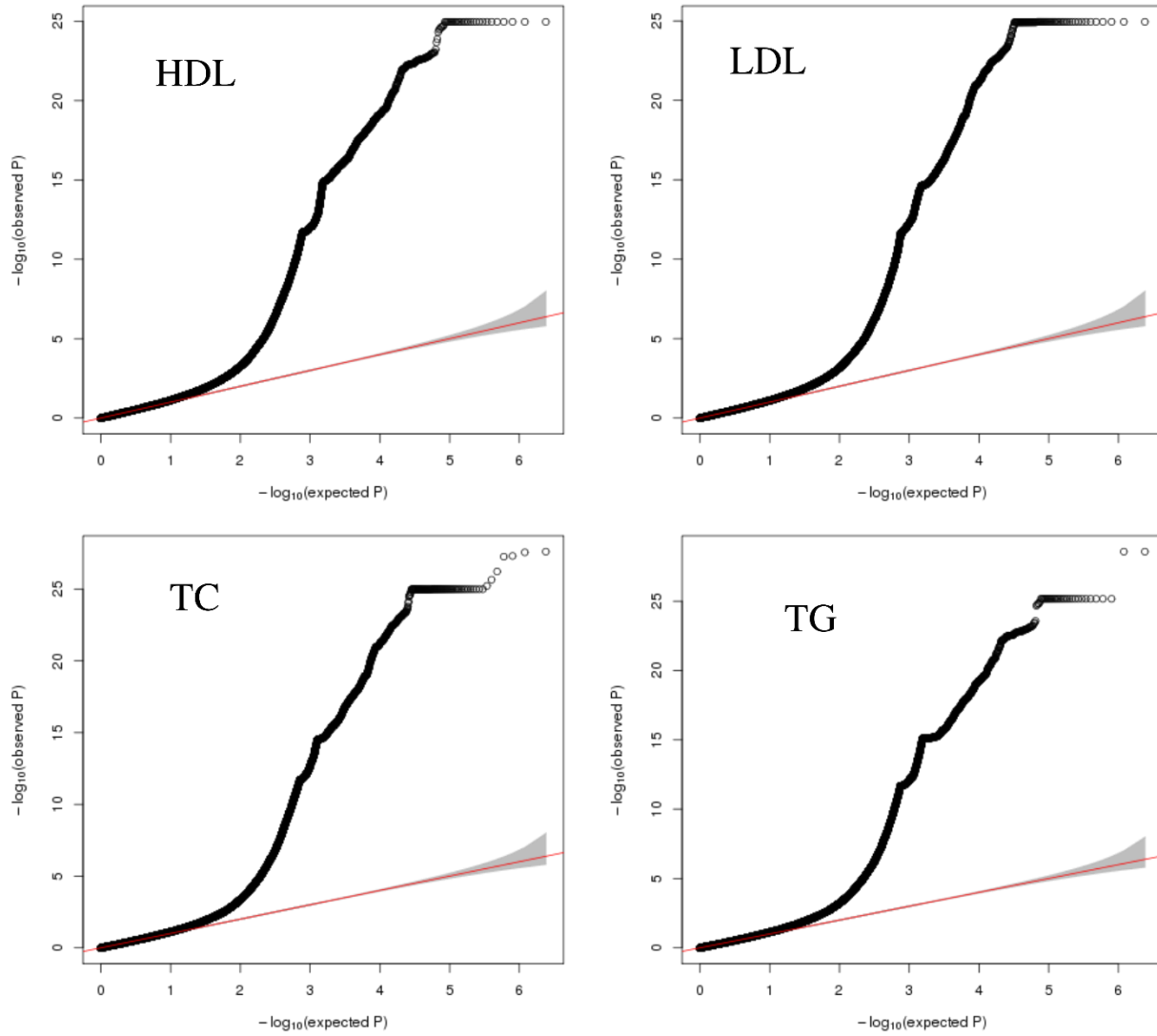
