242,055 (54.1%)	2,369 (41.9%)	239,686 (54.2%)
-2.00 to 1.99 (average)	141,024 (31.5%)	1,930 (34.1%)	139,094 (31.5%)
$\geq$ 2.00 (most deprived)	64,751 (14.5%)	1,353 (23.9%)	63,398 (14.3%)
Current tobacco smoking			
Yes, on most or all days	34,357 (7.7%)	503 (8.9%)	33,854 (7.7%)
Only occasionally	11,928 (2.7%)	150 (2.7%)	11,778 (2.7%)
No	401,851 (89.7%)	4,995 (88.4%)	396,856 (89.7%)
Alcohol intake frequency			
Daily or almost daily	94,706 (21.1%)	764 (13.5%)	93,942 (21.2%)
Three or four times a week	107,623 (24.0%)	785 (13.9%)	106,838 (24.1%)
Once or twice a week	118,248 (26.4%)	1,263 (22.4%)	116,985 (26.4%)
One to three times a month	50,217 (11.2%)	739 (13.1%)	49,478 (11.2%)
Special occasions only	48,011 (10.7%)	1,198 (21.2%)	46,813 (10.6%)
Never	29,246 (6.5%)	892 (15.8%)	28,354 (6.4%)
IPAQ activity group			
Low	66,662 (18.4%)	1,293 (30.0%)	65,369 (18.3%)
Moderate	147,855 (40.9%)	1,698 (39.4%)	146,157 (40.9%)
High	147,225 (40.7%)	1,324 (30.7%)	145,901 (40.8%)
Body mass index (BMI, kg/m ²), mean $\pm$ SD	27.3 $\pm$ 4.7	32.2 $\pm$ 6.2	27.2 $\pm$ 4.7
Systolic blood pressure (SBP, mmHg), mean $\pm$ SD	137.9 $\pm$ 18.6	141.6 $\pm$ 17.4	137.9 $\pm$ 18.7
Diastolic blood pressure (DBP, mmHg), mean $\pm$ SD	82.3 $\pm$ 10.1	80.9 $\pm$ 9.5	82.3 $\pm$ 10.1
Hypertension			
Yes	193,137 (45.9%)	2,934 (54.7%)	190,203 (45.7%)
No	228,031 (54.1%)	2,432 (45.3%)	225,599 (54.3%)
Triglycerides (TG, mmol/L), median $\pm$ IQR	1.5 $\pm$ 1.1	1.9 $\pm$ 1.4	1.5 $\pm$ 1.1
Total cholesterol (TC, mmol/L), mean $\pm$ SD	5.8 $\pm$ 1.1	4.5 $\pm$ 1.0	5.8 $\pm$ 1.1
LDL cholesterol (LDL-C, mmol/L), mean $\pm$ SD	3.6 $\pm$ 0.9	2.7 $\pm$ 0.8	3.6 $\pm$ 0.8
HDL cholesterol (HDL-C, mmol/L), mean $\pm$ SD	1.5 $\pm$ 0.4	1.2 $\pm$ 0.3	1.5 $\pm$ 0.4
Dyslipidemia			
Yes	334,097 (87.1%)	3,657 (76.8%)	330,440 (87.3%)
No	49,365 (12.9%)	1,104 (23.2%)	48,261 (12.7%)

IQR, interquartile range; SD, standard deviation;

Body mass index was calculated as weight in kilograms divided by height in meters squared.

Hypertension: SBP $\geq$ 140mmHg; DBP $\geq$ 90mmHg.

Dyslipidemia: TG >1.7 mmol/L; TC>5.0 mmol/L; LDL-C>3.0 mmol/L; HDL-C< 1.0 mmol/L (male) or 1.2 mmol/L (female).

Supplementary Table 7. Baseline Characteristics of UK Biobank participants by coronary artery disease status at the baseline.

Characteristics	All	With CAD	Without CAD
Total (N)	449,603	15,662	433,941
Sex			
Female	248,373 (55.2%)	4,708 (30.1%)	243,665 (56.2%)
Male	201,230 (44.8%)	10,954 (69.9%)	190,276 (43.8%)
Age at recruitment (years), mean $\pm$ SD	56.5 $\pm$ 8.0	62.0 $\pm$ 5.8	56.3 $\pm$ 8.0
Assessment center			
England	396,794 (88.3%)	13,638 (87.1%)	383,156 (88.3%)
Scotland	33,482 (7.4%)	1,381 (8.8%)	32,101 (7.4%)
Wales	19,327 (4.3%)	643 (4.1%)	18,684 (4.3%)
Average total household income before tax			
<£18,000	82,748 (21.5%)	5,142 (39.9%)	77,606 (20.9%)
£18,000 to £30,999	97,378 (25.3%)	3,646 (28.3%)	93,732 (25.2%)
£31,000 to £51,999	102,351 (26.6%)	2,452 (19.0%)	99,899 (26.8%)
£52,000 to £100,000	80,921 (21.0%)	1,359 (10.5%)	79,562 (21.4%)
>£100,000	21,575 (5.6%)	286 (2.2%)	21,289 (5.7%)
Townsend deprivation index at recruitment			
<2.00 (least deprived)	242,693 (54.0%)	7,394 (47.3%)	235,299 (54.3%)
2.00 to 1.99 (average)	141,239 (31.5%)	4,926 (31.5%)	136,313 (31.5%)
$\geq$ 2.00 (most deprived)	65,129 (14.5%)	3,320 (21.2%)	61,809 (14.3%)
Current tobacco smoking			
Yes, on most or all days	34,271 (7.6%)	1,485 (9.5%)	32,786 (7.6%)
Only occasionally	11,974 (2.7%)	418 (2.7%)	11,556 (2.7%)
No	403,133 (89.7%)	13,746 (87.8%)	389,387 (89.8%)
Alcohol intake frequency			
Daily or almost daily	95,084 (21.2%)	3,200 (20.4%)	91,884 (21.2%)
Three or four times a week	108,398 (24.1%)	3,374 (21.6%)	105,024 (24.2%)
Once or twice a week	118,744 (26.4%)	3,932 (25.1%)	114,812 (26.5%)
One to three times a month	50,189 (11.2%)	1,570 (10.0%)	48,619 (11.2%)
Special occasions only	47,733 (10.6%)	1,989 (12.7%)	45,744 (10.5%)
Never	29,155 (6.5%)	1,584 (10.1%)	27,571 (6.4%)
IPAQ activity group			
Low	66,607 (18.4%)	2,677 (21.9%)	63,930 (18.2%)
Moderate	148,453 (40.9%)	4,904 (40.1%)	143,549 (40.9%)
High	147,788 (40.7%)	4,635 (37.9%)	143,153 (40.8%)
Body mass index (BMI, kg/m ²), mean $\pm$ SD	27.3 $\pm$ 4.7	29.0 $\pm$ 4.8	27.2 $\pm$ 4.7
Systolic blood pressure (SBP, mmHg), mean $\pm$ SD	137.7 $\pm$ 18.6	137.9 $\pm$ 18.9	137.7 $\pm$ 18.6
Diastolic blood pressure (DBP, mmHg), mean $\pm$ SD	82.2 $\pm$ 10.1	79.1 $\pm$ 10.2	82.3 $\pm$ 10.1
Hypertension			
Yes	191,778 (45.4%)	6,571 (45.0%)	185,207 (45.4%)
No	230,564 (54.1%)	8,045 (55.0%)	222,519 (54.6%)
Triglycerides (TG, mmol/L), median $\pm$ IQR	1.5 $\pm$ 1.1	1.6 $\pm$ 1.2	1.5 $\pm$ 1.1
Total cholesterol (TC, mmol/L), mean $\pm$ SD	5.7 $\pm$ 1.1	4.6 $\pm$ 1.1	5.8 $\pm$ 1.1
LDL cholesterol (LDL-C, mmol/L), mean $\pm$ SD	3.6 $\pm$ 0.9	2.8 $\pm$ 0.8	3.6 $\pm$ 0.8
HDL cholesterol (HDL-C, mmol/L), mean $\pm$ SD	1.5 $\pm$ 0.4	1.2 $\pm$ 0.3	1.5 $\pm$ 0.4
Dyslipidemia			
Yes	333,479 (86.7%)	9,377 (70.0%)	324,102 (87.3%)
No	51,090 (13.3%)	4,017 (30.0%)	47,073 (12.7%)

IQR, interquartile range; SD, standard deviation;

Body mass index was calculated as weight in kilograms divided by height in meters squared.

Hypertension: SBP $\geq$ 140mmHg; DBP $\geq$ 90mmHg.

Dyslipidemia: TG >1.7 mmol/L; TC>5.0 mmol/L; LDL-C>3.0 mmol/L; HDL-C< 1.0 mmol/L (male) or 1.2 mmol/L (female).

Supplementary Table 8. Cox proportional hazards regression models on the risk of incident coronary artery disease associated with type 2 diabetes mellitus.

Covariate	Primary analysis			Sensitivity analysis
	Basic model	Basic model + BMI	Full model	Full model
Age	1.08 (1.07 to 1.08)	1.08 (1.08 to 1.08)	1.07 (1.07 to 1.07)	1.07 (1.07 to 1.08)
Sex				
Female	1.00 (ref)	1.00 (ref)	1.00 (ref)	1.00 (ref)
Male	2.04 (1.99 to 2.08)	2.01 (1.97 to 2.06)	2.07 (2.00 to 2.14)	2.07 (2.00 to 2.14)
Assessment center				
England	1.00 (ref)	1.00 (ref)	1.00 (ref)	1.00 (ref)
Scotland	0.77 (0.73 to 0.81)	0.77 (0.73 to 0.81)	0.80 (0.73 to 0.87)	0.79 (0.72 to 0.86)
Wales	0.76 (0.70 to 0.82)	0.74 (0.69 to 0.80)	0.69 (0.63 to 0.77)	0.66 (0.59 to 0.73)
Principal component 1	1.00 (1.00 to 1.00)	1.00 (1.00 to 1.00)	1.00 (1.00 to 1.01)	1.00 (1.00 to 1.01)
Principal component 2	1.00 (1.00 to 1.00)	1.00 (1.00 to 1.00)	1.00 (0.99 to 1.00)	1.00 (0.99 to 1.00)
Principal component 3	1.00 (1.00 to 1.01)	1.00 (1.00 to 1.01)	1.00 (1.00 to 1.01)	1.01 (1.00 to 1.01)
Principal component 4	1.00 (1.00 to 1.01)	1.00 (1.00 to 1.01)	1.01 (1.00 to 1.01)	1.01 (1.00 to 1.01)
Principal component 5	1.01 (1.01 to 1.01)	1.01 (1.01 to 1.01)	1.01 (1.00 to 1.01)	1.00 (1.00 to 1.01)
Principal component 6	1.00 (1.00 to 1.01)	1.00 (1.00 to 1.01)	1.00 (0.99 to 1.01)	1.00 (0.99 to 1.01)
Principal component 7	1.00 (1.00 to 1.00)	1.00 (1.00 to 1.00)	1.00 (0.99 to 1.00)	1.00 (0.99 to 1.00)
Principal component 8	1.00 (1.00 to 1.01)	1.00 (1.00 to 1.00)	1.00 (0.99 to 1.00)	1.00 (0.99 to 1.00)
Principal component 9	1.01 (1.00 to 1.01)	1.01 (1.00 to 1.01)	1.00 (1.00 to 1.01)	1.00 (1.00 to 1.01)
Principal component 10	1.01 (1.00 to 1.01)	1.01 (1.00 to 1.01)	1.01 (1.00 to 1.01)	1.01 (1.00 to 1.01)
Body mass index (BMI)	-	1.04 (1.04 to 1.04)	1.04 (1.03 to 1.04)	1.04 (1.04 to 1.05)
Income				
<£18,000	-	-	1.00 (ref)	1.00 (ref)
£18,000 to £30,999	-	-	0.86 (0.83 to 0.90)	0.85 (0.82 to 0.89)
£31,000 to £51,999	-	-	0.85 (0.81 to 0.89)	0.84 (0.80 to 0.88)
£52,000 to £100,000	-	-	0.77 (0.73 to 0.81)	0.76 (0.72 to 0.81)
>£100,000	-	-	0.73 (0.67 to 0.79)	0.72 (0.66 to 0.79)
Townsend deprivation index				
<-2.00 (least deprived)	-	-	1.00 (ref)	1.00 (ref)
-2.00 to 1.99 (average)	-	-	1.02 (0.98 to 1.05)	1.02 (0.98 to 1.06)
≥2.00 (most deprived)	-	-	1.13 (1.07 to 1.18)	1.12 (1.07 to 1.18)
Smoking				
Yes, on most or all days	-	-	1.59 (1.51 to 1.67)	1.60 (1.52 to 1.69)
Only occasionally	-	-	1.12 (1.02 to 1.23)	1.13 (1.03 to 1.25)
No	-	-	1.00 (ref)	1.00 (ref)
Drinking				
Daily or almost daily	-	-	1.00 (ref)	1.00 (ref)
Three or four times a week	-	-	0.99 (0.95 to 1.04)	0.98 (0.94 to 1.03)
Once or twice a week	-	-	1.08 (1.03 to 1.13)	1.08 (1.03 to 1.13)
One to three times a month	-	-	1.08 (1.02 to 1.15)	1.08 (1.01 to 1.15)
Special occasions only	-	-	1.19 (1.12 to 1.26)	1.20 (1.13 to 1.27)
Never	-	-	1.31 (1.23 to 1.40)	1.33 (1.24 to 1.42)
Physical activity				
Low	-	-	1.00 (ref)	1.00 (ref)
Moderate	-	-	0.92 (0.88 to 0.96)	0.92 (0.88 to 0.96)
High	-	-	0.93 (0.89 to 0.97)	0.93 (0.89 to 0.97)
Hypertension				
No	-	-	1.00 (ref)	1.00 (ref)
Yes	-	-	1.23 (1.19 to 1.27)	1.23 (1.18 to 1.27)
Dyslipidemia				
No	-	-	1.00 (ref)	1.00 (ref)
Yes	-	-	0.98 (0.93 to 1.02)	0.97 (0.93 to 1.02)
Type 2 diabetes mellitus				
No	1.00 (ref)	1.00 (ref)	1.00 (ref)	1.00 (ref)
Yes	2.70 (2.60 to 2.81)	2.28 (2.19 to 2.37)	2.12 (2.01 to 2.24)	1.66 (1.56 to 1.76)

Hazard ratios are provided with 95% confidence intervals.

Supplementary Table 9. Cox proportional hazards regression models on the risk of incident type 2 diabetes mellitus associated with coronary artery disease.

Covariate	Primary analysis			Sensitivity analysis
	Basic model	Basic model + BMI	Full model	Full model
Age	1.05 (1.05 to 1.05)	1.06 (1.05 to 1.06)	1.05 (1.05 to 1.06)	1.06 (1.05 to 1.06)
Sex				
Female	1.00 (ref)	1.00 (ref)	1.00 (ref)	1.00 (ref)
Male	1.58 (1.54 to 1.62)	1.66 (1.61 to 1.71)	1.91 (1.83 to 1.99)	1.95 (1.87 to 2.04)
Assessment center				
England	1.00 (ref)	1.00 (ref)	1.00 (ref)	1.00 (ref)
Scotland	0.54 (0.51 to 0.58)	0.54 (0.50 to 0.58)	0.53 (0.47 to 0.60)	0.53 (0.47 to 0.60)
Wales	0.92 (0.85 to 1.00)	0.82 (0.75 to 0.89)	0.84 (0.75 to 0.93)	0.82 (0.73 to 0.91)
Principal component 1	1.01 (1.00 to 1.01)	1.01 (1.00 to 1.01)	1.00 (1.00 to 1.01)	1.01 (1.00 to 1.01)
Principal component 2	1.00 (1.00 to 1.00)	1.00 (1.00 to 1.01)	1.00 (1.00 to 1.01)	1.00 (1.00 to 1.01)
Principal component 3	1.01 (1.00 to 1.01)	1.00 (1.00 to 1.01)	1.00 (1.00 to 1.01)	1.00 (0.99 to 1.01)
Principal component 4	1.00 (1.00 to 1.01)	1.00 (1.00 to 1.01)	1.00 (1.00 to 1.01)	1.00 (1.00 to 1.01)
Principal component 5	1.00 (1.00 to 1.01)	1.00 (1.00 to 1.00)	1.00 (1.00 to 1.00)	1.00 (1.00 to 1.00)
Principal component 6	0.99 (0.99 to 1.00)	0.99 (0.99 to 1.00)	0.99 (0.98 to 1.00)	0.99 (0.98 to 1.00)
Principal component 7	1.00 (1.00 to 1.01)	1.00 (1.00 to 1.00)	1.00 (0.99 to 1.00)	1.00 (0.99 to 1.00)
Principal component 8	1.00 (1.00 to 1.01)	1.00 (1.00 to 1.01)	1.01 (1.00 to 1.01)	1.01 (1.00 to 1.01)
Principal component 9	1.01 (1.00 to 1.01)	1.01 (1.00 to 1.01)	1.00 (1.00 to 1.01)	1.01 (1.00 to 1.01)
Principal component 10	1.00 (1.00 to 1.01)	1.00 (0.99 to 1.01)	1.00 (0.99 to 1.01)	1.00 (1.00 to 1.01)
Body mass index (BMI)	-	1.15 (1.15 to 1.15)	1.15 (1.14 to 1.15)	1.15 (1.15 to 1.15)
Income				
<£18,000	-	-	1.00 (ref)	1.00 (ref)
£18,000 to £30,999	-	-	0.92 (0.88 to 0.96)	0.91 (0.86 to 0.96)
£31,000 to £51,999	-	-	0.78 (0.73 to 0.82)	0.77 (0.73 to 0.82)
£52,000 to £100,000	-	-	0.70 (0.66 to 0.75)	0.70 (0.65 to 0.75)
>£100,000	-	-	0.52 (0.46 to 0.59)	0.52 (0.46 to 0.59)
Townsend deprivation index				
<-2.00 (least deprived)	-	-	1.00 (ref)	1.00 (ref)
-2.00 to 1.99 (average)	-	-	1.08 (1.04 to 1.13)	1.08 (1.03 to 1.13)
≥2.00 (most deprived)	-	-	1.26 (1.20 to 1.33)	1.26 (1.20 to 1.33)
Smoking				
Yes, on most or all days	-	-	1.64 (1.55 to 1.75)	1.67 (1.57 to 1.78)
Only occasionally	-	-	1.02 (0.91 to 1.15)	1.01 (0.90 to 1.15)
No	-	-	1.00 (ref)	1.00 (ref)
Drinking				
Daily or almost daily	-	-	1.00 (ref)	1.00 (ref)
Three or four times a week	-	-	1.03 (0.97 to 1.10)	1.03 (0.97 to 1.09)
Once or twice a week	-	-	1.19 (1.12 to 1.26)	1.19 (1.12 to 1.27)
One to three times a month	-	-	1.36 (1.26 to 1.45)	1.39 (1.29 to 1.49)
Special occasions only	-	-	1.63 (1.52 to 1.74)	1.64 (1.53 to 1.76)
Never	-	-	1.68 (1.56 to 1.81)	1.69 (1.56 to 1.83)
Physical activity				
Low	-	-	1.00 (ref)	1.00 (ref)
Moderate	-	-	0.86 (0.82 to 0.90)	0.86 (0.82 to 0.90)
High	-	-	0.78 (0.74 to 0.82)	0.78 (0.74 to 0.82)
Hypertension				
No	-	-	1.00 (ref)	1.00 (ref)
Yes	-	-	1.10 (1.05 to 1.14)	1.11 (1.06 to 1.15)
Dyslipidemia				
No	-	-	1.00 (ref)	1.00 (ref)
Yes	-	-	0.77 (0.73 to 0.81)	0.79 (0.75 to 0.83)
Coronary artery disease				
No	1.00 (ref)	1.00 (ref)	1.00 (ref)	1.00 (ref)
Yes	2.44 (2.35 to 2.53)	1.99 (1.92 to 2.06)	1.72 (1.63 to 1.81)	1.48 (1.40 to 1.56)

Hazard ratios are provided with 95% confidence intervals.

Supplementary Table 10. Local heritability of type 2 diabetes mellitus and coronary artery disease, and regions that contribute significant genetic correlation as estimated by ρ -HESS ($P < 0.05/1,703$).

Model	Locus	local h^2_{T2D}	local h^2_{CAD}	local genetic covariance	P
T2DM-CAD	2: 225840004-228119842	1.2×10^{-3} (1.5×10^{-4})	7.4×10^{-5} (3.1×10^{-5})	2.1×10^{-4} (4.5×10^{-5})	3.55×10^{-6}
	5: 55417349-56621102	1.1×10^{-3} (1.5×10^{-4})	1.0×10^{-4} (3.2×10^{-5})	2.3×10^{-4} (4.6×10^{-5})	7.07×10^{-7}
	8: 19492840-20060856	3.0×10^{-4} (1.1×10^{-4})	9.2×10^{-5} (3.2×10^{-5})	1.7×10^{-4} (3.7×10^{-5})	5.38×10^{-6}
	9: 20463534-22206559	1.3×10^{-3} (1.5×10^{-4})	9.6×10^{-4} (6.2×10^{-5})	4.3×10^{-4} (6.9×10^{-5})	4.53×10^{-10}
	12: 119754110-122007651	8.8×10^{-4} (1.4×10^{-4})	1.3×10^{-4} (3.3×10^{-5})	2.0×10^{-4} (4.4×10^{-5})	4.70×10^{-6}
T2DM _{adj} BMI-CAD	2: 225840004-228119842	1.3×10^{-3} (1.9×10^{-4})	7.4×10^{-5} (3.1×10^{-5})	2.3×10^{-4} (4.9×10^{-5})	2.41×10^{-6}
	5: 55417349-56621102	1.4×10^{-3} (2.0×10^{-4})	1.0×10^{-4} (3.2×10^{-5})	2.5×10^{-4} (5.1×10^{-5})	1.68×10^{-6}
	6: 30798168-31571218	1.0×10^{-3} (1.8×10^{-4})	7.5×10^{-5} (3.3×10^{-5})	2.0×10^{-4} (4.9×10^{-5})	2.85×10^{-5}
	8: 19492840-20060856	4.5×10^{-4} (1.5×10^{-4})	9.1×10^{-5} (3.2×10^{-5})	1.8×10^{-4} (4.2×10^{-5})	2.78×10^{-5}
	9: 20463534-22206559	1.5×10^{-3} (2.0×10^{-4})	9.6×10^{-4} (6.2×10^{-5})	4.7×10^{-4} (7.9×10^{-5})	2.07×10^{-9}

Numbers in parentheses represent standard errors of genetic covariance/correlation estimated by ρ -HESS.

Genetic regions marked in red indicate specific loci affecting only T2DM and CAD or T2DM_{adj}BMI and CAD.

T2DM, type 2 diabetes mellitus; CAD, coronary artery disease; T2DM_{adj}BMI, type 2 diabetes mellitus adjusted for body mass index.

Supplementary Table 11. Results from cross-trait meta-analysis of type 2 diabetes mellitus and coronary artery disease (SNPs with P-CPASSOC < 5×10⁻⁸ and single trait P-value < 1×10⁻⁵ are shown).

SNP	CHR	BP	A1	A2	Beta		P-T2DM	P-CAD	P-CPASSOC	Genomic coordinates	Genes within clumping area	Established T2D		Established CAD		Mapped genes
					T2DM	CAD						Literature SNP	r ²	Literature SNP	r ²	
T2DM and CAD																
	Known pleiotropic SNPs: P-T2DM < 5×10 ⁻⁸ and P-CAD < 5×10 ⁻⁸															
rs1399627	2	227083411	A	G	-0.094	-0.034	2.30E-45	2.16E-10	7.63E-50	2: 226866226-227199263	LOC646736	rs2972144	0.95	rs2972146	0.95	-
rs3936510*	5	55860866	T	G	0.068	0.046	1.10E-16	2.60E-13	1.59E-26	5: 55833892-55876283	LOC101928448	rs9687832	0.97	rs3936510	1.00	AC022431.2
rs3130283*	6	32138545	A	C	-0.069	-0.042	9.40E-15	1.37E-08	5.03E-19	6: 32029226-32637680	AGER, AGPAT1, ATF6B, BTNL2, C6orf10, EGFL8, FKBPL, GPSM3, HCG23, HLA-DQA1, HLA-DQB1, HLA-DRA, HLA-DRB1, HLA-DRB5, HLA-DRB6, LOC100507547, MIR6721, MIR6833, NOTCH4, PBX2, PPT2, PPT2-EGFL8, PRRT1, RNF5, RNF5P1, TNXB			rs3130683	0.75	EGFL8, AGPAT1, PPT2-EGFL8, PPT2, XXbac-BCX105D18.9
rs6905288*	6	43758873	A	G	0.040	0.037	6.60E-10	5.02E-13	1.65E-20	6: 43756863-43767274		rs11967262	0.67	rs6905288	1.00	VEGFA
rs17091891	8	19843171	T	C	0.071	0.053	1.30E-12	9.80E-12	1.86E-21	8: 19788675-19955382	LPL	rs10096633	0.97	rs2083636	0.24	-
rs10965199*	9	21954653	T	C	-0.110	-0.082	6.70E-10	2.15E-08	2.89E-15	9: 21954653-22039426	C9orf53, CDKN2A, CDKN2B, CDKN2B-AS1	rs1412830	0.07			RP11-145E5.5
rs12555274*	9	22136440	C	G	0.110	0.034	5.80E-50	1.51E-09	2.80E-57	9: 22131825-22137685		rs10757283	0.45			-
rs507666*	9	136149399	A	G	0.050	0.056	9.30E-10	1.47E-18	4.71E-26	9: 136081319-136339755	ABO, ADAMTS13, C9orf96, CACFD1, MED22, OBP2B, REXO4, RPL7A, SLC2A6, SNORD24, SNORD36A, SNORD36B, SNORD36C, SURF1, SURF2, SURF4, SURF6	rs505922	0.39	rs507666	1.00	ABO
rs1169288*	12	121416650	A	C	-0.049	-0.049	7.30E-13	3.81E-20	6.28E-31	12: 121189116-121485336	C12orf43, HNF1A, HNF1A-AS1, OASL, SPPL3	rs56348580	0.19	rs2244608	0.96	HNF1A, HNF1A-AS1
rs56158042*	12	121455589	A	G	-0.062	-0.031	4.40E-19	1.82E-08	3.86E-22	12: 121068353-121489657	ACADS, C12orf43, CABP1, HNF1A, HNF1A-AS1, MIR4700, MLEC, OASL, SPPL3, UNC119B	rs56348580	0.99	rs2258287	0.22	C12orf43, OASL
rs6564229	16	75236409	C	G	-0.039	-0.032	2.70E-08	2.66E-09	2.58E-15	16: 75233851-75288184	BCAR1, CTRB1, CTRB2, LOC100506281	rs72802342	0.18	rs3851738	0.15	CTRB2
rs9936550	16	75242850	T	C	-0.130	-0.066	1.00E-25	2.08E-11	1.42E-31	16: 75048508-75517115	BCAR1, CFDP1, CHST6, CTRB1, CTRB2, LDHD, LOC100506281, TMEM170A, ZFP1, ZNRF1	rs72802342	0.84	rs3851738	0.10	CTRB2
rs8067439	17	17698254	A	G	-0.041	-0.031	9.00E-10	2.14E-09	1.21E-16	17: 17519037-18036283	ATPAF2, DRG2, GID4, LRRC48, MIR33B, MIR6777, MYO15A, RAI1, SMCR5, SREBF1, TOM1L2	rs4925109	0.64	rs12936927	0.76	RAI1

