# SUPPLEMENTAL MATERIAL to

# Evaluating the Causal Relation of ApoA-IV with Disease-Related Traits - A Bidirectional Two-sample Mendelian Randomization Study

Salome Mack[1], Stefan Coassin[1], Julien Vaucher[2], Florian Kronenberg[1], ApoA-IV-GWAS Consortium, Claudia Lamina[1]*

[1] Division of Genetic Epidemiology, Department of Medical Genetics, Molecular and Clinical Pharmacology, Medical University of Innsbruck, Innsbruck, Austria

[2] Department of Internal Medicine, Lausanne University Hospital, Lausanne, Switzerland

***Address of correspondence:**
Claudia Lamina, PhD
Division of Genetic Epidemiology
Department of Medical Genetics, Molecular and Clinical Pharmacology
Medical University of Innsbruck
Schöpfstr. 41, A-6020 Innsbruck, AUSTRIA
Phone: (+43) 512 9003-70565
Fax: (+43) 512 9003-73560 or -73561
E-mail: Claudia.Lamina@i-med.ac.at

# Content

# Supplementary Text

## Methods: Data sources and SNP selection

### Lipid traits

We used publicly available data from the Global Lipids Genetics Consortium (GLGC; http://csg.sph.umich.edu/abecasis/public/lipids2013/) to select genetic variants, which were genome-wide significantly associated ($p<5x10^{-8}$) with lipid traits (HDL cholesterol [HDL-C], LDL cholesterol [LDL-C] and triglycerides [TG])[1] . The GLGC meta-analyzed data from 23 studies of European ancestry (n=94,595 individuals), using inverse variance-weighted fixed effect models. 196,710 genetic variants were genotyped with genome-wide SNP arrays and additionally 37 studies (n=93,982 individuals) where 5,023 SNPs for HDL-C, 5,055 SNPs for LDL-C, and 5,056 SNPs for TG were genotyped with the Metabochip array [2]. SNPs were imputed using HapMap release 22. When there were multiple SNPs within one locus having a p-value$<5x10^{-8}$, we selected the leading SNP based on the lowest p-value. Hence, we found 71 independent SNPs for HDL-C (sample size ranging from 92,820 to 187,141), 58 independent SNPs for LDL-C (sample size ranging from 80,502 to 173,045) and 40 independent SNPs for TG (sample size ranging from 83,616 to 177,825). All datasets were adjusted for age, age$^2$ and sex. Each dataset included the SNP rs964184, which is located in the *APOA5-A4-C3-A1* gene cluster and is in close proximity to the *APOA4* gene. Since that SNP may directly influence apoA-IV concentrations itself, which would violate a Mendelian randomization assumption, we excluded this SNP in sensitivity analyses.

For all SNPs beta effect estimates, standard errors and p-values were retrieved from the original publication. Beta effect estimates are expressed in standard deviations of inverse-normally transformed values for each increase in number of the effect allele. The effect allele was defined as the allele oriented towards an increase in the investigated lipid trait.

### Kidney function

We used publicly available data from the CKDGen Consortium (https://www.nhlbi.nih.gov/research/intramural/researchers/pi/fox-caroline/datasets) to select genetic variants, which were genome-wide significantly associated ($p<5x10^{-8}$) with estimated glomerular filtration rate (eGFR) based on serum creatinine [3]. This consortium combined genome-wide data from up to 133,413 individuals of European ancestry from 49 predominantly population-based studies in ≈2.5 million SNPs using inverse variance-weighted fixed effect models. In 45 studies, SNPs were imputed using HapMap II CEU and 4 studies were imputed using the 1000 Genomes

Project data. For each locus that was found to be associated with the log-transformed eGFR values with SNPs having a p-value $<5x10^{-8}$, the lead SNP was selected, resulting in a list of 53 independent SNPs (sample size ranging from 115,895 to 133,810). For the single-SNP-analysis, the dataset was adjusted for age and sex. For all SNPs, beta effect estimates, standard errors and p-values were retrieved from the original publication. Beta effect estimates refer to change in log-transformed eGFR for each increase in number of the effect allele. The effect allele was defined as the allele oriented towards an increase in eGFR.

## Adiposity

We used data from the Genetic Investigation of ANthropometric Traits (GIANT) Consortium (http://portals.broadinstitute.org/collaboration/giant/index.php/GIANT_consortium_data_files) to select genetic variants, which were genome-wide significantly associated ($p<5x10^{-8}$) with adiposity-related traits (BMI and WHR adjusted for BMI [4,5]. The dataset used for the investigation of BMI comprised 114 studies including 322,206 individuals of European ancestry and over 2.5 million SNPs genotyped using the Metabochip array [2]. SNPs were imputed using HapMap phase II CEU. When there were multiple SNPs within one locus having a p-value$<5x10^{-8}$, we selected the leading SNP based on the lowest p-value, resulting in 77 independent SNPs (sample size ranging from 205,675 to 322,135). For the single-SNP-analysis, the dataset was adjusted for age, age$^2$ and sex. The 20 SNPs that were found in non-Europeans only were not included in this MR analysis since the dataset from the apoA-IV GWAS included only European populations.

The dataset used for the investigation of WHR, which was adjusted for BMI (WHRadjBMI), combined 57 cohorts including 142,762 individuals of European ancestry that were genotyped with genome-wide SNP arrays and additionally 44 cohorts including 67,326 individuals of European ancestry that were genotyped with the Metabochip array [2]. Genotypes were imputed using CEU haplotypes from HapMap resulting in ≈2.5 million SNPs. When there were multiple SNPs within one locus having a p-value$<5x10^{-8}$, we selected the leading SNP based on the lowest p-value, resulting in 40 independent SNPs (sample size ranging from 191,245 to 231,293). For this analysis sex-specific residuals were calculated and adjusted for age, age$^2$ and BMI. The 8 sex-specific SNPs as well as one SNP found in non-Europeans only were not included in this MR analysis.

For both adiposity-related traits, the beta effect estimates refer to one standard deviation of inverse-normally transformed phenotypes for each increase in number of the effect allele. For all SNPs, beta effect estimates, standard errors and p-values were retrieved from the original publication.

## Glucose

We used data from Scott et al from the Meta-Analyses of Glucose and Insulin-related traits Consortium (MAGIC; www.magicinvestigators.org/) to select genetic variants, which were genome-wide significantly associated ($p<5x10^{-8}$) associated with fasting glucose [6]. This dataset combined genome-wide data from up to 133,010 individuals of European ancestry from 65 population-based studies including SNPs genotyped using the Metabochip array [2]. Single study data were meta-analyzed using inverse variance-weighted fixed effect models. Studies with genome-wide arrays imputed genotypes using the HapMap CEU reference panel. From a total of ≈2.5 million directly genotyped or imputed SNPs, study-specific results for ≈66,000 Metabochip follow-up SNPs were considered for the meta-analyses. When there were multiple SNPs within one locus having a p-value$<5x10^{-8}$, we selected the leading SNP based on the lowest p-value, resulting in 36 independent SNPs (sample size ranging from 106,897 to 132,996). All analyses were adjusted for age, study site and geographical covariates. For all SNPs beta effect estimates, standard errors and p-values were retrieved from the original publication. Beta effect estimates refer to change in mmol/L in fasting glucose levels for each increase in number of the effect allele. The effect allele was defined as the allele oriented towards an increase in fasting glucose.

None of the three apoA-IV-associated SNPs (see next paragraph) was available in the dataset corresponding to the analysis by Scott et al. Therefore, we used data by Manning et al. from the MAGIC consortium to retrieve these apoA-IV-associated SNPs [7]. This dataset combined genome-wide data from up to 58,070 individuals of European ancestry from 29 studies in the first phase of discovery analysis and 38,422 individuals of European ancestry from 23 cohorts in the second phase of analysis. SNPs in the first phase were genotyped using genome-wide SNP arrays. Imputation was performed on the basis of the HapMap Utah residents of Northern and Western European ancestry (CEU) population (Build 36), resulting in ≈2.4 million SNPs that were included in the discovery phase meta-analyses. All single-SNP-analyses were adjusted for age, sex and study-level covariates (see original publication for details). For the follow-up genotyping, studies were invited to participate through either in silico searches with existing genotype data or de novo genotyping. A large percentage of the follow-up cohorts used the Illumina Cardio-Metabochip. For all 3 SNPs found to be associated with apoA-IV, beta effect estimates, standard errors and p-values were retrieved from the original publication. Beta effect estimates refer to log-transformed values of fasting glucose levels for each increase in number of the effect allele.

### ApoA-IV

SNPs associated with lipids, kidney function, adiposity and glucose level (see above) were directly matched with those available from the currently largest genome-wide association studies meta-analysis on apoA-IV [8]. This meta-analysis comprised data of 5 studies with 13,813 individuals of

European ancestry in the discovery stage as well as 2 further studies with 2,267 individuals of European ancestry in the replication stage (altogether n=16,080 for replicated SNPs). In all studies, SNPs were imputed using 1000 Genomes (phase 1, version 3) resulting in >7 million SNPs available for meta-analysis. The quantification of plasma apoA-IV was done in one laboratory (Division of Genetic Epidemiology, Medical University of Innsbruck, Austria) for all 5 GWA studies participating in the meta-analysis. It was based on a double-antibody enzyme-linked immunosorbent assay using an affinity-purified polyclonal rabbit anti-human apoA-IV antibody for coating and the same antibody coupled to horseradish peroxidase for detection. Plasma with a known concentration of apoA-IV was used as the calibration standard [9]. Four control sera with different concentrations were run on each plate in double measurements for control purposes throughout the entire project. The intra- and interassay coefficients of variation were 2.7% and 6.0%, respectively [9]. The apoA-IV concentration values were log-transformed due to their skewed distribution. For the genome-wide SNP-analysis, all datasets were adjusted for age and sex. Beta effect estimates refer to log-transformed apoA-IV concentrations on the original scale(mg/dL).

To investigate the inverse association , namely whether apoA-IV concentration is causally associated with lipid traits, kidney function, adiposity and fasting glucose , we retrieved all SNPs passing a genome-wide threshold (p-value $<5\text{x}10^{-8}$) within each locus that was associated with the log-transformed apoA-IV concentrations . When there were multiple SNPs within one locus having a p-value$<5\text{x}10^{-8}$, we selected the leading SNP based on the lowest p-value. Hence, we found three independent SNPs ($r^2<0.1$), two in the *APOA4* gene region (rs1729407 with an F-statistic of 222 and rs5104 with an F-statistic of 161) and one in the *KLKB1* gene region (rs4241819 with an F-statistic of 71).

# References

1. Global Lipids Genetics Consortium *et al.* Discovery and refinement of loci associated with lipid levels. *Nat. Genet.* **45,** 1274–83 (2013).
2. Voight, B. F. *et al.* The metabochip, a custom genotyping array for genetic studies of metabolic, cardiovascular, and anthropometric traits. *PLoS Genet.* **8,** e1002793 (2012).
3. Pattaro, C. *et al.* Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. *Nat. Commun.* **7,** 10023 (2016).
4. Locke, A. E. *et al.* Genetic studies of body mass index yield new insights for obesity biology. *Nature* **518,** 197–206 (2015).

5. Shungin, D. *et al.* New genetic loci link adipose and insulin biology to body fat distribution. *Nature* **518,** 187–96 (2015).

6. Scott, R. A. *et al.* Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. *Nat. Genet.* **44,** 991–1005 (2012).

7. Manning, A. K. *et al.* A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. *Nat. Genet.* **44,** 659–69 (2012).

8. Lamina, C. *et al.* A genome-wide association meta-analysis on apolipoprotein A-IV concentrations. *Hum. Mol. Genet.* **25,** 3635–3646 (2016).

9. Kronenberg, F., Lobentanz, E. M., König, P., Utermann, G. & Dieplinger, H. Effect of sample storage on the measurement of lipoprotein[a], apolipoproteins B and A-IV, total and high density lipoprotein cholesterol and triglycerides. *J. Lipid Res.* **35,** 1318–28 (1994).

# Supplementary Tables

**Supplementary Table 1:** Characteristics and results of the 71 SNPs associated with HDL-C [1,8]. The table is sorted by the p-value for HDL-C.

| | | | | | | Results from the GWAS meta-analysis on | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | HDL-C | | | ApoA-IV | | |
| SNP | Chr | Pos | Nearest gene | A1 | A2 | Beta* | SE* | P-value | Beta$^{\S}$ | SE$^{\S}$ | P-value |
| rs3764261 | 16 | 56993324 | *CETP* | A | C | 0.2412 | 0.0039 | 1.00E-769 | 0.0043 | 0.0043 | 0.3175 |
| rs1532085 | 15 | 58683366 | *LIPC* | A | G | 0.1068 | 0.0035 | 1.24E-188 | 0.0050 | 0.0038 | 0.1834 |
| rs12678919 | 8 | 19844222 | *LPL* | G | A | 0.1554 | 0.0057 | 1.38E-149 | 0.0095 | 0.0059 | 0.1053 |
| rs1883025 | 9 | 107664301 | *ABCA1* | C | T | 0.0698 | 0.0041 | 1.50E-65 | 0.0010 | 0.0042 | 0.8095 |
| rs16942887 | 16 | 67928042 | *PSKH1* | A | G | 0.0831 | 0.0051 | 8.28E-54 | 0.0164 | 0.0054 | 0.0022 |
| rs964184 | 11 | 116648917 | *ZPR1* | C | G | 0.1065 | 0.0071 | 6.09E-48 | 0.0198 | 0.0052 | 0.0001 |
| rs7241918 | 18 | 47160953 | *LIPG* | T | G | 0.0902 | 0.0064 | 1.11E-44 | 0.0127 | 0.0050 | 0.0114 |
| rs9987289 | 8 | 9183358 | *PPP1R3B* | G | A | 0.0817 | 0.0062 | 1.95E-41 | -0.0017 | 0.0066 | 0.8036 |
| rs4846914 | 1 | 230295691 | *GALNT2* | A | G | 0.0479 | 0.0034 | 3.51E-41 | 0.0021 | 0.0037 | 0.5637 |
| rs6065906 | 20 | 44554015 | *PCIF1* | T | C | 0.0594 | 0.0044 | 5.34E-40 | -0.0040 | 0.0048 | 0.4024 |
| rs1800961 | 20 | 43042364 | *HNF4A* | C | T | 0.1270 | 0.0099 | 1.64E-34 | -0.0059 | 0.0136 | 0.6627 |
| rs838880 | 12 | 125261593 | *SCARB1* | C | T | 0.0484 | 0.0039 | 6.38E-32 | 0.0073 | 0.0051 | 0.1584 |
| rs2954029 | 8 | 126490972 | *TRIB1* | T | A | 0.0401 | 0.0034 | 2.67E-29 | 0.0036 | 0.0036 | 0.3220 |
| rs3136441 | 11 | 46743247 | *F2* | C | T | 0.0545 | 0.0047 | 6.76E-29 | 0.0029 | 0.0056 | 0.6095 |
| rs174546 | 11 | 61569830 | *FADS1* | C | T | 0.0391 | 0.0035 | 8.30E-28 | 0.0028 | 0.0039 | 0.4712 |
| rs386000 | 19 | 54792761 | *LILRA3* | C | G | 0.0479 | 0.0047 | 2.71E-23 | -0.0022 | 0.0057 | 0.6950 |
| rs4420638 | 19 | 45422946 | *APOC1* | A | G | 0.0669 | 0.0068 | 1.72E-21 | 0.0083 | 0.0061 | 0.1780 |
| rs1689800 | 1 | 182168885 | *ZNF648* | A | G | 0.0344 | 0.0036 | 4.77E-20 | 0.0019 | 0.0037 | 0.6055 |
| rs581080 | 9 | 15305378 | *TTC39B* | C | G | 0.0419 | 0.0045 | 1.04E-19 | -0.0017 | 0.0048 | 0.7231 |
| rs2925979 | 16 | 81534790 | *GAN* | C | T | 0.0351 | 0.0037 | 1.32E-19 | -0.0049 | 0.0041 | 0.2277 |
| rs4660293 | 1 | 40028180 | *PABPC4* | A | G | 0.0353 | 0.004 | 2.86E-18 | -0.0017 | 0.0043 | 0.6827 |
| rs113359481 | 22 | 21932068 | *RIMBP3C* | C | T | 0.0379 | 0.0042 | 4.30E-18 | 0.0029 | 0.0046 | 0.5324 |
| rs2972146 | 2 | 227100698 | *IRS1* | G | T | 0.0323 | 0.0035 | 1.85E-17 | -0.0027 | 0.0038 | 0.4814 |
| rs11869286 | 17 | 37813856 | *STARD3* | C | G | 0.0319 | 0.0037 | 2.70E-17 | 0.0073 | 0.0038 | 0.0560 |
| rs2293889 | 8 | 116599199 | *TRPS1* | G | T | 0.0312 | 0.0035 | 4.27E-17 | 0.0047 | 0.0037 | 0.1976 |
| rs4731702 | 7 | 130433384 | *KLF14* | T | C | 0.0294 | 0.0034 | 4.84E-17 | -0.0071 | 0.0037 | 0.0521 |
| rs12748152 | 1 | 27138393 | *PIGV* | C | T | 0.0506 | 0.0062 | 9.74E-16 | 0.0092 | 0.0076 | 0.2281 |
| rs13107325 | 4 | 103188709 | *SLC39A8* | C | T | 0.0708 | 0.0078 | 1.07E-15 | 0.0014 | 0.0072 | 0.8452 |
| rs12328675 | 2 | 165540800 | *COBLL1* | C | T | 0.0447 | 0.0052 | 2.13E-15 | 0.0020 | 0.0055 | 0.7230 |
| rs112302432 | 11 | 122522375 | *UBASH3B* | C | T | 0.0269 | 0.0035 | 1.12E-14 | -0.0025 | 0.0037 | 0.4970 |
| rs7134594 | 12 | 110000193 | *MMAB* | T | C | 0.0354 | 0.0048 | 1.77E-13 | 0.0018 | 0.0036 | 0.6132 |
| rs11613352 | 12 | 57792580 | *R3HDM2* | T | C | 0.0281 | 0.004 | 2.39E-13 | -0.0009 | 0.0044 | 0.8307 |
| rs17695224 | 19 | 52324216 | *FPR3* | G | A | 0.0290 | 0.0039 | 2.42E-13 | -0.0001 | 0.004 | 0.9841 |
| rs17145738 | 7 | 72982874 | *TBL2* | T | C | 0.0408 | 0.0053 | 4.95E-13 | 0.0071 | 0.0057 | 0.2152 |
| rs4148008 | 17 | 66875294 | *ABCA8* | C | G | 0.0280 | 0.0038 | 1.13E-12 | 0.0074 | 0.0039 | 0.0594 |

to be continued…

**Supplementary Table 1 continued**

| | | | | | | Results from the GWAS meta-analysis on | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | HDL-C | | | ApoA-IV | | |
| SNP | Chr | Pos | Nearest gene | A1 | A2 | Beta* | SE* | P-value | Beta$^{§}$ | SE$^{§}$ | P-value |
| rs3822072 | 4 | 89741269 | *FAM13A* | G | A | 0.0251 | 0.0034 | 4.06E-12 | -0.0021 | 0.0037 | 0.5749 |
| rs702485 | 7 | 6449272 | *DAGLB* | G | A | 0.0243 | 0.0034 | 6.45E-12 | 0.0036 | 0.0037 | 0.3231 |
| rs2013208 | 3 | 50129399 | *SEMA3F* | T | C | 0.0254 | 0.0036 | 8.92E-12 | 0.0032 | 0.0036 | 0.3723 |
| rs4142995 | 7 | 17919258 | *SNX13* | G | T | 0.0263 | 0.0037 | 9.37E-12 | -0.0080 | 0.0037 | 0.0299 |
| rs4129767 | 17 | 76403984 | *PGS1* | A | G | 0.0237 | 0.0034 | 2.10E-11 | -0.0027 | 0.0036 | 0.4546 |
| rs998584 | 6 | 43757896 | *VEGFA* | C | A | 0.0260 | 0.0038 | 2.27E-11 | 0.0022 | 0.0042 | 0.5968 |
| rs2652834 | 15 | 63396867 | *LACTB* | G | A | 0.0285 | 0.0043 | 3.59E-11 | -0.0024 | 0.0044 | 0.5868 |
| rs13326165 | 3 | 52532118 | *STAB1* | A | G | 0.0289 | 0.0043 | 9.04E-11 | -0.0067 | 0.0048 | 0.1623 |
| rs11246602 | 11 | 51512090 | *OR4C46* | C | T | 0.0340 | 0.0052 | 1.68E-10 | 0.0036 | 0.0062 | 0.5641 |
| rs970548 | 10 | 46013277 | *MARCH8* | C | A | 0.0258 | 0.0039 | 1.71E-10 | 0.0005 | 0.0041 | 0.9003 |
| rs1936800 | 6 | 127436064 | *RSPO3* | C | T | 0.0200 | 0.0034 | 3.06E-10 | -0.0031 | 0.0036 | 0.3956 |
| rs6450176 | 5 | 53298025 | *ARL15* | G | A | 0.0254 | 0.0039 | 6.88E-10 | 0.0019 | 0.0041 | 0.6483 |
| rs4765127 | 12 | 124460167 | *ZNF664* | T | G | 0.0324 | 0.005 | 7.79E-10 | -0.0076 | 0.0037 | 0.0424 |
| rs1047891 | 2 | 211540507 | *CPS1* | C | A | 0.0269 | 0.0039 | 8.73E-10 | -0.0010 | 0.0041 | 0.7985 |
| rs731839 | 19 | 33899065 | *PEPD* | A | G | 0.0220 | 0.0037 | 3.44E-09 | 0.0019 | 0.0039 | 0.6304 |
| rs2290547 | 3 | 47061183 | *SETD2* | G | A | 0.0297 | 0.0046 | 3.69E-09 | 0.0145 | 0.0059 | 0.0144 |
| rs13076253 | 3 | 131751775 | *CPNE4* | A | C | 0.0283 | 0.0048 | 4.96E-09 | -0.0047 | 0.0052 | 0.3749 |
| rs13076253 | 3 | 131751775 | *CPNE4* | A | C | 0.0283 | 0.0048 | 4.96E-09 | -0.0047 | 0.0052 | 0.3749 |
| rs4650994 | 1 | 178515312 | *C1orf220* | G | A | 0.0210 | 0.0034 | 6.70E-09 | -0.0102 | 0.0036 | 0.0046 |
| rs1121980 | 16 | 53809247 | *FTO* | G | A | 0.0196 | 0.0034 | 6.79E-09 | 0.0041 | 0.0036 | 0.2583 |
| rs4983559 | 14 | 105277209 | *ZBTB42* | G | A | 0.0197 | 0.0036 | 9.57E-09 | 0.0060 | 0.0044 | 0.8870 |
| rs4917014 | 7 | 50305863 | *IKZF1* | G | T | 0.0222 | 0.0036 | 1.03E-08 | -0.0069 | 0.0039 | 0.0758 |
| rs7134375 | 12 | 20473758 | *PDE3A* | A | C | 0.0207 | 0.0035 | 1.05E-08 | -0.0004 | 0.0039 | 0.9112 |
| rs499974 | 11 | 75455021 | *MOGAT2* | C | A | 0.0263 | 0.0044 | 1.12E-08 | 0.0011 | 0.0047 | 0.8164 |
| rs6805251 | 3 | 119560606 | *GSK3B* | T | C | 0.0200 | 0.0035 | 1.33E-08 | -0.0022 | 0.0037 | 0.5399 |
| rs12145743 | 1 | 156700651 | *C1orf66* | G | T | 0.0203 | 0.0036 | 1.80E-08 | -0.0038 | 0.004 | 0.3399 |
| rs7255436 | 19 | 8433196 | *ANGPTL4* | A | C | 0.0316 | 0.0053 | 1.87E-08 | -0.0071 | 0.0046 | 0.1258 |
| rs17173637 | 7 | 150529449 | *ABP1* | T | C | 0.0363 | 0.0057 | 1.90E-08 | 0.0075 | 0.0062 | 0.2311 |
| rs605066 | 6 | 139829666 | *CITED2* | T | C | 0.0281 | 0.0049 | 2.79E-08 | 0.0037 | 0.0037 | 0.3127 |
| rs4759375 | 12 | 123796238 | *SBNO1* | T | C | 0.0560 | 0.0102 | 3.01E-08 | 0.0027 | 0.0062 | 0.6621 |
| rs12801636 | 11 | 65391317 | *PCNXL3* | A | G | 0.0235 | 0.0042 | 3.15E-08 | 0.0038 | 0.0047 | 0.4104 |
| rs12967135 | 18 | 57849023 | *MC4R* | G | A | 0.0262 | 0.0045 | 3.57E-08 | -0.0053 | 0.0042 | 0.2071 |
| rs2606736 | 3 | 11400249 | *ATG7* | C | T | 0.0246 | 0.0043 | 4.80E-08 | 0.0007 | 0.0037 | 0.8523 |
| rs10019888 | 4 | 26062990 | *RBPJ* | A | G | 0.0270 | 0.0046 | 4.90E-08 | -0.0031 | 0.0048 | 0.5123 |
| rs2602836 | 4 | 100014805 | *ADH5* | A | G | 0.0192 | 0.0034 | 4.96E-08 | -0.0013 | 0.0037 | 0.7217 |
| rs2923084 | 11 | 10388782 | *ADM* | A | G | 0.0256 | 0.0045 | 5.02E-08 | 0.0063 | 0.0048 | 0.1907 |

A1: effect allele; A2: other allele.