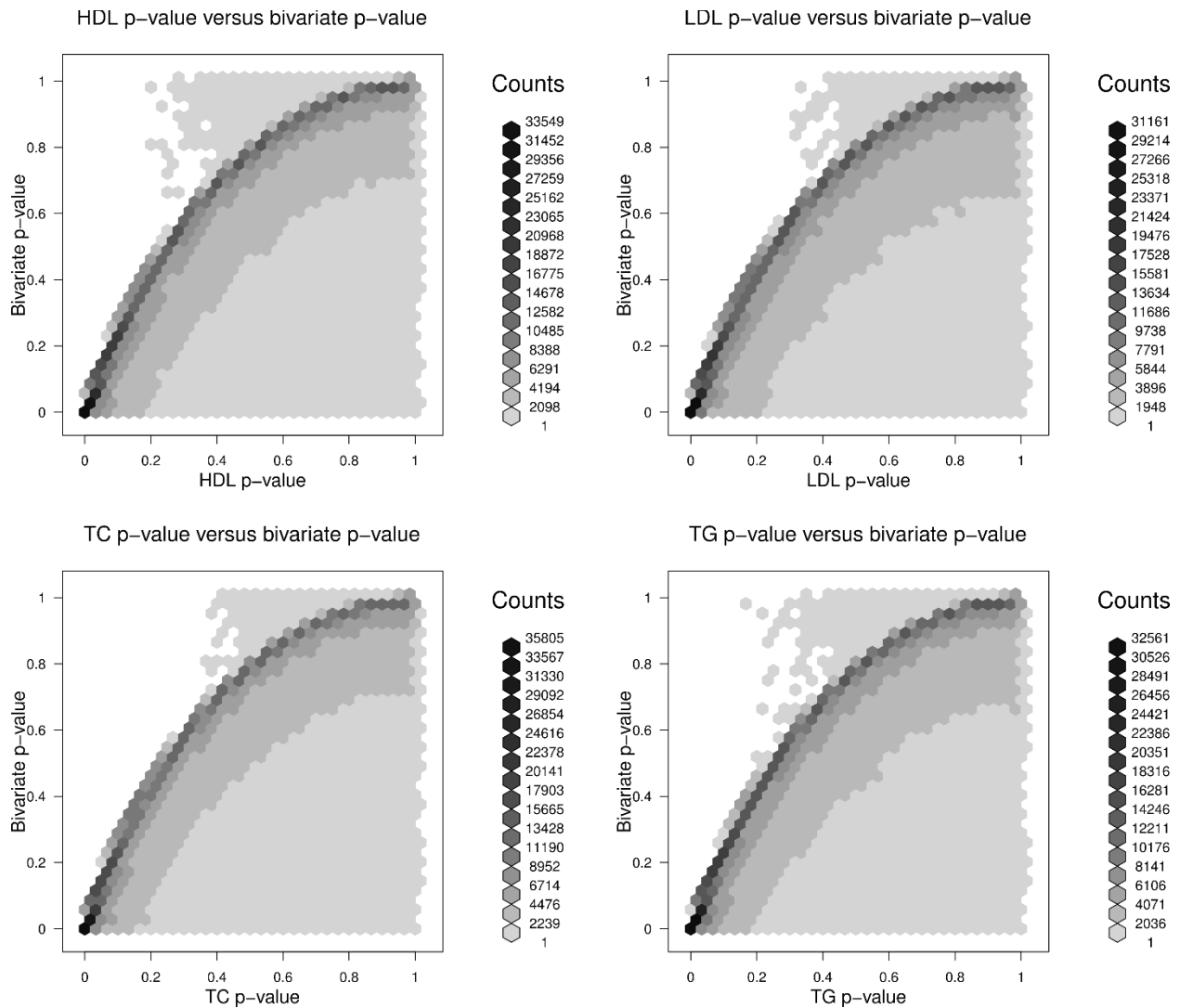