rs646123	17	4072063 2	A	G	0.048	0.032	1.10E-11	8.44E-09	2.14E-17	17: 40555799-40836975	ATP6V0A1, CCR10, CNTNAP1, COASY, FAM134C, HSD17B1, MIR5010, MLX, NAGLU, PLEKHH3, PSMC3IP, PTRF, TUBG1, TUBG2 ATP5G1, CALCOCO2, GIP, IGF2BP1, SNF8, TTLL6, UBE2Z	rs34855406	0.96			MLX, PSMC3IP, COASY
rs1962412*	17	4697025 9	T	C	-0.052	-0.037	1.40E-13	6.20E-12	1.55E-22	17: 46831823-47190299		rs35895680	0.38	rs4643373	0.35	ATP5G1, SUMO2P17
rs12954782	18	5786409 2	C	G	-0.053	-0.030	1.50E-13	2.82E-08	3.83E-18	18: 57728947-57920877		rs523288	0.75	rs476828	0.78	RP11-795H16.2
rs429358	19	4541194 1	T	C	0.080	-0.091	1.80E-18	3.73E-38	5.76E-65	19: 45387459-45428234	APOC1, APOE, PVRL2, TOMM40	rs429358	1.00	rs429358	1.00	APOE, TOMM40
T2DM-driven SNPs: P-T2DM < 5×10 ⁻⁸ and 5×10 ⁻⁸ < P-CAD < 10 ⁻⁵																
rs72979712	2	2270194 16	T	G	-0.097	-0.053	4.90E-11	8.62E-06	8.90E-13	2: 226900882-227019416	LOC646736			rs952227	0.10	-
rs78718224*	2	2271778 27	T	C	-0.130	-0.092	1.40E-08	8.94E-07	1.96E-12	2: 227177827-227177827						-
rs76367336*	2	2272282 51	T	C	0.061	0.039	3.20E-09	1.15E-06	3.56E-13	2: 227200627-227342038						-
rs62271373*	3	1500665 40	A	T	0.088	0.056	1.00E-09	1.14E-06	1.51E-13	3: 150018637-150097635	LINC01214	rs62271373	1.00			-
rs12641981	4	4517988 3	T	C	0.044	0.026	8.50E-12	3.37E-07	1.94E-15	4: 45068929-45186832		rs10938398	0.99			-
rs454424*	6	3128496 3	T	G	-0.038	-0.025	1.50E-08	7.33E-06	1.59E-11	6: 31220567-31362891	HLA-B, HLA-C, MIR6891 ABHD16A, AIF1, APOM, BAG6, C6orf25, C6orf47, CLIC1, CSNK2B, DDAH2, GPANK1, HSPA1A, HSPA1L, LSM2, LY6G5B, LY6G5C, LY6G6C, LY6G6D, LY6G6E, LY6G6F, MIR4646, MIR6832, MSH5, MSH5- SAPCD1, PRRC2A, SAPCD1, SNORA38, VARS, VWA7 ABHD16A, AIF1, APOM, ATF6B, ATP6V1G2, ATP6V1G2-DDX39B, BAG6, C2, C4A, C4B, C4B_2, C6orf25, C6orf47, C6orf48, CCHCR1, CFB, CLIC1, CSNK2B, CYP21A1P, CYP21A2, DDAH2, DDX39B, DXO, EHMT2, FKBP1, GPANK1, HCG26, HCG27, HCP5, HLA-B, HLA-C, HSPA1A, HSPA1B, HSPA1L, LOC102060414, LSM2, LST1, LTA, LTB, LY6G5B, LY6G5C, LY6G6C, LY6G6D, LY6G6E, LY6G6F, MCCD1, MICA, MICB,			rs9266631	0.13	-
rs2260051	6	3159191 8	A	T	-0.046	-0.024	7.40E-13	5.81E-06	1.87E-14	6: 31572956-31786872				rs3130683	0.13	SNORA38, PRRC2A, BX511262.2
rs3115669	6	3161902 4	T	G	-0.073	-0.041	9.20E-16	5.46E-08	4.41E-19	6: 31119889-32112955				rs3130683	0.83	BAG6, APOM, BX511262.2

rs2395153	6	3234559 5	C	G	-0.041	-0.026	2.70E-10	1.71E-06	2.28E-13	6: 32221552-32681161	MIR1236, MIR4646, MIR6832, MIR6891, MSH5, MSH5-SAPCD1, NCR3, NELFE, NEU1, NFKBIL1, POU5F1, PRRC2A, PSORS1C3, SAPCD1, SKIV2L, SLC44A4, SNORA38, SNORD48, SNORD52, SNORD84, SNORD117, STK19, TCF19, TNF, TNXA, TNXB, VARS, VWA7, ZBTB12 BTNL2, C6orf10, HCG23, HLA-DQA1, HLA-DQB1, HLA-DRA, HLA-DRB1, HLA-DRB5, HLA-DRB6	rs601945	0.18	rs3130683	0.05	C6orf10
rs4713587	6	3265953 5	T	G	0.038	0.026	3.70E-09	1.21E-06	7.89E-13	6: 32582601-32674329	HLA-DQA1, HLA-DQB1	rs601945	0.15	rs3130683	0.07	-
rs62405422	6	5079690 5	T	C	-0.056	-0.031	9.10E-12	6.12E-07	5.22E-15	6: 50664180-50977502	TFAP2B, TFAP2D	rs3798519	0.99			TFAP2B
rs11759026	6	1267920 95	A	G	-0.067	0.029	1.30E-18	1.07E-06	3.30E-24	6: 126623947-127201350	CENPW	rs11759026	1.00	rs35510806	0.37	-
rs76011118*	9	2213377 3	A	G	0.190	0.090	1.70E-22	1.14E-07	7.73E-25	9: 22133773-22133773		rs76011118	1.00			-
rs3935875	9	1392388 24	A	G	-0.076	-0.030	4.20E-21	2.08E-06	6.23E-22	9: 139235415-139274523	CARD9, DNLZ, GPSM1, SNAPC4	rs28505901	0.96			GPSM1
rs62618693	11	3295649 2	T	C	-0.110	-0.059	3.90E-11	8.18E-06	1.30E-13	11: 32595598-32956492	CCDC73, EIF3M, PRRG4, QSER1	rs145678014	0.91			QSER1
rs2257813*	12	1214475 19	A	C	-0.040	-0.023	6.60E-10	9.19E-06	3.84E-12	12: 121352974- 121448395	C12orf43, HNF1A, HNF1A-AS1	rs56348580	0.15	rs2258287	0.28	C12orf43
rs8032939*	15	3883403 3	T	C	-0.043	-0.026	8.40E-09	3.65E-06	5.34E-12	15: 38817150-38925195	RASGRP1	rs8032939	1.00			RASGRP1, Y_RNA
rs34127110	15	7731357 1	A	G	0.037	0.024	7.00E-09	1.77E-06	2.51E-12	15: 76818070-77316133	PSTPIP1, RCN2, SCAPER	rs1005752	0.15			PSTPIP1
rs739846	19	1941907 1	A	G	0.092	-0.042	1.20E-14	3.84E-06	1.83E-19	19: 19083483-19793545	ARMC6, ATP13A1, CILP2, GATAD2A, GMIP, HAPLN4, LPAR2, MAU2, MEF2B, MEF2BNB, MEF2BNB- MEF2B, NCAN, NDUFA13, NR2C2AP, PBX4, RFXANK, SLC25A42, SUGP1, SUGP2, TM6SF2, TMEM161A, TSSK6, YJEFN3, ZNF101	rs8107974	0.97			SUGP1
CAD-driven SNPs: $5 \times 10^{-8} < P\text{-T2DM} < 10^{-5}$ and $P\text{-CAD} < 5 \times 10^{-8}$																
rs13079221*	3	1490152 5	C	G	0.029	0.032	4.70E-06	1.60E-10	3.05E-14	3: 14873214-14958126	FGD5			rs748431	0.53	FGD5
rs78629618	3	4688013 0	T	C	-0.050	-0.047	2.30E-06	4.12E-08	7.96E-12	3: 46384204-47305392	ALS2CL, CCDC12, CCR2, CCR5, CCRL2, KIF9, KIF9-AS1, LOC100132146, LRRC2, LRRC2-AS1, LTF, MYL3, NBEAL2, NRADDP, PRSS42, PRSS45, PRSS46, PRSS50,	rs75423501	0.58	rs7633770	0.10	PRSS42

rs1128535	3	4986639 2	T	C	0.033	0.028	3.00E-07	1.42E-08	1.16E-13	3: 49385417-50209053	PTH1R, RTP3, SETD2, TDGF1, TMIE AMIGO3, AMT, APEH, BSN, BSN-AS2, CAMKV, CDHR4, DAG1, FAM212A, GMPPB, GPX1, IP6K1, MIR5193, MON1A, MST1, MST1R, NICN1, RBM5, RBM5- AS1, RBM6, RHOA, RNF123, SEMA3F, TCTA, TRAIIP, UBA7 MSL2, NCK1, NCK1- AS1, PCCB, PPP2R3A, SLC35G2, STAG1 HCG27, HCP5, HLA-B, HLA-C, MICA, MIR6891, POU5F1, PSORS1C3	rs4688760	0.25	rs7623687	0.15	TRAIP
rs7644541	3	1361457 66	A	G	-0.041	-0.045	1.10E-07	4.04E-14	8.99E-20	3: 135798658-136643571			rs667920	0.97	STAG1, RNU6- 1284P	
rs11961408*	6	3131785 0	A	G	0.038	0.035	2.10E-07	5.95E-09	3.77E-14	6: 31136208-31431820			rs9266631	0.06	HLA-B	
rs77899453	8	1978031 0	A	G	-0.047	-0.041	1.00E-06	1.88E-08	9.41E-13	8: 19732374-19806671	LPL	rs10096633	0.13	rs2083636	0.16	LPL
rs301	8	1981693 4	T	C	0.036	0.036	2.00E-06	4.51E-10	2.41E-14	8: 19816934-19816934	LPL	rs10096633	0.10	rs2083636	0.33	LPL
rs28597716	8	1993668 7	A	G	0.039	0.039	1.90E-06	1.56E-09	1.38E-13	8: 19815189-19936687	LPL	rs10096633	0.14	rs66778572	0.49	AC100802.3
rs117197971	9	2195117 5	A	G	-0.069	-0.117	8.30E-06	1.10E-19	4.82E-23	9: 21940070-21951175					RP11-145E5.5	
rs7041637*	9	2196186 6	A	C	0.037	0.103	2.80E-07	1.52E-72	1.93E-79	9: 21961866-21966221		rs1412830	0.16	rs2891168	0.17	RP11-145E5.5
rs3731239*	9	2197421 8	A	G	0.035	0.088	1.80E-07	1.39E-59	5.77E-65	9: 21974218-22019156	CDKN2A, CDKN2B, CDKN2B-AS1	rs1412830	0.18	rs6475608	0.36	CDKN2A, RP11- 145E5.5 CDKN2B, UBA52P6, RP11- 145E5.5, CDKN2B-AS1
rs117626887	9	2201306 3	A	G	-0.110	0.102	6.00E-07	1.11E-09	8.36E-18	9: 22013063-22057530	CDKN2B-AS1					CDKN2B-AS1
rs11790231*	9	2205359 1	A	G	0.058	0.106	6.70E-08	3.39E-35	7.28E-39	9: 21973857-22082375	CDKN2A, CDKN2B, CDKN2B-AS1	rs76011118	0.13	rs2891168	0.13	CDKN2B-AS1
rs2891168	9	2209861 9	A	G	-0.028	-0.174	8.70E-06	1.00E- 200	0.00E+00	9: 21995882-22125913	CDKN2B, CDKN2B-AS1	rs1412830	0.27	rs2891168	1.00	CDKN2B-AS1
rs2306363*	11	6540560 0	T	G	-0.040	-0.041	3.80E-07	1.46E-11	2.78E-16	11: 65365077-65593756	AP5B1, KAT5, MAP3K11, MIR4489, MIR4690, OVOL1, OVOL1-AS1, PCNXL3, RELA, RNASEH2C, SIPAI			rs2306363	1.00	PCNXL3, SIPAI, MIR4690
rs4765127	12	1244601 67	T	G	-0.034	-0.031	6.30E-07	4.93E-09	7.98E-14	12: 124388511- 124501208	CCDC92, DNAH10, ZNF664, ZNF664- FAM101A	rs7978610	1.00	rs7133378	0.88	CCDC92, ZNF664, FAM101A, RP11- 214K3.18
rs10773049*	12	1245066 31	T	C	0.032	0.029	1.00E-06	1.07E-08	3.64E-13	12: 124505444- 124616113	ZNF664-FAM101A	rs825452	1.00			FAM101A
rs2411759	17	4707107 4	T	C	-0.034	-0.029	2.00E-07	1.99E-08	1.19E-13	17: 47050275-47142697	IGF2BP1	rs35895680	0.57	rs4643373	0.42	IGF2BP1, RP11- 501C14.5
rs147711004	19	4533791 8	A	G	-0.087	0.081	8.30E-07	1.22E-08	1.78E-15	19: 45324756-45418486	APOC1, APOE, PVRL2, TOMM40	rs429358	0.10	rs429358	0.10	-
Suggestive SNPs: $5 \times 10^{-8} < P\text{-T2DM/CAD} < 10^{-5}$, and LD with established SNPs ($r^2 \geq 0.05$)																
rs227199	1	2102653 84	C	G	-0.030	-0.023	9.30E-06	7.09E-06	2.57E-09	1: 210068954-210306846	SYT14			rs60154123	0.17	SYT14
rs13027161	2	6060772 8	T	C	0.030	0.024	4.00E-06	5.83E-06	9.26E-10	2: 60602892-60725451	BCL11A, MIR4432	rs243024	0.19	rs243071	0.52	RNU1-32P, AC007381.2

rs78058190	2	219699999	A	G	0.075	0.073	1.30E-06	1.35E-07	1.52E-11	2: 219699999-219859171	CDK5R2, CRYBA2, FEV, LINC00608, LOC101928537, WNT6, WNT10A	rs113414093	0.574			PRKAG3		
rs11692712*	2	227167100	T	C	0.047	0.031	7.30E-08	4.56E-06	3.95E-11	2: 227104535-227182519		rs2972144	0.17	rs2972146	0.18	-		
rs9989973*	3	12499264	C	G	0.031	0.023	1.60E-06	5.48E-06	4.68E-10	3: 12487612-12499264		rs17819328	0.94			-		
rs77481436	3	47506230	A	G	0.060	0.043	1.00E-07	2.49E-06	1.54E-11	3: 47397300-47981735	CSPG5, DHX30, ELP6, MAP4, MIR1226, PTPN23, SCAP, SMARCC1	rs75423501	0.82	rs7633770	0.06	SCAP, snoU13		
rs62260788	3	48068610	T	C	0.059	0.040	1.20E-07	9.77E-06	1.15E-10	3: 48009467-48405661	CAMP, CDC25A, MAP4, MIR4443, NME6, SPINK8, ZNF589	rs75423501	0.64			MAP4		
rs6795831	3	129341403	A	C	0.036	0.029	7.80E-06	2.22E-06	8.20E-10	3: 129281866-129671420	PLXND1, TMCC1, TMCC1-AS1	rs9828772	0.45			-		
rs3796459	4	96116778	T	G	0.037	0.029	2.30E-06	1.06E-06	8.68E-11	4: 96031577-96181240	BMPRI1, UNC5C			rs3775058	0.97	UNC5C		
rs10474433	5	74616843	T	C	0.030	-0.024	8.40E-06	2.10E-06	5.11E-12	5: 74352180-74917862	ANKDD1B, ANKRD31, COL4A3BP, HMGCR, POLK	rs2307111	0.21	rs12916	0.60	CTD-2235C13.2		
											C2, C4A, C4B, C4B_2, CFB, CYP21A1P, CYP21A2, DXO, EHMT2, LOC102060414, MIR1236, NELFE, NEU1, SKIV2L, SLC44A4, STK19, TNXA, TNXB, ZBTB12			rs3130683	0.20	SKIV2L, NELFE, CYP21A2		
rs592229	6	31930441	T	G	0.029	0.028	8.70E-06	1.11E-07	3.18E-11	6: 31826153-32076499				rs3130683	0.20	SKIV2L, NELFE, CYP21A2		
rs7755075	6	126708470	A	G	-0.042	0.033	6.80E-07	7.33E-07	1.23E-13	6: 126545036-127179594	CENPW	rs11759026	0.09	rs1591805	0.26	-		
rs2971672	7	44205906	A	C	-0.031	-0.026	1.90E-06	3.53E-07	3.02E-11	7: 44150119-44219705	AEBP1, GCK, MIR4649, MYL7, POLD2	rs878521	0.05			GCK		
rs12003940*	9	19101350	A	G	-0.038	-0.029	2.00E-07	2.42E-07	2.25E-12	9: 18997136-19105638	FAM154A, HAUS6, RRAGA, SCARNA8	rs7022807	0.46			HAUS6		
rs660549	12	121300988	T	C	0.034	0.023	1.40E-07	3.00E-06	3.50E-11	12: 121187557-121372763	SPPL3	rs56348580	0.13	rs2244608	0.17	SPPL3		
rs2893895	12	121693947	T	C	-0.035	-0.025	6.80E-07	8.62E-06	3.20E-10	12: 121601455-121693947	CAMKK2, P2RX4, P2RX7	rs56348580	0.07			CAMKK2		
											AOC2, AOC3, ATP6V0A1, BECN1, CCR10, CNTD1, CNTNAP1, COA3, COASY, EZH1, FAM134C, HSD17B1, MIR5010, MIR6780A, MIR6781, MLX, NAGLU, PLEKHH3, PSMC3IP, PSME3, PTRF, RAMP2, RAMP2-AS1, STAT3, STAT5A, TUBG1, TUBG2, VPS25, WNK4			rs34855406	0.10	rs8068844	0.27	PTRF
rs72823056	17	40565926	T	G	-0.047	-0.033	3.40E-07	2.47E-06	8.14E-11	17: 40451137-41018481	KDM4B, MIR4747, UHRF1	rs34855406	0.10	rs8068844	0.27	PTRF		
rs17883331*	19	4954455	A	G	0.044	0.033	6.10E-08	1.34E-07	5.80E-13	19: 4920414-5074637		rs7249758	0.84			UHRF1		
Novel SNPs: $5 \times 10^{-8} < P\text{-T2DM/CAD} < 10^{-5}$, and not in LD with established SNPs ($r^2 < 0.05$)																		
rs4135268	3	12437237	C	G	-0.053	-0.044	4.00E-06	1.97E-06	1.64E-10	3: 12026709-12494178	PPARG, SYN2, TIMP4					PPARG		
rs6449	6	32006655	T	C	0.034	0.027	2.00E-06	3.33E-06	3.32E-10	6: 31741659-32189481	AGER, AGPAT1, ATF6B, C2, C4A, C4B, C4B 2,					TNXB, C4B-AS1, CYP21A2, C4B,		

											C6orf48, CFB, CYP21A1P, CYP21A2, DXO, EGFL8, EHMT2, FKBPL, GPSM3, HSPA1A, HSPA1B, HSPA1L, LOC100507547, LOC102060414, LSM2, MIR1236, MIR6721, MIR6833, NELFE, NEU1, NOTCH4, PBX2, PPT2, PPT2-EGFL8, PRRT1, RNF5, RNF5P1, SKIV2L, SLC44A4, SNORD48, SNORD52, STK19, TNXA, TNXB, VARS, VWA7, ZBTB12 CDK12, ERBB2, FBXL20, MED1, MIR4728, NEUROD2, PGAP3, PNMT, PPP1R1B, STARD3, TCAP					XXbac- BPG116M5.15, C4A, C4A-AS1
rs35497503	17	3762062 7	T	C	-0.035	-0.026	3.60E-06	5.74E-06	7.72E-10	17: 37387413-37884037						CDK12
rs12452590	17	6072005 8	T	G	0.032	0.024	2.50E-06	7.63E-06	1.17E-09	17: 60636826-60720058	MRC2, TLK2					MRC2
rs2306527	17	7679815 5	T	C	-0.031	-0.024	1.00E-06	1.71E-06	9.24E-11	17: 76661269-76833916	CYTH1, USP36					USP36
T2DM _{adj} BMI and CAD																
Known pleiotropic SNP: P-T2DM _{adj} BMI < 5×10 ⁻⁸ and P-CAD < 5×10 ⁻⁸																
rs2943656	2	2271219 18	A	G	-0.100	-0.036	1.70E-38	2.51E-12	1.04E-41	2: 226866226-227199263	LOC646736	rs2972144	0.88	rs2972146	0.88	-
rs185244	3	1380928 89	T	C	0.059	0.060	7.00E-09	3.22E-19	1.20E-26	3: 137906532-138276541	ARMC8, CEP70, ESYT3, MRAS, NME9			rs185244	1.00	MRAS
rs3936510*	5	5586086 6	T	G	0.066	0.046	4.00E-12	2.60E-13	1.37E-21	5: 55833892-55876283	LOC101928448	rs9687832	0.97	rs3936510	1.00	AC022431.2
											ABHD16A, AGER, AGPAT1, ATF6B, BTNL2, C2, C4A, C4B, C4B_2, C6orf10, C6orf25, C6orf48, CFB, CLIC1, CYP21A1P, CYP21A2, DDAH2, DXO, EGFL8, EHMT2, FKBPL, GPSM3, HCG23, HLA-DQA1, HLA-DQB1, HLA-DRA, HLA-DRB1, HLA-DRB5, HLA-DRB6, HSPA1A, HSPA1B, HSPA1L, LOC100507547, LOC102060414, LSM2, LY6G5C, LY6G6C, LY6G6D, LY6G6E, LY6G6F, MIR1236, MIR4646, MIR6721, MIR6833, MSH5, MSH5- SAPCD1, NELFE, NEU1, NOTCH4, PBX2, PPT2, PPT2-EGFL8, PRRT1, RNF5, RNF5P1,					
rs3130283*	6	3213854 5	A	C	-0.070	-0.042	3.50E-11	1.37E-08	1.24E-14	6: 31643399-32634405				rs3130683	0.75	EGFL8, AGPAT1, PPT2- EGFL8, PPT2, XXbac- BCX105D18.9

rs6905288*	6	4375873	A	G	0.054	0.037	9.90E-13	5.02E-13	1.64E-21	6: 43756863-43767274	SAPCD1, SKIV2L, SLC44A4, SNORD48, SNORD52, STK19, TNXA, TNXB, VARS, VWA7, ZBTB12	rs11967262	0.67	rs6905288	1.00	VEGFA
rs1591805	6	126717064	A	G	-0.057	0.030	4.50E-14	4.13E-09	1.82E-20	6: 126623947-127080700	CENPW	rs11759026	0.35	rs1591805	1.00	-
rs12555274*	9	22136440	C	G	0.120	0.034	3.10E-47	1.51E-09	3.49E-49	9: 22131825-22137685		rs10757283	0.45			-
rs1169288*	12	121416650	A	C	-0.055	-0.049	6.80E-12	3.81E-20	1.01E-29	12: 121189116-121485336	C12orf43, HNF1A, HNF1A-AS1, OASL, SPPL3	rs56348580	0.19	rs2244608	0.96	HNF1A, HNF1A-AS1
rs56158042*	12	121455589	A	G	-0.052	-0.031	1.30E-10	1.82E-08	1.49E-14	12: 121197124-121471931	C12orf43, HNF1A, HNF1A-AS1, OASL, SPPL3	rs56348580	0.99	rs2258287	0.22	C12orf43, OASL
rs7133378	12	124409502	A	G	-0.049	-0.031	1.10E-09	3.96E-09	5.63E-15	12: 124390681-124538302	CCDC92, DNAH10, ZNF664, ZNF664-FAM101A	rs7978610	0.88	rs7133378	1.00	DNAH10, DNAH10OS, CCDC92, RP11-380L11.4
rs10773049*	12	124506631	T	C	0.043	0.029	1.20E-08	1.07E-08	9.33E-14	12: 124505444-124620185	ZNF664-FAM101A	rs825452	1.00			FAM101A
rs72802342	16	75234872	A	C	-0.160	-0.061	2.70E-29	7.82E-10	1.98E-32	16: 75048508-75517115	BCAR1, CFDP1, CHST6, CTRB1, CTRB2, LDHD, LOC100506281, TMEM170A, ZFP1, ZNRF1	rs72802342	1.00	rs3851738	0.09	CTRB2
rs9937988	16	75248803	A	G	-0.051	-0.036	5.90E-10	4.36E-11	1.84E-17	16: 75233851-75299437	BCAR1, CTRB1, CTRB2, LOC100506281	rs72802342	0.16	rs3851738	0.20	CTRB1
rs116843064	19	8429323	A	G	-0.160	-0.177	1.10E-08	3.56E-21	6.31E-29	19: 8410381-8627569	ANGPTL4, HNRNPM, MARCH2, MIR4999, MYO1F, PRAM1, RAB11B, RAB11B-AS1, ZNF414			rs116843064	1.00	ANGPTL4
T2DM-driven SNPs: P-T2DM _{adj} BMI < 5×10 ⁻⁸ and 5×10 ⁻⁸ < P-CAD < 10 ⁻⁵																
rs115528845	2	43927374	A	G	0.180	-0.101	3.10E-09	2.88E-06	4.17E-13	2: 43541071-44037396	DYNC2LI1, LOC728819, PLEKHH2, THADA	rs80147536	0.12			PLEKHH2
rs113414093	2	219859171	A	G	0.120	0.070	6.60E-09	8.73E-07	9.22E-12	2: 219699999-219859171	CDK5R2, CRYBA2, FEV, LINC00608, LOC101928537, WNT6, WNT10A	rs113414093	1.00			CRYBA2
rs9989973*	3	12499264	C	G	0.042	0.023	2.50E-08	5.48E-06	3.33E-10	3: 12487612-12499264		rs17819328	0.94			-
rs62271373*	3	150066540	A	T	0.099	0.056	2.50E-09	1.14E-06	2.22E-11	3: 150047893-150097635		rs62271373	1.00			-
rs76011118*	9	22133773	A	G	0.230	0.090	2.70E-22	1.14E-07	5.73E-25	9: 22133773-22133773		rs76011118	1.00			-
rs28505901	9	139241030	A	G	-0.080	-0.028	2.80E-19	7.28E-06	2.74E-20	9: 139235415-139266221	CARD9, DNLZ, GPSM1	rs28505901	1.00			GPSM1
rs11257655	10	12307894	T	C	0.095	0.026	7.70E-26	9.97E-06	9.43E-28	10: 12239456-12328010	CDC123	rs11257655	1.00	rs61848342	0.44	RN7SL232P
rs12778642	10	94464307	T	G	-0.120	-0.024	1.10E-56	2.46E-06	5.17E-63	10: 94202905-94499577	HHEX, IDE, KIF11	rs10882101	0.94			-
rs35519679	10	114818754	A	G	0.260	0.026	8.70E-199	6.04E-06	1.75E-218	10: 114803307-114823426	TCF7L2	rs7903146	0.45			TCF7L2
rs2257813*	12	121447519	A	C	-0.042	-0.023	4.60E-08	9.19E-06	9.82E-10	12: 121352974-121448395	C12orf43, HNF1A, HNF1A-AS1	rs56348580	0.15	rs2258287	0.28	C12orf43
CAD-driven SNPs: 5×10 ⁻⁸ < P-T2DM _{adj} BMI < 10 ⁻⁵ and P-CAD < 5×10 ⁻⁸																

rs79567528	2	227038586	T	C	0.062	0.050	7.10E-08	1.36E-10	2.39E-15	2: 227002100-227038586	LOC646736	rs2972144	0.21	rs952227	0.24	-
rs13079221*	3	14901525	C	G	0.034	0.032	7.00E-06	1.60E-10	2.48E-14	3: 14873214-14958126	FGD5			rs748431	0.53	FGD5
rs11961408*	6	31317850	A	G	0.042	0.035	7.80E-07	5.95E-09	4.56E-13	6: 31045717-31431820	C6orf15, CCHCR1, CDSN, HCG27, HCP5, HLA-B, HLA-C, MICA, MIR6891, POU5F1, PSORS1C1, PSORS1C2, PSORS1C3, TCF19, ABHD16A, AIF1, APOM, ATP6V1G2, ATP6V1G2-DDX39B, BAG6, C6orf15, C6orf25, C6orf47, C6orf48, CCHCR1, CDSN, CLIC1, CSNK2B, DDAH2, DDR1, DDX39B, DPCR1, GPANK1, GTF2H4, HCG22, HCG26, HCG27, HCP5, HLA-B, HLA-C, HSPA1A, HSPA1B, HSPA1L, LSM2, LST1, LTA, LTB, LY6G5B, LY6G5C, LY6G6C, LY6G6D, LY6G6E, LY6G6F, MCCD1, MICA, MICB, MIR4646, MIR6832, MIR6891, MSH5, MSH5-SAPCD1, MUC21, MUC22, NCR3, NEU1, NFKBIL1, POU5F1, PRRC2A, PSORS1C1, PSORS1C2, PSORS1C3, SAPCD1, SFTA2, SLC44A4, SNORA38, SNORD48, SNORD52, SNORD84, SNORD117, TCF19, TNF, VARS, VARS2, VWA7			rs9266631	0.06	HLA-B
rs9266631	6	31346898	A	G	-0.049	-0.043	1.50E-07	5.92E-11	6.24E-16	6: 30861729-31845985	LY6G6F, MCCD1, MICA, MICB, MIR4646, MIR6832, MIR6891, MSH5, MSH5-SAPCD1, MUC21, MUC22, NCR3, NEU1, NFKBIL1, POU5F1, PRRC2A, PSORS1C1, PSORS1C2, PSORS1C3, SAPCD1, SFTA2, SLC44A4, SNORA38, SNORD48, SNORD52, SNORD84, SNORD117, TCF19, TNF, VARS, VARS2, VWA7			rs9266631	1.00	ZDHHC20P2, HLA-S, FGFR3P1, AL671883.1, FGFR3P
rs2292334	6	160858188	A	G	0.037	0.071	1.50E-06	1.47E-44	3.12E-51	6: 160712194-160969738	LPA, LPAL2, SLC22A3			rs56195640	0.22	SLC22A3
rs15285	8	19824667	T	C	-0.041	-0.044	8.30E-07	4.66E-16	2.92E-21	8: 19742204-19934339	LPL	rs10096633	0.43	rs2083636	0.79	LPL
rs66778572	8	19916120	A	G	-0.041	-0.039	6.90E-07	1.33E-12	1.94E-17	8: 19720833-19939049	LPL	rs10096633	0.21	rs66778572	1.00	-
rs10965199*	9	21954653	T	C	-0.110	-0.082	2.00E-07	2.15E-08	8.49E-13	9: 21954653-22039426	C9orf53, CDKN2A, CDKN2B, CDKN2B-AS1	rs1412830	0.07			RP11-145E5.5
rs7041637*	9	21961866	A	C	0.039	0.103	4.50E-06	1.52E-72	1.01E-79	9: 21961866-21966221		rs1412830	0.16	rs2891168	0.17	RP11-145E5.5
rs3731239*	9	21974218	A	G	0.036	0.088	4.40E-06	1.39E-59	6.23E-66	9: 21952926-22019156	C9orf53, CDKN2A, CDKN2B, CDKN2B-AS1	rs1412830	0.18	rs6475608	0.36	CDKN2A, RP11-145E5.5
rs11790231*	9	22053591	A	G	0.062	0.106	8.30E-07	3.39E-35	1.89E-41	9: 21973857-22082375	CDKN2A, CDKN2B, CDKN2B-AS1	rs76011118	0.13	rs2891168	0.13	CDKN2B-AS1
rs507666*	9	136149399	A	G	0.042	0.056	6.80E-06	1.47E-18	3.68E-23	9: 136137065-136339755	ABO, ADAMTS13, C9orf96, CACFD1, MED22, REXO4, RPL7A, SLC2A6, SNORD24,	rs505922	0.39	rs507666	1.00	ABO