*units in SD; $^{§}$units in log(apoA-IV).

**Supplementary Table 2:** Characteristics and results of the 58 SNPs associated with LDL-C [1,8]. The table is sorted by the p-value for LDL-C.

| | | | | | | Results from the GWAS meta-analysis on | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | LDL-C | | | ApoA-IV | | |
| **SNP** | **Chr** | **Pos** | **Nearest gene** | **A1** | **A2** | **Beta*** | **SE*** | **P-value** | **Beta§** | **SE§** | **P-value** |
| rs6511720 | 19 | 11202306 | *LDLR* | G | T | 0.2209 | 0.0061 | 3.85E-262 | -0.0060 | 0.0070 | 0.3900 |
| rs629301 | 1 | 109818306 | *CELSR2* | T | G | 0.1669 | 0.0049 | 5.40E-241 | -0.0102 | 0.0044 | 0.0192 |
| rs1367117 | 2 | 21263900 | *APOB* | A | G | 0.1186 | 0.0040 | 9.48E-183 | 0.0013 | 0.0039 | 0.7356 |
| rs4420638 | 19 | 45422946 | *APOC1* | G | A | 0.2251 | 0.0077 | 1.51E-178 | -0.0083 | 0.0061 | 0.1780 |
| rs12916 | 5 | 74656539 | *HMGCR* | C | T | 0.0733 | 0.0038 | 7.79E-78 | -0.0055 | 0.0038 | 0.1423 |
| rs4299376 | 2 | 44072576 | *ABCG8* | G | T | 0.0812 | 0.0045 | 3.94E-72 | -0.0046 | 0.0042 | 0.2746 |
| rs10401969 | 19 | 19407718 | *SF4* | T | C | 0.1184 | 0.0072 | 2.65E-54 | -0.0107 | 0.0071 | 0.1351 |
| rs2954029 | 8 | 126490972 | *TRIB1* | A | T | 0.0564 | 0.0036 | 2.10E-50 | -0.0036 | 0.0036 | 0.3220 |
| rs2479409 | 1 | 55504650 | *PCSK9* | G | A | 0.0642 | 0.0041 | 2.52E-50 | -0.0034 | 0.0041 | 0.3978 |
| rs635634 | 9 | 136155000 | *ABO* | T | C | 0.0772 | 0.0055 | 1.83E-41 | -0.0060 | 0.0047 | 0.2010 |
| rs2000999 | 16 | 72108093 | *HPR* | A | G | 0.0650 | 0.0046 | 4.22E-41 | 0.0030 | 0.0046 | 0.5177 |
| rs174546 | 11 | 61569830 | *FADS1* | C | T | 0.0512 | 0.0038 | 1.63E-39 | 0.0028 | 0.0039 | 0.4712 |
| rs3764261 | 16 | 56993324 | *CETP* | C | A | 0.0528 | 0.0042 | 2.22E-34 | -0.0043 | 0.0043 | 0.3175 |
| rs2131925 | 1 | 63025942 | *DOCK7* | T | G | 0.0489 | 0.0039 | 2.98E-32 | -0.0026 | 0.0039 | 0.4977 |
| rs6882076 | 5 | 156390297 | *TIMD4* | C | T | 0.0456 | 0.0038 | 3.31E-31 | 0.0009 | 0.0037 | 0.8102 |
| rs964184 | 11 | 116648917 | *ZPR1* | G | C | 0.0855 | 0.0078 | 2.01E-26 | -0.0198 | 0.0052 | 0.0001 |
| rs9987289 | 8 | 9183358 | *PPP1R3B* | G | A | 0.0714 | 0.0066 | 8.53E-24 | -0.0017 | 0.0066 | 0.8036 |
| rs1564348 | 6 | 160578860 | *SLC22A1* | C | T | 0.0481 | 0.0050 | 2.76E-21 | -0.0009 | 0.0051 | 0.8666 |
| rs1169288 | 12 | 121416650 | *HNF1A* | C | A | 0.0375 | 0.0040 | 6.45E-21 | 0.0034 | 0.0040 | 0.3915 |
| rs11220462 | 11 | 126243952 | *ST3GAL4* | A | G | 0.0590 | 0.0059 | 6.61E-21 | 0.0041 | 0.0054 | 0.4493 |
| rs6029526 | 20 | 39672618 | *TOP1* | A | T | 0.0436 | 0.0052 | 4.81E-18 | -0.0067 | 0.0036 | 0.0676 |
| rs3757354 | 6 | 16127407 | *MYLIP* | C | T | 0.0382 | 0.0044 | 2.09E-17 | -0.0053 | 0.0045 | 0.2464 |
| rs3177928 | 6 | 32412435 | *HLA-DRB5* | A | G | 0.0452 | 0.0052 | 3.10E-17 | 0.0025 | 0.0074 | 0.7396 |
| rs2072183 | 7 | 44579180 | *NPC1L1* | C | G | 0.0386 | 0.0047 | 7.12E-16 | 0.0044 | 0.0058 | 0.4475 |
| rs8017377 | 14 | 24883887 | *NYNRIN* | A | G | 0.0303 | 0.0038 | 2.52E-15 | -0.0041 | 0.0041 | 0.3241 |
| rs12027135 | 1 | 25775733 | *TMEM57* | T | A | 0.0300 | 0.0038 | 2.27E-14 | 0.0028 | 0.0039 | 0.4757 |
| rs4722551 | 7 | 25991826 | *MIR148A* | C | T | 0.0391 | 0.0049 | 3.95E-14 | 0.0058 | 0.0051 | 0.2603 |
| rs12670798 | 7 | 21607352 | *DNAH11* | C | T | 0.0344 | 0.0043 | 4.81E-14 | -0.0017 | 0.0045 | 0.7081 |
| rs1800562 | 6 | 26093141 | *HFE* | G | A | 0.0615 | 0.0080 | 8.25E-14 | -0.0061 | 0.0084 | 0.4723 |
| rs2255141 | 10 | 113933886 | *GPAM* | A | G | 0.0299 | 0.0040 | 1.32E-13 | 0.0008 | 0.004 | 0.8374 |
| rs10490626 | 2 | 118835841 | *INSIG2* | G | A | 0.0508 | 0.0069 | 1.70E-12 | -0.0144 | 0.0069 | 0.0378 |
| rs12748152 | 1 | 27138393 | *PIGV* | T | C | 0.0499 | 0.0066 | 3.21E-12 | -0.0092 | 0.0076 | 0.2281 |
| rs4530754 | 5 | 122855416 | *CSNK1G3* | A | G | 0.0275 | 0.0036 | 3.58E-12 | -0.0047 | 0.0037 | 0.2002 |
| rs11136341 | 8 | 145043543 | *PLEC* | G | A | 0.0447 | 0.0062 | 7.11E-12 | -0.0081 | 0.0047 | 0.0893 |
| rs514230 | 1 | 234858597 | *IRF2BP2* | T | A | 0.0364 | 0.0054 | 9.24E-12 | -0.0010 | 0.0036 | 0.7856 |
| rs1801689 | 17 | 64210580 | *APOH* | C | A | 0.1028 | 0.0139 | 9.81E-12 | 0.0023 | 0.0153 | 0.8829 |
| rs11065987 | 12 | 112072424 | *BRAP* | A | G | 0.0269 | 0.0038 | 1.20E-11 | 0.0043 | 0.0039 | 0.2691 |
| rs4942486 | 13 | 32953388 | *BRCA2* | T | C | 0.0243 | 0.0037 | 2.26E-11 | 0.0092 | 0.0037 | 0.0124 |
| rs10102164 | 8 | 55421614 | *SOX17* | A | G | 0.0316 | 0.0045 | 3.74E-11 | 0.0018 | 0.0047 | 0.7096 |
| rs2642442 | 1 | 220973563 | *MOSC1* | T | C | 0.0360 | 0.0054 | 5.27E-11 | -0.0009 | 0.0040 | 0.8301 |

to be continued…

**Supplementary Table 2 continued**

| | | | | | | Results from the GWAS meta-analysis on | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | LDL-C | | | ApoA-IV | |
| **SNP** | **Chr** | **Pos** | **Nearest gene** | **A1** | **A2** | **Beta*** | **SE*** | **P-value** | **Beta$^{\S}$** | **SE$^{\S}$** | **P-value** |
| rs314253 | 17 | 7091650 | *DLG4* | T | C | 0.0242 | 0.0038 | 3.44E-10 | -0.0029 | 0.0038 | 0.4430 |
| rs364585 | 20 | 12962718 | *SPTLC3* | G | A | 0.0249 | 0.0038 | 4.28E-10 | -0.0020 | 0.0039 | 0.6034 |
| rs3780181 | 9 | 2640759 | *VLDLR* | A | G | 0.0445 | 0.0074 | 1.76E-09 | 0.0021 | 0.0073 | 0.7707 |
| rs17404153 | 3 | 132163200 | *DNAJC13* | G | T | 0.0336 | 0.0054 | 1.83E-09 | -0.0033 | 0.0055 | 0.5492 |
| rs267733 | 1 | 150958836 | *ANXA9* | A | G | 0.0331 | 0.0053 | 5.29E-09 | 0.0046 | 0.0053 | 0.3867 |
| rs2328223 | 20 | 17845921 | *SNX5* | C | A | 0.0299 | 0.0050 | 5.63E-09 | -0.0056 | 0.0050 | 0.2627 |
| rs2710642 | 2 | 63149557 | *EHBP1* | A | G | 0.0239 | 0.0038 | 6.09E-09 | -0.0018 | 0.0038 | 0.6415 |
| rs2030746 | 2 | 121309488 | *GLI2* | T | C | 0.0214 | 0.0038 | 8.61E-09 | -0.0005 | 0.0040 | 0.9047 |
| rs7640978 | 3 | 32533010 | *CMTM6* | C | T | 0.0392 | 0.0069 | 9.84E-09 | -0.0023 | 0.0067 | 0.7310 |
| rs5763662 | 22 | 30378703 | *MTMR3* | T | C | 0.0767 | 0.0121 | 1.19E-08 | 0.0067 | 0.0121 | 0.5835 |
| rs1250229 | 2 | 216304384 | *FN1* | C | T | 0.0243 | 0.0042 | 3.13E-08 | -0.0032 | 0.0042 | 0.4513 |
| rs4253772 | 22 | 46627603 | *PPARA* | T | C | 0.0313 | 0.0060 | 4.33E-08 | 0.0061 | 0.0056 | 0.2760 |
| rs11563251 | 2 | 234679384 | *HEATR7B1* | T | C | 0.0345 | 0.0062 | 4.50E-08 | 0.0058 | 0.0068 | 0.3954 |
| rs2081687 | 8 | 59388565 | *CYP7A1* | T | C | 0.0311 | 0.0054 | 1.19E-07 | -0.0014 | 0.0038 | 0.7159 |
| rs9488822 | 6 | 116312893 | *FRK* | A | T | 0.0311 | 0.0054 | 1.69E-07 | -0.0017 | 0.0039 | 0.6638 |
| rs7206971 | 17 | 45425115 | *C17orf57* | A | G | 0.0292 | 0.0055 | 3.05E-07 | 0.0097 | 0.0036 | 0.0076 |
| rs6831256 | 4 | 3473139 | *DOK7* | G | A | 0.0188 | 0.0038 | 9.07E-07 | -0.0063 | 0.0043 | 0.1401 |
| rs2277862 | 20 | 34152782 | *FER1L4* | C | T | 0.0271 | 0.0054 | 1.30E-06 | 0.0046 | 0.0050 | 0.3519 |

A1: effect allele; A2: other allele.

*units in SD; $^{\S}$units in log(apoA-IV).

**Supplementary Table 3:** Characteristics and results of the 40 SNPs associated with TG [1,8]. The table is sorted by the p-value for TG.

| | | | | | | **Results from the GWAS meta-analysis on** | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | **TG** | | | **ApoA-IV** | |
| **SNP** | **Chr** | **Pos** | **Nearest gene** | **A1** | **A2** | **Beta*** | **SE*** | **P-value** | **Beta§** | **SE§** | **P-value** |
| rs1260326 | 2 | 27730940 | *GCKR* | T | C | 0.1148 | 0.0034 | 2.29E-239 | -0.0058 | 0.0036 | 0.1092 |
| rs964184 | 11 | 116648917 | *ZPR1* | G | C | 0.2341 | 0.0069 | 6.55E-224 | -0.0198 | 0.0052 | 0.0001 |
| rs12678919 | 8 | 19844222 | *LPL* | A | G | 0.1702 | 0.0056 | 1.82E-199 | -0.0095 | 0.0059 | 0.1053 |
| rs2954029 | 8 | 126490972 | *TRIB1* | A | T | 0.0764 | 0.0033 | 1.02E-107 | -0.0036 | 0.0036 | 0.3220 |
| rs17145738 | 7 | 72982874 | *TBL2* | C | T | 0.1149 | 0.0053 | 9.42E-99 | -0.0071 | 0.0057 | 0.2152 |
| rs2131925 | 1 | 63025942 | *DOCK7* | T | G | 0.0657 | 0.0035 | 3.05E-74 | -0.0026 | 0.0039 | 0.4977 |
| rs10401969 | 19 | 19407718 | *SF4* | T | C | 0.1210 | 0.0065 | 9.70E-70 | -0.0107 | 0.0071 | 0.1351 |
| rs174546 | 11 | 61569830 | *FADS1* | T | C | 0.0447 | 0.0034 | 7.42E-38 | -0.0028 | 0.0039 | 0.4712 |
| rs6065906 | 20 | 44554015 | *PCIF1* | C | T | 0.0534 | 0.0043 | 2.36E-34 | 0.0040 | 0.0048 | 0.4024 |
| rs4846914 | 1 | 230295691 | *GALNT2* | G | A | 0.0401 | 0.0034 | 7.20E-31 | -0.0021 | 0.0037 | 0.5637 |
| rs3764261 | 16 | 56993324 | *CETP* | C | A | 0.0395 | 0.0038 | 1.58E-25 | -0.0043 | 0.0043 | 0.3175 |
| rs442177 | 4 | 88030261 | *AFF1* | T | G | 0.0309 | 0.0033 | 1.32E-18 | 0.0057 | 0.0037 | 0.1230 |
| rs9686661 | 5 | 55861786 | *MAP3K1* | T | C | 0.0379 | 0.0044 | 2.54E-16 | 0.0032 | 0.0046 | 0.4889 |
| rs6882076 | 5 | 156390297 | *TIMD4* | C | T | 0.0286 | 0.0035 | 1.51E-15 | 0.0009 | 0.0037 | 0.8102 |
| rs2972146 | 2 | 227100698 | *IRS1* | T | G | 0.0281 | 0.0034 | 2.97E-15 | 0.0027 | 0.0038 | 0.4814 |
| rs998584 | 6 | 43757896 | *VEGFA* | A | C | 0.0293 | 0.0037 | 3.42E-15 | -0.0022 | 0.0042 | 0.5968 |
| rs11613352 | 12 | 57792580 | *R3HDM2* | C | T | 0.0280 | 0.0039 | 9.40E-14 | 0.0009 | 0.0044 | 0.8307 |
| rs6831256 | 4 | 3473139 | *DOK7* | G | A | 0.0258 | 0.0035 | 1.60E-12 | -0.0063 | 0.0043 | 0.1401 |
| rs1832007 | 10 | 5254847 | *AKR1C4* | A | G | 0.0327 | 0.0047 | 1.72E-12 | 0.0004 | 0.0052 | 0.9346 |
| rs645040 | 3 | 135926622 | *MSL2* | T | G | 0.0293 | 0.004 | 1.83E-12 | -0.0045 | 0.0043 | 0.2965 |
| rs1495741 | 8 | 18272881 | *NAT2* | G | A | 0.0399 | 0.0056 | 2.73E-12 | 0.0002 | 0.0043 | 0.9535 |
| rs10761731 | 10 | 65027610 | *JMJD1C* | A | T | 0.0312 | 0.0047 | 8.40E-12 | -0.0108 | 0.0037 | 0.0039 |
| rs2412710 | 15 | 42683787 | *CAPN3* | A | G | 0.0988 | 0.0132 | 1.66E-11 | -0.0148 | 0.0121 | 0.2219 |
| rs2068888 | 10 | 94839642 | *CYP26A1* | G | A | 0.0241 | 0.0034 | 1.68E-11 | -0.0077 | 0.0040 | 0.0555 |
| rs11776767 | 8 | 10683929 | *SOX7* | C | G | 0.0220 | 0.0035 | 2.87E-11 | 0.0063 | 0.0038 | 0.0958 |
| rs7248104 | 19 | 7224431 | *INSR* | G | A | 0.0222 | 0.0034 | 5.05E-10 | -0.0025 | 0.0037 | 0.4870 |
| rs12748152 | 1 | 27138393 | *PIGV* | T | C | 0.0372 | 0.0059 | 1.10E-09 | -0.0092 | 0.0076 | 0.2281 |
| rs4722551 | 7 | 25991826 | *MIR148A* | T | C | 0.0267 | 0.0044 | 1.58E-09 | -0.0058 | 0.0051 | 0.2603 |
| rs2929282 | 15 | 44245931 | *FRMD5* | T | A | 0.0725 | 0.0121 | 1.95E-09 | -0.0035 | 0.0083 | 0.6703 |
| rs731839 | 19 | 33899065 | *PEPD* | G | A | 0.0224 | 0.0036 | 2.65E-09 | -0.0019 | 0.0039 | 0.6304 |
| rs8077889 | 17 | 41878166 | *MPP3* | C | A | 0.0252 | 0.0042 | 9.88E-09 | 0.0052 | 0.0043 | 0.2333 |
| rs38855 | 7 | 116358044 | *MET* | A | G | 0.0187 | 0.0033 | 2.11E-08 | -0.0022 | 0.0036 | 0.5377 |
| rs3198697 | 16 | 15129940 | *PDXDC1* | C | T | 0.0198 | 0.0034 | 2.21E-08 | -0.0015 | 0.0037 | 0.6871 |
| rs4765127 | 12 | 124460167 | *ZNF664* | G | T | 0.0286 | 0.0049 | 2.41E-08 | 0.0076 | 0.0037 | 0.0424 |
| rs5756931 | 22 | 38546033 | *PLA2G6* | T | C | 0.0203 | 0.0035 | 2.52E-08 | -0.0011 | 0.0038 | 0.7652 |
| rs11649653 | 16 | 30918487 | *MIR762* | C | G | 0.0274 | 0.0050 | 1.56E-07 | -0.007 | 0.0037 | 0.0609 |
| rs1936800 | 6 | 127436064 | *RSPO3* | T | C | 0.0175 | 0.0033 | 3.79E-07 | 0.0031 | 0.0036 | 0.3956 |
| rs1121980 | 16 | 53809247 | *FTO* | A | G | 0.0171 | 0.0034 | 1.52E-06 | -0.0041 | 0.0036 | 0.2583 |
| rs13238203 | 7 | 72129667 | *TYW1B* | C | T | 0.0592 | 0.0140 | 3.07E-06 | -0.0102 | 0.0168 | 0.5455 |
| rs838880 | 12 | 125261593 | *SCARB1* | T | C | 0.0059 | 0.0037 | 0.3064 | -0.0073 | 0.0051 | 0.1584 |

A1: effect allele; A2: other allele.

*units in SD; §units in log(apoA-IV).