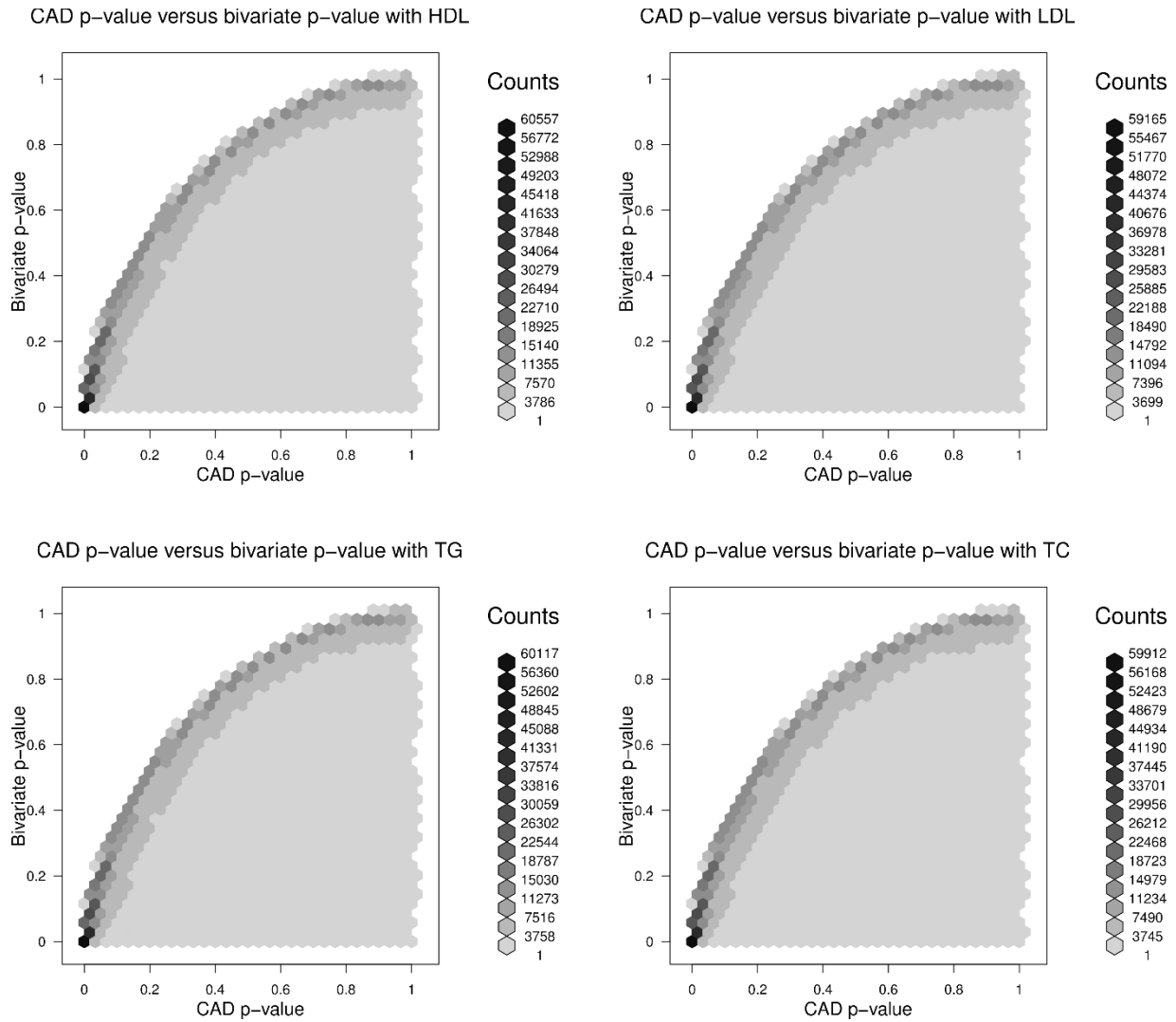
SUPPLEMENTAL MATERIAL



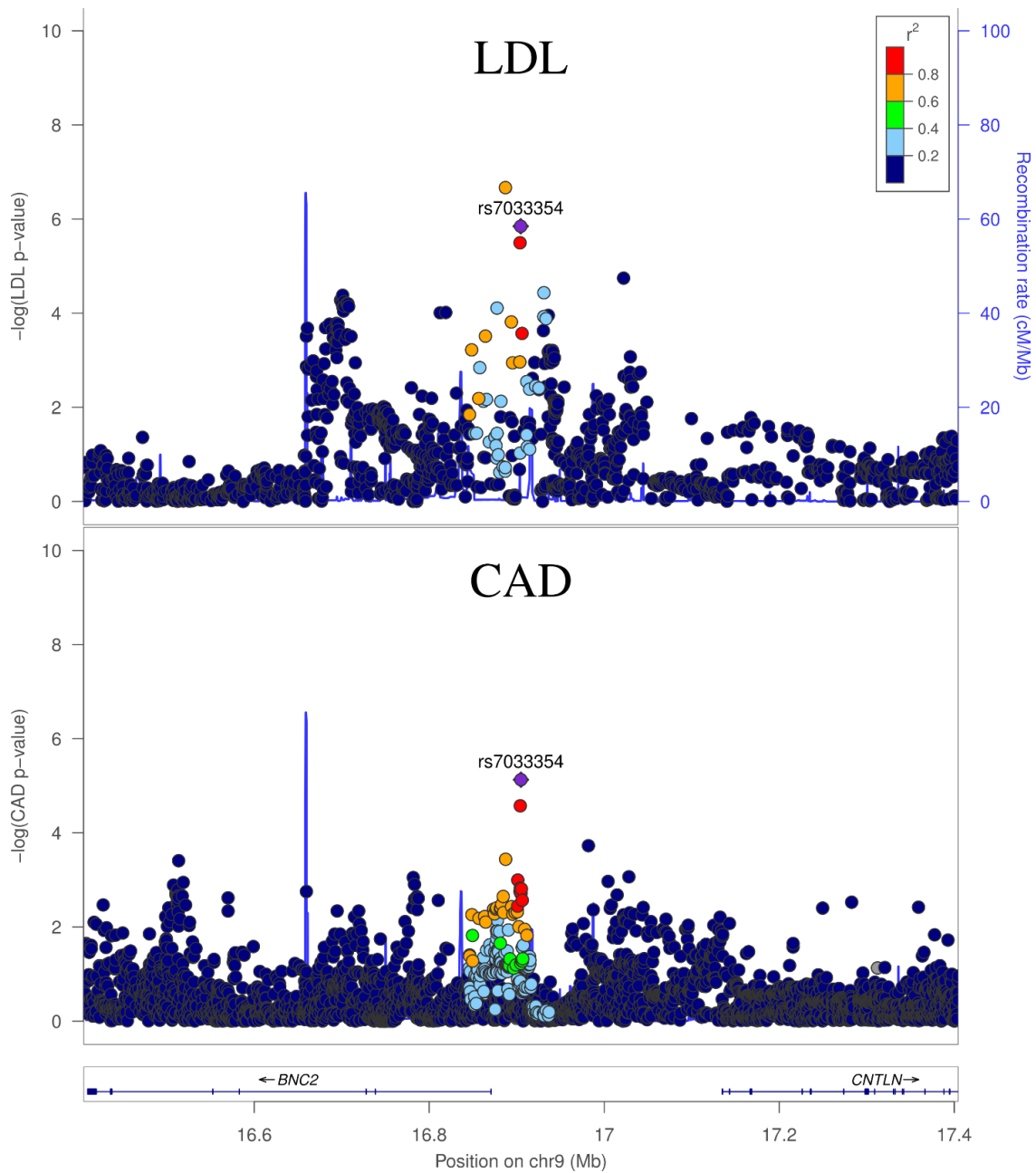
**Supplementary Figure 1:** QQ plots of p-values for each bivariate GWAS scan between Coronary Artery Disease (CAD) and each of four lipid traits (HDL: High-Density Lipoprotein Cholesterol, LDL: Low-Density Lipoprotein cholesterol, TC: Total Cholesterol, TG: Triglycerides).