rs2306363*	11	6540560 0	T	G	-0.049	-0.041	1.80E-07	1.46E-11	1.46E-16	11: 65365077-65593756	SNORD36A, SNORD36B, SNORD36C, SURF1, SURF2, SURF4, SURF6 AP5B1, KAT5, MAP3K11, MIR4489, MIR4690, OVOL1, OVOL1-AS1, PCNXL3, RELA, RNASEH2C, SIPA1 ACAD10, ADAM1A, ALDH2, ATXN2, BRAP, CUX2, FAM109A, MAPKAPK5, MAPKAPK5-AS1, MIR6760, MIR6761, SH2B3 BCAR1	rs2306363	1.00	PCNXL3, SIPA1, MIR4690		
rs4766578	12	1119043 71	A	T	-0.041	-0.057	6.20E-08	2.03E-28	6.25E-36	12: 111426615- 112355949		rs10774625	1.00	ATXN2		
rs7188857	16	7530344 4	A	G	0.044	0.034	1.30E-06	1.45E-08	1.56E-12	16: 75269534-75303444	BCAR1	rs33928862	0.23	BCAR1		
rs37601	16	7550477 5	A	G	-0.050	-0.045	2.60E-06	2.60E-10	4.15E-14	16: 75504775-75510212	CHST6	rs72802342	0.21	rs3851738	0.19	-
rs9891957	17	1774443 9	A	G	-0.040	-0.032	2.60E-07	7.68E-10	2.14E-14	17: 17519037-18036283	ATPAF2, DRG2, GID4, LRRC48, MIR33B, MIR6777, MYO15A, RAI1, SMCR5, SREBF1, TOM1L2 ATP6V0A1, COASY, FAM134C, HSD17B1, MIR5010, MLX, NAGLU, PLEKHH3, PSMC3IP, PTRF, STAT3, TUBG1, TUBG2 ATP5G1, CALCOCO2, GIP, IGF2BP1, SNF8, TTLL6, UBE2Z	rs4925109	0.52	rs12936927	0.94	SREBF1, TOM1L2
rs8068844	17	4057128 4	T	C	-0.035	-0.032	8.90E-06	6.96E-10	1.88E-13	17: 40514201-40824834		rs34855406	0.72	rs8068844	1.00	PTRF
rs1962412*	17	4697025 9	T	C	-0.038	-0.037	3.00E-06	6.20E-12	4.25E-16	17: 46831823-47145848		rs35895680	0.38	rs4643373	0.35	ATP5G1, SUMO2P17
Suggestive SNPs: $5 \times 10^{-8} < P\text{-T2DM}_{adj}BMI/CAD < 10^{-5}$, and LD with established SNPs ($r^2 \geq 0.05$)																
rs11692712*	2	2271671 00	T	C	0.049	0.031	1.40E-06	4.56E-06	1.77E-09	2: 227068430-227181188		rs2972144	0.17	rs2972146	0.18	-
rs78718224*	2	2271778 27	T	C	-0.130	-0.092	3.90E-06	8.94E-07	2.92E-10	2: 227177827-227177827						-
rs76367336*	2	2272282 51	T	C	0.063	0.039	1.40E-07	1.15E-06	1.17E-10	2: 227200627-227346475						-
rs9853950	3	1293360 57	A	T	0.044	0.028	4.20E-06	3.69E-06	2.77E-09	3: 129292948-129670844	PLXND1, TMCC1, TMCC1-AS1	rs9828772	0.45			-
rs3869098	6	3100245 2	A	G	-0.036	-0.024	2.30E-06	6.54E-06	4.28E-09	6: 31002452-31002527	MUC22		rs9266631	0.14	MUC22, XXbac- BPG118E17.9, AL663093.2, AL805909.3, BX248321.1	
rs454424*	6	3128496 3	T	G	-0.038	-0.025	8.00E-07	7.33E-06	3.47E-09	6: 31275289-31315755		rs9266631	0.13			-
rs2857702	6	3157728 3	C	G	0.045	0.033	1.60E-06	3.77E-07	9.44E-11	6: 31572956-32006655	ABHD16A, AIF1, APOM, BAG6, C2, C4A, C4B, C4B_2, C6orf25, C6orf47, C6orf48, CFB, CLIC1, CSNK2B, CYP21A1P, CYP21A2, DDAH2, DXO, EHMT2, GPANK1, HSPA1A, HSPA1B, HSPA1L, LOC102060414, LSM2,	rs601945	0.05			UQCRHP1, BX511262.2

											LY6G5B, LY6G5C, LY6G6C, LY6G6D, LY6G6E, LY6G6F, MIR1236, MIR4646, MIR6832, MSH5, MSH5- SAPCD1, NELFE, NEU1, PRRC2A, SAPCD1, SKIV2L, SLC44A4, SNORA38, SNORD48, SNORD52, STK19, TNXA, TNXB, VARS, VWA7, ZBTB12					
rs2941383	6	1608704 76	A	C	-0.044	-0.030	4.80E-06	2.03E-06	1.51E-09	6: 160697762-160906440	LPAL2, SLC22A3	rs474513	0.22	rs1998043	0.16	SLC22A3, LPAL2
rs12003940*	9	1910135 0	A	G	-0.043	-0.029	6.10E-07	2.42E-07	3.44E-11	9: 18997136-19101350	FAM154A, HAUS6, RRAGA, SCARNA8	rs7022807	0.46			HAUS6
rs8032939*	15	3883403 3	T	C	-0.042	-0.026	9.20E-07	3.65E-06	1.40E-09	15: 38817150-38869666	RASGRP1	rs8032939	1.00			RASGRP1, Y_RNA
rs17883331*	19	4954455	A	G	0.044	0.033	3.40E-06	1.34E-07	4.89E-11	19: 4920414-5074637	KDM4B, MIR4747, UHRF1	rs7249758	0.84			UHRF1
rs12625329	20	6270927 4	A	G	-0.036	-0.024	1.80E-06	1.75E-06	8.30E-10	20: 62690683-62761699	LKAAEAR1, MIR6813, NPBWR2, OPRL1, RGS19, TCEA2	rs59944054	0.26			RGS19, OPRL1
Novel SNPs: $5 \times 10^{-8} < P\text{-T2DM}_{\text{adj}}\text{BMI/CAD} < 10^{-5}$, and not in LD with established SNPs ($r^2 < 0.05$)																
rs4762753	12	2057996 9	T	G	-0.042	-0.031	5.70E-06	4.83E-07	3.17E-10	12: 20578881-20586395	PDE3A					PDE3A

*27 SNPs identified in the T2DM-CAD CPASSOC analysis remained significant in the T2DM_{adj}BMI-CAD CPASSOC analysis.

Measuring linkage disequilibrium (LD) with r^2 . LD ($r^2 \geq 0.05$) with previous reported SNPs were presented.

SNP, single nucleotide polymorphisms; CHR, chromosome; BP, physical position of SNP (base-pairs); A1, effect allele; A2, non-effect allele; Beta, effect allele beta coefficient.

T2DM, type 2 diabetes mellitus; CAD, coronary artery disease; T2DM_{adj}BMI, type 2 diabetes mellitus adjusted for body mass index.

Supplementary Table 12. Previously reported genome-wide significant loci for type 2 diabetes mellitus, with and without adjust for BMI, among European ancestry.

Chromosome	Position (Build 37 bp)	SNP	Nearest gene	Primary/Secondary	PMID
1	40035928	rs3768321	<i>MACF1</i>	Primary	30297969
1	51256091	rs58432198	<i>FAF1</i>	Primary	30297969
1	62579891	rs12140153	<i>PATJ</i>	Primary	30297969
1	115144899	rs184660829	<i>DENND2C</i>	Primary	30297969
1	117532790	rs1127215	<i>PTGFRN</i>	Primary	30297969
1	120526982	rs1493694	<i>NOTCH2</i>	Primary	30297969
1	147121000	rs79489938	.	Primary	32541925
1	150786038	rs10305745	<i>FAM63A</i>	Secondary	30297969
1	151017991	rs145904381	<i>FAM63A</i>	Primary	30297969
1	177889025	rs539515	<i>SEC16B</i>	Primary	30297969
1	205114873	rs12048743	<i>DSTYK</i>	Primary	30297969
1	206593900	rs9430095	<i>SRGAP2</i>	Primary	30297969
1	214150821	rs79687284	<i>PROX1</i>	Secondary	30297969
1	214159256	rs340874	<i>PROX1</i>	Primary	30297969
1	214175531	rs114526150	<i>PROX1</i>	Secondary	30297969
1	219584164	rs553014999	<i>LYPLAL1</i>	Secondary	30297969
1	219748818	rs2820446	<i>LYPLAL1</i>	Primary	30297969
1	229672955	rs348330	<i>ABCB10</i>	Primary	30297969
1	235690800	rs291367	<i>GNG4</i>	Primary	30297969
2	422144	rs62107261	<i>TMEM18</i>	Primary	30297969
2	653575	rs35913461	<i>TMEM18</i>	Secondary	30297969
2	16574669	rs11680058	<i>FAM49A</i>	Primary	30297969
2	25643221	rs17802463	<i>DTNB</i>	Primary	30297969
2	27730940	rs1260326	<i>GCKR</i>	Primary	30297969
2	43207872	rs28525376	<i>THADA</i>	Secondary	30297969
2	43430440	rs6708643	<i>THADA</i>	Secondary	30297969
2	43698028	rs80147536	<i>THADA</i>	Primary	30297969
2	58981064	rs10193538	<i>BNIP1</i>	Secondary	30297969
2	59307725	rs6545714	<i>BNIP1</i>	Primary	30297969
2	60583665	rs243024	<i>BCL11A</i>	Primary	30297969
2	65287896	rs2249105	<i>CEP68</i>	Primary	30297969
2	65355270	rs2052261	<i>CEP68</i>	Secondary	30297969
2	65655012	rs2028150	<i>CEP68</i>	Secondary	30297969
2	96913918	rs79046683	<i>TMEM127</i>	Primary	30297969
2	118071061	rs562386202	<i>DDX18</i>	Primary	30297969
2	121318166	rs11688931	<i>GLI2</i>	Secondary	30297969
2	121347612	rs11688682	<i>GLI2</i>	Primary	30297969

2	121378852	rs66477705	<i>GLI2</i>	Secondary	30297969
2	147861633	rs35999103	<i>PABPC1P2</i>	Primary	30297969
2	158339550	rs13426680	<i>CYTIP</i>	Primary	30297969
2	161135544	rs3772071	<i>RBMS1</i>	Primary	30297969
2	165513091	rs10195252	<i>GRB14/COBLL1</i>	Primary	30297969
2	165573194	rs13024606	<i>GRB14/COBLL1</i>	Secondary	30297969
2	219859171	rs113414093	<i>CRYBA2</i>	Primary	30297969
2	227101411	rs2972144	<i>IRS1</i>	Primary	30297969
3	3649850	rs9842137	.	Primary	32541925
3	12336507	rs11709077	<i>PPARG</i>	Primary	30297969
3	12489342	rs17819328	<i>PPARG</i>	Secondary	30297969
3	23455582	rs35352848	<i>UBE2E2</i>	Primary	30297969
3	23510044	rs17013314	<i>UBE2E2</i>	Secondary	30297969
3	36870230	rs11129735	.	Primary	32541925
3	46925539	rs11926707	<i>KIF9</i>	Primary	30297969
3	47242923	rs75423501	<i>KIF9</i>	Secondary	30297969
3	49980596	rs4688760	<i>RBM6</i>	Primary	30297969
3	53127677	rs2581787	<i>RFT1</i>	Primary	30297969
3	54828827	rs76263492	<i>CACNA2D3</i>	Primary	30297969
3	63962339	rs3774723	<i>PSMD6</i>	Primary	30297969
3	64460694	rs74368513	<i>PSMD6</i>	Secondary	30297969
3	64701146	rs9860730	<i>ADAMTS9</i>	Primary	30297969
3	72865183	rs13085136	<i>SHQ1</i>	Primary	30297969
3	77671721	rs2272163	<i>ROBO2</i>	Primary	30297969
3	89986280	rs11716527	.	Primary	32541925
3	123065778	rs11708067	<i>ADCY5</i>	Primary	30297969
3	124926637	rs649961	<i>SLC12A8</i>	Primary	30297969
3	128579324	rs181752889	.	Primary	32541925
3	129333182	rs9828772	<i>TMCC1</i>	Primary	30297969
3	129470067	rs559138871	<i>TMCC1</i>	Secondary	30297969
3	150066540	rs62271373	<i>TSC22D2</i>	Primary	30297969
3	152086533	rs13065698	<i>MBNL1</i>	Primary	30297969
3	152417881	rs74653713	<i>MBNL1</i>	Secondary	30297969
3	152433628	rs35497231	<i>MBNL1</i>	Secondary	30297969
3	168218841	rs7629630	<i>EGFEM1P</i>	Primary	30297969
3	170733076	rs9873618	<i>SLC2A2</i>	Primary	30297969
3	183738460	rs2872246	<i>ABCC5</i>	Primary	30297969
3	185503456	rs6780171	<i>IGF2BP2</i>	Primary	30297969
3	185514421	rs150111048	<i>IGF2BP2</i>	Secondary	30297969

3	185541213	rs11717959	<i>IGF2BP2</i>	Secondary	30297969
3	185829891	rs1516728	<i>IGF2BP2</i>	Secondary	30297969
3	186665645	rs3887925	<i>ST6GAL1</i>	Primary	30297969
3	186675277	rs7645517	<i>ST6GAL1</i>	Secondary	30297969
3	187740899	rs4686471	<i>LPP</i>	Primary	30297969
4	616608	rs111827885	<i>PCGF3</i>	Secondary	30297969
4	744972	rs1531583	<i>PCGF3</i>	Primary	30297969
4	1010077	rs35654957	<i>PCGF3</i>	Secondary	30297969
4	1784403	rs56337234	<i>MAEA</i>	Primary	30297969
4	3241845	rs362307	<i>HTT</i>	Primary	30297969
4	6302519	rs1801212	<i>WFS1</i>	Secondary	30297969
4	6306763	rs10937721	<i>WFS1</i>	Primary	30297969
4	17792869	rs12640250	<i>LCORL</i>	Primary	30297969
4	45186139	rs10938398	<i>GNPDA2</i>	Primary	30297969
4	52818664	rs2102278	<i>USP46</i>	Primary	30297969
4	53207093	rs114447556	<i>USP46</i>	Secondary	30297969
4	83578271	rs12642790	<i>SCD5</i>	Primary	30297969
4	89740894	rs1903002	<i>FAM13A</i>	Primary	30297969
4	89857291	rs576406049	<i>FAM13A</i>	Secondary	30297969
4	91243865	rs7656001	.	Primary	32541925
4	95091911	rs6821438	<i>SMARCAD1</i>	Primary	30297969
4	104140848	rs1580278	<i>SLC9B1</i>	Primary	30297969
4	137083193	rs1296328	<i>PABPC4L</i>	Primary	30297969
4	153513369	rs7669833	<i>TMEM154</i>	Primary	30297969
4	157652753	rs28819812	<i>PDGFC</i>	Primary	30297969
4	185717759	rs58730668	<i>ACSL1</i>	Primary	30297969
5	14610134	rs3845281	<i>ANKH</i>	Secondary	30297969
5	14751305	rs146886108	<i>ANKH</i>	Primary	30297969
5	14753745	rs17250977	<i>ANKH</i>	Secondary	30297969
5	14768092	rs6885132	<i>ANKH</i>	Secondary	30297969
5	14768766	rs76549217	<i>ANKH</i>	Secondary	30297969
5	44534364	rs62368490	<i>MRPS30</i>	Secondary	30297969
5	44682589	rs6884702	<i>MRPS30</i>	Primary	30297969
5	51791225	rs17261179	<i>ITGA1</i>	Secondary	30297969
5	52100489	rs3811978	<i>ITGA1</i>	Primary	30297969
5	52315682	rs62357230	<i>ITGA1</i>	Secondary	30297969
5	52774510	rs62370480	<i>ARL15</i>	Secondary	30297969
5	53271420	rs702634	<i>ARL15</i>	Primary	30297969
5	53412620	rs279744	<i>ARL15</i>	Secondary	30297969

5	55808475	rs465002	ANKRD55	Primary	30297969
5	55848669	rs2431115	ANKRD55	Secondary	30297969
5	55861595	rs9687832	ANKRD55	Secondary	30297969
5	56196604	rs96844	ANKRD55	Secondary	30297969
5	67714246	rs4976033	PIK3R1	Primary	30297969
5	75003678	rs2307111	POC5	Primary	30297969
5	76424949	rs4457053	ZBED3	Primary	30297969
5	78430607	rs1316776	DMGDH	Primary	30297969
5	86577352	rs7719891	RASA1	Primary	30297969
5	101232944	rs138337556	SLCO6A1	Primary	30297969
5	102338739	rs78408340	PAM	Secondary	30297969
5	102422968	rs115505614	PAM	Primary	30297969
5	133414622	rs244665	PHF15	Secondary	30297969
5	133864599	rs329122	PHF15	Primary	30297969
5	157928196	rs3934712	EBF1	Primary	30297969
6	7035734	rs112498319	RREB1	Secondary	30297969
6	7231843	rs9379084	RREB1	Primary	30297969
6	7255650	rs9505097	RREB1	Secondary	30297969
6	20679709	rs7756992	CDKAL1	Primary	30297969
6	32573415	rs601945	MHC	Primary	30297969
6	34247047	rs77136196	HMGA1	Primary	30297969
6	34524698	rs2233632	HMGA1	Secondary	30297969
6	40409243	rs34298980	LRFN2	Primary	30297969
6	41012405	rs4714422	.	Primary	32541925
6	43760327	rs11967262	VEGFA	Secondary	30297969
6	43814190	rs6458354	VEGFA	Primary	30297969
6	50788778	rs3798519	TFAP2B	Primary	30297969
6	51180765	rs2465043	TFAP2B	Secondary	30297969
6	67387490	rs555402748	SLC25A51P1	Primary	30297969
6	107431688	rs4946812	BEND3	Primary	30297969
6	126792095	rs11759026	CENPW	Primary	30297969
6	127416930	rs2800733	SOGA3	Primary	30297969
6	137300960	rs9494624	SLC35D3	Primary	30297969
6	139835329	rs2982521	MIR3668	Primary	30297969
6	140249466	rs616279	MIR3668	Secondary	30297969
6	160770312	rs474513	SLC22A3	Primary	30297969
6	164133001	rs4709746	QKI	Primary	30297969
7	1872921	rs4721089	.	Primary	32541925
7	2760750	rs798549	.	Primary	32541925

7	14898282	rs17168486	DGKB	Secondary	30297969
7	15063569	rs10228066	DGKB	Primary	30297969
7	15206239	rs2908334	DGKB	Secondary	30297969
7	23434606	rs78840640	IGF2BP3	Secondary	30297969
7	23512896	rs4279506	IGF2BP3	Primary	30297969
7	28198677	rs1708302	JAZF1	Primary	30297969
7	30728452	rs917195	CRHR2	Primary	30297969
7	44255643	rs878521	GCK	Primary	30297969
7	44365549	rs116913033	GCK	Secondary	30297969
7	102038318	rs56376556	FBXL13	Secondary	30297969
7	102486254	rs11496066	FBXL13	Primary	30297969
7	102987583	rs62482405	RELN	Secondary	30297969
7	103444978	rs39328	RELN	Primary	30297969
7	117495667	rs6976111	CTTNBP2	Primary	30297969
7	130027037	rs2268382	KLF14	Secondary	30297969
7	130457914	rs1562396	KLF14	Primary	30297969
7	150537635	rs62492368	AOC1	Primary	30297969
7	156930550	rs6459733	MNX1	Primary	30297969
8	4186731	rs117173251	.	Primary	32541925
8	9974824	rs17689007	MSRA	Primary	30297969
8	10808687	rs57327348	XKR6	Primary	30297969
8	19830921	rs10096633	LPL	Primary	30297969
8	30863938	rs10954772	PURG	Primary	30297969
8	41508577	rs13262861	ANK1	Primary	30297969
8	41509915	rs4736819	ANK1	Secondary	30297969
8	41552046	rs148766658	ANK1	Secondary	30297969
8	95685147	rs11786992	TP53INP1	Secondary	30297969
8	95961626	rs10097617	TP53INP1	Primary	30297969
8	96092422	rs187936726	TP53INP1	Secondary	30297969
8	97737741	rs149364428	CPQ	Primary	30297969
8	110123183	rs12680028	TRHR	Primary	30297969
8	118185025	rs3802177	SLC30A8	Primary	30297969
8	118404672	rs80244329	SLC30A8	Secondary	30297969
8	128711742	rs17772814	CASC11	Primary	30297969
8	129568078	rs1561927	PVT1	Primary	30297969
8	145507304	rs4977213	BOP1	Primary	30297969
8	145879883	rs12719778	BOP1	Secondary	30297969
9	3965689	rs510807	GLIS3	Secondary	30297969
9	4243045	rs79103584	GLIS3	Secondary	30297969

9	4291928	rs10974438	GLIS3	Primary	30297969
9	19067833	rs7022807	HAUS6	Primary	30297969
9	20241069	rs7867635	FOCAD	Primary	30297969
9	20662703	rs7847880	FOCAD	Secondary	30297969
9	22043612	rs1412830	CDKN2A/B	Secondary	30297969
9	22133773	rs76011118	CDKN2A/B	Secondary	30297969
9	22134068	rs10811660	CDKN2A/B	Primary	30297969
9	22134172	rs10757283	CDKN2A/B	Secondary	30297969
9	22157908	rs1333052	CDKN2A/B	Secondary	30297969
9	22301092	rs1575972	CDKN2A/B	Secondary	30297969
9	28410683	rs1412234	LINGO2	Primary	30297969
9	34074476	rs12001437	UBAP2	Primary	30297969
9	81359113	rs11137820	MTND2P8	Primary	30297969
9	81905590	rs17791513	TLE4	Primary	30297969
9	84308948	rs2796441	TLE1	Primary	30297969
9	97001682	rs55653563	ZNF169	Primary	30297969
9	97497494	rs12236906	ZNF169	Secondary	30297969
9	126586563	rs1752169	.	Primary	32541925
9	136149229	rs505922	ABO	Primary	30297969
9	139235606	rs78403475	GPSM1	Secondary	30297969
9	139241030	rs28505901	GPSM1	Primary	30297969
9	139507212	rs11793035	GPSM1	Secondary	30297969
9	139737088	9:139737088:G:A	GPSM1	Secondary	30297969
10	12307894	rs11257655	CDC123/CAMK1D	Primary	30297969
10	71321279	rs177045	NEUROG3	Secondary	30297969
10	71321658	rs61850200	NEUROG3	Secondary	30297969
10	71332301	rs41277236	NEUROG3	Secondary	30297969
10	71347311	rs549498088	NEUROG3	Secondary	30297969
10	71466578	rs2642588	NEUROG3	Primary	30297969
10	73835274	rs12773019	.	Primary	32541925
10	80952826	rs703972	ZMIZ1	Primary	30297969
10	81096589	rs1317617	ZMIZ1	Secondary	30297969
10	89769340	rs11202627	PTEN	Primary	30297969
10	93924663	rs7078559	HHEX/IDE	Secondary	30297969
10	94462427	rs10882101	HHEX/IDE	Primary	30297969
10	94479107	rs1112718	HHEX/IDE	Secondary	30297969
10	114699835	rs536643418	TCF7L2	Secondary	30297969
10	114702962	rs140242150	TCF7L2	Secondary	30297969
10	114703136	rs7918400	TCF7L2	Secondary	30297969

10	114740337	rs184509201	<i>TCF7L2</i>	Secondary	30297969
10	114751173	rs180988137	<i>TCF7L2</i>	Secondary	30297969
10	114757956	rs78025551	<i>TCF7L2</i>	Secondary	30297969
10	114758349	rs7903146	<i>TCF7L2</i>	Primary	30297969
10	114871594	rs34855922	<i>TCF7L2</i>	Secondary	30297969
10	122915345	rs72631105	<i>WDR11</i>	Primary	30297969
10	124193181	rs2280141	<i>PLEKHA1</i>	Primary	30297969
11	1704596	rs12802972	<i>INS/IGF2</i>	Secondary	30297969
11	2118860	rs11042596	<i>INS/IGF2</i>	Secondary	30297969
11	2151761	rs555759341	<i>INS/IGF2</i>	Secondary	30297969
11	2182519	rs571342427	<i>INS/IGF2</i>	Secondary	30297969
11	2197286	rs4929965	<i>INS/IGF2</i>	Primary	30297969
11	2372356	rs4930091	<i>KCNQ1</i>	Secondary	30297969
11	2579163	rs2283164	<i>KCNQ1</i>	Secondary	30297969
11	2634177	rs80102379	<i>KCNQ1</i>	Secondary	30297969
11	2672821	rs231349	<i>KCNQ1</i>	Secondary	30297969
11	2691500	rs231361	<i>KCNQ1</i>	Secondary	30297969
11	2755548	rs2283220	<i>KCNQ1</i>	Secondary	30297969
11	2850828	rs234853	<i>KCNQ1</i>	Secondary	30297969
11	2857194	rs2237895	<i>KCNQ1</i>	Primary	30297969
11	2858546	rs2237897	<i>KCNQ1</i>	Secondary	30297969
11	2908754	rs445084	<i>KCNQ1</i>	Secondary	30297969
11	14763828	rs141521721	<i>PDE3B</i>	Primary	30297969
11	17408404	rs5213	<i>KCNJ11</i>	Primary	30297969
11	17470143	rs67254669	<i>KCNJ11</i>	Secondary	30297969
11	28534898	rs4923543	<i>METTL15</i>	Primary	30297969
11	32460873	rs7943101	<i>QSER1</i>	Secondary	30297969
11	32927778	rs145678014	<i>QSER1</i>	Primary	30297969
11	33091735	rs528122639	<i>QSER1</i>	Secondary	30297969
11	34642668	rs286925	<i>PDHX</i>	Secondary	30297969
11	34982148	rs2767036	<i>PDHX</i>	Primary	30297969
11	43877934	rs1061810	<i>HSD17B12</i>	Primary	30297969
11	45912013	rs7115753	<i>CRY2</i>	Primary	30297969
11	47529947	rs7124681	<i>CELF1</i>	Primary	30297969
11	65294799	rs1783541	<i>MAP3K11</i>	Primary	30297969
11	68997225	rs61881115	<i>CCND1</i>	Secondary	30297969
11	69448758	rs11820019	<i>CCND1</i>	Primary	30297969
11	72460398	rs77464186	<i>CENTD2/ARAP1</i>	Primary	30297969
11	74625997	rs480840	.	Primary	32541925