**Supplementary Table 4:** Characteristics and results of the 53 SNPs associated with eGFR [3,8]. The table is sorted by the p-value for eGFR.

| | | | | | | **Results from the GWAS meta-analysis on** | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | **eGFR** | | | **ApoA-IV** | |
| **SNP** | **Chr** | **Pos** | **Nearest gene** | **A1** | **A2** | **Beta*** | **SE*** | **P-value** | **Beta$^{\S}$** | **SE$^{\S}$** | **P-value** |
| rs13329952 | 16 | 20366507 | *UMOD* | T | C | -0.0160 | 0.0011 | 9.50E-43 | -0.0129 | 0.0048 | 0.0069 |
| rs2467853 | 15 | 45698793 | *SPATA5L1* | T | G | 0.0130 | 0.0009 | 1.00E-42 | -0.0069 | 0.0037 | 0.0636 |
| rs17319721 | 4 | 77368847 | *SHROOM3* | A | G | -0.0110 | 0.0009 | 1.30E-37 | -0.0056 | 0.0037 | 0.1266 |
| rs7805747 | 7 | 151407801 | *PRKAG2* | A | G | -0.0130 | 0.0011 | 8.00E-29 | -0.0027 | 0.0040 | 0.4942 |
| rs7422339 | 2 | 211540507 | *CPS1* | A | C | -0.0110 | 0.0010 | 2.20E-23 | -0.0010 | 0.0041 | 0.7985 |
| rs6420094 | 5 | 176817636 | *SLC34A1* | A | G | 0.0096 | 0.0010 | 4.90E-22 | -0.0068 | 0.0050 | 0.1754 |
| rs11657044 | 17 | 59450105 | *BCAS3* | T | C | -0.0110 | 0.0012 | 7.90E-22 | -0.0098 | 0.0050 | 0.0486 |
| rs11959928 | 5 | 39397132 | *FYB* | A | T | -0.0083 | 0.0009 | 1.70E-20 | 0.0008 | 0.0037 | 0.8314 |
| rs6546838 | 2 | 73679280 | *ALMS1* | A | G | -0.0093 | 0.0010 | 7.70E-20 | -0.0004 | 0.0043 | 0.9222 |
| rs316009 | 6 | 160675764 | *SLC22A2* | T | C | 0.0130 | 0.0014 | 4.40E-19 | 0.0015 | 0.0061 | 0.8113 |
| rs963837 | 11 | 30749090 | *DCDC5* | T | C | -0.0078 | 0.0009 | 5.70E-18 | -0.0033 | 0.0037 | 0.3795 |
| rs3758086 | 8 | 23714992 | *STC1* | A | G | -0.0071 | 0.0009 | 1.70E-15 | -0.0058 | 0.0037 | 0.1161 |
| rs491567 | 15 | 53946593 | *WDR72* | A | C | -0.0084 | 0.0010 | 2.90E-15 | 0.0007 | 0.0045 | 0.8697 |
| rs9472135 | 6 | 43809802 | *VEGFA* | T | C | -0.0080 | 0.0010 | 3.30E-15 | -0.0023 | 0.0042 | 0.5823 |
| rs4744712 | 9 | 71434707 | *PIP5K1B* | A | C | -0.0071 | 0.0009 | 4.30E-15 | 0.0048 | 0.0037 | 0.1918 |
| rs9916302 | 17 | 37499949 | *FBXL20* | T | C | -0.0080 | 0.0010 | 4.80E-15 | -0.0078 | 0.0042 | 0.0631 |
| rs1260326 | 2 | 27730940 | *GCKR* | T | C | 0.0068 | 0.0009 | 3.40E-14 | -0.0058 | 0.0036 | 0.1092 |
| rs1394125 | 15 | 76158983 | *UBE2Q2* | A | G | -0.0073 | 0.0010 | 5.50E-14 | -0.0005 | 0.0042 | 0.9061 |
| rs2861422 | 3 | 141724644 | *TFDP2* | T | C | 0.0074 | 0.0010 | 9.10E-14 | -0.0063 | 0.0041 | 0.1226 |
| rs12460876 | 19 | 33356891 | *SLC7A9* | T | C | -0.0066 | 0.0009 | 1.90E-13 | -0.0077 | 0.0038 | 0.0414 |
| rs267734 | 1 | 150951477 | *ANXA9* | T | C | -0.0079 | 0.0011 | 4.00E-13 | -0.0062 | 0.0045 | 0.1740 |
| rs17216707 | 20 | 52732362 | *CYP24A1* | T | C | -0.0084 | 0.0011 | 6.00E-13 | -0.0090 | 0.0047 | 0.0533 |
| rs848490 | 7 | 77555005 | *PHTF2* | C | G | 0.0073 | 0.0010 | 7.80E-13 | -0.0041 | 0.0041 | 0.3122 |
| rs10774021 | 12 | 349298 | *SLC6A13* | T | C | -0.0063 | 0.0009 | 4.80E-12 | -0.0003 | 0.0039 | 0.9478 |
| rs807601 | 2 | 15793014 | *DDX1* | T | G | 0.0064 | 0.0009 | 6.60E-12 | -0.0095 | 0.0038 | 0.0129 |
| rs1044261 | 10 | 1065710 | *C10orf110* | T | C | -0.011 | 0.0016 | 1.20E-11 | 0.0010 | 0.0075 | 0.8948 |
| rs4014195 | 11 | 65506822 | *KRT8P26* | C | G | 0.0061 | 0.0009 | 2.20E-11 | -0.0063 | 0.0038 | 0.0970 |
| rs2453580 | 17 | 19438321 | *SLC47A1* | T | C | 0.0064 | 0.0009 | 2.90E-11 | 0.0003 | 0.0046 | 0.9433 |
| rs10277115 | 7 | 1285195 | *UNCX* | A | T | 0.0095 | 0.0014 | 1.10E-10 | -0.0098 | 0.0065 | 0.1315 |
| rs10994860 | 10 | 52645424 | *A1CF* | T | C | 0.0075 | 0.0011 | 1.20E-10 | -0.0002 | 0.0048 | 0.9694 |
| rs6459680 | 7 | 156258568 | *C7orf13* | T | G | -0.0065 | 0.0010 | 2.00E-10 | -0.0025 | 0.0042 | 0.5552 |
| rs10491967 | 12 | 3368093 | *TSPAN9* | A | G | -0.0092 | 0.0014 | 3.00E-10 | 0.0074 | 0.006 | 0.2179 |
| rs228611 | 4 | 103561709 | *NFKB1* | A | G | -0.0055 | 0.0009 | 4.70E-10 | -0.0045 | 0.0037 | 0.2149 |
| rs6088580 | 20 | 33285053 | *TP53INP2* | C | G | -0.0055 | 0.0009 | 7.20E-10 | -0.0026 | 0.0037 | 0.4764 |
| rs1800615 | 1 | 15832281 | *CASP9* | T | C | -0.0058 | 0.0009 | 1.90E-09 | -0.0033 | 0.0039 | 0.4011 |
| rs7956634 | 12 | 15321194 | *RERG* | T | C | -0.0068 | 0.0011 | 2.50E-09 | -0.0032 | 0.0051 | 0.5277 |
| rs3850625 | 1 | 201016296 | *CACNA1S* | A | G | 0.008 | 0.0014 | 6.40E-09 | -0.0055 | 0.0056 | 0.3264 |
| rs476633 | 15 | 41392134 | *INO80* | C | G | 0.0051 | 0.0009 | 8.90E-09 | -0.0004 | 0.0037 | 0.9220 |
| rs6795744 | 3 | 13906850 | *WNT7A* | A | G | 0.0071 | 0.0012 | 9.60E-09 | -0.0031 | 0.0052 | 0.5444 |
| rs163160 | 11 | 2789955 | *KCNQ1* | A | G | 0.0067 | 0.0011 | 9.70E-09 | -0.0053 | 0.0048 | 0.2710 |

to be continued…

**Supplementary Table 4 continued**

| | | | | | | Results from the GWAS meta-analysis on | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | eGFR | | | ApoA-IV | | |
| **SNP** | **Chr** | **Pos** | **Nearest gene** | **A1** | **A2** | **Beta*** | **SE*** | **P-value** | **Beta$^{§}$** | **SE$^{§}$** | **P-value** |
| rs2712184 | 2 | 217682779 | *TNP1* | A | C | -0.0049 | 0.0009 | 2.70E-08 | -0.0002 | 0.0037 | 0.9498 |
| rs1106766 | 12 | 57809456 | *R3HDM2* | T | C | 0.0062 | 0.0011 | 4.70E-08 | -0.0009 | 0.0044 | 0.8303 |
| rs716877 | 13 | 72347448 | *DACH1* | C | G | 0.0049 | 0.0009 | 6.20E-08 | 0.0082 | 0.0038 | 0.0317 |
| rs2802729 | 1 | 243501763 | *SDCCAG8* | A | C | -0.005 | 0.0009 | 7.40E-08 | -0.0051 | 0.0038 | 0.1819 |
| rs11666497 | 19 | 38464262 | *SIPA1L3* | T | C | -0.0064 | 0.0012 | 8.60E-08 | -0.0009 | 0.0047 | 0.8406 |
| rs164748 | 16 | 89708292 | *CHMP1A* | C | G | 0.0047 | 0.0009 | 9.30E-08 | -0.0039 | 0.0037 | 0.2925 |
| rs10513801 | 3 | 185822353 | *ETV5* | T | G | 0.007 | 0.0013 | 9.30E-08 | 0.0001 | 0.0056 | 0.9805 |
| rs12136063 | 1 | 110014170 | *SYPL2* | A | G | 0.0049 | 0.0009 | 2.30E-07 | 0.0035 | 0.0039 | 0.3633 |
| rs4667594 | 2 | 170008506 | *LRP2* | A | T | -0.0045 | 0.0009 | 2.40E-07 | 0.0045 | 0.0036 | 0.2112 |
| rs3750082 | 7 | 32919927 | *RP9P* | A | T | 0.0049 | 0.0009 | 2.50E-07 | 0.0045 | 0.0039 | 0.2509 |
| rs7759001 | 6 | 27341409 | *ZNF391* | A | G | -0.0053 | 0.0010 | 2.60E-07 | 0.0001 | 0.0043 | 0.9842 |
| rs8091180 | 18 | 77164243 | *NFATC1* | A | G | -0.0054 | 0.0010 | 3.50E-07 | -0.0058 | 0.0056 | 0.2970 |
| rs9682041 | 3 | 170091902 | *SKIL* | T | C | -0.0067 | 0.0013 | 3.80E-07 | -0.0037 | 0.0054 | 0.4933 |

A1: effect allele; A2: other allele.

*units in log(eGFR); $^{§}$units in log(apoA-IV).

**Supplementary Table 5:** Characteristics and results of the 77 SNPs associated with BMI [4,8]. The table is sorted by the p-value for BMI.

| | | | | | | Results from the GWAS meta-analysis on | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | BMI | | | ApoA-IV | | |
| **SNP** | **Chr** | **Pos** | **Nearest gene** | **A1** | **A2** | **Beta*** | **SE*** | **P-value** | **Beta$^{\S}$** | **SE$^{\S}$** | **P-value** |
| rs1558902 | 16 | 53803574 | *FTO* | A | T | 0.0818 | 0.0031 | 7.51E-153 | -0.0047 | 0.0037 | 0.2020 |
| rs6567160 | 18 | 57829135 | *MC4R* | C | T | 0.0556 | 0.0036 | 3.93E-53 | 0.0053 | 0.0042 | 0.2124 |
| rs13021737 | 2 | 632348 | *TMEM18* | A | G | -0.0601 | 0.0040 | 1.11E-50 | -0.0023 | 0.0047 | 0.6214 |
| rs10938397 | 4 | 45182527 | *GNPDA2* | A | G | -0.0402 | 0.0031 | 3.21E-38 | -0.0032 | 0.0038 | 0.3917 |
| rs543874 | 1 | 177889480 | *SEC16B* | G | A | 0.0482 | 0.0039 | 2.62E-35 | 0.0066 | 0.0047 | 0.1650 |
| rs2207139 | 6 | 50845490 | *TFAP2B* | G | A | 0.0447 | 0.0040 | 4.13E-29 | 0.0011 | 0.0049 | 0.8146 |
| rs11030104 | 11 | 27684517 | *LIN7C* | A | G | 0.0414 | 0.0038 | 5.56E-28 | 0.0014 | 0.0043 | 0.7515 |
| rs3101336 | 1 | 72751185 | *NEGR1* | T | C | -0.0334 | 0.0031 | 2.66E-26 | 0.0059 | 0.0038 | 0.1250 |
| rs7138803 | 12 | 50247468 | *BCDIN3D* | G | A | -0.0315 | 0.0031 | 8.15E-24 | 0.0032 | 0.0038 | 0.4074 |
| rs10182181 | 2 | 25150296 | *ADCY3* | A | G | -0.0307 | 0.0031 | 8.78E-24 | 0.0022 | 0.0037 | 0.5530 |
| rs3888190 | 16 | 28889486 | *ATP2A1* | A | C | 0.0309 | 0.0031 | 3.14E-23 | 0.0046 | 0.0046 | 0.3185 |
| rs1516725 | 3 | 185824004 | *TRA2B* | T | C | -0.0451 | 0.0046 | 1.89E-22 | 0.0000 | 0.0055 | 0.9956 |
| rs12446632 | 16 | 19935389 | *GPRC5B* | A | G | -0.0403 | 0.0046 | 1.48E-18 | -0.0043 | 0.0052 | 0.4029 |
| rs2287019 | 19 | 46202172 | *QPCTL* | C | T | 0.0360 | 0.0042 | 4.59E-18 | 0.0089 | 0.0057 | 0.1169 |
| rs16951275 | 15 | 68077168 | *MAP2K5* | C | T | -0.0311 | 0.0037 | 1.91E-17 | 0.0034 | 0.0043 | 0.4360 |
| rs3817334 | 11 | 47650993 | *MTCH2* | C | T | -0.0262 | 0.0031 | 5.15E-17 | -0.0003 | 0.0037 | 0.9354 |
| rs2112347 | 5 | 75015242 | *C5orf37* | G | T | -0.0261 | 0.0031 | 6.19E-17 | -0.0001 | 0.0038 | 0.9795 |
| rs12566985 | 1 | 75002193 | *LRRC53* | G | A | 0.0242 | 0.0031 | 3.28E-15 | -0.0003 | 0.0036 | 0.9285 |
| rs3810291 | 19 | 47569003 | *ZC3H4* | A | G | 0.0283 | 0.0036 | 4.81E-15 | -0.0035 | 0.0043 | 0.4228 |
| rs7141420 | 14 | 79899454 | *NRXN3* | T | C | 0.0235 | 0.0031 | 1.23E-14 | -0.0006 | 0.0036 | 0.8679 |
| rs13078960 | 3 | 85807590 | *CADM2* | T | G | -0.0297 | 0.0039 | 1.74E-14 | -0.0069 | 0.0046 | 0.1286 |
| rs10968576 | 9 | 28414339 | *LINGO2* | G | A | 0.0249 | 0.0033 | 6.61E-14 | -0.0013 | 0.0040 | 0.7444 |
| rs17024393 | 1 | 110154688 | *GNAT2* | C | T | 0.0658 | 0.0088 | 7.03E-14 | 0.0005 | 0.0108 | 0.9598 |
| rs657452 | 1 | 49589847 | *AGBL4* | A | G | 0.0227 | 0.0031 | 5.48E-13 | 0.0026 | 0.0037 | 0.4835 |
| rs12429545 | 13 | 54102206 | *OLFM4* | G | A | -0.0334 | 0.0047 | 1.09E-12 | -0.0085 | 0.0060 | 0.1528 |
| rs12286929 | 11 | 115022404 | *CADM1* | G | A | 0.0217 | 0.0031 | 1.31E-12 | -0.0040 | 0.0036 | 0.2720 |
| rs13107325 | 4 | 103188709 | *SLC39A8* | C | T | -0.0477 | 0.0068 | 1.83E-12 | -0.0014 | 0.0072 | 0.8452 |
| rs11165643 | 1 | 96924097 | *PTBP2* | C | T | -0.0218 | 0.0031 | 2.07E-12 | -0.0013 | 0.0036 | 0.7126 |
| rs7903146 | 10 | 114758349 | *TCF7L2* | T | C | -0.0234 | 0.0034 | 1.11E-11 | -0.0074 | 0.0040 | 0.0626 |
| rs10132280 | 14 | 25928179 | *STXBP6* | A | C | -0.0230 | 0.0034 | 1.14E-11 | 0.0092 | 0.0040 | 0.0209 |
| rs17405819 | 8 | 76806584 | *HNF4G* | C | T | -0.0224 | 0.0033 | 2.07E-11 | -0.0044 | 0.0039 | 0.2583 |
| rs1016287 | 2 | 59305625 | *EIF3FP3* | T | C | 0.0229 | 0.0034 | 2.25E-11 | -0.0041 | 0.0040 | 0.3092 |
| rs4256980 | 11 | 8673939 | *TRIM66* | G | C | 0.0209 | 0.0031 | 2.90E-11 | -0.0047 | 0.0037 | 0.2026 |
| rs17094222 | 10 | 102395440 | *HIF1AN* | C | T | 0.0249 | 0.0038 | 5.94E-11 | 0.0032 | 0.0047 | 0.4966 |
| rs12401738 | 1 | 78446761 | *FUBP1* | A | G | 0.0211 | 0.0033 | 1.15E-10 | -0.0009 | 0.0040 | 0.8132 |
| rs7599312 | 2 | 213413231 | *MIR548F2* | G | A | 0.0220 | 0.0034 | 1.17E-10 | 0.0030 | 0.0041 | 0.4586 |
| rs2365389 | 3 | 61236462 | *FHIT* | C | T | 0.0200 | 0.0031 | 1.63E-10 | -0.0022 | 0.0037 | 0.5494 |
| rs205262 | 6 | 34563164 | *C6orf106* | A | G | -0.0221 | 0.0035 | 1.75E-10 | 0.0031 | 0.0041 | 0.4481 |
| rs2820292 | 1 | 201784287 | *NAV1* | A | C | -0.0195 | 0.0031 | 1.83E-10 | 0.0030 | 0.0037 | 0.4210 |
| rs12885454 | 14 | 29736838 | *PRKD1* | C | A | 0.0207 | 0.0033 | 1.94E-10 | 0.0004 | 0.0038 | 0.9144 |

to be continued…

**Supplementary Table 5 continued**

| | | | | | | Results from the GWAS meta-analysis on | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | BMI | | | ApoA-IV | | |
| **SNP** | **Chr** | **Pos** | **Nearest gene** | **A1** | **A2** | **Beta*** | **SE*** | **P-value** | **Beta$^{\S}$** | **SE$^{\S}$** | **P-value** |
| rs12016871 | 13 | 28017782 | *MTIF3* | C | T | -0.0298 | 0.0047 | 2.29E-10 | -0.0091 | 0.0046 | 0.0480 |
| rs16851483 | 3 | 141275436 | *RASA2* | G | T | -0.0483 | 0.0077 | 3.55E-10 | 0.0060 | 0.0077 | 0.4360 |
| rs1167827 | 7 | 75163169 | *HIP1* | A | G | -0.0202 | 0.0033 | 6.33E-10 | 0.0033 | 0.0045 | 0.4617 |
| rs758747 | 16 | 3627358 | *NLRC3* | C | T | -0.0225 | 0.0037 | 7.47E-10 | -0.0011 | 0.0051 | 0.8256 |
| rs1928295 | 9 | 120378483 | *TLR4* | C | T | -0.0188 | 0.0031 | 7.91E-10 | 0.0051 | 0.0036 | 0.1570 |
| rs9925964 | 16 | 31129895 | *MYST1* | G | A | -0.0192 | 0.0031 | 8.11E-10 | -0.0067 | 0.0038 | 0.0726 |
| rs11126666 | 2 | 26928811 | *KCNK3* | G | A | -0.0207 | 0.0034 | 1.33E-09 | -0.0009 | 0.0042 | 0.8208 |
| rs2650492 | 16 | 28333411 | *SBK1* | A | G | 0.0207 | 0.0035 | 1.92E-09 | 0.0050 | 0.0052 | 0.3342 |
| rs6804842 | 3 | 25106437 | *RARB* | A | G | -0.0185 | 0.0031 | 2.48E-09 | -0.0013 | 0.0037 | 0.7170 |
| rs12940622 | 17 | 78615571 | *RPTOR* | A | G | -0.0182 | 0.0031 | 2.49E-09 | -0.0006 | 0.0036 | 0.8686 |
| rs11847697 | 14 | 30515112 | *PRKD1* | T | C | 0.0492 | 0.0084 | 3.99E-09 | 0.0013 | 0.0094 | 0.8854 |
| rs4740619 | 9 | 15634326 | *C9orf93* | T | C | 0.0179 | 0.0031 | 4.56E-09 | 0.0058 | 0.0036 | 0.1126 |
| rs13191362 | 6 | 163033350 | *PARK2* | A | G | 0.0277 | 0.0048 | 7.34E-09 | -0.0029 | 0.0058 | 0.6145 |
| rs3736485 | 15 | 51748610 | *DMXL2* | A | G | 0.0176 | 0.0031 | 7.41E-09 | 0.0077 | 0.0037 | 0.0371 |
| rs17001654 | 4 | 77129568 | *SCARB2* | C | G | -0.0306 | 0.0053 | 7.76E-09 | 0.0041 | 0.0049 | 0.4050 |
| rs11191560 | 10 | 104869038 | *NT5C2* | T | C | -0.0308 | 0.0053 | 8.45E-09 | -0.0006 | 0.0060 | 0.9178 |
| rs1528435 | 2 | 181550962 | *UBE2E3* | T | C | 0.0178 | 0.0031 | 1.20E-08 | 0.0043 | 0.0038 | 0.2632 |
| rs2075650 | 19 | 45395619 | *TOMM40* | A | G | 0.0258 | 0.0045 | 1.25E-08 | 0.0061 | 0.0062 | 0.3222 |
| rs1000940 | 17 | 5283252 | *RABEP1* | G | A | 0.0192 | 0.0034 | 1.28E-08 | -0.0007 | 0.0040 | 0.8663 |
| rs2033529 | 6 | 40348653 | *LRFN2* | G | A | 0.0190 | 0.0033 | 1.39E-08 | 0.0026 | 0.0040 | 0.5126 |
| rs11583200 | 1 | 50559820 | *ELAVL4* | C | T | 0.0177 | 0.0031 | 1.48E-08 | 0.0075 | 0.0038 | 0.0455 |
| rs9400239 | 6 | 108977663 | *FOXO3* | C | T | 0.0188 | 0.0033 | 1.61E-08 | 0.0007 | 0.0039 | 0.8503 |
| rs10733682 | 9 | 129460914 | *LMX1B* | A | G | 0.0174 | 0.0031 | 1.83E-08 | -0.0011 | 0.0040 | 0.7850 |
| rs11688816 | 2 | 63053048 | *EHBP1* | A | G | -0.0172 | 0.0031 | 1.89E-08 | -0.0015 | 0.0036 | 0.6785 |
| rs11057405 | 12 | 122781897 | *CLIP1* | A | G | -0.0307 | 0.0055 | 2.02E-08 | 0.0041 | 0.0076 | 0.5888 |
| rs2121279 | 2 | 143043285 | *LRP1B* | T | C | 0.0245 | 0.0044 | 2.31E-08 | 0.0058 | 0.0055 | 0.2909 |
| rs29941 | 19 | 34309532 | *KCTD15* | A | G | -0.0182 | 0.0033 | 2.41E-08 | 0.0019 | 0.0039 | 0.6265 |
| rs11727676 | 4 | 145659064 | *HHIP* | C | T | -0.0358 | 0.0064 | 2.55E-08 | 0.0149 | 0.0082 | 0.0680 |
| rs3849570 | 3 | 81792112 | *GBE1* | A | C | 0.0188 | 0.0034 | 2.60E-08 | -0.0102 | 0.0039 | 0.0090 |
| rs6477694 | 9 | 111932342 | *EPB41L4B* | C | T | 0.0174 | 0.0031 | 2.67E-08 | 0.0021 | 0.0037 | 0.5772 |
| rs7899106 | 10 | 87410904 | *GRID1* | A | G | -0.0395 | 0.0071 | 2.96E-08 | 0.0071 | 0.0086 | 0.4130 |
| rs2176598 | 11 | 43864278 | *HSD17B12* | T | C | 0.0198 | 0.0036 | 2.97E-08 | -0.0039 | 0.0043 | 0.3622 |
| rs2245368 | 7 | 76608143 | *PMS2L11* | T | C | -0.0317 | 0.0057 | 3.19E-08 | 0.0016 | 0.0075 | 0.8352 |
| rs17724992 | 19 | 18454825 | *PGPEP1* | A | G | 0.0194 | 0.0035 | 3.42E-08 | -0.0011 | 0.0042 | 0.7885 |
| rs7243357 | 18 | 56883319 | *GRP* | G | T | -0.0217 | 0.004 | 3.86E-08 | -0.0014 | 0.0048 | 0.7725 |
| rs1808579 | 18 | 21104888 | *C18orf8* | T | C | -0.0167 | 0.0031 | 4.17E-08 | -0.0018 | 0.0036 | 0.6117 |
| rs2033732 | 8 | 85079709 | *RALYL* | C | T | 0.0192 | 0.0035 | 4.89E-08 | -0.0058 | 0.0042 | 0.1696 |

A1: effect allele; A2: other allele.