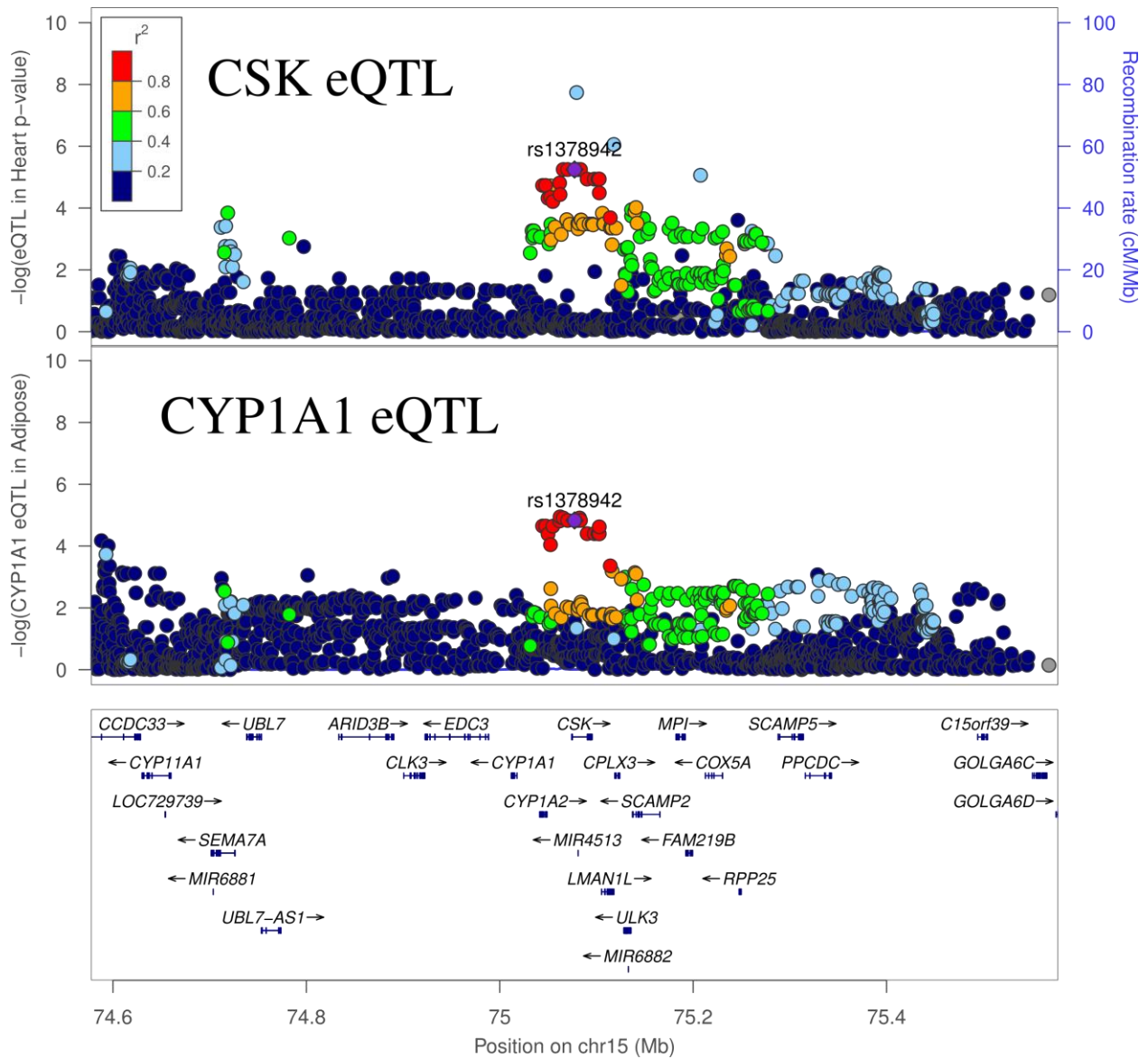
**Supplementary Figure 2:** Hexagonal binning plot between single trait lipid GWAS p-value and p-values from the bivariate GWAS with CAD and each lipid trait. Each hexagon is colored based on the number of genetic variants with P-values within the range represented by that space on the plot.



**Supplementary Figure 3:** Hexagonal binning plot between single trait CAD GWAS p-value and P-values from the bivariate GWAS with CAD. Each hexagon is colored based on the number of genetic variants with P-values within the range represented by that space on the plot.



**Supplementary Figure 4:** GWAS signals for LDL cholesterol and Coronary Artery Disease (CAD) upstream of the *BNC2* gene.



**Supplementary Figure 5:** eQTL signals for the CSK (in the left ventricle of the heart) and CYP1A1 (in adipose subcutaneous) genes around rs1378942, a lead bivariate GWAS hit for total cholesterol and CAD.

	HDL/CAD	LDL/CAD	TC/CAD	TG/CAD
Estimate of $\mu$ : $Z_{Lipid}$	-0.0020	0.0054	0.0043	0.0021
Estimate of $\mu$ : $Z_{CAD}$	-0.0029	-0.0021	-0.0029	-0.0027
Estimate of $\sigma^2$ : Lipid	1.0063	1.0192	1.0287	0.9896
Estimate of $\sigma^2$ : CAD	1.2748	1.2823	1.2756	1.2784
Covariance	-0.0727	0.0629	0.0570	0.0722

Supplementary Table 1: Estimates of bivariate normal parameters for each scan

Variant	chr	Position (hg19)	Lipid Trait	PP3	PP4
rs895953	12	122249048	TG	0.17	0.26
rs895953*	12	122249048	TG	0.00	0.32
rs3741782	12	109095137	LDL	0.00	0.98
rs7033354	9	16904846	LDL	0.01	0.84
rs12423664	12	133069894	TG	0.02	0.53
rs2908290	7	44216137	TG	0.06	0.77
rs2908290*	7	44216137	TG	0.00	0.87
rs1378942	15	75077367	TC	0.14	0.44

\* denotes 200kb window (100kb on either side of variant), chosen to exclude nearby independent GWAS peaks, instead of default 1MB region

Supplementary Table 2: Colocalization probabilities between CAD and Lipid GWAS signals at each lead SNP (**Methods**). PP3 denotes the posterior probability that both traits are associated in the region, but with different causal variants. PP4 denotes the posterior probability that both traits are associated and share a single causal variant.