11	92708710	rs10830963	<i>MTNR1B</i>	Primary	30297969
11	93013531	rs57235767	<i>MTNR1B</i>	Secondary	30297969
11	128042575	rs10893829	<i>ETS1</i>	Secondary	30297969
11	128234144	rs10750397	<i>ETS1</i>	Secondary	30297969
11	128398938	rs67232546	<i>ETS1</i>	Primary	30297969
11	128583975	rs112595469	<i>ETS1</i>	Secondary	30297969
12	4031104	rs10848958	<i>CCND2</i>	Secondary	30297969
12	4300172	rs11063028	<i>CCND2</i>	Secondary	30297969
12	4376089	rs4238013	<i>CCND2</i>	Secondary	30297969
12	4384696	rs3217792	<i>CCND2</i>	Secondary	30297969
12	4384844	rs76895963	<i>CCND2</i>	Primary	30297969
12	4399050	rs3217860	<i>CCND2</i>	Secondary	30297969
12	12871099	rs2066827	<i>CDKN1B</i>	Primary	30297969
12	26453283	rs718314	<i>ITPR2</i>	Primary	30297969
12	27965150	rs10842994	<i>KLHDC5</i>	Primary	30297969
12	66221060	rs2258238	<i>HMGA2</i>	Primary	30297969
12	66358347	rs1042725	<i>HMGA2</i>	Secondary	30297969
12	71522953	rs1796330	<i>TSPAN8/LGR5</i>	Primary	30297969
12	95928560	rs2197973	<i>USP44</i>	Primary	30297969
12	97562756	rs759111467	<i>RMST</i>	Secondary	30297969
12	97779248	rs557027608	<i>RMST</i>	Secondary	30297969
12	97848775	rs77864822	<i>RMST</i>	Primary	30297969
12	108629780	rs1426371	<i>WSCD2</i>	Primary	30297969
12	118412373	rs34965774	<i>KSR2</i>	Primary	30297969
12	118489636	rs12578639	<i>KSR2</i>	Secondary	30297969
12	121297815	rs11065299	<i>HNF1A</i>	Secondary	30297969
12	121380541	rs73226260	<i>HNF1A</i>	Secondary	30297969
12	121416864	rs1800574	<i>HNF1A</i>	Secondary	30297969
12	121432117	rs56348580	<i>HNF1A</i>	Primary	30297969
12	121501461	rs28638142	<i>HNF1A</i>	Secondary	30297969
12	121882395	rs73224262	<i>HNF1A</i>	Secondary	30297969
12	123450765	rs4148856	<i>MPHOSPH9</i>	Primary	30297969
12	124468572	rs7978610	<i>ZNF664</i>	Primary	30297969
12	124509177	rs825452	<i>ZNF664</i>	Secondary	30297969
12	133069698	rs12811407	<i>FBRSL1</i>	Primary	30297969
13	26776999	rs34584161	<i>RNF6</i>	Primary	30297969
13	28245127	rs9319382	.	Primary	32541925
13	31042452	rs11842871	<i>HMGB1</i>	Primary	30297969
13	33554302	rs576674	<i>KL</i>	Primary	30297969

13	51096095	rs963740	<i>DLEU1</i>	Primary	30297969
13	58366634	rs9537803	<i>PCDH17</i>	Primary	30297969
13	58965435	rs9569864	<i>PCDH17</i>	Secondary	30297969
13	59077406	rs9563615	<i>SRGAP2D</i>	Primary	30297969
13	59184234	rs76251711	<i>SRGAP2D</i>	Secondary	30297969
13	80717156	rs1359790	<i>SPRY2</i>	Primary	30297969
13	109947213	rs7987740	<i>IRS2</i>	Primary	30297969
13	110431626	rs4771648	<i>IRS2</i>	Secondary	30297969
14	23288935	rs17122772	<i>SLC7A7</i>	Primary	30297969
14	33302882	rs17522122	<i>AKAP6</i>	Primary	30297969
14	38848419	rs8017808	<i>CLEC14A</i>	Primary	30297969
14	79932041	rs17836088	<i>NRXN3</i>	Primary	30297969
14	91963722	rs8010382	<i>SMEK1</i>	Primary	30297969
14	103894071	rs62007683	<i>MARK3</i>	Primary	30297969
15	36392562	rs11073147	.	Primary	32541925
15	38834033	rs8032939	<i>RASGRP1</i>	Secondary	30297969
15	38873115	rs34715063	<i>RASGRP1</i>	Primary	30297969
15	41809205	rs11070332	<i>LTK</i>	Primary	30297969
15	42201410	rs543786825	<i>LTK</i>	Secondary	30297969
15	53091553	rs2456530	<i>ONECUT1</i>	Primary	30297969
15	53747228	rs528350911	<i>WDR72</i>	Primary	30297969
15	57456802	rs117483894	<i>TCF12</i>	Primary	30297969
15	60938816	rs8033609	.	Primary	32541925
15	62394264	rs8037894	<i>C2CD4A/B</i>	Primary	30297969
15	63871292	rs7178762	<i>USP3</i>	Primary	30297969
15	67260238	rs1874832	.	Primary	32541925
15	68080886	rs4776970	<i>MAP2K5</i>	Primary	30297969
15	75932129	rs13737	<i>PTPN9</i>	Primary	30297969
15	77818128	rs1005752	<i>HMG20A</i>	Primary	30297969
15	90423293	rs4932265	<i>AP3S2</i>	Primary	30297969
15	91511260	rs12910825	<i>PRC1</i>	Primary	30297969
16	295795	rs6600191	<i>ITFG3</i>	Primary	30297969
16	3583173	rs3751837	<i>CLUAP1</i>	Primary	30297969
16	28915217	rs8046545	<i>ATP2A1</i>	Primary	30297969
16	30045789	rs11642430	<i>FAM57B</i>	Primary	30297969
16	30419384	rs199795270	<i>FAM57B</i>	Secondary	30297969
16	53501946	rs4281707	<i>FTO</i>	Secondary	30297969
16	53758720	rs78020297	<i>FTO</i>	Secondary	30297969
16	53800954	rs1421085	<i>FTO</i>	Primary	30297969

16	69651866	rs862320	NFAT5	Primary	30297969
16	75234872	rs72802342	BCAR1	Primary	30297969
16	75516534	rs3115960	BCAR1	Secondary	30297969
16	81534790	rs2925979	CMIP	Primary	30297969
16	89564055	rs12920022	SPG7	Primary	30297969
17	3828086	rs1043246	ZZEF1	Secondary	30297969
17	3860356	rs3826482	ZZEF1	Secondary	30297969
17	4045440	rs1377807	ZZEF1	Primary	30297969
17	7549681	rs1641523	ATP1B2	Primary	30297969
17	7740170	rs62059712	ATP1B2	Secondary	30297969
17	9785187	rs7222481	GLP2R	Primary	30297969
17	17661802	rs4925109	RAI1	Primary	30297969
17	29413019	rs71372253	NF1	Primary	30297969
17	36046451	rs10962	HNF1B	Secondary	30297969
17	36063685	rs2189301	HNF1B	Secondary	30297969
17	36099952	rs10908278	HNF1B	Primary	30297969
17	40731411	rs34855406	MLX	Primary	30297969
17	47060322	rs35895680	TTL6	Primary	30297969
17	52140805	rs569511541	KIF2B	Primary	30297969
17	61965043	rs2727301	ACE	Secondary	30297969
17	62203304	rs60276348	ACE	Primary	30297969
17	65648427	rs11657492	BPTF	Secondary	30297969
17	65820153	rs558308082	BPTF	Secondary	30297969
17	65892507	rs61676547	BPTF	Primary	30297969
17	75386909	rs1656794	.	Primary	32541925
17	77895311	rs9912236	.	Primary	32541925
18	7070642	rs7240767	LAMA1	Primary	30297969
18	13271367	rs11662800	.	Primary	32541925
18	36278709	rs62080313	COMMD9	Primary	30297969
18	52604955	rs76197067	TCF4	Secondary	30297969
18	53050646	rs72926932	TCF4	Primary	30297969
18	53452144	rs28719468	TCF4	Secondary	30297969
18	54675384	rs17684074	WDR7	Primary	30297969
18	56876228	rs9957145	GRP	Primary	30297969
18	57848369	rs523288	MC4R	Primary	30297969
18	58056566	rs74452128	MC4R	Secondary	30297969
18	60668270	rs10469140	BCL2A	Secondary	30297969
18	60845884	rs12454712	BCL2A	Primary	30297969
19	4948862	rs7249758	UHRF1	Primary	30297969

19	5224998	rs116953931	<i>PTPRS</i>	Secondary	30297969
19	7240848	rs75253922	<i>INSR</i>	Primary	30297969
19	7970635	rs4804833	<i>MAP2K7</i>	Primary	30297969
19	12938471	rs755734872	<i>FARSA</i>	Secondary	30297969
19	13038415	rs3111316	<i>FARSA</i>	Primary	30297969
19	19388500	rs8107974	<i>TM6SF2</i>	Primary	30297969
19	19396616	rs188247550	<i>TM6SF2</i>	Secondary	30297969
19	33890838	rs10406327	<i>PEPD</i>	Primary	30297969
19	44938870	rs745903616	<i>TOMM40/APOE</i>	Secondary	30297969
19	45411941	rs429358	<i>TOMM40/APOE</i>	Primary	30297969
19	46157019	rs10406431	<i>GIPR</i>	Primary	30297969
19	46178661	rs2238689	<i>GIPR</i>	Secondary	30297969
19	46351837	rs533172266	<i>GIPR</i>	Secondary	30297969
19	47569003	rs3810291	<i>ZC3H4</i>	Primary	30297969
20	21466795	rs13041756	<i>NKX2.2</i>	Primary	30297969
20	32596704	rs2268078	<i>RALY</i>	Primary	30297969
20	42905415	rs76811102	<i>HNF4A</i>	Secondary	30297969
20	43001721	rs4810426	<i>HNF4A</i>	Secondary	30297969
20	43023355	rs191830490	<i>HNF4A</i>	Secondary	30297969
20	43042364	rs1800961	<i>HNF4A</i>	Primary	30297969
20	43233649	rs11696357	<i>HNF4A</i>	Secondary	30297969
20	45317678	rs560716466	<i>EYA2</i>	Secondary	30297969
20	45598564	rs6063048	<i>EYA2</i>	Primary	30297969
20	48832135	rs11699802	<i>CEBPB</i>	Primary	30297969
20	51223594	rs34454109	<i>TSHZ2</i>	Primary	30297969
20	57394628	rs6070625	<i>GNAS</i>	Primary	30297969
20	57551099	rs862016	<i>GNAS</i>	Secondary	30297969
20	62450664	rs6011155	<i>ZBTB46</i>	Secondary	30297969
20	62693175	rs59944054	<i>TCEA2</i>	Primary	30297969
21	47767295	rs75756987	.	Primary	32541925
22	30609554	rs6518681	<i>MTMR3/ASCC2</i>	Primary	30297969
22	32348841	rs117001013	<i>YWHAH</i>	Primary	30297969
22	41489920	rs5758223	<i>EP300</i>	Primary	30297969
22	44324730	rs738408	<i>PNPLA3</i>	Primary	30297969
22	50356850	rs1801645	<i>PIM3</i>	Primary	30297969
22	50604696	rs112915006	<i>PIM3</i>	Secondary	30297969

BMI, body mass index.

Supplementary Table 13. Previously reported genome-wide significant loci for coronary artery disease among European ancestry.

Chromosome	Position (Build 37 bp)	SNP	Nearest gene/Locus	PMID
1	2245570	rs2843152	<i>SKI</i>	36474045
1	2252205	rs36096196	<i>MORN1</i>	29212778
1	2985885	rs7413494	<i>PRDM16</i>	36474045
1	3325912	rs2493298	<i>PRDM16</i>	29212778
1	27284913	rs79598313	<i>KDF1</i>	36474045
1	38461319	rs61776719	<i>FHL3</i>	29212778
1	55489542	rs34232196	<i>BSND</i>	36474045
1	55505647	rs11591147	<i>PCSK9</i>	28714975
1	55521313	rs472495	<i>PCSK9</i>	36474045
1	56877509	rs11206803	<i>PPAP2B</i>	36474045
1	57016131	rs56170783	<i>PPAP2B</i>	28714975
1	59433354	rs71646019	<i>LOC100131060</i>	36474045
1	109817192	rs7528419	<i>SORT1</i>	28714975
1	109817590	rs12740374	<i>CELSR2</i>	36474045
1	114173410	rs1230666	<i>MAGI3</i>	36474045
1	115753482	rs11806316	<i>NGF</i>	29212778
1	115902514	rs61797068	<i>NGF</i>	36474045
1	149995265	rs67807996	<i>OTUD7B</i>	36474045
1	150572037	rs11585169	<i>MCL1</i>	36474045
1	151762308	rs11810571	<i>TDRKH</i>	28584231
1	154395946	rs6689306	<i>IL6R</i>	28714975
1	154419843	rs6686750	<i>IL6R</i>	36474045
1	169094459	rs1892094	<i>ATP1B1</i>	28530674
1	169314833	rs61806987	<i>NME7</i>	36474045
1	200646073	rs6700559	<i>DDX59-CAMSAP2</i>	28530674
1	201872264	rs2820315	<i>LMOD1</i>	28530674
1	210468999	rs60154123	<i>HHA</i>	29212778
1	222823743	rs67180937	<i>MIA3</i>	28714975
1	222828704	rs17163363	<i>MIA3</i>	36474045
1	230845794	rs699	<i>AG</i>	29212778
2	19942473	rs16986953	<i>AK097927</i>	28714975
2	21270554	rs585967	<i>APOB</i>	28714975
2	21286057	rs515135	<i>APOB</i>	36474045
2	44072576	rs4299376	<i>ABCG5/ABCG8</i>	28714975
2	44074431	rs4245791	<i>ABCG8</i>	36474045
2	44075483	rs76866386	<i>ABCG8</i>	36474045
2	45896437	rs582384	<i>PRKCE</i>	29212778

2	60619028	rs243071	<i>MIR4432</i>	36474045
2	85762048	rs10176176	<i>PARTICL</i>	36474045
2	85788175	rs7568458	<i>VAMP5/ VAMP8/ GGCX</i>	28714975
2	128785663	rs114192718	<i>SAP130</i>	36474045
2	144186475	rs4662330	<i>ARHGAP15</i>	36474045
2	145270592	rs6740731	<i>ZEB2</i>	36474045
2	145286559	rs17678683	<i>ZEB2/ AC074093.1</i>	28714975
2	145831428	rs10928241	<i>TEX41</i>	36474045
2	148377860	rs35611688	<i>ACVR2A</i>	36474045
2	164930382	rs10930115	<i>FIGN</i>	36474045
2	164957251	rs12999907	<i>FIGN</i>	29212778
2	188196469	rs840616	<i>CALCRL</i>	29212778
2	203831212	rs114123510	<i>WDR12</i>	28714975
2	203877233	rs148812085	<i>NBEAL1</i>	36474045
2	216291359	rs17517928	<i>FN1</i>	28714974
2	216299629	rs1250247	<i>FN1</i>	36474045
2	218680529	rs2161967	<i>TNSI</i>	36474045
2	218683154	rs2571445	<i>TNS1a</i>	28530674
2	227062080	rs952227	<i>LOC646736</i>	36474045
2	227100698	rs2972146	<i>LOC646736</i>	28714974
2	230005505	rs4140748	<i>PID1</i>	36474045
2	233584109	rs13003675	<i>KCNJ13/ GIGYF2</i>	28714975
2	233645691	rs283485	<i>GIGYF2</i>	36474045
2	238223955	rs11677932	<i>COL6A3</i>	29212778
3	14926351	rs34991912	<i>FGD5</i>	36474045
3	14928077	rs748431	<i>FGD5</i>	28714974
3	46688562	rs7633770	<i>ALS2CL</i>	29212778
3	48193515	rs7617773	<i>CDC25A</i>	29212778
3	49162284	rs34759087	<i>LAMB2</i>	36474045
3	49448566	rs7623687	<i>RHOA</i>	28714974
3	52848207	rs77347777	<i>ITIH4</i>	36474045
3	124453022	rs17843797	<i>UMPS-ITGB5</i>	28714974
3	124475201	rs142695226	<i>UMPS/ITGB5</i>	28584231
3	132257961	rs10512861	<i>DNAJC13</i>	29212778
3	135800409	rs34330586	<i>PPP2R3A</i>	36474045
3	136069472	rs667920	<i>STAG1</i>	29212778
3	138092889	rs185244	<i>MRAS</i>	36474045
3	138099161	rs139016349	<i>MRAS</i>	28714975
3	153839866	rs12493885	<i>ARHGEF26</i>	28714974

3	153937753	rs357494	<i>ARHGEF26</i>	36474045
3	153980130	rs433903	<i>ARHGEF26/DHX36e</i>	28584231
3	156852592	rs4266144	<i>CCNL1</i>	29212778
3	172115902	rs12897	<i>FNDC3B</i>	29212778
3	172117455	rs34229028	<i>FNDC3B</i>	36474045
4	3449652	rs16844401	<i>HGFAC</i>	29212778
4	54572066	rs17083333	<i>LNXI</i>	36474045
4	57781754	rs781663	<i>REST</i>	36474045
4	57839051	rs72627509	<i>REST/NOA1</i>	28714975
4	77416627	rs12500824	<i>SHROOM3</i>	29212778
4	81181072	rs10857147	<i>FGF5</i>	28714974
4	82587050	rs11099493	<i>HNRNPD</i>	29212778
4	82625720	rs36002015	<i>RASGEF1B</i>	36474045
4	96117371	rs3775058	<i>UNC5C</i>	29212778
4	120901336	rs11723436	<i>MAD2L1/PDE5A</i>	28584231
4	120909501	rs7678555	<i>MAD2L1</i>	28714974
4	146782837	rs35879803	<i>ZNF827</i>	28584231
4	146784774	rs13124853	<i>ZNF827</i>	36474045
4	148273397	rs13120678	<i>EDNRA</i>	36474045
4	148401190	rs6841581	<i>EDNRA</i>	28714975
4	156433520	rs7440763	<i>MAP9</i>	36474045
4	156638073	rs3796587	<i>GUCY1A3</i>	36474045
4	156638573	rs2306556	<i>GUCY1A3</i>	28714975
4	169687725	rs7696431	<i>PALLD</i>	29212778
4	169688000	rs869396	<i>PALLD</i>	36474045
5	9552338	rs17263917	<i>SNORD123</i>	36474045
5	9556694	rs1508798	<i>SEMA5A</i>	29212778
5	52193125	rs4074793	<i>ITGA1</i>	36474045
5	55441571	rs62362364	<i>ANKRD55</i>	36474045
5	55860781	rs3936511	<i>MAP3K1</i>	29212778
5	55860866	rs3936510	<i>MAP3K1</i>	36474045
5	74656539	rs12916	<i>HMGCR</i>	36474045
5	108085190	rs112949822	<i>FER</i>	36474045
5	118448279	rs13169691	<i>DMXL1</i>	36474045
5	121278751	rs4345341	<i>SRFBP1</i>	36474045
5	121413208	rs1800449	<i>LOX</i>	28714974
5	127926190	rs6883598	<i>FBN2</i>	36474045
5	131759825	rs77335401	<i>SLC22A4/SLC22A5</i>	28714975
5	131795310	rs10477741	<i>IRF-AS1</i>	36474045

5	141915692	rs249760	<i>FGF1</i>	36474045
5	142494165	rs3776307	<i>ARHGAP26</i>	36474045
5	142516897	rs246600	<i>ARHGAP26</i>	28530674
6	1617143	rs9501744	<i>FOXC1</i>	29212778
6	1617327	rs72836800	<i>FOXC1</i>	36474045
6	11327021	rs742115	<i>ADTRP/ C6orf105</i>	28714975
6	12903957	rs9349379	<i>PHACTR1</i>	28714975
6	22583856	rs35541991	<i>HDGFL1</i>	28584231
6	22612629	rs6909752	<i>HDGFL1</i>	36474045
6	31346898	rs9266631	<i>MICA</i>	36474045
6	31888367	rs3130683	<i>C2</i>	28714975
6	34769765	rs4472337	<i>ANKS1A</i>	28714975
6	34793124	rs9469899	<i>UHRF1BP1</i>	36474045
6	36638636	rs1321309	<i>CDKN1A</i>	29212778
6	39152041	rs56015508	<i>KCNK5</i>	28714975
6	39171862	rs733701	<i>KCNK5</i>	36474045
6	43068370	rs1034246	<i>PTK7</i>	36474045
6	43758873	rs6905288	<i>VEGFA</i>	29212778
6	57145562	rs11752218	<i>PRIM2</i>	36474045
6	57160572	rs9367716	<i>PRIM2</i>	29212778
6	82595959	rs9361867	<i>FAM46A</i>	36474045
6	82612271	rs4613862	<i>FAM46A</i>	29212778
6	97029871	rs2983896	<i>FHL5</i>	36474045
6	126678331	rs35510806	<i>CENPW</i>	36474045
6	126717064	rs1591805	<i>CENPW</i>	29212778
6	133999868	rs6919211	<i>TARID</i>	36474045
6	134173151	rs12202017	<i>TCF21</i>	28714975
6	134202690	rs2327426	<i>TCF21</i>	36474045
6	134378151	rs2492304	<i>SLC2A12</i>	36474045
6	150997401	rs17080091	<i>PLEKHG1</i>	29212778
6	150997440	rs17080093	<i>PLEKHG1</i>	36474045
6	160535878	rs6932293	<i>SLC22A1</i>	36474045
6	160720747	rs56195640	<i>SLC22A2</i>	36474045
6	161010118	rs10455872	<i>SLC22A3/ LPAL2/ LPA/ PLG</i>	28714975
6	161017363	rs73596816	<i>LPA</i>	36474045
6	161024291	rs79018195	<i>LPA</i>	36474045
6	161032250	rs192425087	<i>LPA</i>	36474045
6	161097871	rs1998043	<i>LPA</i>	36474045
6	161104918	rs28867400	<i>LPA</i>	36474045

6	161111700	rs186696265	<i>PLG</i>	36474045
6	161177756	rs184278183	<i>PLG</i>	36474045
7	1911281	rs62435159	<i>MAD1L1</i>	36474045
7	1937261	rs10267593	<i>MAD1L1</i>	29212778
7	6446027	rs10951983	<i>RAC1</i>	36474045
7	6486067	rs7797644	<i>DAGLB</i>	29212778
7	12261911	rs11509880	<i>TMEM106B</i>	29212778
7	19049388	rs2107595	<i>HDAC9</i>	28714975
7	20300416	rs10486389	<i>MACC1</i>	36474045
7	35277093	rs2215614	<i>TBX20</i>	36474045
7	45077978	rs2107732	<i>CCM2</i>	29212778
7	106941324	rs12112877	<i>COG5</i>	36474045
7	107176780	rs112370447	<i>7q22</i>	28714975
7	117100046	rs13222797	<i>CFTR</i>	36474045
7	117332914	rs975722	<i>CTTNBP2</i>	29212778
7	129663496	rs11556924	<i>ZC3HC1</i>	28714975
7	139757136	rs10237377	<i>PARP12</i>	28530674
7	139760540	rs756142636	<i>PARP12</i>	36474045
7	150690176	rs3918226	<i>NOS3</i>	28714975
8	18260431	rs4646249	<i>NAT2</i>	36474045
8	18286997	rs6997340	<i>NAT2</i>	29212778
8	19813529	rs268	<i>LPL</i>	36474045
8	19865263	rs2083636	<i>LPL</i>	28714975
8	19865747	rs894211	<i>LPL</i>	36474045
8	19916120	rs66778572	<i>SLC18A1</i>	36474045
8	22033615	rs6984210	<i>BMP1</i>	29212778
8	22048490	rs56408342	<i>BMP1</i>	36474045
8	25061807	rs1510758	<i>DOCK5</i>	36474045
8	95278307	rs34917849	<i>GEM</i>	36474045
8	106565414	rs10093110	<i>ZFPM2</i>	29212778
8	126478450	rs2001846	<i>TRIB1</i>	36474045
8	126490972	rs2954029	<i>TRIB1</i>	28714975
9	13724051	rs10961206	<i>C9orf146</i>	36474045
9	19436055	rs10811183	<i>ACER2</i>	36474045
9	21843842	rs11523031	<i>MTAP</i>	36474045
9	22011083	rs76959412	<i>CDKN2B-AS1</i>	36474045
9	22098619	rs2891168	<i>CDKN2BAS</i>	28714975
9	22101702	rs6475608	<i>CDKN2B-AS1</i>	36474045
9	110517794	rs944172	<i>KLF4</i>	29212778

9	110530324	rs1967604	<i>KLF4</i>	36474045
9	113169775	rs111245230	<i>SVEP1</i>	28714975
9	123726749	rs41312891	<i>C5</i>	36474045
9	124420173	rs885150	<i>DAB2IP</i>	29212778
9	136149399	rs507666	<i>ABO</i>	28714975
9	136153875	rs651007	<i>ABO</i>	36474045
10	12275947	rs17566555	<i>CDC123</i>	36474045
10	12303813	rs61848342	<i>CDC123</i>	29212778
10	30317073	rs9337951	<i>JCAD</i>	36474045
10	30321598	rs1887318	<i>KIAA1462</i>	28714975
10	44480811	rs1870634	<i>CXCL12</i>	28714975
10	44740010	rs2457480	<i>CXCL12</i>	36474045
10	44741256	rs494207	<i>CXCL12</i>	36474045
10	82251514	rs17680741	<i>TSPAN14</i>	29212778
10	91004886	rs2246942	<i>LIPA</i>	28714975
10	91007360	rs1051338	<i>LIPA</i>	36474045
10	96029170	rs55753709	<i>PLCE1</i>	36474045
10	99923763	rs884811	<i>R3HCC1L</i>	36474045
10	104604916	rs11191416	<i>CYP17A1/ CNM2/ NT5C2</i>	28714975
10	104776205	rs77787671	<i>CNM2</i>	36474045
10	105643223	rs2067831	<i>OBFC1</i>	36474045
10	105693644	rs4918072	<i>STN1</i>	29212778
10	124230750	rs2672592	<i>HTRA1</i>	36474045
10	124237612	rs4752700	<i>HTRA1</i>	29212778
11	5701074	rs11601507	<i>TRIM5</i>	29212778
11	9323353	rs4537761	<i>TMEM41B</i>	36474045
11	9751196	rs10840293	<i>SWAP70</i>	28714975
11	9762274	rs360153	<i>SWAP70</i>	36474045
11	10284499	rs201267813	<i>MRV11/CTR9</i>	28714975
11	13295751	rs11316597	<i>ARNTL</i>	36474045
11	13301548	rs1351525	<i>ARNTL</i>	28584231
11	32380521	rs7118294	<i>WT1</i>	36474045
11	43696917	rs7116641	<i>HSD17B12</i>	29212778
11	65391317	rs12801636	<i>PCNX3</i>	28530674
11	65405600	rs2306363	<i>SIPA1</i>	36474045
11	75274150	rs590121	<i>SERPINH1</i>	28530674
11	75277628	rs584961	<i>SERPINH1</i>	36474045
11	100593538	rs633185	<i>ARHGAP42</i>	36474045
11	100624599	rs7947761	<i>ARHGAP42</i>	29212778

11	102795606	rs1892971	<i>MMP13</i>	36474045
11	103673294	rs2839812	<i>PDGFD</i>	28714975
11	110244360	rs10488763	<i>FDX1</i>	36474045
11	116648917	rs964184	<i>ZNF259/ APOA5/ APOA1</i>	28714975
11	118949331	rs1177562	<i>VPS11</i>	36474045
11	120363937	rs4938809	<i>ARHGEF12</i>	36474045
11	126262638	rs10790800	<i>ST3GAL4</i>	36474045
12	7175872	rs11838267	<i>CIS</i>	29212778
12	7178440	rs72447384	<i>CIS</i>	36474045
12	20220033	rs10841443	<i>RP11-664H17.1</i>	28714974
12	54513915	rs11170820	<i>HOXC4</i>	28584231
12	54521594	rs75160195	<i>LOC400043</i>	36474045
12	57843711	rs2229357	<i>LRP1</i>	28714975
12	90008959	rs2681472	<i>ATP2B1</i>	28714975
12	95355541	rs7306455	<i>NDUFA12</i>	29212778
12	95507971	rs11107903	<i>FGD6</i>	36474045
12	111910219	rs10774625	<i>SH2B3</i>	28714975
12	115353368	rs34606058	<i>TBX3</i>	36474045
12	118265441	rs11830157	<i>KSR2</i>	28714975
12	121416988	rs2244608	<i>HNF1A</i>	28714974
12	121454313	rs2258287	<i>C12orf43-HNF1A</i>	28530674
12	124409502	rs7133378	<i>DNAH10</i>	36474045
12	124427306	rs11057401	<i>CCDC92</i>	28714974
12	125307053	rs11057830	<i>SCARB1</i>	28530674
12	125315647	rs7485656	<i>SCARB1</i>	36474045
12	125336956	rs7296737	<i>SCARB1</i>	36474045
13	28962686	rs17086617	<i>FLT1</i>	36474045
13	29022645	rs1924981	<i>FLT1</i>	28714975
13	33058333	rs9591012	<i>N4BP2L2</i>	29212778
13	33126074	rs7991314	<i>N4BP2L2</i>	36474045
13	99434810	rs8000794	<i>DOCK9</i>	36474045
13	110818102	rs11617955	<i>COL4A1/ COL4A2</i>	28714975
13	110834746	rs3783113	<i>COL4A1</i>	36474045
13	110918660	rs11619113	<i>COL4A1</i>	36474045
13	110954353	rs4773141	<i>COL4A1</i>	36474045
13	111049623	rs9515203	<i>COL4A2</i>	36474045
13	111108436	rs7333991	<i>COL4A2</i>	36474045
13	113618496	rs4907571	<i>MCF2L-ASI</i>	36474045
13	113631780	rs1317507	<i>MCF2L</i>	29212778