*units in SD; $^{\S}$units in log(apoA-IV).

**Supplementary Table 6:** Characteristics and results of the 40 SNPs associated with WHR [5,8]. The table is sorted by the p-value for WHR.

| | | | | | | Results from the GWAS meta-analysis on | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | WHR | | | ApoA-IV | |
| **SNP** | **Chr** | **Pos** | **Nearest gene** | **A1** | **A2** | **Beta** | **SE** | **P-value** | **Beta** | **SE** | **P-value** |
| rs2645294 | 1 | 119574587 | *WARS2* | C | T | -0.032 | 0.0034 | 1.30E-20 | -0.0049 | 0.0036 | 0.1733 |
| rs979012 | 20 | 6623374 | *BMP2* | T | C | 0.033 | 0.0036 | 5.40E-20 | -0.0057 | 0.0039 | 0.1381 |
| rs1936805 | 6 | 127452116 | *RSPO3* | T | C | 0.029 | 0.0034 | 8.40E-18 | 0.0022 | 0.0036 | 0.5481 |
| rs10245353 | 7 | 25858614 | *MIR148A* | A | C | 0.033 | 0.0043 | 5.80E-15 | 0.0070 | 0.0048 | 0.1440 |
| rs1358980 | 6 | 43764551 | *VEGFA* | T | C | 0.027 | 0.0036 | 3.20E-14 | -0.0031 | 0.0042 | 0.4577 |
| rs17451107 | 3 | 156797609 | *LEKR1* | T | C | 0.026 | 0.0036 | 1.30E-13 | -0.0013 | 0.0037 | 0.7138 |
| rs6556301 | 5 | 176527577 | *FGFR4* | T | G | 0.028 | 0.0039 | 1.80E-12 | 0.0050 | 0.0047 | 0.2934 |
| rs12679556 | 8 | 72514228 | *MSC* | G | T | 0.026 | 0.0039 | 1.30E-11 | -0.0015 | 0.0042 | 0.7189 |
| rs7801581 | 7 | 27223771 | *HOXA11* | T | C | 0.027 | 0.0042 | 8.00E-11 | 0.0008 | 0.0049 | 0.8637 |
| rs7705502 | 5 | 173320815 | *CPEB4* | A | G | 0.023 | 0.0036 | 9.10E-11 | 0.0072 | 0.0040 | 0.0715 |
| rs2371767 | 3 | 64718258 | *ADAMTS9* | G | C | 0.022 | 0.0039 | 6.40E-09 | -0.0016 | 0.0039 | 0.6857 |
| rs4765219 | 12 | 124440110 | *CCDC92* | C | A | 0.020 | 0.0035 | 9.40E-09 | -0.0071 | 0.0038 | 0.0574 |
| rs12608504 | 19 | 18389135 | *JUND* | A | G | 0.020 | 0.0036 | 1.50E-08 | 0.0013 | 0.0040 | 0.7379 |
| rs2276824 | 3 | 52637486 | *PBRM1* | C | G | 0.020 | 0.0035 | 1.50E-08 | -0.0007 | 0.0038 | 0.8511 |
| rs2294239 | 22 | 29449477 | *ZNRF3* | A | G | 0.019 | 0.0035 | 3.50E-08 | 0.0045 | 0.0037 | 0.2189 |
| rs1385167 | 2 | 66200648 | *MEIS1* | G | A | 0.024 | 0.0049 | 5.80E-07 | -0.0039 | 0.0055 | 0.4706 |
| rs4081724 | 19 | 33824946 | *CEBPG* | G | A | 0.025 | 0.0050 | 8.70E-07 | 0.0021 | 0.0051 | 0.6760 |
| rs8030605 | 15 | 56504598 | *RFX7* | A | G | 0.024 | 0.0052 | 2.70E-06 | 0.0094 | 0.0053 | 0.0791 |
| rs10842707 | 12 | 26471364 | *ITPR2* | T | C | 0.018 | 0.0040 | 5.80E-06 | -0.0033 | 0.0044 | 0.4530 |
| rs1443512 | 12 | 54342684 | *HOXC13* | A | C | 0.017 | 0.0039 | 9.20E-06 | -0.0075 | 0.0043 | 0.0786 |
| rs7759742 | 6 | 32381736 | *HLA-DRB5* | A | T | 0.014 | 0.0034 | 3.40E-05 | 0.0037 | 0.0049 | 0.4530 |
| rs10991437 | 9 | 107735920 | *ABCA1* | A | C | 0.021 | 0.0053 | 5.80E-05 | -0.0121 | 0.0058 | 0.0374 |
| rs714515 | 1 | 172352990 | *C1orf105* | G | A | 0.012 | 0.0033 | 3.00E-04 | 0.0074 | 0.0037 | 0.0420 |
| rs10919388 | 1 | 170372503 | *GORAB* | A | C | -0.014 | 0.0040 | 0.00034 | -0.0008 | 0.0040 | 0.8457 |
| rs8042543 | 15 | 31708263 | *KLF13* | C | T | 0.015 | 0.0042 | 0.00035 | -0.0043 | 0.0054 | 0.4221 |
| rs10195252 | 2 | 165513091 | *COBLL1* | T | C | 0.0110 | 0.0034 | 0.00094 | -0.0001 | 0.0038 | 0.9822 |
| rs1294410 | 6 | 6738752 | *LY86* | C | T | 0.0110 | 0.0035 | 0.00094 | -0.0024 | 0.0038 | 0.5321 |
| rs303084 | 4 | 124066948 | *SPATA5* | A | G | 0.0140 | 0.0042 | 0.0012 | -0.0020 | 0.0043 | 0.6436 |
| rs4646404 | 17 | 17420199 | *PEMT* | G | A | 0.0120 | 0.0039 | 0.0015 | -0.0008 | 0.0041 | 0.8485 |
| rs905938 | 1 | 154991389 | *DCST2* | C | T | -0.0120 | 0.0040 | 0.0021 | 0.0068 | 0.0046 | 0.1386 |
| rs6090583 | 20 | 45558831 | *EYA2* | A | G | 0.0100 | 0.0034 | 0.0022 | 0.0001 | 0.0037 | 0.9851 |
| rs224333 | 20 | 34023962 | *GDF5* | G | A | -0.0100 | 0.0036 | 0.0053 | 0.0005 | 0.0038 | 0.8961 |
| rs1569135 | 2 | 188115398 | *CALCRL* | A | G | 0.0094 | 0.0034 | 0.0056 | 0.0005 | 0.0036 | 0.8909 |
| rs11231693 | 11 | 63862612 | *MACROD1* | A | G | 0.0200 | 0.0075 | 0.0085 | 0.0200 | 0.0084 | 0.0177 |
| rs1440372 | 15 | 67033151 | *SMAD6* | C | T | 0.0094 | 0.0037 | 0.0120 | 0.0008 | 0.0043 | 0.8515 |
| rs1045241 | 5 | 118729286 | *TNFAIP8* | C | T | 0.0065 | 0.0037 | 0.0830 | -0.0058 | 0.0040 | 0.1520 |
| rs9991328 | 4 | 89713121 | *FAM13A* | T | C | 0.0058 | 0.0034 | 0.0890 | 0.0035 | 0.0037 | 0.3434 |
| rs17819328 | 3 | 12489342 | *PPARG* | G | T | 0.0054 | 0.0035 | 0.1200 | -0.0016 | 0.0037 | 0.6706 |
| rs10804591 | 3 | 129334233 | *PLXND1* | A | C | -0.0026 | 0.0042 | 0.5400 | 0.0013 | 0.0045 | 0.7707 |
| rs2820443 | 1 | 219753509 | *ZC3H11B* | C | T | -0.0001 | 0.0037 | 0.9800 | 0.0005 | 0.0041 | 0.8998 |

A1: effect allele; A2: other allele.

*units in SD; $^{\S}$units in log(apoA-IV).

**Supplementary Table 7:** Characteristics and results of the 36 SNPs associated with fasting glucose [6,8]. The table is sorted by the p-value for fasting glucose.

| | | | | | | Results from the GWAS meta-analysis on | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | Fasting Glucose | | | ApoA-IV | | |
| **SNP** | **Chr** | **Pos** | **Nearest gene** | **A1** | **A2** | **Beta*** | **SE*** | **P-value** | **Beta$^{\S}$** | **SE$^{\S}$** | **P-value** |
| rs10830963 | 11 | 92708710 | *MTNR1B* | C | G | -0.078 | 0.0025 | 1.07E-215 | -0.0043 | 0.0043 | 0.3218 |
| rs560887 | 2 | 169763148 | *ABCB11* | C | T | 0.071 | 0.0025 | 1.40E-178 | 0.0014 | 0.0040 | 0.7196 |
| rs2908289 | 7 | 44223942 | *GCK* | G | A | -0.057 | 0.0029 | 3.32E-88 | -0.0013 | 0.0048 | 0.7923 |
| rs2191349 | 7 | 15064309 | *DGKB* | G | T | -0.029 | 0.0021 | 1.28E-42 | 0.0001 | 0.0036 | 0.9722 |
| rs780094 | 2 | 27741237 | *GCKR* | C | T | 0.027 | 0.0021 | 2.58E-37 | 0.0074 | 0.0036 | 0.0411 |
| rs11558471 | 8 | 118185733 | *SLC30A8* | A | G | 0.029 | 0.0023 | 7.80E-37 | -0.0019 | 0.0041 | 0.6405 |
| rs4502156 | 15 | 62383155 | *C2CD4A* | T | C | 0.022 | 0.0021 | 1.38E-25 | -0.0016 | 0.0037 | 0.6682 |
| rs11607883 | 11 | 45839709 | *SLC35C1* | G | A | 0.021 | 0.0021 | 6.32E-24 | -0.0024 | 0.0036 | 0.5115 |
| rs11039182 | 11 | 47346723 | *MADD* | T | C | 0.023 | 0.0024 | 4.82E-22 | -0.0013 | 0.0040 | 0.7400 |
| rs7903146 | 10 | 114758349 | *TCF7L2* | C | T | -0.022 | 0.0024 | 2.71E-20 | 0.0074 | 0.0040 | 0.0626 |
| rs174576 | 11 | 61603510 | *FADS2* | C | A | 0.020 | 0.0022 | 1.18E-18 | 0.0020 | 0.0040 | 0.6230 |
| rs11708067 | 3 | 123065778 | *ADCY5* | A | G | 0.023 | 0.0026 | 1.30E-18 | 0.0146 | 0.0045 | 0.0011 |
| rs11195502 | 10 | 113039667 | *ADRA2A* | C | T | 0.032 | 0.0037 | 1.97E-18 | -0.0062 | 0.0065 | 0.3403 |
| rs10811661 | 9 | 22134094 | *CDKN2B* | T | C | 0.024 | 0.0028 | 5.65E-18 | -0.0025 | 0.0048 | 0.6096 |
| rs1280 | 3 | 170713290 | *SLC2A2* | T | C | 0.026 | 0.0031 | 8.56E-18 | -0.0058 | 0.0052 | 0.2686 |
| rs4869272 | 5 | 95539448 | *MIR583* | C | T | -0.018 | 0.0022 | 1.02E-15 | -0.0011 | 0.0039 | 0.7699 |
| rs11619319 | 13 | 28487599 | *PDX1* | A | G | -0.020 | 0.0024 | 1.33E-15 | 0.0017 | 0.0045 | 0.6953 |
| rs983309 | 8 | 9177732 | *PPP1R3B* | G | T | -0.026 | 0.0033 | 6.29E-15 | 0.0007 | 0.0059 | 0.9056 |
| rs10814916 | 9 | 4293150 | *GLIS3* | C | A | 0.016 | 0.0022 | 2.26E-13 | 0.0088 | 0.0036 | 0.0149 |
| rs6943153 | 7 | 50791579 | *GRB10* | C | T | -0.015 | 0.0022 | 1.63E-12 | -0.0003 | 0.0040 | 0.9421 |
| rs11603334 | 11 | 72432985 | *ARAP1* | G | A | 0.019 | 0.0028 | 1.12E-11 | -0.0108 | 0.0052 | 0.0363 |
| rs6113722 | 20 | 22557099 | *FOXA2* | G | A | 0.035 | 0.0053 | 2.49E-11 | 0.0092 | 0.0085 | 0.2802 |
| rs16913693 | 9 | 111680359 | *IKBKAP* | T | G | 0.043 | 0.0066 | 3.51E-11 | 0.0039 | 0.0107 | 0.7181 |
| rs3829109 | 9 | 139256766 | *GPSM1* | G | A | 0.017 | 0.0027 | 1.13E-10 | -0.0042 | 0.0055 | 0.4413 |
| rs3783347 | 14 | 100839261 | *WARS* | G | T | 0.017 | 0.0026 | 1.32E-10 | -0.0055 | 0.0045 | 0.2199 |
| rs340874 | 1 | 214159256 | *PROX1* | C | T | 0.013 | 0.0022 | 4.08E-10 | 0.002 | 0.0039 | 0.6108 |
| rs2302593 | 19 | 46196634 | *QPCTL* | C | G | 0.014 | 0.0023 | 9.26E-10 | 0.0052 | 0.0045 | 0.2390 |
| rs9368222 | 6 | 20686996 | *CDKAL1* | C | A | -0.014 | 0.0023 | 1.00E-09 | 0.0074 | 0.0041 | 0.0673 |
| rs10747083 | 12 | 133041618 | *FBRSL1* | A | G | 0.013 | 0.0023 | 7.57E-09 | 0.0072 | 0.0054 | 0.1833 |
| rs6072275 | 20 | 39743905 | *TOP1* | G | A | -0.016 | 0.0028 | 1.66E-08 | 0.0015 | 0.0051 | 0.7704 |
| rs7651090 | 3 | 185513392 | *IGF2BP2* | A | G | -0.013 | 0.0023 | 1.75E-08 | 0.0019 | 0.0039 | 0.6353 |
| rs576674 | 13 | 33554302 | *KL* | G | A | 0.017 | 0.0030 | 2.26E-08 | -0.0034 | 0.0051 | 0.5075 |
| rs11715915 | 3 | 49455330 | *AMT* | C | T | 0.012 | 0.0022 | 4.90E-08 | -0.0051 | 0.0039 | 0.1901 |
| rs17762454 | 6 | 7213200 | *RREB1* | C | T | -0.012 | 0.0023 | 1.88E-07 | -0.0010 | 0.0042 | 0.8072 |
| rs7708285 | 5 | 76425867 | *SNORA47* | G | A | 0.011 | 0.0025 | 4.89E-06 | 0.0053 | 0.0043 | 0.2217 |
| rs2657879 | 12 | 56865338 | *GLS2* | A | G | -0.012 | 0.0027 | 5.69E-06 | -0.0012 | 0.0045 | 0.7896 |

A1: effect allele; A2: other allele.

*units in mmol/L; $^{\S}$units in log(apoA-IV).

**Supplementary Table 8:** Location and association p-values for the SNPs associated with HDL-C (Trait 1) that are in LD ($r^2>0.8$) with SNPs associated with the other traits (denoted as Trait 2). The table is sorted by Trait 2 and within Trait 2 by the SNP name of Trait 1.

| Trait 1 | SNP | Chr | Pos | Nearest gene | P-value | Trait 2 | SNP | Chr | Pos | Nearest gene | P-value | $R^2$ |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **HDL-C** | rs1121980 | 16 | 53809247 | *FTO* | 6.79E-09 | **BMI** | rs1558902 | 16 | 53803574 | *FTO* | 7.51E-153 | 0.956547 |
| **HDL-C** | rs12967135 | 18 | 57849023 | *MC4R* | 3.57E-08 | **BMI** | rs6567160 | 18 | 57829135 | *MC4R* | 3.93E-53 | 1 |
| **HDL-C** | rs13107325 | 4 | 103188709 | *SLC39A8* | 1.07E-15 | **BMI** | rs13107325 | 4 | 103188709 | *SLC39A8* | 1.83E-12 | 1 |
| **HDL-C** | rs1047891 | 2 | 211540507 | *CPS1* | 8.73E-10 | **eGFR** | rs7422339 | 2 | 211540507 | *CPS1* | 2.20E-23 | 1 |
| **HDL-C** | rs11613352 | 12 | 57792580 | *R3HDM2* | 2.39E-13 | **eGFR** | rs1106766 | 12 | 57809456 | *R3HDM2* | 4.70E-08 | 1 |
| **HDL-C** | rs174546 | 11 | 61569830 | *FADS1* | 8.30E-28 | **Fasting Glucose** | rs174576 | 11 | 61603510 | *FADS2* | 1.18E-18 | 0.936276 |
| **HDL-C** | rs12748152 | 1 | 27138393 | *PIGV* | 9.74E-16 | **LDL-C** | rs12748152 | 1 | 27138393 | *PIGV* | 3.21E-12 | 1 |
| **HDL-C** | rs174546 | 11 | 61569830 | *FADS1* | 8.30E-28 | **LDL-C** | rs174546 | 11 | 61569830 | *FADS1* | 1.63E-39 | 1 |
| **HDL-C** | rs2954029 | 8 | 126490972 | *TRIB1* | 2.67E-29 | **LDL-C** | rs2954029 | 8 | 126490972 | *TRIB1* | 2.10E-50 | 1 |
| **HDL-C** | rs3764261 | 16 | 56993324 | *CETP* | 1.00E-769 | **LDL-C** | rs3764261 | 16 | 56993324 | *CETP* | 2.22E-34 | 1 |
| **HDL-C** | rs4420638 | 19 | 45422946 | *APOC1* | 1.72E-21 | **LDL-C** | rs4420638 | 19 | 45422946 | *APOC1* | 1.51E-178 | 1 |
| **HDL-C** | rs964184 | 11 | 116648917 | *ZNF259* | 6.09E-48 | **LDL-C** | rs964184 | 11 | 116648917 | *ZNF259* | 2.01E-26 | 1 |
| **HDL-C** | rs9987289 | 8 | 9183358 | *PPP1R3B* | 1.95E-41 | **LDL-C** | rs9987289 | 8 | 9183358 | *PPP1R3B* | 8.53E-24 | 1 |
| **HDL-C** | rs1121980 | 16 | 53809247 | *FTO* | 6.79E-09 | **TG** | rs1121980 | 16 | 53809247 | *FTO* | 1.52E-06 | 1 |
| **HDL-C** | rs11613352 | 12 | 57792580 | *R3HDM2* | 2.39E-13 | **TG** | rs11613352 | 12 | 57792580 | *R3HDM2* | 9.40E-14 | 1 |
| **HDL-C** | rs12678919 | 8 | 19844222 | *LPL* | 1.38E-149 | **TG** | rs12678919 | 8 | 19844222 | *LPL* | 1.82E-199 | 1 |
| **HDL-C** | rs12748152 | 1 | 27138393 | *PIGV* | 9.74E-16 | **TG** | rs12748152 | 1 | 27138393 | *PIGV* | 1.10E-09 | 1 |
| **HDL-C** | rs17145738 | 7 | 72982874 | *TBL2* | 4.95E-13 | **TG** | rs17145738 | 7 | 72982874 | *TBL2* | 9.42E-99 | 1 |
| **HDL-C** | rs174546 | 11 | 61569830 | *FADS1* | 8.30E-28 | **TG** | rs174546 | 11 | 61569830 | *FADS1* | 7.42E-38 | 1 |
| **HDL-C** | rs1936800 | 6 | 127436064 | *RSPO3* | 3.06E-10 | **TG** | rs1936800 | 6 | 127436064 | *RSPO3* | 3.79E-07 | 1 |
| **HDL-C** | rs2954029 | 8 | 126490972 | *TRIB1* | 2.67E-29 | **TG** | rs2954029 | 8 | 126490972 | *TRIB1* | 1.02E-107 | 1 |
| **HDL-C** | rs2972146 | 2 | 227100698 | *IRS1* | 1.85E-17 | **TG** | rs2972146 | 2 | 227100698 | *IRS1* | 2.97E-15 | 1 |
| **HDL-C** | rs3764261 | 16 | 56993324 | *CETP* | 1.00E-769 | **TG** | rs3764261 | 16 | 56993324 | *CETP* | 1.58E-25 | 1 |
| **HDL-C** | rs4765127 | 12 | 124460167 | *ZNF664* | 7.79E-10 | **TG** | rs4765127 | 12 | 124460167 | *ZNF664* | 2.41E-08 | 1 |
| **HDL-C** | rs4846914 | 1 | 230295691 | *GALNT2* | 3.51E-41 | **TG** | rs4846914 | 1 | 230295691 | *GALNT2* | 7.20E-31 | 1 |
| **HDL-C** | rs6065906 | 20 | 44554015 | *PCIF1* | 5.34E-40 | **TG** | rs6065906 | 20 | 44554015 | *PCIF1* | 2.36E-34 | 1 |
| **HDL-C** | rs731839 | 19 | 33899065 | *PEPD* | 3.44E-09 | **TG** | rs731839 | 19 | 33899065 | *PEPD* | 2.65E-09 | 1 |
| **HDL-C** | rs838880 | 12 | 125261593 | *SCARB1* | 6.38E-32 | **TG** | rs838880 | 12 | 125261593 | *SCARB1* | 0.3064 | 1 |
| **HDL-C** | rs964184 | 11 | 116648917 | *ZNF259* | 6.09E-48 | **TG** | rs964184 | 11 | 116648917 | *ZNF259* | 6.55E-224 | 1 |
| **HDL-C** | rs998584 | 6 | 43757896 | *VEGFA* | 2.27E-11 | **TG** | rs998584 | 6 | 43757896 | *VEGFA* | 3.42E-15 | 1 |

to be continued…

**Supplementary Table 8 continued**

| Trait 1 | SNP | Chr | Pos | Nearest gene | P-value | Trait 2 | SNP | Chr | Pos | Nearest gene | P-value | R² |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **HDL-C** | rs1936800 | 6 | 127436064 | *RSPO3* | 3.06E-10 | **WHR** | rs1936805 | 6 | 127452116 | *RSPO3* | 8.40E-18 | 0.876715 |
| **HDL-C** | rs3822072 | 4 | 89741269 | *FAM13A* | 4.06E-12 | **WHR** | rs9991328 | 4 | 89713121 | *FAM13A* | 0.089 | 0.960722 |
| **HDL-C** | rs4765127 | 12 | 124460167 | *ZNF664* | 7.79E-10 | **WHR** | rs4765219 | 12 | 124440110 | *CCDC92* | 9.40E-09 | 0.987213 |
| **HDL-C** | rs998584 | 6 | 43757896 | *VEGFA* | 2.27E-11 | **WHR** | rs1358980 | 6 | 43764551 | *VEGFA* | 3.20E-14 | 0.829246 |