SNP	Gene	Effect Allele / Other Allele	TG Beta / p-value	CAD Beta / p-value	Fasting glucose adj. for BMI Beta / p-value	Glycated Hemoglobin Beta / p-value	Type II Diabetes Beta / p-value
rs2908290	GCK	A/G	0.017 / $1.5 \times 10^{-6}$	0.023 / $1.4 \times 10^{-5}$	0.032 / $5.0 \times 10^{-23}$	0.014 / $1.1 \times 10^{-19}$	0.034 / $3.2 \times 10^{-4}$
rs1260326	GCKR	C/T	-0.11 / $2.3 \times 10^{-239}$	-0.018 / $1.9 \times 10^{-3}$	0.03 / $1.3 \times 10^{-24}$	0.0059 / $3.7 \times 10^{-4}$	0.049 / $2.3 \times 10^{-6}$

Supplementary Table 3: Association between GCK and GCKR alleles and cardiometabolic phenotypes.



SNP	Lipid Trait	Gene	Tissue	eQTL x CAD PP3	eQTL x CAD PP4	eQTL x Lipid PP3	eQTL x Lipid PP4			
rs3741782	LDL	CORO1C	Adipose Visceral Omentum	0.066	0.717	0.022	0.942			
			Adrenal Gland	0.085	0.601	0.018	0.926			
		SSH1	Whole Blood	0.097	0.586	0.068	0.823			
rs895953	TG	RHOF	Adipose Subcutaneous	0.402	0.057	0.009	0.990			
			Artery Coronary	0.358	0.058	0.009	0.990			
			Artery Tibial	0.398	0.064	0.009	0.990			
		HPD	Adipose Subcutaneous	0.403	0.047	0.023	0.974			
			Muscle Skeletal	0.427	0.002	0.830	0.080			
			Whole Blood	0.427	0.002	0.877	0.030			
		BCL7A	Muscle Skeletal	0.424	0.010	0.903	0.001			
			rs895953	HDL	RHOF	Adipose Subcutaneous	0.402	0.057	0.011	0.969
						Artery Coronary	0.358	0.058	0.012	0.946
Artery Tibial	0.398	0.064				0.013	0.964			
HPD	Adipose Subcutaneous	0.403			0.047	0.020	0.945			
	Muscle Skeletal	0.427			0.002	0.159	0.585			
	Whole Blood	0.427			0.002	0.354	0.078			
BCL7A	Muscle Skeletal	0.424	0.010	0.356	0.070					
	rs895953 (100 kb window on either side)	TG	RHOF	Adipose Subcutaneous	0.006	0.055	0.009	0.990		
				Artery Coronary	0.005	0.055	0.012	0.979		
Artery Tibial				0.006	0.064	0.009	0.990			
HPD			Adipose Subcutaneous	0.006	0.045	0.023	0.974			
			Muscle Skeletal	0.006	0.001	0.830	0.080			
			Whole Blood	0.006	0.002	0.877	0.030			
BCL7A			Muscle Skeletal	0.006	0.005	0.901	0.002			
			rs12423664	TG	FBRSL1	Pancreas	0.157	0.388	0.000	1.000
Whole Blood						0.251	0.020	0.635	0.252	
rs1378942	TC	CSK	Adipose Subcutaneous	0.121	0.625	0.039	0.914			
			Heart Left Ventricle	0.094	0.637	0.080	0.765			
		CYP1A1	Adipose Subcutaneous	0.127	0.431	0.059	0.786			
			Muscle Skeletal	0.193	0.441	0.090	0.821			

Supplementary Table 4: Colocalization at lead SNPS between eQTL and GWAS signals using the coloc method (**Methods**). Default window was 500kb on either side of the variant of interest.

Phenotype 1	Phenotype 2	PP3	PP4
LDL	CAD	0.07	0.11
TC	CAD	0.14	0.44
SBP	CAD	0.02	0.97
SBP	LDL	0.07	0.56
SBP	TC	0.05	0.91
LDL	TC	0.03	0.66

Supplementary Table 5: Evidence of colocalization of GWAS association signals at the CSK variant rs1378942. Performed using the coloc package (**Methods**).