14	58794001	rs2145598	<i>ARID4A</i>	29212778
14	75446879	rs10131894	<i>EIF2B2</i>	36474045
14	75614504	rs3832966	<i>TMED10/ZC2HC1C/RPS6KL1/NEK9/EIF2B2/ACYP1</i>	28584231
14	94838142	rs112635299	<i>SERPINA2</i>	29212778
14	100123487	rs36033161	<i>HHIPL1</i>	36474045
14	100145710	rs10139550	<i>HHIPL1</i>	28714975
15	58730498	rs588136	<i>LIPC</i>	36474045
15	65024204	rs6494488	<i>OAZ2, RBPMS2</i>	28530674
15	67441750	rs72743461	<i>SMAD3</i>	28714975
15	67455630	rs56062135	<i>SMAD3</i>	36474045
15	79051705	rs112238647	<i>ADAMTS7</i>	36474045
15	79065380	rs7177201	<i>ADAMTS7</i>	36474045
15	79123054	rs7164479	<i>ADAMTS7</i>	28714975
15	79141784	rs7173743	<i>MORF4L1</i>	36474045
15	81385552	rs2683260	<i>CFAP161</i>	36474045
15	89565257	rs1807214	<i>ABHD2</i>	36474045
15	89574484	rs2083460	<i>MFGE8/ ABHD2</i>	28714975
15	91428197	rs2071382	<i>FURIN/ FES</i>	28714975
15	91428589	rs7183988	<i>FES</i>	36474045
15	96146414	rs17581137	<i>LOC145820</i>	36474045
16	15909513	rs12691049	<i>MYH11</i>	36474045
16	56987015	rs12446515	<i>CETP</i>	36474045
16	56989590	rs247616	<i>CETP</i>	28714975
16	72130815	rs1050362	<i>DHX38</i>	28530674
16	72148419	rs12445401	<i>DHX38</i>	36474045
16	75308440	rs33928862	<i>BCAR1</i>	28584231
16	75387533	rs3851738	<i>CFDPI</i>	28714974
16	75442143	rs8046696	<i>CFDPI</i>	36474045
16	81510742	rs10493891	<i>CMIP</i>	36474045
16	81906423	rs7199941	<i>PLCG2</i>	29212778
16	81907867	rs7189462	<i>PLCG2</i>	36474045
16	83045790	rs7500448	<i>CDH13</i>	28714974
17	2068932	rs4790881	<i>SMG6</i>	36474045
17	2088848	rs113348108	<i>SMG6</i>	28714975
17	17593453	rs9897596	<i>RAI1/ PEMT/ RASD1</i>	28714975
17	17726965	rs12936927	<i>SREBF1</i>	36474045
17	27938424	rs11080107	<i>ANKRD13B</i>	36474045
17	27941886	rs13723	<i>CORO6</i>	29212778
17	30033514	rs76954792	<i>COPRS</i>	29212778

17	40257163	rs2074158	<i>DHX58</i>	29212778
17	40270081	rs12952244	<i>KAT2A</i>	36474045
17	40571284	rs8068844	<i>PTRF</i>	36474045
17	45013271	rs17608766	<i>GOSR2</i>	28530674
17	47123423	rs4643373	<i>UBE2Z</i>	28714975
17	47417942	rs5820757	<i>ZNF652</i>	36474045
17	59232365	rs11655024	<i>BCAS3</i>	36474045
17	59286644	rs8068952	<i>BCAS3</i>	28714975
17	62387091	rs1867624	<i>PECAM1</i>	28530674
17	62392403	rs11079536	<i>PECAM1</i>	36474045
17	66463985	rs2909217	<i>WIP1I</i>	36474045
17	73841285	rs2410859	<i>UNC13D</i>	36474045
18	20009691	rs9951447	<i>CTAGE1</i>	36474045
18	46515916	rs9945890	<i>SMAD7</i>	36474045
18	47213682	rs12965923	<i>LIPG</i>	36474045
18	47229717	rs9964304	<i>ACAA2</i>	29212778
18	56960510	rs11663411	<i>CPLX4</i>	36474045
18	57832856	rs35614134	<i>PMAIP1/MC4R</i>	28714975
18	57852587	rs476828	<i>MC4R</i>	36474045
19	8429323	rs116843064	<i>ANGPTL4</i>	28714975
19	11188117	rs55997232	<i>LDLR</i>	36474045
19	11202306	rs6511720	<i>LDLR</i>	28714975
19	11216617	rs10422256	<i>LDLR</i>	36474045
19	11231203	rs72658867	<i>LDLR</i>	36474045
19	11526765	rs167479	<i>RGL3</i>	36474045
19	17219105	rs7246865	<i>MYO9B</i>	36474045
19	17829608	rs10410487	<i>MAP1S</i>	36474045
19	17855763	rs73015714	<i>MAP1S</i>	29212778
19	18575193	rs78030362	<i>ELL</i>	36474045
19	33386556	rs10417115	<i>ZNF507/LOC400684</i>	28714975
19	41790086	rs138120077	<i>HNRNPUL1/TGFB1ed/CCDC97</i>	28584231
19	41790086	rs768453105	<i>HNRNPUL1</i>	36474045
19	41837615	rs11466359	<i>TGFB1</i>	36474045
19	41854534	rs8108632	<i>TGFB1</i>	28714974
19	41860296	rs1800469	<i>B9D2</i>	36474045
19	45411941	rs429358	<i>APOE</i>	36474045
19	45412079	rs7412	<i>APOE/APOC1</i>	28714975
19	45742498	rs183657985	<i>EXOC3L2</i>	36474045
19	46301479	rs8108474	<i>RSPH6A</i>	36474045

20	17596155	rs1132274	<i>RRBP1</i>	36474045
20	33358499	rs6088595	<i>NCOA6</i>	36474045
20	33764554	rs867186	<i>PROCRa</i>	28530674
20	33799176	rs17406518	<i>MMP24</i>	36474045
20	39142516	rs2207132	<i>MAFB</i>	36474045
20	39924279	rs6102343	<i>ZHX3</i>	29212778
20	44586023	rs3827066	<i>PCIF1</i>	29212778
20	44608901	rs8124182	<i>ZNF335</i>	36474045
20	47433150	rs2008614	<i>PREX1</i>	36474045
20	57714025	rs260020	<i>ZNF831</i>	29212778
20	57739469	rs6026739	<i>ZNF831</i>	36474045
21	30533076	rs2832227	<i>MAP3K7CL</i>	29212778
21	35593827	rs28451064	<i>KCNE2</i>	28714975
21	35605863	rs149487184	<i>NCRNA00310</i>	36474045
22	19960184	rs71313931	<i>ARVCF</i>	36474045
22	24555861	rs12484557	<i>CABIN1</i>	36474045
22	24658858	rs180803	<i>POM121L9P/ADORA2A</i>	28714975
22	24677831	rs5760309	<i>SPECCIL</i>	36474045
22	30669883	rs6006426	<i>OSM</i>	36474045
22	43623972	rs139012	<i>SCUBE1</i>	36474045

Supplementary Table 14. Detailed annotation of genome-wide significant SNPs identified by cross-trait meta-analysis.

SNP	Location	Consequence	IMPACT	SYMBOL	Feature type	BIOTYPE
T2DM and CAD						
rs227199	1: 210265384-210265384	intron_variant, non_coding_transcript_variant	MODIFIER	<i>SYT14</i>	Transcript	processed_transcript
rs227199	1: 210265384-210265384	intron_variant	MODIFIER	<i>SYT14</i>	Transcript	protein_coding
rs62618693	11: 32956492-32956492	missense_variant	MODERATE	<i>QSER1</i>	Transcript	protein_coding
rs62618693	11: 32956492-32956492	downstream_gene_variant	MODIFIER	<i>QSER1</i>	Transcript	processed_transcript
rs62618693	11: 32956492-32956492	downstream_gene_variant	MODIFIER	<i>QSER1</i>	Transcript	protein_coding
rs2306363	11: 65405600-65405600	downstream_gene_variant	MODIFIER	<i>PCNXL3</i>	Transcript	protein_coding
rs2306363	11: 65405600-65405600	upstream_gene_variant	MODIFIER	<i>SIPA1</i>	Transcript	protein_coding
rs2306363	11: 65405600-65405600	downstream_gene_variant	MODIFIER	<i>PCNXL3</i>	Transcript	retained_intron
rs2306363	11: 65405600-65405600	downstream_gene_variant	MODIFIER	<i>PCNXL3</i>	Transcript	processed_transcript
rs2306363	11: 65405600-65405600	5_prime_UTR_variant	MODIFIER	<i>SIPA1</i>	Transcript	protein_coding
rs2306363	11: 65405600-65405600	upstream_gene_variant	MODIFIER	<i>SIPA1</i>	Transcript	retained_intron
rs2306363	11: 65405600-65405600	downstream_gene_variant	MODIFIER	<i>MIR4690</i>	Transcript	miRNA
rs2306363	11: 65405600-65405600	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	promoter
rs2306363	11: 65405600-65405600	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	CTCF_binding_site
rs660549	12: 121300988-121300988	intron_variant	MODIFIER	<i>SPPL3</i>	Transcript	protein_coding
rs1169288	12: 121416650-121416650	missense_variant	MODERATE	<i>HNFI1A</i>	Transcript	protein_coding
rs1169288	12: 121416650-121416650	intron_variant, non_coding_transcript_variant	MODIFIER	<i>HNFI1A-AS1</i>	Transcript	antisense
rs1169288	12: 121416650-121416650	intron_variant	MODIFIER	<i>HNFI1A</i>	Transcript	protein_coding
rs1169288	12: 121416650-121416650	splice_region_variant, intron_variant	LOW	<i>HNFI1A</i>	Transcript	protein_coding
rs1169288	12: 121416650-121416650	missense_variant, NMD_transcript_variant	MODERATE	<i>HNFI1A</i>	Transcript	nonsense_mediated_decay
rs1169288	12: 121416650-121416650	splice_region_variant, intron_variant, NMD_transcript_variant	LOW	<i>HNFI1A</i>	Transcript	nonsense_mediated_decay
rs1169288	12: 121416650-121416650	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	promoter
rs2257813	12: 121447519-121447519	intron_variant	MODIFIER	<i>C12orf43</i>	Transcript	protein_coding
rs2257813	12: 121447519-121447519	upstream_gene_variant	MODIFIER	<i>C12orf43</i>	Transcript	retained_intron
rs2257813	12: 121447519-121447519	intron_variant, non_coding_transcript_variant	MODIFIER	<i>C12orf43</i>	Transcript	retained_intron
rs2257813	12: 121447519-121447519	intron_variant, NMD_transcript_variant	MODIFIER	<i>C12orf43</i>	Transcript	nonsense_mediated_decay
rs2257813	12: 121447519-121447519	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	promoter_flanking_region
rs2257813	12: 121447519-121447519	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	CTCF_binding_site
rs56158042	12: 121455589-121455589	downstream_gene_variant	MODIFIER	<i>OASL</i>	Transcript	protein_coding
rs56158042	12: 121455589-121455589	upstream_gene_variant	MODIFIER	<i>C12orf43</i>	Transcript	protein_coding
rs56158042	12: 121455589-121455589	upstream_gene_variant	MODIFIER	<i>C12orf43</i>	Transcript	retained_intron
rs56158042	12: 121455589-121455589	upstream_gene_variant	MODIFIER	<i>C12orf43</i>	Transcript	nonsense_mediated_decay
rs2893895	12: 121693947-121693947	intron_variant	MODIFIER	<i>CAMKK2</i>	Transcript	protein_coding
rs2893895	12: 121693947-121693947	intron_variant, non_coding_transcript_variant	MODIFIER	<i>CAMKK2</i>	Transcript	processed_transcript
rs4765127	12: 124460167-124460167	upstream_gene_variant	MODIFIER	<i>CCDC92</i>	Transcript	protein_coding
rs4765127	12: 124460167-124460167	intron_variant	MODIFIER	<i>ZNF664</i>	Transcript	protein_coding
rs4765127	12: 124460167-124460167	intron_variant, non_coding_transcript_variant	MODIFIER	<i>ZNF664</i>	Transcript	processed_transcript
rs4765127	12: 124460167-124460167	downstream_gene_variant	MODIFIER	<i>ZNF664</i>	Transcript	retained_intron
rs4765127	12: 124460167-124460167	intron_variant	MODIFIER	<i>FAM101A</i>	Transcript	protein_coding
rs4765127	12: 124460167-124460167	intron_variant, non_coding_transcript_variant	MODIFIER	<i>FAM101A</i>	Transcript	processed_transcript
rs4765127	12: 124460167-124460167	upstream_gene_variant	MODIFIER	<i>RP11-214K3.18</i>	Transcript	sense_intronic
rs4765127	12: 124460167-124460167	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	promoter
rs10773049	12: 124506631-124506631	intron_variant	MODIFIER	<i>FAM101A</i>	Transcript	protein_coding
rs10773049	12: 124506631-124506631	intron_variant, non_coding_transcript_variant	MODIFIER	<i>FAM101A</i>	Transcript	processed_transcript

rs10773049	12: 124506631-124506631	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	CTCF_binding_site
rs8032939	15: 38834033-38834033	intron_variant	MODIFIER	<i>RASGRP1</i>	Transcript	protein_coding
rs8032939	15: 38834033-38834033	upstream_gene_variant	MODIFIER	<i>Y_RNA</i>	Transcript	misc_RNA
rs8032939	15: 38834033-38834033	intron_variant, NMD_transcript_variant	MODIFIER	<i>RASGRP1</i>	Transcript	nonsense_mediated_decay
rs34127110	15: 77313571-77313571	intron_variant	MODIFIER	<i>PSTPIP1</i>	Transcript	protein_coding
rs34127110	15: 77313571-77313571	intron_variant, NMD_transcript_variant	MODIFIER	<i>PSTPIP1</i>	Transcript	nonsense_mediated_decay
rs34127110	15: 77313571-77313571	intron_variant, non_coding_transcript_variant	MODIFIER	<i>PSTPIP1</i>	Transcript	retained_intron
rs34127110	15: 77313571-77313571	intron_variant, non_coding_transcript_variant	MODIFIER	<i>PSTPIP1</i>	Transcript	processed_transcript
rs6564229	16: 75236409-75236409	downstream_gene_variant	MODIFIER	<i>CTRB2</i>	Transcript	protein_coding
rs6564229	16: 75236409-75236409	downstream_gene_variant	MODIFIER	<i>CTRB2</i>	Transcript	retained_intron
rs9936550	16: 75242850-75242850	upstream_gene_variant	MODIFIER	<i>CTRB2</i>	Transcript	protein_coding
rs9936550	16: 75242850-75242850	upstream_gene_variant	MODIFIER	<i>CTRB2</i>	Transcript	retained_intron
rs8067439	17: 17698254-17698254	synonymous_variant	LOW	<i>RAI1</i>	Transcript	protein_coding
rs8067439	17: 17698254-17698254	downstream_gene_variant	MODIFIER	<i>RAI1</i>	Transcript	protein_coding
rs8067439	17: 17698254-17698254	upstream_gene_variant	MODIFIER	<i>RAI1</i>	Transcript	protein_coding
rs35497503	17: 37620627-37620627	intron_variant	MODIFIER	<i>CDK12</i>	Transcript	protein_coding
rs35497503	17: 37620627-37620627	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	promoter
rs72823056	17: 40565926-40565926	intron_variant	MODIFIER	<i>PTRF</i>	Transcript	protein_coding
rs646123	17: 40720632-40720632	intron_variant	MODIFIER	<i>MLX</i>	Transcript	protein_coding
rs646123	17: 40720632-40720632	downstream_gene_variant	MODIFIER	<i>PSMC3IP</i>	Transcript	protein_coding
rs646123	17: 40720632-40720632	downstream_gene_variant	MODIFIER	<i>COASY</i>	Transcript	protein_coding
rs646123	17: 40720632-40720632	intron_variant, non_coding_transcript_variant	MODIFIER	<i>MLX</i>	Transcript	retained_intron
rs646123	17: 40720632-40720632	downstream_gene_variant	MODIFIER	<i>PSMC3IP</i>	Transcript	nonsense_mediated_decay
rs646123	17: 40720632-40720632	non_coding_transcript_exon_variant	MODIFIER	<i>MLX</i>	Transcript	retained_intron
rs646123	17: 40720632-40720632	downstream_gene_variant	MODIFIER	<i>COASY</i>	Transcript	retained_intron
rs646123	17: 40720632-40720632	downstream_gene_variant	MODIFIER	<i>PSMC3IP</i>	Transcript	retained_intron
rs646123	17: 40720632-40720632	downstream_gene_variant	MODIFIER	<i>MLX</i>	Transcript	retained_intron
rs646123	17: 40720632-40720632	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	promoter
rs1962412	17: 46970259-46970259	intron_variant	MODIFIER	<i>ATP5G1</i>	Transcript	protein_coding
rs1962412	17: 46970259-46970259	5_prime_UTR_variant	MODIFIER	<i>ATP5G1</i>	Transcript	protein_coding
rs1962412	17: 46970259-46970259	upstream_gene_variant	MODIFIER	<i>ATP5G1</i>	Transcript	retained_intron
rs1962412	17: 46970259-46970259	upstream_gene_variant	MODIFIER	<i>ATP5G1</i>	Transcript	protein_coding
rs1962412	17: 46970259-46970259	intron_variant, non_coding_transcript_variant	MODIFIER	<i>SUMO2P17</i>	Transcript	processed_transcript
rs1962412	17: 46970259-46970259	intron_variant, non_coding_transcript_variant	MODIFIER	<i>ATP5G1</i>	Transcript	retained_intron
rs1962412	17: 46970259-46970259	non_coding_transcript_exon_variant	MODIFIER	<i>ATP5G1</i>	Transcript	processed_transcript
rs1962412	17: 46970259-46970259	upstream_gene_variant	MODIFIER	<i>ATP5G1</i>	Transcript	processed_transcript
rs1962412	17: 46970259-46970259	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	promoter
rs2411759	17: 47071074-47071074	upstream_gene_variant	MODIFIER	<i>IGF2BP1</i>	Transcript	protein_coding
rs2411759	17: 47071074-47071074	downstream_gene_variant	MODIFIER	<i>RP11-501C14.5</i>	Transcript	antisense
rs2411759	17: 47071074-47071074	upstream_gene_variant	MODIFIER	<i>IGF2BP1</i>	Transcript	processed_transcript
rs2411759	17: 47071074-47071074	TF_binding_site_variant	MODIFIER	-	MotifFeature	-
rs12452590	17: 60720058-60720058	intron_variant	MODIFIER	<i>MRC2</i>	Transcript	protein_coding
rs12452590	17: 60720058-60720058	intron_variant, non_coding_transcript_variant	MODIFIER	<i>MRC2</i>	Transcript	retained_intron
rs2306527	17: 76798155-76798155	intron_variant	MODIFIER	<i>USP36</i>	Transcript	protein_coding
rs2306527	17: 76798155-76798155	upstream_gene_variant	MODIFIER	<i>USP36</i>	Transcript	nonsense_mediated_decay
rs2306527	17: 76798155-76798155	downstream_gene_variant	MODIFIER	<i>USP36</i>	Transcript	non_stop_decay
rs2306527	17: 76798155-76798155	upstream_gene_variant	MODIFIER	<i>USP36</i>	Transcript	protein_coding
rs2306527	17: 76798155-76798155	intron_variant, NMD_transcript_variant	MODIFIER	<i>USP36</i>	Transcript	nonsense_mediated_decay
rs12954782	18: 57864092-57864092	non_coding_transcript_exon_variant	MODIFIER	<i>RP11-795H16.2</i>	Transcript	processed_pseudogene

rs12954782	18: 57864092-57864092	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	enhancer
rs739846	19: 19419071-19419071	intron_variant	MODIFIER	<i>SUGP1</i>	Transcript	protein_coding
rs739846	19: 19419071-19419071	intron_variant, NMD_transcript_variant	MODIFIER	<i>SUGP1</i>	Transcript	nonsense_mediated_decay
rs739846	19: 19419071-19419071	intron_variant, non_coding_transcript_variant	MODIFIER	<i>SUGP1</i>	Transcript	processed_transcript
rs739846	19: 19419071-19419071	upstream_gene_variant	MODIFIER	<i>SUGP1</i>	Transcript	retained_intron
rs739846	19: 19419071-19419071	intron_variant, non_coding_transcript_variant	MODIFIER	<i>SUGP1</i>	Transcript	retained_intron
rs739846	19: 19419071-19419071	upstream_gene_variant	MODIFIER	<i>SUGP1</i>	Transcript	nonsense_mediated_decay
rs147711004	19: 45337918-45337918	intergenic_variant	MODIFIER	-	-	-
rs429358	19: 45411941-45411941	missense_variant	MODERATE	<i>APOE</i>	Transcript	protein_coding
rs429358	19: 45411941-45411941	downstream_gene_variant	MODIFIER	<i>TOMM40</i>	Transcript	protein_coding
rs429358	19: 45411941-45411941	downstream_gene_variant	MODIFIER	<i>APOE</i>	Transcript	retained_intron
rs17883331	19: 4954455-4954455	non_coding_transcript_exon_variant	MODIFIER	<i>UHRF1</i>	Transcript	processed_transcript
rs78058190	2: 219699999-219699999	upstream_gene_variant	MODIFIER	<i>PRKAG3</i>	Transcript	nonsense_mediated_decay
rs78058190	2: 219699999-219699999	upstream_gene_variant	MODIFIER	<i>PRKAG3</i>	Transcript	protein_coding
rs78058190	2: 219699999-219699999	upstream_gene_variant	MODIFIER	<i>PRKAG3</i>	Transcript	retained_intron
rs78058190	2: 219699999-219699999	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	enhancer
rs72979712	2: 227019416-227019416	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	promoter_flanking_region
rs72979712	2: 227019416-227019416	intergenic_variant	MODIFIER	-	-	-
rs1399627	2: 227083411-227083411	intergenic_variant	MODIFIER	-	-	-
rs11692712	2: 227167100-227167100	intergenic_variant	MODIFIER	-	-	-
rs78718224	2: 227177827-227177827	intergenic_variant	MODIFIER	-	-	-
rs76367336	2: 227228251-227228251	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	enhancer
rs76367336	2: 227228251-227228251	intergenic_variant	MODIFIER	-	-	-
rs13027161	2: 60607728-60607728	upstream_gene_variant	MODIFIER	<i>RNU1-32P</i>	Transcript	snRNA
rs13027161	2: 60607728-60607728	intron_variant, non_coding_transcript_variant	MODIFIER	<i>AC007381.2</i>	Transcript	lincRNA
rs13027161	2: 60607728-60607728	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	promoter_flanking_region
rs4135268	3: 12437237-12437237	intron_variant	MODIFIER	<i>PPARG</i>	Transcript	protein_coding
rs4135268	3: 12437237-12437237	intron_variant, NMD_transcript_variant	MODIFIER	<i>PPARG</i>	Transcript	nonsense_mediated_decay
rs4135268	3: 12437237-12437237	intron_variant, non_coding_transcript_variant	MODIFIER	<i>PPARG</i>	Transcript	retained_intron
rs9989973	3: 12499264-12499264	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	promoter_flanking_region
rs9989973	3: 12499264-12499264	intergenic_variant	MODIFIER	-	-	-
rs6795831	3: 129341403-129341403	intergenic_variant	MODIFIER	-	-	-
rs7644541	3: 136145766-136145766	intron_variant	MODIFIER	<i>STAG1</i>	Transcript	protein_coding
rs7644541	3: 136145766-136145766	downstream_gene_variant	MODIFIER	<i>RNU6-1284P</i>	Transcript	snRNA
rs7644541	3: 136145766-136145766	intron_variant, NMD_transcript_variant	MODIFIER	<i>STAG1</i>	Transcript	nonsense_mediated_decay
rs13079221	3: 14901525-14901525	intron_variant	MODIFIER	<i>FGD5</i>	Transcript	protein_coding
rs62271373	3: 150066540-150066540	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	promoter_flanking_region
rs62271373	3: 150066540-150066540	intergenic_variant	MODIFIER	-	-	-
rs78629618	3: 46880130-46880130	upstream_gene_variant	MODIFIER	<i>PRSS42</i>	Transcript	protein_coding
rs77481436	3: 47506230-47506230	intron_variant	MODIFIER	<i>SCAP</i>	Transcript	protein_coding
rs77481436	3: 47506230-47506230	intron_variant, NMD_transcript_variant	MODIFIER	<i>SCAP</i>	Transcript	nonsense_mediated_decay
rs77481436	3: 47506230-47506230	upstream_gene_variant	MODIFIER	<i>snoU13</i>	Transcript	snoRNA
rs77481436	3: 47506230-47506230	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	promoter_flanking_region
rs62260788	3: 48068610-48068610	intron_variant	MODIFIER	<i>MAP4</i>	Transcript	protein_coding
rs62260788	3: 48068610-48068610	intron_variant, non_coding_transcript_variant	MODIFIER	<i>MAP4</i>	Transcript	processed_transcript
rs62260788	3: 48068610-48068610	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	enhancer
rs1128535	3: 49866392-49866392	3_prime_UTR_variant	MODIFIER	<i>TRAIP</i>	Transcript	protein_coding
rs1128535	3: 49866392-49866392	downstream_gene_variant	MODIFIER	<i>TRAIP</i>	Transcript	protein_coding
rs1128535	3: 49866392-49866392	downstream_gene_variant	MODIFIER	<i>TRAIP</i>	Transcript	nonsense_mediated_decay

rs1128535	3: 49866392-49866392	downstream_gene_variant	MODIFIER	<i>TRAIP</i>	Transcript	retained_intron
rs1128535	3: 49866392-49866392	non_coding_transcript_exon_variant	MODIFIER	<i>TRAIP</i>	Transcript	retained_intron
rs12641981	4: 45179883-45179883	intergenic_variant	MODIFIER	-	-	-
rs3796459	4: 96116778-96116778	intron_variant	MODIFIER	<i>UNC5C</i>	Transcript	protein_coding
rs3936510	5: 55860866-55860866	intron_variant	MODIFIER	<i>AC022431.2</i>	Transcript	protein_coding
rs3936510	5: 55860866-55860866	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	promoter_flanking_region
rs3936510	5: 55860866-55860866	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	CTCF_binding_site
rs10474433	5: 74616843-74616843	intron_variant, non_coding_transcript_variant	MODIFIER	<i>CTD-2235C13.2</i>	Transcript	antisense
rs10474433	5: 74616843-74616843	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	promoter_flanking_region
rs10474433	5: 74616843-74616843	TF_binding_site_variant	MODIFIER	-	MotifFeature	-
rs7755075	6: 126708470-126708470	intergenic_variant	MODIFIER	-	-	-
rs11759026	6: 126792095-126792095	intergenic_variant	MODIFIER	-	-	-
rs454424	6: 31284963-31284963	intergenic_variant	MODIFIER	-	-	-
rs11961408	6: 31317850-31317850	downstream_gene_variant	MODIFIER	<i>HLA-B</i>	Transcript	protein_coding
rs11961408	6: 31317850-31317850	downstream_gene_variant	MODIFIER	<i>HLA-B</i>	Transcript	retained_intron
rs2260051	6: 31591918-31591918	downstream_gene_variant	MODIFIER	<i>SNORA38</i>	Transcript	snoRNA
rs2260051	6: 31591918-31591918	intron_variant	MODIFIER	<i>PRRC2A</i>	Transcript	protein_coding
rs2260051	6: 31591918-31591918	upstream_gene_variant	MODIFIER	<i>PRRC2A</i>	Transcript	retained_intron
rs2260051	6: 31591918-31591918	intron_variant, non_coding_transcript_variant	MODIFIER	<i>PRRC2A</i>	Transcript	processed_transcript
rs3115669	6: 31619024-31619024	intron_variant	MODIFIER	<i>BAG6</i>	Transcript	protein_coding
rs3115669	6: 31619024-31619024	upstream_gene_variant	MODIFIER	<i>APOM</i>	Transcript	protein_coding
rs3115669	6: 31619024-31619024	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	promoter
rs592229	6: 31930441-31930441	intron_variant	MODIFIER	<i>SKIV2L</i>	Transcript	protein_coding
rs592229	6: 31930441-31930441	upstream_gene_variant	MODIFIER	<i>NELFE</i>	Transcript	protein_coding
rs592229	6: 31930441-31930441	intron_variant, NMD_transcript_variant	MODIFIER	<i>SKIV2L</i>	Transcript	nonsense_mediated_decay
rs592229	6: 31930441-31930441	upstream_gene_variant	MODIFIER	<i>SKIV2L</i>	Transcript	processed_transcript
rs592229	6: 31930441-31930441	intron_variant, non_coding_transcript_variant	MODIFIER	<i>SKIV2L</i>	Transcript	retained_intron
rs592229	6: 31930441-31930441	upstream_gene_variant	MODIFIER	<i>NELFE</i>	Transcript	retained_intron
rs592229	6: 31930441-31930441	upstream_gene_variant	MODIFIER	<i>SKIV2L</i>	Transcript	retained_intron
rs592229	6: 31930441-31930441	downstream_gene_variant	MODIFIER	<i>SKIV2L</i>	Transcript	processed_transcript
rs592229	6: 31930441-31930441	upstream_gene_variant	MODIFIER	<i>NELFE</i>	Transcript	nonsense_mediated_decay
rs592229	6: 31930441-31930441	downstream_gene_variant	MODIFIER	<i>SKIV2L</i>	Transcript	retained_intron
rs6449	6: 32006655-32006655	downstream_gene_variant	MODIFIER	<i>TNXB</i>	Transcript	protein_coding
rs6449	6: 32006655-32006655	upstream_gene_variant	MODIFIER	<i>C4B-AS1</i>	Transcript	antisense
rs6449	6: 32006655-32006655	intron_variant	MODIFIER	<i>CYP21A2</i>	Transcript	protein_coding
rs6449	6: 32006655-32006655	downstream_gene_variant	MODIFIER	<i>C4B</i>	Transcript	protein_coding
rs6449	6: 32006655-32006655	upstream_gene_variant	MODIFIER	<i>CYP21A2</i>	Transcript	retained_intron
rs6449	6: 32006655-32006655	downstream_gene_variant	MODIFIER	<i>C4B</i>	Transcript	retained_intron
rs6449	6: 32006655-32006655	intron_variant, non_coding_transcript_variant	MODIFIER	<i>CYP21A2</i>	Transcript	retained_intron
rs6449	6: 32006655-32006655	intron_variant, NMD_transcript_variant	MODIFIER	<i>CYP21A2</i>	Transcript	nonsense_mediated_decay
rs6449	6: 32006655-32006655	non_coding_transcript_exon_variant	MODIFIER	<i>CYP21A2</i>	Transcript	retained_intron
rs6449	6: 32006655-32006655	downstream_gene_variant	MODIFIER	<i>TNXB</i>	Transcript	retained_intron
rs3130283	6: 32138545-32138545	downstream_gene_variant	MODIFIER	<i>EGFL8</i>	Transcript	protein_coding
rs3130283	6: 32138545-32138545	intron_variant	MODIFIER	<i>AGPAT1</i>	Transcript	protein_coding
rs3130283	6: 32138545-32138545	downstream_gene_variant	MODIFIER	<i>PPT2-EGFL8</i>	Transcript	nonsense_mediated_decay
rs3130283	6: 32138545-32138545	3_prime_UTR_variant, NMD_transcript_variant	MODIFIER	<i>PPT2-EGFL8</i>	Transcript	nonsense_mediated_decay
rs3130283	6: 32138545-32138545	downstream_gene_variant	MODIFIER	<i>PPT2</i>	Transcript	protein_coding
rs3130283	6: 32138545-32138545	downstream_gene_variant	MODIFIER	<i>PPT2-EGFL8</i>	Transcript	processed_transcript
rs3130283	6: 32138545-32138545	downstream_gene_variant	MODIFIER	<i>EGFL8</i>	Transcript	retained_intron