**Supplementary Table 9:** Location and association p-values for the SNPs associated with LDL-C (Trait 1) that are in LD ($r^2$>0.8) with SNPs associated with the other traits (denoted as Trait 2). The table is sorted by Trait 2 and within Trait 2 by the SNP name of Trait 1.

| Trait 1 | SNP | Chr | Pos | Nearest gene | P-value | Trait 2 | SNP | Chr | Pos | Nearest gene | P-value | R² |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **LDL-C** | rs174546 | 11 | 61569830 | *FADS1* | 1.63E-39 | **Fasting Glucose** | rs174576 | 11 | 61603510 | *FADS2* | 1.18E-18 | 0.936276 |
| **LDL-C** | rs12748152 | 1 | 27138393 | *PIGV* | 3.21E-12 | **HDL-C** | rs12748152 | 1 | 27138393 | *PIGV* | 9.74E-16 | 1 |
| **LDL-C** | rs174546 | 11 | 61569830 | *FADS1* | 1.63E-39 | **HDL-C** | rs174546 | 11 | 61569830 | *FADS1* | 8.30E-28 | 1 |
| **LDL-C** | rs2954029 | 8 | 126490972 | *TRIB1* | 2.10E-50 | **HDL-C** | rs2954029 | 8 | 126490972 | *TRIB1* | 2.67E-29 | 1 |
| **LDL-C** | rs3764261 | 16 | 56993324 | *CETP* | 2.22E-34 | **HDL-C** | rs3764261 | 16 | 56993324 | *CETP* | 0 | 1 |
| **LDL-C** | rs4420638 | 19 | 45422946 | *APOC1* | 1.51E-178 | **HDL-C** | rs4420638 | 19 | 45422946 | *APOC1* | 1.72E-21 | 1 |
| **LDL-C** | rs964184 | 11 | 116648917 | *ZNF259* | 2.01E-26 | **HDL-C** | rs964184 | 11 | 116648917 | *ZNF259* | 6.09E-48 | 1 |
| **LDL-C** | rs9987289 | 8 | 9183358 | *PPP1R3B* | 8.53E-24 | **HDL-C** | rs9987289 | 8 | 9183358 | *PPP1R3B* | 1.95E-41 | 1 |
| **LDL-C** | rs10401969 | 19 | 19407718 | *SF4* | 2.65E-54 | **TG** | rs10401969 | 19 | 19407718 | *SF4* | 9.70E-70 | 1 |
| **LDL-C** | rs12748152 | 1 | 27138393 | *PIGV* | 3.21E-12 | **TG** | rs12748152 | 1 | 27138393 | *PIGV* | 1.10E-09 | 1 |
| **LDL-C** | rs174546 | 11 | 61569830 | *FADS1* | 1.63E-39 | **TG** | rs174546 | 11 | 61569830 | *FADS1* | 7.42E-38 | 1 |
| **LDL-C** | rs2131925 | 1 | 63025942 | *DOCK7* | 2.98E-32 | **TG** | rs2131925 | 1 | 63025942 | *DOCK7* | 3.05E-74 | 1 |
| **LDL-C** | rs2954029 | 8 | 126490972 | *TRIB1* | 2.10E-50 | **TG** | rs2954029 | 8 | 126490972 | *TRIB1* | 1.02E-107 | 1 |
| **LDL-C** | rs3764261 | 16 | 56993324 | *CETP* | 2.22E-34 | **TG** | rs3764261 | 16 | 56993324 | *CETP* | 1.58E-25 | 1 |
| **LDL-C** | rs4722551 | 7 | 25991826 | *MIR148A* | 3.95E-14 | **TG** | rs4722551 | 7 | 25991826 | *MIR148A* | 1.58E-09 | 1 |
| **LDL-C** | rs6831256 | 4 | 3473139 | *DOK7* | 9.07E-07 | **TG** | rs6831256 | 4 | 3473139 | *DOK7* | 1.60E-12 | 1 |
| **LDL-C** | rs6882076 | 5 | 156390297 | *TIMD4* | 3.31E-31 | **TG** | rs6882076 | 5 | 156390297 | *TIMD4* | 1.51E-15 | 1 |
| **LDL-C** | rs964184 | 11 | 116648917 | *ZNF259* | 2.01E-26 | **TG** | rs964184 | 11 | 116648917 | *ZNF259* | 6.55E-224 | 1 |

**Supplementary Table 10:** Location and association p-values for the SNPs associated with TG (Trait 1) that are in LD ($r^2>0.8$) with SNPs associated with the other traits (denoted as Trait 2). The table is sorted by Trait 2 and within Trait 2 by the SNP name of Trait 1.

| Trait 1 | SNP | Chr | Pos | Nearest gene | P-value | Trait 2 | SNP | Chr | Pos | Nearest gene | P-value | $R^2$ |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **TG** | rs1121980 | 16 | 53809247 | *FTO* | 1.52E-06 | **BMI** | rs1558902 | 16 | 53803574 | *FTO* | 7.51E-153 | 0.956547 |
| **TG** | rs11613352 | 12 | 57792580 | *R3HDM2* | 9.40E-14 | **eGFR** | rs1106766 | 12 | 57809456 | *R3HDM2* | 4.70E-08 | 1 |
| **TG** | rs1260326 | 2 | 27730940 | *GCKR* | 2.29E-239 | **eGFR** | rs1260326 | 2 | 27730940 | *GCKR* | 3.40E-14 | 1 |
| **TG** | rs1260326 | 2 | 27730940 | *GCKR* | 2.29E-239 | **FG** | rs780094 | 2 | 27741237 | *GCKR* | 2.58E-37 | 0.911673 |
| **TG** | rs174546 | 11 | 61569830 | *FADS1* | 7.42E-38 | **FG** | rs174576 | 11 | 61603510 | *FADS2* | 1.18E-18 | 0.936276 |
| **TG** | rs1121980 | 16 | 53809247 | *FTO* | 1.52E-06 | **HDL-C** | rs1121980 | 16 | 53809247 | *FTO* | 6.79E-09 | 1 |
| **TG** | rs11613352 | 12 | 57792580 | *R3HDM2* | 9.40E-14 | **HDL-C** | rs11613352 | 12 | 57792580 | *R3HDM2* | 2.39E-13 | 1 |
| **TG** | rs12678919 | 8 | 19844222 | *LPL* | 1.82E-199 | **HDL-C** | rs12678919 | 8 | 19844222 | *LPL* | 1.38E-149 | 1 |
| **TG** | rs12748152 | 1 | 27138393 | *PIGV* | 1.10E-09 | **HDL-C** | rs12748152 | 1 | 27138393 | *PIGV* | 9.74E-16 | 1 |
| **TG** | rs17145738 | 7 | 72982874 | *TBL2* | 9.42E-99 | **HDL-C** | rs17145738 | 7 | 72982874 | *TBL2* | 4.95E-13 | 1 |
| **TG** | rs174546 | 11 | 61569830 | *FADS1* | 7.42E-38 | **HDL-C** | rs174546 | 11 | 61569830 | *FADS1* | 8.30E-28 | 1 |
| **TG** | rs1936800 | 6 | 127436064 | *RSPO3* | 3.79E-07 | **HDL-C** | rs1936800 | 6 | 127436064 | *RSPO3* | 3.06E-10 | 1 |
| **TG** | rs2954029 | 8 | 126490972 | *TRIB1* | 1.02E-107 | **HDL-C** | rs2954029 | 8 | 126490972 | *TRIB1* | 2.67E-29 | 1 |
| **TG** | rs2972146 | 2 | 227100698 | *IRS1* | 2.97E-15 | **HDL-C** | rs2972146 | 2 | 227100698 | *IRS1* | 1.85E-17 | 1 |
| **TG** | rs3764261 | 16 | 56993324 | *CETP* | 1.58E-25 | **HDL-C** | rs3764261 | 16 | 56993324 | *CETP* | 0 | 1 |
| **TG** | rs4765127 | 12 | 124460167 | *ZNF664* | 2.41E-08 | **HDL-C** | rs4765127 | 12 | 124460167 | *ZNF664* | 7.79E-10 | 1 |
| **TG** | rs4846914 | 1 | 230295691 | *GALNT2* | 7.20E-31 | **HDL-C** | rs4846914 | 1 | 230295691 | *GALNT2* | 3.51E-41 | 1 |
| **TG** | rs6065906 | 20 | 44554015 | *PCIF1* | 2.36E-34 | **HDL-C** | rs6065906 | 20 | 44554015 | *PCIF1* | 5.34E-40 | 1 |
| **TG** | rs731839 | 19 | 33899065 | *PEPD* | 2.65E-09 | **HDL-C** | rs731839 | 19 | 33899065 | *PEPD* | 3.44E-09 | 1 |
| **TG** | rs838880 | 12 | 125261593 | *SCARB1* | 0.3064 | **HDL-C** | rs838880 | 12 | 125261593 | *SCARB1* | 6.38E-32 | 1 |
| **TG** | rs964184 | 11 | 116648917 | *ZNF259* | 6.55E-224 | **HDL-C** | rs964184 | 11 | 116648917 | *ZNF259* | 6.09E-48 | 1 |
| **TG** | rs998584 | 6 | 43757896 | *VEGFA* | 3.42E-15 | **HDL-C** | rs998584 | 6 | 43757896 | *VEGFA* | 2.27E-11 | 1 |
| **TG** | rs10401969 | 19 | 19407718 | *SF4* | 9.70E-70 | **LDL-C** | rs10401969 | 19 | 19407718 | *SF4* | 2.65E-54 | 1 |
| **TG** | rs12748152 | 1 | 27138393 | *PIGV* | 1.10E-09 | **LDL-C** | rs12748152 | 1 | 27138393 | *PIGV* | 3.21E-12 | 1 |
| **TG** | rs174546 | 11 | 61569830 | *FADS1* | 7.42E-38 | **LDL-C** | rs174546 | 11 | 61569830 | *FADS1* | 1.63E-39 | 1 |
| **TG** | rs2131925 | 1 | 63025942 | *DOCK7* | 3.05E-74 | **LDL-C** | rs2131925 | 1 | 63025942 | *DOCK7* | 2.98E-32 | 1 |
| **TG** | rs2954029 | 8 | 126490972 | *TRIB1* | 1.02E-107 | **LDL-C** | rs2954029 | 8 | 126490972 | *TRIB1* | 2.10E-50 | 1 |
| **TG** | rs3764261 | 16 | 56993324 | *CETP* | 1.58E-25 | **LDL-C** | rs3764261 | 16 | 56993324 | *CETP* | 2.22E-34 | 1 |
| **TG** | rs4722551 | 7 | 25991826 | *MIR148A* | 1.58E-09 | **LDL-C** | rs4722551 | 7 | 25991826 | *MIR148A* | 3.95E-14 | 1 |

to be continued…

**Supplementary Table 10 continued**

| Trait 1 | SNP | Chr | Pos | Nearest gene | P-value | Trait 2 | SNP | Chr | Pos | Nearest gene | P-value | R² |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **TG** | rs6831256 | 4 | 3473139 | *DOK7* | 1.60E-12 | **LDL-C** | rs6831256 | 4 | 3473139 | *DOK7* | 9.07E-07 | 1 |
| **TG** | rs6882076 | 5 | 156390297 | *TIMD4* | 1.51E-15 | **LDL-C** | rs6882076 | 5 | 156390297 | *TIMD4* | 3.31E-31 | 1 |
| **TG** | rs964184 | 11 | 116648917 | *ZNF259* | 6.55E-224 | **LDL-C** | rs964184 | 11 | 116648917 | *ZNF259* | 2.01E-26 | 1 |
| **TG** | rs1936800 | 6 | 127436064 | *RSPO3* | 3.79E-07 | **WHR** | rs1936805 | 6 | 127452116 | *RSPO3* | 8.40E-18 | 0.876715 |
| **TG** | rs4765127 | 12 | 124460167 | *ZNF664* | 2.41E-08 | **WHR** | rs4765219 | 12 | 124440110 | *CCDC92* | 9.40E-09 | 0.987213 |
| **TG** | rs998584 | 6 | 43757896 | *VEGFA* | 3.42E-15 | **WHR** | rs1358980 | 6 | 43764551 | *VEGFA* | 3.20E-14 | 0.829246 |

**Supplementary Table 11:** Location and association p-values for the SNPs associated with eGFR (Trait 1) that are in LD ($r^2>0.8$) with SNPs associated with the other traits (denoted as Trait 2). The table is sorted by Trait 2 and within Trait 2 by the SNP name of Trait 1.

| Trait 1 | SNP | Chr | Pos | Nearest gene | P-value | Trait 2 | SNP | Chr | Pos | Nearest gene | P-value | R² |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **eGFR** | rs10513801 | 3 | 185822353 | *ETV5* | 9.30E-08 | **BMI** | rs1516725 | 3 | 185824004 | *TRA2B* | 1.89E-22 | 1 |
| **eGFR** | rs1260326 | 2 | 27730940 | *GCKR* | 3.40E-14 | **Fasting Glucose** | rs780094 | 2 | 27741237 | *GCKR* | 2.58E-37 | 0.911673 |
| **eGFR** | rs7422339 | 2 | 211540507 | *CPS1* | 2.20E-23 | **HDL-C** | rs1047891 | 2 | 211540507 | *CPS1* | 8.73E-10 | 1 |
| **eGFR** | rs1106766 | 12 | 57809456 | *R3HDM2* | 4.70E-08 | **HDL-C** | rs11613352 | 12 | 57792580 | *R3HDM2* | 2.39E-13 | 1 |
| **eGFR** | rs1106766 | 12 | 57809456 | *R3HDM2* | 4.70E-08 | **TG** | rs11613352 | 12 | 57792580 | *R3HDM2* | 9.40E-14 | 1 |
| **eGFR** | rs1260326 | 2 | 27730940 | *GCKR* | 3.40E-14 | **TG** | rs1260326 | 2 | 27730940 | *GCKR* | 2.29E-239 | 1 |

**Supplementary Table 12:** Location and association p-values for the SNPs associated with BMI (Trait 1) that are in LD ($r^2$>0.8) with SNPs associated with the other traits (denoted as Trait 2). The table is sorted by Trait 2 and within Trait 2 by the SNP name of Trait 1.

| Trait 1 | SNP | Chr | Pos | Nearest gene | P-value | Trait 2 | SNP | Chr | Pos | Nearest gene | P-value | $R^2$ |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **BMI** | rs1516725 | 3 | 185824004 | TRA2B | 1.89E-22 | **eGFR** | rs10513801 | 3 | 185822353 | ETV5 | 9.30E-08 | 1 |
| **BMI** | rs7903146 | 10 | 114758349 | TCF7L2 | 1.11E-11 | **Fasting Glucose** | rs7903146 | 10 | 114758349 | TCF7L2 | 2.71E-20 | 1 |
| **BMI** | rs13107325 | 4 | 103188709 | SLC39A8 | 1.83E-12 | **HDL-C** | rs13107325 | 4 | 103188709 | SLC39A8 | 1.07E-15 | 1 |
| **BMI** | rs1558902 | 16 | 53803574 | FTO | 7.51E-153 | **HDL-C** | rs1121980 | 16 | 53809247 | FTO | 6.79E-09 | 0.956547 |
| **BMI** | rs6567160 | 18 | 57829135 | MC4R | 3.93E-53 | **HDL-C** | rs12967135 | 18 | 57849023 | MC4R | 3.57E-08 | 1 |
| **BMI** | rs1558902 | 16 | 53803574 | FTO | 7.51E-153 | **TG** | rs1121980 | 16 | 53809247 | FTO | 1.52E-06 | 0.956547 |

**Supplementary Table 13:** Location and association p-values for the SNPs associated with WHR (Trait 1) that are in LD ($r^2$>0.8) with SNPs associated with the other traits (denoted as Trait 2). The table is sorted by Trait 2 and within Trait 2 by the SNP name of Trait 1.

| Trait 1 | SNP | Chr | Pos | Nearest gene | P-value | Trait 2 | SNP | Chr | Pos | Nearest gene | P-value | $R^2$ |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **WHR** | rs1358980 | 6 | 43764551 | *VEGFA* | 3.20E-14 | **HDL-C** | rs998584 | 6 | 43757896 | *VEGFA* | 2.27E-11 | 0.829246 |
| **WHR** | rs1936805 | 6 | 127452116 | *RSPO3* | 8.40E-18 | **HDL-C** | rs1936800 | 6 | 127436064 | *RSPO3* | 3.06E-10 | 0.876715 |
| **WHR** | rs4765219 | 12 | 124440110 | *CCDC92* | 9.40E-09 | **HDL-C** | rs4765127 | 12 | 124460167 | *ZNF664* | 7.79E-10 | 0.987213 |
| **WHR** | rs9991328 | 4 | 89713121 | *FAM13A* | 0.089 | **HDL-C** | rs3822072 | 4 | 89741269 | *FAM13A* | 4.06E-12 | 0.960722 |
| **WHR** | rs1358980 | 6 | 43764551 | *VEGFA* | 3.20E-14 | **TG** | rs998584 | 6 | 43757896 | *VEGFA* | 3.42E-15 | 0.829246 |
| **WHR** | rs1936805 | 6 | 127452116 | *RSPO3* | 8.40E-18 | **TG** | rs1936800 | 6 | 127436064 | *RSPO3* | 3.79E-07 | 0.876715 |
| **WHR** | rs4765219 | 12 | 124440110 | *CCDC92* | 9.40E-09 | **TG** | rs4765127 | 12 | 124460167 | *ZNF664* | 2.41E-08 | 0.987213 |

**Supplementary Table 14:** Location and association p-values for the SNPs associated with fasting glucose (Trait 1) that are in LD ($r^2>0.8$) with SNPs associated with the other traits (denoted as Trait 2). The table is sorted by Trait 2 and within Trait 2 by the SNP name of Trait 1.

| Trait 1 | SNP | Chr | Pos | Nearest gene | P-value | Trait 2 | SNP | Chr | Pos | Nearest gene | P-value | $R^2$ |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Fasting Glucose** | rs7903146 | 10 | 114758349 | *TCF7L2* | 2.71E-20 | **BMI** | rs7903146 | 10 | 114758349 | *TCF7L2* | 1.11E-11 | 1 |
| **Fasting Glucose** | rs780094 | 2 | 27741237 | *GCKR* | 2.58E-37 | **eGFR** | rs1260326 | 2 | 27730940 | *GCKR* | 3.40E-14 | 0.911673 |
| **Fasting Glucose** | rs174576 | 11 | 61603510 | *FADS2* | 1.18E-18 | **HDL-C** | rs174546 | 11 | 61569830 | *FADS1* | 8.30E-28 | 0.936276 |
| **Fasting Glucose** | rs174576 | 11 | 61603510 | *FADS2* | 1.18E-18 | **LDL-C** | rs174546 | 11 | 61569830 | *FADS1* | 1.63E-39 | 0.936276 |
| **Fasting Glucose** | rs174576 | 11 | 61603510 | *FADS2* | 1.18E-18 | **TG** | rs174546 | 11 | 61569830 | *FADS1* | 7.42E-38 | 0.936276 |
| **Fasting Glucose** | rs780094 | 2 | 27741237 | *GCKR* | 2.58E-37 | **TG** | rs1260326 | 2 | 27730940 | *GCKR* | 2.29E-239 | 0.911673 |

**Supplementary Table 15:** Causal effect estimates of lipid traits, adiposity-related traits and fasting glucose on apoA-IV concentrations, contrasting the results from the conventional Mendelian randomization approach (MR-IVW) with those from the sensitivity analyses using the proxy search approach.

| | **Causal effect of phenotype on apoA-IV** | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | **All SNPs** | | | | **Without potentially pleiotropic SNPs (proxy search**)** | | | |
| **Phenotype (exposure)** | **No. of SNPs** | **Beta*** | **95% CI*** | **P-value** | **No. of SNPs** | **Beta*** | **95% CI*** | **P-value** |
| *Lipid traits* | | | | | | | | |
| HDL-C, unadjusted | 71 | 0.0341 | [0.0142, 0.0540] | **0.0008** | 48 | 0.0324 | [0.0007, 0.0641] | 0.0453 |
| HDL-C, adjusted for LDL-C and TG (multivariable MR) | 71 | 0.0195 | [-0.0084, 0.0475] | 0.1706 | 61[§] | 0.0224 | [-0.0059, 0.0507] | 0.1212 |
| LDL-C, unadjusted | 58 | -0.0376 | [-0.0572, -0.0179] | **0.0002** | 46 | -0.0293 | [-0.0528, -0.0058] | 0.0144 |
| LDL-C, adjusted for LDL-C and TG (multivariable MR) | 58 | -0.0225 | [-0.0441, -0.0010] | 0.0406 | 57[§] | -0.0234 | [-0.0457, -0.0011] | 0.0395 |
| TG, unadjusted | 40 | -0.0600 | [-0.0834, -0.0366] | **4.8e-07** | 17 | -0.0576 | [-0.1262, 0.0111] | 0.1003 |
| TG, adjusted for HDL-C and LDL-C (multivariable MR) | 40 | -0.0597 | [-0.0962, -0.0232] | **0.0014** | 33[§] | -0.0625 | [-0.1057, -0.0192] | **0.0047** |
| *Kidney function* | | | | | | | | |
| eGFR | 53 | -0.3890 | [-0.5367, -0.2413] | **2.4e-07** | 49 | -0.3987 | [-0.5528, -0.2447] | **3.9e-07** |
| *Adiposity-related parameters* | | | | | | | | |
| BMI | 77 | 0.0067 | [-0.0266, 0.0400] | 0.6946 | 72 | 0.0179 | [-0.0201, 0.0560] | 0.3558 |
| WHR | 40 | 0.0761 | [0.0093, 0.1429] | 0.0255 | 36 | 0.0745 | [0.0017, 0.1473] | 0.0450 |
| *Fasting Glucose* | | | | | | | | |
| Fasting Glucose | 36 | 0.0146 | [-0.0364, 0.0656] | 0.5742 | 33 | -0.0047 | [-0.0578, 0.0483] | 0.8613 |

*in log(apoA-IV) per change in SD for the lipid and obesity traits, in log(apoA-IV) per change in log(eGFR) for kidney function, in log(apoA-IV) per change in mmol/L for fasting glucose.