rs3130283	6: 32138545-32138545	intron_variant, non_coding_transcript_variant	MODIFIER	<i>AGPAT1</i>	Transcript	processed_transcript
rs3130283	6: 32138545-32138545	downstream_gene_variant	MODIFIER	<i>PPT2-EGFL8</i>	Transcript	retained_intron
rs3130283	6: 32138545-32138545	downstream_gene_variant	MODIFIER	<i>EGFL8</i>	Transcript	processed_transcript
rs2395153	6: 32345595-32345595	intergenic_variant	MODIFIER	-	-	-
rs4713587	6: 32659535-32659535	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	enhancer
rs4713587	6: 32659535-32659535	intergenic_variant	MODIFIER	-	-	-
rs6905288	6: 43758873-43758873	downstream_gene_variant	MODIFIER	<i>VEGFA</i>	Transcript	protein_coding
rs6905288	6: 43758873-43758873	downstream_gene_variant	MODIFIER	<i>VEGFA</i>	Transcript	retained_intron
rs62405422	6: 50796905-50796905	intron_variant	MODIFIER	<i>TFAP2B</i>	Transcript	protein_coding
rs62405422	6: 50796905-50796905	downstream_gene_variant	MODIFIER	<i>TFAP2B</i>	Transcript	protein_coding
rs2971672	7: 44205906-44205906	intron_variant	MODIFIER	<i>GCK</i>	Transcript	protein_coding
rs2971672	7: 44205906-44205906	intron_variant, non_coding_transcript_variant	MODIFIER	<i>GCK</i>	Transcript	processed_transcript
rs77899453	8: 19780310-19780310	intron_variant	MODIFIER	<i>LPL</i>	Transcript	protein_coding
rs301	8: 19816934-19816934	intron_variant	MODIFIER	<i>LPL</i>	Transcript	protein_coding
rs17091891	8: 19843171-19843171	intergenic_variant	MODIFIER	-	-	-
rs28597716	8: 19936687-19936687	upstream_gene_variant	MODIFIER	<i>AC100802.3</i>	Transcript	antisense
rs507666	9: 136149399-136149399	intron_variant, non_coding_transcript_variant	MODIFIER	<i>ABO</i>	Transcript	processed_transcript
rs507666	9: 136149399-136149399	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	promoter
rs3935875	9: 139238824-139238824	intron_variant	MODIFIER	<i>GPSM1</i>	Transcript	protein_coding
rs3935875	9: 139238824-139238824	downstream_gene_variant	MODIFIER	<i>GPSM1</i>	Transcript	protein_coding
rs12003940	9: 19101350-19101350	intron_variant	MODIFIER	<i>HAUS6</i>	Transcript	protein_coding
rs12003940	9: 19101350-19101350	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	promoter
rs117197971	9: 21951175-21951175	intron_variant, NMD_transcript_variant	MODIFIER	<i>RP11-145E5.5</i>	Transcript	nonsense_mediated_decay
rs10965199	9: 21954653-21954653	intron_variant, NMD_transcript_variant	MODIFIER	<i>RP11-145E5.5</i>	Transcript	nonsense_mediated_decay
rs7041637	9: 21961866-21961866	intron_variant, NMD_transcript_variant	MODIFIER	<i>RP11-145E5.5</i>	Transcript	nonsense_mediated_decay
rs3731239	9: 21974218-21974218	intron_variant	MODIFIER	<i>CDKN2A</i>	Transcript	protein_coding
rs3731239	9: 21974218-21974218	upstream_gene_variant	MODIFIER	<i>CDKN2A</i>	Transcript	processed_transcript
rs3731239	9: 21974218-21974218	intron_variant, NMD_transcript_variant	MODIFIER	<i>CDKN2A</i>	Transcript	nonsense_mediated_decay
rs3731239	9: 21974218-21974218	intron_variant, NMD_transcript_variant	MODIFIER	<i>RP11-145E5.5</i>	Transcript	nonsense_mediated_decay
rs3731239	9: 21974218-21974218	upstream_gene_variant	MODIFIER	<i>CDKN2A</i>	Transcript	protein_coding
rs3731239	9: 21974218-21974218	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	promoter
rs117626887	9: 22013063-22013063	upstream_gene_variant	MODIFIER	<i>CDKN2B</i>	Transcript	protein_coding
rs117626887	9: 22013063-22013063	downstream_gene_variant	MODIFIER	<i>UBA52P6</i>	Transcript	processed_pseudogene
rs117626887	9: 22013063-22013063	intron_variant, NMD_transcript_variant	MODIFIER	<i>RP11-145E5.5</i>	Transcript	nonsense_mediated_decay
rs117626887	9: 22013063-22013063	intron_variant, non_coding_transcript_variant	MODIFIER	<i>CDKN2B-AS1</i>	Transcript	antisense
rs11790231	9: 22053591-22053591	intron_variant, non_coding_transcript_variant	MODIFIER	<i>CDKN2B-AS1</i>	Transcript	antisense
rs11790231	9: 22053591-22053591	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	CTCF_binding_site
rs11790231	9: 22053591-22053591	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	promoter_flanking_region
rs2891168	9: 22098619-22098619	intron_variant, non_coding_transcript_variant	MODIFIER	<i>CDKN2B-AS1</i>	Transcript	antisense
rs2891168	9: 22098619-22098619	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	promoter_flanking_region
rs76011118	9: 22133773-22133773	intergenic_variant	MODIFIER	-	-	-
rs12555274	9: 22136440-22136440	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	promoter_flanking_region
rs12555274	9: 22136440-22136440	intergenic_variant	MODIFIER	-	-	-
rs507666	HG79_PATCH: 136149518-136149518	intron_variant	MODIFIER	<i>ABO</i>	Transcript	protein_coding
rs3935875	HG998_2_PATCH: 139252274-139252274	downstream_gene_variant	MODIFIER	<i>GPSM1</i>	Transcript	protein_coding
rs3935875	HG998_2_PATCH: 139252274-139252274	intron_variant	MODIFIER	<i>GPSM1</i>	Transcript	protein_coding

rs3130283	HSCHR6_MHC_APD: 32149889-32149889	downstream_gene_variant	MODIFIER	<i>EGFL8</i>	Transcript	protein_coding
rs3130283	HSCHR6_MHC_APD: 32149889-32149889	intron_variant	MODIFIER	<i>AGPAT1</i>	Transcript	protein_coding
rs3130283	HSCHR6_MHC_APD: 32149889-32149889	intron_variant, non_coding_transcript_variant	MODIFIER	<i>AGPAT1</i>	Transcript	processed_transcript
rs3130283	HSCHR6_MHC_APD: 32149889-32149889	3_prime_UTR_variant, NMD_transcript_variant	MODIFIER	<i>PPT2</i>	Transcript	nonsense_mediated_decay
rs3130283	HSCHR6_MHC_APD: 32149889-32149889	downstream_gene_variant	MODIFIER	<i>EGFL8</i>	Transcript	retained_intron
rs3130283	HSCHR6_MHC_APD: 32149889-32149889	downstream_gene_variant	MODIFIER	<i>PPT2</i>	Transcript	nonsense_mediated_decay
rs3130283	HSCHR6_MHC_APD: 32149889-32149889	downstream_gene_variant	MODIFIER	<i>EGFL8</i>	Transcript	processed_transcript
rs3130283	HSCHR6_MHC_APD: 32149889-32149889	downstream_gene_variant	MODIFIER	<i>PPT2</i>	Transcript	protein_coding
rs2395153	HSCHR6_MHC_APD: 32356581-32356581	intergenic_variant	MODIFIER	-	-	-
rs454424	HSCHR6_MHC_COX: 31275997-31275997	intergenic_variant	MODIFIER	-	-	-
rs11961408	HSCHR6_MHC_COX: 31308332-31308332	downstream_gene_variant	MODIFIER	<i>HLA-B</i>	Transcript	protein_coding
rs11961408	HSCHR6_MHC_COX: 31308332-31308332	downstream_gene_variant	MODIFIER	<i>HLA-B</i>	Transcript	retained_intron
rs2260051	HSCHR6_MHC_COX: 31579329-31579329	intron_variant	MODIFIER	<i>PRRC2A</i>	Transcript	protein_coding
rs2260051	HSCHR6_MHC_COX: 31579329-31579329	upstream_gene_variant	MODIFIER	<i>PRRC2A</i>	Transcript	retained_intron
rs2260051	HSCHR6_MHC_COX: 31579329-31579329	intron_variant, non_coding_transcript_variant	MODIFIER	<i>PRRC2A</i>	Transcript	processed_transcript
rs2260051	HSCHR6_MHC_COX: 31579329-31579329	downstream_gene_variant	MODIFIER	<i>SNORA38</i>	Transcript	snoRNA
rs3115669	HSCHR6_MHC_COX: 31606439-31606439	upstream_gene_variant	MODIFIER	<i>APOM</i>	Transcript	protein_coding
rs3115669	HSCHR6_MHC_COX: 31606439-31606439	intron_variant	MODIFIER	<i>BAG6</i>	Transcript	protein_coding
rs3115669	HSCHR6_MHC_COX: 31606439-31606439	intron_variant, non_coding_transcript_variant	MODIFIER	<i>BAG6</i>	Transcript	processed_transcript
rs592229	HSCHR6_MHC_COX: 31917993-31917993	upstream_gene_variant	MODIFIER	<i>NELFE</i>	Transcript	protein_coding
rs592229	HSCHR6_MHC_COX: 31917993-31917993	intron_variant	MODIFIER	<i>SKIV2L</i>	Transcript	protein_coding
rs592229	HSCHR6_MHC_COX: 31917993-31917993	upstream_gene_variant	MODIFIER	<i>NELFE</i>	Transcript	retained_intron
rs592229	HSCHR6_MHC_COX: 31917993-31917993	upstream_gene_variant	MODIFIER	<i>SKIV2L</i>	Transcript	retained_intron
rs592229	HSCHR6_MHC_COX: 31917993-31917993	upstream_gene_variant	MODIFIER	<i>SKIV2L</i>	Transcript	processed_transcript

rs592229	HSCHR6_MHC_COX: 31917993-31917993	downstream_gene_variant	MODIFIER	<i>SKIV2L</i>	Transcript	processed_transcript
rs592229	HSCHR6_MHC_COX: 31917993-31917993	intron_variant, non_coding_transcript_variant	MODIFIER	<i>SKIV2L</i>	Transcript	processed_transcript
rs592229	HSCHR6_MHC_COX: 31917993-31917993	downstream_gene_variant	MODIFIER	<i>SKIV2L</i>	Transcript	retained_intron
rs592229	HSCHR6_MHC_COX: 31917993-31917993	intron_variant, non_coding_transcript_variant	MODIFIER	<i>SKIV2L</i>	Transcript	retained_intron
rs592229	HSCHR6_MHC_COX: 31917993-31917993	upstream_gene_variant	MODIFIER	<i>NELFE</i>	Transcript	processed_transcript
rs6449	HSCHR6_MHC_COX: 31955102-31955102	downstream_gene_variant	MODIFIER	<i>TNXB</i>	Transcript	protein_coding
rs6449	HSCHR6_MHC_COX: 31955102-31955102	downstream_gene_variant	MODIFIER	<i>TNXB</i>	Transcript	retained_intron
rs6449	HSCHR6_MHC_COX: 31955102-31955102	downstream_gene_variant	MODIFIER	<i>C4B</i>	Transcript	protein_coding
rs6449	HSCHR6_MHC_COX: 31955102-31955102	upstream_gene_variant	MODIFIER	<i>XXbac- BPG116M5.15</i>	Transcript	processed_transcript
rs6449	HSCHR6_MHC_COX: 31955102-31955102	intron_variant	MODIFIER	<i>CYP21A2</i>	Transcript	protein_coding
rs6449	HSCHR6_MHC_COX: 31955102-31955102	downstream_gene_variant	MODIFIER	<i>C4B</i>	Transcript	retained_intron
rs6449	HSCHR6_MHC_COX: 31955102-31955102	intron_variant, non_coding_transcript_variant	MODIFIER	<i>CYP21A2</i>	Transcript	processed_transcript
rs6449	HSCHR6_MHC_COX: 31955102-31955102	non_coding_transcript_exon_variant	MODIFIER	<i>CYP21A2</i>	Transcript	retained_intron
rs6449	HSCHR6_MHC_COX: 31955102-31955102	intron_variant, non_coding_transcript_variant	MODIFIER	<i>CYP21A2</i>	Transcript	retained_intron
rs6449	HSCHR6_MHC_COX: 31955102-31955102	downstream_gene_variant	MODIFIER	<i>C4B</i>	Transcript	processed_transcript
rs6449	HSCHR6_MHC_COX: 31955102-31955102	downstream_gene_variant	MODIFIER	<i>TNXB</i>	Transcript	processed_transcript
rs3130283	HSCHR6_MHC_COX: 32087022-32087022	downstream_gene_variant	MODIFIER	<i>EGFL8</i>	Transcript	protein_coding
rs3130283	HSCHR6_MHC_COX: 32087022-32087022	intron_variant	MODIFIER	<i>AGPAT1</i>	Transcript	protein_coding
rs3130283	HSCHR6_MHC_COX: 32087022-32087022	downstream_gene_variant	MODIFIER	<i>XXbac- BCX105D18.9</i>	Transcript	nonsense_mediated_decay
rs3130283	HSCHR6_MHC_COX: 32087022-32087022	downstream_gene_variant	MODIFIER	<i>EGFL8</i>	Transcript	processed_transcript
rs3130283	HSCHR6_MHC_COX: 32087022-32087022	3_prime_UTR_variant, NMD_transcript_variant	MODIFIER	<i>XXbac- BCX105D18.9</i>	Transcript	nonsense_mediated_decay
rs3130283	HSCHR6_MHC_COX: 32087022-32087022	intron_variant, non_coding_transcript_variant	MODIFIER	<i>AGPAT1</i>	Transcript	processed_transcript
rs3130283	HSCHR6_MHC_COX: 32087022-32087022	downstream_gene_variant	MODIFIER	<i>EGFL8</i>	Transcript	retained_intron
rs3130283	HSCHR6_MHC_COX: 32087022-32087022	downstream_gene_variant	MODIFIER	<i>PPT2</i>	Transcript	protein_coding

rs2395153	HSCHR6_MHC_COX: 32293835-32293835	intergenic_variant	MODIFIER	-	-	-
rs4713587	HSCHR6_MHC_COX: 32582982-32582982	intergenic_variant	MODIFIER	-	-	-
rs11961408	HSCHR6_MHC_DBB: 31299785-31299785	intergenic_variant	MODIFIER	-	-	-
rs2260051	HSCHR6_MHC_DBB: 31574093-31574093	intron_variant	MODIFIER	<i>PRRC2A</i>	Transcript	protein_coding
rs2260051	HSCHR6_MHC_DBB: 31574093-31574093	upstream_gene_variant	MODIFIER	<i>PRRC2A</i>	Transcript	retained_intron
rs2260051	HSCHR6_MHC_DBB: 31574093-31574093	intron_variant, non_coding_transcript_variant	MODIFIER	<i>PRRC2A</i>	Transcript	processed_transcript
rs2260051	HSCHR6_MHC_DBB: 31574093-31574093	downstream_gene_variant	MODIFIER	<i>SNORA38</i>	Transcript	snoRNA
rs3115669	HSCHR6_MHC_DBB: 31601202-31601202	intron_variant	MODIFIER	<i>BAG6</i>	Transcript	protein_coding
rs3115669	HSCHR6_MHC_DBB: 31601202-31601202	upstream_gene_variant	MODIFIER	<i>APOM</i>	Transcript	protein_coding
rs3115669	HSCHR6_MHC_DBB: 31601202-31601202	intron_variant, non_coding_transcript_variant	MODIFIER	<i>BAG6</i>	Transcript	processed_transcript
rs592229	HSCHR6_MHC_DBB: 31912627-31912627	upstream_gene_variant	MODIFIER	<i>NELFE</i>	Transcript	protein_coding
rs592229	HSCHR6_MHC_DBB: 31912627-31912627	intron_variant	MODIFIER	<i>SKIV2L</i>	Transcript	protein_coding
rs592229	HSCHR6_MHC_DBB: 31912627-31912627	downstream_gene_variant	MODIFIER	<i>SKIV2L</i>	Transcript	processed_transcript
rs592229	HSCHR6_MHC_DBB: 31912627-31912627	upstream_gene_variant	MODIFIER	<i>NELFE</i>	Transcript	processed_transcript
rs592229	HSCHR6_MHC_DBB: 31912627-31912627	upstream_gene_variant	MODIFIER	<i>SKIV2L</i>	Transcript	retained_intron
rs592229	HSCHR6_MHC_DBB: 31912627-31912627	upstream_gene_variant	MODIFIER	<i>NELFE</i>	Transcript	retained_intron
rs592229	HSCHR6_MHC_DBB: 31912627-31912627	intron_variant, non_coding_transcript_variant	MODIFIER	<i>SKIV2L</i>	Transcript	processed_transcript
rs592229	HSCHR6_MHC_DBB: 31912627-31912627	upstream_gene_variant	MODIFIER	<i>SKIV2L</i>	Transcript	processed_transcript
rs592229	HSCHR6_MHC_DBB: 31912627-31912627	downstream_gene_variant	MODIFIER	<i>SKIV2L</i>	Transcript	retained_intron
rs592229	HSCHR6_MHC_DBB: 31912627-31912627	intron_variant, non_coding_transcript_variant	MODIFIER	<i>SKIV2L</i>	Transcript	retained_intron
rs6449	HSCHR6_MHC_DBB: 31982474-31982474	downstream_gene_variant	MODIFIER	<i>TNXB</i>	Transcript	retained_intron
rs6449	HSCHR6_MHC_DBB: 31982474-31982474	intron_variant	MODIFIER	<i>CYP21A2</i>	Transcript	protein_coding
rs6449	HSCHR6_MHC_DBB: 31982474-31982474	upstream_gene_variant	MODIFIER	<i>XXbac- BPG116M5.15</i>	Transcript	processed_transcript
rs6449	HSCHR6_MHC_DBB: 31982474-31982474	downstream_gene_variant	MODIFIER	<i>TNXB</i>	Transcript	protein_coding

rs6449	HSCHR6_MHC_DBB: 31982474-31982474	downstream_gene_variant	MODIFIER	<i>C4B</i>	Transcript	protein_coding
rs6449	HSCHR6_MHC_DBB: 31982474-31982474	downstream_gene_variant	MODIFIER	<i>C4B</i>	Transcript	retained_intron
rs6449	HSCHR6_MHC_DBB: 31982474-31982474	intron_variant, non_coding_transcript_variant	MODIFIER	<i>CYP21A2</i>	Transcript	processed_transcript
rs6449	HSCHR6_MHC_DBB: 31982474-31982474	intron_variant, non_coding_transcript_variant	MODIFIER	<i>CYP21A2</i>	Transcript	retained_intron
rs6449	HSCHR6_MHC_DBB: 31982474-31982474	downstream_gene_variant	MODIFIER	<i>C4B</i>	Transcript	processed_transcript
rs6449	HSCHR6_MHC_DBB: 31982474-31982474	downstream_gene_variant	MODIFIER	<i>TNXB</i>	Transcript	processed_transcript
rs6449	HSCHR6_MHC_DBB: 31982474-31982474	non_coding_transcript_exon_variant	MODIFIER	<i>CYP21A2</i>	Transcript	retained_intron
rs2395153	HSCHR6_MHC_DBB: 32321114-32321114	intergenic_variant	MODIFIER	-	-	-
rs4713587	HSCHR6_MHC_DBB: 32637889-32637889	intergenic_variant	MODIFIER	-	-	-
rs11961408	HSCHR6_MHC_MANN: 31360907-31360907	downstream_gene_variant	MODIFIER	<i>HLA-B</i>	Transcript	protein_coding
rs11961408	HSCHR6_MHC_MANN: 31360907-31360907	downstream_gene_variant	MODIFIER	<i>HLA-B</i>	Transcript	retained_intron
rs2260051	HSCHR6_MHC_MANN: 31631405-31631405	intron_variant	MODIFIER	<i>PRRC2A</i>	Transcript	protein_coding
rs2260051	HSCHR6_MHC_MANN: 31631405-31631405	upstream_gene_variant	MODIFIER	<i>PRRC2A</i>	Transcript	retained_intron
rs2260051	HSCHR6_MHC_MANN: 31631405-31631405	intron_variant, non_coding_transcript_variant	MODIFIER	<i>PRRC2A</i>	Transcript	processed_transcript
rs2260051	HSCHR6_MHC_MANN: 31631405-31631405	downstream_gene_variant	MODIFIER	<i>SNORA38</i>	Transcript	snoRNA
rs3115669	HSCHR6_MHC_MANN: 31658516-31658516	intron_variant	MODIFIER	<i>BAG6</i>	Transcript	protein_coding
rs3115669	HSCHR6_MHC_MANN: 31658516-31658516	upstream_gene_variant	MODIFIER	<i>APOM</i>	Transcript	protein_coding
rs3115669	HSCHR6_MHC_MANN: 31658516-31658516	intron_variant, non_coding_transcript_variant	MODIFIER	<i>BAG6</i>	Transcript	processed_transcript
rs3130283	HSCHR6_MHC_MANN: 32177972-32177972	intron_variant	MODIFIER	<i>AGPAT1</i>	Transcript	protein_coding
rs3130283	HSCHR6_MHC_MANN: 32177972-32177972	downstream_gene_variant	MODIFIER	<i>EGFL8</i>	Transcript	protein_coding
rs3130283	HSCHR6_MHC_MANN: 32177972-32177972	intron_variant, non_coding_transcript_variant	MODIFIER	<i>AGPAT1</i>	Transcript	processed_transcript
rs3130283	HSCHR6_MHC_MANN: 32177972-32177972	downstream_gene_variant	MODIFIER	<i>EGFL8</i>	Transcript	retained_intron
rs3130283	HSCHR6_MHC_MANN: 32177972-32177972	downstream_gene_variant	MODIFIER	<i>EGFL8</i>	Transcript	processed_transcript
rs3130283	HSCHR6_MHC_MANN: 32177972-32177972	3_prime_UTR_variant, NMD_transcript_variant	MODIFIER	<i>PPT2</i>	Transcript	nonsense_mediated_decay

rs3130283	HSCHR6_MHC_MANN: 32177972-32177972	downstream_gene_variant	MODIFIER	<i>PPT2</i>	Transcript	nonsense_mediated_decay
rs3130283	HSCHR6_MHC_MANN: 32177972-32177972	downstream_gene_variant	MODIFIER	<i>PPT2</i>	Transcript	protein_coding
rs2395153	HSCHR6_MHC_MANN: 32385027-32385027	intron_variant	MODIFIER	<i>C6orf10</i>	Transcript	protein_coding
rs4713587	HSCHR6_MHC_MANN: 32813827-32813827	intergenic_variant	MODIFIER	-	-	-
rs454424	HSCHR6_MHC_MCF: 31362068-31362068	intergenic_variant	MODIFIER	-	-	-
rs11961408	HSCHR6_MHC_MCF: 31394233-31394233	downstream_gene_variant	MODIFIER	<i>HLA-B</i>	Transcript	protein_coding
rs11961408	HSCHR6_MHC_MCF: 31394233-31394233	downstream_gene_variant	MODIFIER	<i>HLA-B</i>	Transcript	retained_intron
rs2260051	HSCHR6_MHC_MCF: 31668209-31668209	intron_variant	MODIFIER	<i>PRRC2A</i>	Transcript	protein_coding
rs2260051	HSCHR6_MHC_MCF: 31668209-31668209	upstream_gene_variant	MODIFIER	<i>PRRC2A</i>	Transcript	retained_intron
rs2260051	HSCHR6_MHC_MCF: 31668209-31668209	intron_variant, non_coding_transcript_variant	MODIFIER	<i>PRRC2A</i>	Transcript	processed_transcript
rs2260051	HSCHR6_MHC_MCF: 31668209-31668209	downstream_gene_variant	MODIFIER	<i>SNORA38</i>	Transcript	snoRNA
rs3115669	HSCHR6_MHC_MCF: 31695301-31695301	intron_variant	MODIFIER	<i>BAG6</i>	Transcript	protein_coding
rs3115669	HSCHR6_MHC_MCF: 31695301-31695301	upstream_gene_variant	MODIFIER	<i>APOM</i>	Transcript	protein_coding
rs3115669	HSCHR6_MHC_MCF: 31695301-31695301	intron_variant, non_coding_transcript_variant	MODIFIER	<i>BAG6</i>	Transcript	processed_transcript
rs592229	HSCHR6_MHC_MCF: 32006888-32006888	intron_variant	MODIFIER	<i>SKIV2L</i>	Transcript	protein_coding
rs592229	HSCHR6_MHC_MCF: 32006888-32006888	upstream_gene_variant	MODIFIER	<i>NELFE</i>	Transcript	protein_coding
rs592229	HSCHR6_MHC_MCF: 32006888-32006888	upstream_gene_variant	MODIFIER	<i>NELFE</i>	Transcript	retained_intron
rs592229	HSCHR6_MHC_MCF: 32006888-32006888	upstream_gene_variant	MODIFIER	<i>NELFE</i>	Transcript	processed_transcript
rs592229	HSCHR6_MHC_MCF: 32006888-32006888	downstream_gene_variant	MODIFIER	<i>SKIV2L</i>	Transcript	retained_intron
rs592229	HSCHR6_MHC_MCF: 32006888-32006888	upstream_gene_variant	MODIFIER	<i>SKIV2L</i>	Transcript	retained_intron
rs592229	HSCHR6_MHC_MCF: 32006888-32006888	upstream_gene_variant	MODIFIER	<i>SKIV2L</i>	Transcript	processed_transcript
rs592229	HSCHR6_MHC_MCF: 32006888-32006888	downstream_gene_variant	MODIFIER	<i>SKIV2L</i>	Transcript	processed_transcript
rs592229	HSCHR6_MHC_MCF: 32006888-32006888	intron_variant, non_coding_transcript_variant	MODIFIER	<i>SKIV2L</i>	Transcript	processed_transcript
rs592229	HSCHR6_MHC_MCF: 32006888-32006888	intron_variant, non_coding_transcript_variant	MODIFIER	<i>SKIV2L</i>	Transcript	retained_intron