**The search for proxies was performed using SNiPA (http://snipa.helmholtz-muenchen.de/snipa/index.php?task=proxy_search) with an LD threshold of 0.8.

[§] Removing all SNPs included in the SNP set or in LD with any SNP in the SNP set of the non-lipid traits.

**Supplementary Table 16:** Causal effect estimates of lipid traits, adiposity-related traits and fasting glucose on apoA-IV concentrations, contrasting the results from the conventional Mendelian randomization approach (MR-IVW) with those from sensitivity analyses (MR-Egger regression and weighted median estimation).

| Phenotype | No. of SNPs | Beta* | 95% CI* | P-value |
|---|---|---|---|---|
| **HDL-C** | | | | |
| ***Main analysis:*** | | | | |
| MR-IVW | 71 | 0.0341 | [0.0142, 0.0540] | **0.0008** |
| ***Sensitivity analyses:*** | | | | |
| 1) MR-Egger regression | 71 | 0.0611 | [0.0254, 0.0969] | **0.0008** |
| 2) Weighted median estimation | 71 | 0.0193 | [-0.0129, 0.0516] | 0.2405 |
| 3) MR-IVW excluding rs964184** | 70 | 0.0271 | [ 0.0067, 0.0474] | 0.0091 |
| **LDL-C** | | | | |
| ***Main analysis:*** | | | | |
| MR-IVW | 58 | -0.0376 | [-0.0572, -0.0179] | **0.0002** |
| ***Sensitivity analyses:*** | | | | |
| 1) MR-Egger regression | 58 | -0.0555 | [-0.0910, -0.0200] | **0.0022** |
| 2) Weighted median estimation | 58 | -0.0427 | [-0.0733, -0.0121] | **0.0062** |
| 3) MR-IVW excluding rs964184 | 57 | -0.0320 | [-0.0519, -0.0121] | **0.0016** |
| **TG** | | | | |
| ***Main analysis:*** | | | | |
| MR-IVW | 40 | -0.0600 | [-0.0834, -0.0366] | **4.8e-07** |
| ***Sensitivity analyses:*** | | | | |
| 1) MR-Egger regression | 40 | -0.0709 | [-0.1075, -0.0343] | **0.0001** |
| 2) Weighted median estimation | 40 | -0.0600 | [-0.0926, -0.0274] | **0.0003** |
| 3) MR-IVW excluding rs964184 | 39 | -0.0498 | [-0.0776, -0.0220] | **0.0004** |
| **eGFR** | | | | |
| ***Main analysis:*** | | | | |
| MR-IVW | 53 | -0.3890 | [-0.5367, -0.2413] | **2.4e-07** |
| ***Sensitivity analyses:*** | | | | |
| 1) MR-Egger regression | 53 | -0.6694 | [-1.1460, -0.1928] | **0.0059** |
| 2) Weighted median estimation | 53 | -0.4894 | [-0.7116, -0.2671] | **1.59e-05** |
| **BMI** | | | | |
| ***Main analysis:*** | | | | |
| MR-IVW | 77 | 0.0067 | [-0.0266, 0.0400] | 0.6946 |
| ***Sensitivity analyses:*** | | | | |
| 1) MR-Egger regression | 77 | -0.0079 | [-0.0910, 0.0753] | 0.8532 |
| 2) Weighted median estimation | 77 | -0.0196 | [-0.0730, 0.0337] | 0.4705 |
| **WHR** | | | | |
| ***Main analysis:*** | | | | |
| MR-IVW | 40 | 0.0761 | [0.0093, 0.1429] | 0.0255 |
| ***Sensitivity analyses:*** | | | | |
| 1) MR-Egger regression | 40 | 0.1025 | [-0.0519, 0.2570] | 0.1933 |
| 2) Weighted median estimation | 40 | 0.0735 | [-0.0253, 0.1723] | 0.1446 |
| **Fasting Glucose** | | | | |
| ***Main analysis:*** | | | | |
| MR-IVW | 36 | 0.0146 | [-0.0364, 0.0656] | 0.5742 |
| ***Sensitivity analyses:*** | | | | |
| 1) MR-Egger regression | 36 | -0.0439 | [-0.1517, 0.0639] | 0.4246 |
| 2) Weighted median estimation | 36 | -0.0214 | [-0.0966, 0.0539] | 0.5775 |

* in log(apoA-IV) per change in SD for the lipid and obesity traits, in log(apoA-IV) per change in log(eGFR) for kidney function, in log(apoA-IV) per change in mmol/L for fasting glucose.

** SNP excluded based on the gtx-package used for testing presence of pleiotropy.

**Bold:** significant after Bonferroni correction (α=0.00625).

**Supplementary Table 17**: Intercept estimates of MR-Egger regressions for detection of directional pleiotropy of the genetic instruments associated with lipid traits, kidney function, adiposity-related traits and fasting glucose.

| Phenotype | No. of SNPs | MR-Egger intercept estimate* | 95% CI* | P-value |
|---|---|---|---|---|
| HDL-C | 71 | -0.0018 | [-0.0036, 1.7e-05] | 0.0522 |
| LDL-C | 58 | 0.0013 | [-0.0008, 0.0035] | 0.2203 |
| TG | 40 | 0.0008 | [-0.0012, 0.0029] | 0.4276 |
| eGFR | 53 | 0.0023 | [-0.0014, 0.0060] | 0.2253 |
| BMI | 77 | 0.0005 | [-0.0019, 0.0028] | 0.7074 |
| WHR | 40 | -0.0006 | [-0.0036, 0.0024] | 0.7076 |
| Fasting Glucose | 36 | 0.0020 | [-0.0011, 0.0050] | 0.2035 |

*in log(apoA-IV) per change in SD for the lipid and obesity traits, in log(apoA-IV) per change in log(eGFR) for kidney function, in log(apoA-IV) per change in mmol/L for fasting glucose.

**Supplementary Table 18**: Adapted I²-statistic ($I^2_{GX}$) and the corrected MR-Egger estimates based on the method of Simulation Extrapolation (SIMEX). Here, apoA-IV was considered as the outcome and the phenotypes were considered as the exposure.

| | | Unadjusted MR-Egger estimate | | | Adjusted MR-Egger estimate (SIMEX) | | |
|---|---|---|---|---|---|---|---|
| **Phenotype** | $I^2_{GX}$ | **Beta*** | **95% CI*** | **P-value** | **Beta*** | **95% CI*** | **P-value** |
| HDL-C | 0.9846 | 0.0611 | [0.0254, 0.0969] | **0.0008** | 0.0621 | [0.0251, 0.0990] | **0.0013** |
| LDL-C | 0.9817 | -0.0555 | [-0.0910, -0.0200] | **0.0022** | -0.0564 | [-0.0933, -0.0194] | **0.0035** |
| TG | 0.9865 | -0.0709 | [-0.1075, -0.0343] | **0.0001** | -0.0718 | [-0.1101, -0.0335] | **0.0005** |
| eGFR | 0.8213 | -0.6694 | [-1.1460, -0.1928] | **0.0059** | -0.7973 | [-1.3370, -0.2576] | **0.0046** |
| BMI | 0.9072 | -0.0079 | [-0.0910, 0.0753] | 0.8532 | -0.0089 | [-0.1007, 0.0829] | 0.8478 |
| WHR | 0.8105 | 0.1025 | [-0.0519, 0.2570] | 0.1933 | 0.1230 | [-0.0637, 0.3096] | 0.1902 |
| Fasting Glucose | 0.9723 | -0.0439 | [-0.1517, 0.0639] | 0.4246 | -0.0446 | [-0.1585, 0.0692] | 0.4314 |

*in log(apoA-IV) per change in SD for the lipid and obesity traits, in log(apoA-IV) per change in log(eGFR) for kidney function, in log(apoA-IV) per change in mmol/L for fasting glucose.

**Bold:** significant after Bonferroni correction ($\alpha$=0.00625).

**Supplementary Table 19:** Characteristics and meta-analysis results of the 3 SNPs associated with apoA-IV [8].

| | | | | | Results from the GWAS meta-analysis on | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | **apoA-IV** | | **HDL-C** | | **LDL-C** | | **TG** | |
| **SNP** | **Chr** | **Pos** | **Nearest Gene** | **A1/ A2[#]** | **Beta* (SE*)** | **P-value** | **Beta* (SE*)** | **P-value** | **Beta* (SE*)** | **P-value** | **Beta* (SE*)** | **P-value** |
| rs1729407 | 11 | 116677370 | *APOA4* | G/ C | -0.0459 (0.0033) | **6.77e-44** | 0.0233 (0.0054) | **7.06e-07** | -0.0061 (0.0059) | 0.4332 | -0.0015 (0.0053) | 0.9608 |
| rs5104[§] | 11 | 116684028 | *APOA4* | C/ T | -0.0479 (0.0047) | **1.79e-24** | | | | | | |
| rs4253311 | 4 | 187174683 | *KLKB1* | G/ A | 0.0256 (0.0034) | **5.63e-14** | -0.0034 (0.0048) | 0.5394 | 0.0088 (0.0052) | 0.0894 | -0.0090 (0.0047) | 0.0677 |

| | | | | | Results from the GWAS meta-analysis on | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | **eGFR** | | **BMI** | | **WHR** | | **Fasting Glucose** | |
| **SNP** | **Chr** | **Pos** | **Nearest Gene** | **A1/ A2[#]** | **Beta* (SE*)** | **P-value** | **Beta* (SE*)** | **P-value** | **Beta* (SE*)** | **P-value** | **Beta* (SE*)** | **P-value** |
| rs1729407 | 11 | 116677370 | *APOA4* | G/ C | -0.0008 (0.0009) | 0.4200 | 0.0046 (0.0042) | 0.2734 | 0.0028 (0.0048) | 0.5600 | -0.0037 (0.0034) | 0.2760 |
| rs5104[§] | 11 | 116684028 | *APOA4* | C/ T | | | | | | | 0.0087 (0.8317) | 8.7e-03 |
| rs4253311 | 4 | 187174683 | *KLKB1* | G/ A | 0.0008 (0.0009) | 0.3500 | 0.0035 (0.0037) | 0.3442 | 0.0049 (0.0042) | 0.2400 | 0.0031 (0.9359) | 3.1e-03 |

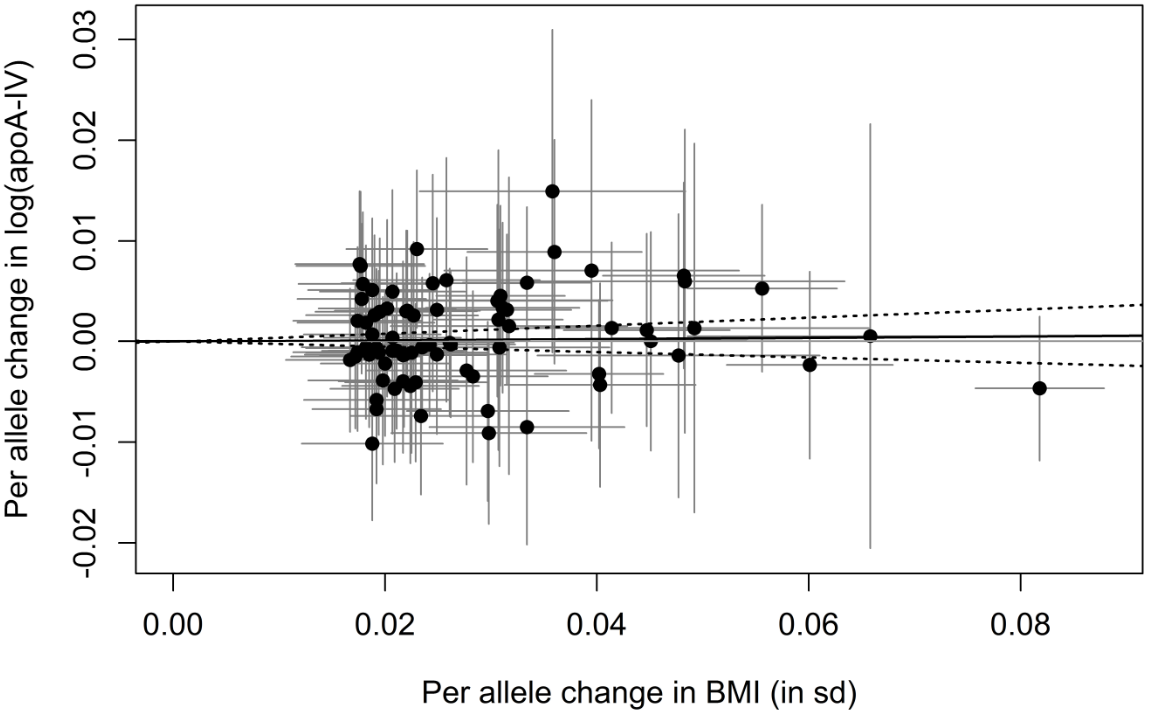
[#] A1: effect allele; A2: other allele.

*in log(apoA-IV) for apoA-IV, in SD for the lipid and obesity traits, in log(eGFR) for kidney function, in mmol/L for fasting glucose.

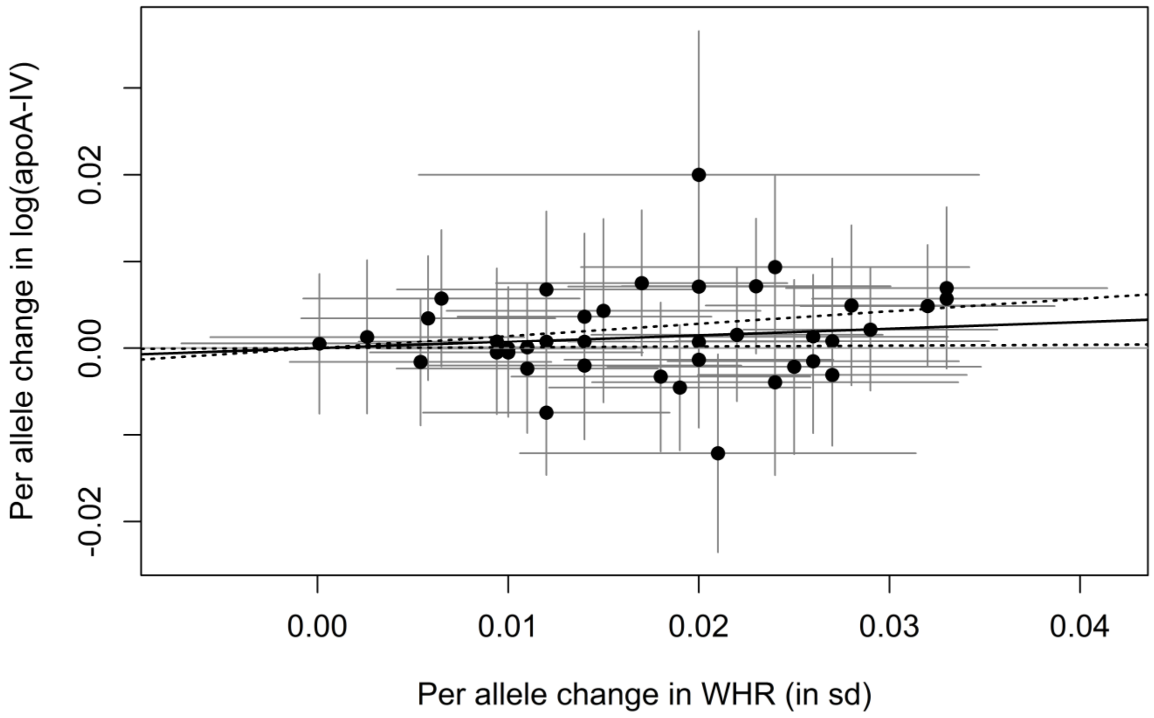
[§] rs5104 was not present in any of the other GWAs consortia for the other traits. For fasting glucose, the results from one proxy SNP (rs7396835, $r^2$=0.95 with rs5104) could be retrieved. For the other phenotypes no proxies for SNP rs5104 were present in the datasets.

**Bold:** significant after Bonferroni correction ($\alpha$=0.00625).

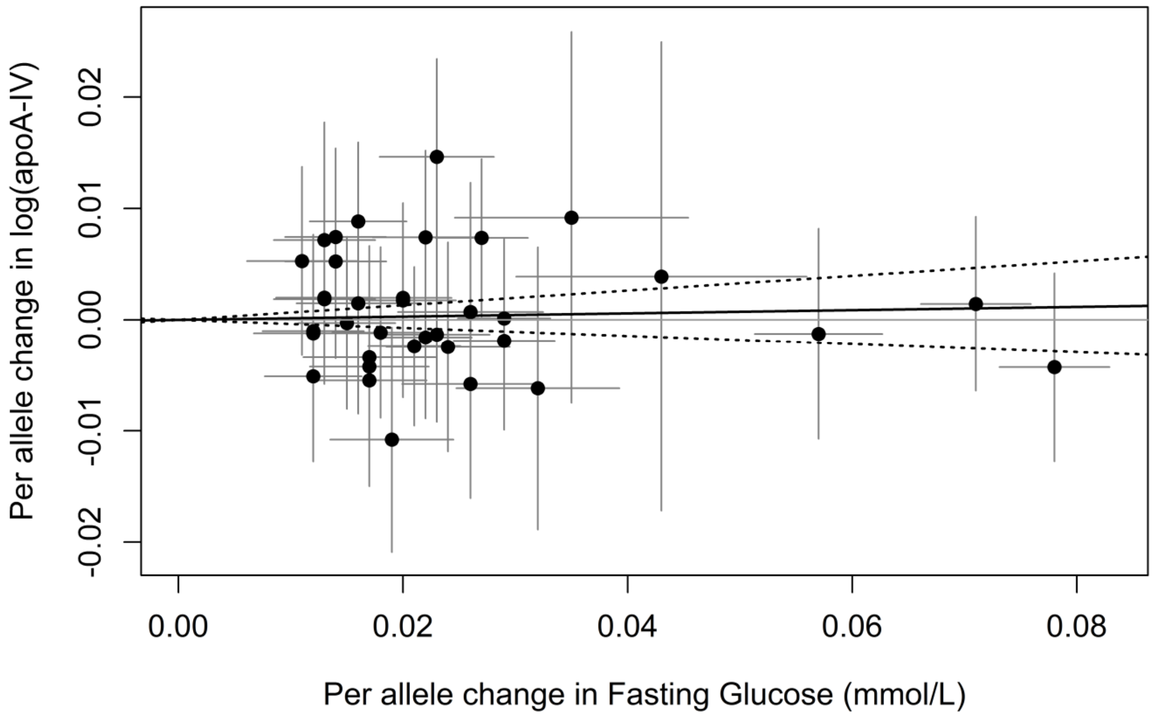
# Supplementary Figures



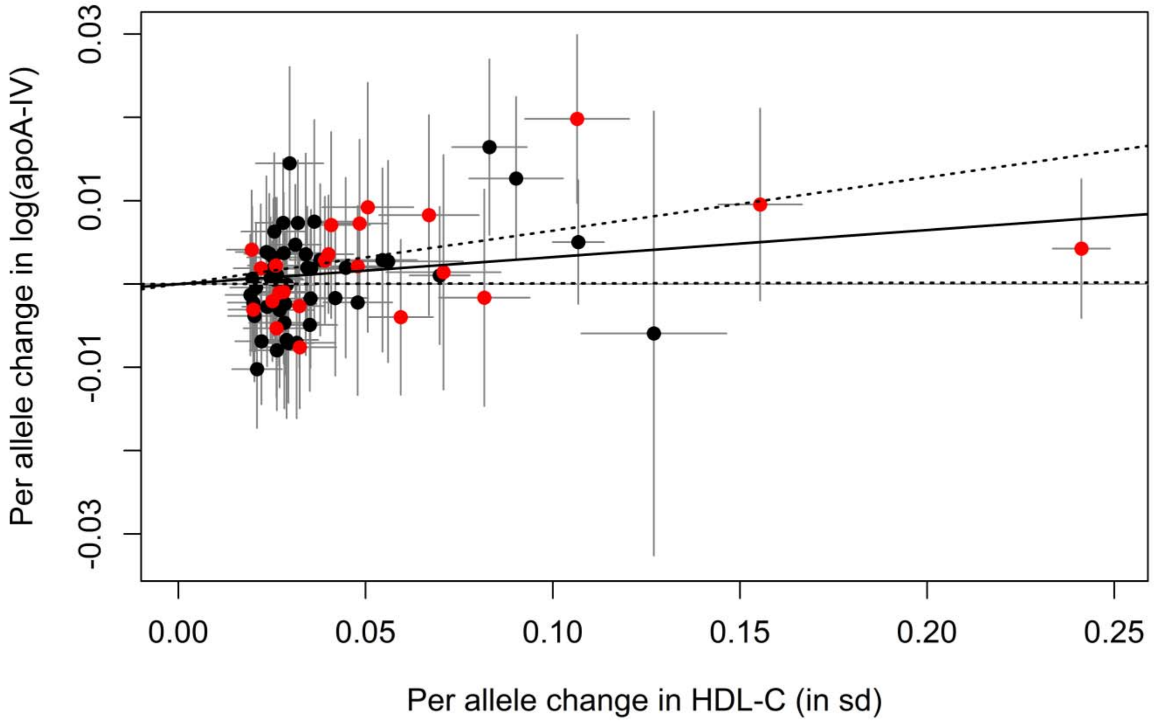
**Supplementary Figure 1:** Scatterplot showing the effect estimates of SNP-BMI (body-mass index) associations (95% CI) on the x- and SNP-apoA-IV (apolipoprotein A-IV) associations (95% CI) on the y-axis for all 77 SNPs. The continuous black line represents the MR-IVW estimate of BMI on apoA-IV (dashed lines represent the 95% CI).