rs6449	HSCHR6_MHC_MCF: 32083100-32083100	downstream_gene_variant	MODIFIER	C4A	Transcript	protein_coding
rs6449	HSCHR6_MHC_MCF: 32083100-32083100	downstream_gene_variant	MODIFIER	TNXB	Transcript	protein_coding
rs6449	HSCHR6_MHC_MCF: 32083100-32083100	upstream_gene_variant	MODIFIER	C4A-AS1	Transcript	processed_transcript
rs6449	HSCHR6_MHC_MCF: 32083100-32083100	intron_variant	MODIFIER	CYP21A2	Transcript	protein_coding
rs6449	HSCHR6_MHC_MCF: 32083100-32083100	downstream_gene_variant	MODIFIER	C4A	Transcript	retained_intron
rs6449	HSCHR6_MHC_MCF: 32083100-32083100	intron_variant, non_coding_transcript_variant	MODIFIER	CYP21A2	Transcript	retained_intron
rs6449	HSCHR6_MHC_MCF: 32083100-32083100	intron_variant, non_coding_transcript_variant	MODIFIER	CYP21A2	Transcript	processed_transcript
rs6449	HSCHR6_MHC_MCF: 32083100-32083100	downstream_gene_variant	MODIFIER	TNXB	Transcript	retained_intron
rs6449	HSCHR6_MHC_MCF: 32083100-32083100	downstream_gene_variant	MODIFIER	TNXB	Transcript	processed_transcript
rs6449	HSCHR6_MHC_MCF: 32083100-32083100	downstream_gene_variant	MODIFIER	C4A	Transcript	processed_transcript
rs6449	HSCHR6_MHC_MCF: 32083100-32083100	non_coding_transcript_exon_variant	MODIFIER	CYP21A2	Transcript	retained_intron
rs3130283	HSCHR6_MHC_MCF: 32214977-32214977	downstream_gene_variant	MODIFIER	EGFL8	Transcript	protein_coding
rs3130283	HSCHR6_MHC_MCF: 32214977-32214977	intron_variant	MODIFIER	AGPAT1	Transcript	protein_coding
rs3130283	HSCHR6_MHC_MCF: 32214977-32214977	intron_variant, non_coding_transcript_variant	MODIFIER	AGPAT1	Transcript	processed_transcript
rs3130283	HSCHR6_MHC_MCF: 32214977-32214977	downstream_gene_variant	MODIFIER	EGFL8	Transcript	retained_intron
rs3130283	HSCHR6_MHC_MCF: 32214977-32214977	3_prime_UTR_variant, NMD_transcript_variant	MODIFIER	PPT2	Transcript	nonsense_mediated_decay
rs3130283	HSCHR6_MHC_MCF: 32214977-32214977	downstream_gene_variant	MODIFIER	EGFL8	Transcript	processed_transcript
rs3130283	HSCHR6_MHC_MCF: 32214977-32214977	downstream_gene_variant	MODIFIER	PPT2	Transcript	nonsense_mediated_decay
rs3130283	HSCHR6_MHC_MCF: 32214977-32214977	downstream_gene_variant	MODIFIER	PPT2	Transcript	protein_coding
rs2395153	HSCHR6_MHC_MCF: 32421778-32421778	intergenic_variant	MODIFIER	-	-	-
rs4713587	HSCHR6_MHC_MCF: 32692524-32692524	intergenic_variant	MODIFIER	-	-	-
rs454424	HSCHR6_MHC_QBL: 31275049-31275049	intergenic_variant	MODIFIER	-	-	-
rs11961408	HSCHR6_MHC_QBL: 31307967-31307967	downstream_gene_variant	MODIFIER	HLA-B	Transcript	protein_coding
rs11961408	HSCHR6_MHC_QBL: 31307967-31307967	downstream_gene_variant	MODIFIER	HLA-B	Transcript	retained_intron

rs2260051	HSCHR6_MHC_QBL: 31582160-31582160	intron_variant	MODIFIER	<i>PRRC2A</i>	Transcript	protein_coding
rs2260051	HSCHR6_MHC_QBL: 31582160-31582160	upstream_gene_variant	MODIFIER	<i>PRRC2A</i>	Transcript	retained_intron
rs2260051	HSCHR6_MHC_QBL: 31582160-31582160	intron_variant, non_coding_transcript_variant	MODIFIER	<i>PRRC2A</i>	Transcript	processed_transcript
rs2260051	HSCHR6_MHC_QBL: 31582160-31582160	downstream_gene_variant	MODIFIER	<i>SNORA38</i>	Transcript	snoRNA
rs3115669	HSCHR6_MHC_QBL: 31609267-31609267	intron_variant	MODIFIER	<i>BAG6</i>	Transcript	protein_coding
rs3115669	HSCHR6_MHC_QBL: 31609267-31609267	upstream_gene_variant	MODIFIER	<i>APOM</i>	Transcript	protein_coding
rs3115669	HSCHR6_MHC_QBL: 31609267-31609267	intron_variant, non_coding_transcript_variant	MODIFIER	<i>BAG6</i>	Transcript	processed_transcript
rs592229	HSCHR6_MHC_QBL: 31920833-31920833	intron_variant	MODIFIER	<i>SKIV2L</i>	Transcript	protein_coding
rs592229	HSCHR6_MHC_QBL: 31920833-31920833	upstream_gene_variant	MODIFIER	<i>NELFE</i>	Transcript	protein_coding
rs592229	HSCHR6_MHC_QBL: 31920833-31920833	upstream_gene_variant	MODIFIER	<i>NELFE</i>	Transcript	processed_transcript
rs592229	HSCHR6_MHC_QBL: 31920833-31920833	intron_variant, non_coding_transcript_variant	MODIFIER	<i>SKIV2L</i>	Transcript	retained_intron
rs592229	HSCHR6_MHC_QBL: 31920833-31920833	upstream_gene_variant	MODIFIER	<i>NELFE</i>	Transcript	retained_intron
rs592229	HSCHR6_MHC_QBL: 31920833-31920833	upstream_gene_variant	MODIFIER	<i>SKIV2L</i>	Transcript	retained_intron
rs592229	HSCHR6_MHC_QBL: 31920833-31920833	downstream_gene_variant	MODIFIER	<i>SKIV2L</i>	Transcript	processed_transcript
rs592229	HSCHR6_MHC_QBL: 31920833-31920833	intron_variant, non_coding_transcript_variant	MODIFIER	<i>SKIV2L</i>	Transcript	processed_transcript
rs592229	HSCHR6_MHC_QBL: 31920833-31920833	intron_variant, non_coding_transcript_variant	MODIFIER	<i>CYP21A2</i>	Transcript	processed_transcript
rs592229	HSCHR6_MHC_QBL: 31920833-31920833	downstream_gene_variant	MODIFIER	<i>SKIV2L</i>	Transcript	retained_intron
rs592229	HSCHR6_MHC_QBL: 31920833-31920833	upstream_gene_variant	MODIFIER	<i>SKIV2L</i>	Transcript	processed_transcript
rs3130283	HSCHR6_MHC_QBL: 32096168-32096168	intron_variant	MODIFIER	<i>AGPAT1</i>	Transcript	protein_coding
rs3130283	HSCHR6_MHC_QBL: 32096168-32096168	downstream_gene_variant	MODIFIER	<i>EGFL8</i>	Transcript	protein_coding
rs3130283	HSCHR6_MHC_QBL: 32096168-32096168	3_prime_UTR_variant, NMD_transcript_variant	MODIFIER	<i>EGFL8</i>	Transcript	nonsense_mediated_decay
rs3130283	HSCHR6_MHC_QBL: 32096168-32096168	downstream_gene_variant	MODIFIER	<i>EGFL8</i>	Transcript	retained_intron
rs3130283	HSCHR6_MHC_QBL: 32096168-32096168	downstream_gene_variant	MODIFIER	<i>EGFL8</i>	Transcript	nonsense_mediated_decay
rs3130283	HSCHR6_MHC_QBL: 32096168-32096168	intron_variant, non_coding_transcript_variant	MODIFIER	<i>AGPAT1</i>	Transcript	processed_transcript

rs3130283	HSCHR6_MHC_QBL: 32096168-32096168	downstream_gene_variant	MODIFIER	<i>EGFL8</i>	Transcript	processed_transcript
rs2395153	HSCHR6_MHC_QBL: 32303064-32303064	intergenic_variant	MODIFIER	-	-	-
rs4713587	HSCHR6_MHC_QBL: 32588243-32588243	intergenic_variant	MODIFIER	-	-	-
rs454424	HSCHR6_MHC_SSTO: 31277815-31277815	intergenic_variant	MODIFIER	-	-	-
rs11961408	HSCHR6_MHC_SSTO: 31310749-31310749	downstream_gene_variant	MODIFIER	<i>HLA-B</i>	Transcript	protein_coding
rs11961408	HSCHR6_MHC_SSTO: 31310749-31310749	downstream_gene_variant	MODIFIER	<i>HLA-B</i>	Transcript	retained_intron
rs2260051	HSCHR6_MHC_SSTO: 31581861-31581861	intron_variant	MODIFIER	<i>PRRC2A</i>	Transcript	protein_coding
rs2260051	HSCHR6_MHC_SSTO: 31581861-31581861	upstream_gene_variant	MODIFIER	<i>PRRC2A</i>	Transcript	retained_intron
rs2260051	HSCHR6_MHC_SSTO: 31581861-31581861	intron_variant, non_coding_transcript_variant	MODIFIER	<i>PRRC2A</i>	Transcript	processed_transcript
rs2260051	HSCHR6_MHC_SSTO: 31581861-31581861	intron_variant	MODIFIER	<i>BX511262.2</i>	Transcript	protein_coding
rs2260051	HSCHR6_MHC_SSTO: 31581861-31581861	downstream_gene_variant	MODIFIER	<i>SNORA38</i>	Transcript	snoRNA
rs3115669	HSCHR6_MHC_SSTO: 31608971-31608971	intron_variant	MODIFIER	<i>BAG6</i>	Transcript	protein_coding
rs3115669	HSCHR6_MHC_SSTO: 31608971-31608971	upstream_gene_variant	MODIFIER	<i>APOM</i>	Transcript	protein_coding
rs3115669	HSCHR6_MHC_SSTO: 31608971-31608971	intron_variant, non_coding_transcript_variant	MODIFIER	<i>BAG6</i>	Transcript	processed_transcript
rs3115669	HSCHR6_MHC_SSTO: 31608971-31608971	intron_variant	MODIFIER	<i>BX511262.2</i>	Transcript	protein_coding
rs592229	HSCHR6_MHC_SSTO: 31922293-31922293	intron_variant	MODIFIER	<i>SKIV2L</i>	Transcript	protein_coding
rs592229	HSCHR6_MHC_SSTO: 31922293-31922293	upstream_gene_variant	MODIFIER	<i>NELFE</i>	Transcript	protein_coding
rs592229	HSCHR6_MHC_SSTO: 31922293-31922293	upstream_gene_variant	MODIFIER	<i>NELFE</i>	Transcript	retained_intron
rs592229	HSCHR6_MHC_SSTO: 31922293-31922293	intron_variant, non_coding_transcript_variant	MODIFIER	<i>SKIV2L</i>	Transcript	processed_transcript
rs592229	HSCHR6_MHC_SSTO: 31922293-31922293	upstream_gene_variant	MODIFIER	<i>SKIV2L</i>	Transcript	retained_intron
rs592229	HSCHR6_MHC_SSTO: 31922293-31922293	upstream_gene_variant	MODIFIER	<i>NELFE</i>	Transcript	processed_transcript
rs592229	HSCHR6_MHC_SSTO: 31922293-31922293	intron_variant, non_coding_transcript_variant	MODIFIER	<i>SKIV2L</i>	Transcript	retained_intron
rs592229	HSCHR6_MHC_SSTO: 31922293-31922293	downstream_gene_variant	MODIFIER	<i>SKIV2L</i>	Transcript	retained_intron
rs592229	HSCHR6_MHC_SSTO: 31922293-31922293	downstream_gene_variant	MODIFIER	<i>SKIV2L</i>	Transcript	processed_transcript

rs592229	HSCHR6_MHC_SSTO: 31922293-31922293	upstream_gene_variant	MODIFIER	<i>SKIV2L</i>	Transcript	processed_transcript
rs6449	HSCHR6_MHC_SSTO: 31998505-31998505	downstream_gene_variant	MODIFIER	<i>C4B</i>	Transcript	protein_coding
rs6449	HSCHR6_MHC_SSTO: 31998505-31998505	downstream_gene_variant	MODIFIER	<i>TNXB</i>	Transcript	protein_coding
rs6449	HSCHR6_MHC_SSTO: 31998505-31998505	upstream_gene_variant	MODIFIER	<i>C4A-AS1</i>	Transcript	processed_transcript
rs6449	HSCHR6_MHC_SSTO: 31998505-31998505	intron_variant	MODIFIER	<i>CYP21A2</i>	Transcript	protein_coding
rs6449	HSCHR6_MHC_SSTO: 31998505-31998505	downstream_gene_variant	MODIFIER	<i>TNXB</i>	Transcript	retained_intron
rs6449	HSCHR6_MHC_SSTO: 31998505-31998505	downstream_gene_variant	MODIFIER	<i>TNXB</i>	Transcript	processed_transcript
rs6449	HSCHR6_MHC_SSTO: 31998505-31998505	downstream_gene_variant	MODIFIER	<i>C4B</i>	Transcript	retained_intron
rs6449	HSCHR6_MHC_SSTO: 31998505-31998505	intron_variant, non_coding_transcript_variant	MODIFIER	<i>CYP21A2</i>	Transcript	retained_intron
rs6449	HSCHR6_MHC_SSTO: 31998505-31998505	non_coding_transcript_exon_variant	MODIFIER	<i>CYP21A2</i>	Transcript	retained_intron
rs6449	HSCHR6_MHC_SSTO: 31998505-31998505	downstream_gene_variant	MODIFIER	<i>C4B</i>	Transcript	processed_transcript
rs6449	HSCHR6_MHC_SSTO: 31998505-31998505	intron_variant, non_coding_transcript_variant	MODIFIER	<i>CYP21A2</i>	Transcript	processed_transcript
rs3130283	HSCHR6_MHC_SSTO: 32145415-32145415	downstream_gene_variant	MODIFIER	<i>EGFL8</i>	Transcript	protein_coding
rs3130283	HSCHR6_MHC_SSTO: 32145415-32145415	intron_variant	MODIFIER	<i>AGPAT1</i>	Transcript	protein_coding
rs3130283	HSCHR6_MHC_SSTO: 32145415-32145415	downstream_gene_variant	MODIFIER	<i>PPT2</i>	Transcript	nonsense_mediated_decay
rs3130283	HSCHR6_MHC_SSTO: 32145415-32145415	downstream_gene_variant	MODIFIER	<i>PPT2</i>	Transcript	processed_transcript
rs3130283	HSCHR6_MHC_SSTO: 32145415-32145415	intron_variant, non_coding_transcript_variant	MODIFIER	<i>AGPAT1</i>	Transcript	processed_transcript
rs3130283	HSCHR6_MHC_SSTO: 32145415-32145415	downstream_gene_variant	MODIFIER	<i>EGFL8</i>	Transcript	retained_intron
rs3130283	HSCHR6_MHC_SSTO: 32145415-32145415	3_prime_UTR_variant, NMD_transcript_variant	MODIFIER	<i>PPT2</i>	Transcript	nonsense_mediated_decay
rs3130283	HSCHR6_MHC_SSTO: 32145415-32145415	downstream_gene_variant	MODIFIER	<i>EGFL8</i>	Transcript	processed_transcript
rs3130283	HSCHR6_MHC_SSTO: 32145415-32145415	downstream_gene_variant	MODIFIER	<i>PPT2</i>	Transcript	protein_coding
rs2395153	HSCHR6_MHC_SSTO: 32352202-32352202	intergenic_variant	MODIFIER	-	-	-
rs4713587	HSCHR6_MHC_SSTO: 32750160-32750160	intergenic_variant	MODIFIER	-	-	-
T2DM _{adj} BMI and CAD						
rs35519679	10: 114818754-114818754	intron_variant	MODIFIER	<i>TCF7L2</i>	Transcript	protein_coding
rs11257655	10: 12307894-12307894	downstream_gene_variant	MODIFIER	<i>RN7SL232P</i>	Transcript	misc_RNA

rs11257655	10: 12307894-12307894	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	CTCF_binding_site
rs11257655	10: 12307894-12307894	TF_binding_site_variant	MODIFIER	-	MotifFeature	-
rs12778642	10: 94464307-94464307	intergenic_variant	MODIFIER	-	-	-
rs2306363	11: 65405600-65405600	downstream_gene_variant	MODIFIER	<i>PCNXL3</i>	Transcript	protein_coding
rs2306363	11: 65405600-65405600	upstream_gene_variant	MODIFIER	<i>SIPA1</i>	Transcript	protein_coding
rs2306363	11: 65405600-65405600	downstream_gene_variant	MODIFIER	<i>PCNXL3</i>	Transcript	retained_intron
rs2306363	11: 65405600-65405600	downstream_gene_variant	MODIFIER	<i>PCNXL3</i>	Transcript	processed_transcript
rs2306363	11: 65405600-65405600	5_prime_UTR_variant	MODIFIER	<i>SIPA1</i>	Transcript	protein_coding
rs2306363	11: 65405600-65405600	upstream_gene_variant	MODIFIER	<i>SIPA1</i>	Transcript	retained_intron
rs2306363	11: 65405600-65405600	downstream_gene_variant	MODIFIER	<i>MIR4690</i>	Transcript	miRNA
rs2306363	11: 65405600-65405600	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	promoter
rs2306363	11: 65405600-65405600	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	CTCF_binding_site
rs4766578	12: 111904371-111904371	intron_variant	MODIFIER	<i>ATXN2</i>	Transcript	protein_coding
rs4766578	12: 111904371-111904371	intron_variant, non_coding_transcript_variant	MODIFIER	<i>ATXN2</i>	Transcript	retained_intron
rs4766578	12: 111904371-111904371	intron_variant, NMD_transcript_variant	MODIFIER	<i>ATXN2</i>	Transcript	nonsense_mediated_decay
rs4766578	12: 111904371-111904371	downstream_gene_variant	MODIFIER	<i>ATXN2</i>	Transcript	retained_intron
rs1169288	12: 121416650-121416650	missense_variant	MODERATE	<i>HNF1A</i>	Transcript	protein_coding
rs1169288	12: 121416650-121416650	intron_variant, non_coding_transcript_variant	MODIFIER	<i>HNF1A-AS1</i>	Transcript	antisense
rs1169288	12: 121416650-121416650	intron_variant	MODIFIER	<i>HNF1A</i>	Transcript	protein_coding
rs1169288	12: 121416650-121416650	splice_region_variant, intron_variant	LOW	<i>HNF1A</i>	Transcript	protein_coding
rs1169288	12: 121416650-121416650	missense_variant, NMD_transcript_variant	MODERATE	<i>HNF1A</i>	Transcript	nonsense_mediated_decay
rs1169288	12: 121416650-121416650	splice_region_variant, intron_variant, NMD_transcript_variant	LOW	<i>HNF1A</i>	Transcript	nonsense_mediated_decay
rs1169288	12: 121416650-121416650	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	promoter
rs2257813	12: 121447519-121447519	intron_variant	MODIFIER	<i>C12orf43</i>	Transcript	protein_coding
rs2257813	12: 121447519-121447519	upstream_gene_variant	MODIFIER	<i>C12orf43</i>	Transcript	retained_intron
rs2257813	12: 121447519-121447519	intron_variant, non_coding_transcript_variant	MODIFIER	<i>C12orf43</i>	Transcript	retained_intron
rs2257813	12: 121447519-121447519	intron_variant, NMD_transcript_variant	MODIFIER	<i>C12orf43</i>	Transcript	nonsense_mediated_decay
rs2257813	12: 121447519-121447519	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	promoter_flanking_region
rs2257813	12: 121447519-121447519	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	CTCF_binding_site
rs56158042	12: 121455589-121455589	downstream_gene_variant	MODIFIER	<i>OASL</i>	Transcript	protein_coding
rs56158042	12: 121455589-121455589	upstream_gene_variant	MODIFIER	<i>C12orf43</i>	Transcript	protein_coding
rs56158042	12: 121455589-121455589	upstream_gene_variant	MODIFIER	<i>C12orf43</i>	Transcript	retained_intron
rs56158042	12: 121455589-121455589	upstream_gene_variant	MODIFIER	<i>C12orf43</i>	Transcript	nonsense_mediated_decay
rs7133378	12: 124409502-124409502	intron_variant	MODIFIER	<i>DNAH10</i>	Transcript	protein_coding
rs7133378	12: 124409502-124409502	upstream_gene_variant	MODIFIER	<i>DNAH10</i>	Transcript	retained_intron
rs7133378	12: 124409502-124409502	downstream_gene_variant	MODIFIER	<i>DNAH10OS</i>	Transcript	protein_coding
rs7133378	12: 124409502-124409502	intron_variant, non_coding_transcript_variant	MODIFIER	<i>CCDC92</i>	Transcript	processed_transcript
rs7133378	12: 124409502-124409502	downstream_gene_variant	MODIFIER	<i>RP11-380L11.4</i>	Transcript	antisense
rs10773049	12: 124506631-124506631	intron_variant	MODIFIER	<i>FAM101A</i>	Transcript	protein_coding
rs10773049	12: 124506631-124506631	intron_variant, non_coding_transcript_variant	MODIFIER	<i>FAM101A</i>	Transcript	processed_transcript
rs10773049	12: 124506631-124506631	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	CTCF_binding_site
rs4762753	12: 20579969-20579969	intron_variant	MODIFIER	<i>PDE3A</i>	Transcript	protein_coding
rs4762753	12: 20579969-20579969	intron_variant, non_coding_transcript_variant	MODIFIER	<i>PDE3A</i>	Transcript	retained_intron
rs8032939	15: 38834033-38834033	intron_variant	MODIFIER	<i>RASGRP1</i>	Transcript	protein_coding
rs8032939	15: 38834033-38834033	upstream_gene_variant	MODIFIER	<i>Y RNA</i>	Transcript	misc RNA
rs8032939	15: 38834033-38834033	intron_variant, NMD_transcript_variant	MODIFIER	<i>RASGRP1</i>	Transcript	nonsense_mediated_decay
rs72802342	16: 75234872-75234872	downstream_gene_variant	MODIFIER	<i>CTRB2</i>	Transcript	protein_coding
rs72802342	16: 75234872-75234872	downstream_gene_variant	MODIFIER	<i>CTRB2</i>	Transcript	retained_intron

rs72802342	16: 75234872-75234872	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	promoter_flanking_region
rs9937988	16: 75248803-75248803	upstream_gene_variant	MODIFIER	<i>CTRB1</i>	Transcript	protein_coding
rs7188857	16: 75303444-75303444	upstream_gene_variant	MODIFIER	<i>BCAR1</i>	Transcript	protein_coding
rs7188857	16: 75303444-75303444	upstream_gene_variant	MODIFIER	<i>BCAR1</i>	Transcript	nonsense_mediated_decay
rs37601	16: 75504775-75504775	intergenic_variant	MODIFIER	-	-	-
rs9891957	17: 17744439-17744439	upstream_gene_variant	MODIFIER	<i>SREBF1</i>	Transcript	protein_coding
rs9891957	17: 17744439-17744439	downstream_gene_variant	MODIFIER	<i>TOM1L2</i>	Transcript	protein_coding
rs9891957	17: 17744439-17744439	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	promoter
rs8068844	17: 40571284-40571284	intron_variant	MODIFIER	<i>PTRF</i>	Transcript	protein_coding
rs1962412	17: 46970259-46970259	intron_variant	MODIFIER	<i>ATP5G1</i>	Transcript	protein_coding
rs1962412	17: 46970259-46970259	5_prime_UTR_variant	MODIFIER	<i>ATP5G1</i>	Transcript	protein_coding
rs1962412	17: 46970259-46970259	upstream_gene_variant	MODIFIER	<i>ATP5G1</i>	Transcript	retained_intron
rs1962412	17: 46970259-46970259	upstream_gene_variant	MODIFIER	<i>ATP5G1</i>	Transcript	protein_coding
rs1962412	17: 46970259-46970259	intron_variant, non_coding_transcript_variant	MODIFIER	<i>SUMO2P17</i>	Transcript	processed_transcript
rs1962412	17: 46970259-46970259	intron_variant, non_coding_transcript_variant	MODIFIER	<i>ATP5G1</i>	Transcript	retained_intron
rs1962412	17: 46970259-46970259	non_coding_transcript_exon_variant	MODIFIER	<i>ATP5G1</i>	Transcript	processed_transcript
rs1962412	17: 46970259-46970259	upstream_gene_variant	MODIFIER	<i>ATP5G1</i>	Transcript	processed_transcript
rs1962412	17: 46970259-46970259	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	promoter
rs17883331	19: 4954455-4954455	non_coding_transcript_exon_variant	MODIFIER	<i>UHRF1</i>	Transcript	processed_transcript
rs116843064	19: 8429323-8429323	missense_variant	MODERATE	<i>ANGPTL4</i>	Transcript	protein_coding
rs116843064	19: 8429323-8429323	5_prime_UTR_variant	MODIFIER	<i>ANGPTL4</i>	Transcript	protein_coding
rs116843064	19: 8429323-8429323	missense_variant, NMD_transcript_variant	MODERATE	<i>ANGPTL4</i>	Transcript	nonsense_mediated_decay
rs116843064	19: 8429323-8429323	non_coding_transcript_exon_variant	MODIFIER	<i>ANGPTL4</i>	Transcript	retained_intron
rs116843064	19: 8429323-8429323	intron_variant, non_coding_transcript_variant	MODIFIER	<i>ANGPTL4</i>	Transcript	retained_intron
rs116843064	19: 8429323-8429323	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	promoter
rs113414093	2: 219859171-219859171	upstream_gene_variant	MODIFIER	<i>CRYBA2</i>	Transcript	protein_coding
rs113414093	2: 219859171-219859171	upstream_gene_variant	MODIFIER	<i>CRYBA2</i>	Transcript	processed_transcript
rs113414093	2: 219859171-219859171	upstream_gene_variant	MODIFIER	<i>CRYBA2</i>	Transcript	retained_intron
rs113414093	2: 219859171-219859171	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	CTCF_binding_site
rs79567528	2: 227038586-227038586	intergenic_variant	MODIFIER	-	-	-
rs2943656	2: 227121918-227121918	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	promoter_flanking_region
rs2943656	2: 227121918-227121918	intergenic_variant	MODIFIER	-	-	-
rs11692712	2: 227167100-227167100	intergenic_variant	MODIFIER	-	-	-
rs78718224	2: 227177827-227177827	intergenic_variant	MODIFIER	-	-	-
rs76367336	2: 227228251-227228251	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	enhancer
rs76367336	2: 227228251-227228251	intergenic_variant	MODIFIER	-	-	-
rs115528845	2: 43927374-43927374	missense_variant	MODERATE	<i>PLEKHH2</i>	Transcript	protein_coding
rs115528845	2: 43927374-43927374	non_coding_transcript_exon_variant	MODIFIER	<i>PLEKHH2</i>	Transcript	retained_intron
rs115528845	2: 43927374-43927374	downstream_gene_variant	MODIFIER	<i>PLEKHH2</i>	Transcript	nonsense_mediated_decay
rs12625329	20: 62709274-62709274	intron_variant	MODIFIER	<i>RGS19</i>	Transcript	protein_coding
rs12625329	20: 62709274-62709274	upstream_gene_variant	MODIFIER	<i>OPRL1</i>	Transcript	protein_coding
rs12625329	20: 62709274-62709274	intron_variant, non_coding_transcript_variant	MODIFIER	<i>RGS19</i>	Transcript	processed_transcript
rs12625329	20: 62709274-62709274	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	promoter
rs9989973	3: 12499264-12499264	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	promoter_flanking_region
rs9989973	3: 12499264-12499264	intergenic_variant	MODIFIER	-	-	-
rs9853950	3: 129336057-129336057	intergenic_variant	MODIFIER	-	-	-
rs185244	3: 138092889-138092889	intron_variant	MODIFIER	<i>MRAS</i>	Transcript	protein_coding
rs185244	3: 138092889-138092889	downstream_gene_variant	MODIFIER	<i>MRAS</i>	Transcript	protein_coding
rs13079221	3: 14901525-14901525	intron_variant	MODIFIER	<i>FGD5</i>	Transcript	protein_coding