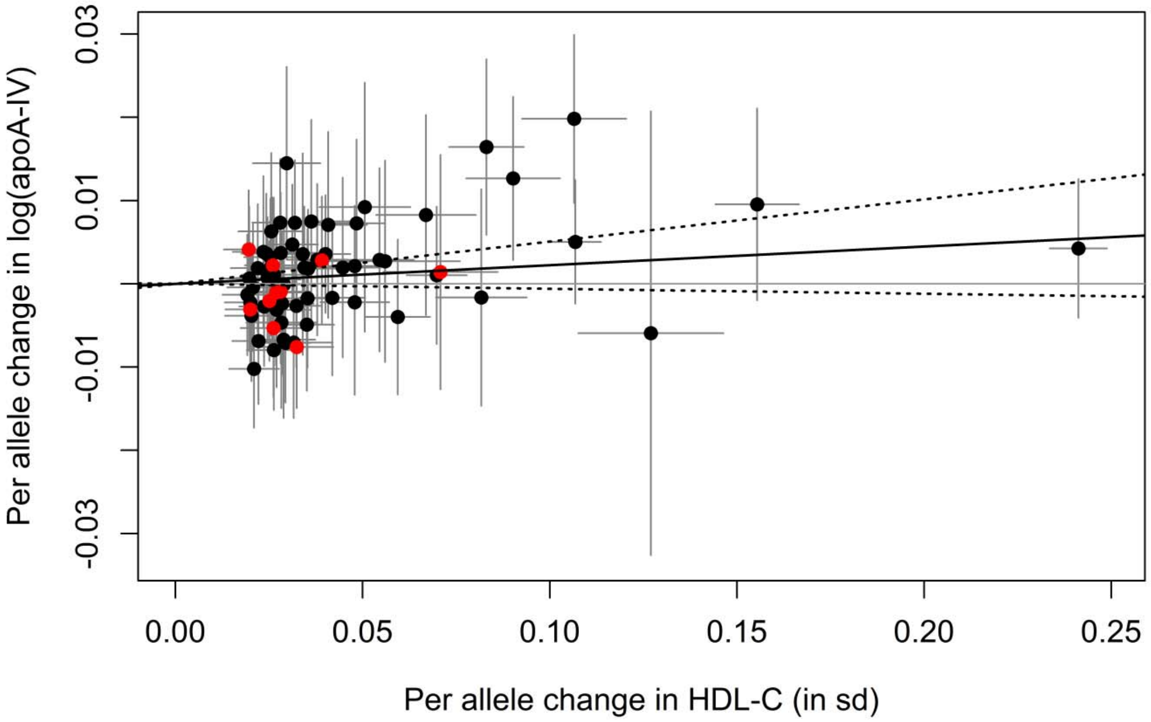
**Supplementary Figure 2:** Scatterplot showing the effect estimates of SNP-WHR (waist-hip-ratio) associations (95% CI) on the x- and SNP-apoA-IV (apolipoprotein A-IV) associations (95% CI) on the y-axis for all 40 SNPs. The continuous black line represents the MR-IVW estimate of WHR on apoA-IV (dashed lines represent the 95% CI).



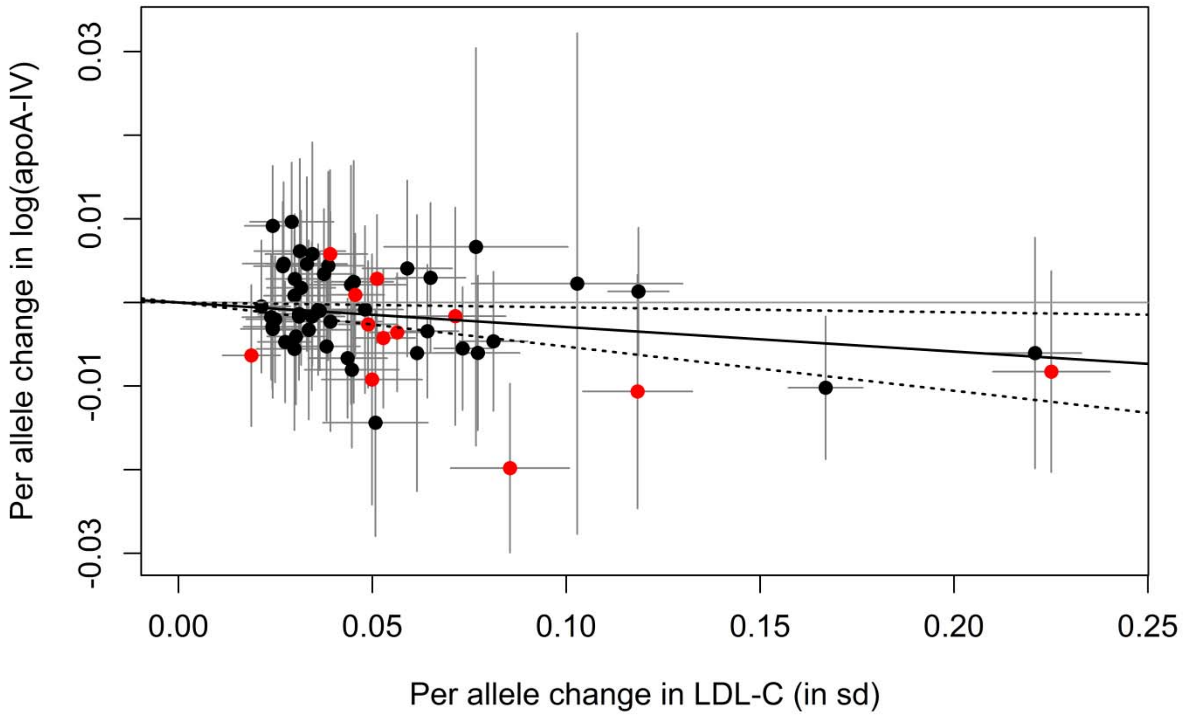
**Supplementary Figure 3:** Scatterplot showing the effect estimates of SNP-Fasting Glucose associations (95% CI) on the x- and SNP-apoA-IV (apolipoprotein A-IV) associations (95% CI) on the y-axis for all 36 SNPs. The continuous black line represents the MR-IVW estimate of Fasting Glucose on apoA-IV (dashed lines represent the 95% CI).



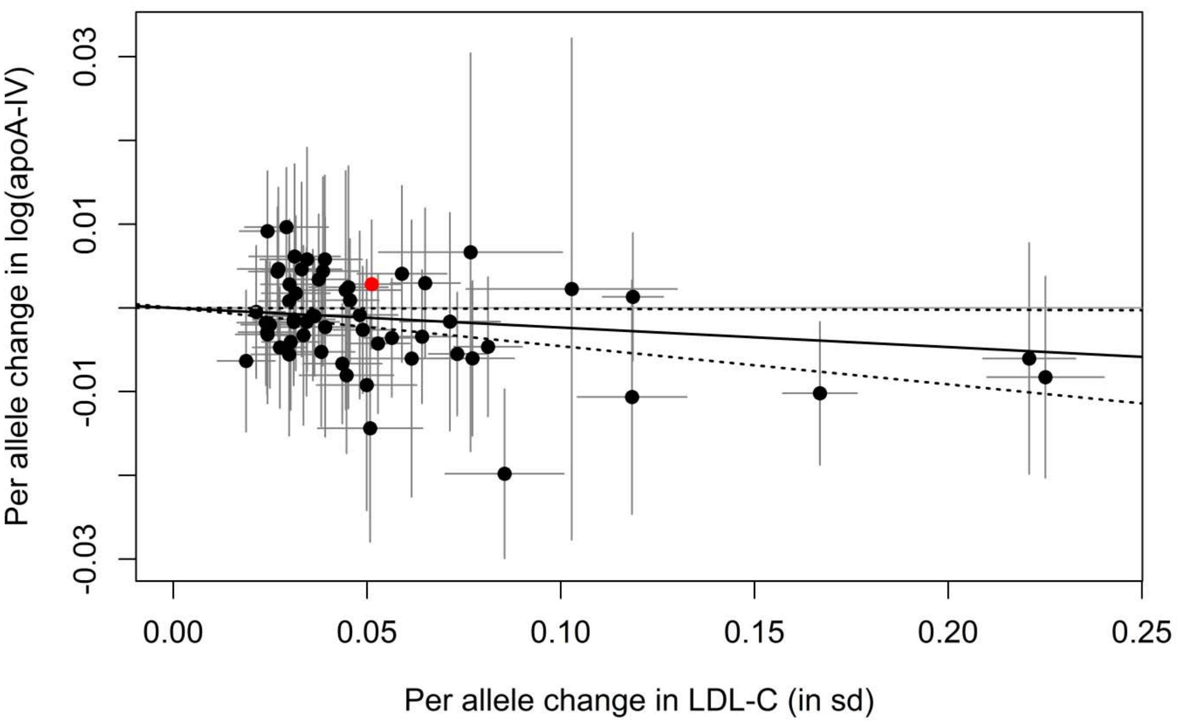
**Supplementary Figure 4:** Scatterplot showing the effect estimates of SNP-HDL-C associations (95% CI) on the x- and SNP-apoA-IV (apolipoprotein A-IV) associations (95% CI) on the y-axis for all 71 SNPs. Red points indicate the 23 SNPs that were in LD with SNPs associated with any of the other traits. The continuous black line represents the MR-IVW estimate of HDL-C on apoA-IV based on the 48 SNPs not associated with any other trait (dashed lines represent the 95% CI).



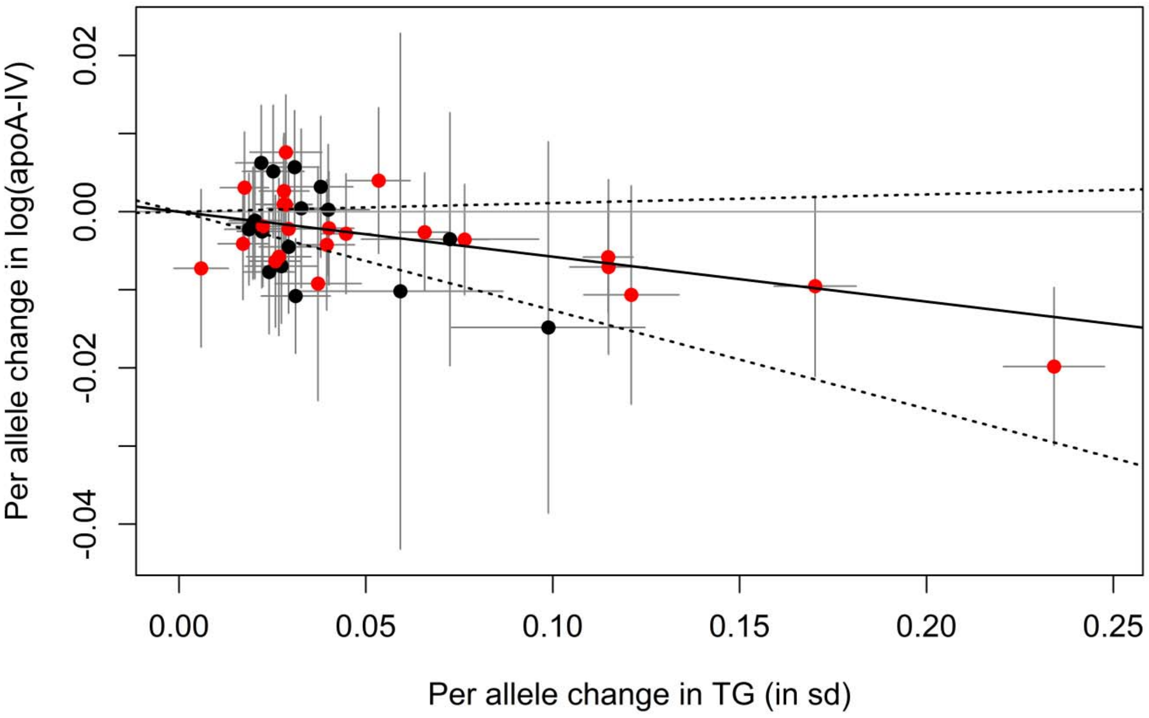
**Supplementary Figure 5:** Scatterplot showing the effect estimates of SNP-HDL-C associations (95% CI) on the x- and SNP-apoA-IV (apolipoprotein A-IV) associations (95% CI) on the y-axis for all 71 SNPs. Red points indicate the 10 SNPs that were in LD with SNPs associated with the non-lipid traits. The continuous black line represents the causal estimate of HDL-C on apoA-IV after application of the multivariable Mendelian randomization approach based on the 61 SNPs not associated with any non-lipid-trait (dashed lines represent the 95% CI).



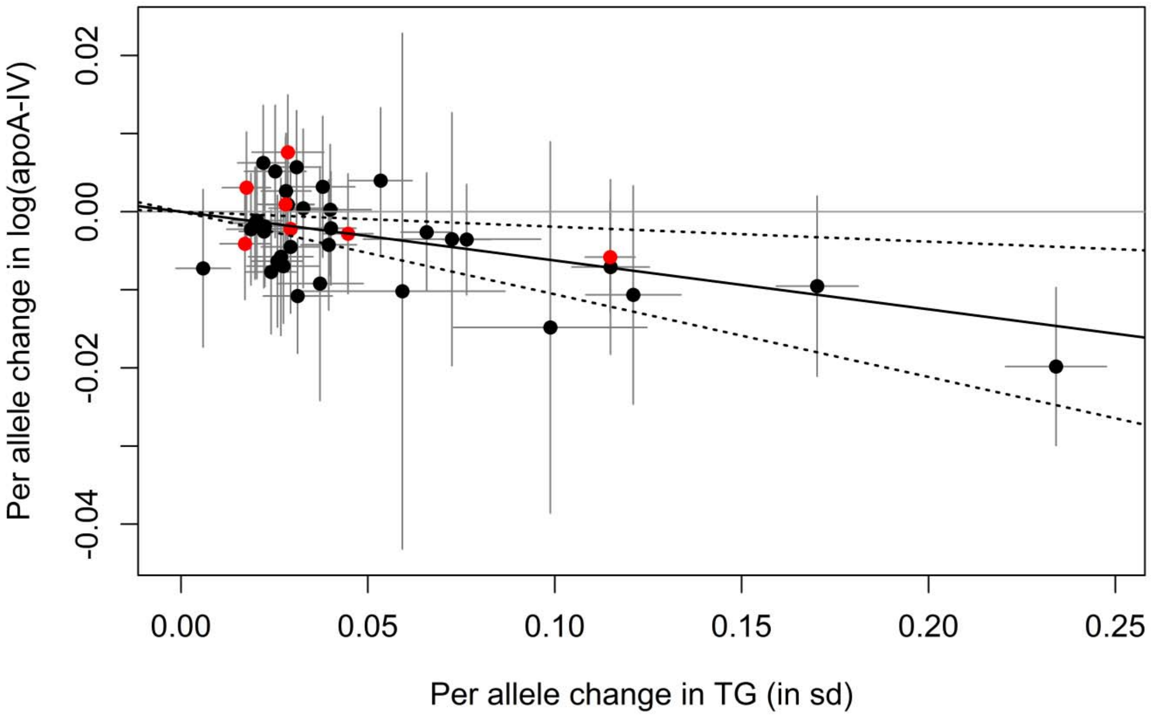
**Supplementary Figure 6:** Scatterplot showing the effect estimates of SNP-LDL-C associations (95% CI) on the x- and SNP-apoA-IV (apolipoprotein A-IV) associations (95% CI) on the y-axis for all 58 SNPs. Red points indicate the 12 SNPs that were in LD with SNPs associated with any of the other traits. The continuous black line represents the MR-IVW estimate of LDL-C on apoA-IV based on the 46 SNPs not associated with any other trait (dashed lines represent the 95% CI).



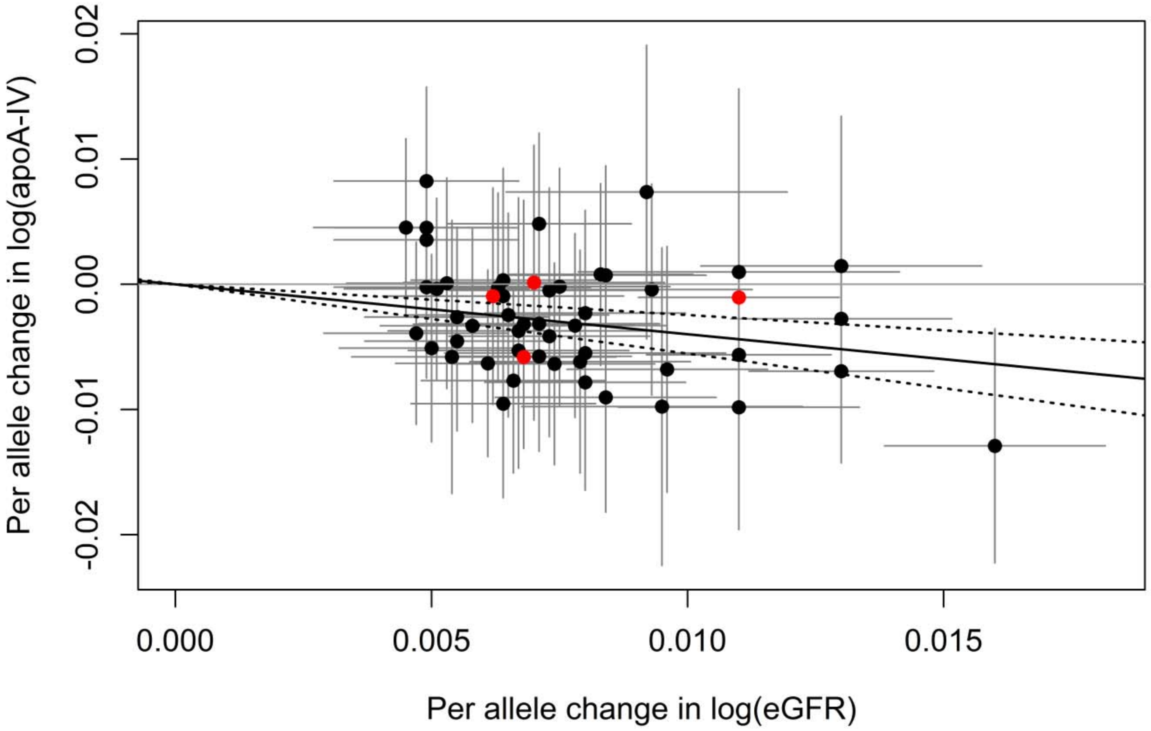
**Supplementary Figure 7:** Scatterplot showing the effect estimates of SNP-LDL-C associations (95% CI) on the x- and SNP-apoA-IV (apolipoprotein A-IV) associations (95% CI) on the y-axis for all 58 SNPs. The red point indicates the one SNP that was in LD with SNPs associated with the non-lipid traits. The continuous black line represents the causal estimate of LDL-C on apoA-IV after application of the multivariable Mendelian randomization approach based on the 57 SNPs not associated with any non-lipid-trait (dashed lines represent the 95% CI).



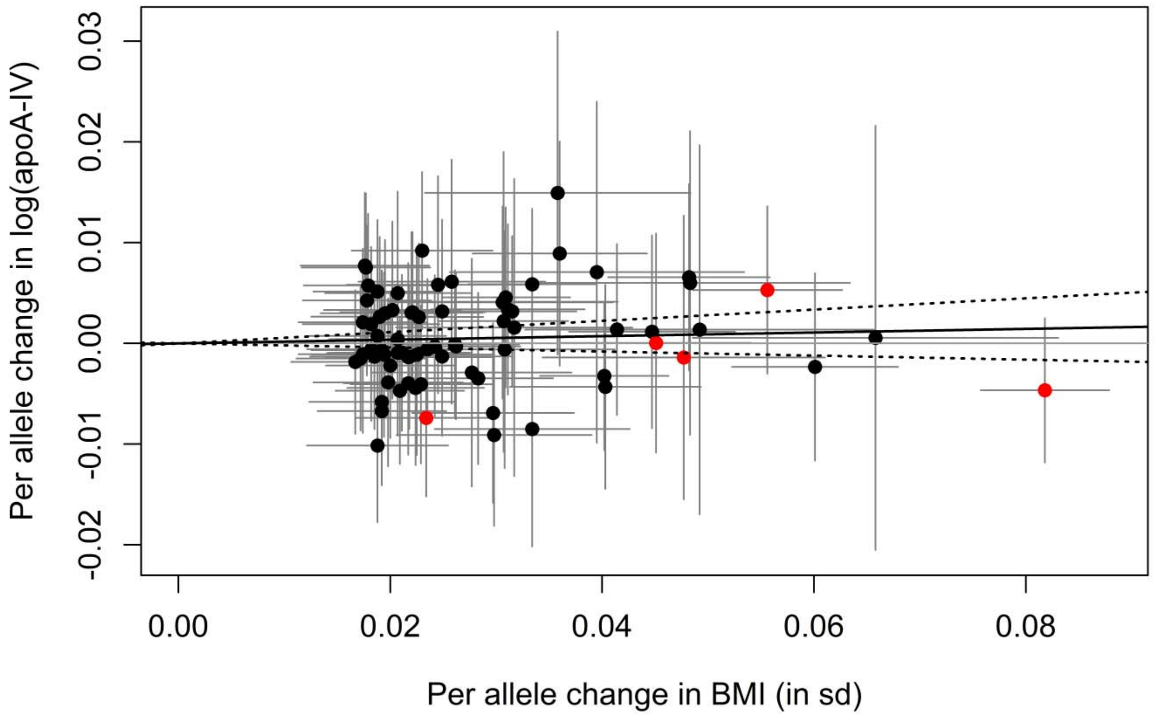
**Supplementary Figure 8:** Scatterplot showing the effect estimates of SNP-TG associations (95% CI) on the x- and SNP-apoA-IV (apolipoprotein A-IV) associations (95% CI) on the y-axis for all 40 SNPs. Red points indicate the 23 SNPs that were in LD with SNPs associated with any of the other traits. The continuous black line represents the MR-IVW estimate of TG on apoA-IV based on the 17 SNPs not associated with any other trait (dashed lines represent the 95% CI).



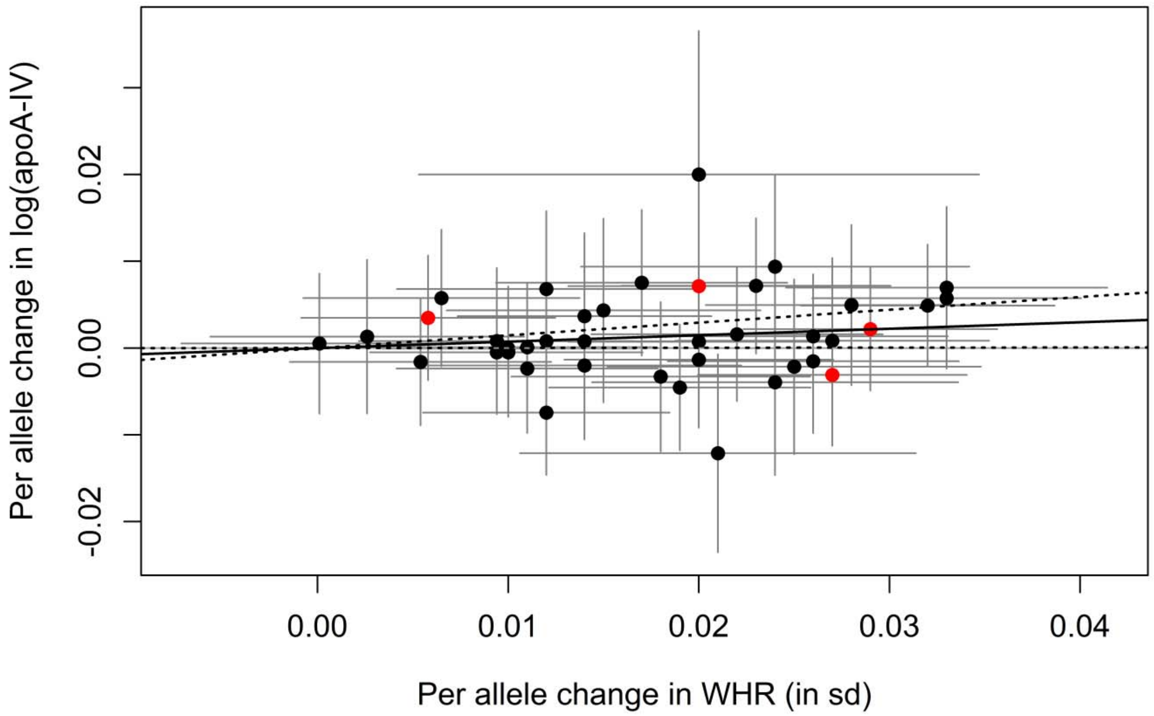
**Supplementary Figure 9:** Scatterplot showing the effect estimates of SNP-TG associations (95% CI) on the x- and SNP-apoA-IV (apolipoprotein A-IV) associations (95% CI) on the y-axis for all 40 SNPs. Red points indicate the 7 SNPs that were in LD with SNPs associated with the non-lipid traits. The continuous black line represents the causal estimate of TG on apoA-IV after application of the multivariable Mendelian randomization approach based on the 33 SNPs not associated with any non-lipid-trait (dashed lines represent the 95% CI).