rs62271373	3: 150066540-150066540	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	promoter_flanking_region
rs62271373	3: 150066540-150066540	intergenic_variant	MODIFIER	-	-	-
rs3936510	5: 55860866-55860866	intron_variant	MODIFIER	AC022431.2	Transcript	protein_coding
rs3936510	5: 55860866-55860866	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	promoter_flanking_region
rs3936510	5: 55860866-55860866	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	CTCF_binding_site
rs1591805	6: 126717064-126717064	intergenic_variant	MODIFIER	-	-	-
rs2292334	6: 160858188-160858188	synonymous_variant	LOW	SLC22A3	Transcript	protein_coding
rs2941383	6: 160870476-160870476	intron_variant	MODIFIER	SLC22A3	Transcript	protein_coding
rs2941383	6: 160870476-160870476	downstream_gene_variant	MODIFIER	LPAL2	Transcript	transcribed_unprocessed_pseudogene
rs3869098	6: 31002452-31002452	missense_variant	MODERATE	MUC22	Transcript	protein_coding
rs454424	6: 31284963-31284963	intergenic_variant	MODIFIER	-	-	-
rs11961408	6: 31317850-31317850	downstream_gene_variant	MODIFIER	HLA-B	Transcript	protein_coding
rs11961408	6: 31317850-31317850	downstream_gene_variant	MODIFIER	HLA-B	Transcript	retained_intron
rs9266631	6: 31346898-31346898	upstream_gene_variant	MODIFIER	ZDHHC20P2	Transcript	processed_pseudogene
rs9266631	6: 31346898-31346898	downstream_gene_variant	MODIFIER	HLA-S	Transcript	unprocessed_pseudogene
rs9266631	6: 31346898-31346898	downstream_gene_variant	MODIFIER	FGFR3P1	Transcript	processed_pseudogene
rs9266631	6: 31346898-31346898	upstream_gene_variant	MODIFIER	AL671883.1	Transcript	miRNA
rs2857702	6: 31577283-31577283	downstream_gene_variant	MODIFIER	UQCRHP1	Transcript	processed_pseudogene
rs3130283	6: 32138545-32138545	downstream_gene_variant	MODIFIER	EGFL8	Transcript	protein_coding
rs3130283	6: 32138545-32138545	intron_variant	MODIFIER	AGPAT1	Transcript	protein_coding
rs3130283	6: 32138545-32138545	downstream_gene_variant	MODIFIER	PPT2-EGFL8	Transcript	nonsense_mediated_decay
rs3130283	6: 32138545-32138545	3_prime_UTR_variant, NMD_transcript_variant	MODIFIER	PPT2-EGFL8	Transcript	nonsense_mediated_decay
rs3130283	6: 32138545-32138545	downstream_gene_variant	MODIFIER	PPT2	Transcript	protein_coding
rs3130283	6: 32138545-32138545	downstream_gene_variant	MODIFIER	PPT2-EGFL8	Transcript	processed_transcript
rs3130283	6: 32138545-32138545	downstream_gene_variant	MODIFIER	EGFL8	Transcript	retained_intron
rs3130283	6: 32138545-32138545	intron_variant, non_coding_transcript_variant	MODIFIER	AGPAT1	Transcript	processed_transcript
rs3130283	6: 32138545-32138545	downstream_gene_variant	MODIFIER	PPT2-EGFL8	Transcript	retained_intron
rs3130283	6: 32138545-32138545	downstream_gene_variant	MODIFIER	EGFL8	Transcript	processed_transcript
rs6905288	6: 43758873-43758873	downstream_gene_variant	MODIFIER	VEGFA	Transcript	protein_coding
rs6905288	6: 43758873-43758873	downstream_gene_variant	MODIFIER	VEGFA	Transcript	retained_intron
rs15285	8: 19824667-19824667	3_prime_UTR_variant	MODIFIER	LPL	Transcript	protein_coding
rs66778572	8: 19916120-19916120	intergenic_variant	MODIFIER	-	-	-
rs507666	9: 136149399-136149399	intron_variant, non_coding_transcript_variant	MODIFIER	ABO	Transcript	processed_transcript
rs507666	9: 136149399-136149399	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	promoter
rs28505901	9: 139241030-139241030	intron_variant	MODIFIER	GPSM1	Transcript	protein_coding
rs28505901	9: 139241030-139241030	downstream_gene_variant	MODIFIER	GPSM1	Transcript	protein_coding
rs28505901	9: 139241030-139241030	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	CTCF_binding_site
rs12003940	9: 19101350-19101350	intron_variant	MODIFIER	HAUS6	Transcript	protein_coding
rs12003940	9: 19101350-19101350	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	promoter
rs10965199	9: 21954653-21954653	intron_variant, NMD_transcript_variant	MODIFIER	RP11-145E5.5	Transcript	nonsense_mediated_decay
rs7041637	9: 21961866-21961866	intron_variant, NMD_transcript_variant	MODIFIER	RP11-145E5.5	Transcript	nonsense_mediated_decay
rs3731239	9: 21974218-21974218	intron_variant	MODIFIER	CDKN2A	Transcript	protein_coding
rs3731239	9: 21974218-21974218	upstream_gene_variant	MODIFIER	CDKN2A	Transcript	processed_transcript
rs3731239	9: 21974218-21974218	intron_variant, NMD_transcript_variant	MODIFIER	CDKN2A	Transcript	nonsense_mediated_decay
rs3731239	9: 21974218-21974218	intron_variant, NMD_transcript_variant	MODIFIER	RP11-145E5.5	Transcript	nonsense_mediated_decay
rs3731239	9: 21974218-21974218	upstream_gene_variant	MODIFIER	CDKN2A	Transcript	protein_coding
rs3731239	9: 21974218-21974218	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	promoter
rs11790231	9: 22053591-22053591	intron_variant, non_coding_transcript_variant	MODIFIER	CDKN2B-AS1	Transcript	antisense
rs11790231	9: 22053591-22053591	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	CTCF_binding_site

rs11790231	9: 22053591-22053591	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	promoter_flanking_region
rs76011118	9: 22133773-22133773	intergenic_variant	MODIFIER	-	-	-
rs12555274	9: 22136440-22136440	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	promoter_flanking_region
rs12555274	9: 22136440-22136440	intergenic_variant	MODIFIER	-	-	-
rs507666	HG79_PATCH: 136149518-136149518	intron_variant	MODIFIER	<i>ABO</i>	Transcript	protein_coding
rs28505901	HG998_2_PATCH: 139254479-139254479	intron_variant	MODIFIER	<i>GPSM1</i>	Transcript	protein_coding
rs3869098	HSCHR6_MHC_APD: 31011035-31011035	non_coding_transcript_exon_variant	MODIFIER	<i>XXbac-BPG118E17.9</i>	Transcript	processed_transcript
rs2857702	HSCHR6_MHC_APD: 31588624-31588624	downstream_gene_variant	MODIFIER	<i>UQCRHP1</i>	Transcript	processed_pseudogene
rs3130283	HSCHR6_MHC_APD: 32149889-32149889	downstream_gene_variant	MODIFIER	<i>EGFL8</i>	Transcript	protein_coding
rs3130283	HSCHR6_MHC_APD: 32149889-32149889	intron_variant	MODIFIER	<i>AGPAT1</i>	Transcript	protein_coding
rs3130283	HSCHR6_MHC_APD: 32149889-32149889	intron_variant, non_coding_transcript_variant	MODIFIER	<i>AGPAT1</i>	Transcript	processed_transcript
rs3130283	HSCHR6_MHC_APD: 32149889-32149889	3_prime_UTR_variant, NMD_transcript_variant	MODIFIER	<i>PPT2</i>	Transcript	nonsense_mediated_decay
rs3130283	HSCHR6_MHC_APD: 32149889-32149889	downstream_gene_variant	MODIFIER	<i>EGFL8</i>	Transcript	retained_intron
rs3130283	HSCHR6_MHC_APD: 32149889-32149889	downstream_gene_variant	MODIFIER	<i>PPT2</i>	Transcript	nonsense_mediated_decay
rs3130283	HSCHR6_MHC_APD: 32149889-32149889	downstream_gene_variant	MODIFIER	<i>EGFL8</i>	Transcript	processed_transcript
rs3130283	HSCHR6_MHC_APD: 32149889-32149889	downstream_gene_variant	MODIFIER	<i>PPT2</i>	Transcript	protein_coding
rs3869098	HSCHR6_MHC_COX: 30992271-30992271	non_coding_transcript_exon_variant	MODIFIER	<i>XXbac-BPG118E17.9</i>	Transcript	processed_transcript
rs3869098	HSCHR6_MHC_COX: 30992271-30992271	intron_variant	MODIFIER	<i>AL663093.2</i>	Transcript	protein_coding
rs454424	HSCHR6_MHC_COX: 31275997-31275997	intergenic_variant	MODIFIER	-	-	-
rs11961408	HSCHR6_MHC_COX: 31308332-31308332	downstream_gene_variant	MODIFIER	<i>HLA-B</i>	Transcript	protein_coding
rs11961408	HSCHR6_MHC_COX: 31308332-31308332	downstream_gene_variant	MODIFIER	<i>HLA-B</i>	Transcript	retained_intron
rs9266631	HSCHR6_MHC_COX: 31337355-31337355	downstream_gene_variant	MODIFIER	<i>HLA-S</i>	Transcript	unprocessed_pseudogene
rs9266631	HSCHR6_MHC_COX: 31337355-31337355	downstream_gene_variant	MODIFIER	<i>FGFR3P</i>	Transcript	processed_pseudogene
rs9266631	HSCHR6_MHC_COX: 31337355-31337355	upstream_gene_variant	MODIFIER	<i>ZDHHC20P2</i>	Transcript	processed_pseudogene
rs2857702	HSCHR6_MHC_COX: 31564701-31564701	downstream_gene_variant	MODIFIER	<i>UQCRHP1</i>	Transcript	processed_pseudogene
rs3130283	HSCHR6_MHC_COX: 32087022-32087022	downstream_gene_variant	MODIFIER	<i>EGFL8</i>	Transcript	protein_coding

rs3130283	HSCHR6_MHC_COX: 32087022-32087022	intron_variant	MODIFIER	<i>AGPAT1</i>	Transcript	protein_coding
rs3130283	HSCHR6_MHC_COX: 32087022-32087022	downstream_gene_variant	MODIFIER	<i>XXbac-BCX105D18.9</i>	Transcript	nonsense_mediated_decay
rs3130283	HSCHR6_MHC_COX: 32087022-32087022	downstream_gene_variant	MODIFIER	<i>EGFL8</i>	Transcript	processed_transcript
rs3130283	HSCHR6_MHC_COX: 32087022-32087022	3_prime_UTR_variant, NMD_transcript_variant	MODIFIER	<i>XXbac-BCX105D18.9</i>	Transcript	nonsense_mediated_decay
rs3130283	HSCHR6_MHC_COX: 32087022-32087022	intron_variant, non_coding_transcript_variant	MODIFIER	<i>AGPAT1</i>	Transcript	processed_transcript
rs3130283	HSCHR6_MHC_COX: 32087022-32087022	downstream_gene_variant	MODIFIER	<i>EGFL8</i>	Transcript	retained_intron
rs3130283	HSCHR6_MHC_COX: 32087022-32087022	downstream_gene_variant	MODIFIER	<i>PPT2</i>	Transcript	protein_coding
rs3869098	HSCHR6_MHC_DBB: 30993509-30993509	non_coding_transcript_exon_variant	MODIFIER	<i>XXbac-BPG118E17.9</i>	Transcript	processed_transcript
rs11961408	HSCHR6_MHC_DBB: 31299785-31299785	intergenic_variant	MODIFIER	-	-	-
rs2857702	HSCHR6_MHC_DBB: 31559451-31559451	downstream_gene_variant	MODIFIER	<i>UQCRHP1</i>	Transcript	processed_pseudogene
rs3869098	HSCHR6_MHC_MANN: 31047413-31047413	non_coding_transcript_exon_variant	MODIFIER	<i>XXbac-BPG118E17.9</i>	Transcript	processed_transcript
rs11961408	HSCHR6_MHC_MANN: 31360907-31360907	downstream_gene_variant	MODIFIER	<i>HLA-B</i>	Transcript	protein_coding
rs11961408	HSCHR6_MHC_MANN: 31360907-31360907	downstream_gene_variant	MODIFIER	<i>HLA-B</i>	Transcript	retained_intron
rs9266631	HSCHR6_MHC_MANN: 31389950-31389950	downstream_gene_variant	MODIFIER	<i>FGFR3P</i>	Transcript	processed_pseudogene
rs9266631	HSCHR6_MHC_MANN: 31389950-31389950	upstream_gene_variant	MODIFIER	<i>ZDHHC20P2</i>	Transcript	processed_pseudogene
rs9266631	HSCHR6_MHC_MANN: 31389950-31389950	downstream_gene_variant	MODIFIER	<i>HLA-S</i>	Transcript	unprocessed_pseudogene
rs2857702	HSCHR6_MHC_MANN: 31616773-31616773	intergenic_variant	MODIFIER	-	-	-
rs3130283	HSCHR6_MHC_MANN: 32177972-32177972	intron_variant	MODIFIER	<i>AGPAT1</i>	Transcript	protein_coding
rs3130283	HSCHR6_MHC_MANN: 32177972-32177972	downstream_gene_variant	MODIFIER	<i>EGFL8</i>	Transcript	protein_coding
rs3130283	HSCHR6_MHC_MANN: 32177972-32177972	intron_variant, non_coding_transcript_variant	MODIFIER	<i>AGPAT1</i>	Transcript	processed_transcript
rs3130283	HSCHR6_MHC_MANN: 32177972-32177972	downstream_gene_variant	MODIFIER	<i>EGFL8</i>	Transcript	retained_intron
rs3130283	HSCHR6_MHC_MANN: 32177972-32177972	downstream_gene_variant	MODIFIER	<i>EGFL8</i>	Transcript	processed_transcript
rs3130283	HSCHR6_MHC_MANN: 32177972-32177972	3_prime_UTR_variant, NMD_transcript_variant	MODIFIER	<i>PPT2</i>	Transcript	nonsense_mediated_decay
rs3130283	HSCHR6_MHC_MANN: 32177972-32177972	downstream_gene_variant	MODIFIER	<i>PPT2</i>	Transcript	nonsense_mediated_decay

rs3130283	HSCHR6_MHC_MANN: 32177972-32177972	downstream_gene_variant	MODIFIER	<i>PPT2</i>	Transcript	protein_coding
rs3869098	HSCHR6_MHC_MCF: 31081002-31081002	non_coding_transcript_exon_variant	MODIFIER	<i>XXbac-BPG118E17.9</i>	Transcript	processed_transcript
rs454424	HSCHR6_MHC_MCF: 31362068-31362068	intergenic_variant	MODIFIER	-	-	-
rs11961408	HSCHR6_MHC_MCF: 31394233-31394233	downstream_gene_variant	MODIFIER	<i>HLA-B</i>	Transcript	protein_coding
rs11961408	HSCHR6_MHC_MCF: 31394233-31394233	downstream_gene_variant	MODIFIER	<i>HLA-B</i>	Transcript	retained_intron
rs3130283	HSCHR6_MHC_MCF: 32214977-32214977	downstream_gene_variant	MODIFIER	<i>EGFL8</i>	Transcript	protein_coding
rs3130283	HSCHR6_MHC_MCF: 32214977-32214977	intron_variant	MODIFIER	<i>AGPAT1</i>	Transcript	protein_coding
rs3130283	HSCHR6_MHC_MCF: 32214977-32214977	intron_variant, non_coding_transcript_variant	MODIFIER	<i>AGPAT1</i>	Transcript	processed_transcript
rs3130283	HSCHR6_MHC_MCF: 32214977-32214977	downstream_gene_variant	MODIFIER	<i>EGFL8</i>	Transcript	retained_intron
rs3130283	HSCHR6_MHC_MCF: 32214977-32214977	3_prime_UTR_variant, NMD_transcript_variant	MODIFIER	<i>PPT2</i>	Transcript	nonsense_mediated_decay
rs3130283	HSCHR6_MHC_MCF: 32214977-32214977	downstream_gene_variant	MODIFIER	<i>EGFL8</i>	Transcript	processed_transcript
rs3130283	HSCHR6_MHC_MCF: 32214977-32214977	downstream_gene_variant	MODIFIER	<i>PPT2</i>	Transcript	nonsense_mediated_decay
rs3130283	HSCHR6_MHC_MCF: 32214977-32214977	downstream_gene_variant	MODIFIER	<i>PPT2</i>	Transcript	protein_coding
rs3869098	HSCHR6_MHC_QBL: 30992511-30992511	non_coding_transcript_exon_variant	MODIFIER	<i>XXbac-BPG118E17.9</i>	Transcript	processed_transcript
rs3869098	HSCHR6_MHC_QBL: 30992511-30992511	intron_variant	MODIFIER	<i>AL805909.3</i>	Transcript	protein_coding
rs454424	HSCHR6_MHC_QBL: 31275049-31275049	intergenic_variant	MODIFIER	-	-	-
rs11961408	HSCHR6_MHC_QBL: 31307967-31307967	downstream_gene_variant	MODIFIER	<i>HLA-B</i>	Transcript	protein_coding
rs11961408	HSCHR6_MHC_QBL: 31307967-31307967	downstream_gene_variant	MODIFIER	<i>HLA-B</i>	Transcript	retained_intron
rs9266631	HSCHR6_MHC_QBL: 31337013-31337013	downstream_gene_variant	MODIFIER	<i>HLA-S</i>	Transcript	unprocessed_pseudogene
rs9266631	HSCHR6_MHC_QBL: 31337013-31337013	upstream_gene_variant	MODIFIER	<i>ZDHHC20P2</i>	Transcript	processed_pseudogene
rs9266631	HSCHR6_MHC_QBL: 31337013-31337013	downstream_gene_variant	MODIFIER	<i>FGFR3P</i>	Transcript	processed_pseudogene
rs2857702	HSCHR6_MHC_QBL: 31567530-31567530	downstream_gene_variant	MODIFIER	<i>UQCRHP1</i>	Transcript	processed_pseudogene
rs3130283	HSCHR6_MHC_QBL: 32096168-32096168	intron_variant	MODIFIER	<i>AGPAT1</i>	Transcript	protein_coding
rs3130283	HSCHR6_MHC_QBL: 32096168-32096168	downstream_gene_variant	MODIFIER	<i>EGFL8</i>	Transcript	protein_coding

rs3130283	HSCHR6_MHC_QBL: 32096168-32096168	3_prime_UTR_variant, NMD_transcript_variant	MODIFIER	<i>EGFL8</i>	Transcript	nonsense_mediated_decay
rs3130283	HSCHR6_MHC_QBL: 32096168-32096168	downstream_gene_variant	MODIFIER	<i>EGFL8</i>	Transcript	retained_intron
rs3130283	HSCHR6_MHC_QBL: 32096168-32096168	downstream_gene_variant	MODIFIER	<i>EGFL8</i>	Transcript	nonsense_mediated_decay
rs3130283	HSCHR6_MHC_QBL: 32096168-32096168	intron_variant, non_coding_transcript_variant	MODIFIER	<i>AGPAT1</i>	Transcript	processed_transcript
rs3130283	HSCHR6_MHC_QBL: 32096168-32096168	downstream_gene_variant	MODIFIER	<i>EGFL8</i>	Transcript	processed_transcript
rs3869098	HSCHR6_MHC_SSTO: 30993850-30993850	non_coding_transcript_exon_variant	MODIFIER	<i>XXbac- BPG118E17.9</i>	Transcript	processed_transcript
rs3869098	HSCHR6_MHC_SSTO: 30993850-30993850	intron_variant	MODIFIER	<i>BX248321.1</i>	Transcript	protein_coding
rs454424	HSCHR6_MHC_SSTO: 31277815-31277815	intergenic_variant	MODIFIER	-	-	-
rs11961408	HSCHR6_MHC_SSTO: 31310749-31310749	downstream_gene_variant	MODIFIER	<i>HLA-B</i>	Transcript	protein_coding
rs11961408	HSCHR6_MHC_SSTO: 31310749-31310749	downstream_gene_variant	MODIFIER	<i>HLA-B</i>	Transcript	retained_intron
rs9266631	HSCHR6_MHC_SSTO: 31339784-31339784	downstream_gene_variant	MODIFIER	<i>HLA-S</i>	Transcript	unprocessed_pseudogene
rs9266631	HSCHR6_MHC_SSTO: 31339784-31339784	upstream_gene_variant	MODIFIER	<i>ZDHHC20P2</i>	Transcript	processed_pseudogene
rs9266631	HSCHR6_MHC_SSTO: 31339784-31339784	downstream_gene_variant	MODIFIER	<i>FGFR3P</i>	Transcript	processed_pseudogene
rs2857702	HSCHR6_MHC_SSTO: 31567235-31567235	downstream_gene_variant	MODIFIER	<i>UQCRHP1</i>	Transcript	processed_pseudogene
rs2857702	HSCHR6_MHC_SSTO: 31567235-31567235	intron_variant	MODIFIER	<i>BX511262.2</i>	Transcript	protein_coding
rs3130283	HSCHR6_MHC_SSTO: 32145415-32145415	downstream_gene_variant	MODIFIER	<i>EGFL8</i>	Transcript	protein_coding
rs3130283	HSCHR6_MHC_SSTO: 32145415-32145415	intron_variant	MODIFIER	<i>AGPAT1</i>	Transcript	protein_coding
rs3130283	HSCHR6_MHC_SSTO: 32145415-32145415	downstream_gene_variant	MODIFIER	<i>PPT2</i>	Transcript	nonsense_mediated_decay
rs3130283	HSCHR6_MHC_SSTO: 32145415-32145415	downstream_gene_variant	MODIFIER	<i>PPT2</i>	Transcript	processed_transcript
rs3130283	HSCHR6_MHC_SSTO: 32145415-32145415	intron_variant, non_coding_transcript_variant	MODIFIER	<i>AGPAT1</i>	Transcript	processed_transcript
rs3130283	HSCHR6_MHC_SSTO: 32145415-32145415	downstream_gene_variant	MODIFIER	<i>EGFL8</i>	Transcript	retained_intron
rs3130283	HSCHR6_MHC_SSTO: 32145415-32145415	3_prime_UTR_variant, NMD_transcript_variant	MODIFIER	<i>PPT2</i>	Transcript	nonsense_mediated_decay
rs3130283	HSCHR6_MHC_SSTO: 32145415-32145415	downstream_gene_variant	MODIFIER	<i>EGFL8</i>	Transcript	processed_transcript
rs3130283	HSCHR6_MHC_SSTO: 32145415-32145415	downstream_gene_variant	MODIFIER	<i>PPT2</i>	Transcript	protein_coding

T2DM, type 2 diabetes mellitus; CAD, coronary artery disease; T2DM_{adj}BMI, type 2 diabetes mellitus adjusted for body mass index.

Supplementary Table 15. Previously reported phenotypes associated with novel SNPs identified by cross-trait meta-analysis between type 2 diabetes mellitus and coronary artery disease.

Model	SNP	Phenotypes
T2DM and CAD	rs4135268	BMI-adjusted waist-hip ratio. Eosinophil count; Eosinophil percentage of granulocytes; Eosinophil percentage of white cells; Granulocyte count; Lymphocyte count; Monocyte count; Myeloid white cell count; Neutrophil count; Neutrophil percentage of granulocytes; Sum basophil neutrophil counts; Sum eosinophil basophil counts; Sum neutrophil eosinophil counts; White blood cell count; IgA deficiency; Arm fat-free mass left; Arm fat-free mass right; Arm predicted mass left; Arm predicted mass right; Asthma; Basal metabolic rate; Comparative height size at age 10; Forced vital capacity; Forced vital capacity, best measure; Hand grip strength left; Hand grip strength right; Height; Impedance of arm left; Impedance of arm right; Impedance of leg left; Impedance of leg right; Impedance of whole body; Intestinal malabsorption; Leg fat-free mass left; Leg fat-free mass right; Leg predicted mass left; Leg predicted mass right; Medication for cholesterol, blood pressure or diabetes: none of the above; Multiple sclerosis; No blood clot, bronchitis, emphysema, asthma, rhinitis, eczema or allergy diagnosed by doctor; Number of treatments or medications taken; Other rheumatoid arthritis; Self-reported asthma; Self-reported hypertension; Self-reported hyperthyroidism or thyrotoxicosis; Self-reported hypothyroidism or myxoedema; Self-reported malabsorption or coeliac disease; Self-reported multiple sclerosis; Self-reported rheumatoid arthritis; Sitting height; Systolic blood pressure; Treatment with methotrexate; Trunk fat-free mass; Trunk predicted mass; Vascular or heart problems diagnosed by doctor: high blood pressure; Vascular or heart problems diagnosed by doctor: none of the above; Whole body fat-free mass; Whole body water mass; Worrier or anxious feelings; Rheumatoid arthritis
	rs6449	
	rs35497503	Refractive error; Immature fraction of reticulocytes; Mean corpuscular volume; Red blood cell count.
	rs12452590	Heel bone mineral density; Lung function (FEV1/FVC); Lung function (FVC); Migraine; Comparative height size at age 10; Forced vital capacity, best measure; Height; Sitting height; Trunk fat-free mass; Trunk predicted mass.
	rs2306527	Heart failure; Arm fat-free mass left; Arm fat-free mass right; Arm predicted mass left; Arm predicted mass right; Basal metabolic rate; Diastolic blood pressure; Height; Leg fat-free mass left; Leg fat-free mass right; Leg predicted mass left; Leg predicted mass right; Systolic blood pressure; Trunk fat-free mass; Trunk predicted mass; Weight; Whole body fat-free mass; Whole body water mass.
T2DM _{adj} BMI and CAD	rs4762753	-

Previously reported phenotypes ($P < 5 \times 10^{-8}$) were extracted from GWAS Catalog and PhenoScanner V2.

T2DM, type 2 diabetes mellitus; CAD, coronary artery disease; T2DM_{adj}BMI, type 2 diabetes mellitus adjusted for body mass index.

Supplementary Table 16. Univariable Mendelian randomization analysis between body mass index, systolic blood pressure, taking HMG CoA reductase inhibitors, type 2 diabetes mellitus, and coronary artery disease.

Exposure	Outcome	N _{SNPs}	Beta	Se	OR (95%CI)	P
BMI	T2DM	1832	0.963	0.027	2.62 (2.49-2.76)	9.08E-284
BMI	CAD	1833	0.370	0.017	1.45 (1.40-1.50)	1.36E-108
BMI	SBP	1653	-0.671	0.160	0.51 (0.37-0.70)	2.91E-05
BMI	C10AA	1738	0.378	0.020	1.46 (1.40-1.52)	3.06E-77
T2DM	SBP	305	0.749	0.091	2.12 (1.77-2.53)	2.01E-16
SBP	CAD	230	0.030	0.003	1.03 (1.02-1.04)	6.49E-24
CAD	C10AA	211	0.551	0.036	1.73 (1.61-1.86)	9.82E-52
C10AA	T2DM	97	0.213	0.080	1.24 (1.06-1.45)	7.59E-03

T2DM, type 2 diabetes mellitus; CAD, coronary artery disease; SBP, systolic blood pressure; BMI, body mass index; C10AA, HMG CoA reductase inhibitors.

Supplementary Table 17. Multivariable Mendelian randomization analysis between body mass index, systolic blood pressure, taking HMG CoA reductase inhibitors, type 2 diabetes mellitus, and coronary artery disease.

Exposure	Outcome	N _{SNPs}	Beta	Se	OR (95%CI)	P
T2DM	CAD	1242	0.157	0.013	1.17 (1.14-1.20)	7.02E-35
BMI			0.201	0.026	1.22 (1.16-1.29)	1.58E-14
CAD	T2DM	1231	0.211	0.026	1.23 (1.17-1.30)	1.18E-15
BMI			0.855	0.039	2.35 (2.18-2.54)	3.97E-106
T2DM	CAD	1249	0.072	0.010	1.07 (1.05-1.10)	8.48E-14
BMI			0.304	0.025	1.36 (1.29-1.42)	2.17E-33
SBP			0.034	0.002	1.03 (1.03-1.04)	2.27E-42
CAD			0.020	0.035	1.02 (0.95-1.09)	0.563061
BMI	T2DM	1206	0.755	0.040	2.13 (1.97-2.30)	3.51E-78
C10AA			0.401	0.039	1.49 (1.38-1.61)	3.30E-24

T2DM, type 2 diabetes mellitus; CAD, coronary artery disease; SBP, systolic blood pressure; C10AA, HMG CoA reductase inhibitors.

Supplementary Table 18. Mediation analysis between type 2 diabetes mellitus, systolic blood pressure, taking HMG CoA reductase inhibitors, and coronary artery disease.

Mediator	Total effect (c)					Direct effect (c')					Indirect effect (c-c')			Proportion mediated					
	exposure	outcome	beta	se	var	exposure	outcome	beta	se	var	beta	se	var	PM	se (PM)	var (PM)	lower PM	upper PM	P
SBP	T2DM	CAD	0.157	0.013	1.63E-04	T2DM	CAD	0.072	0.010	9.37E-05	0.085	0.022	5.05E-04	0.541	0.149	0.022	0.249	0.834	1.44E-04
C10AA	CAD	T2DM	0.211	0.026	6.94E-04	CAD	T2DM	0.020	0.035	1.22E-03	0.191	0.061	3.75E-03	0.904	0.312	0.097	0.293	1.515	1.86E-03

T2DM, type 2 diabetes mellitus; CAD, coronary artery disease; SBP, systolic blood pressure; C10AA, HMG CoA reductase inhibitors. All models are extensively adjusted for BMI.