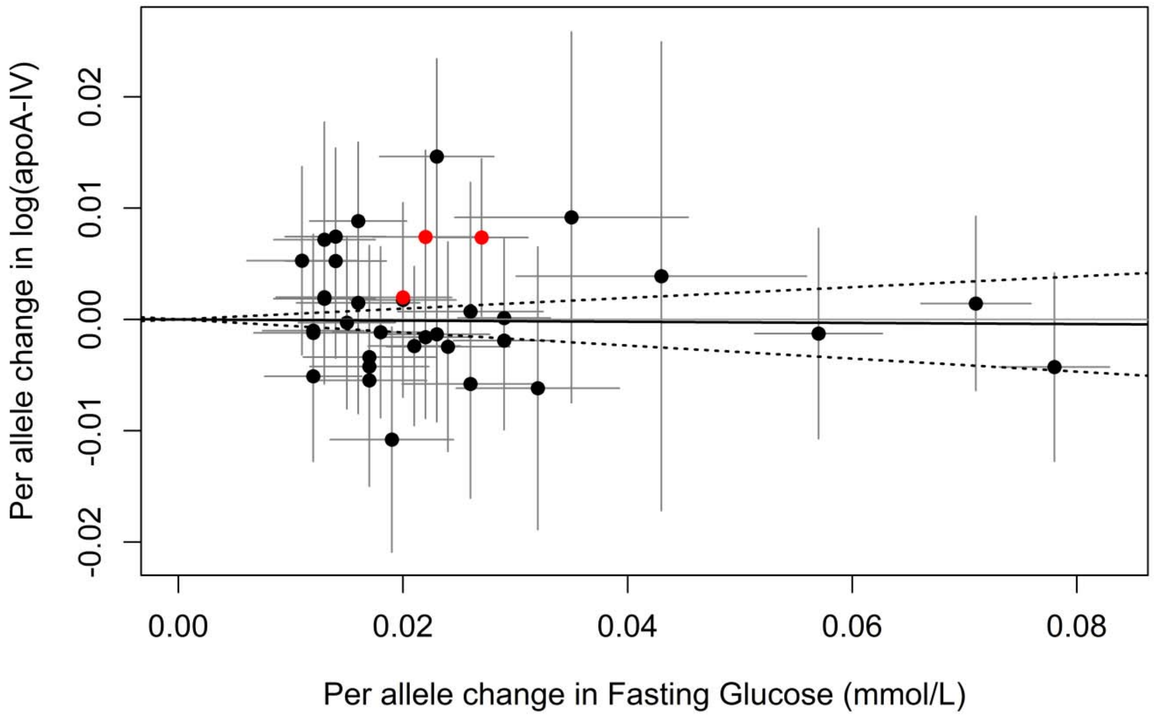
**Supplementary Figure 10:** Scatterplot showing the effect estimates of SNP-eGFR associations (95% CI) on the x- and SNP-apoA-IV (apolipoprotein A-IV) associations (95% CI) on the y-axis for all 53 SNPs. Red points indicate the 4 SNPs that were in LD with SNPs associated with any of the other traits. The continuous black line represents the MR-IVW estimate of eGFR on apoA-IV based on the 49 SNPs not associated with any other trait (dashed lines represent the 95% CI).



**Supplementary Figure 11:** Scatterplot showing the effect estimates of SNP-BMI associations (95% CI) on the x- and SNP-apoA-IV (apolipoprotein A-IV) associations (95% CI) on the y-axis for all 77 SNPs. Red points indicate the 5 SNPs that were in LD with SNPs associated with any of the other traits. The continuous black line represents the MR-IVW estimate of BMI on apoA-IV based on the 72 SNPs not associated with any other trait (dashed lines represent the 95% CI).



**Supplementary Figure 12:** Scatterplot showing the effect estimates of SNP-WHR associations (95% CI) on the x- and SNP-apoA-IV (apolipoprotein A-IV) associations (95% CI) on the y-axis for all 40 SNPs. Red points indicate the 4 SNPs that were in LD with SNPs associated with any of the other traits. The continuous black line represents the MR-IVW estimate of WHR on apoA-IV based on the 36 SNPs not associated with any other trait (dashed lines represent the 95% CI).

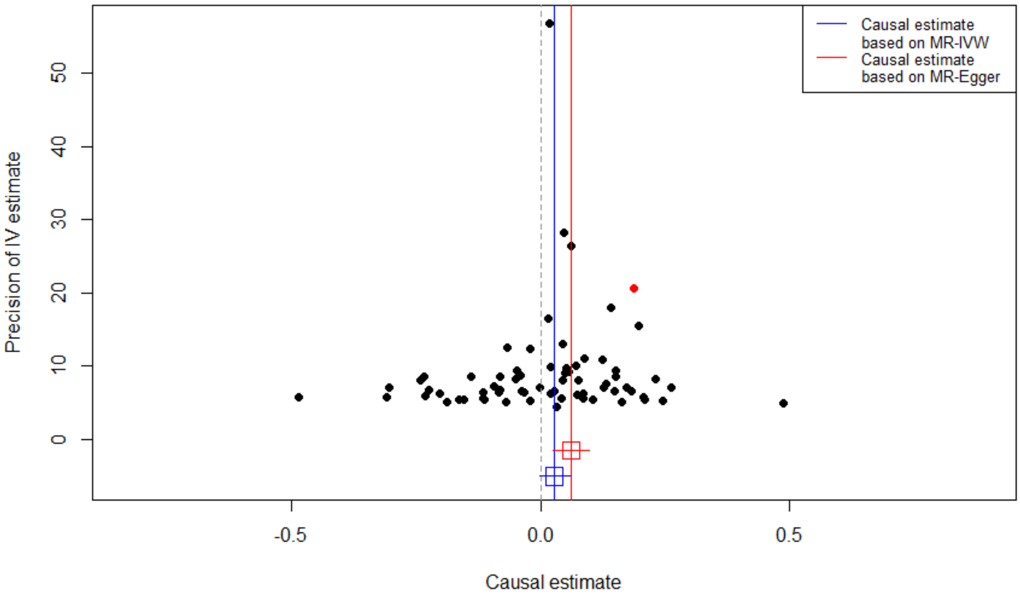


**Supplementary Figure 13:** Scatterplot showing the effect estimates of SNP-Fasting Glucose associations (95% CI) on the x- and SNP-apoA-IV (apolipoprotein A-IV) associations (95% CI) on the y-axis for all 36 SNPs. Red points indicate the 3 SNPs that were in LD with SNPs associated with any of the other traits. The continuous black line represents the MR-IVW estimate of Fasting Glucose on apoA-IV based on the 33 SNPs not associated with any other trait (dashed lines represent the 95% CI).

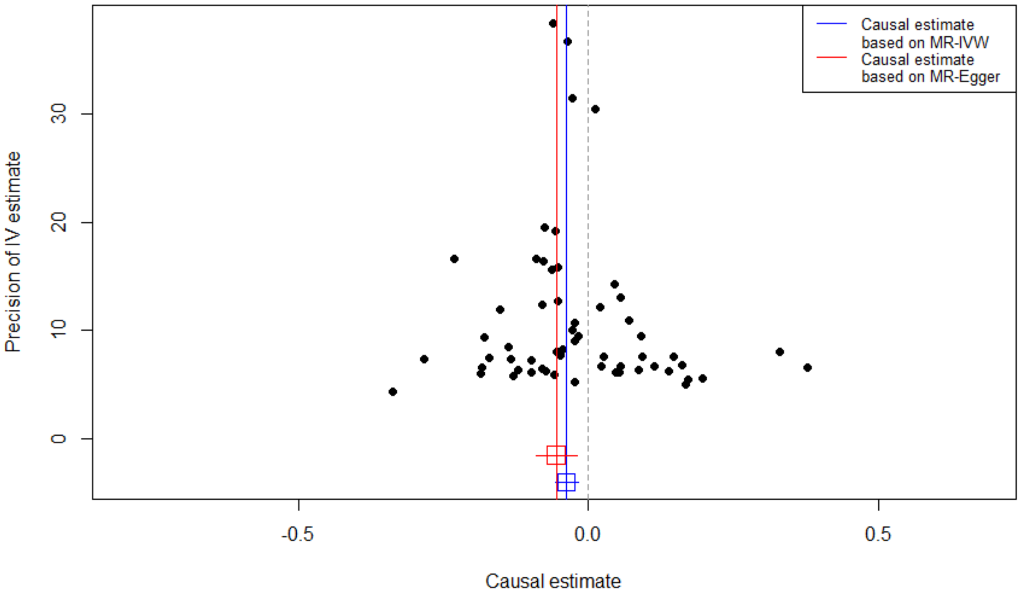
**Supplementary Figure 14:** Reported correlation of SNPs in the *APOA5-A4-C3-A1* gene cluster with rs964184 (given as $r^2$ as reported by SNiPA using 1000 Genomes phase 3v5 data). *APOA4* gene is highlighted. **A.** Whole genomic region (225 kb; chr11:116,530,000-116,755,000, hg19). **B.** Close-up view of region spanning *ZPR1, APOA5* and *APOA4.*

Both panels. Row 1: bar plot showing the $r^2$ value with rs964184 for the SNPs reported in row 1. The solid horizontal lines delines $r^2$=0.25 level. Row 2: rs-IDs of the SNPs. Row 3: $r^2$ values of the plot bars in row 1 are reported. The red arrow marks rs964184.

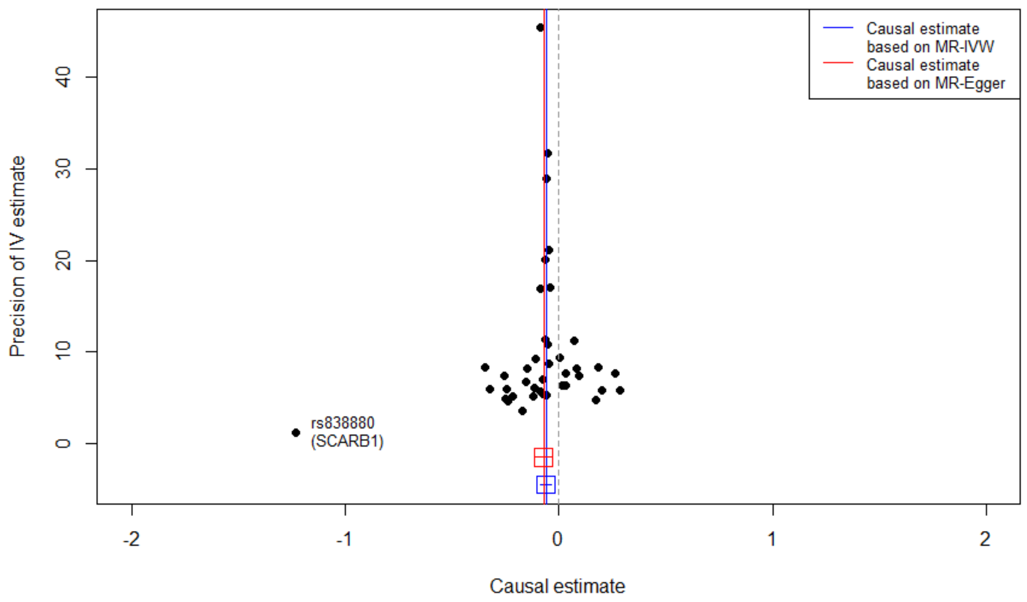
rs964184 is relatively independent with no SNPs with $r^2 > 0.52$. If any, rs964184 might rather tag variant in *APOA5*, while *APOA4* variants show very low $r^2$ (max $r^2$=0.2). It is therefore unlikely, that 964184 will directly affect *APOA4* expression.



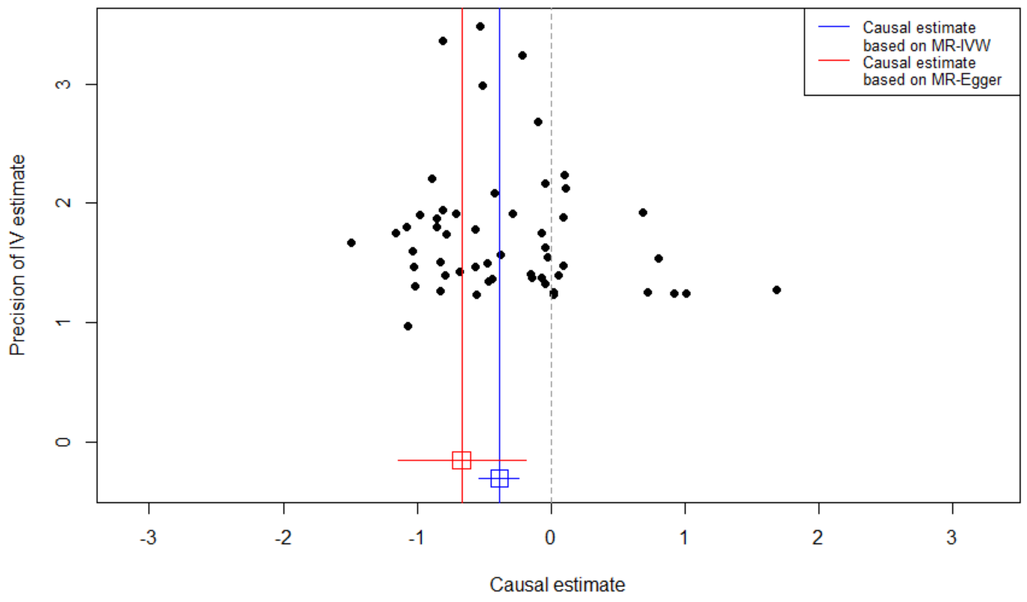
**Supplementary Figure 15:** Funnel plot of genetic associations with HDL-C. The MR-IVW estimate (blue) as well as the MR-Egger regression estimate (red) are shown. The causal estimates are represented by the boxes and the vertical lines, and the corresponding 95%-CIs are displayed by the horizontal lines. The red SNP denotes rs964184, the potential pleiotropic SNP identified by the gtx package.



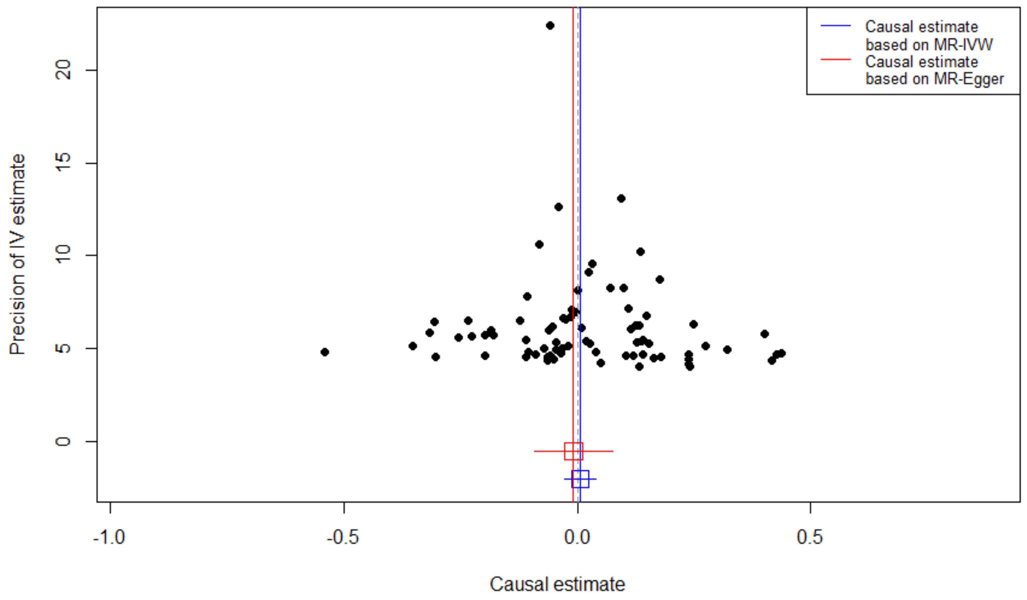
**Supplementary Figure 16:** Funnel plot of genetic associations with LDL-C. The MR-IVW estimate (blue) as well as the MR-Egger regression estimate (red) are shown. The causal estimates are represented by the boxes and the vertical lines, and the corresponding 95%-CIs are displayed by the horizontal lines.



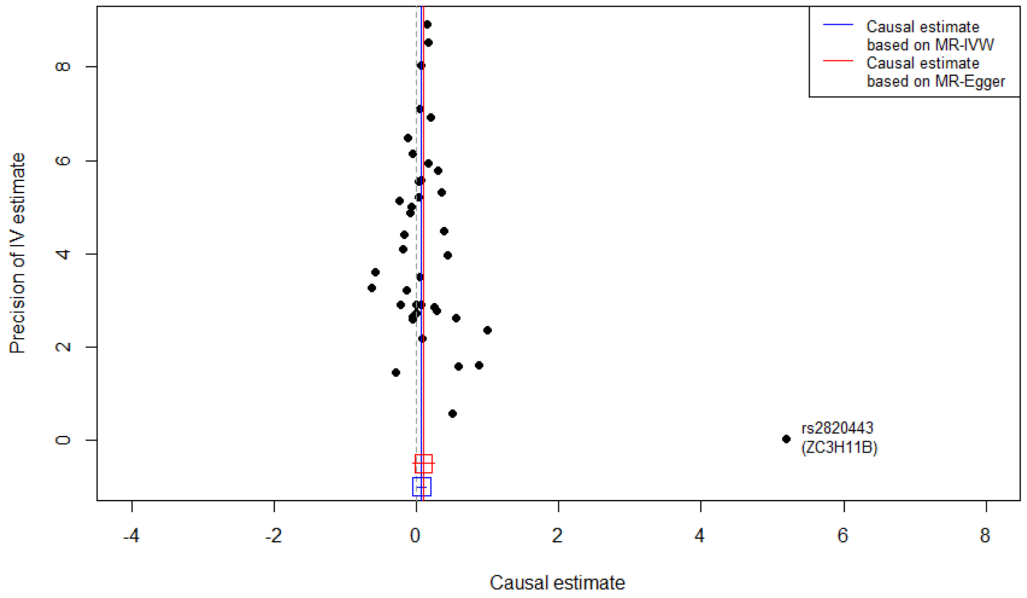
**Supplementary Figure 17:** Funnel plot of genetic associations with TG. The MR-IVW estimate (blue) as well as the MR-Egger regression estimate (red) are shown. The causal estimates are represented by the boxes and the vertical lines, and the corresponding 95%-CIs are displayed by the horizontal lines.



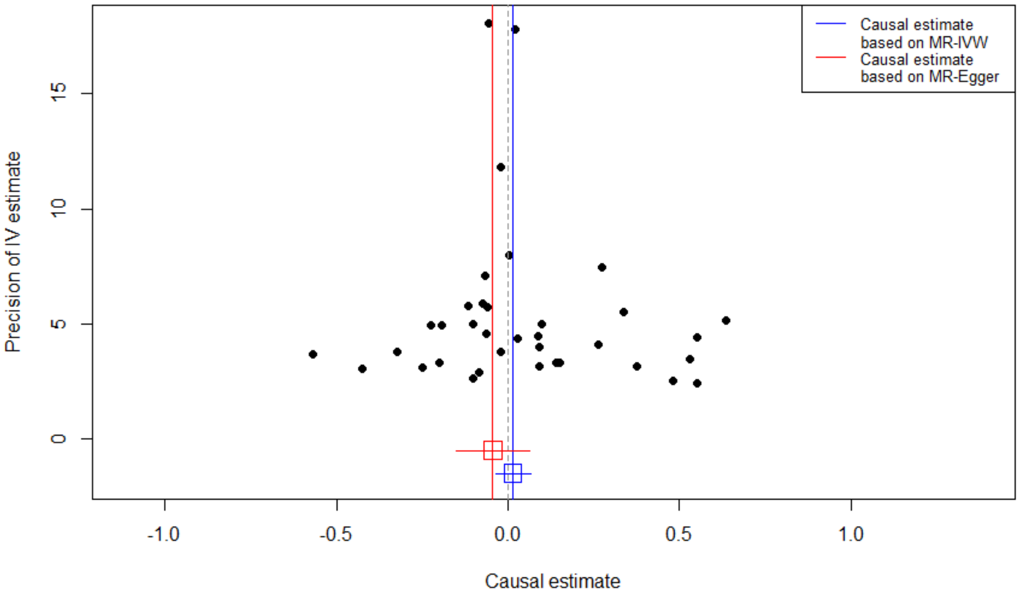
**Supplementary Figure 18:** Funnel plot of genetic associations with eGFR. The MR-IVW estimate (blue) as well as the MR-Egger regression estimate (red) are shown. The causal estimates are represented by the boxes and the vertical lines, and the corresponding 95%-CIs are displayed by the horizontal lines.



**Supplementary Figure 19:** Funnel plot of genetic associations with BMI. The MR-IVW estimate (blue) as well as the MR-Egger regression estimate (red) are shown. The causal estimates are represented by the boxes and the vertical lines, and the corresponding 95%-CIs are displayed by the horizontal lines.



**Supplementary Figure 20:** Funnel plot of genetic associations with WHR. The MR-IVW estimate (blue) as well as the MR-Egger regression estimate (red) are shown. The causal estimates are represented by the boxes and the vertical lines, and the corresponding 95%-CIs are displayed by the horizontal lines.



**Supplementary Figure 21:** Funnel plot of genetic associations with Fasting Glucose. The MR-IVW estimate (blue) as well as the MR-Egger regression estimate (red) are shown. The causal estimates are represented by the boxes and the vertical lines, and the corresponding 95%-CIs are displayed by the horizontal lines.